EVALUATION OF CYTOPLASMIC MALE STERILE LINES OF CHILLI PEPPER (*Capsicum annuum* L.) AND THEIR UTILIZATION IN HETEROSIS BREEDING

Dissertation

Submitted to the Punjab Agricultural University
in partial fulfillment of the requirements
for the degree of

DOCTOR OF PHILOSOPHY
in
VEGETABLE SCIENCE
(Minor Subject: Plant Breeding and Genetics)

By

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(L-2013-A-27-D)

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CERTIFICATE I

This is to certify that the dissertation entitled, **''Evaluation of cytoplasmic male sterile lines of chilli pepper (*Capsicum annuum* L.) and their utilization in heterosis breeding''** submitted for the degree of **Doctor of Philosophy,** in the subject of **Vegetable Science** (Minor subject: **Plant Breeding and Genetics**) to the Punjab Agricultural University, Ludhiana, is a bonafide research work carried out by **Om Prakash Meena (L-2013-A-27-D)** under my supervision and that no part of this dissertation has been submitted for any other degree.

The assistance and help received during the course of investigation have been fully acknowledged.

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CERTIFICATE II

This is to certify that the dissertation entitled, **''Evaluation of cytoplasmic male sterile lines of chilli pepper (*Capsicum annuum* L.) and their utilization in heterosis breeding''** submitted by **Om Prakash Meena (L-2013-A-27-D)** to the Punjab Agricultural University, Ludhiana, in partial fulfillment of the requirements for the degree of **Doctor of Philosophy,** in the subject of **Vegetable Science** (Minor subject: **Plant Breeding and Genetics**) has been approved by the Student's Advisory Committee along with Head of the Department after an oral examination on the same.

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Place: ....
Date: ....

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ABSTRACT

A total of 17 cytoplasmic male sterile (CMS) lines were evaluated under the low (E_1 and E_3) and the high (E_2 and E_4) temperature regimes of 2014-15 and 2015-16. Based on pollen sterility and pollen release score, 10 lines namely CMS4611A, CMS4614A, CMS4622A, CMS4624A, CMS4626A, CMS46213A, CMS463D2A, CMS463D13A, CMS463D14A and CMS463L5A have been identified as temperature stable. The lines showed normal fruit and seed setting ability under the open pollination conditions, and have commercially acceptable fruit traits. The marker analysis of three selected CMS A- and their respective CMS B-lines showed that the genome recovery of the recurrent parent in CMS4611A, CMS4626A and CMS463D13A was estimated to be 98.8, 98.9 and 96.6%, respectively. Three CMS lines and 20 potential restorer lines were evaluated in a Line × tester mating design to estimate combing ability and heterosis over the better parent and two standard checks over three environments *viz.* the early season (E_1), the main season (E_2) and the late season (E_3). Over the environments, the estimates due to GCA lines, GCA testers and SCA crosses were significant for all the 15 plant growth, yield and quality traits, except due to GCA lines for number of primary branches plant^{-1}. The magnitude of the additive variance (σ^2A) was more than the non-additive variance (σ^2D) for all the traits studied except for number of primary branches plant^{-1} in E_2, E_3, and across the three environments; and for plant height, plant spread and number of fruits plant^{-1} in E_3. The CMS line CMS463D13A and the testers SL 475, IS 268, PP 402, FL 201 and C 142 were identified for use in breeding to develop high yielding genotypes with superior horticultural traits for early, main and late season environments. Hybrids were identified for different crop seasons and for different purposes. Pooled across the environments, the cross CMS463D13A × IS 268 was good specific combiner for total yield palnt^{-1}, number of primary branches plant^{-1}, fruit weight, number of seed fruit^{-1}, capsaicin content and SHU, and involved good × good GCA parents. The maximum mean better parent heterosis over environments was exhibited for total yield plant^{-1} (35.29%), followed by number of primary branches plant^{-1} (17.96%), number of seed fruit^{-1} (12.46) and number of fruits plant^{-1} (11.43%). The crosses CMS463D13A × SL 475, CMS463D13A × VR 523, CMS463D13A × YL 581 and CMS463D13A × IS 268 performed consistently superior over environments in respect of *per se* and standard heterosis for total yield plant^{-1}, fruit weight and fruit length, and CMS463D13A × SL 475 for total yield plant^{-1}, capsaicin content and SHU. These crosses are recommended for multi-location testing.

Keywords: *Capsicum annuum*, cytoplasmic male sterility, heterosis breeding, combining ability, G × E interaction, SSR markers

Signature of Major Advisor

Signature of the Student

ਖੋਜ ਦਾ ਸਿਰਲੇਖ : ਮਿਰਚਾਂ ਦੀਆਂ ਸਾਇਟੋਪਲਾਜ਼ਮਿਕ ਨਰ ਮੁਰਦਾਰ (ਬਾਂਝਪਣ) ਲਾਇਨਾਂ ਦਾ ਮੁਲਾਂਕਨ ਅਤੇ ਇਨਾਂ ਦੀ ਹੈਟਰੌਸਿਸ ਬ੍ਰੀਡਿੰਗ ਵਿੱਚ ਵਰਤੋਂ

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ਸਾਰ-ਅੰਸ਼

ਸਾਲ 2014-2015 ਅਤੇ ਸਾਲ 2015-16 ਦੇ ਘੱਟ (E_1 ਅਤੇ E_3) ਅਤੇ ਵੱਧ (E_2 ਅਤੇ E_4) ਤਾਪਮਾਨ ਵਿੱਚ ਕੁੱਲ 17 ਸਾਇਟੋਪਲਾਜ਼ਮਿਕ ਨਰ ਮੁਰਦਾਰ (CMS) ਲਾਇਨਾਂ ਦਾ ਮੁਲਾਂਕਣ ਕੀਤਾ ਗਿਆ। ਪਰਾਗ਼ ਬਾਝਪਨ ਅਤੇ ਪਰਾਗ਼ ਜਾਰੀ ਸਕੋਰ ਦੇ ਆਧਾਰ ਤੇ, 10 ਲਾਇਨਾਂ, CMS4611A, CMS4614A, CMS4622A, CMS4624A, CMS4626A, CMS46213A, CMS463D2A, CMS463D13A, CMS463D14A ਅਤੇ CMS463L5A ਨੂੰ ਤਾਪਮਾਨ ਸਥਿਰ ਦੇ ਤੌਰ ਤੇ ਪਹਿਚਾਣਿਆ ਗਿਆ। ਖੁਲ੍ਹੇ ਹਾਲਾਤਾਂ ਵਿੱਚ ਇਹਨਾਂ ਲਾਇਨਾਂ ਨੇ ਦਰੁਸਤ ਫ਼ਲ ਅਤੇ ਬੀਜ ਸੈਟਿੰਗ ਯੋਗਤਾ ਦਿਖਾਈ ਅਤੇ ਇਹਨਾਂ ਵਿੱਚ ਵਪਾਰਕ ਤੌਰ ਤੇ ਸਵੀਕਾਰਨਯੋਗ ਫ਼ਲ ਵਿਸ਼ੇਸ਼ਤਾਵਾਂ ਸਨ। ਤਿੰਨ ਚੌਣਵੇਂ CMSA ਅਤੇ ਉਹਨਾਂ ਦੀਆਂ CMSB ਲਾਇਨਾਂ ਦੇ ਮਾਰਕਰ ਵਿਸ਼ਲੇਸ਼ਣ CMS4611A, CMS4626A ਅਤੇ CMS463D13A ਵਿਚ ਆਵਰਤਕ ਜਣਨ ਦੀ ਜੀਨੋਮ ਦੀ ਪ੍ਰਾਪਤੀ ਸਮਰੱਥਾ ਕ੍ਰਮਵਾਰ 98.8, 98.9 ਅਤੇ 96.6% ਦਿਖਾਉਂਦਾ ਹੈ। ਕੰਬਾਈਨਿੰਗ ਸਮਰੱਥਾ ਅਤੇ ਹੈਟਰੋਸਿਸ ਦਾ ਉੱਤਮ ਜਣਨ ਅਤੇ ਤਿੰਨ ਵਾਤਾਵਰਣਕ ਹਲਾਤਾਂ ਜਿਵੇਂ ਕਿ ਅਗੇਤਾ ਸੀਜ਼ਨ (E_1), ਮੁੱਖ ਸੀਜ਼ਨ (E_2) ਅਤੇ ਪਿਛੇਤੇ ਸੀਜ਼ਨ (E_3) ਵਿੱਚ ਦੋ ਮਿਆਰੀ ਚੈੱਕ ਅੰਦਾਜ਼ਾ ਲਗਾਉਣ ਲਈ ਤਿੰਨ CMS ਲਾਈਆਂ ਅਤੇ 20 ਸਮਰੱਥਾ ਰਿਸਟੋਰਰ (ਮੁੜ ਭੰਡਾਰਨ) ਲਈਨਾਂ ਨੂੰ ਲਾਈਨ × ਟੈਸਟਰ ਮੇਟਿੰਗ (ਮਿਲਾਪ) ਡਿਜ਼ਾਇਨ ਤੇ ਪਰਖਿਆ ਗਿਆ। ਇਨ੍ਹਾਂ ਵਾਤਾਵਰਣਕ ਸਥਿਤੀਆਂ ਵਿੱਚ GCA ਲਾਈਨਾਂ, GCA ਟੈਸਟਰਜ਼ ਅਤੇ SCA ਕਰਾਸਿਸ ਸਦਕਾ ਸਾਰੇ 15 ਪੌਦਿਆਂ ਦੇ ਵਿਕਾਸ, ਝਾੜ ਅਤੇ ਗੁਣਵਤਾ ਵਿਸ਼ੇਸ਼ਤਾਵਾਂ, ਸਿਰਫ GCA ਲਾਈਆਂ ਕਰਕੇ ਪੌਦੇ ਦੀਆਂ ਮੁੱਢਲੀਆਂ ਸਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ ਨੂੰ ਛੱਡ ਕੇ ਬਾਕੀ ਅੰਦਾਜ਼ੇ ਮਹੱਤਵਪੂਰਨ ਰਹੇ। ਤਿੰਨੇ ਵਾਤਾਵਰਣਕ ਸਥਿਤੀਆਂ ਵਿੱਚ E_2, E_3 ਦੀਆਂ ਮੁੱਢਲੀਆਂ ਪੌਦ ਸ਼ਾਖਾਵਾਂ ਦੀ ਗਿਣਤੀ ਨੂੰ ਛੱਡ ਕੇ ਅਤੇ E_3 ਵਿੱਚ ਪੌਦੇ ਦੀ ਉਚਾਈ, ਫੈਲਾਅ ਅਤੇ ਫਲਾਂ ਦੀ ਗਿਣਤੀ ਤੋਂ ਇਲਾਵਾ ਅਧਿਐਨ ਕੀਤੀਆਂ ਗਈਆਂ ਸਾਰੀਆਂ ਵਿਸ਼ੇਸ਼ਤਾਵਾਂ ਵਿੱਚ ਯੋਗਤਾਮਕ ਵਿਭਿੰਨਤਾ (σ^2A) ਦਾ ਦਾਇਰਾ ਅਯੋਗਾਤਮਕ ਵਿਭਿੰਨਤਾ (σ^2D) ਨਾਲੋਂ ਵੱਧ ਸੀ। ਅਗੇਤੇ, ਮੁੱਖ ਅਤੇ ਪਿਛੇਤੇ ਸੀਜ਼ਨ ਲਈ ਬਿਹਤਰ ਬਾਗਬਾਨੀ ਗੁਣਾ ਵਾਲੇ ਵੱਧ ਝਾੜ ਦੇਣ ਵਾਲੇ ਜੀਨੋਟਾਇਪ ਤਿਆਰ ਕਰਨ ਲਈ ਬਰੀਡਿੰਗ ਲਈ CMS ਲਾਇਨ, CMS463D13A ਅਤੇ ਟੈਸਟਰ SL 475, IS 268, PP 402, FL 201 ਅਤੇ C 142 ਦੀ ਪਹਿਚਾਣ ਕੀਤੀ ਗਈ। ਵੱਖ-ਵੱਖ ਫਸਲੀ ਸੀਜ਼ਨ ਤੇ ਵਰਤੋਂ ਲਈ ਹਾਇਬਰਿਡ ਪਹਿਚਾਣੇ ਗਏ। ਵਾਤਾਵਰਣਿਕ ਸਥਿਤੀਆਂ ਦੌਰਾਨ ਇਕੱਤਰ ਕਰਨ ਤੇ ਪ੍ਰਤੀ ਪੌਦਾ ਝਾੜ, ਪ੍ਰਤੀ ਪੌਦਾ ਪ੍ਰਮੁੱਖ ਸਾਖਾਵਾਂ, ਫ਼ਲ ਭਾਰ, ਪ੍ਰਤੀ ਫ਼ਲ ਬੀਜ, ਕੈਪਸਾਇਸਿਨ ਮਾਤਰਾ ਅਤੇ SHU ਲਈ CMS463D13A × IS 268 ਇੱਕ ਵਧੀਆ ਕੰਬਾਇਨਰ ਸੀ। ਵਾਤਾਵਰਣਿਕ ਪ੍ਰਸਥਿਤੀਆਂ ਦੌਰਾਨ ਵੱਧ ਤੋਂ ਵੱਧ ਭਾਵ ਬਿਹਤਰ ਜਣਨ ਹੈਟਰੋਸਿਸ ਪ੍ਰਤੀ ਪੌਦਾ ਕੁਲ ਝਾੜ (32.29%) ਲਈ ਅਤੇ ਇਸ ਤੋਂ ਬਾਅਦ ਪ੍ਰਤੀ ਪੌਦਾ ਪ੍ਰਮੁੱਖ ਸ਼ਾਖਾਵਾਂ (17.96%), ਪ੍ਰਤੀ ਫਲ ਬੀਜ (12.46) ਅਤੇ ਪ੍ਰਤੀ ਪੌਦਾ ਫ਼ਲ ਦੀ ਸੰਖਿਆ (11.43%) ਲਈ ਪਾਇਆ ਗਿਆ। CMS463D13A × SL 475, CMS463D13A × VR 523, CMS463D13A × YL 581 ਅਤੇ CMS463D13A × IS 268 ਸਾਰੇ ਵਾਤਾਵਰਨ ਵਿਚ ਪ੍ਰਤੀ ਪੌਦਾ ਝਾੜ, ਫ਼ਲ ਭਾਰ ਅਤੇ ਫ਼ਲ ਮਾਤਰਾ, SHU ਲਈ CMS463DBA × SL 475 ਬਿਹਤਰੀਨ ਸਾਬਿਤ ਹੋਏ। ਇਹਨਾਂ ਕਰਾਸ ਨੂੰ ਬਹੁ-ਸਥਾਨਾਂ ਤੇ ਪਰਖਣ ਲਈ ਸਿਫਾਰਿਸ਼ ਕੀਤਾ ਜਾਂਦਾ ਹੈ ।

ਮੁੱਖ ਸ਼ਬਦ: ਸਾਇਟੋਪਲਾਜਮਿਕ ਨਰ ਮੁਰਦਾਰ, ਹੈਟਰੋਸਿਸ ਬਰੀਡਿੰਗ, ਸੁਮੇਲ ਸਮਰੱਥਾ, G × E ਸਬੰਧ, SSR ਮਾਰਕਰ

ਪ੍ਰਮੁੱਖ ਸਲਾਹਕਾਰ ਦੇ ਹਸਤਾਖਰ

ਵਿਦਿਆਰਥੀ ਦੇ ਹਸਤਾਖਰ

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

CHAPTER I

INTRODUCTION

Chilli, a member of the plant genus *Capsicum* in the family Solanaceae, is native to Central and South America (Pickersgill 1991) and comprises at least 32-34 species (Barboza *et al* 2011, Qin *et al* 2014 and da Costa Batista 2016). Of the *Capsicum* species, five are cultivated which include *Capsicum annuum* L., *C. frutescens* L., *C. chinense* Jacq., *C. pubescens* Ruiz. & Pavon and *C. baccatum* L. Ruiz. & Pavon (Bosland 1992). Of the five domesticated species, *C. annuum* is the most widely cultivated that includes both the chilli (pepper) and the bell pepper. Most of the cultivated and the wild species of *Capsicum* have chromosome number $2n=2x=24$ (Pickersgill 1997). Chilli was first introduced into India by the Portuguese traders towards the end of 15th century and its cultivation became popular in the 17th century (Dhaliwal *et al* 2014a). In economic terms, chilli is the second largest commodity after black pepper (*Piper nigrum* L.) in the international spice trade. It is an important source of vitamins C and E, minerals, and phytoceuticals like carotenoids and flavonoids (Cichewicz and Thorpe 1996, Bosland and Votava 2000, Maoka *et al* 2001 and Dhaliwal 2017). These nutrients have great benefits for human health (Matsufuji *et al* 2007). From breeding point of view, chilli is considered as a facultative cross pollinating species, although out-crossing to the extent of 90% has been reported (Tanksley 1984).

Global production of chilli in 2014 reached 3.8 million tonnes dried pods harvested from 1.68 million hectares (FAO 2014). India is the largest producer, consumer and exporter of chillies in the world. In India, it is cultivated over 0.83 million hectare with annual production of 1.87 million tonnes of dry chillies (Anonymous 2017). The dry chilli productivity of India has increased by about 90% from 1.18 tonnes ha^{-1} in 2000 to 2.25 tonnes ha^{-1} in 2016 (Anonymous 2017). Cultivation of high yielding F_1 hybrids in place of open pollinated varieties is an important reason for increased productivity (Singh *et al* 2014). Globally, heterosis breeding has been shown to increase fruit yield in chilli by 35-50% (Dhaliwal and Jindal 2014).

In some parts of the world, hybrid seed is still produced manually using hand emasculation and pollination. This is laborious and time consuming. Additionally, it increases cost of hybrid seed and seed purity cannot be assured owing to chance self-pollination. The exploitation of male sterility (MS) systems in production of hybrid seed can eliminate emasculation and reduces the hybrid seed cost up to 50% (Yang *et al* 2008). Two types of MS, the genic or nuclear male sterility (GMS) and the cytoplasmic or cytogenic male sterility (CMS) have been documented and exploited to produce hybrid seed in crop plants. Both the GMS and the CMS are available in peppers (Dhaliwal and Jindal 2014). The GMS in pepper was first documented by Martin and Crawford (1951) in Cayenne strain No. 4526, strain No.

69a, and strain No. 4558 of *C. frutescens*. Till today, approximately twenty such independently inherited GMS genes have been reported in *Capsicum* (Dhaliwal and Jindal 2014). At Punjab Agricultural University, Ludhiana nuclear male sterility gene '*ms-10*' (originally designated as *mc 509*, Pochard 1970) was transferred from a French introduction to 'Punjab Lal', a multiple disease resistant variety, and a GMS line named 'MS 12' was developed (Singh and Kaur 1986). The GMS line 'MS-12' was utilized to develop three commercial hybrid cultivars *viz.*, 'CH-1' (Hundal and Khurana 1993), 'CH-3' (Hundal and Khurana 2002), and 'CH-27' (Dhaliwal *et al* 2015a). The limitation of the GMS is that the progeny segregates into male fertile (MF) and male sterile (MS) in equal proportion and the MF plants must be identified and removed from the hybrid seed production block at flowering. This increases cost of hybrid seed and the seed might suffer from genetic impurities resulting from improper identification of MS and MF plants (Dhaliwal and Jindal 2014).

The CMS is determined by the interaction between the sterile cytoplasm and the recessive '*rf*' gene, but it maintains female fertility (Hanson and Folkerts 1992, Linke and Börner 2005, Lee *et al* 2008a and Min *et al* 2009). The CMS in chilli pepper was first documented by Peterson (1958) in the accession USDA PI 164835 introduced from India. This CMS pepper has been the only usable source for F_1 hybrid seed production (Shifriss 1997). The CMS usually involves three lines (A, B, and C) for hybrid seed production. A-line is genetically S*rfrf*, B-line or the maintainer is N*rfrf*, and the C-line or the restorer is N/S*RfRf*. The A-line is propagated by crossing it with the maintainer line. The resultant progeny are 100% male sterile. To hybrid seed, A-line is crossed with the restorer line. The restorer line has the ability to restore fertility in the resultant F_1 hybrid. The CMS also ensures genetic purity of the seed as self-pollination is prevented due to lack of viable pollen.

There are reports that the CMS is sensitive to environmental fluctuations, especially the temperature (Peterson 1958, Yazawa *et al* 2002 and Kim *et al* 2013). When day and night temperature falls below 25°C and 17°C, respectively, fertility of the CMS is partially restored (Shifriss 1997). Partial fertility of CMS might also be influenced by some of the modifier genes (Zhang *et al* 2000) or by the interaction between the nuclear genes and the cytoplasm (Yu 1985). The modifier genes in favourable temperature conditions may lead to alterations in fertility ranging from complete sterility to partial fertility. This causes self-pollination in the female parent resulting in genetic impurity in the hybrid seed (Gulyas *et al* 2006).

To assure genetically pure F_1 hybrid seed production, the commercial use of CMS needs highly stable male sterility. Stable CMS lines could be developed by growing single plant progeny, retaining only those maintainer genotypes producing 100% male sterility, and by screening under the environmental conditions that ensures selection for the highest level of male sterility (Yu 1985 and Lee 2001).

During the last two decades or so, CMS lines has been developed and utilized for commercial F_1 seed production in Israel, South Korea, China, Taiwan and India (Shifriss and Guri 1979, Lee 2001, Madhavi Reddy *et al* 2002, Gong *et al* 2008, Gniffke *et al* 2009 and Anonymous 2010). Following selection of the maintainer plants and screening for sterility under low temperature conditions, 17 CMS lines have been developed at the Punjab Agricultural University by transferring S-cytoplasm from 'CCA 4261', an introduction from the World Vegetable Center, Taiwan, into elite chilli backgrounds. Stability and combining ability of these lines need to be investigated for their utilization in hybrid breeding programmes of chilli.

Chilli exhibits wide range of variability for various economic and quality traits (Borgohain *et al* 2005) encouraging the breeders to exploit the variation for genetic improvement of the crop. With the availability of CMS lines and elite breeding lines as potential restorers of fertility, there is considerable scope of genetic improvement in yield and quality traits of chilli through hybrid breeding. To develop potential F_1 hybrids, the most important task for the plant breeder is the proper choice of parental lines. The usual approach to select the parental lines on the basis of *per se* performance is not appropriate. Such parental lines do not necessarily produce promising hybrids. The ability of the lines or parents to nick well depends on the genes, which can't be merely adjudged by *per se* performance of the parents (Allard 1960). To exploit heterosis in chilli using CMS system in the hybrid breeding program, breeders need to test the combining ability between CMS A-line and the potential C-lines.

Combining ability analysis is an effective approach for selection of the potentially good parents and for identification of the promising hybrids. The general combining ability (GCA) effects indicates importance of the additive gene action and specific combining ability (SCA) indicates importance of the non-additive gene action (Falconer and Mackay 1996). Further, the components of variation analysis highlight the relative importance of the additive gene action and the non-additive gene action in inheritance of the traits.

Given the two set of parental lines, line × tester mating design is appropriate to assess heterosis and combing ability of the CMS lines and fertility restoration ability of the elite breeding lines. The mating design can evaluate relatively more number of lines at a time than the diallel or the partial diallel crosses. The knowledge of the relative importance of the additive and the non-additive gene effects will be useful to identify CMS based F_1 hybrids for commercial cultivation, and to generate populations for selection of the promising true breeding lines.

Keeping these points in view, this investigation was undertaken with the following objectives:

- To study stability of the newly developed CMS lines
- To check the genetic similarity between CMS A- and B- lines
- To estimate combining ability effects of parental lines and hybrids for important horticultural traits
- To identify promising hybrid combinations for commercial exploitation

CHAPTER II

REVIEW OF LITERATURE

The literature pertinent to the present investigation entitled "Evaluation of cytoplasmic male sterile lines of chilli pepper (*Capsicum annuum* L.) and their utilization in heterosis breeding" has been reviewed under the following heads:

2.1 Inheritance of cytoplasmic male sterility (CMS)
2.2 Development and evaluation of CMS lines
2.3 Heterosis breeding
2.4 Combining ability studies
2.5 Components of genetic variance

2.1 Inheritance of CMS

Peterson (1958) isolated a male-sterile plant in an Indian introduction USDA 'PI 164835'. He grouped various degrees of sterility, from 1 or 2 to 10 or 15 functional pollen grains per anther. The sterility was found to be controlled by a major recessive *rf* gene interacting with a specific S-plasmatype. A dominant *Rf* allele is essential to restore the fertility. Therefore, from the cross (S)*rfrf* × (N)*RfRf* one should obtain fertile (S)*Rfrf* progeny only. Whereas, from several test crosses a di-hybrid ratio was obtained (3:1, fertile: sterile) suggesting an additional duplicate *Rf* locus, *Rf*2*rf*2. Shifriss and Frankel (1971) developed 23 crosses and produce 23 F_2 populations by selfing the crosses and concluded that two types of S-cytoplasm might be identical in pepper because pepper lines 1005 and 1006 known to be restorers, and non-restorers behaved similarly. In a cross of *C. frutescens* × *C. annuum*, Yu (1990) found a third type of S-cytoplasm and it was identical to Peterson cytoplasm (Peterson 1958).

Working with Peterson's male sterile (MS) plants, Novak *et al* (1971) reported 2 contradictory digenic interpretations to his data. On the basis of 1 fertile: 3 sterile ratios under test crosses and 9 fertile: 7 sterile ratio in F_2 populations, a complementary gene action was suggested. On the contrary, 3:1 test cross data indicated independent gene action of the Rf_1 and Rf_2 loci. With the end concept, one would expect a 15:1 F_2 ratio, but such F_2 segregation was never documented. Whereas *Rf* allele was found in most of the wild hot pepper genotypes, the *rf* allele seem to be present in various sweet and large fruited lines (Peterson 1958, Novak *et al* 1971, Ohta 1971 and Yu 1985).

Two mitochondrial genes, *atp6* (Kim and Kim 2006) and *orf456* (Kim *et al* 2007) have been identified as candidates potentially responsible for CMS in chilli pepper. The CMS line exhibited an approximately 17 kDa product while the level of expression of this protein was severely reduced in the restorer line. Jo *et al* (2009) developed a novel CMS specific marker, accD-U from a deletion in a chloroplast derived sequence in the mitochondrial genome of a CMS pepper line and it was most efficient than the previously reported markers by Kim and Kim (2005). Ji *et al* (2014) developed a SCAR marker for early identification of S-cytoplasm based on mitochondrial SRAP analysis in pepper. On the basis of SRAP analysis of CMS lines and maintainer lines, a $SCAR_{130}$ marker was developed. Four markers ($SCAR_{130}$ and three previously reported) were used on different pepper lines and found out that the $SCAR_{130}$, was the most reliable than the other three previously reported markers namely, SCAR $atp6_{607}$, SCAR $coxII_{708}$ and accD-U (Kim and Kim 2005 and Jo *et al* 2009).

Various types of unstable CMS have been reported and their inheritance patterns in pepper were studied (Shifriss and Guri 1979 and Yu 1985). Lee (2001) suggested one locus *St* with three alleles, St^2, St^u and St^1) related to stability of CMS independent from the *Rf* locus and classified the unstable lines based on two different phenotypes. One was unstable CMS that produces extremely few amounts of pollen and other type was unstable CMS that produces more pollen grains than that of unstable CMS lines but less than that of normal fertile lines. The amount of pollen grains of those two types appear to be influenced by temperature but it was not clear whether they were restored at low temperature. By self-pollination and selection, both stable maintainer and restorer lines were recovered (Yu 1985), indicating that the unstable CMS lines might be heterozygous for sterility modifier gene(s) and that their progeny reacted to yearly or seasonal variations. In addition, another locus, *partial-restoration* (*pr*), producing a mix of normal and aborted pollen grains from normal anthers, that is closely linked to *Rf* was identified by Lee *et al* (2008a). The trait was expressed only when the pepper plant had the sterile (S-) cytoplasm and homozygous recessive (*pr*) alleles. The homozygous dominant (*PrPr*) alleles determined full fertility.

To understand the role of the major *Rf* gene, the minor genes and the environmental factors such as temperature, Wang *et al* (2004) determined quantitative trait loci (QTL) for fertility restoration (Lee *et al* 2009). One major QTL for CMS fertility restoration was mapped on the upper terminus of chromosome 6 (P6). The QTL accounted for 20-69% of the phenotypic variation and four additional minor QTLs identified on other chromosomes (P5, P2, linkage group PY3 and PY1), accounted for 7-17% of the phenotypic variation (Lefebvre *et al* 2002 and Jo *et al* 2010).

The F_2 populations of cultivars Buja and Tamna were used for the development of a linkage map by Min *et al* (2009). Three additional *Rf* linked molecular markers, AFRF1, AFRF3 and AFRF4, were identified. The marker AFRF4 was the closest to the *Rf* locus. The previous allelic testing observed the existence of a third haplotype, $Rfls^{7701}$, which can function as dominant (*Rf*) or recessive (*rf*). Min *et al* (2008) suggested that $Rfls^{7701}$ was linked to instability of CMS. However, Min *et al* (2009) found out that unstable CMS was induced by a gene residing at another locus rather than by $Rfls^{7701}$ haplotype linked allele.

Various reports have emerged indicating development of molecular markers linked to the *restorer-of-fertility* (*Rf*) gene. However, the calculated genetic distances of linked molecular markers have varied between the research groups. The characteristics of molecular markers linked to the *Rf* gene are summarized in Table 2.1.

Table 2.1: Characteristics of the molecular markers linked to the CMS-associated genes in pepper

Marker	**Type**	**Gene**	**Fragment size (bp)**	**Distance cM**	**Reference(s)**
coxII SCAR	SCAR	*coxII*	708	-	Kim and Kim (2005)
atp6-2 SCAR	SCAR	*atp6-2*	607	-	Kim and Kim (2005)
$SCAR_{130}$	SCAR	*orf456*	130	-	Ji *et al* (2014)
accD-U	-	*accD*	1082	-	Jo *et al* (2009)
$OP13_{1400}$	RAPD	*Rf*	1400	0.37	Zhang *et al* (2000)
$OW19_{800}$	RAPD	*Rf*	800	8.12	Zhang *et al* (2000)
OPP13-CAPS	CAPS	*Rf*	1400	1.1	Kim *et al* (2006) and Min *et al* (2008)
CRF3SIS	SCAR	*Rf*	870	4.8-5.3*	Gulyas *et al* (2006)
AFRF8CAPS	CAPS	*Rf*	737	1.8	Kim *et al* (2006)
CaRf-FL-M2	STS	*Rf*	650	0.5	Min *et al* (2009)
AFRF4	AFLP	*Rf*	218	0.1	Min *et al* (2009)
AFRF1	AFLP	*Rf*	478	1.1	Min *et al* (2009)
AFRF3	AFLP	*Rf*	261	18.3	Min *et al* (2009)
CRF-SCAR	SCAR	*Rf*	556	1.4	Jo *et al* (2010)
PR-CAPS	CAPS	*pr*	122	1.8	Lee *et al* (2008b)

*****5.3 cM in the F_3 generation and 4.8 cM in the F_4 generation (Source: Dhaliwal and Jindal 2014)

2.2 Development and evaluation of CMS lines

The bell pepper genotypes are known to possess the fertility restorer (*rf*) gene (Shifriss and Frankel 1971, Yu 1985, 1990, Shifriss 1997, Zhang *et al* 2000 and Kumar *et al* 2007), a CMS line can be developed by transferring the maintainer gene from the bell pepper to newly identified source of S-cytoplasm (Shifriss and Frankel 1971). Shifriss and Frankel (1971) crossed 23 small fruited hot pepper lines with 3 bell pepper lines possessing the *rf* gene, for search the new sources of S-cytoplasm. The segregation pattern in two populations, 1005 and 1006, indicated dominance of MF over MS and confirmed that sterility was controlled by a single recessive gene.

Four cytoplasmic-genetic male sterile lines namely, MS-1, MS-2, MS-3 and MS-4 and their counterpart CMS B-lines were developed by Madhavi Reddy *et al* (2002) and found stable for sterility in various seasons' *viz*., *kharif and rabi*. Pákozdi *et al* (2002) also reported that the CMS lines No. 202, 203, 204 and 205 did not form viable or functional pollen during three growing seasons viz. May, June-July and August-September. Yazawa *et al* (2002) succeeded in breeding of two stable CMS pepper, 'P-MS' and 'Murasaki-MS' with no fruit set. Liu and Gniffke (2004) bred three CMS lines, 'CCA4759', 'CCA4757' and 'CCA5273' with little viable pollen and the lines set no fruits with seed under low temperature (< 23.8 °C/ 14.3 °C day/night) at the World Vegetable Center, Taiwan. Five CMS sterile lines were evaluated by Gniffke *et al* (2009) at the World Vegetable Center. They found that 2 lines, 'CCA7234' and 'CCA7235', displayed stable sterility on all winter observation temperature dates. Gong *et al* (2008) developed several CMS lines in chilli pepper, as well as their maintainers and restorers, by a combination of inter-specific crossing and induced mutations.

There are reports that the CMS could be unstable due to environmental fluctuations, especially under the low temperature (<25°/17 °C day/night) and its genetic background (Peterson 1958, Novak *et al* 1971, Shifriss and Guri 1979, Yu 1985, Kubisova and Haslbachova 1991, Ledo *et al* 1992 and Shifriss 1997). High temperatures are the most critical environment for the expression of sterility in pepper (Peterson 1958). The instability of the CMS trait was attributed to an interaction between temperature and sterility modifier genes (Yu 1985). Stable CMS lines could be developed by selecting maintainer plants (B-lines) that are tolerant to temperature variations, selection against modifier genes, incorporation of seedling markers for the early exclusions of progenies resulting from self-pollinations and sampling of the environmental conditions that produced the maximum level of MS (Yu 1985, Shifriss and Guri 1979 and Lee 2001). Min *et al* (2009) reported that during the summer season (June-August) a greater number of unstable MS flowers appeared; however, most of stable MS flowers appeared during the cooler season (fall to spring).

To assess the MF of hybrids synthesized from cross between the Peterson's MS plants and 270 pepper inbred lines, Yu (1985) observed 152 lines to be stable maintainer lines (B-lines), *i.e.*, (N)*rfrf*; 66 to be restorer lines (N/S)*RfRf* and rest of the lines were classified as unstable (Yu 1990). Upon self-pollination and selection, both the stable maintainer and restorer lines were recovered, suggesting that the unstable lines might be heterozygous for the sterility modifier genes and that their progeny reacted to yearly or seasonal variations.

A thermo-sensitive cytoplasmic male sterile (TCMS) line (Milyang A) of chilli pepper was evaluated by Kim *et al* (2013). They observed that the line was sterile at temperatures above 15 ºC but its fertility was restored when night temperatures fell below 13 ºC. The self-crossed fruit-setting rate of 200A × 206B, 201A × 200B, 201A × 206B, 203A ×

200B, 206A × 200B, 206A × 201B were nil and the 6 F_1 hybrids of pepper did not have normal pollen or traces of pollen, indicating that the F_1 hybrids were sterile (Ma *et al* 2013). Suryawanshi *et al* (2013) reported that a hot pepper 'CMS-A (0246)' plants did not set any fruit across locations. By using marker assisted selection (MAS), Mulyantoro *et al* (2014) introgressed the S-type cytoplasm and the *Rf* allele from hot pepper to bell pepper and converted the NMS system to the CMS system.

2.3 Heterosis breeding

Heterosis describes the performance of heterozygous F_1 hybrid plants in terms of increased or decreased vigor, size, yield, uniformity, speed of development, fertility, wider adaptability, resistance to disease and to insect pests, in comparison to their genetically different homozygous parents (Shull 1908 and East 1936). Powers in 1944 suggested that the term heterosis should be used when F_1 hybrid is superior or inferior to both of the parents, other phenomenon regarded as dominance or partial dominance. In the post-Mendelian era of plant breeding, systematic chilli pepper breeding research in India started in the 1930s with efforts to understand the inheritance of important traits (Ramiah and Pillai 1935). In chilli, the cltivation of F_1 hybrid is more profitable than open-pollinated varieties. Bosland and Votava (2000) reported that chilli grown from hybrid seed are uniform and usually higher yielding.

Ten CMS based F_1 hybrids were evaluated at two locations in Thailand by Milerue and Nikornpun (2000). Three F_1 hybrids, CF 21789 × Fang (261.58%), KY 1-1 × Fang (237.93%) and KY 1-1 × Bang-Chang (233.97 %) were promising for fruit yield, while for pungency levels the hybrids KY 1-1 × Nhum Khiew Maejo, CF 21789 × Nhurn Khiew and KY 1-1 × Nhum Khiew had the high levels of heterosis. Zewdie and Bosland (2001) reported high estimates of heterosis for nornordihydrocapsaicin (34%), nordihydrocapsaicin (42%), capsaicin (153%), dihydrocapsaicin (33%) and total capsaicinoids (71%) in a hybrid, NMCA80004 × NMCA80058. Sousa and Maluf (2003) noted that the cross BGH-4285 × BGH-433 was the superior performing for number of seed fruit^{-1}, fruit dry weight plant^{-1} and total fruit yield. According to Geleta and Labuschagne (2004a) three-way and double cross hybrids could be used in pepper breeding, because the yield potential of three-way and double cross hybrids was higher than single cross hybrids. Overall the three-way crossed hybrids exhibited 36.1 and 13.6% heterosis for fruit yield and fruit length, respectively, while double crossed hybrids showed high mean heterosis for fruit weight (16.9%), fruit number (24.0%) and fruit yield (35.6%).

Geleta and Labuschagne (2004b) showed that mean values of mid-parent heterosis and standard heterosis were high and significantly positive for fruit yield, plant height, fruit diameter, fruit weight, pericarp thickness and fruit number plant^{-1}, similarly the high significant positive parent heterosis was recorded in plant height and fruit yield plant^{-1}. Out of

21 F_1 hybrids, 12 crosses expressed standard heterosis, ranging from 28.0 to 68.8% for fruit yield. The highest standard heterosis exhibited by the cross combinations, Szegedi 178 × Pepper 1976 followed by Bakko Local × Pepper 1976 and Bakko Local × Mareko Shote for fruit yield plant^{-1}. Khalil *et al* (2004) identified 5-27 × Yolo Wonder (63.2%) as the most promising hybrids for total yield. Patel *et al* (2004) demonstrated that the range of heterosis over better parent and standard checks varied from 87.20 to 472.09% and 77.37 to 138.32% for green fruit yield, respectively. Of the 48 crosses, 7 and 5 showed significant better parent and standard heterosis (over check, S-49), respectively.

Millawithanachchi *et al* (2006) noted that out of 28 F_1 hybrids, the cross IR × MI 2 expressed the highest significant and positive heterosis over their better parent for total yield (113.24%), total number of pods plant^{-1} (22.59%) and early flowering; while the hybrid KA 2 × MI 2 showed maximum heterobeltiosis for dry matter content (10.53%). To develop the male sterility based F_1 hybrids in chilli, Shankarnag *et al* (2006) crossed 3 CGMS lines with 7 testers using line × tester mating design and evaluated for plant growth, earliness and early green fruit yield. Out of 21 F_1 hybrids, the cross L3 × T16 was most heterotic over two standard checks for stem girth, plant spread and number of tertiary branches, L1 × T16 for number of secondary branches, L3 × T15 for plant height, L1 × T14 for days to first and 50% flowering and L5 × T14 for early green fruit yield. Cruz-Pérez *et al* (2007) reported that the cross Puebla × Huatusco manifested maximum heterosis over their respective better parent for capsaicinoid content (224.72%) at 96 days of development after flowering. The heterosis for vitamin C content was significant negative for all the three crosses Puebla × Chiapas, Puebla × Zongolica and Puebla × Huatusco.

Performance evaluation trail conducted by Prasath and Ponnuswami (2008) on 30 F_1 hybrids indicated that heterosis was ranged from 40.35 to 126.32% over their respective better parent for dry yield ha^{-1}. The hybrids Bydagi Kaddi × Arka Abir and MDU Y × Co 4 were found promising in term of total extractable colour, low capsaicin besides dry yield and other contributing traits. Marame *et al* (2009) produced 66 F_1 hybrids involving 12 parents (nine Asian and three Ethiopian) of hot pepper by using half-diallel mating design. They found that the cross PBC 223 × Marekoshote displayed the highest standard heterosis of 92.05% for fruit yield plant^{-1}, 136.36% for number of fruits plant^{-1} while, the highest better parent heterosis for fruit yield plant^{-1} was expressed by the cross-combination PBC 602 × ICPN9#16 (163.8%), for number of fruits plant^{-1} by ICPN10#5 × Bakolocal (79.61%), for fruit weight (50.29%) and for number of branches plant^{-1} (55.63%) by PBC 223 × Marekofana, for fruit length by PBC 223 × Bakolocal (26.59%) and for plant height by the cross PBC 223 × PBC 580 (18.24%).

Pérez-Grajales *et al* (2009) evaluated 21 genotypes including 15 hybrids and 6 parental lines of manzano hot pepper (*C. pubescens* R & P) to estimates heterosis and combining ability for different yield and quality traits. They found that the hybrid Zongolica × Puebla had higher magnitude of heterobeltiosis for fruit yield (51%), Peru × Chiapas for fruit volume (33%), Puebla × Peru for number of seed fruit^{-1} (22%) and Puebla × Chiapas for seed weight (38%) and locule number (18%). Sitaresmi *et al* (2010) reported that the highest better parent heterosis value for fruit weight plant^{-1} recorded in the cross IPB C2 × IPB C15 (25.60%). The cross IPB C8 × IPB C15 had shown the highest heterosis over better parent for number of fruits plant^{-1} (63%).

In a study conducted by Prajapati and Agalodia (2011), the hybrid JCh-676 × JCh-659 exhibited the highest mid-parent (83.21%) and better parent heterosis (78.38%) for dry fruit yield. The cross combinations JCh-730 × JCh-725 and JCh-676 × JCh-659 were identified as promising hybrids for green and dry fruit yield and its component traits. To estimate the magnitude of heterosis and heterobeltiosis Shrestha *et al* (2011) tested 23 F_1 hybrids and their parents for yield and its component traits of sweet pepper. The maximum significant and positive heterobeltiosis was exhibited by the hybrid 5AVS7 × SP32 (87.2%) and SP12 × SP38 (119.3%) for number of fruits palnt^{-1} and fruit yield, respectively, while 5AVS7 × SP45, 5AVS7 × SP32 and 5AVS8 × SP48 have shown the highest standard heterosis over the varieties Special, Fiesta and President for fruit yield plant^{-1}.

Tembhurne and Rao (2012) conducted an experiment to identify the most heterotic CMS based F_1 hybrids in chilli pepper. Total of 51 F_1 hybrids were generated using 3 lines and 17 testers, crossed in line × tester fashion. Eight hybrids namely, JNA1 × BVC-37 (48.47%), JNA1 × PantC1 (25.76%), JNA1 × LCA334 (25.33%), JNA1 × LCA960 (24.02%), JNA1 × PSBR (22.77%), JNA1 × GUK-2-1(16.59%), ACA2 × LCA960 (13.10%) and ACA1 × LCA960 (6.99%) exhibited significant and positive heterosis over standard check (VNR 332) for dry fruit weight plant^{-1}.

Butcher *et al* (2013) developed 29 F_1 Paprika and Serrano pepper hybrids by controlled pollinations involving 19 parents. Among 'Paprika' parents, PapP30 depicted a significantly higher fruit length (188.33 mm) and PapP27 had maximum fruit weight (38.45 g) as well fruit diameter (35.9 mm). Among the crosses PapP27 × PapP67 exhibited the maximum fruit diameter (42.0 mm), pericarp thickness (3.2 mm) and fruit weight (62.95 g) and the F_1 hybrid PapP27 × PapP30 exhibited the maximum fruit length (188.8 mm). Among the 'Serrano' types, the line SP128 had the highest means for fruit weight (19.18 g), fruit diameter (24.9 mm) and pericarp thickness (3.9 mm), whereas the line SP50 had the maximum fruit length (116.2 mm). Among the hybrids, SP15 × SP5 expressed the highest mean value for fruit weight (17.09 g), the hybrid SP50 × SP15 for fruit length (109.8 mm) and the F_1 hybrid SP5 × SP73 for fruit diameter (20.0 mm) and pericarp thickness (4.2 mm). The F_1 hybrid SP16 × SP57 exhibited the highest mid-parent heterosis for capsaicin (1289.23%) and the cross SP16 × SP15 for total capsaicinoid (902.32%). The hybrid SP16 × SP15 showed the maximum high-parent heterosis for capsaicin (814.95%) and total capsaicinoid (604.81%), SP41 × SP95 for ascorbic acid (75.91%), SP15 × SP5 for fruit weight (64.96%), SP15 × SP128 for fruit length (24.49%), PapP27 × PapP67 for fruit diameter (16.99%) and SP5 × SP73 for pericarp thickness (16.67%).

Chaudhary *et al* (2013) also found significant positive heterois for yield and quality characters. Out of 25 F_1's, the cross combination Pusa Jwala × DC-16 (161.55%) had shown the highest better parent heterosis for number of fruits plant^{-1} followed by Pusa Jwala × VR-339 (127.63%) and Japani Longi × DC-16 (96.43%), while the hybrids Pusa Jwala × VR-339 (220.53%), Pusa Jwala × DC-16 (205.53%) and Pant C-1 × VR-339 (239%) had shown the highest better parent heterosis for yield plant^{-1}. Khalil and Hatem (2014) indicated that the hybrid LS 5-6 × B 23-5, LS 2-2 × W 5-15 and Big Dipper × B 16-10 expressed the desired heterosis over their respective better parent for early fruit weight plant^{-1}, W 5-15 × B 23-5 and W 5-15 × LS 5-6 for total fruit number plant^{-1}, LS 2-2 × W 5-15 followed by W 5-15 × B 23-5, LS 2-2 × B 16-10 for total fruit weight, Big Dipper × B 23-5 for fruit length, LS 2-2 × W 5-15 for average fruit weight and Big Dipper × B 16-10 and Big Dipper × LS 2-2 for vitamin C. Hasanuzzaman *et al* (2013) developed 15 F_1's in a diallel fashion (excluding the reciprocals) involving 6 parental lines of chilli. They found that the cross BARI Morich 1 × CCA 19 and CCA 5 × BARI Morich 1 expressed heterosis for fruit length, number of seed fruit^{-1}, number of fruits plant^{-1}, plant canopy and yield plant^{-1}.

Sharma *et al* (2013) noted that the highest fruit weight heterosis of 102.73 and 49.50% over better parent and standard check were recorded by the cross Rani Sel-1 × Sel-12-2-1 and PRC-1 × Rani Sel-1, respectively, 30.64 and 17.81% by the cross Rani Sel-1 × Sel-12-2-1 and Sel-12-2- 1 × SP-316 for fruit diameter, 40.76 and 61.18% by the cross SSP × SP-316 for fruit length, 25.71 and 17.56% by SSP × Sel-12-2-1 and Rani Sel-1 × SSP for fruit girth, 156.61 and 155.98% by California Wonder × SP-316 for number of fruits plant^{-1}, 70.31 and 33.52% by Rani Sel-1 × Sel-12-2-1 and California Wonder × SP-316 for pericarp thickness, 51.13 and 18.74% by PRC-1 × SSP and Rani Sel-1 × SSP for number of branches plant^{-1} and 58.84 and 170.37% by the cross Rani Sel-1 × Sel-12-2-1 and PRC-1 × Rani Sel-1 for marketable fruit yield plant^{-1}.

Krishnamurthy *et al* (2013) developed 150 F_1 hybrids via line × tester mating design involving five lines and 30 testers to estimate the mid-parent heterosis at two locations. Fifty-six per cent of the crosses exhibited significant mid-parent heterosis for green and red fruit yield plant^{-1}. Hybrids namely, CMS 8A × Pusa Sadabahar, CMS 8A × Tiwari, CMS 8A ×

LCA 273, CMS 2A × LAM 333, CMS 8A × Arka Suphal, CMS 3A × CA 9 and CMS 8A × Vangara showed significant and positive mid-parent heterosis for green fruit yield plant^{-1}. Twenty four F_1 crosses of bell pepper produced in line × tester mating design involving 8 lines and 3 testers were evaluated by Sood and Kumar (2013). They observed the highest heterosis of 114.49% over their respective better parent for yield plant^{-1} in the cross EC 464107 × Yolo Wonder, SKAU-SP 633-1 × Yolo Wonder for number of fruits plant^{-1} (84.86%) and marketable fruits plant^{-1} (82.39%) and HC 201 × California Wonder for pericarp thickness (28.17%).

Medeiros *et al* (2014) estimated the gene effects and heterosis in *C. baccatum* var. *pendulum* involving 5 parents (lady's finger and cambuci types) and their10 F_1 hybrids developed in full diallel mating design without reciprocals. The cross UENF 1639 × UENF 1732 (cambuci × cambuci) obtained higher yield plant^{-1} than that of the better parent. Among the crosses between lady's finger and cambuci types, most of the hybrids showed positive heterosis for fruit length except UENF 1616 × UENF 1639. Pandey and Chura (2014) reported that out of 25 F_1 hybrids, the cross 09/ Cvar 2 × DARL 74 exhibited heterosis over better parent for fruit length (38.55%) and 09/ Cvar 1 × DARL 74 for number of fruits palnt^{-1} (60.08%), fruit yield (198.11%) and 09/ Cvar 3 × DARL 74 for ascorbic acid content (148.22%).

Sixty-six F_1 hybrids of hot pepper developed in half-diallel set involving 12 genetically diverse parents, including a GMS and a CGMS line, were evaluated by Singh *et al* (2014) to study heterosis for earliness, plant growth, yield and fruit traits. For number of fruits plant^{-1}, the better parent heterosis ranged from -79.30 in EL 181 × PP 402 to 205.95% in CC 141 × VR 521, from -4.72 in SL 462 × US 501 to 39.64% in CC 141 × PP 402 for fruit length, from -20.60 in DL 161 × US 501 to 10.41% in EL 181 × PA 401 for fruit width, from -28.65 in US 501 × PS 403 to 57.52% in CC 141 × VR 521 for fruit weight, from -37.98 in US 501 × PS 403 to 14.39 in SL 462 × DL 161 for pericarp thickness, from -80.70 in CC 141 × SD 463 to 89.94% in SL 462 × PP 402 for number of seed fruit^{-1}, from -1.80 in MS 341 × VR 521 to 32.21% in DL 161 × US 501 for plant height, from -13.77 in US 501 × SD 463 to 20.66% in EL 181 × US 501 for plant spread and from -71.82 in PA 401 × PS 403 to 331.11% in CC 141 × VR 521 for total yield plant^{-1}.

Bhutia *et al* (2015) conducted a trial involving 10 F_1 hybrids and their 5 genetically diverse parental lines to estimates mode of gene action, percent heterosis and combining ability effects for 14 quantitative traits. The range of heterosis over the better parent varied between -39.54 to 2.08% for plant height, -46.41 to 20.05% for number of primary branches plant^{-1}, -44.77 to 0.29% for number of fruits plant^{-1}, -37.88 to 4.49% for fruit girth, -64.66 to 6.14% for fruit length, -40.0 to 7.24% for number of seed fruit^{-1}, -36.36 to 2.68% for test weight of seed, -69.44 to 28.93% for vitamin C content, -31.43 to 46.67% for capsaicin content and -49.45 to 71.06% for fruit yield plant^{-1}. The highest better parent heterosis for fruit yield plant^{-1} along with fruit length, number of fruits plant^{-1}, number of seed fruit^{-1} and vitamin C content was recorded by the F_1 hybrid BCCH Sel-4 × AC-575.

Naresh *et al* (2016) crossed ten lines in a half-diallel mating design and the resultant 45 hybrids were tested to identify promising crosses. The maximum heterosis over better parent and standard check, respectively was observed in the cross IHR 3849 × IHR 3448 (291.47%) and IHR 3849 × IHR 3453 (35.42%) for dry fruit yield plant^{-1}, IHR 3453 × IHR 4507 and IHR 4507 × IHR 3476 (31.36 and 33.33%) for fruit length and IHR 3849 × IHR 2451 (15.84%) and IHR 4507 × IHR 3476 (165.0%) for fruit width. Kaur *et al* (2017) studied 28 F_1 hybrids developed in a half diallel mating design excluding reciprocals for 10 agro-morphological traits. They found that the range of heterosis over their better parent varied from -24.29 to 26.05% for fruit length, -25.12 to 31.81% for fruit weight, -38.03 to 35.16% for pericarp thickness, -58.41 to 82.64% for seed fruit^{-1} and -23.44 to 110.62% for fruit yield plant^{-1}. The top most heterotic combinations over the superior standard check were SL 461 × VR 521 for fruit length, SD 463 × PP 402 for pericarp thickness, MS 341 × SL 461 for fruit weight, fruit width and seed fruit^{-1} and SD 463 × PP 403 for early yield, fruit yield plant^{-1} and 100 seed weight.

Heterosis for fruit yield and other related traits of 30 F_1 hybrids of hot pepper derived from a 6 × 6 full diallel set were investigated by Rohini *et al* (2017a). The cross combinations Pusa Jwala × PKM 1 had shown the highest significant and positive better parent heterosis for plant height (25.05%), number of fruits plant^{-1} (96.15%), fresh fruit weight (65.86%), fresh fruit yield plant^{-1} (248.72%) and dry pod yield plant^{-1} (140.83%). The F_1 hybrid, Arka Lohit × LCA 334 depicted the highest heterosis over better parent for branches plant^{-1} (92.86%) and fruit length (21.43%).

2.4 Combining ability studies

Selection of parents to be used in a crop breeding programme is one of the most important tasks to a plant breeder. The concept of combining ability was given by Sprague and Tatum (1942). Combining ability analysis is important genetic parameter, which is useful to study the nature and magnitude of gene actions and has been used by the plant breeders to select suitable parents for breeding programmes (Chezhian *et al* 2000). According to Arunachalam (1976) and Baker (1978), combining ability is an important biometrical tool to circumvent the plant breeding programme. Knowledge regarding to general (GCA) and specific combining ability (SCA) are of a great worth in plant breeding programme for the species which are responsible to the development of F_1 hybrid. The GCA is defined as the average performance of a line or a parent in hybrid combinations and it estimates the role of the additive portion of the genetic effects and means that the particular line has good genes in general. The SCA is used to designate those cases in which certain cross-combinations do selectively better or worse than would be expected based on the average performance of the lines or parents involved and it estimates the role of the non-additive gene action to the total genetic variation (Falconer and Mackay 1996). Expression of the heterosis is highly correlated with SCA of crosses. The significance of the study of combining ability in autogamous crops was emphasized by Allard (1960).

Legesse (2000) crossed seven diverse genotypes in a half-diallel mating design to produce 21 F_1 hybrids of chilli pepper. The parent, Bako Local showed good GCA values for fruit weight, fruit length and fruit yield, the parental line PBC 972 for plant height and canopy width, Mareko Fana for fruit diameter and fruit weight, PBC 485 for days to flowering, canopy width and number of fruits plant^{-1} and PBC 510 for fruit length and days to flowering. Based on SCA effects, the F_1 hybrids Bako Local × PBC 485, PBC 731 × PBC 510, Mareko Fana × PBC 485, Mareko Fana × PBC 972, PBC 972 × PBC 510 and PBC 364 × PBC 972 were the best for improving the fruit yield.

Lohithaswa *et al* (2000) studied half diallel mating design to find out GCA effects of parents and SCA effects of crosses over three environments. The GCA × Environment and SCA × Environment were significant for plant height, fruit weight, number of fruits palnt^{-1}, dry fruit yield plant^{-1} and capsaicin content. The genotype, Pant C-1, Arka Lohit and X-235 were found to be good general combiners for number of fruits plant^{-1} and dry fruit yield. The cross-combination Pant C-1 × Pusa Jwala expressed highest significant SCA effects for plant height (5.76), number of fruits palnt^{-1} (25.85) and capsaicin content (0.33), X-235 × Pusa Jwala for dry fruit yield plant^{-1} (17.75) and RHRC-16-5 × Arka Lohit for fruit weight (0.12).

Zewdie and Bosland (2001) studied the inheritance of capsaicinoid content in five *C. pubescens* Ruiz & Pavon genotypes using diallel analysis. The results revealed significant GCA and SCA effects for capsaicinoids, indicating the importance of both the additive and non-additive gene actions. Parents which have high capsaicinoid content also had significant positive GCA effects. A hybrid, NMCA80049 × NMCA80062, involving both high capsaicinoid content parents had positive SCA values for nornordihydrocapsaicin, nordihydrocapsaicin and isomer of dihydrocapsaicin.

Khalil *et al* (2004) reported that the lines Feherozon, 25-1, Yolo Wonder and Greygo were good general combiners for early yield, and Sweet Banana, Marconi Rrosso, Casca Dura and Avelar for total yield. The cross-combinations Feherozon × Sweet Banana (511.2) were regarded as the best specific combiner for early yield, 5-27 × Yolo Wonder (1.43) for total fruit yield, Greygo × Suptol and 5-27 × Yolo Wonder for heavy fruit and Suptol × Avelar and Casca Dura × Yellow Wonder for light fruit. Patel *et al* (2004) developed 48 F_1 hybrids using

4 GMS line and 12 testers and evaluated to estimates the GCA and SCA effects of parents and hybrids, respectively for different yield and its component traits. The GMS line, ACMS-4 was good general combiner for plant height, number of fruits plant^{-1}, fruit length, fruit girth and green fruit yield. The testers, ACG-77, ACS 92-3, ACS 2000-2, ACS 2000-3, Punjab Guchhedar, RHRC-Pendent and Resham Patti were considered as good general combiner for number of fruits palnt^{-1} and green fruit yield. The cross-combination ACMS-2 × RHRC-Pendent was best specific combiner for plant height (13.03), fruit girth (0.34) and green fruit yield plant^{-1} (1.91), ACMS-4 × ACG-77 for number of fruits plant^{-1} (42.93) and ACMS-4 × ACS 2000-3 for fruit weight (0.41).

Saritha *et al* (2005) studied combining ability of parents and hybrids for 12 fruit yield and quality traits. The GCA and SCA variance were significant for plant height, fruit length, number of fruits plant^{-1}, fruit yield plant^{-1}, ascorbic acid content and oleoresin content and non-significant for number of primary branches plant^{-1} and number of seed fruit^{-1}. The significant SCA effects for number of fruits plant^{-1} and fresh fruit yield plant^{-1} were expressed by the cross PMR-14 × PMR-57 (205.55 and 425.40%, respectively) and AVRDC-95-06 × Byadgi Dabbi (120.52 and 314.70%, respectively). The cross PMR-19 × Arka Lohit had shown the maximum significant positive SCA value for dry fruit yield plant^{-1} (75.14%).

Geleta and Labuschagne (2006a) developed 21 hybrids through non-reciprocal crosses using 7 genetically diverse pepper accessions and evaluated under greenhouse and field conditions. Mean squares due to GCA and SCA were significant for fruit length, fruit weight, pericarp thickness and number of fruits palnt^{-1} and non-significant for fruit diameter (in greenhouse) and fruit yield (in field). The SCA effects were non-significant, indicating the importance of additive gene effects. The parents with elongated fruit, bigger size and thicker pericarp depicted positive GCA effects and round, small and thin pericarp parents showed high negative GCA values. The parental line, Pepper 1976 had shown high positive GCA values for fruit diameter, fruit weight, pericarp thickness, fruit length and fruit yield. Out of 21 cross combinations, 5 hybrids exhibited positive SCA effects over the locations for fruit length. The crosses Kalocsai "M" Csereszyne × Bakko Local and Mareko Shote × PBC 142A involved contrasting GCA parents for fruit length. Six hybrids depicted highly significant positive SCA effects for fruit yield under greenhouse only.

Geleta and Labuschagne (2006b) reported that the GCA effects in desired direction were expressed by the parents Mareko Shote and PBC 142A for vitamin C. The F_1 hybrids Kalocsai 'M' Cseresznye × Bakko Local and Kalocsai 'M' Cseresznye × Szegedi 178 exhibited the highest significant positive SCA effects for vitamin C content. Prasath and Ponnuswami (2008) adjudged the parent MDU Y as good general combiner for fruit length, fruit girth, number of seed fruit^{-1}, individual green fruit weight and individual dry fruit weight and the parent Bydagi Kaddi for short plant stature (plant height), fresh yield plant^{-1} and dry yield ha^{-1}. Significant positive SCA effects were observed in the hybrid MDU Y × Co 4 for yield and quality traits like fresh yield, dry yield and capsaicin content (%).

do Rego *et al* (2009) crossed 8 diverse lines of peppers in a complete diallel design to estimate GCA and SCA by measuring fruit yield and quality parameters. The ANOVA for combining ability showed that the GCA and SCA effects were significant for plant height, fruit weight, fruit width, fruit length, fruit wall thickness and yield. For height of first bifurcation, only SCA was significant. The parental line CB 24 had shown positive GCA effects for fruit length, highest fruit width, fruit weight, plant height, plant canopy width between plants and rows, and fruit yield, the line 50 showed good GCA effects for fruit wall thickness and yield, and the line 04 expressed the positive GCA effects for fruit yield and wall thickness. Of the 56 F_1 hybrids, the crosses CB 24 × CB 50, CB 04 × CB 24 and CB 44 × CB 56 performed better for fruit weight, fruit wall thickness and fruit yield.

Marchesan *et al* (2009) produced ten hybrids of sweet pepper via a partial diallel to evaluate for agronomic performance and resistance to powdery mildew. The parent, Platero expressed the highest magnitude of positive GCA effects for fruit weight and wall thickness, whereas P36-R was good general combiner for fruit length and fruit width. F_1 hybrid P36-R × HV-12 had maximum SCA value for fruit weight and fruit, and the hybrids Quantum-R × HV-12, P36-R × HV-12 and Rubia-R × HV-12 for fruit length. Pérez-Grajales *et al* (2009) identified the landrace Puebla as the best parent based on the overall performance for yield and fruit quality in a series of hybrid combinations with other landraces of manzano hot pepper. The hybrids namely, Zongolica × Puebla had higher SCA value for fruit yield and fruit number. The cross Puebla × Peru depicted the highest SCA effects for pericarp thickness, fruit volume, number of seed fruit^{-1} and seed weight.

Sánchez-Sánchez *et al* (2010) studied diallel design to find out GCA and SCA effects of parents and hybrids, respectively for different capsaicinoids content in manzano hot pepper (*Capsicum pubescens* R. and P.). The SCA effects were significant for nordihydrocapsaicin, dihydrocapsaicin, capsaicin and total capsaicinoids, whereas the GCA effects were non-significant except for nordihydrocapsaicin. The parent Tacámbaro had the maximum positive GCA values for nordihydrocapsaicin, Zongolica for capsaicin and total capsaicinoids and Huatusco for dihydrocapsaicin. The cross combinations Puebla ×Tacámbaro, Tacámbaro ×Perú and Huatusco × Zongolica were identified as a good specific combiners for capsaicin, dihydrocapsaicin and total capsaicinoids content.

Sitaresmi *et al* (2010) observed that the parent IPB C19 had the highest GCA values for fruit weight plant^{-1} (90.13) and IPB C8 for number of fruits^{-1} (13.51). A study by Hasanuzzaman *et al* (2012) identified the parental lines CCA 5, BARI Morich 1 and CCA 19 as good general combiners for fruit yield plant^{-1}, while the hybrids BARI Morich 1 × CCA 19 and CCA 5 × BARI Morich 1 were identified as the promising for number of fruits plant^{-1} and fruit yield plant^{-1} based on SCA effects. Based on GCA effects, Tembhurne and Rao (2012) selected the parental lines namely, LCA960, BVC37, LCA334, PantC1 and JNA1 for green fruit yield and dry fruit yield. The cross JNA1 × BVC37 was adjudged as good specific combiner for green and dry fruit yield due to its highest significant SCA effects.

The combining ability of 10 F_1 hybrids of *C. baccatum* developed using complete diallel mating design without reciprocals involving 5 parents were evaluated by Rodrigues *et al* (2012) on twelve agronomic parameters. The parent UENF 1639 depicted the significant and positive GCA effects for plant height and fruit diameter, the parent UENF 1616 for fruit length and fruit yield plant^{-1}, the line UENF 1629 for fruit weight and the line UENF 1732 for number of fruits plant^{-1}. The crosses namely UENF 1629 × UENF 1732, UENF 1616 × UENF 1732 and UENF 1624 × UENF 1639 were adjudged the best specific combiners for total yield plant^{-1}. By using line × tester mating design Savitha *et al* (2013) estimated the combining ability of chilli genotypes. The parental lines namely, CA 197 and CA 192 among the lines, and Kashi Anmol among the tester were regarded as good general combiners for number of fruits plant^{-1} and dry fruit yield plant^{-1} and the line CA 197 and CA 71, and the tester CA 97 for capsaicin content, while the cross combination CA 172 × Kashi Anmol was found to be the best for dry yield plant^{-1} and ascorbic acid based on highest SCA effects, and the hybrid CA 192 × CA 97 for capsaicin content and oleoresin content.

do Nascimento *et al* (2014) reported that out of 30 F_1 hybrids, the significant and negative SCA value for placenta length was expressed by cross combination UFPB 77.2 × UFPB 134 (-0.16). The cross UFPB 132 × UFPB 134 was identified as the best for fruit weight and UFPB 77.2 × UFPB 132 for fruit length with SCA effects of 0.45 and 0.72, respectively. The reciprocal cross UFPB 137 × UFPB 77.1 showed the highest positive SCA values for vitamin C (30.38). The parental line UFPB 77.1 had shown significantly positive GCA effect for vitamin C (18.49). Khalil and Hatem (2014) evaluated six parents and their 15 F_1 hybrids in pepper. They found that B 16-10 and Big Dipper showed highest GCA effects for early fruit weight, W 5-15 and Big Dipper for early fruit number, W 5-15 and LS 2-2 for number of fruits and fruit weight, B 16-10 and Big Dipper for average fruit weight, LS 5-6 and B 16-10 for fruit length and Big Dipper for fruit diameter, pericarp thickness and vitamin C. The estimates of SCA effects expressed that the F_1 hybrid Big Dipper × B 16-10 depicted the positive significant value for early fruit number, early fruit weight, total fruit number, fruit length, fruit weight, pericarp thickness and vitamin C.

Medeiros *et al* (2014) demonstrated that the line UENF 1624 depicted the highest GCA values for number of fruits plant^{-1} (38.48) and yield plant^{-1} (0.13) and UENF 1629

(7.57) and UENF 1616 (2.3) for fruit weight. The crosses UENF 1616 × UENF 1629 and UENF 1616 × UENF 1732 were regarded as the best specific combiners for number of fruits plant^{-1}, UENF 1629 × UENF 1639 for fruit weight, UENF 1639 × UENF 1732 for yield plant^{-1}, UENF 1616 × UENF 1629 for fruit length. Pandey and Chura (2014) reported that the sweet pepper line DARL 82 was good general combiner for fruit length, 09/Cvar 4 for fruit weight, 09/Cvar3 for number of fruit plant^{-1}, 09/Cvar 4 for pericarp thickness, 09/Cvar 3 for fruit yield plant^{-1}, DARL 82 for plant height and 09/Cvar 5 for ascorbic acid content.

To identify the most promising parental lines and hybrids Singh *et al* (2014) conducted an experiment using CGMS and GMS lines. They found that the GMS line MS 341 had significant GCA effects for early yield, number of fruits plant^{-1}, fruit length and number of seed fruit^{-1} and was therefore, considered as good general combiner. The CGMS line CC 141 exhibited desired GCA for plant height, plant spread and fruit length. The line SD463 was a good general combiner for fruit weight, pericarp thickness, fruit length, fruit width, plant spread and total yield plant^{-1}, the line SL 461 for fruit length and total fruit yield, the line PP 402 for early yield and fruit width and the line DL 161 for number of fruits palnt^{-1}. The highest significant and positive SCA effects were exhibited by the hybrid MS 341 × PP 402 for plant height, by SD 463 × PS 403 for plant spread, by EL 181 × PA 401 for fruit width and pericarp thickness, by PP 402 × PS 403 for fruit weight, by US 501 × SD 463 for number of seed fruit^{-1} and by CC 141 × VR 521 for total yield plant^{-1}.

Bhutia *et al* (2015) evaluated 10 hybrids produced by crossing 5 parental lines in a diallel fashion design excluding the reciprocals for fresh fruit yield and quality traits. No single parental line had good GCA effects for all the studied traits. The line BCCH Sel-4 expressed significant GCA values in desirable directions for plant height, number of fruits plant^{-1}, fruit length, fruit yield plant^{-1} and vitamin C and thus was considered as a good general combiner. The hybrid BCCH Sel-4 × AC-575 showed the highest SCA effects for number of fruits plant^{-1} (24.57), fruit length (1.32), fruit yield plant^{-1} (177.86) and vitamin C (49.46).

Naresh *et al* (2016) estimated the general combining ability and specific combining ability effects of 10 parents and their 45 hybrids. The parental lines IHR500, IHR2451 and IHR4516 were considered as good general combiners for fresh-to-dry recovery, and IHR500, IHR3448 and IHR4507 for dry fruit yield plant^{-1}. The cross IHR3849 × IHR3448 was the best specific combiner for dry fruit yield plant^{-1} with the SCA effects of 209.59, the cross IHR3448 × IHR4516 for total capsaicinoid content (43002.46) and for dihydrocapsaicin content (16943.29), the cross IHR3849 × IHR4503 for capsaicin content (25602.53) and the cross IHR3849 × IHR3453 for nor-dihydrocapsaicin content (3234.72).

Rohini *et al* (2017b) estimated the GCA effects of parents and SCA effects of hybrids by using 6 parental lines and their 30 F_1 hybrids developed in a full diallel fashion with reciprocals. The MS due to GCA, SCA and RCA were highly significant for all the traits. This suggested that the parents performed differently among different cross combinations indicating the interallelic interactions. The lines LCA625, K1 and PKM1 were adjudged as good general combiners for number of fruits palnt^{-1} and dry pod yield. The crosses LCA625 × K1, K1 × Arka Lohit and Pusa Jwala × PKM1 were found to be good specific combiners for number of fruits palnt^{-1}, dry pod weight, dry pod yield plant^{-1}, ascorbic acid and capsaicin content.

2.5 Components of genetic variance

In chilli, both the additive and non-additive type of gene action governs the inheritance of agro-morphological traits. The predominant role of additive gene action was reported for genetic control of plant height (Rodrigues *et al* 2012), number of fruits plant^{-1} (Bento *et al* 2016), fruit weight (Ben-Chaim and Paran 2000, Prasath and Ponnuswami 2008, Rodrigues *et al* 2012 and Medeiros *et al* 2014), fruit length (Ben-Chaim and Paran 2000, do Rego *et al* 2009, Pérez-Grajales *et al* 2009, Syukur *et al* 2010 and Medeiros *et al* 2014), fruit width (Ben-Chaim and Paran 2000, Ahmed *et al* 2003, Nandadevi and Hosamani 2003, Sabita and Baruah 2003, Sousa and Maluf 2003, Anand and Subbaraman 2006, Syukur *et al* 2010 and Medeiros *et al* 2014), pericarp thickness (Ben-Chaim and Paran 2000, Rodrigues *et al* 2012 and Bento *et al* 2016), total yield plant^{-1} (Geleta *et al* 2004, Syukur *et al* 2010 and Chaudhary *et al* 2013). Non-additive gene effects were important for plant height (Shukla *et al* 1999 and do Rego *et al* 2009), plant spread (Singh *et al* 2014), fruit weight (Lippert 1975), number of fruits plant^{-1} (Shukla *et al* 1999), pericarp thickness (do Nascimento *et al* 2014) and total yield plant^{-1} (Shukla *et al* 1999, do Rego *et al* 2009, do Nascimento *et al* 2014, Medeiros *et al* 2014 and Singh *et al* 2014) in chilli. The additive and non-additive gene effects were important in genetic control of number of fruits plant^{-1}, fruit length, fruit width and total yield plant^{-1} (Rodrigues *et al* 2012).

CHAPTER III

MATERIAL AND METHODS

The present study entitled, "Evaluation of cytoplasmic male sterile lines of chilli pepper (*Capsicum annuum* L.) and their utilization in heterosis breeding" was carried out at the Vegetable Research Farm and the Molecular Breeding Laboratory of the Department of Vegetable Science, Punjab Agricultural University (PAU), Ludhiana, India, during the period 2014-2016. The major objectives of the study were to evaluate the newly developed CMS lines of chilli for stability of sterility and estimate heterosis and combining ability of these lines for important plant growth, fruit, yield and quality traits.

Three experiments were carried out to fulfill the objectives formulated for the present study. Details of the materials used and the methodologies adopted to accomplish these objectives are described below:

3.1 Stability analysis of newly developed CMS lines of chilli pepper

3.2 Assessment of reconstitution of the recurrent parent (A-line) genome by using molecular markers

3.3 Evaluation of newly developed CMS lines of chilli pepper in hybrid combinations

3.1 Stability analysis of newly developed CMS lines of chilli pepper

3.1.1 Experimental site

The experiment was conducted at the Vegetable Research Farm, PAU, Ludhiana, India. The Farm is located at 30°54' N, 70°45' E and 247 m above sea level. The soil of the research Farm is loamy sand in texture, high in available potassium, medium in available phosphorus and low in available nitrogen and organic matter (Garg and Cheema 2011).

3.1.2 Plant materials

The experiment involved 17 cytoplasmic male sterile (CMS) or A-lines of chilli pepper and their corresponding maintainer or B-lines, which were developed by the PAU, Ludhiana following six cycles of backcrossing and selection (Table 3.1).

3.1.3 Planting design and field managements

The newly developed 17 CMS A-lines and the maintainer B-lines were evaluated in the open field conditions over four environments (E_1- E_4) comprising two date of sowing and two crop seasons. In the first crop season (2014-15), the first sowing (E_1) was done on 15thSeptember, 2014 and transplanted on 30th October, 2014 and the second sowing (E_2) on 1st February, 2015 and transplanted on 15th March, 2015. In the second crop season (2015-16), the first sowing (E_3) was done on 15th September, 2015 and transplanted on 30th October, 2015; and the second sowing (E_4) was done on 1st February, 2016 and transplanted on 15th

March, 2016. The seedlings were transplanted on ridges spaced 90 cm from row-to-row and 45 cm from plant-to-plant. The experiment was laid out in a randomized complete block design (RCBD) with seven replications. Plants were protected from insect-mediated cross pollination with 24-mesh net cages. Flowering in E_1 and E_3 coincided with low temperature and that of E_2 and E_4 coincided with high temperature.

Table 3.1: List of newly developed CMS lines of chilli pepper and their maintainer lines used for stability of sterility

CMS A-Line	Pedigree	B-Line	Pedigree
CMS4611A	4261SL461-BC_6-P1	CMS4611B	SL461-P1
CMS4614A	4261SL461-BC_6-P4	CMS4614B	SL461-P4
CMS46113A	4261SL461-BC_6-P13	CMS46113B	SL461-P13
CMS4622A	4261SL462-BC_6-P2	CMS4622B	SL462-P2
CMS4623A	4261SL462-BC_6-P3	CMS4623B	SL462-P3
CMS4624A	4261SL462-BC_6-P4	CMS4624B	SL462-P4
CMS4626A	4261SL462-BC_6-P6	CMS4626B	SL462-P6
CMS4627A	4261SL462-BC_6-P7	CMS4627B	SL462-P7
CMS46213A	4261SL462-BC_6-P13	CMS46213B	SL462-P13
CMS46214A	4261SL462-BC_6-P14	CMS46214B	SL462-P14
CMS463D2A	4261SD463DG-BC_6-P2	CMS463D2B	SD463DG -P2
CMS463D13A	4261SD463DG-BC_6-P13	CMS463D13B	SD463DG -P13
CMS463D14A	4261SD463DG-BC_6-P14	CMS463D14B	SD463DG -P14
CMS463L3A	4261SD463LG-BC_6-P3	CMS463L3B	SD463LG -P3
CMS463L5A	4261SD463LG-BC_6-P5	CMS463L5B	SD463LG -P5
CMS463L9A	4261SD463LG-BC_6-P9	CMS463L9B	SD463LG -P9
CMS463L11A	4261SD463LG-BC_6-P11	CMS463L11B	SD463LG -P11

3.1.4 Observations recorded

3.1.4.1 Evaluation of CMS A-lines for pollen sterility

Pollen sterility in CMS A-lines was observed at weekly intervals for seven weeks, starting from third week of March in first date of sowing (E_1 and E_3); and first week of June in second date of sowing (E_2 and E_4) in the two crop seasons. Male sterility was scored following four methods:

3.1.4.1.1 Pollen staining technique

Five plants from each CMS A-line were randomly selected for scoring for pollen sterility. From each plant, five well-developed unopened flower buds from different branches were collected before anthesis (9 AM) in a vial containing 70% ethanol. Anthers from each bud were crushed on a glass slide and stained with a drop of 2% I_2-KI (prepared by dissolving 2 g of iodine and 4 g of potassium iodide in 100 ml distilled water). After removing the debris, a cover slip was placed over the pollen material and the slide was observed under a light microscope of 10× magnification. Three microscopic fields were examined per slide. The round, well-filled and dark stained pollen grains were considered as fertile, while the unstained, half stained, shriveled, deformed and empty pollen grains were scored as sterile. Progeny means of all the microscopic fields were calculated and pollen sterility was expressed in percentage. The technique is similar to the one used by Shinjyo (1969) in rice.

Based on of the scale outlined by Virmani *et al* (1997), CMS A-lines were classified as below;

Pollen sterility (%)	**Pollen sterility/fertility classes**
100	Completely sterile
91-99	Sterile
71-90	Partially sterile
31-70	Partially fertile
21-30	Fertile
0-20	Fully fertile

3.1.4.1.2 Pollen release score (visual observation)

Five plants from each CMS A-line were randomly selected for scoring on the basis of quantum of pollen released. Between 9 - 11 AM, 10 freshly opened flowers from each plant were observed visually and scored for pollen release as per the scale given by Liu and Gniffke (2004) where; 0 = no pollen released, 1 = some pollen released but adhering to anther and 2 = pollen released freely.

3.1.4.1.3 Fruit setting (%) under caged conditions

Fruit setting percentage of each CMS line was assessed by tagging 50 well-developed unopened flower buds of three randomly selected plants and per cent fruit set was worked out as the number of set fruits divided by the total number of flower buds tagged × 100.

3.1.4.1.4 Number of seed fruit^{-1}

The total number of seed extracted manually from 10 randomly taken fruits per replication was counted and average number of seed fruit^{-1} was worked out.

3.1.4.2 Evaluation of CMS A-lines for fruit traits

CMS A-lines planted in open field were evaluated for following traits.

3.1.4.2.1 Fruit setting (%)

Fruit setting percentage of each CMS line was assessed by tagging 50 well-developed unopened flower buds and it was expressed in percentage.

3.1.4.2.2 Number of fruits plant^{-1}

The number of red ripe fruits from each picking were counted, added and divided by five (number of plants from which fruit was harvested) to obtain average number of fruits plant^{-1}.

3.1.4.2.3 Number of seed fruit^{-1}

The total number of seed extracted manually from 10 randomly taken fruits was counted and average number of seed fruit^{-1} was worked out.

3.1.4.2.4 Fruit weight (g)

The weight of 10 randomly taken fruits was measured on electronic balance and average fruit weight was worked out.

3.1.4.2.5 Fruit length (cm)

The length of 10 randomly taken red ripe fruits was measured in centimeters from base of the fruit to its tip and the average was taken as fruit length.

3.1.4.2.6 Fruit width (mm)

The width of 10 fruits used for measurement of fruit length was recorded at the middle portion of the fruit with the help of a 'vernier caliper' and average width was calculated.

3.1.4.2.7 Pericarp thickness (mm)

The thickness of pericarp of 10 fruits used for measurement of fruit length was measured in millimeters at the middle portion of the fruit with the help of a 'vernier caliper' and average pericarp thickness was calculated.

3.1.5 Statistical analyses

The percent data on pollen sterility and fruit setting were subjected to 'arcsin' transformation before statistical analysis. Data on pollen release score were transformed using square-root transformation by adding 0.5 to the score.

Pooled analysis of variance (ANOVA) for pollen sterility, pollen release score, fruit setting and number of seed fruit^{-1} over four environments under the caged conditions; and for important fruit traits under open pollination conditions was carried out using the generalized linear model procedure of SAS (Version 9.2, SAS Inst., Cary, NC, USA). Significance of differences among the lines was determined following the Duncan’s multiple range test. Stability of the CMS lines over environments was determined following the biplot analysis of Yan *et al* (2000). Pearson’s correlation analysis was performed to determine the relationships between two methods used for screening of CMS A-lines for pollen sterility viz. the staining method *vis-a-vis* the visual pollen release score.

3.2 Assessment of reconstitution of the recurrent parent (A-line) genome by using molecular markers

3.2.1 Location/place of work

CMS-A and CMS-B lines were raised at the Vegetable Research Farm, PAU, Ludhiana. The molecular analysis was conducted at the Molecular Breeding Laboratory of the Department of Vegetable Science, PAU, Ludhiana, India

3.2.2 Plant material

The experiment involved 3 selected CMS (A-) lines and their alloplasmic maintainer (B-) lines of chilli pepper

3.2.3 Experimental methodology

3.2.3.1 Collection of plant samples and DNA extraction

Genomic DNA of 3 CMS A-lines and their counterpart maintainer lines (CMS B-lines) were isolated from the young leaf tissues. Leaf samples were collected from 30 day old plants in butter paper bags and transported from the field to the laboratory in ice box. The samples were surface sterilized with 70% alcohol and stored at -80°C till isolation of DNA. The DNA was isolated as per the method described by Singh *et al* (2009) with slight modifications. Samples were crushed finely to make dry powder with pastel and mortar using liquid nitrogen. Step wise procedure for DNA extraction is given below:

a. Grinded powder of the leaf was transferred to a 2 ml properly labeled eppendorf tube upto one fourth of the tube capacity. Simultaneously, in each tube, 900 µl of 2X CTAB buffer (Table 3.2) was added and gently mixed by inverting for few minutes to homogenize

b. Sample tubes were incubated at 65°C in a water bath for 50 minutes and during incubation the tubes were gently shaken after each 10-15 minutes for proper mixing of contents

c. After that 800 µl of chloroform: isoamyl alcohol (24:1) was added in each tube and mixed the contents thoroughly on a shaker for 20 min

d. Then tubes were spun/ centrifuged for 7 minutes at 13, 000 rpm in microcentrifuge (Eppendorf centrifuge 5415D) at room temperature

e. With the help of micropipette, the supernatant/ upper aqueous phase was pipetted out and transferred to fresh labeled eppendorf tube (1.5 ml) and after that 600 µl of chilled isopropanol was added, mixed slowly till formation of the DNA loop and refrigerated overnight at -20°C

f. The eppendorf tubes were centrifuged at 10,000 rpm for 5 minutes to pellet the DNA

g. After discarding the supernatant, DNA pellet was washed with 200 µl of 70% ethanol by centrifuged for 5 min at 10,000 rpm. After discarding the ethanol the tubes were air dried by inverting them on blotting paper

h. After drying DNA pellets were dissolved in 100 µl of 1X TE buffer and stored at -20 ºC

Table 3.2: Composition of 2X CTAB extraction buffer (100 ml) used for DNA extraction

Component	**Quantity/litre**	**Final Concentration**
5M NaCl	28.0 ml	1.4M
1M Tris, pH 8.0	20.0 ml	100mM
0.5M EDTA	4.0 ml	20mM
10% CTAB	20.0 ml	2.0%
B-Mercaptoethanol	1.0 g	1.0%
dd H_2O	28.0 ml	-

3.2.3.2 Genomic DNA quantification

The quantity and quality of extracted DNA was quantified by Nanodrop spectrophotometer as follows:

i. Initiation of the spectrophotometer was done by 2 µl of distilled/nanopure water
ii. The blank measurement was performed with 2 µl of 1X TE buffer
iii. Two micro litre (2 µl) of nucleic acid sample was loaded on Nanodrop spectrophotometer pedestal to measure the quantity of genomic DNA
iv. The DNA quality in ng.µl^{-1} and optical density (OD) value for each sample was noted

The samples which showing adequate DNA concentration (50ng.µl^{-1}, and above) and quality (260/280 = 1.7 to 2.0) were selected for PCR amplification.

3.2.3.3 Screening of CMS A- and maintainer B-lines with SSR markers

Screening of the CMS A-lines and the maintainer B-lines was carried out for identification of polymorphism. The DNA from 3 CMS A-lines and their maintainer B-lines were subjected to PCR amplification with the selected 120 PCR based SSR markers 10 from each linkage group. The SSR primers used for this study were selected from the linkage maps developed by Lee *et al* (2004), Minamiyama *et al* (2006), Yi *et al* (2006) and Ince *et al* (2010). The selected primers were well distributed covering all the linkage groups. The list of SSR markers used in this study is presented in APPENDIX I.

3.2.3.4 PCR conditions for amplifying of genomic SSR alleles

Primers were diluted by giving a brief spin to collect the amorphous primer stock at the bottom of tubes supplied by the company and then Nanopure water was added to prepare stock solution of 100 µM. The tubes were incubated at 37°C for 30 minutes. Then, the working solution of 5 µM concentration was prepared.

3.2.3.5 DNA amplification

The polymorphism between the CMS A- and the respective B-lines was assessed by amplifying genomic DNA with SSR primer pairs. For a 25µl volume reaction mixture components are presented in Table 3.3.

Table 3.3: The composition of reaction components used in PCR

Reaction component	**Stock concentration**	**Volume (µl)**
DNA template	50 ng.μl^{-1}	2.0
PCR buffer (Promega, USA)	5X	5.0
$MgCl_2$ (Promega, USA)	25Mm	1.5
dNTPs (Promega, USA)	10mM	0.5
Primer-Forward	5 µM	1.5
Primer-Reverse	5 µM	1.5
Taq (Promega, USA)	5U.μl^{-1}	0.12
Nuclease free water	-	12.88
Total	-	25

PCR reaction was carried out using profile as given in Table 3.4. The reaction was performed in Master Cycler 5331-Eppendorf version 2.30. 31-09, Germany.

Table 3.4: Touchdown PCR profile used for amplification of DNA

Step	**Temperature (°C)**	**Time**
Initial denaturation	94	3 min
Denaturation	94	30 sec
Primer annealing	60	1 min
Primer extension	72	1 min
10 cycles from step 2 to step 4 with 0.5˚C decrement in annealing temperature in each cycle		
Denaturation	94	30 sec
Primer annealing	55	1 min
Primer extension	72	1 min
30 cycles from step 5 to step 7		
Final extension	72	5 min
Storage	4	∞

3.2.3.6 Electrophoresis

Separation and visualization of PCR products of CMS A- and maintainer B-lines was done on 2.5% agarose gel.

3.2.3.6.1 Agarose gel electrophoresis

Agarose gel electrophoresis was done for fractionation of SSR markers. Agarose was casted in 2.5% gels in TAE buffer (1X). The slabs were casted in a horizontal gel frame; products were visualized by incorporating 1 µl (10mg.ml^{-1}) ethidium bromide per 10 ml of gel and visualized under the gel documentation system. The step-wise procedure followed for gel electrophoresis is as follows:

i. The Perspex tray and comb were thoroughly cleaned with 70% alcohol using tissue paper

ii. The ends of Perspex tray were sealed with spacers and comb was inserted

iii. Agarose gel was prepared by adding 2.5 g agarose to 100 ml of TAE (1X) buffer (EDTA 0.5M at pH 8)

iv. The solution was boiled by keeping the flask in microwave oven and allowed to cool to 60°C

v. Ethidium bromide (10 µl of conc. 10mg.ml^{-1}) was added to the gel and mixed gently

vi. The gel was poured into the tray and air bubbles were removed by using pipette. When the gel was completely set, then the gel was removed from casting tray and placed into the electrophoresis tank

vii. Approximately 500 ml of TAE (1X) buffer was poured into the electrophoresis tank, enough to cover the gel to a depth of 5 mm

viii. Comb was removed carefully

ix. About 1/10th volume of loading dye (6x) bromophenol blue was added to DNA samples and mixed by tapping and spinning for 2-3 sec in a micro centrifuge

x. DNA samples were loaded onto the wells and the 80 V was applied to run the gel

xi. The power supply was switched off when loading dye was about 2 cm from positive end and the gel was removed from the gel apparatus

xii. The gel was viewed and photographed by using gel documentation system (UVI Tech England)

3.2.4 Observations recorded

Based on the banding pattern, genetic similarity between the CMS A- and B-lines was stdied and reconstitution of the CMS A-lines of chilli pepper was established.

3.3 Evaluation of newly developed CMS lines of chilli pepper in hybrid combinations

3.3.1 Research site

The experiment was carried out at the Vegetable Research Farm, PAU, Ludhiana, India.

3.3.2 Plant material

The plant material consisted of three recently developed CMS A-lines namely, 'CMS4611A', 'CMS4626A' and 'CMS463D13A', and 20 potential restorers (CMS C- lines), selected based on their *per se* performance (Singh 2011, Yadav 2013, Dhaliwal *et al* 2015b and Kaur 2015). Salient features of the three CMS A-lines and 20 potential restorer lines are described in Table 3.5.

3.3.3 Development of crosses

The parental lines were sown in finely-prepared nursery beds of 1.0 m wide and 15 cm high. Seed treated with Captan @ 2-3 $g.kg^{-1}$ of seed were sown on 15th September, 2014 at a depth of 1-2 cm. Before transplanting, seedlings were hardened by withholding water 5 days before transplanting. The seedlings were transplanted in the crossing block on 30th October, 2014. Sixty crosses were developed by manually pollinating 3 CMS A-lines with 20 CMS C-lines, following line × tester mating design where each A-line was crossed with each C-line. The parental lines were protected from insect-mediated cross pollination with 24-mesh net cages. Between 9 AM-11.30 AM, the fresh fully opened flowers of CMS A-lines (female lines) were selected and pollinated with pollen collected from the fresh fully opened male (C-line) flowers. The petals of the pollen-source flower were removed so that the staminal columns and anthers were uncovered. To transfer pollen, anthers of the male parent were taken and gently touched on tip of the stigmatic surface of the female flowers (A-line). The pollinated flowers were tagged mentioning name of the cross and date and time of pollination. Cross seed was extracted manually from the red ripe fruits.

3.3.4 Evaluation of crosses

In 2015-16, 60 crosses were evaluated along with their 23 parents (3 CMS A-lines and 20 restorer lines) and two check hybrids (CH-27 and Soldier) over three environments *viz*., the early season (E_1), the main season (E_2) and the late season (E_3). The early season sowing (E_1) was done on 15th September, 2015 and transplanted on 30th October, 2015; the main season sowing (E_2) was done on 15th October, 2015 and transplanted on 25th February, 2016 and the late season sowing (E_3) was done on 15th February, 2016 and transplanted on 05th April, 2016. The seedlings were transplanted on ridges spaced 75 cm between rows and 45 cm between plants. The experiment was laid out in a randomized complete block design (RCBD) with three replications. There were 10 plants of each entry in each replication. The E_1 crop was protected from frost by covering plants with the polythene sheet from December to mid-February. Cultural practices such as fertilization, irrigation, weed control, disease and insect-pest control were performed as per the Package of Practices for Cultivation of Vegetable Crops (Anonymous 2015). Mean weekly agro-meteorological data recorded during the crop seasons are presented in APPENDIX II.

Table 3.5: Salient features of the three CMS A-lines and 20 potential restorer lines involved in hybrid development in chilli pepper

Parental line	**Alternate ID**	**Fertility status**	**Fruit colour**	**Fruit length**	**Fruit width**
CMS4611A	S/SL461-1	Cytoplasmic male sterile (S*rfrf*)	Light green	Short	Medium thick
CMS4626A	S/SL462-6	Cytoplasmic male sterile (S*rfrf*)	Dark green	Medium long	Medium thick
CMS463D13A	S/SD463D-13	Cytoplasmic male sterile (S*rfrf*)	Dark green	Medium long	Medium thick
AC 102	ACC-2-1	Male fertile	Light green	Medium long	Medium thick
SL 475	Selection-20-1	Male fertile	Dark green	Medium long	Medium thick
PL 412	PLS-13	Male fertile	Light green	Medium long	Medium thick
IS 263	ICPN-21-5	Male fertile	Light green	Medium long	Medium thick
VR 523	VNR-314-2-1-4	Male fertile	Light green	Medium long	Medium thick
DL 161	DCL-524	Male fertile	Light green	Medium long	Medium thick
IS 267	ICPN-21-4	Male fertile	Light green	Medium long	Medium thick
YL 581	YLYS	Male fertile	Yellowish green	Medium long	Medium thick
SL 473	Selection-40	Male fertile	Light green	Medium long	Medium thick
IS 262	ICPN-20-5	Male fertile	Light green	Medium long	Medium thick
VR 521	VR-16	Male fertile	Dark green	Medium long	Medium thick
FL 201	Faslima	Male fertile	Light green	Very long	Medium thick
PP 402	Pepsi-17-2	Male fertile	Dark green	Medium long	Medium thick
C 142	C-31-1	Male fertile	Light green	Medium long	Medium thick
PP 414	PP-0237-7508	Male fertile	Light green	Medium long	Medium thick
VR 522	VNR-314-1-1-1	Male fertile	Light green	Medium long	Medium thick
PL 406	PLS-1	Male fertile	Light green	Medium long	Medium thick
E 183	EC-532390	Male fertile	Light green	Short	Medium thick
IS 268	ICPN-20-4	Male fertile	Light green	Medium long	Medium thick
IS 261	Imported Selection	Male fertile	Dark green	Medium long	Medium thick

3.3.5 Observations recorded

The data were recorded on the following traits from five randomly selected plants excluding the two border plants, one on each side.

3.3.5.1 Plant height (cm)

The plant height was measured from ground level to the highest plant tip of five randomly selected plants in each parent/cross and the mean value was worked out. The measurement was done at the time of last harvest.

3.3.5.2 Plant spread (cm)

The maximum spread of the plant at final harvest in all the four directions was measured from the same five plants selected for plant height and the mean value was worked out.

3.3.5.3 Number of primary branches plant^{-1}

Number of primary branches plant^{-1} was counted at the time of last harvest and the mean value was worked out.

3.3.5.4 Fruit weight (g)

The weight of 10 randomly taken fruits from second harvest was recorded on the electronic balance and average fruit weight was worked out.

3.3.5.5 Fruit length (cm)

The length of 10 randomly taken red ripe fruits from the second harvest was measured from base to tip of fruit and average fruit length was worked out.

3.3.5.6 Fruit width (mm)

The width of 10 randomly taken fruits from second harvest was recorded at the middle portion of the fruit with a 'vernier caliper' and average fruit width was worked out.

3.3.5.7 Pericarp thickness (mm)

The pericarp thickness of 10 randomly taken red ripe fruits from second harvest was measured at middle portion of the fruit with a 'vernier caliper' and average pericarp thickness was calculated.

3.3.5.8 Number of fruits plant^{-1}

From five randomly selected plants, number of red ripe fruits from each harvest was counted, added over harvests and number of fruit plant^{-1} was worked out.

3.3.5.9 Number of seed fruit^{-1}

Total number of seed harvested manually from 10 randomly taken fruits from second harvest was counted and average number of seed fruit^{-1} worked out.

3.3.5.10 *1000 seed weight (g)*

Manually harvested seeds were counted and 1000 seed weighed on an electronic balance.

3.3.5.11 *Total yield plant^{-1}(kg)*

Total yield plant^{-1} was calculated by adding the weight of fresh red ripe fruits from each harvest and dividing by five (number of plants from which harvesting was done).

3.3.5.12 *Ascorbic acid (mg.100g^{-1})*

Ascorbic acid content (mg.100g^{-1}) in green chilli was estimated by 2,6-dichlorophenol indophenols titration methods (AOAC 1970). Ascorbic acid content was calculated using formula given below

$$\text{Ascorbic acid (mg.100g}^{-1}\text{)} = \frac{\text{Dye factor} \times \text{volume make up} \times \text{titration reading}}{\text{Sample weigh} \times \text{aliquot taken for estimation}} \times 100$$

3.3.5.13 *Oleoresin content (%)*

The oleoresin content was isolated according to the method given by Tandon *et al* (1964). Soxhlet extraction apparatus was used for extraction of chilli oleoresin. Forty g of chilli powder was swathed in a filter paper and kept in the extractor. Two-hundred ml of acetone was taken in a flask. The apparatus consisting of distillation, extraction and flask was set up and put on a heater. The distillation part was connected with water connection for regular running of water. The heater was turned on and temperature was adjusted to 60 °C and heating process continued for 5 h. Oleoresin was accumulated in pre weighed flask with acetone from the extraction. The acetone was collected in the extractor for re-use. The flask was removed from the apparatus and acetone was further evaporated by slow heating. After complete evaporation of the solvent, weight of oleoresin was noted. Oleoresin content (%) was calculated using formula given below;

Oleoresin content (%) = {Weight of oleoresin (g)/ weight of powder taken (g)} × 100

3.3.5.14 *Capsaicin content (%)*

Capsaicin content (%) in chilli powder was determined as per the method given by Bajaj and Kaur (1979). Five-hundred mg of dried powder was taken in a volumetric flask and volume was made to 25 ml by adding ethyl acetate. The content was mixed well and kept for 24 h under dark at room temperature. Two ml of extract was passed via a basic alumina column, Brockman Grade I, of the size 10.0cm × 1.0cm. The column was washed/ cleaned 3 times by 5 ml of acetone after loading and the washings were discarded. Pure capsaicin was eluted with methanol: acetone: water mixture (75:25:1) and volume was made to 50 ml. From this stock solution, 10 ml of aliquot was evaporated to dryness at room temperature. To develop color, 0.5 ml of Folin-Ciocalteu reagent along with 6.5 ml of distilled water were added and kept for 3 min. After that, 1.0 ml of saturated Na_2CO_3 (sodium carbonate) solution was added to it and mixed well. The volume was made to 10 ml with distilled water in a volumetric flask. After keeping in dark for 1 h at room temperature, the absorbance was measured at 760 nm. Capsaicin content (%) was calculated as per standard curve prepared by using pure capsaicin.

3.3.5.15 Scoville heat units (SHU) conversion

The commonly acceptable Scoville organoleptic test, the pungency strength of the studied samples was computed by converting the capsaicin content expressed in grams of capsaicin per gram of chilli. This conversion of capsaicin content to SHU was done by multiplying the capsaicin content in dry chilli by the coefficient corresponding to the heat value for pure capsaicin, which is 1.6×10^7 (Othman *et al* 2011).

3.3.6 Statistical analyses

The means of the progeny were used for statistical analysis, using the computer software program WINDOSTAT 9.2 (INDOSTAT services Ltd. Hyderabad, India).

The data were subjected to the following statistical analyses:

3.3.6.1 Analysis of variance for design of the experiment
3.3.6.2 Combining ability analysis
3.3.6.3 Estimation of heterosis

3.3.6.1 Analysis of variance for design of the experiment

To test the significance of differences among 83 genotypes (60 crosses and 23 parents) for various traits, the data were analyzed based on following model;

$$p_{ij} = m + g_i + b_j + e_{ij}$$

Where, p_{ij}= phenotypic value of i^{th} genotype grown in j^{th} replication

m = general mean

g_i= effect of i^{th} genotype

b_j= effect of j^{th} block and

e_{ij}= error associated with ij^{th} observation

Total variation among the hybrids and parents was divided into replications and genotypes as per the following expectations;

Source of variation	df	Sum of squares (SS)	Mean squares (MS)	
			Observed	Expected
Replication	(r-1)	$Sr = \frac{\sum x^2.j}{g} - \frac{\sum x^2}{N}$	Mr = Sr/(r-1)	Ve+gVr
Genotype	(g-1)	$Sg = \frac{\sum xi.^2}{r} - \frac{\sum x^2}{N}$	Mg = Sg/(g-1)	Ve+rVg
Error	(r-1)(g-1)	Se=St-Sr-Sg	Me = Se/ (r-1)(g-1)	Ve
Total	gr-1	S_t		

where, r = number of replications; g = number of genotypes; N = total number of observations; Se = error SS; St = total SS; Vr = replication variance; Vg = genotype variance; Ve = error variance

The genotype variance was tested against error variance by 'F' test at (g-1) and (r-1) (g-1) degree of freedom. The replication variance was tested against error variance at (r-1) and (r-1) (g-1) degree of freedom.

3.3.6.2 Combining ability analysis

The replication wise means of 60 crosses were subjected to statistical analysis by using the following model suggested by Kempthorne (1957).

$$y_{ijk} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

where, y_{ijk} = value of the ijk^{th} observation of the cross involving i^{th} line and j^{th} tester in k^{th} replication

μ = general mean (effect common to whole crosses in all the replications)

g_i = GCA effects of i^{th} line

g_j = GCA effects of j^{th} tester

S_{ij} = SCA effects of cross involving i^{th} line and j^{th} tester and

e_{ijk} = error associated with ijk^{th} observation. i = i^{th} line (1, 2, 3); j = j^{th} tester (1, 2, 3...20) and k = k^{th} replication (1, 2, 3).

Analysis of variance for combining ability was done as per following ANOVA

Source of variation	**df**	**Sum of square**	**Mean square**	**Expected MS**
Replication	(r-1)	$\sum_{k=1}^{r}\frac{(x...k)2}{LT}-\frac{x2...}{LTr}$	-	-
Crosses	(LT-1)	$\sum_{ij=1}^{LT}\frac{(xij)2}{r}-\frac{x2...}{LTr}$	-	-
Lines	(L-1)	$\sum_{i=1}^{L}\frac{(xi.)2}{Tr}-\frac{x2...}{LTr}$	M_L	$\sigma^2_e + r\,\sigma^2_{\mathrm{LT}} + r\,T\sigma^2_L$
Testers	(T-1)	$\sum_{j=1}^{T}\frac{(xj.)2}{Lr}-\frac{x2...}{LTr}$	M_T	$\sigma^2_e + r\,\sigma^2_{\mathrm{LT}} + r\,L\sigma^2_T$
Lines × Testers	(L-1)(T-1)	$\sum_{ij=1}^{LT}\frac{(xij)2}{r}-\sum_{i=1}^{L}\frac{(xi.)2}{Tr}-\sum_{j=1}^{T}\frac{(xj.)2}{Lr}+\frac{x2...}{LTr}$	M_{LT}	$\sigma_e^{2} + r\sigma^{2}_{\mathrm{LT}}$
Error	(LT-1)(r-1)	By differences	M_e	σ^2_e
Total	(LTr-1)	$\sum_{i=1}^{L}\sum_{j=1}^{T}\sum_{k=1}^{r}x2_{ijk}-\frac{x2}{LTr}$	-	-

where, L = number of lines/females; T = number of testers/males; $x\,.\,.\,.\,k$ = sum of replication of crosses; $x\,.\,.\,.$ = sum of all crosses involving all lines and testers over all replications; x_{ij}= sum of ij^{th} cross-combination over all replications; $x_{i}.$ = sum of i^{th} line over all testers and replications; $x_{\,j.}$= sum of j^{th} tester over all lines and replications; x_{ijk} = ij^{th} observation in k^{th} replication; M_L = MS due to lines/females; M_T = MS due to testers/males; M_{LT} = MS due to line × tester interactions; Me = error MS; σ^2_L = variance due to lines/progeny variance arising from differences among lines/female parents; σ^2_T = variance due to testers/ progeny variance arising from the interaction of the contribution of female and male parents and $\sigma^2 e$ = environmental variance/ error variance among individuals from SCA effects.

3.3.6.2.1 Estimation of general combining ability (GCA) and specific combining ability (SCA) effects

The general combining ability effects and specific combining ability effects were computed from the two way table of female parents *vs* male parents in which every figure was total over replications. The individual effects were estimated as follows

(1) GCA effects of i^{th} line

$$g_i=(x_{i.}\,/\,T\,r) - (x\,.\,.\,/LT\,r)$$

where, $x.\ .$ = sum total of all the crosses; $x_{i.}$ = total of i^{th} line over all the testers and replications; r = number of replications; L = number of lines/female parents and T = number of testers/ male parents.

(2) GCA effects of j^{th} tester

$$g_j=(x_{j.}\,/Lr) - (x.\,.\,/LT\,r)$$

where, $x_{j.}$ = total of j^{th} male parent over all females and replications

(3) SCA effects of ij^{th} cross

$$Sij = (xij\,/r) - (xi.\,/T\,r) - (xj.\,/Lr) + (x..\,/LT\,r)$$

where, x_{ij} = ij^{th} combination total over all replications

(4) Standard error (SE) for different combining ability effects

(a) SE (g_i) lines = $(Me/T\,r)^{1/2}$

(b) SE (g_i) testers = $(Me/Lr)^{1/2}$

(c) SE (S_{ij}) crosses = $(Me/r)^{1/2}$

(d) SE (g - g_i) lines = $(2Me/T\,r)^{1/2}$ = SE (D1)

(e) SE (g_i - g_j) tester = $(2Me/Lr)^{1/2}$ = SE (D2)

(f) SE (S_{ij} - S_{kl}) crosses = $(2Me/r)^{1/2}$ = SE (D3)

where, Me = MS due to error

3.3.6.2.2 Analysis of variance for combining ability

(1) Estimation of general mean

$\mu = x.../T\,Lr\,E$

where, $x...$ = total of all the crosses over all replications in all environments

(2) GCA effect of i^{th} line

$$g_i=(x_{i.}/T\,r\,E)-(x.../T\,lr\,E)$$

where, $x_{i.}$ = sum of the i^{th} line over all testers, replications and environments and E = number of environments

(3) GCA effect of j^{th} tester

$$g_j=(x_{j.}/Lr\,E)-(x.../T\,lr\,E)$$

where, $x_{j.}$ = sum of the j^{th} tester over all lines, replication and environments

(4) SCA effect of ij^{th} cross

$$S_{ij}=(x_{ij}/r\,E)-(x_{i.}/T\,r\,E)-(x_{j.}/Lr\,E)-(x.../T\,Lr\,E)$$

where, x_{ij} = ij^{th} cross total over all the replications and environments

(5) Standard errors (SE) for combining ability effects

(a) SE combined (g_i) line = $(Me/\,r\,T\,E)^{1/2}$

(b) SE combined (g_i) tester = $(Me/\,r\,L\,E)^{1/2}$

(c) SE combined (S_{ij}) crosses = $(Me/\,r\,E)^{1/2}$

(d) SE ($g_i - g_j$) lines = $(2Me/T\,r\,E)^{1/2}$ = SE (D1a)

(e) SE ($g_i - g_j$) testers = $(2Me/\,Lr\,E)^{1/2}$ = SE (D2a)

(f) SE ($S_{ij} - S_{kl}$) crosses = $(2Me/\,r\,E)^{1/2}$ = SE (D3a)

(g) Test of significance for GCA and SCA effects

i. T_i (cal) for GCA of lines (females) = $(\mathrm{g_i} - 0)/\mathrm{SE}(\mathrm{g_i})$

ii. T_j (cal) for GCA of testers (males) = $(\mathrm{g_j} - 0)/\ \mathrm{SE}(\mathrm{g_j})$

iii. T_{ij} (cal) for SCA of crosses = $(S_{ij} - 0)/ SE(S_{ij})$

where, T_i (cal), T_j (cal) and T_{ij} (cal) are the calculated '*t*' values; g_i = GCA effects of i^{th} line; g_j = GCA effects of j^{th} tester and S_{ij} = SCAeffects of ij^{th} cross

The GCA effects of lines and testers and SCA effects of crosses were marked significant (*) when the values of t_i (cal), t_j (cal) and t_{ij} (cal) were ≥ tabulated '*t*' value at error degree of freedom (df) of individual environment or combined over environments at $P = 0.05$

(h) Critical difference (CD) for comparing GCA effects of lines/testers and SCA effects of crosses/hybrids

i. CD for GCA (lines) = SE (D1) or SE (D1a) × '*t*' tab (error df, $P = 0.05$)

ii. CD for GCA (testers) = SE (D2) or SE (D2a) × '*t*' tab (error df, $P = 0.05$)

iii. CD for SCA (crosses) = SE (D3) or SE (D3a) × '*t*' tab (error df, $P = 0.05$)

The differences between GCA of any two lines/ testers and SCA of any two crosses were considered significant when the differences were ≥ respective CD values.

3.3.6.2.3 Estimation of variance components

The covariance of full-sibs and half-sibs were estimated as per method suggested by Singh and Chaudhary (1985) and Dabholkar (1992).

(1) Individual environment

$$\text{Cov (HS)} = \sigma^2_L \ \text{(Lines)} = \frac{(M_L - M_{LT})}{T\,r}$$

$$\text{Cov (HS)} = \sigma^2_T \ \text{(Testers)} = \frac{(M_T - M_{LT})}{L\,r}$$

$$\sigma^2_{LT} \ \text{(lines × testers)} = \frac{(M_{LT} - M_e)}{r} = \sigma^2_{sca}$$

Estimation of Cov HS (average) and Cov (FS): These were calculated as

$$\text{Cov HS (average)} = \frac{(T\,\sigma^2_L + L\sigma^2_T)}{(L + T)}$$

$$\text{Cov FS} = \sigma^2_{LT} + 2\ \text{Cov (HS)}$$

These could also be calculated from the expectations of MS as

$$\text{Cov HS (average)} = \frac{(M_L + M_T - 2M_{LT})}{r\,(L + T)}$$

$$\text{Cov FS} = \frac{[M_L + M_T + M_{LT} - 3Me + 6r\ \text{Cov HS} - r\,(L + T)\ \text{Cov (HS)}]}{3r}$$

(2) Combined over environments

$$\text{Cov (HS)} \quad = \quad \sigma^2_L \text{ (Lines)} \quad = \quad \frac{(M_L - M_{LT})}{T\,r\,E}$$

$$= \quad \sigma^2_L \times E \text{ (Lines × Environments)} \quad = \quad \frac{(M_LE - M_{LT}E)}{Lr}$$

$$\text{Cov (HS)} \quad = \quad \sigma^2_T \text{ (Testers)} \quad = \quad \frac{(M_T - M_{LT})}{Lr\,E}$$

$$= \quad \sigma^2_T \times E \text{ (Testers × Environments)} \quad = \quad \frac{(M_TE - M_{LT}E)}{Lr}$$

$$\sigma^2_{LT} \text{ (Lines × Testers)} \quad = \quad \frac{(M_{LT} - Me)}{r\,E} \quad = \quad \sigma^2_{\text{sca}}$$

$$\sigma^2_{LT} \times E \text{ [(Lines × Testers) × Environments]} \quad = \quad \frac{(M_{LT}E - Me)}{r} \quad = \quad \sigma^2_{\text{sca}} \times E$$

3.3.6.2.4 Estimation of Cov HS (average) and Cov (FS)

$$\text{Cov HS (average)} \quad = \quad \frac{(T\,\sigma^2_L + L\,\sigma^2_T)}{(L + T)}$$

$$\text{Cov HS (average) × environments} \quad = \quad \frac{(T\,\sigma^2_{LE} + L\,\sigma^2_{TE})}{(L + T)}$$

$$\text{Cov FS} = \sigma^2_{LT} + 2 \text{ Cov HS}$$

$$\text{Cov FS × environments} = \sigma^2_{LT}E + 2 \text{ Cov HS×environments}$$

These could also be calculated from the expectations of MS as

$$\text{Cov HS (average)} \quad = \quad \frac{(M_L + M_T - 2M_{LT})}{r\,E\,(L + T)}$$

$$\text{Cov HS (average) × environments} \quad = \quad \frac{(M_L E + M_TE + 2M_{LT}E)}{r\,(L + T)}$$

These could also be calculated from the expectations of MS as

$$\text{Cov(FS)} \quad = \quad \frac{[M_L + MT + M_{LT} - 3Me + 6r\,E \text{ Cov (HS)} - r\,E(L + T) \text{ Cov (HS)}]}{3r\,E}$$

$$\text{Cov(FS)} \quad = \quad \frac{[M_LE + M_TE + M_{LT}E - 3Me + 6r \text{ Cov (HS)} \times E - r\,(L + T) \text{ Cov(HS)} \times E]}{3r}$$

Pooled analysis of variance for combining ability was done as per following ANOVA

Source of variation	**df**	**Sum of square**	**Mean square**	**Expected MS**
Environments	(E-1)	$\sum_{n=1}^{E}\frac{(x...n)}{TLr}-\frac{x2...}{TLrE}$	-	-
Lines	(L-1)	$\sum_{i=1}^{L}\frac{(xi.)2}{TrE}-\frac{x2...}{TLrE}$	M_1	$\sigma^2_e + r\ \sigma^2_{\mathrm{LTE}} + r\ E\sigma^2_{TL} + rET\sigma^2_{LT}$
Testers	(T-1)	$\sum_{j=1}^{t}\frac{(xj.)2}{TrE}-\frac{x2...}{TLrE}$	M_2	$\sigma^2_e + r\ \sigma^2_{\mathrm{LTE}} + r\ E\sigma^2_{LT}$
Lines × Testers	(L-1) (T-1)	$\sum_{ij=1}^{LT}\frac{(xij)2}{TrE}-\sum_{j=1}^{T}\frac{(xi.)2}{LrE}-\sum_{i=1}^{L}\frac{(xi.)2}{TrE}+\frac{x2...}{TLrE}$	M_3	$\sigma_e{}^2 + r\sigma^2_{\mathrm{LTE}} + rE\sigma^2_{TL}$
Tester × Environment	(T-1) (E-1)	$\sum_{jn=1}^{TE}\frac{xj...n}{Lr}-\sum_{n=1}^{E}\frac{x2...n}{TLr}-\sum_{j=1}^{T}\frac{x2j.}{LrE}+\frac{x2...}{TLrE}=A$	M_4	$\sigma_e{}^2 + r\sigma^2_{\mathrm{LTE}} + rL\sigma^2_{TE}$
Lines × Environment	(L-1) (E-1)	$\sum_{in=1}^{LE}\frac{x2i...n}{Tr}-\sum_{n=1}^{E}\frac{x2...n}{Lr}-\sum_{i=1}^{L}\frac{x2i.}{LrE}+\frac{x2...}{TLrE}=B$	M_5	$\sigma_e{}^2 + r\sigma^2_{\mathrm{LTE}} + rE\sigma^2_{LE}$
Lines × Testers × Environment	(T-1) (L-1) (E-1)	$\sum_{ijn=1}^{Ttle}\frac{x2ij...n}{Tr}-\sum_{ij=1}^{TL}\frac{x2ij}{rE}-\sum_{n=1}^{E}\frac{x2...n}{TLr}+\frac{x2...}{TLrE}=A-B$	M_6	$\sigma_e{}^2 + r\sigma^2_{LTE}$
Pooled error	E (TL-1) (r-1)	Error as at environment − I + error as at environment – II + error as at environment – III	M_e	σ^2_e

where, T = number of testers/males; L = number of lines/females; E = number of environments; r = number of replications in each environment; $x. . .$ = sum of all the crosses of all lines, testers, replication and over all environments; $x. . .n$ = sum of all the crosses of all lines and testers over replications; $x_{j.}$ = sum of j^{th}testers over all lines, replications and environments; x_i = sum of i^{th} line over all testers and replications and environments; x_{ij} = sum of ij^{th} cross over all replications and environments; $x_{j...n}$ = sum of j^{th} tester over all lines and replications at n^{th} environments; $x_{i\,j...n}$ = sum of ij^{th} cross over replications at n^{th} environments and Me = combined error MS

(1) Estimation of GCA and SCA variances

From the estimates of Cov (HS) and Cov (FS), variance due to GCA and SCA were calculated as

$$\sigma^2_{\text{gca}} = \text{Cov (HS)} = \frac{(M_L + M_{T} - 2M_{LT})}{r\,E\,(L + T)}$$

$$\sigma^2_{\text{gca}} \times \text{Environment} = \text{Cov (HS)} \times \text{Environments} = \frac{(M_L E + M_T E - 2M_{gT}E)}{r\,(L + T)}$$

$$\sigma^2_{\text{sca}} = \text{Cov (FS) - 2Cov (HS)} = \frac{(M_{LT} - Me)}{r\,E}$$

$$\sigma^2_{\text{sca}} \times \text{Environment} = \text{Cov (FS)} \times \text{Environments - 2Cov (HS)} \times \text{Environments} = \frac{(M_{LT}E - Me)}{r}$$

(2) Estimation of additive (σ^2_A) and dominance (σ^2_D) components of variance

Additive (σ^2_A) and dominance (σ^2_D) components of variances were calculated following Singh and Chaudhary (1985) and Dabholkar (1992).

$$\sigma^2_{gca} = \frac{(1 + F)}{4}\,\sigma^2_A = 1/\,2\sigma^2_A$$

So, $\sigma^2_A = 2\sigma^2_{gca}$

$$\sigma^2_{sca} = \left(\frac{(1 + F)}{2}\right)^2 \sigma^2_D = \sigma^2_D$$

So, $\sigma^2_D = \sigma^2_{sca}$

where, F (inbreeding coefficient) = 1.0, since chilli being self-pollinated crop, it does not suffer from inbreeding depression

3.3.6.2.5 Percent contribution of lines, testers and their interactions

These were computed as per the formulae suggested by Singh and Chaudhary (1985)

a. Per cent contribution of lines = SS (lines)/ SS (crosses) × 100
b. Per cent contribution of testers = SS (testers)/ SS (crosses) × 100

Per cent contribution of lines × testers = SS (lines × testers)/ SS (crosses) × 100

3.3.6.3 Estimation of heterosis

The heterosis was expressed as per cent deviation of F_1 hybrid performance from the mid-parent, better parent and standard check

$$\text{Per cent heterosis over mid-parent} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

where, F_1 and MP are mean values of F_1 hybrid and mid-parent, respectively

$$\text{Per cent heterosis over better parent} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

where, F_1 and BP are mean values of F_1 hybrid and better parent, respectively

$$\text{Per cent heterosis over standard check} = \frac{\overline{F}_1 - \overline{SC}}{SC} \times 100$$

where, F_1 and SC are mean values of F_1 hybrid and standard check, respectively

3.3.6.3.1 Test of significance for heterosis over mid-parent, better parent and standard check

To test the significance of heterosis, least square differences (LSD) were calculated as below;

LSD = SE (d) × '*t*' value

where,

$$\text{SE (d)} = \text{SD}_d = \pm\sqrt{2\frac{\text{MSE}}{\text{r}}}$$

MSE = error MS as computed in RCBD using F_1*'s*, parents and standard checks

r = number of replication

The LSD was calculated by multiplying the SD_d with '*t*' value at error df at both $P \leq 0.05$ and $P \leq 0.01$ level of significance.

CHAPTER IV

RESULTS AND DISCUSSION

The present study entitled "Evaluation of cytoplasmic male sterile lines of chilli pepper (*Capsicum annuum* L.) and their utilization in heterosis breeding" was conducted to identify temperature stable cytoplasmic male sterile (CMS) lines of chilli pepper and, to identify suitable parents for hybrid chilli breeding. Superior performing crosses were identified on the basis of expressed heterosis and specific combining ability (SCA) effects; and the potential parents for hybrid breeding were identified on the basis of mean performance and general combining ability (GCA) effects. The results are reported and discussed under the following sub-heads:

4.1 Evaluation of CMS A-lines of chilli pepper over environments
  4.1.1 Analysis of variance for pollen sterility and associated traits
  4.1.2 Performance of CMS A-lines over environments
  4.1.3 Stability performance of CMS A-lines based on GGE biplot analysis
  4.1.4 Evaluation of CMS A-lines for fruit and seed setting under open pollination conditions
  4.1.5 Evaluation of CMS A-lines for important fruit traits
4.2 Assessment of reconstitution of the recurrent parent (A-line) genome by using molecular markers
4.3 Estimation of combining ability effects
  4.3.1 Analysis of variance for the experimental design
  4.3.2 Analysis of variance for combining ability
  4.3.3 Estimation of general combining ability effects of parents
  4.3.4 Estimation of specific combining ability effects of crosses
4.4 Estimation of components of genetic variance
4.5 Estimation of heterosis

4.1 Evaluation of CMS A-lines of chilli pepper over the environments

In chilli, CMS is one of the most effective and economical methods for hybrid seed production (Duvick 1959 and Ma *et al* 2013). The basic principle of CMS is the interaction of nuclear *rf* gene and S-cytoplasm (Hanson and Folkerts 1992 and Linke and Börner 2005). Peterson (1958) and Shifriss (1997) reported that the expression of the male sterility in CMS could be affected by environmental conditions, especially the low temperature (<25°/17 °C day/night) (Shifriss and Guri 1979 and Yazawa *et al* 2002). Partial sterility of pollen, which may be affected by the environment or influenced by the modifier gene(s), was first reported by Zhang *et al* (2000). Thus, changes in temperature may lead to alterations in fertility ranging from complete sterility to partial fertility, which may also lead to CMS lines self-crossing or being crossed as the male parent (Gulyas *et al* 2006). Commercial use of CMS needs highly stable male sterility, to assure genetically uniform/pure F_1 hybrid seed production and reduce the risk of incomplete pollen sterility under low as well as high temperature conditions. Stable CMS lines could be developed by selecting maintainer plants (B-lines) that were tolerant to temperature fluctuations, selection against modifier gene(s), incorporation of the seedling markers for the early elimination of progenies resulting from self-pollination and sampling of environmental conditions that produced the highest level of male sterility (Shifriss and Guri 1979, Lee 2001 and Dhaliwal and Jindal 2014). The present study attempted to evaluate the newly developed CMS lines of chilli pepper under the variable temperature conditions and to identify the temperature stable CMS lines with superior horticultural traits for their utilization in hybrid development programs. The G × E interaction effects are of special interest for identifying the most stable genotype with respect to target environments or locations.

4.1.1 Analysis of variance for pollen sterility and fruit traits

The mean squares (MS) due to genotypes, environments and genotype × environment interaction for pollen sterility (%), pollen release score, fruit setting and seed setting under caged conditions are given in Table 4.1. The pooled analysis of variance (ANOVA) showed highly significant differences for pollen sterility (%), pollen release score, fruit setting (%), and number of seed fruit^{-1} due to genotypes. This suggested that there existed significant differences among CMS lines in their mean performance for male sterility associated traits. The analysis further showed that the MS due to environments were also significant for all traits signifying the important role played by the environment in expression of these traits. The MS due to G × E interaction was significant for pollen sterility (%), fruit setting and number of seed fruit^{-1}, and non-significant for pollen release score. This indicated that apart from genotypic differences, change of environment influenced the mean performance of the CMS lines for pollen sterility, fruit setting and seed setting, and the CMS lines responded differently to the variation in environmental conditions. The results indicated previous reports that CMS in chilli is influenced by the temperature. The CMS lines could be unstable due to environmental conditions or different genetic background of the lines or both. Further, the magnitude of MS attributed to genotypes was much higher than the MS due to environments and genotype × environment interaction for all the traits.

Table 4.1: Analysis of variance for pollen sterility, pollen release score, fruit setting and seed setting in CMS A- lines of chilli pepper over environments

Source of variance	**Pollen sterility (%)**			**Pollen release score**			**Fruit setting (%)**			**Number of seed fruit^{-1}**		
	df	**Mean Square**	**F-ratio**	**df**	**Mean Square**	**F-ratio**	**df**	**Mean Square**	**F-ratio**	**df**	**Mean Square**	**F-ratio**
Genotypes	16	982.69*	21.93	16	1.463*	15.52	16	59.05*	744.78	16	250.46*	749.1
Environments	3	589.96*	13.17	3	0.487*	5.17	3	11.09*	139.80	3	126.35*	377.91
Genotype × Environment	48	94.31*	2.11	48	0.101^{ns}	1.08	48	3.47*	43.79	48	20.97*	62.72
Error	408	44.81		408	0.094		68	0.079		68	0.334	

Where *, significant at *p*=0.05; ns, non-significant at *p*=0.05

4.1.2 Performance of CMS A-lines over environments

Performance of 17 CMS A-lines for pollen sterility, pollen release score, fruit setting and seed setting over environments under caged conditions during 2014-15 and 2015-16 is given in Table 4.3. Maximum and minimum weekly temperature recorded during period of pollen viability study during low temperature in 2014-15 (E_1), during high temperature in 2014-15 (E_2), during low temperature in 2015-16 (E_3) and during high temperature in 2015-16 (E_4) is given in Fig. 4.1a-d. Effect of environments on pollen sterility, pollen release score, fruit setting and seed setting under caged condition during 2014-15 and 2015-16 is given in Table 4.2.

4.1.2.1 Evaluation of CMS A-lines for pollen sterility

Performance of 17 CMS A-lines of chilli pepper for pollen sterility (%) under low (E_1 and E_3) and high temperature (E_2 and E_4) environments, and that pooled across the four environments is given in Table 4.3. Pollen viability evaluation of CMS A-lines exhibiting complete or partial sterility and that of CMS B-lines exhibiting abundance of fertile pollen under 10× magnification with 2% I_2-KI stain is shown in Plate 4.1a-c. Across the genotypes, pollen sterility in general was lower under E_1 and E_3 when compared with E_2 and E_4, indicating that the expression of pollen sterility in CMS lines was less under low temperature as compared to high temperature (Table 4.2). Shifriss (1997) suggested that under low temperature, meiotic breakdown is either stopped or delayed, resulting in pollen fertility. The results are in agreement with earlier reports in that high temperature presents the most critical environment for expression of sterility in pepper (Peterson 1958, Wang *et al* 2006 and Kim *et al* 2013). The Duncan's multiple range test (DMRT) indicated that the differences for pollen sterility under E_3 (low temperature environment) from E_2 and E_4 (high temperature environments) were non-significant. By contrast, a large number of viable/fertile pollen grains were observed in the maintainer/ B- lines, consistently throughout the study, indicating that pollen sterility in CMS A-lines is genetically inherited. Screening under low temperature is critical for the development of stable CMS lines.

Pollen sterility of CMS A-lines varied from 74.37 to 100% in E_1; 92.10 to 100% in E_2; 78.48 to 100% in E_3 and 87 to 100% in E_4. Under low temperature environments E_1 and E_3, 100% pollen sterility was recorded in 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A' and 'CMS463L5A'. These 10 lines along with 'CMS463L3A' also showed 100% pollen sterility under high temperature E_2 and E_4 environments. 'CMS46214A' recorded 92.3% pollen sterility in E_1; 98.43% in E_2 and 100% in E_3 and E_4. The pooled ANOVA indicated that these 12 lines recorded more than 97% pollen sterility across the environments and were statistically at par. Of the remaining 5 lines, pollen sterility across the environments ranged from 84.35% in 'CMS463L9A' to 92.24% in 'CMS46113A'. Based on the scale of Virmani *et al* (1997), 10 lines namely 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A' and 'CMS463L5A' scoring 100% pollen sterility over environments were regarded as completely male sterile. These lines were stable under the variable temperature stress conditions ranging from 24.1 °C/ 12.1 °C to 41.1 °C/ 28.5 °C day/ night temperature.

Earlier, Yazawa *et al* (2002) succeeded in breeding of two stable CMS pepper lines, 'P-MS' and 'Murasaki-MS'. Liu and Gniffke (2004) identified two lines 'CCA4757' and 'CCA4759' stable under low temperatures (< 23.8 °C/ 14.3 °C day/night). Gong *et al* (2008) developed several CMS lines as well as their maintainer and restorer lines by a combination of inter-specific crossing and induced mutations. Five CMS sterile lines were evaluated by Gniffke *et al* (2009) at The World Vegetable Center and found that two lines, 'CCA7234' and 'CCA7235', displayed stable sterility on all winter observation temperature dates. Suryawanshi *et al* (2013) regarded a line 'CMS-A(0246)' as highly stable across locations.

Among the seven lines producing viable pollen, the widest range for pollen sterility across the environments (74.37% to 93.05%) was recorded in 'CMS463L9A', indicating that this CMS line was more sensitive to change in temperature conditions. The narrowest range (96.89% to 100%) was found in 'CMS463L3A'. This indicated more consistence performance under all the four environments as compared to the other unstable CMS lines. Three lines namely 'CMS46113A', 'CMS46214A' and 'CMS463L3A' scoring pollen sterility between 92 to 99% were regarded as male sterile and the remaining 4 lines namely 'CMS4623A', 'CMS4627A', 'CMS463L9A' and 'CMS463L11A' scoring pollen sterility between 84 to 87% were regarded as partially male sterile. Under low temperature conditions, these lines produce viable pollen when temperature was relatively low (<26°C/ 14 °C average day/night temperature) during the initial few weeks of screening, but did not produce viable pollen grains with the onset of high temperature (mean temperature around 32-35°C/ 23-25 °C day/ night). Under high temperature conditions also, these lines showed partially sterility during initial stages of screening. However, the level of fertility was much lowers the high temperature than under the low temperature regime.

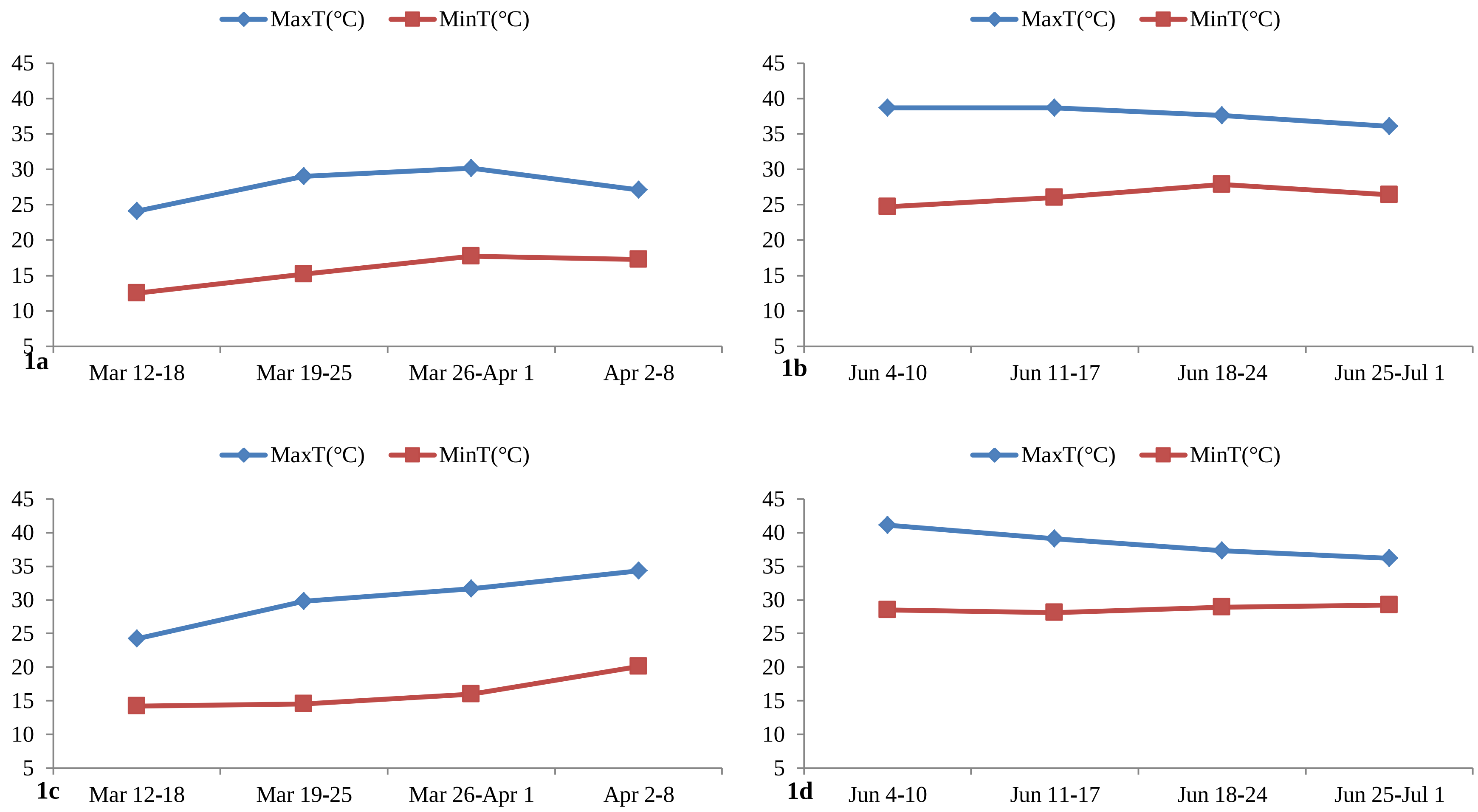

Figure 4.1: Maximum and minimum weekly temperature recorded during period of pollen viability study, 1a, during low temperature 2014-15 (E_1), 1b, during high temperature 2014-15 (E_2), 1c, during low temperature 2015-16 (E_3), 1d, during high temperature 2015-16 (E_4)

Production of viable pollen during initial stages of screening by these CMS lines may be due to exposure of plants to temperatures < 25 °C/ 15 °C day/night during December to mid-March or due to the presence of modifier gene(s) or both. Activity of the modifier gene(s) slows down with increase in temperature and stops completely at advanced stage of plant growth. Kaul (1988), Tan *et al* (1990) and Lee *et al* (2008a) opined that restoration of partial fertility in CMS lines of chilli is genotype specific influenced by the genetic background and might be influenced by temperature, photo-period or both.

In almost all the unstable CMS lines the pollen sterility (%) increased under E_3 when compared with E_1 (both low temperature regimes), whereas under E_4 the pollen sterility decreased as compare to E_2 (both high temperature regimes). The average variation for temperatures between E_1 and E_3 was 2.5 °C/ 0.06 °C day/night and between E_2 and E_4 was 0.65°C/ 1.54 °C day/night, means E_3 and E_4 experienced comparatively higher temperature compare to E_1 and E_2. This might have affected the pollen sterility status of the unstable CMS lines over the two years of evaluation. It is speculated that with few more cycles of backcrossing and selection, sterility of these lines can be improved. This is substantiated by the fact that two lines 'CMS46214A' and 'CMS463L3A' which were partially male sterile during the first year of evaluation were completely male sterile in the second year, expectedly due to one additional cycle of selection and backcrossing.

4.1.2.2 Evaluation of CMS A-lines for pollen release score

The amount of pollen released is generally associated with the combined total number of viable and aborted pollen grains seen adhering to the anther lobes. Performance of CMS lines of chilli pepper for pollen release score under the caged conditions is given in Table 4.3. Under the two low temperature environments E_1 and E_3, 10 lines namely 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A', and 'CMS463L5A' had ‘zero’ pollen release score. These 10 lines and 'CMS463L3A' recorded ‘zero’ pollen release score under the two high temperature environments E_2 and E_4. The line 'CMS463L3A' recorded ‘zero’ pollen release score under low temperature environment E_3 but had 0.17 score under E_1. The line 'CMS46214A' had ‘zero’ pollen release score under two environments E_3 and E_4 in the second crop season but scored 0.29 and 0.11 under E_1 and E_2 in the first crop season. Other lines with small amount of pollen tightly adhered to anthers during early weeks/dates of screening included 'CMS46113A', 'CMS4623A', 'CMS4627A', 'CMS463L9A', and 'CMS463L11A'. The pollen release score of these lines ranged from 0.11 under E_2 in 'CMS46214A' to 0.89 under E_3 in 'CMS463L9A'. The pooled analysis indicated that among the 7 partially male fertile

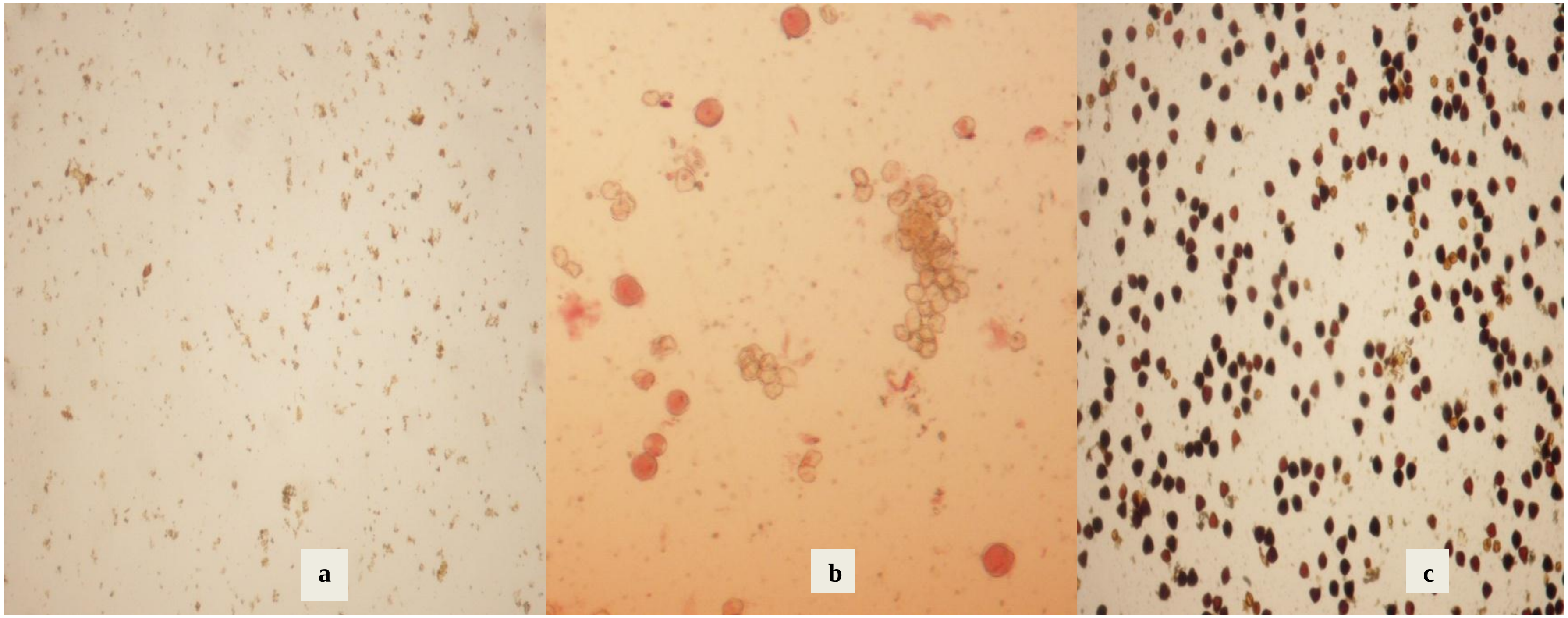

Plate 4.1a-c: Pollen viability evaluation of CMS lines with 2% I_2-KI stain under 10× magnification; a) Aborted pollen of completely male sterile A-line, b) mostly aborted pollen of partially male sterile A-lines, and c) Abundant fertile pollen of fully fertile CMS B-line

lines, minimum pollen release score of 0.04 across the four environments was recorded by 'CMS463L3A'. This was followed by 'CMS46214A' (0.10), 'CMS46113A' (0.37), 'CMS4627A' (0.48), 'CMS463L11A' (0.49) and 'CMS4623A' (0.51). The maximum pollen release score of 0.59 was recorded by 'CMS463L9A'. Based on the Liu and Gniffke (2004) scale of pollen release score, 10 CMS lines namely 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A', and 'CMS463L5A' were regarded as completely male sterile across the four environments.

During early weeks/dates of screening in E_1 when temperature was around 25 °C/ 15 °C day/ night, the lines 'CMS46113A', 'CMS4623A', 'CMS46214A', 'CMS463L9A' and 'CMS463L11A' had 10% of the plants, and 'CMS4627A' had 30% of the plants with some amount of pollen seen on surface of the anthers of few flowers. In E_2, the 'CMS463L11A' and 'CMS4623A' had 10% and 20% plants, respectively with few pollen grains seen on surface of the anthers when temperature was around 38 °C/ 26 °C day/ night. In E_3, the 'CMS4623A' had 10% plants; 'CMS46113A' and 'CMS4627A' each had 20% plants; 'CMS463L11A' had 30% plants and 'CMS463L9A' had 40% plants with few amount of pollen grains seen on the anther surface when temperature was around 25 °C/ 14 °C day/ night. In E_4, the 'CMS4627A' and 'CMS463L11A' each had 10% plants; 'CMS4623A' and 'CMS463L9A' each had 20% plants and 'CMS46113A' had 30% plants with few amount of pollen seen on surface of the anthers of some flowers when temperature was around 40 °C/ 28 °C day/ night. In contrast, during the last week/dates of screening, none of the plants showed pollen on the anthers.

Production of some pollen grains in some plants could occur due to favorable (low) temperature and photoperiod and presence of modifier gene(s). Screening of CMS lines under low temperature conditions and removal of fertile plants would enhance stability of CMS lines for male sterility. Kim *et al* (2013) observed few tightly adhered abnormal pollen grains on anthers when night temperature above 15 °C (sterile TCMS), and produced abundant amount of pollen grains on anthers as in their maintainer plants when night temperature of 13 °C (fertile TCMS). On the other hand, CMS sterile anthers never produced as abundant amount of pollen as their corresponding maintainer lines. Further, the dehiscence was never complete even in those lines in which sterility reversal was the highest under the low temperature.

Table 4.2: Effect of environments on pollen sterility, pollen release score, fruit setting and seed setting under caged condition during 2014-15 and 2015-16)

Environment	Pollen sterility (%)	Pollen release score	Fruit setting (%)	Number of seed fruit^{-1}
E_1	93.17 c	0.22 a	2.29 a	6.04 a
E_2	98.32 a	0.08 c	0.95 d	1.42 d
E_3	95.91 b	0.18 ab	1.76 c	3.79 c
E_4	97.25 ab	0.12 bc	1.96 b	4.53 b

[†]values are presented as mean. Values in columns followed by the same letter are not significantly different at p <0.01 according to the Duncan's multiple range test

Table 4.3: Performance of CMS A- lines of chilli pepper for pollen sterility, pollen release score, fruit setting and seed setting under caged conditions over environments

CMS line	Pollen sterility (%)[†]				
	E_1	E_2	E_3	E_4	Pooled mean
CMS4611A	100.00 A[y]	100.00 A	100.00 A	100.00 A	100.00 a[z]
CMS4614A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS46113A	81.83 B	99.17 A	96.59 A	91.37 AB	92.24 b
CMS4622A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS4623A	79.68 B	93.73 A	90.14 AB	87.00 AB	87.64 c
CMS4624A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS4626A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS4627A	76.44 B	94.99 A	83.15 B	92.86 A	86.86 c
CMS46213A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS46214A	92.30 A	98.43 A	100.00 A	100.00 A	97.68 a
CMS463D2A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS463D13A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS463D14A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS463L3A	96.89 A	100.00 A	100.00 A	100.00 A	99.22 a
CMS463L5A	100.00 A	100.00 A	100.00 A	100.00 A	100.00 a
CMS463L9A	74.37 B	93.05 A	78.48 B	91.48 A	84.35 c
CMS463L11A	82.34 A	92.10 A	82.10 A	90.50 A	86.76 c

Table 4.3 (*Cont'd.*)

CMS line	**Pollen release score**†				
	E_1	**E_2**	**E_3**	**E_4**	**Pooled mean**
CMS4611A	0.00 A[y]	0.00 A	0.00 A	0.00 A	0.00 c[z]
CMS4614A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS46113A	0.69 A	0.00 B	0.37 AB	0.43 AB	0.37 b
CMS4622A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS4623A	0.74 A	0.37 A	0.43 A	0.51 A	0.51 ab
CMS4624A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS4626A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS4627A	0.71 A	0.14 B	0.74 A	0.34 AB	0.48 ab
CMS46213A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS46214A	0.29 A	0.11 A	0.00 A	0.00 A	0.10 c
CMS463D2A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS463D13A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS463D14A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS463L3A	0.17 A	0.00 A	0.00 A	0.00 A	0.043 c
CMS463L5A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 c
CMS463L9A	0.69 AB	0.34 B	0.89 A	0.43 B	0.59 a
CMS463L11A	0.51 AB	0.37 B	0.69 A	0.37 B	0.49 ab

Table 4.3 (*Cont'd.*)

CMS lines	**Fruit setting (%)**[†]				
	E_1	**E_2**	**E_3**	**E_4**	**Pooled mean**
CMS4611A	0.00 A[y]	0.00 A	0.00 A	0.00 A	0.00 h[z]
CMS4614A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS46113A	4.66 A	0.00 C	2.66 B	3.33 AB	2.66 e
CMS4622A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS4623A	4.66 B	3.85 B	3.33 B	8.66 A	5.12 d
CMS4624A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS4626A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS4627A	7.66 A	1.33 B	8.66 A	5.33 A	5.74 c
CMS46213A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS46214A	5.33 A	0.00 B	0.00 B	0.00 B	1.33 f
CMS463D2A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS463D13A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS463D14A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS463L3A	2.00 A	0.00 B	0.00 B	0.00 B	0.50 g
CMS463L5A	0.00 A	0.00 A	0.00 A	0.00 A	0.00 h
CMS463L9A	8.33 A	5.83 A	8.66 A	6.66 A	7.37 a
CMS463L11A	6.33 AB	5.12 B	6.66 AB	9.31 A	6.85 b
CMS lines	**Number of seed fruit^{-1}**[†][+]				
CMS46113A	15.66	0.00 C[y]	11.51 B	17.40 A	11.14 c[z]
CMS4623A	14.38	6.06 B	11.60 AB	17.07 A	12.27 ab
CMS4627A	16.87	1.15 B	14.84 A	14.25 A	11.78 bc
CMS46214A	14.14	0.00 B	0.00 B	0.00 B	3.53 d
CMS463L3A	10.22	0.00 B	0.00 B	0.00 B	2.55 e
CMS463L9A	15.72	7.95 B	13.70 A	14.30 A	12.92 a
CMS463L11A	15.75	8.96 A	12.85 A	14.06 A	12.90 a

[†] Values are presented as mean

[+] Data's presented only those CMS lines which set seed

[y] Average means of a genotype followed by the same upper case letters between environments are not significantly different at *p* <0.01 according to the Duncan's multiple range test

[z] Across environments means (pooled means) followed by the same lower case letter are not significantly different at *p* <0.01 according to the Duncan's multiple range test

Correlation coefficient between pollen sterility and pollen release score was highly significant and negative (-0.932). As the pollen sterility percent increased, pollen release score would decrease and the vice-versa. Since pollen viability test is laborious and time consuming, it is suggested that pollen release score can be used for initial screening of large populations.

4.1.2.3 Evaluation of CMS A-lines for fruit setting

CMS lines were evaluated for sterility performance by covering the plants by 24-mesh net cages and observing for fruit setting ability under the caged conditions. CMS lines without fruit setting or erratic fruit setting and fruit setting without seed under caged conditions were considered as male sterile. Inability of setting fruit under the caged conditions was attributed to the non-viability of pollen grains. Mean performance of CMS A-lines for fruit setting (%) over environments under the caged conditions is given in Table 4.3.

Ten lines namely 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A' and 'CMS463L5A' did not set any fruit irrespective of the environmental conditions. Among the remaining lines, 'CMS46214A' and 'CMS463L3A' recorded fruit setting under E_1 only. Four lines namely 'CMS4623A', 'CMS4627A', 'CMS463L9A', and 'CMS463L11A' set fruits across the four environments and 'CMS46113A' across three (E_1, E_3 and E_4) environments. Across the environments, fruit setting in these lines varied from 1.33% in 'CMS4627A' under E_2 to 9.31% in 'CMS463L11A' under E_4. Among the lines which set fruits, the minimum fruit setting across the four environments was recorded by 'CMS463L3A' (0.5%). This was followed by 'CMS46214A' (1.33%), 'CMS46113A' (2.66%), 'CMS4623A' (5.12%), 'CMS4627A' (5.74%) and 'CMS463L11A' (6.85%), and the maximum fruit setting was recorded by 'CMS463L9A' (7.37%).

The fruit setting results of present study were comparable with the pollen staining results in that the stable or completely sterile lines lacked viable pollen, failed to set fruits or produced few fruits without seed. The lines regarded as partially fertile resulted in self-pollination with varying degrees of fruit set. Liu and Gniffke (2004) reported that the CMS lines without viable pollen grain failed to set any fruit. Ma *et al* (2013) reported the self-pollinated fruit-setting rate of 200A × 206B, 201A × 200B, 201A × 206B, 203A × 200B, 206A × 200B, 206A × 201B were ‘zero’ and these 6 F_1 hybrids of pepper did not have normal pollen or traces of pollen. Suryawanshi *et al* (2013) reported that a hot pepper 'CMS-A(0246)' line did not set any fruit across the locations.

4.1.2.4 Number of seed fruit^{-1}

Among the seven lines those could set fruit under the caged conditions, number of seed fruit^{-1} varied from 1.15 in 'CMS4627A' under E_2 to 17.4 in 'CMS46113A' under E_4. The pooled analysis indicated that the minimum number of seed fruit^{-1} was recorded in 'CMS463L3A'. This was followed by 'CMS46214A', 'CMS46113A', 'CMS4627A', 'CMS4623A', 'CMS463L11A' and 'CMS463L9A'.

4.1.3 Stability performance of CMS lines based on GGE biplot analysis

The results of the principal component analysis (PCA) of genotype × environment interaction (GEI) showed that the first two principal components (PCs) in the biplot explained 98.2% of the total variation in GEI. Stability performance of the 17 CMS lines of chilli pepper based on GGE biplot analysis is shown in Fig. 4.2. The CMS line location closer to average-environment coordination (AEC) indicated highest mean for pollen sterility. The line that passes through the origin and is perpendicular to the average-environment axis (AEA) represents the stability of the genotype. Distance in either direction away from the biplot origin on AEA axis indicates greater genotype × environment interaction and reduced stability. The single arrowed line is the AEA that points to higher pollen sterility over environments. For selection based on biplot analysis, the ideal CMS lines would be those with both high mean pollen sterility and high stability. The lines 'CMS4611A' (G1), 'CMS4614A' (G2), 'CMS463D2A' (G11), 'CMS463D13A' (G12), 'CMS463D14A' (G13), 'CMS4624A' (G6), 'CMS463L5A' (G15), 'CMS4622A' (G4), 'CMS46213A' (G9) and 'CMS4626A' (G7) had the 100% pollen sterility and the shortest distance from AEA. The line 'CMS463L9A' (G16) had the lowest pollen sterility and was located farthest from the origin on left side of perpendicular line with greater distance from AEA. The double arrowed line is the AEC ordinate points to greater variability (poorer stability) in either direction. Thus, the lines 'CMS46113A' (G3) and 'CMS4623A' (G5) were highly unstable because the relative performance of these lines was not consistent across the environments. The lines 'CMS4611A' (G1), 'CMS4614A' (G2), 'CMS463D2A' (G11), 'CMS463D13A' (G12), 'CMS463D14A' (G13), 'CMS4624A' (G6), 'CMS463L5A' (G15), 'CMS4622A' (G4), 'CMS46213A' (G9), and 'CMS4626A' (G7) were highly stable for pollen sterility.

The ideal test environment for high pollen sterility screening can be identified from the Fig. 4.3. The average environment (represented by the small circle at the end of the arrow) has the average coordinate of all the test environments and AEA is the line that passes through the average environment and the biplot origin. An "ideal test environment" for selection of fully sterile CMS lines would be the center of the concentric circles. Since E_1 is closest to this point, so this environment is the most suitable for screening of breeding material for selection of fully sterile CMS lines. During the E_1, day/ night temperature of the initial week was 24.1 ºC/ 12.5 ºC, the relative humidity and sunshine hours were 78% and 6.1 h, respectively. Contrary to this, E_2 is farthest from the point of ideal test environment and thus is the least suitable for screening of CMS genotypes.

4.1.4 Evaluation of CMS A-lines for fruit setting and seed setting under open pollination conditions

A pre-requisite for a female parent to be used in hybrid seed production is its ability to have good fruit setting with normal seed set under the open pollination conditions. The number of seed fruit^{-1} is one of the most important criteria in the eyes of breeders and producers for hybrid seed production. The number of seed fruit^{-1} depends on the potentiality of the female parent and the male parent that provided the pollen. The performance of CMS A-lines for fruit setting (%), number of fruits plant^{-1} and number of seed fruit^{-1} recorded under the open pollination conditions are presented in Table 4.4.

Under low temperature environments (E_1 and E_3), fruit setting (%) ranged from 19.33 in 'CMS4614A' to 50.66% in 'CMS463D13A' under E_1 and from 20.66 in 'CMS4623A' to 53.33% in 'CMS463D13A' under E_3. The number of fruits plant^{-1} ranged from 43.62 in 'CMS463L9A' to 159.50 in 'CMS463D13A' and from 40.50 in 'CMS463L9A' to 167.80 in 'CMS463D13A' under E_1 and E_3, respectively. The number of seed fruit^{-1} varied from 27.40 in 'CMS463L11A' to 79.80 in 'CMS463D13A' under E_1 and from 28.10 in 'CMS463L3A' to 76.30 in 'CMS463D13A' under E_3.

Under high temperature environments, fruit setting (%) ranged from 9.33 in 'CMS4614A' to 31.33% in 'CMS463D13A' under E_2 and from 11.33 in 'CMS4611A' to 33.56% in 'CMS463D13A' under E_4. The number of fruits plant^{-1} ranged from 25.66 in 'CMS4614A' to 72.44 in 'CMS463D13A' and from 23.50 in 'CMS4626A' to 73.28 in 'CMS463D13A' under E_2 and E_4, respectively. The number of seed fruit^{-1} ranged from 20.70 in 'CMS4622A' to 47.20 in 'CMS463D13A' under E_2 and from 17.40 in 'CMS4622A' to 68.65 in 'CMS463D13A' under E_4.

The pooled analysis indicated that all the CMS lines had sufficient fruit setting ability (18.09 to 42.22%), number of fruits plant^{-1} (47.00 to 118.25) and number of seed fruit^{-1} (27.50 to 67.99) under the open pollination conditions. This indicated that the female fertility of the CMS lines is normal. The good female fertility of the CMS lines would contribute to economic production of hybrid seed. Yazawa *et al* (2002) also reported more than 50% fruit setting when CMS line 'P-MS' and 'Murasaki-MS' were crossed with fertile pollen. Dahal *et al* (2006) recorded that the fruit setting in chilli ranged from 6.66 to 41.33%. Kaur *et al* (2016) reported the fruit set (%) among hot pepper genotypes varied from 26 to 86% and number of seed fruit^{-1} ranged from 16.8 to 69.7 at optimum temperature regime (34 °C / 16 °C day/night). Rodrigues *et al* (2012) observed the highest number of fruits plant^{-1} for 'UENF 1624 × UENF 1639' with 108.9 fruits plant^{-1}. Wang *et al* (2006) also observed fruits with

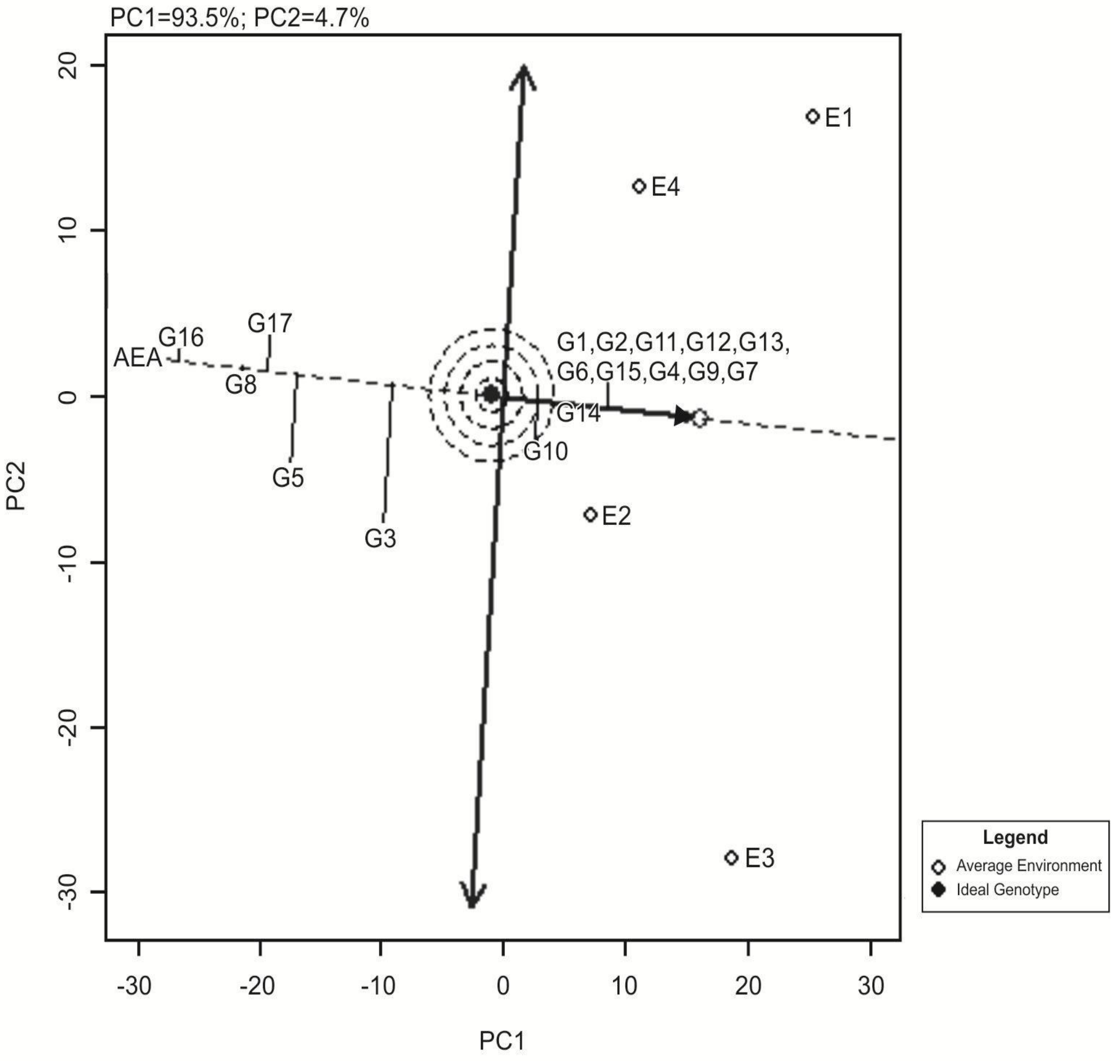

Figure 4.2: GGE biplot showing ranking of CMS lines for pollen sterility with 2% I_2-KI staining method and stability performance over the environments

Where, **G1:** CMS4611A; **G2:** CMS4614A; **G3:** CMS46113A; **G4:** CMS4622A; **G5:** CMS4623A; **G6:** CMS4624A; **G7:** CMS4626A; **G8:** CMS4627A; **G9:** CMS46213A; **G10:** CMS46214A; **G11:** CMS463D2A; **G12:** CMS463D13A; **G13:** CMS463D14A; **G14:** CMS463L3A; **G15:** CMS463L5A; **G16:** CMS463L9A; **G17:** CMS463L11A

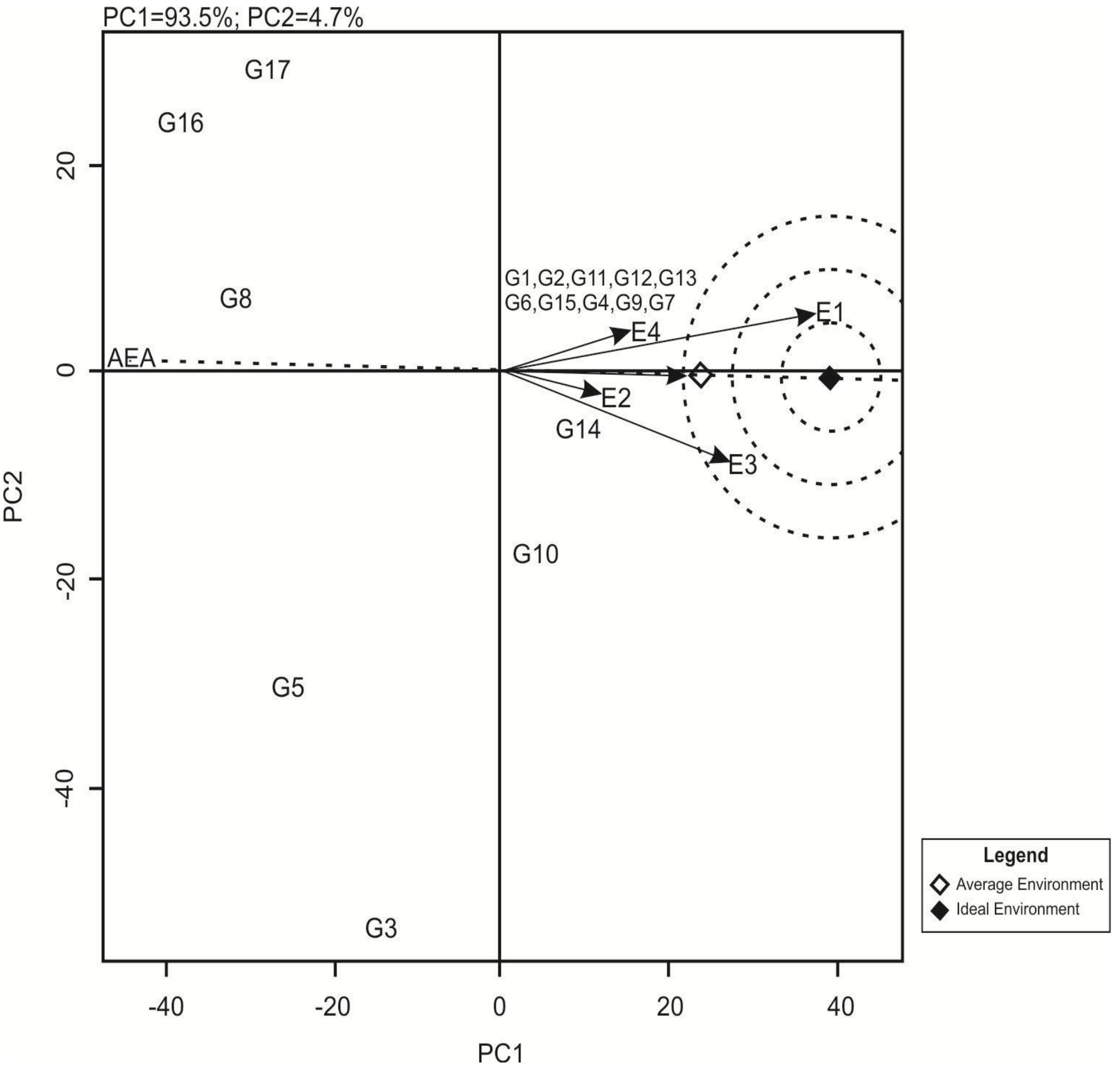

Figure 4.3: The view of the GGE biplot to rank test environments relative to an ideal test environment (represented by center of the concentric circles) (2% I_2-KI staining method)

Table 4.4: Mean performance of CMS chilli pepper lines for fruit setting, number of fruit plant^{-1} and number of seed plant^{-1} in open pollination conditions

CMS line	Fruit setting (%)[†]				
	E_1	E_2	E_3	E_4	Pooled mean
CMS4611A	29.33 A[y]	12.66 B	36.66	11.33 B	22.49 f[z]
CMS4614A	19.33 AB	9.33 C	27.33	16.37 BC	18.09 h
CMS46113A	37.33 A	12.66 B	42.66	18.66 B	27.82 cd
CMS4622A	24.00 A	22.66 A	21.33	24.00 A	22.99 ef
CMS4623A	24.66 A	19.75 A	20.66	22.66 A	21.93 fg
CMS4624A	31.00 A	18.66 B	34.66	21.33 B	26.41 cde
CMS4626A	22.00 AB	16.66 AB	22.66	14.66 B	18.99 gh
CMS4627A	26.66 A	17.33 A	29.33	24.66 A	24.49 def
CMS46213A	45.33 A	24.66 B	46.66	27.33 AB	35.99 b
CMS46214A	32.66 AB	21.33 BC	35.33	19.33 C	27.16 cd
CMS463D2A	43.33 A	27.40 A	37.33	28.66 A	34.18 b
CMS463D13A	50.66 A	31.33 A	53.33	33.56 A	42.22 a
CMS463D14A	47.33 A	28.66 A	46.00	26.66 A	37.16 b
CMS463L3A	22.00 A	26.66 A	31.33	27.33 A	26.83 cd
CMS463L5A	27.33 A	23.05 A	24.66	22.66 A	24.42 def
CMS463L9A	29.33 A	27.96 A	27.33	29.33 A	28.49 c
CMS463L11A	34.00 A	29.07 A	30.66	23.23 A	29.24 c

Table 4.4 (*Cont'd.*)

CMS line	Number of fruits plant^{-1}[†]				
	E_1	E_2	E_3	E_4	Pooled mean
CMS4611A	75.20 A[y]	37.90 B	89.56 A	35.66 B	59.58 gh[z]
CMS4614A	69.00 A	25.66 B	76.50 A	40.01 B	52.79 hi
CMS46113A	108.25 A	44.67 B	115.28 A	51.50 B	79.93 cd
CMS4622A	99.50 A	53.00 BC	91.66 AB	36.50 C	70.16 ef
CMS4623A	88.00 A	43.87 B	106.33 A	35.20 B	68.35 efg
CMS4624A	133.00 A	39.50 B	136.50 A	27.66 B	84.16 c
CMS4626A	99.00 A	29.50 B	110.66 A	23.50 B	65.66 fg
CMS4627A	91.50 A	37.66 B	119.82 A	54.66 B	75.91 cde
CMS46213A	157.50 A	55.25 B	148.33 A	48.50 B	102.39 b
CMS46214A	151.50 A	49.50 B	154.50 A	25.50 B	95.25 b
CMS463D2A	147.25 A	58.89 C	130.67 AB	69.33 BC	101.53 b
CMS463D13A	159.50 A	72.44 B	167.80 A	73.28 B	118.25 a
CMS463D14A	133.33 A	67.25 B	142.50 A	49.50 B	98.14 b
CMS463L3A	66.50 A	58.33 A	75.82 A	62.50 A	65.78 fg
CMS463L5A	56.62 A	52.77 A	53.66 A	40.22 A	50.82 hi
CMS463L9A	43.62 A	57.19 A	40.50 A	46.70 A	47.00 i
CMS463L11A	107.00 A	59.30 B	83.75 AB	45.80 B	73.96 def

Table 4.4 (*Cont'd.*)

CMS line	**Number of seed fruit^{-1}†**				
	E_1	**E_2**	**E_3**	**E_4**	**Pooled mean**
CMS4611A	35.70 A[y]	24.60 A	31.90 A	20.90 A	28.27 f[z]
CMS4614A	31.70 A	21.30 A	37.40 A	23.28 A	28.42 f
CMS46113A	41.30 A	32.70 A	40.50 A	34.20 A	37.17 e
CMS4622A	39.30 A	20.70 B	41.70 A	17.40 B	29.77 f
CMS4623A	47.78 AB	26.95 B	51.40 AB	66.90 A	48.26 c
CMS4624A	30.70 A	21.60 A	28.60 A	29.10 A	27.50 f
CMS4626A	47.90 A	28.40 B	40.50 AB	32.50 AB	37.32 e
CMS4627A	66.90 A	42.60 A	58.70 A	60.30 A	57.12 b
CMS46213A	45.10 A	40.60 A	49.20 A	33.60 A	42.12 d
CMS46214A	45.80 A	34.30 A	50.30 A	41.60 A	43.00 d
CMS463D2A	50.90 B	38.28 C	55.60 B	63.10 A	51.97 c
CMS463D13A	79.80 A	47.20 A	76.30 A	68.65 A	67.99 a
CMS463D14A	65.90 A	38.50 A	69.50 A	53.90 A	56.95 b
CMS463L3A	35.90 A	25.70 A	28.10 A	29.80 A	29.87 f
CMS463L5A	40.30 AB	21.29 B	47.20 A	31.70 AB	35.12 e
CMS463L9A	36.40 AB	35.65 B	38.90 AB	59.40 A	42.58 d
CMS463L11A	27.40 B	28.10 B	30.50 B	58.82 A	36.20 e

† Values are presented as mean

[y] Average means of a genotype followed by the same upper case letters between environments are not significantly different at $p < 0.01$ according to the Duncan's multiple range test

[z] Across environments means (pooled means) followed by the same lower case letter are not significantly different at $p < 0.01$ according to the Duncan's multiple range test

sufficient amount of seed in pepper under open field of spring season. The seed number fruit^{-1} of hot pepper genotypes varied from 16.33 to 59.67 (Singh *et al* 2014). The fruit setting (%), number of fruits plant^{-1} and number of seed plant^{-1} of CMS lines under the normal temperature conditions (high temperature regime, E_2 and E_4) is comparable with the previous reports and, therefore, are suitable for their use in hybrid seed production programs of chilli.

4.1.5 Evaluation of CMS A-lines for important fruit traits

The fruit traits of CMS A-lines were measured and compared by LSD-test in BC_6F_1 generation. The traits like fruit weight, fruit length, fruit width and pericarp thickness directly contribute towards total yield. Performance of the parental lines determines performance of the resultant hybrids. Besides fruit weight and fruit length are important for consumer acceptance. A thick pericarp is vital for green chilli and chilli paste, the medium thickness is more suitable for dry chilli production as it takes comparatively lesser time for drying.

The ANOVA for fruit traits of CMS A- lines of chilli pepper evaluated during 2015-16 is given in Table 4.5. The ANOVA revealed significant differences in performance of the CMS lines for the fruit traits studied, indicating diversity among the CMS lines which can be exploited in hybrid breeding. Mean performance of CMS A-lines for fruit weight (g), fruit length (cm), fruit width (mm) and pericarp thickness (mm) are given in Table 4.6.

4.1.5.1 Fruit weight (g)

The average fruit weight of CMS A-lines varied from 2.81 to 7.48 g with overall mean of 5.23 g. The maximum fruit weight was recorded in 'CMS463D14A' (7.48 g) followed by 'CMS463D13A' (7.19 g), 'CMS463D2A' (7.13 g) and 'CMS463L5A (6.38 g)', while the minimum was shown by 'CMS46113A' (2.81 g).

4.1.5.2 Fruit length (cm)

Among the CMS lines, the maximum fruit length (8.29 cm) was recorded in 'CMS463D13A' whereas the minimum fruit length was observed in 'CMS4611A' (4.28 cm) followed by 'CMS463L11A' (4.82 cm), 'CMS46113A' (4.98 cm) and 'CMS463L5A' (5.02 cm).

4.1.5.3 Fruit width (mm)

The fruit width of CMS lines varied from 7.88 to 13.01 mm with overall mean of 10.55 mm. The line, 'CMS463D13A' recorded maximum fruit width (13.01 mm) which was statistically at par with 'CMS463D2A' (12.91 mm), while the minimum fruit width (7.88 mm) was observed in 'CMS463L5A'. This was followed by 'CMS463L11A' (8.35 mm), 'CMS4627A' (8.53 mm) and 'CMS46113A' (8.62 mm).

Table 4.5: Analysis of variance for fruit traits of CMS A- lines of chilli pepper evaluated during 2015-16

Source of variance	**df**	**Fruit weight (g)**		**Fruit length (cm)**		**Fruit width (mm)**		**Pericarp thickness (mm)**	
		Mean Square	F-ratio	Mean Square	F-ratio	Mean Square	F-ratio	Mean Square	F-ratio
Replication	1	0.0018	0.01	0.0071	0.05	0.71	2.34	0.0017	0.64
Genotypes	16	3.92*	19.92	3.20*	24.40	5.11*	16.74	0.051*	19.08
Error	16	0.20		0.13		0.31		0.003	

Where *, significant at p=0.05

Table 4.6: Performance of CMS A- lines of chilli pepper for important fruit traits in open field conditions

CMS lines	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)
CMS4611A	3.66±0.24 ghi	4.28±0.18 g	9.43±0.46 fg	0.78±0.03 fg
CMS4614A	3.07±0.14 hi	5.79±0.22 de	10.17±0.34 def	0.72±0.02 gh
CMS46113A	2.81±0.20 i	4.98±0.22 fg	8.62±0.35 gh	0.90±0.03 de
CMS4622A	4.76±0.25 ef	6.11±0.20 d	10.27±0.41 def	0.74±0.02 g
CMS4623A	5.07±0.26 de	5.92±0.18 de	11.52±0.48 bc	0.62±0.03 h
CMS4624A	5.26±0.34 de	7.00±0.24 c	11.89±0.36 ab	0.79±0.02 efg
CMS4626A	5.86±0.34 cd	7.29±0.25 bc	10.71±0.36 cde	1.00±0.03 cd
CMS4627A	4.10±0.21 fg	5.58±0.22 def	8.53±0.27 gh	0.80±0.03 efg
CMS46213A	5.37±0.33 de	7.75±0.31 abc	11.34±0.33 bcd	1.04±0.05 bc
CMS46214A	5.21±0.29 de	7.10±0.35 c	10.59±0.53 cdef	1.11±0.05 ab
CMS463D2A	7.13±0.34 ab	7.91±0.38 ab	12.91±0.43 a	1.09±0.04 abc
CMS463D13A	7.19±0.33 ab	8.29±0.27 a	13.01±0.45 a	1.18±0.06 a
CMS463D14A	7.48±0.41 a	7.93±0.29 ab	11.96±0.37 ab	1.06±0.03 bc
CMS463L3A	5.80±0.30 cd	5.16±0.26 ef	10.04±0.45 ef	1.01±0.04 bc
CMS463L5A	6.38±0.35 bc	5.01±0.17 fg	7.88±0.40 h	0.98±0.05 cd
CMS463L9A	5.87±0.50 cd	5.83±0.22 de	12.07±0.46 ab	0.86±0.04 ef
CMS463L11A	3.85±0.16 fgh	4.81±0.22 fg	8.35±0.41 gh	0.90±0.04 de
Mean	5.23	6.28	10.55	0.92
CD (p<0.05)	0.94	0.77	1.17	0.11
CV (%)	8.49	5.76	5.24	5.62

Values in columns followed by the same letter are not significantly different at p <0.05 according to the least significant difference (LSD) test

4.1.5.4 Pericarp thickness (mm)

The pericarp thickness of CMS lines varied from 0.62 to 1.19 mm with an average of 0.92 mm. The minimum pericarp thickness was observed in 'CMS4623A' (0.62 mm), whereas the maximum pericarp thickness was recorded in 'CMS463D13A' (1.19 mm) followed by 'CMS46214A' (1.12 mm) and 'CMS463D2A' (1.09 mm).

Based on the results of fruit traits, the CMS line 'CMS463D13A' recorded maximum fruit length, fruit width and pericarp thickness which was statistically at par with 'CMS463D2A'. These lines are identified as the most promising parental material to initiate hybrid breeding program for the development of heterotic hybrids of chilli pepper.

4.2 Assessment of reconstitution of the recurrent parent (A-line) genome by using molecular markers

In this experiment, the genetic similarity or homology between three selected CMS A- and their corresponding CMS B-lines was examined by using SSR markers. The purpose was to assess whether genome of the recurrent parent has been fully recovered. For this purpose, 120 markers covering the whole *Capsicum* genome were screened. The list of SSR markers used in this study is presented in APPENDIX I. Out of 120 markers screened, 84 markers (70.0%) were amplified in 'CMS4611A' (both A and B-), 90 markers (75.0%) in 'CMS4626A' (both A and B-) and 88 markers (73.3%) in 'CMD463D13A' (both A and B-).

Almost all the amplified markers showed monomorphic bands between the A- and the B- lines on superfine 2.5% agarose gel (Plate 4.2). Between 'CMS463D13A' and 'CMS463D13B' (alloplasmic maintainer line) and between 'CMS4626A' and 'CMS4626B', polymorphic banding patterns were observed by a marker (GPMS 191) for chromosome 1; one marker showed polymorphic bands between 'CMS463D13A' and 'CMS463D13B' for chromosome 1 (CAMS 679) and chromosome 2 (CAMS 177) and one marker (HpmsE 065) between 'CMS4611A' and 'CMS4611B' for chromosome 10, but the percentage of marker which showed the polymorphic bands, were negligible. The probable reasons could be either some genetic drag between lines or due to the technological limitations.

After five cycles of backcrossing and selection, the genome recovery of the recurrent parent in 'CMS4611A', 'CMS4626A' and 'CMS463D13A' was estimated to be 98.8, 98.9 and 96.6%, respectively, measured by percentage of the monomorphic marker ratios. Since the CMS lines are maintained by backcrossing the respective maintainer lines, 100% genome the recurrent parent will be recovered with additional one or two backcrosses.

4.3 Estimation of combining ability effects

4.3.1 Analysis of variance for the experimental design

The results pertaining to the analysis of variance (ANOVA) for the experimental design are presented in Table 4.7. The mean squares (MS) due to genotypes over the three environments were significant for all the traits studied, suggesting that there existed significant differences among the genotypic means that included 23 parents and their 60 crosses. The pooled MS due to genotypes for all the traits studied over the three environments were significant revealing inherent variability among the genotypes. Therefore, the analysis for combining ability was performed for all the plant growth, yield and quality traits. It might also be noted that diversity in parental lines resulted in sufficient amount of variability in performance of the crosses. The pooled ANOVA for the experimental design for different traits showed that the MS due to environments were significant for all the traits which mean

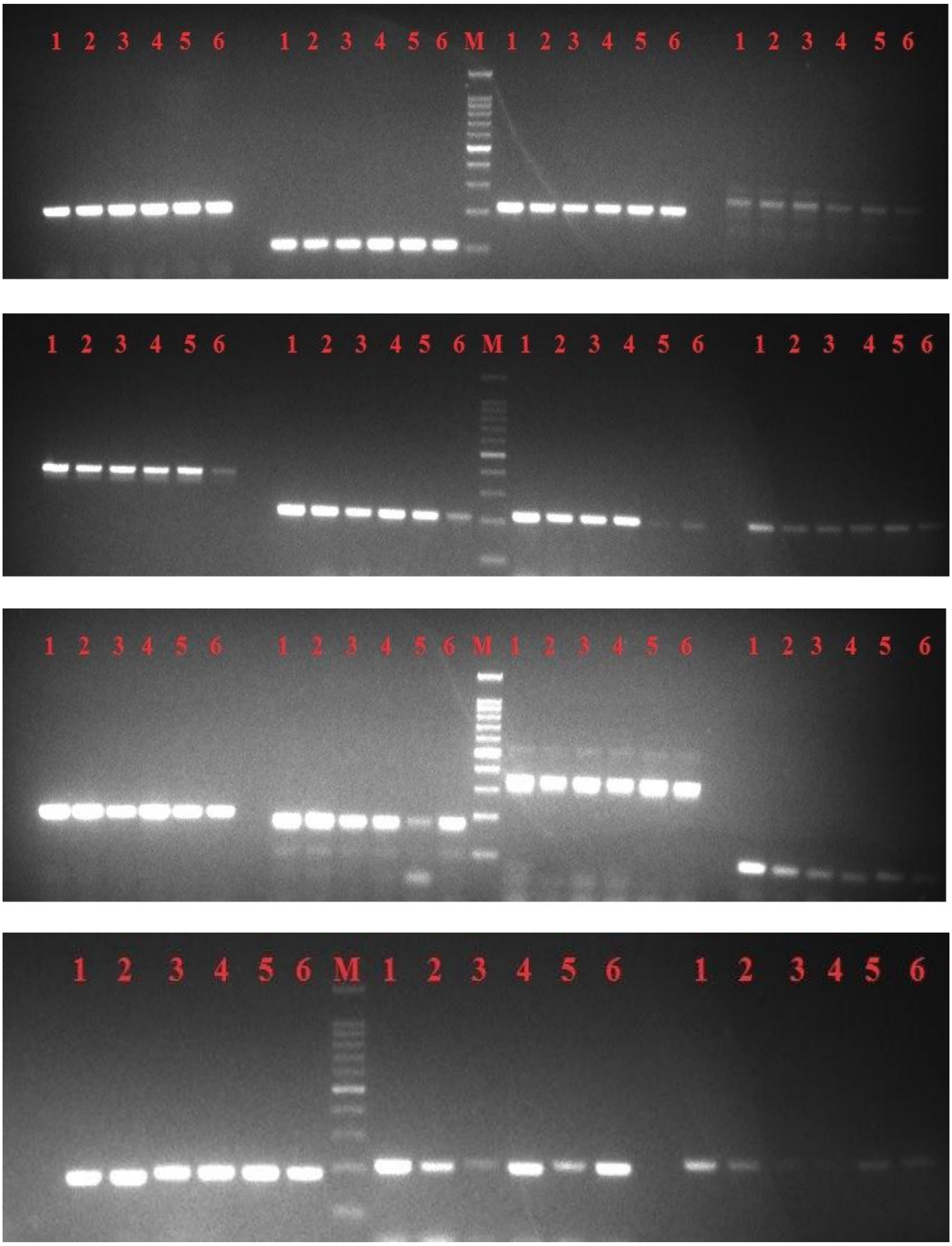

Plate 4.2: SSR markers showing genetic similarity between the A and B- lines

where, 1: CMS463D13A; 2: CMS463D13B; 3: CMS4626A; 4: CMS4626B; 5: CMS4611A; 6: CMS4611B; M: 100bp DNA ladder that the environments in three seasons were different from one another, signifying the important role played by environments in the expression of the traits. There is need to pursue environment specific breeding strategy for genetic improvement of the crop. Previous studies in which yield related traits were measured have showed significant genetic differences among the progenies (Geleta and Labuschagne 2006a, do Nascimento *et al* 2014, Medeiros *et al* 2014 and Singh *et al* 2014).

The MS due to the genotype × environment interaction effects were non-significant for 1000 seed weight and significant for rest of the traits. This indicated differential response of genotypes to change in the environment. However, 1000 seed weight of all genotypes responded similarly for change in the environment. The magnitude of MS attributed to the genotypes was much higher than the MS due to environments and the G × E interaction effects for all the traits. While evaluating 13 genotypes of chilli pepper at two locations, Dhaliwal *et al* (2014b) have reported significant G × E interactions for fruit weight, fruit length, number of seed fruit^{-1} and fruit yield plant^{-1}.

Average weekly day/ night temperature of the experimental site in E_1, E_2 and E_3 ranged from 13.0/ 4.9 to 42.6/ 29.2 °C with an average of 29.22/16.14 °C, from 24.2/ 11.7 to 42.6/ 29.2 °C with an average of 34.58/ 22.70 °C and from 32.2/ 18.0 to 42.6/ 29.2 °C with an average of 36.55/ 25.30 °C, respectively (APPENDIX II).

4.3.2 Analysis of variance for combining ability

The ANOVA for combining ability for 15 plant growth, yield and quality traits over three environments and pooled across the environments is presented in Table 4.8a-d. The total genetic variability was partitioned into the general combining ability (GCA) and the specific combining ability (SCA) effects. The ANOVA showed highly significant MS due to the parents, testers and crosses for all the traits studied over the three environments. The MS due to lines was non-significant for number of primary branches plant^{-1}, fruit width and 1000 seed weight in E_1, 1000 seed weight and total yield plant^{-1} in E_2 and plant height, plant spread, number of primary branches plnat^{-1} and 1000 seed weight in E_3, and significant for rest of the traits under the three environments.

The MS due to GCA lines were non-significant for number of primary branches plant^{-1} and number of seed fruit^{-1} in E_2, for plant height, plant spread and number of primary branches plant^{-1} in E_3, and significant for rest of the traits studied over the three environments. The MS due to GCA testers were significant for most of the traits studied except for number of primary branches plant^{-1} in E_1 and E_3. The MS due to SCA crosses were highly significant for all the traits studied over the three environments except for fruit width in E_2 and 1000 seed weight in E_2 and E_3. Significance of the MS due to GCA lines and GCA testers, and SCA crosses for all the traits studied indicated that both additive and non-additive types of gene action were involved in the genetic control of the traits.

The pooled ANOVA showed that the MS due to parents, testers and crosses were highly significant for all the traits studied. However, the MS due to lines were non-significant for number of primary branches plant^{-1} and 1000 seed weight, and significant for rest of the traits. The parent × environment interaction effects were non-significant for number of seed fruit^{-1} and 1000 seed weight, crosses × environments and line × tester × environment effects for 1000 seed weight, and significant for rest of the traits. This suggested that the performance of the parents and the crosses across the environments for most of the traits studied was influenced by the environment.

Through the diallel cross analysis, do Nascimento *et al* (2014) and Singh *et al* (2014) found significant differences due to GCA parents and SCA crosses for fruit weight, fruit length, fruit diameter, pericarp thickness and fruit yield plant^{-1}. Significant differences due to parent × environment and cross × environment have also been reported by Singh *et al* (2014). The GCA effects for lines were observed to be significant for all the traits except number of primary branches plant^{-1}. The GCA testers and SCA crosses were significant for all the plant growth, yield and quality traits studied. Evaluation of progenies over environments is, therefore, important to select parent and crosses suitable for specific environments and those stable over the environments.

4.3.3 Estimation of general combining ability (GCA) effects of parents

The success of any crop breeding program is highly dependent on right choice of parents. The genetic worth of any parent is estimated by comparing the *per se* performance and combining ability of the parents. Effects due to GCA are the result of simple additive nature of gene action or additive × additive interaction and can be fixed through selection. The parental lines which show significant positive values of GCA effects are considered as good general combiners and are used for breeding superior recombinants (Comstock *et al* 1949). Parents evaluated in the current study and identified with desirable GCA effects and superior *per se* performance could be used in breeding program for improvement of plant growth, yield and quality traits in chilli. In majority of the cases, good general combiners expressed better mean performance, indicating that the parents may be selected either on the basis of GCA estimates, mean performance or both. Parental means and GCA effects for plant growth, yield and quality traits over the three environments estimated through the line × tester analysis are given in Table 4.9a-o.

Table 4.7: Analysis of variance for the experimental design for plant growth, yield and quality traits in chilli over environments

Source of variance	df	Plant height (cm)	Plant spread (cm)	Number of primary branches plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)	Number of fruits plant^{-1}
E$_1$									
Replication	2	51.61	12.16	0.24	0.31	0.56	1.54	0.00	822.85
Genotypes	82	771.47**	267.08**	1.67**	16.38**	5.70**	11.95**	0.33**	7899.94**
Error	164	61.59	29.10	0.17	0.31	0.42	1.00	0.01	462.70
E$_2$									
Replication	2	3.48	7.42	0.50*	0.38	0.05	0.03	0.00	492.84
Genotypes	82	514.99**	242.91**	5.24**	13.63**	3.26**	3.82**	0.19**	12083.33**
Error	164	37.32	16.38	0.15	0.15	0.25	0.76	0.01	454.49
E$_3$									
Replication	2	4.59	1.70	0.19	0.29	0.02	0.24	0.00	42.72
Genotypes	82	273.57**	110.57**	3.69**	2.73**	3.10**	5.30**	0.16**	9670.97**
Error	164	26.37	15.44	0.24	0.12	0.22	0.53	0.00	137.24
Pooled									
Replication	2	28.19	9.50	0.83*	0.00	0.36	0.76	0.00	149.32
Genotypes	82	1164.47**	402.89**	4.73**	25.87**	9.17**	16.81**	0.51**	18797.27**
Environments	2	71455.23**	27597.61**	43.39**	204.53**	326.97**	646.98**	11.95**	1150129.25**
Genotypes × Environments	164	197.78**	108.83**	2.94**	3.44**	1.44**	2.13**	0.08**	5428.48**
Pooled error	492	41.76	20.31	0.19	0.19	0.30	0.76	0.01	351.48

Table 4.7 (*Cont'd.*)

Source of variance	**df**	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg.100g^{-1})**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
E$_1$								
Replication	2	3.98	0.07	0.00	60.62	0.44	0.00	2391698.0
Genotypes	82	709.01**	2.52**	0.24**	2900.95**	18.63**	0.09**	2240130560.0**
Error	164	20.03	0.14	0.01	25.84	0.33	0.00	12286826.0
E$_2$								
Replication	2	0.05	0.16	0.00	9.66	0.19	0.00	8673145.0
Genotypes	82	594.00**	2.55**	0.18**	3212.30**	20.78**	0.08**	1990282752.0**
Error	164	12.92	0.13	0.00	32.58	0.33	0.00	15341746.0
E$_3$								
Replication	2	11.59	0.10	0.00	9.79	0.20	0.00	22815460.0
Genotypes	82	516.37**	2.68**	0.08**	2735.74**	8.52**	0.07**	1743941120.0**
Error	164	9.68	0.14	0.00	25.26	0.20	0.00	17999746.0
Pooled								
Replication	2	9.09	0.09	0.00	12.49	0.45	0.00	6386744.0
Genotypes	82	1758.39**	7.73**	0.33**	7836.85**	38.77**	0.18**	4611280384.0**
Environments	2	18867.34**	14.12**	13.74**	34045.07**	744.37**	1.31**	33479694336.0**
Genotypes × Environments	164	30.49**	0.01	0.08**	506.07**	4.59**	0.03**	681537152.0**
Pooled error	492	14.21	0.13	0.00	27.89	0.29	0.00	15209439.0

Data's are mean sums of squares; *significant at *p*=0.05; **significant at *p*=0.01

Table 4.8a: Analysis of variance for combining ability in line × tester design for plant growth, yield and quality traits in chilli under E_1

Source of variance	df	Plant height (cm)	Plant spread (cm)	Number of primary branches plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)	Number of fruits plant^{-1}
Parents	22	617.86**	130.18**	0.89**	16.57**	6.65**	14.35**	0.44**	6662.05**
Lines	2	927.03**	93.84*	0.16	8.13**	3.46**	2.52	0.12**	5243.06**
Testers	19	611.59**	140.70**	0.89**	17.47**	5.64**	14.65**	0.47**	6735.15**
Crosses	59	598.68**	212.96**	1.63**	16.49**	5.00**	10.86**	0.29**	7637.91**
Lines vs Testers	1	118.64	2.99	2.22**	16.30**	32.32**	32.30**	0.55**	8111.23**
Parents vs Crosses	1	14345.32**	6471.80**	20.99**	5.85**	25.73**	23.21**	0.05*	50593.39**
GCA lines	2	6236.26**	2628.74**	11.90**	246.37**	44.17**	90.26**	4.09**	14112.10**
GCA testers	19	955.68**	211.44**	1.64	18.10**	8.32**	19.72**	0.35**	18618.25**
SCA crosses	38	123.47**	86.58**	1.09**	3.58**	1.28**	2.26**	0.06**	1806.98**
Error	164	61.59	29.10	0.17	0.31	0.42	1.00	0.01	462.70

Table 4.8a (*Cont'd.*)

Source of variance	**df**	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg 100^{-1} g)**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
Parents	22	417.04**	3.59**	0.11**	3300.57**	6.99**	0.08**	2027265920.00**
Lines	2	154.90**	0.04	0.02*	1204.64**	2.07**	0.01**	295563392.00**
Testers	19	449.68**	4.05**	0.11**	3263.61**	7.44**	0.09**	2311625472.00**
Crosses	59	607.93**	2.11**	0.23**	2721.66**	20.00**	0.08**	2081867008.00**
Lines vs Testers	1	321.34**	1.82**	0.18**	8194.76**	8.12**	0.00**	87839912.00**
Parents vs Crosses	1	13096.28**	3.27**	3.55**	4687.59**	193.96**	0.64**	16260703232.00**
GCA lines	2	741.54**	3.39**	1.27**	4668.16**	19.56*	0.14**	3640065024.00**
GCA testers	19	1551.18**	5.76**	0.47**	7205.40**	49.46**	0.20**	5181727232.00**
SCA crosses	38	129.27**	0.21*	0.05**	377.34**	5.29**	0.02**	449926528.00**
Error	164	20.03	0.14	0.01	25.84	0.33	0.00	12286826.00

Data's are mean sums of squares; *significant at p=0.05; **significant at p=0.01

Table 4.8b: Analysis of variance for combining ability in line × tester design for plant growth, yield and quality traits in chilli E_2

Source of variance	df	Plant height (cm)	Plant spread (cm)	Number of primary branches plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)	Number of fruits plant^{-1}
Parents	22	306.44**	211.72**	3.46**	17.35**	5.79**	4.33**	0.27**	4507.58**
Lines	2	285.52**	81.42**	1.16**	6.32**	3.29**	5.52**	0.05**	2300.06**
Testers	19	313.49**	226.39**	3.88**	18.85**	6.09**	4.36**	0.30**	4596.46**
Crosses	59	523.83**	207.88**	5.10**	12.48**	2.23**	3.17**	0.16**	11628.90**
Lines vs Testers	1	214.47*	193.55**	0.01	10.83**	5.23**	1.31	0.03*	7233.89**
Parents vs Crosses	1	4581.27**	2995.85**	52.93**	0.18	8.24**	31.37**	0.31**	205561.38**
GCA lines	2	680.06*	943.31**	4.74	81.62**	9.48**	38.58**	0.57**	72264.62**
GCA testers	19	1197.15**	334.40**	7.53*	23.30**	4.75**	4.23**	0.34**	14426.97*
SCA crosses	38	178.94**	105.91**	3.90**	3.43**	0.59**	0.77	0.05**	7038.51**
Error	164	37.32	16.38	0.15	0.15	0.25	0.76	0.01	454.49

Table 4.8b (*Cont'd.*)

Source of variance	**df**	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg 100^{-1} g)**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
Parents	22	394.55**	3.52**	0.05**	3727.00**	11.32**	0.08**	2078196096.00**
Lines	2	203.68**	0.03	0.00	1124.52**	4.42**	0.02**	394126688.00**
Testers	19	419.92**	3.98**	0.05**	3691.91**	12.60**	0.09**	2362548480.00**
Crosses	59	504.25**	2.16**	0.18**	2940.31**	20.50**	0.07**	1757225856.00**
Lines vs Testers	1	294.19**	1.94**	0.02**	9598.62**	0.78	0.00	43637440.00
Parents vs Crosses	1	10277.30**	3.68**	3.01**	7936.25**	245.72**	0.54**	13806545920.00**
GCA lines	2	271.15	3.10**	0.58**	1047.69	17.17*	0.04**	1035555264.00**
GCA testers	19	1333.18**	6.01**	0.38**	8345.06**	52.32**	0.20**	5076744192.00**
SCA crosses	38	102.05**	0.19	0.06**	337.55**	4.77**	0.01**	135449328.00**
Error	164	12.92	0.13	0.00	32.58	0.33	0.00	15341746.00

Data's are mean sums of squares; *significant at *p*=0.05; **significant at *p*=0.01

Table 4.8c: Analysis of variance for combining ability in line × tester design for plant growth, yield and quality traits in chilli E_3

Source of variance	df	Plant height (cm)	Plant spread (cm)	Number of primary branches plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)	Number of fruits plant^{-1}
Parents	22	172.37**	90.46**	1.68**	2.70**	3.76**	7.01**	0.24**	5734.01**
Lines	2	71.33	19.30	0.46	1.97**	2.36**	5.83**	0.03**	983.50**
Testers	19	189.36**	100.32**	1.80**	2.80**	3.77**	7.41**	0.24**	6531.28**
Crosses	59	253.39**	89.11**	3.58**	2.74**	2.83**	4.67**	0.13**	9561.35**
Lines vs Testers	1	51.74	45.47	1.68**	2.25**	6.25**	1.71	0.51**	87.07
Parents vs Crosses	1	3690.97**	1818.87**	54.69**	2.24**	4.87**	4.73**	0.01	102751.78**
GCA lines	2	405.38	34.91	0.96	30.07**	18.05**	37.21**	0.40**	15661.70*
GCA testers	19	480.83**	192.91**	5.08	3.74**	4.49**	8.59**	0.29**	19813.29**
SCA crosses	38	131.67**	40.06**	2.97**	0.81**	1.19**	1.00**	0.03**	4114.31**
Error	164	26.37	15.44	0.24	0.12	0.22	0.53	0.00	137.24

Table 4.8c (*Cont'd.*)

Source of variance	**df**	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg 100^{-1} g)**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
Parents	22	402.14**	3.62**	0.05**	3074.70**	6.11**	0.07**	1882922880.00**
Lines	2	161.44**	0.02	0.03**	1146.03**	1.35**	0.01**	334370144.00**
Testers	19	434.86**	4.09**	0.05**	3042.40**	6.69**	0.08**	2143960960.00**
Crosses	59	450.70**	2.31**	0.07**	2526.63**	8.13**	0.06**	1577946368.00**
Lines vs Testers	1	261.81**	1.92**	0.00	7545.72**	4.68**	0.00	20302804.00
Parents vs Crosses	1	6903.46**	3.84**	0.70**	7615.95**	85.10**	0.33**	8480034816.00**
GCA lines	2	248.91**	3.73**	0.10**	2823.61**	20.58**	0.15**	3950941952.00**
GCA testers	19	1303.01**	6.40**	0.18**	7053.58**	20.86**	0.16**	4035913984.00**
SCA crosses	38	35.17**	0.19	0.02**	247.53**	1.10**	0.01**	224068112.00**
Error	164	9.68	0.14	0.00	25.26	0.20	0.00	17999746.00

Data's are mean sums of squares; *significant at *p*=0.05; **significant at *p*=0.01

Table 4.8d: Analysis of variance for combining ability in line × tester design for plant growth, yield and quality traits in chilli over environment

Source of variance	df	Plant height (cm)	Plant spread (cm)	Number of primary branches plant^{-1}	Fruit weight (g)	Fruit length (cm)	Fruit width (mm)	Pericarp thickness (mm)	Number of fruits plant^{-1}
Parents	22	821.60**	278.65**	2.26**	30.96**	13.39**	20.26**	0.76**	10640.21**
Lines (L)	2	714.71**	160.55**	0.39	14.61**	8.40**	13.35**	0.19**	2203.60**
Testers (T)	19	875.88**	304.36**	2.44**	32.94**	12.70**	21.45**	0.81**	11606.10**
Crosses	59	963.98**	277.39**	3.64**	24.34**	7.17**	14.91**	0.42**	16520.55**
Lines vs Testers	1	3.95	26.39	2.43**	25.97**	36.55**	11.40**	0.90**	9161.37**
Parent vs Crosses	1	20536.14**	10541.18**	123.55**	4.05**	34.34**	52.87**	0.15**	332578.91**
GCA lines	2	4885.65**	2470.83**	4.38	293.22**	62.50**	157.26**	3.69**	64455.76**
GCA testers	19	2124.28**	465.68**	6.61**	36.78**	13.58**	25.95**	0.81**	33928.28**
SCA crosses	38	177.43**	67.79**	2.12**	3.96**	1.06**	1.89**	0.05**	5293.79**
Parents × Environments	44	137.54**	76.85**	1.88**	2.83**	1.41**	2.71**	0.09**	3131.72**
Crosses × Environments	118	205.96**	116.28**	3.33**	3.69**	1.44**	1.90**	0.08**	6153.80**
L × T × Environments effects	76	128.32**	82.38**	2.92**	1.93**	1.01**	1.07*	0.05**	3833.01**
Pooled error	492	41.76	20.31	0.19	0.19	0.30	0.76	0.01	351.48

Table 4.8d (*Cont'd.*)

Source of variance	**d.f.**	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg 100^{-1} g)**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
Parents	22	1201.75**	10.73**	0.13**	9107.72**	19.16**	0.17**	4348357120.00**
Lines (L)	2	509.46**	0.09	0.03**	3470.72**	6.20**	0.04**	970141760.00**
Testers (T)	19	1291.78**	12.11**	0.14**	8850.18**	21.23**	0.19**	4925458432.00**
Crosses	59	1490.99**	6.56**	0.30**	7157.17**	38.22**	0.16**	4145440768.00**
Lines vs Testers	1	875.80**	5.69**	0.03**	25275.03**	5.68**	0.01**	139865056.00**
Parent vs Crosses	1	29781.01**	10.77**	6.62**	19979.10**	502.52**	1.48**	37880111104.00**
GCA lines	2	1172.24**	10.21**	1.27**	7027.66**	25.45*	0.31**	7872519168.00**
GCA testers	19	4098.92**	18.14**	0.71**	20473.27**	104.71**	0.45**	11402295296.00**
SCA crosses	38	203.80**	0.57**	0.05**	505.93**	5.64**	0.01**	320851680.00**
Parents × Environments	44	5.99	0.004	0.04**	497.27**	2.63**	0.03**	820013888.00**
Crosses × Environments	118	35.95**	0.01	0.09**	515.72**	5.20**	0.02**	635799232.00**
L × T × Environments effects	76	31.35**	0.01	0.04**	228.25**	2.76**	0.01**	244296144.00**
Pooled error	492	14.21	0.13	0.00	27.89	0.29	0.00	15209439.00

Data's are mean sums of squares; *significant at *p*=0.05; **significant at *p*=0.01

4.3.3.1 Plant height (cm)

The plant height of CMS lines varied from 64.83 cm (CMS4626A) to 98.57 cm (CMS463D13A) in E_1, from 65.09 cm (CMS4626A) to 84.60 cm (CMS4611A) in E_2, from 46.57 cm (CMS4626A) to 55.52 cm (CMS463D13A) in E_3 and from 58.83 cm (CMS4626A) to 76.27 cm (CMS463D13A) when pooled across the environments. The mean performance of the testers ranged from 55.18 cm (FL 201) to 112.04 cm (IS 262) in E_1, from 50.06 cm (YL 581) to 86.23 cm (PL 412) in E_2, from 37.81 cm (FL 201) to 68.12 cm (C 142) in E_3 and from 49.43 cm (FL 201) to 85.35 cm (C 142) across the environments (Table 4.9a). Eight parents (one CMS line and seven testers) exhibited significant positive and eight parents (one CMS line and seven testers) showed significant negative GCA effects in E_1, 10parents (two CMS lines and eight testers) have shown significant positive values and six parents (one CMS line and five testers) exhibited significant negative GCA values in E_2, 10 parents (one CMS line and nine testers) showed significant positive and eight parents (one CMS line and seven testers) exhibited significant negative GCA values in E_3 and 10 (one CMS line and nine testers) and nine (one CMS line and eight testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for plant height ranged from -9.43 (CMS4626A) to 10.82 (CMS463D13A) in E_1, from -3.87 (CMS4626A) to 2.25 (CMS463D13A) in E_2, from -2.98 (CMS4626A) to 1.82 (CMS463D13A) in E_3 and from -5.43 (CMS4626A) to 4.96 (CMS463D13A) over the three environments. The GCA effects of testers for plant height varied from -16.63 (FL 201) to 18.44 (IS 268) inE_1, from -23.97 (AC 102) to 22.29 (IS 268) inE_2, from -14.47 (AC 102) to 10.32 (SL 475) in E_3 and from -17.08 (AC 102) to 16.50 (IS 268) across the environments.

The results illustrated that among the CMS lines, CMS463D13A exhibited the highest GCA estimates for plant height in E_1, E_2, E_3 and across the environments. Among the testers, IS 268 was found to be the best general combiner for plant height with the highest GCA estimates followed by PL 406, PL 412 and IS 267 in E_1, IS 268 followed by PL 412, SL 475 and C 142 in E_2, SL 475 followed by IS 261, IS 268 and C 142 in E_3. Over the environments, the testers IS 268 followed by PL 412, C 142 and PL 406 were regarded as the good general combiners for plant height. Among the CMS lines, CMS463D13A and among the testers IS 268, C 142, PL 406, IS 267 and VR 521 performed consistently superior across the environments in respect of both the positive GCA effects and the *per se* performances. Therefore, these parental lines could be involved in hybrid breeding program to obtain genotypes with higher plant height.

The CMS line CMS4626A showed the significant negative GCA effects for plant height in E_1, E_2, E_3 and pooled across the environments. The tester E 183 exhibited the significant negative GCA estimates followed by VR 521, IS 263 and PP 414 in E_1, AC 102 followed by YL 581, DL 161 and FL 201 in E_2, AC 102 followed by DL 161, IS 262 and YL 581 in E_3 and AC 102 followed by DL 161, FL 201 and YL 581 across the environments. These parents can be recommended in crosses to breed for smaller plant stature. Plants with such phenotype have a great commercial value in chilli as they tend to be early in maturity.

Earlier, the parent PBC 972 was identified as good general combiner for plant height by Legesse (2000), Chickballapur by Lohithaswa *et al* (2000), ACMS-4 by Patel *et al* (2004), CB 38 by do Rego *et al* (2009), CCA 2 by Hasanuzzaman *et al* (2012), UENF 1639 by Rodrigues *et al* (2012), CC 141 by Singh *et al* (2014), BCCH Sel-4 by Bhutia *et al* (2015), and UFPB 132 by Ferreira *el al* (2015).

4.3.3.2 Plant spread (cm)

For plant spread, the mean values of CMS lines ranged from 51.60 cm in CMS4626A to 62.78 cm in CMS463D13A under E_1, from 45.58 cm in CMS4626A to 55.26 cm in CMS4611A under E_2, from 34.42 cm in CMS4626A to 39.14 cm in CMS463D13A under E_3 and from 43.87 cm in CMS4626A to 51.89 cm in CMS463D13A across the three environments. The mean performance of the testers varied from 44.59 cm (IS 268) to 72.22 cm (IS 261) in E_1, from 30.27 cm (YL 581) to 57.97 cm (VR 522) in E_2, from 28.38 cm (FL 201) to 48.12 cm (PL 406) in E_3 and from 37.47 cm (IS 268) to 58.07 cm (IS 261) across the environments (Table 4.9b). Seven parents (one CMS line and six testers) exhibited significant positive and six parents (one CMS line and five testers) showed significant negative GCA effects in E_1, seven parents (two CMS lines and five testers) had shown significant positive values and seven parents (one CMS line and six testers) exhibited significant negative GCA values in E_2, five parents (all testers) showed significant positive and eight parents (all testers) exhibited significant negative GCA values in E_3 and six (one CMS line and five testers) and nine (one CMS line and eight testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines ranged from -6.53 in CMS4626A to 6.70 in CMS463D13A under E_1, from -4.50 in CMS4626A to 2.99 in CMS463D13A under E_2, from -0.57 in CMS4626A to 0.87 in CMS463D13A under E_3 and from -3.87 in CMS4626A to 3.52 in CMS463D13A over the environments. The GCA effects of testers varied from -8.64 in VR 522 to 7.41 in IS 261 under E_1, from -8.64 in E 183 to 12.89 in SL 475 under E_2, from -7.16 in E 183 to 9.58 in SL 475 under E_3 and from -5.89 in IS 262 to 9.20 in IS 261 across the environments.

Among the lines, CMS463D13A showed the highest GCA estimates for plant spread in E_1, E_2, E_3, and over the environments. Among the testers, IS 261 was found to be the best general combiner with the highest GCA effects followed by VR 523, PL 412 and PL 406 in

E_1, SL 475 followed by IS 261, VR 522 and VR 523 in E_2, SL 475 followed by IS 261, PL 406 and VR 521 in E_3 and IS 261 followed by SL 475, VR 523 and PL 406 were the good general combiners over the environments. Among the parents, the testers IS 261, VR 523 and PL 406 performed consistently superior across the environments in respect of GCA effects and *per se* performance for plant spread. Thus, these parents can be used in hybrid breeding program to generate recombinants with wider plant spread. do Rego *et al* (2009) identified CB 4, CB 24, CB 58 and CB 38 as good combiners for plant spread. Singh *et al* (2014) from a half-diallel analysis involving CGMS and GMS lines reported that the lines CC 141, SD 463 and PP 402 have good GCA effects for plant spread.

The line CMS4626A expressed significantly negative GCA estimates in E_1, E_2 and pooled across the environments. The tester VR 522 had the significant negative GCA values. This was followed by IS 262, PP 402 and VR 521 in E_1, E 183 followed by YL 581, VR 521 and IS 262 in E_2, E 183 followed by PP 414, IS 262 and AC 102 in E_3 and IS 262 followed by E 183, PP 414 and PP 402 across the three environments. These parents can be used in crosses to breed for compact plant types. Such plant phenotypes are desirable for early maturity and high density planting and indirectly contributing to the higher yields.

4.3.3.3 Number of primary branches plant^{-1}

The CMS lines CMS4611A and CMS4626A (3.56) recorded minimum number of primary branches plant^{-1} in E_1, CMS4626A (4.05) in E_2, CMS463D13A (3.68) in E_3 and CMS4626A (4.0) over the three environments, while the maximum number of primary branches plant^{-1} was observed in CMS463D13A (3.96) under E_1, CMS4611A (5.30) under E_2, CMS4626A (4.38) under E_3 and CMS4611A (4.40) across the three environments. Mean performance of the testers ranged from 3.22 in C 142 to 5.27 in PL 406 under E_1, from 2.67 in PP 414 to 7.01 in E 183 under E_2, from 3.56 in PL 412 to 6.49 in YL 581 under E_3 and from 3.68 in IS 263 to 5.69 in YL 581 across the environments (Table 4.9c). Four (one CMS line and three testers) and eight parents (one CMS line and seven testers) in E_1, eight (one CMS line and seven testers) and 10 (one CMS line and nine testers) parents in E_2, five (one CMS line and four testers) and seven (all testers) parents in E_3 and 11 (two CMS lines and nine testers) and nine (one CMS line and eight testers) parents across the environments exhibited significant positive and negative GCA effects, respectively. The GCA effects of CMS lines for number of primary branches plant^{-1} varied from -0.41 in CMS4626A to 0.47 in CMS463D13A under E_1, from -0.26 in CMS4626A to 0.30 in CMS4611A under E_2, from -0.11 in CMS463D13A to 0.14 in CMS4626A under E_3 and from -0.18 in CMS4626A to 0.11 in CMS463D13A across the environments. The GCA effects of testers ranged from -0.44 in IS 268 to 1.25 in PL 406 under E_1, from -1.11 in AC 102 to 2.20 in VR 523 under E_2, from -

1.30 in IS 262 to 1.35 in VR 521 under E_3 and from -0.81 in SL 473 to 0.86 in SL 475 over the environments.

The highest positive values of GCA for number of primary branches plant^{-1} was recorded by CMS463D13A in E_1, by CMS4611A in E_2, by CMS4626A in E_3 and by CMS463D13A across the environments. Among the testers, PL 406 was found to be the best general combiner for number of primary branches plant^{-1} with the highest GCA effects followed by IS 267 and DL 161 in E_1, VR 523 followed by SL 475, E 183 and IS 268 in E_2, VR 521 followed by SL 475, PP 402 and PL 406 in E_3 and SL 475 followed by VR 523, PL 406 and VR 521 when means were pooled over the environments. Patel *et al* (2004) reported ACS 92-3, and Prasath and Ponnuswami (2008) reported Arka Lohit as good combiner for number of primary branches palnt^{-1}.

4.3.3.4 Fruit weight (g)

The fruit weight of CMS lines ranged from 2.82 g in CMS4611A to 6.05 g in CMS463D13A under E_1, from 2.73 g in CMS4611A to 5.55 g in CMS463D13A under E_2, from 2.83 g in CMS4611A to 4.42 g in CMS463D13A under E_3 and from 2.79 g in CMS4611A to 5.34 g in CMS463D13A over the three environments. The means of testers varied from 2.02 g in VR 521 to 12.81 g in FL 201 under E_1, from 1.41 g in VR 521 to 12.50 g in FL 201 underE_2, from 2.68 g in VR 521 to 7.25 g in FL 201 under E_3 and from 2.04 g in VR 521 to 10.85 g in FL 201 across the environments (Table 4.9d). Nine parents (one CMS line and eight testers) showed significant positive and eight parents (two CMS lines and six testers) exhibited significant negative GCA effects in E_1, eight parents (two CMS lines and six testers) had shown significant positive values and 12 parents (one CMS line and 11 testers) exhibited significant negative GCA values in E_2, 10 parents (two CMS lines and eight testers) showed significant positive and eight parents (one CMS line and seven testers) exhibited significant negative GCA values in E_3 and nine (one CMS line and eight testers) and 10 (one CMS line and nine testers) parents have shown significant positive and negative GCA values, respectively across the three environments. The GCA effects of CMS lines varied from -1.83 in CMS4611A to 2.18 in CMS463D13A under E_1, from -1.26 in CMS4611A to 1.04 in CMS463D13A under E_2, from -0.80 in CMS4611A to 0.55 in CMS463D13A under E_3 and from -1.29 in CMS4611A to 1.26 in CMS463D13A over the environments. The GCA effects of testers ranged from -2.33 in VR 521 to 2.80 in PP 402 under E_1, from -2.90 in VR 521 to 3.06 in PP 402 under E_2, from -1.11 in VR 521 to 1.01 in PP 402 under E_3 and from -2.11 in VR 521 to 2.29 in PP 402 over the three environments.

Under E_1, E_2, E_3 and over the environments the CMS line CMS463D13A showed the highest positive values of GCA for fruit weight. The tester PP 402 was found to be the best general combiner for fruit weight with the highest GCA effects followed by FL 201, YL 581, IS 268 and VR 522 in E_1, PP 402 followed by FL 201, IS 261, IS 268 and YL 581 in E_2, PP 402 followed by FL 201, VR 523, SL 475 and YL 581 in E_3 and PP 402 followed by FL 201, YL 581, IS 268 and SL 475 were the superior general combiners across the environments. The CMS line CMS463D13A and testers PP 402, FL 201, YL 581, IS 268 and SL 475 performed consistently superior across the environments in respect of GCA effects and *per se* performance. Involving these parents in hybridization would be result in the identification of superior cross-combinations with higher fruit weight. Parent Mareko Fana was identified as good general combiner for fruit weight by Legesse (2000), Pepper 1976 by Geleta and Labuschagne (2006a), MDU Y by Prasath and Ponnuswami (2008), CB 24 and CB 50 by do Rego *et al* (2009), UFPB 137 and UFPB 132 by do Nascimento *et al* (2014), UENF 1629 and UENF 1616 by Medeiros *et al* (2014), and SD 463 and PP 402 by Singh *et al* (2014).

4.3.3.5 Fruit length (cm)

The CMS line CMS463D13A produced the largest fruit in E_1 (6.98 cm), E_2 (6.65 cm), E_3 (6.13 cm) and over the three environments (6.59 cm). The CMS4611A produced the smallest fruit with the mean values of 4.89 cm, 4.70 cm, 4.37 cm and 4.65 cm under E_1, E_2, E_3 and across the environments, respectively. The fruit length of testers ranged from 5.93 cm in VR 521 to 12.17 cm in FL 201 under E_1, from 3.83 cm in VR 521 to 10.67 cm in FL 201 under E_2, from 4.61 cm in IS 263 to 9.49 cm in FL 201 under E_3 and from 4.85 cm in VR 521 to 10.77 cm in FL 201 across the environments (Table 4.9e). Seven (one CMS line and six testers) and eight parents (one CMS line and seven testers) under E_1, seven (one CMS line and six testers) and eight (one CMS line and seven testers) parents under E_2, 10 (two CMS lines and eight testers) and eight (one CMS line and seven testers) parents under E_3 and 11 (one CMS line and 10 testers) and nine (one CMS line and eight testers) parents over the three environments showed significant positive and negative GCA values, respectively. The GCA estimates of CMS lines for fruit length ranged from -0.85 in CMS4611A to 0.87 in CMS463D13A under E_1, from -0.38 in CMS4611A to 0.41 in CMS463D13A under E_2, from -0.63 in CMS4611A to 0.38 in CMS463D13A under E_3 and from -0.62 in CMS4611A to 0.55 in CMS463D13A over the environments. The GCA effects of testers varied from -1.70 in E 183 to 2.20 in FL 201 under E_1, from -1.34 in E 183 to 1.21 in FL 201 under E_2, from -1.42 in IS 263 to 1.08 in SL 475 under E_3 and from -1.21 in E 183 to 1.29 in FL 201 across the environments.

Among the lines, CMS463D13A showed the highest positive values of GCA for fruit length under E_1, E_2, E_3 and over the environments. Among the testers, FL 201 had the highest GCA values, and was therefore, adjudged to be the best general combiner. This was followed by SL 475, IS 261 and VR 523 under E_1, FL 201 followed by SL 475, IS 261 and YL 581 under E_2, SL 475 followed by YL 581, VR 523 and VR 522 under E_3 and FL 201 followed by SL 475, IS 261 and YL 581 over the environments. The CMS line CMS463D13A and the testers FL 201, SL 475, IS 261 and PL 412 performed consistently superior across the environments in respect of GCA effects and *per se* performance. These parents can be utilized for the development of true breeding lines with long fruits. Patel *et al* (2004) from a line × tester analysis reported ACMS 4 among the lines and ACS 2000-02 among the testers as the good general combiners for fruit length. Geleta and Labuschagne (2006a) from diallel cross analysis reported that parents Bakko Local and Mareko Shote were good combiners for fruit length. Prasath and Ponnuswami (2008) identified parents MDU Y and Bydagi Kaddi, do Rego *et al* (2009) identified CB 24, do Nascimento *et al* (2014) identified UFPB 132, Medeiros *et al* (2014) identified UENF 1629 and UENF 1616, Bhutia *et al* (2015) identified BCCH Sel-4, and Naresh *et al* (2016) identified IHR 4507 and IHR 3849 as good general combiners for fruit length.

The line CMS4611A exhibited the significant negative values of GCA for fruit length in E_1, E_2, E_3 and pooled across the environments. The tester E 183 have shown significant negative GCA effects followed by VR 521, PP 414 and SL 473 in E_1, E 183 followed by DL 161, AC 102 and SL 473 in E_2, IS 263 and VR 521, AC 102 and IS 262 in E_3 and E 183 followed by VR 521, IS 263 and AC 102 across the environments. These parents can be utilized in hybrid breeding to develop genotypes with short fruited chilli suitable for processing by the spice pepper industry for the production of dehydrated products.

4.3.3.6 Fruit width (mm)

The CMS line CMS4611A recorded minimum fruit width under E_1 (9.70 mm), E_2 (9.0 mm), E_3 (7.95 mm) and over the three environments (8.88 mm). The maximum fruit width was observed by CMS463D13A with the mean values of 11.53 mm in E_1, 11.71 mm in E_2, 10.70 mm in E_3 and 11.31 mm across the environments. Mean performance of the testers ranged from 8.26 mm in VR 521 to 18.48 mm in FL 201 under E_1, from 6.92 mm in VR 521 to 13.16 mm in FL 201 under E_2, from 6.66 mm in VR 521 to 12.93 mm in FL 201 under E_3 and from 7.28 mm in VR 521 to 14.85 mm in FL 201 across the environments (Table 4.9f). Eight parents (one CMS line and seven testers) showed significant positive and seven parents (one CMS line and six testers) exhibited significant negative GCA effects in E_1, six parents (one CMS line and five testers) had shown significant positive values and four (one CMS line and three testers) exhibited significant negative GCA values in E_2, seven parents (two CMS lines and five testers) showed significant positive and six parents (one CMS line and five testers) exhibited significant negative GCA values in E_3 and seven (two CMS lines and five testers) and eight (one CMS line and seven testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for fruit width varied from -1.30 in CMS4611A to 1.14 in CMS463D13A under E_1, from -0.81 in CMS4611A to 0.79 in CMS463D13A under E_2, from -0.88 in CMS4611A to 0.64 in CMS463D13A under E_3 and from -1.0 in CMS4611A to 0.86 in CMS463D13A over the three environments. The GCA estimates of testers ranged from -2.50 in VR 521 to 2.56 in PP 402 under E_1, from -1.57 in VR 521 to 1.21 in PP 402 under E_2, from -1.76 in VR 521 to 2.01 in YL 581 under E_3 and from -1.94 in VR 521 to 1.72 in PP 402 across the environments.

Under E_1, E_2, E_3 and across the environments the CMS line CMS463D13A showed the highest positive values of GCA for fruit width. Among the testers, PP 402 was found to be the best general combiner for fruit width with the highest GCA effects followed by YL 581, FL 201, IS 268 and IS 262 in E_1, PP 402 followed by FL 201, IS 268, IS 267 and YL 581 in E_2, YL 581 followed by PP 402, IS 268, FL 201 and PL 406 in E_3 and PP 402 followed by YL 581, FL 201, IS 268 and SL 473 were the good general combiners over the environments. Among the line CMS463D13A and among the testers PP 402, YL 581, FL 201 and IS 268 performed consistently superior across the environments in respect of GCA effects and *per se* performances. These parents may be exploited in hybrid breeding program for increasing fruit width. Prasath and Ponnuswami (2008) reported the parents MDU Y and Bydagi Kaddi, Rodrigues *et al* (2012) observed UENF 1639 and UENF 1732, do Nascimento *et al* (2014) reported UFPB 137, Medeiros *et al* (2014) observed UENF 1639 and UENF 1732, and Singh *et al* (2014) reported PP 402 and US 501 with significant positive GCA effects for fruit width.

4.3.3.7 Pericarp thickness (mm)

The pericarp thickness of CMS lines varied from 0.80 mm to 1.20 mm in E_1, from 0.84 mm to 1.10 mm in E_2, from 0.49 mm to 0.70 mm in E_3 and from 0.71 mm to 1.0 mm across the environments. The CMS line CMS463D13A and CMS4611A recorded maximum and minimum pericarp thickness, respectively under all the three environments. The means of testers ranged from 0.71 mm in VR 521 to 2.21 mm in FL 201 under E_1, from 0.61 mm in VR 521 to 1.84 mm in FL 201 under E_2, from 0.50 mm in VR 521 to 1.69 mm in FL 201 under E_3 and from 0.61 mm in VR 521 to 1.92 mm in FL 201 across the environments (Table 4.9g). Eight (one CMS line and seven testers) and 10 (two CMS lines and eight testers) parents in E_1, seven (one CMS line and six testers) and 11 (two CMS lines and nine testers) parents in E_2, nine (two CMS lines and seven testers) and 11 (one CMS line and 10 testers) parents in E_3 and eight (one CMS line and seven testers) and 11 (two CMS lines and nine testers) parents across the environments exhibited significant positive and negative GCA effects, respectively. The GCA effects of CMS lines for pericarp thickness ranged from -0.22 in CMS4611A to

0.29 in CMS463D13A in E_1, from -0.06 in CMS4611A to 0.11 in CMS463D13A in E_2, from -0.09 in CMS4611A to 0.07 in CMS463D13A in E_3 and from -0.12 in CMS4611A to 0.16 in CMS463D13A over the environments. The GCA estimates of testers varied from -0.34 in VR 521 to 0.45 in PP 402 under E_1, from -0.26 in IS 262 to 0.49 in FL 201 under E_2, from -0.28 in VR 521 to 0.28 in FL 201 under E_3 and from -0.28 in VR 521 to 0.29 in YL 581 and FL 201 across the environments.

The results illustrated that among the CMS lines, CMS463D13A expressed the highest GCA estimates for pericarp thickness in E_1, E_2, E_3 and across the environments. Among the testers, PP 402 was found to be the best general combiner for pericarp thickness with the highest GCA estimates followed by YL 581, SL 475, IS 268 and FL 201 in E_1, FL 201 followed by YL 581, PP 402, SL 475 and IS 267 in E_2, FL 201 followed by YL 581, IS 268, SL 475 and VR 523 in E_3. Over the environments, the tester YL 581 followed by FL 201, PP 402, SL 475 and IS 268 were regarded as the good general combiners for pericarp thickness. Among the CMS lines, CMS463D13A and among the testers YL 581, FL 201, PP 402 and SL 475 performed consistently superior across the environments in respect of both the GCA effects and the *per se* performances. These parents can be involved in hybrid breeding programs to develop the cultivars of chilli with thicker pericarp. From a diallel analysis, Geleta and Labuschagne (2006a) identified the parents Pepper 1976 and Kalocsai "M" as the good combiner for pericarp thickness, do Rego *et al* (2009) identified CB 50, CB 4 and CB 24, Khalil and Hatem (2014) identified Big Dipper, Pandey and Chura (2014) identified 09/Cvar 4, and Singh *et al* (2014) identified SD 463 and PP 402 as good general combiner for pericarp thickness.

The CMS line CMS4611A exhibited highest significant negative values of GCA for pericarp thickness in E_1, E_2, E_3 and across the environments. The tester VR 521 showed maximum significant negative GCA effects followed by E 183, DL 161 and IS 263 in E_1, IS 262 followed by VR 521, E 183 and PP 414 in E_2, VR 521 followed by E 183, SL 473 and IS 263 in E_3 and VR 521 followed by E 183, AC 102 and IS 263 across the environments. These parents can be used as a donor parent to develop genotypes with thinner pericarp in chilli. Chilli with thin pericarp is facilitate quick drying and therefore, is desirable for processing into powder.

4.3.3.8 Number of fruits plant^{-1}

The number of fruits plant^{-1} produced by the CMS lines ranged from 216.49 in CMS463D13A to 296.34 in CMS4626A under E_1, from 178.25 in CMS463D13A to 233.63 in CMS4611A under E_2, from 79.69 in CMS4611A to 113.06 in CMS463D13A under E_3 and from 169.27 in CMS463D13A to 197.07 in CMS4611A across the environments. Mean performance of the testers varied from 144.97 in E 183 to 303.21 in PP 414 under E_1, from

93.32 in PP 402 to 253.71 in VR 521 under E_2, from 34.38 in FL 201 to 207.56 in VR 523 under E_3 and from 95.89 in PP 402 to 227.74 in DL 161 across the environments (Table 4.9h). Nine parents (one CMS line and eight testers) exhibited significant positive and 10 parents (one CMS line and nine testers) showed significant negative GCA effects in E_1, 10 parents (two CMS lines and eight testers) had shown significant positive values and seven parents (one CMS line and six testers) exhibited significant negative GCA values in E_2, seven parents (one CMS line and six testers) showed significant positive and 11 parents (two CMS lines and nine testers) exhibited significant negative GCA values in E_3 and 10 (two CMS lines and eight testers) and seven (one CMS line and six testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for number of fruits plant^{-1} ranged from -14.65 in CMS463D13A to 15.94 in CMS4611A under E_1, from -39.31 in CMS463D13A to 26.38 in CMS4626A under E_2, from -9.75 in CMS4626A to 18.65 in CMS4611A under E_3 and from -20.95 in CMS463D13A to 15.84 in CMS4611A over the environments. The GCA effects of testers varied from -81.07 in E 183 to 89.96 in DL 161 under E_1, from -75.55 in E 183 to 72.91 in PL 412 under E_2, from -72.0 in FL 201 to 106.01 in DL 161 under E_3 and from -61.71 in E 183 to 74.99 in DL 161 across the environments.

The highest positive values of GCA for number of fruits plant^{-1} was recorded by CMS4611A in E_1, E_3 and across the environments and by CMS4626A in E_2. Among the testers, DL 161 was found to be the best general combiner for number of fruits plant^{-1} with the highest GCA effects followed by C 142, PL 412 and IS 268 in E_1, PL 412 followed by YL 581, IS 267 and DL 161 in E_2, DL 161 followed by SL 475, C 142 and VR 523 in E_3 and DL 161 followed by C 142, PL 412 and SL 475 when means were pooled across the three environments. The CMS line CMS4611A and testers DL 161, C 142 and IS 268 performed consistently superior across the environments in respect of both the GCA effects and the *per se* performances. Thus, these parental lines can be involved in hybrid breeding to generate chilli genotypes with more number of fruits plant^{-1}. From line × tester analysis, Patel *et al* (2004) observed ACMS-4 among the lines and ACS 2000-3 among the testers as good general combiners for number of fruits plant^{-1}. Parents CCA 19 and BARI Morich 1 were identified as good combiner by Hasanuzzaman *et al* (2012), UENF 1732 by Rodrigues *et al* (2012), UENF 1624 and UENF 1732 by Medeiros *et al* (2014), and DL 161 and VR 521 by Singh *et al* (2014).

4.3.3.9 Number of seed fruit^{-1}

Among the CMS lines the maximum number of seed fruit^{-1} was observed by CMS463D13A under E_1 (59.33), E_2 (53.07), E_3 (45.33) and over the environments (52.58).

The CMS4626A possessed minimum number of seed fruit^{-1} with the mean values of 44.97 in E_1, 37.53 in E_2, 30.93 in E_3 and 37.81 across the environments. The means of testers ranged from 26.67 in FL 201 to 64.73 in SL 475 under E_1, from 20.83 in FL 201 to 55.43 in IS 261 under E_2, from 15.13 in FL 201 to 50.93 in IS 261 under E_3 and from 20.88 in FL 201 to 56.20 in SL 475 across the environments (Table 4.9i). Eleven parents (one CMS line and 10 testers) exhibited significant positive and 11 parents (one CMS line and 10 testers) showed significant negative GCA effects in E_1, 10 parents (one CMS line and nine testers) had shown significant positive values and 11 (one CMS line and 10 testers) exhibited significant negative GCA values in E_2, 10 parents (one CMS line and nine testers) showed significant positive and 11 parents (two CMS lines and nine testers) exhibited significant negative GCA values in E_3 and 10 (one CMS line and nine testers) and 12 (two CMS lines and 10 testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for number of seed fruit^{-1} ranged from -2.83 (CMS4611A) to 3.94 (CMS463D13A) in E_1, from -1.87 (CMS4611A) to 2.31 (CMS463D13A) in E_2, from -1.44 (CMS4611A) to 2.33 (CMS463D13A) in E_3 and from -2.04 (CMS4611A) to 2.86 (CMS463D13A) over the environments. The GCA effects of testers varied from -22.0 (E 183) to 21.75 (IS 261) under E_1, from -20.88 (E 183) to 17.59 (SL 475) under E_2, from -16.98 (E 183) to 15.84 (IS 261) under E_3 and from -19.95 (E 183) to 18.05 (SL 475) across the environments.

Among the lines, CMS463D13A exhibited highest values of GCA for number of seed fruit^{-1} in E_1, E_2, E_3 and across the environments. Among the testers, IS 261 was found to be the best general combiner for number of seed fruit^{-1} with the highest GCA estimates followed by SL 475, PL 406 and IS 268 in E_1, SL 475 followed by IS 261, PL 412 and IS 267 in E_2, IS 261 followed by SL 475, PL 412 and PL 406 in E_3. Over the environments, the tester SL 475 followed by IS 261, PL 412 and PL 406 were adjudged as the good general combiners for number of seed fruit^{-1}. Among the CMS lines, CMS463D13A and among the testers, SL 475, IS 261, PL 412, PL 406, IS 267, IS 268, C 142, VR 521 and VR 523 performed consistently superior across the environments in respect of GCA effects and *per se* performances. To increase the number of seed fruit^{-1} in chilli, genotypes mentioned above can be utilized as donor parents in hybridization program. Prasath and Ponnuswami (2008) from diallel cross analysis observed that the parents MDU Y and Bydagi Kaddi were good general combiner for number of seed fruit^{-1}. Hasanuzzaman *et al* (2012) identified CCA 2, Singh *et al* (2014) identified MS 341, and Kaur *et al* (2017) identified MS 341 as good combiner for number of seed fruit^{-1}.

4.3.3.10 1000 seed weight (g)

For 1000 seed weight, the mean values of CMS lines varied from 4.66 g in CMS4611A to 4.89 g in CMS463D13A under E_1, from 4.35 g in CMS4611A to 4.56 g in CMS463D13A under E_2, from 4.19 g in CMS4611A to 4.34 g in CMS463D13A under E_3 and from 4.40 g in CMS4611A to 4.60 g in CMS463D13A across the environments. The mean performance of the testers ranged from 3.21 g in VR 521 to 7.51 g in FL 201 under E_1, from 2.89 g in VR 521 to 7.05 g in FL 201 under E_2, from 2.71 g in VR 521 to 6.89 g in FL 201 under E_3 and from 2.94 g in VR 521 to 7.15 g in FL 201 across the environments (Table 4.9j). Eleven (one CMS line and 10 testers) and eight (one CMS line and seven testers) parents in each E_1, E_2 and E_3 and 13 (one CMS line and 12 testers) and eight (one CMS line and seven testers) parents across the environments exhibited significant positive and negative GCA values, respectively. The GCA estimates of CMS lines ranged from -0.21 in CMS4611A to 0.26 in CMS463D13A under E_1, from -0.20 in CMS4611A to 0.25 in CMS463D13A under E_2, from -0.21 in CMS4611A to 0.27 in CMS463D13A under E_3 and from -0.21 in CMS4611A to 0.26 in CMS463D13A over the environments. The GCA effects of testers varied from -1.51 in VR 521 to 1.03 in FL 201 under E_1, from -1.56 in VR 521 to 1.05 in IS 263 under E_2, from -1.63 in VR 521 to 1.06 in IS 263 under E_3 and from -1.57 in VR 521 to 1.04 in IS 263 across the environments.

The results illustrated that among the CMS lines, CMS463D13A showed the highest GCA estimates for 1000 seed weight in E_1, E_2, E_3 and across the environments. Among the testers, FL 201 was found to be the best general combiner with the highest GCA effects followed by IS 263, YL 581 and IS 261 in E_1, IS 263 followed by YL 581, FL 201 and IS 261 in E_2 and E_3. Over the environments, the tester IS 263 followed by FL 201, YL 581 and IS 261 were the superior general combiners for 1000 seed weight. The CMS line CMS463D13A and testers IS 263, FL 201, YL 581, IS 261, PP 402, IS 262, SL 475, IS 268 and VR 522 performed consistently superior across the environments in respect of GCA effects and *per se* performances. Therefore, these parental lines can be utilized for the development of true breeding genotypes with higher seed weight. From the half-diallel analysis, Kaur *et al* (2017) found that the lines MS 341 and SD 463 as good combiner for seed weight.

4.3.3.11 Total yield plant^{-1} (kg)

The total yield plant^{-1} of CMS lines varied from 0.45 kg in CMS4611A to 0.61 kg in CMS463D13A under E_1, from 0.45 kg in CMS4626A to 0.47 kg in CMS463D13A under E_2, from 0.19 kg in CMS4611A to 0.39 kg in CMS463D13A under E_3 and from 0.37 kg in CMS4611A to 0.49 kg in CMS463D13A across the environments. The mean performance of the testers ranged from 0.27 kg in E 183 to 1.07 kg in PL 412 under E_1, from 0.24 kg in VR

521 to 0.73 kg in SL 475 under E_2, from 0.16 kg in IS 263 to 0.61 kg in SL 475 under E_3 and from 0.25 kg in VR 521 and E 183 to 0.76 kg in SL 475 across the environments (Table 4.9k). Eleven parents (one CMS line and 10 testers) exhibited significant positive and 11 parents (two CMS lines and nine testers) showed significant negative GCA effects in E_1, 10 parents (two CMS lines and eight testers) have shown significant positive values and nine (one CMS line and eight testers) parents exhibited significant negative GCA values in E_2, 11 parents (one CMS line and 10 testers) showed significant positive and 10 (one CMS line and nine testers) parents exhibited significant negative GCA values in E_3 and 11 (one CMS line and 10 testers) and seven (one CMS line and six testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for total yield plant^{-1} ranged from -0.10 in CMS4611A to 0.17 in CMS463D13A under E_1, from -0.11 in CMS4611A to 0.07 in CMS4626A under E_2, from -0.04 in CMS4611A to 0.04 in CMS463D13A under E_3 and from -0.09 in CMS4611A to 0.08 in CMS463D13A over the environments. The GCA estimates of testers varied from -0.47 in E 183 to 0.36 in IS 268 under E_1, from -0.39 in E 183 to 0.29 in YL 581 under E_2, from -0.23 in PP 414 to 0.27 in SL 475 under E_3 and from -0.33 in E 183 to 0.19 in IS 268 and SL 475 across the environments.

Among the CMS lines, the highest positive values of GCA exhibited by CMS463D13A in E_1, E_3 and across the environments and by CMS4626A in E_2. Among the testers, IS 268 have the highest GCA effects followed by DL 161, C 142 and IS 262 in E_1, YL 581 followed by PP 402, SL 475 and FL 201 in E_2, SL 475 followed by VR 523, DL 161 and C 142 in E_3 and IS 268 followed by SL 475, DL 161 and C 142 across the environments. The CMS line CMS463D13A and the testers IS 268, C 142 and PP 402 performed consistently superior across the environments in respect of both the GCA effects and the *per se* performance. Involvement of the identified parental lines with good GCA effects in single and multiple crosses are expected to generate high yielding recombinants in chilli.

From line × tester analysis, Patel *et al* (2004) identified ACMS-4 and Punjab Guchhedar as the good general combiners for green fruit yield plant^{-1}. Parents Pepper 1976 and Bakko Local were reported as good combiners for total yield by Geleta and Labuschagne (2006a), Bydagi Kaddi and Co 4 by Prasath and Ponnuswami (2008), CB 04, CB 24 and CB 50 by do Rego *et al* (2009), UENF 1616 and UENF 1639 by Rodrigues *et al* (2012), CA 197 among the lines and Kashi Anmol among the testers by Savitha *et al* (2013), UFPB 137 and UFPB 132 by do Nascimento *et al* (2014), UENF 1624 and UENF 1732 by Medeiros *et al* (2014), 09/Cvar 3 and 09/Cvar 4 by Pandey and Chura (2014), SL 461, DL 161 and PP 402 by Singh *et al* (2014), and IHR500, IHR3448 and IHR4507 by Naresh *et al* (2016).

4.3.3.12 Ascorbic acid (mg.100g^{-1})

For ascorbic acid content, the mean values of CMS lines ranged from 86.33 mg.100g^{-1} in CMS4611A to 125.51 mg.100g^{-1} in CMS463D13A under E_1, from 92.56 mg.100g^{-1} in CMS4611A to 129.7 mg.100g^{-1} in CMS463D13A under E_2, from 73.03 mg.100g^{-1} in CMS4611A to 111.16 mg.100g^{-1} in CMS463D13A under E_3 and from 83.97 mg.100g^{-1} in CMS4611A to 122.12 mg.100g^{-1} in CMS463D13A across the three environments. The means of testers varied from 69.34 mg.100g^{-1} in YL 581 to 182.0 mg.100g^{-1} in IS 268 under E_1, from 74.16 mg.100g^{-1} in YL 581 to 195.76 mg.100g^{-1} in PL 412 under E_2, from 56.21 mg.100g^{-1} in YL 581 to 166.42 mg.100g^{-1} in PL 406 under E_3 and from 66.57 mg.100g^{-1} in YL 581 to 171.15 mg.100g^{-1} in PL 412 across the environments (Table 4.9l). Eleven parents (two CMS lines and nine testers) exhibited significant positive and 10 parents (one CMS line and nine testers) showed significant negative GCA effects in E_1, 10 parents (one CMS line and nine testers) had shown significant positive values and 10 (two CMS lines and eight testers) exhibited significant negative GCA values in E_2, 13 parents (two CMS lines and 11 testers) showed significant positive and 10 parents (one CMS line and nine testers) exhibited significant negative GCA values in E_3 and 13 (two CMS lines and 11 testers) and nine (one CMS line and eight testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines ranged from -9.80 in CMS4611A to 7.30 in CMS463D13A under E_1, from -2.94 in CMS4611A to 4.78 in CMS463D13A under E_2, from -7.92 in CMS4611A to 4.08 in CMS4626A under E_3 and from -6.89 in CMS4611A to 5.31 in CMS463D13A over the environments. The GCA estimates of testers varied from -45.51 in PP 414 to 47.82 in IS 268 under E_1, from -54.43 in PP 414 to 41.0 in VR 521 under E_2, from -47.64 in YL 581 to 34.71 in IS 261 under E_3 and from -48.92 in PP 414 to 30.24 in IS 268 across the environments.

Among the lines, CMS463D13A showed the highest positive values of GCA for ascorbic acid in E_1, E_2 and across the environments and CMS4626A in E_3. Among the testers, IS 268 was found to be the best general combiner with the highest GCA effects followed by PL 412, IS 267, PL 406 and IS 263 in E_1, VR 521 followed by IS 261, VR 523, SL 475 and PL 406 in E_2, IS 261 followed by VR 521, PL 406, PL 412 and IS 268 in E_3 and IS 268 followed by PL 412, IS 261, PL 406 and VR 521 were the good general combiners across the environments. Among the CMS line CMS463D13A and among the testers IS 268, PL 412, IS 261, PL 406, IS 263, VR 523 and C 142 performed consistently superior across the environments in respect of GCA effects and *per se* performances. These parental lines can be involved in hybrid breeding program to develop chilli genotypes with high ascorbic acid content.

Geleta and Labuschagne (2006b) identified Mareko Shote as the good general combiner for ascorbic acid content, Savitha *et al* (2013) identified Kashi Anmol, do Nascimento *et al* (2014) identified UFPB 77.1, UFPB 01 and UFPB 77.2, Khalil and Hatem (2014) identified Big Dipper, and Pandey and Chura (2014) identified 09/Cvar 5 and 09/Cvar 4 as good general combiners for ascorbic acid content.

4.3.3.13 Oleoresin content (%)

The oleoresin content of CMS lines ranged from 9.73 (CMS4611A) to 11.32% (CMS4626A) in E_1, from 9.29 (CMS4611A) to 11.68% (CMS463D13A) in E_2, from 7.82 (CMS4611A) to 9.03% (CMS463D13A) in E_3 and from 8.95 (CMS4611A) to 10.55% (CMS463D13A) across the environments. The mean performance of the testers varied from 7.32 in IS 262 to 12.11% in DL 161 under E_1, from 7.12 in E 183 to 14.66% in VR 523 under E_2, from 5.42 in IS 262 to 10.2% in C 142 under E_3 and from 6.9 in E 183 to 11.51% in PP 402 across the environments (Table 4.9m). Nine parents (one CMS line and eight testers) exhibited significant positive and 13 parents (one CMS line and 12 testers) showed significant negative GCA effects in E_1, 11 parents (one CMS line and 10 testers) had shown significant positive values and 10 parents (one CMS line and nine testers) exhibited significant negative GCA values in E_2, 12 parents (two CMS lines and 10 testers) showed significant positive and 10 parents (one CMS line and nine testers) exhibited significant negative GCA values in E_3 and 11 (one CMS line and 10 testers) and 10 (one CMS line and nine testers) parents have shown significant positive and negative GCA values, respectively across the environments. The GCA effects of CMS lines for oleoresin content ranged from -0.61 (CMS4611A) to 0.52 (CMS4626A) in E_1, from -0.57 (CMS4626A) to 0.49 (CMS463D13A) in E_2, from -0.66 (CMS4611A) to 0.47 (CMS463D13A) in E_3 and from -0.40 (CMS4611A) to 0.35 (CMS463D13A) across the environments. The GCA effects of testers varied from -3.19 (E 183) to 4.26 (VR 523) in E_1, from -4.05 (E 183) to 4.71 (VR 523) in E_2, from -2.40 (PP 414) to 2.08 (SL 475) in E_3 and from -3.18 (E 183) to 3.33 (VR 523) across the environments.

The highest positive values of GCA for oleoresin content was recorded by CMS4626A in E_1, by CMS463D13A in E_2, E_3 and across the environments. Among the testers, VR 523 was found to be the best general combiner for oleoresin content with the highest GCA effects followed by SL 475, C 142 and DL 161 in E_1, VR 523 followed by IS 261, SL 475 and DL 161 in E_2, SL 475 followed by VR 522, DL 161 and C 142 in E_3 and VR 523 followed by SL 475, DL 161 and C 142 when means were pooled across the environments. Among the testers VR 523, SL 475, DL 161, C 142, VR 521, PL 406 and PP 402 performed consistently superior across the three environments in respect of GCA values and *per se* performances for oleoresin content. Thus, these parental lines can be involved in hybrid breeding for the development of chilli lines with higher oleoresin content.

Prasath and Ponnuswami (2008) from the diallel analysis found Arka Abir and Co 4 as good general combiner for oleoresin content. Savitha *et al* (2013) illustrated that the parental line Kashi Anmol was the best general combiner for oleoresin content.

4.3.3.14 Capsaicin content (%)

For capsaicin content, the CMS line CMS4626A produced the highly pungent fruit in E_1 (0.61%), E_2 (0.65%) and over the three environments (0.59%) and CMS463D13A in E_3 (0.51%). The CMS4611A produced the lowest pungent fruit with the mean values of 0.49, 0.52, 0.39 and 0.47% under E_1, E_2, E_3 and across the environments, respectively. The capsaicin content of testers ranged from 0.32 in YL 581 to 0.86% in SL 475 under E_1, from 0.34 in FL 201 to 0.85% in DL 161 under E_2, from 0.22 in FL 201 to 0.78% in VR 523 under E_3 and from 0.29 in FL 201 to 0.72% in SL 475 across the environments (Table 4.9n). Ten (two CMS lines and eight testers) and 11 parents (one CMS line and 10 testers) in E_1, 11 (two CMS lines and nine testers) and 11 (one CMS line and 10 testers) parents inE_2, 12 (two CMS lines and 10 testers) and nine (one CMS line and eight testers) parents in E_3 and 12 (two CMS lines and 10 testers) and nine (one CMS line and eight testers) parents across the three environments showed significant positive and negative GCA effects, respectively. The GCA effects of CMS lines for capsaicin content ranged from -0.05 (CMS4611A) to 0.04 (CMS4626A) in E_1, from -0.03 (CMS4611A) to 0.02 (CMS463D13A) in E_2, from -0.06 (CMS4611A) to 0.03 (CMS463D13A) in E_3 and from -0.05 (CMS4611A) to 0.03 (CMS4626A) over the environments. The GCA effects of testers for capsaicin content varied from -0.22 (YL 581) to 0.25 (SL 475) in E_1, from -0.20 (FL 201) to 0.27 (DL 161) in E_2, from -0.21 (E 183) to 0.18 (VR 523) in E_3 and from -0.21 (E 183) to 0.19 (SL 475) across the environments.

The results of GCA under three environments illustrated that the CMS line CMS4626A showed the highest positive values of GCA for capsaicin content under E_1 and across the three environments and CMS463D13A under E_2 and E_3. Among the testers, SL 475 had the highest GCA values, and was therefore, adjudged to be the best general combiner. This was followed by DL 161, IS 262 and IS 263 under E_1, DL 161 followed by IS 261, C 142 and SL 475 under E_2, VR 523 followed by PL 412, IS 263 and PL 406 under E_3 and SL 475 followed by IS 262, DL 161 and IS 263 over the environments. The CMS line CMS4626A and CMS463D13A and the testers SL 475, IS 262, IS 263, C 142 and PL 406 performed consistently superior across the environments in respect of GCA effects and *per se* performances, reflecting their true breeding value in increasing capsaicin content in chilli. Lohithaswa *et al* (2000) illustrated that the genotype Pusa Jwala was the good general combiner for capsaicin content. The parent NMCA80049 was identified as the good general combiner for capsaicin content by Zewdie and Bosland (2001), S 1 and Arka Lohit by Prasath and Ponnuswami (2008) and Zongolica and Tacámbaro by Sánchez-Sánchez *et al* (2010). From the line × tester analysis, Savitha *et al* (2013) identified CA 197 among the line and CA 97 among the tester as good combiner for capsaicin content in chilli.

4.3.3.15 Scoville heat units (SHU)

The CMS line CMS4626A with SHU values of 98346.66, 104613.34 and 94497.78 in E_1, E_2 and across the environment, respectively produced the most pungent fruits. The line CMS463D13A with SHU values of 82026.66 produced the most pungent fruits in E_3. The least pungent fruits with the mean SHU values of 78506.66, 82938.66, 63040.0 and 74828.45 under E_1, E_2, E_3 and across the environments, respectively were produced by CMS4611A. The SHU of testers ranged from 50720.0 in YL 581 to 137973.33 in SL 475 under E_1, from 53978.67 in FL 201 to 135690.67 in DL 161 under E_2, from 35093.33 in FL 201 to 124320.0 in VR 523 under E_3 and from 47059.55 in FL 201 to 114487.11 in SL 475 across the environments (Table 4.9o). Ten (two CMS lines and eight testers) and 11 parents (one CMS line and 10 testers) under E_1, 11 (two CMS lines and nine testers) and 11 (one CMS line and 10 testers) parents under E_2, 12 (two CMS lines and 10 testers) and nine (one CMS line and eight testers) parents under E_3 and 12 (two CMS lines and 10 testers) and nine (one CMS line and eight testers) parents over the three environments showed significant positive and negative GCA values, respectively. The GCA effects of CMS lines for SHU ranged from -8671.11 in CMS4611A to 6403.56 in CMS4626A under E_1, from -4792.44 in CMS4611A to 2579.56 in CMS463D13A under E_2, from -9366.22 in CMS4611A to 4916.44 in CMS463D13A under E_3 and from -7609.93 in CMS4611A to 4355.41 in CMS4626A over the three environments. The GCA effects of testers varied from -35444.45 in YL 581 to 39577.78 in SL 475 under E_1, from -32720.80 in FL 201 to 42461.42 in DL 161 under E_2, from -33842.67 in E 183 to 28735.11 in VR 523 under E_3 and from -33363.23 in E 183 to 30732.18 in SL 475 across the environments.

The CMS line CMS4626A showed the highest positive values of GCA estimates for SHU in E_1 and over the environments and CMS463D13A exhibited the highest values in E_2 and E_3. Among the testers, SL 475 had the highest GCA effects, and was therefore, regarded to be the best general combiner. This was followed by DL 161, IS 262 and IS 263 under E_1, DL 161 followed by IS 261, C 142 and SL 475 under E_2, VR 523 followed by PL 412, IS 263 and PL 406 under E_3 and SL 475 followed by IS 262, DL 161 and IS 263 across the environments. The CMS lines CMS4626A and CMS463D13A and the testers SL 475, IS 262, IS 263, C 142 and PL 406 performed consistently superior across the environments in respect of both the GCA effects and the *per se* performances for SHU. These parents can be involved in hybrid breeding programs to increase pungency in chilli for industrial uses such as the elaboration of medicines, sauces, canned goods and for food industry (for wines). Naresh *et al* (2016) from half-diallel analysis reported that the parental lines IHR4503, IHR500 and IHR2451 were good general combiners for high capsaicin content.

The CMS line CMS4611A registered maximum significant negative GCA effects for SHU in E_1, E_2, E_3 and across the environments. The tester YL 581 have shown highest significant negative values of GCA followed by E 183, FL 201 and SL 473 in E_1, FL 201 followed by E 183, YL 581 and PP 414 in E_2, E 183 followed by YL 581, FL 201 and PP 402 in E_3 and E 183 followed by YL 581, FL 201 and PP 402 based on pooled means. These parents can be used in hybrid breeding program to generate recombinants with less pungent fruits in chilli and effectively used in food industries as natural food colorant and for fresh consumption.

The selection of parents based on their general combining ability and understanding the genetic control of key traits ensures the efficiency of a breeding program. In the present study, the GCA effects manifested that all the parental lines had significantly desirable GCA values for at least one trait. High total yield plant^{-1} is one of the most important breeding goals in any crop breeding program. All the parental lines selected for further use in breeding program have high GCA effects for total yield plant^{-1}.

Besides, high GCA estimates for total yield plant^{-1} in early season planted (E_1) crop, the line CMS463D13A was a good general combiner for all the studied traits except number of fruits plant^{-1} and oleoresin content. Involving this CMS line in hybridization would be result in the identification of superior cross-combinations with higher yield. The tester namely IS 268 was found to be good general combiner for plant height, fruit weight, fruit width, pericarp thickness, number of fruits palnt^{-1}, number of seed fruit^{-1}, 1000 seed weight, ascorbic acid, capsaicin content and SHU. Thus, this line can be used in hybrid breeding program to generate high yielding recombinants in chilli with pungent fruits for early planting. The parental lines C 142, VR 523 and PL 406 were good general combiners for plant spread, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU, while C 142 and PL 406 also showed good GCA effects for plant height and number of fruits pant^{-1}. The testers IS 267 and PL 412 have shown significantly positive GCA effects for plant height, fruit length, number of fruits plant^{-1}, number of seed fruit^{-1} and ascorbic acid and significant negative GCA estimates for oleoresin content, capsaicin content and SHU. These parents can be involved in hybrid breeding for the development of mildly pungent chilli used for fresh consumption. The tester PP 402 was a good general combiner for fruit weight, fruit width, pericarp thickness, 1000 seed weight and oleoresin content and exhibited negatively significant GCA values for plant spread, capsaicin content and SHU. This parental line can be useful to breed for plant type with compact canopy and for oleoresin extraction, utilized in food industries as natural food colorant. The tester DL 161 showed significantly positive GCA effects for number of primary branches plant^{-1}, number of fruits plant^{-1}, oleoresin content, capsaicin content and SHU and significant negative GCA values for plant height, fruit length and pericarp thickness. This parent can be used in hybrid breeding program to generate recombinants with short plant stature and small-sized pungent fruits with thinner pericarp. The testers namely PL 406, VR 522, IS 262, C 142, IS 268 and PP 402 were considered as average general combiners for fruit length with higher total yield plant^{-1}. Therefore, these parental lines could be involved in hybrid breeding program to obtain high yielding lines with medium sized fruits suitable for early season planting. The medium sized fruits have better shelf life. For vegetable and paprika production also medium sized fleshy fruits are preferred.

In main-season planted (E_2) crop, the CMS lines, CMS4626A and CMS463D13A were considered as good general combiner for total yield plant^{-1}. The line CMS463D13A also exhibited significantly positive GCA estimates for all other studied traits except number of primary branches plant^{-1} and number of fruits plant^{-1}. The line CMS4626A showed significantly negative values of GCA for plant height, plant spread and pericarp thickness. This line can be useful to breed for plant type with small height, compact canopy and fruits with thin pericarp. Such plant types of be of immense agronomic use for multiple cropping systems and industrial uses such as processing for powder making. The tester SL 475 was found to be good general combiner for all the studied traits except fruit width. Hence, this parental line can be utilized for breeding high yielding chilli with important plant growth and quality traits. The testers YL 581 and PP 402 expressed significantly positive GCA effects for fruit weight, fruit width, pericarp thickness and 1000 seed weight and significant negative GCA values for capsaicin content and SHU. The testers PP 402 and IS 267 have good GCA values for oleoresin content and significantly negative values of GCA for capsaicin content and SHU. Therefore, these parental lines are used in hybrid breeding programs to develop the cultivars of chilli for non-pungent oleoresin extraction, used for paprika production. The tester

IS 268 was considered as good general combiner for plant height, number of primary branches plant^{-1}, fruit weight, fruit width, number of fruits plant^{-1}, number of seed fruit^{-1}, 1000 seed weight, ascorbic acid, capsaicin content and SHU; IS 267 and PL 412 for plant height, fruit length, number of fruits plant^{-1} and number of seed fruit^{-1}; FL 201 for number of primary branches plant^{-1}, fruit weight, fruit length, fruit width, pericarp thickness and 1000 seed weight and C 142 for plant height, number of fruits plant^{-1} and number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU. These parental lines can be involved in hybrid breeding for the development of chilli lines with higher yield. The parents namely PP 402, IS 268 and C 142 produced medium-sized fruits.

In late season planted (E_3) crop, the CMS line, CMS463D13A had the good GCA values for all the traits studied except number of primary branches plant^{-1}, plant spread and number of fruits plant^{-1}. The testers SL 475 and VR 523 were regarded as good general combiner for plant spread, fruit weight, fruit length, pericarp thickness, number of fruits plant^{-1}, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU suggested that these parental lines can be effectively utilized for breeding high yielding pungent chilli cultivars for late season cultivation. The testers namely C 142, PL 406 and VR 522 were registered good GCA values for plant height, ascorbic acid, oleoresin content, capsaicin content and SHU; C 142 and SL 473 for number of fruits plant^{-1} and VR 522 for fruit weight, fruit length and 1000 seed weight. The tester PP 402 showed significantly positive GCA effects for plant height, number of primary branches plant^{-1}, fruit weight, fruit width, pericarp thickness, 1000 seed weight and oleoresin content and significant negative GCA estimates for plant spread, capsaicin content and SHU. This parental line can be used in hybrid breeding program to generate recombinants with mildly pungent fruits in chilli and effectively used for paprika production and fresh consumption. The tester IS 268 was a good general combiner for plant height, fruit weight, fruit width, pericarp thickness, number of fruits plant^{-1}, number of seed fruit^{-1}, 1000 seed weight and ascorbic acid. The tester YL 581 exhibited significant positive values of GCA for fruit weight, fruit length, fruit width, pericarp thickness and 1000 seed weight and significantly negative GCA effects for plant height, oleoresin content, capsaicin content and SHU. This parent can be recommended in crosses to breed for smaller plant stature with mildly pungent fruits in chilli. The testers DL 161 expressed significantly positive values of GCA for number of fruits plant^{-1} and oleoresin content and significant negative GCA effects for capsaicin content and SHU. Therefore, this parent is used in hybrid breeding programs to develop high yielding cultivars of chilli for non-pungent oleoresin extraction. The average general combiners for fruit length were the parents DL 161, C 142, SL 473, PP 402 and IS 268.

Pooled across the environments, the line CMS463D13A was regarded as good general combiner for all the studied traits except number of fruits plant^{-1}. The tester SL 475 was found to be good general combiner for all the traits studied except fruit width. This parent can be utilized for the development of true breeding lines with higher yield and quality traits. The testers IS 268 and VR 523 exhibited good GCA effects for number of primary branches plant^{-1}, pericarp thickness, number of fruits plant^{-1}, number of seed fruit^{-1}, 1000 seed weight, ascorbic acid, capsaicin content and SHU and the testers IS 267 and PL 412 for plant height, number of primary branches palnt^{-1}, fruit length, number of fruits plant^{-1}, number of seed fruit^{-1} and ascorbic acid. The parental lines DL 161 and C 142 showed significantly positive GCA values for number of fruits plant^{-1}, oleoresin content, capsaicin content and SHU and significant negative GCA effects for pericarp thickness. These parents can be used as a donor parent to develop high yielding pungent genotypes with thin pericarp. Chilli with thin pericarp is facilitate quick drying and therefore, is desirable for processing into power. The testers namely PP 402 and VR 522 exhibited significantly positive values of GCA for fruit weight, fruit length, 1000 seed weight and oleoresin content and significant negative values of GCA for capsaicin content and SHU. These parental lines can be used in crosses to breed for high yielding cultivars with mildly pungent fruits, used in oleoresin extraction. The parents that possessed average GCA effects for fruit length were IS 268 and C 142.

Based on the overall GCA estimates, the line CMS463D13A and the testers SL 475, PP 402, IS 268, FL 201 and C 142 could be utilized for breeding high yielding chilli for all the three environments, and to identify superior recombinants for fruit weight, fruit length, fruit width, pericarp thickness, number of seed fruit^{-1}, oleoresin content, capsaicin content and SHU. In some cases, parents that demonstrated the best *per se* performance were not the best general combiners. This is substantiated by the fact that the testers IS 262 had highest *per se* performance for plant height but the GCA effects was significantly negative in E_1. For plant spread, the tester AC 102 exhibited well *per se* performance but the GCA estimates was negative in E_2. Similar trend was observed for number of primary branches plant^{-1} by the tester YL 581 in E_2, E_3 and across the environments, for fruit length by IS 263 in E_1, for number of fruits plant^{-1} by PP 414 in E_1 and for total yield plant^{-1} by DL 161 in E_2. Hence, the selection of the parents should mainly be based on their actual GCA effects with some emphasis on *per se* performance of the parents for the development of superior F_1 hybrids.

Table 4.9a: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for plant height (cm) in 23 parental lines of chilli

Parental lines	**Plant height (cm)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	73.14	-1.38	1.91	698.79	84.60	1.62*	2.62	422.72
CMS4626A	64.83	-9.43**	88.98	420.11	65.09	-3.87**	14.98	795.76
CMS463D13A	98.57	10.82**	116.99	445.02	74.73	2.25**	5.07	1048.14
Testers								
AC 102	67.16	-12.80**	163.91	13.58	54.82	-23.97**	574.69	160.00
SL 475	77.78	-0.89	0.79	99.69	62.50	11.97**	143.32	20.98
PL 412	94.70	13.01**	169.36	149.89	86.23	17.27**	298.41	202.16
IS 263	76.44	-6.47*	41.83	27.13	63.68	-3.41	11.62	49.82
VR 523	73.12	1.56	2.45	43.44	65.88	-2.69	7.22	48.05
DL 161	68.53	-14.28**	203.93	20.86	54.80	-15.92**	253.49	267.26
IS 267	90.33	12.00**	143.89	42.72	74.57	4.26*	18.18	82.51
YL 581	73.47	-3.60	12.94	5.92	50.06	-15.93**	253.74	10.13
SL 473	78.57	-12.41**	154.01	111.58	75.62	-4.55*	20.74	19.81
IS 262	112.04	-5.44*	29.59	0.73	74.73	-3.81	14.55	3.71
VR 521	92.41	5.80*	33.68	103.57	67.96	4.69*	21.99	356.80
FL 201	55.18	-16.63**	276.59	4.71	55.31	-13.76**	189.45	49.35
PP 402	64.18	0.33	0.11	117.31	67.87	0.72	0.52	146.71
C 142	105.21	10.35**	107.20	79.68	82.71	10.15**	103.00	331.72
PP 414	94.28	7.87**	61.95	78.49	78.36	1.66	2.75	30.32
VR 522	76.10	-4.11	16.87	48.55	68.50	1.09	1.19	108.15
PL 406	90.45	13.32**	177.49	144.20	76.24	6.02**	36.19	45.97
E 183	85.74	2.55	6.53	118.43	81.31	-4.02	16.17	34.24
IS 268	83.73	18.44**	340.05	31.50	74.91	22.29**	496.88	15.39
IS 261	95.40	-8.63**	74.39	321.96	75.39	7.95**	63.20	283.54
p=0.05 GCA line		2.01				1.56		
p=0.05 GCA tester		5.18				4.03		

Table 4.9a (*Cont'd.*)

Parental lines	Plant height (cm)							
	E$_3$			Pooled				
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	54.39	1.16	1.35	719.33	70.71	0.46	0.22	212.13
CMS4626A	46.57	-2.98**	8.86	276.83	58.83	-5.43**	29.45	123.41
CMS463D13A	55.52	1.82**	3.30	671.62	76.27	4.96**	24.62	413.61
Testers								
AC 102	41.96	-14.47**	209.31	21.42	54.65	-17.08**	291.76	25.84
SL 475	57.32	10.32**	106.52	11.27	65.87	7.13**	50.90	11.22
PL 412	54.98	0.32	0.10	31.16	78.64	10.20**	104.10	64.73
IS 263	48.50	-4.86**	23.66	33.36	62.87	-4.91**	24.14	0.03
VR 523	54.11	2.66	7.07	38.14	64.37	0.51	0.26	13.15
DL 161	48.33	-9.92**	98.40	32.97	57.22	-13.37**	178.86	53.31
IS 267	60.83	4.61**	21.25	26.20	75.24	6.96**	48.39	11.37
YL 581	47.84	-8.19**	67.02	123.90	57.12	-9.24**	85.33	9.15
SL 473	56.41	-3.10	9.62	42.39	70.20	-6.69**	44.73	18.70
IS 262	55.51	-8.85**	78.24	4.99	80.76	-6.03**	36.40	0.42
VR 521	56.61	4.50**	20.24	18.61	72.33	5.00**	24.98	121.16
FL 201	37.81	-6.14**	37.69	2.79	49.43	-12.18**	148.31	7.75
PP 402	50.58	4.46*	19.88	130.32	60.87	1.84	3.37	51.87
C 142	68.12	7.55**	57.07	67.05	85.35	9.35**	87.47	64.90
PP 414	66.46	-0.36	0.13	46.45	79.70	3.05*	9.33	5.35
VR 522	49.84	3.71*	13.79	128.54	64.82	0.23	0.05	3.37
PL 406	57.18	5.41**	29.23	79.91	74.62	8.25**	68.03	10.47
E 183	66.37	-6.35**	40.36	447.37	77.81	-2.61*	6.79	156.56
IS 268	63.00	8.75**	76.64	33.98	73.88	16.50**	272.10	20.36
IS 261	52.84	9.94**	98.87	346.98	74.54	3.09*	9.54	99.46
p=0.05 GCA line		1.31				0.99		
p=0.05 GCA tester		3.39				2.56		

*, significant at p=0.05; **, significant at p=0.01

Table 4.9b: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for plant spread (cm) in 23 parental lines of chilli

Parental lines	**Plant spread (cm)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	56.83	-0.17	0.03	421.06	55.26	1.51**	2.27	2.27
CMS4626A	51.60	-6.53**	42.68	196.17	45.58	-4.50**	20.23	20.23
CMS463D13A	62.78	6.70**	44.92	479.46	53.76	2.99**	8.95	8.95
Testers								
AC 102	56.29	2.48	6.17	36.46	54.93	-4.67**	21.78	177.84
SL 475	64.11	-0.56	0.32	35.84	53.32	12.89**	166.11	179.37
PL 412	51.82	5.30**	28.07	98.59	54.80	-2.37	5.60	26.74
IS 263	60.28	4.09*	16.74	65.18	46.14	1.72	2.97	50.84
VR 523	59.57	7.13**	50.78	173.31	52.75	6.03**	36.40	16.85
DL 161	55.10	-0.25	0.06	2.45	56.81	-0.43	0.19	18.81
IS 267	52.07	-2.09	4.38	49.02	33.18	-0.26	0.07	59.43
YL 581	50.49	1.53	2.33	126.05	30.27	-8.27**	68.40	2.80
SL 473	61.66	-2.69	7.22	9.48	52.96	1.20	1.43	13.28
IS 262	57.39	-8.16**	66.56	23.08	48.19	-5.19**	26.89	44.78
VR 521	58.06	-5.32**	28.28	39.14	38.20	-7.34**	53.84	109.38
FL 201	51.88	-4.49*	20.12	3.10	38.30	-2.13	4.54	8.73
PP 402	52.78	-6.11**	37.36	43.27	45.33	-0.62	0.39	92.64
C 142	56.49	3.85*	14.86	1.87	51.20	-2.20	4.85	7.56
PP 414	48.66	-0.15	0.02	48.26	34.37	-4.92**	24.24	52.57
VR 522	61.33	-8.64**	74.70	11.10	57.97	7.75**	60.08	125.46
PL 406	66.89	4.86**	23.59	19.71	45.56	4.98**	24.77	134.68
E 183	47.39	-1.12	1.26	9.36	46.33	-8.64**	74.73	20.35
IS 268	44.59	2.94	8.65	88.07	35.94	1.20	1.43	155.32
IS 261	72.22	7.41**	54.89	213.37	54.60	11.28**	127.26	44.04
p=0.05 GCA line		1.38				1.03		
p=0.05 GCA tester		3.56				2.67		

Table 4.9b (*Cont'd.*)

Parental lines	**Plant spread (cm)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	38.39	-0.30	0.09	205.72	50.16	0.35	0.12	103.69
CMS4626A	34.42	-0.57	0.32	146.41	43.87	-3.87**	14.94	80.41
CMS463D13A	39.14	0.87	0.75	155.35	51.89	3.52**	12.39	102.15
Testers								
AC 102	38.36	-4.33**	18.73	19.29	49.86	-2.17*	4.71	36.45
SL 475	46.50	9.58**	91.71	50.06	54.65	7.30**	53.29	4.07
PL 412	43.19	1.97	3.88	25.52	49.94	1.63	2.67	29.61
IS 263	34.29	-0.55	0.30	76.39	46.90	1.76*	3.08	4.97
VR 523	44.80	2.84*	8.04	4.58	52.37	5.33**	28.43	19.99
DL 161	41.48	1.10	1.21	41.52	51.13	0.14	0.02	13.99
IS 267	34.18	1.43	2.05	13.79	39.81	-0.31	0.09	8.19
YL 581	37.96	-2.47	6.11	18.51	39.57	-3.07**	9.44	20.77
SL 473	40.49	-2.93*	8.57	32.73	51.70	-1.47	2.17	2.72
IS 262	39.89	-4.33**	18.79	26.20	48.49	-5.89**	34.73	6.37
VR 521	43.22	2.88*	8.29	67.04	46.49	-3.26**	10.62	68.36
FL 201	28.38	-2.74*	7.52	12.33	39.52	-3.12**	9.73	0.71
PP 402	30.76	-3.46**	12.00	3.90	42.96	-3.40**	11.56	3.65
C 142	45.90	2.57	6.62	41.81	51.20	1.41	1.98	9.39
PP 414	42.44	-6.54**	42.80	5.70	41.82	-3.87**	14.99	15.51
VR 522	34.79	2.15	4.64	23.90	51.36	0.42	0.18	13.66
PL 406	48.12	4.69**	22.01	1.37	53.52	4.84**	23.44	7.19
E 183	40.57	-7.16**	51.22	9.99	44.76	-5.64**	31.82	1.87
IS 268	31.89	-3.62**	13.13	18.04	37.47	0.17	0.03	10.12
IS 261	47.39	8.92**	79.65	14.80	58.07	9.20**	84.73	8.66
p=0.05 GCA line		1.00				0.68		
p=0.05 GCA tester		2.59				1.75		

Table 4.9c: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for number of primary branches plant^{-1} in 23 parental lines

Parental lines	**Number of primary branches plant^{-1}**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	3.56	-0.06	0.00	2.70	5.30	0.30**	0.09	14.26
CMS4626A	3.56	-0.41**	0.17	6.13	4.05	-0.26**	0.07	15.19
CMS463D13A	3.96	0.47**	0.22	4.98	4.66	-0.03	0.00	19.97
Testers								
AC 102	4.22	-0.42**	0.17	0.62	6.01	-1.11**	1.24	1.35
SL 475	4.44	-0.15	0.02	1.03	5.34	1.40**	1.97	3.15
PL 412	4.54	0.25	0.06	0.27	4.33	0.21	0.04	2.32
IS 263	3.67	-0.33*	0.11	0.44	3.37	-0.24	0.06	1.15
VR 523	3.78	-0.17	0.03	0.28	6.67	2.20**	4.86	7.26
DL 161	4.78	0.38**	0.14	1.87	4.37	-0.67**	0.45	0.34
IS 267	4.84	0.81**	0.66	2.17	3.63	-0.52**	0.27	1.82
YL 581	4.22	0.06	0.00	0.40	6.36	-0.54**	0.29	0.38
SL 473	3.71	-0.36*	0.13	0.17	4.32	-1.00**	0.99	0.14
IS 262	3.78	0.03	0.00	1.25	4.33	-1.10**	1.20	1.64
VR 521	4.00	0.20	0.04	0.36	3.68	-0.18	0.03	1.14
FL 201	4.84	-0.03	0.00	0.87	4.38	0.57**	0.33	2.39
PP 402	3.44	-0.30*	0.09	0.25	3.98	-0.43**	0.19	1.41
C 142	3.22	0.11	0.01	0.32	4.33	-0.91**	0.82	0.32
PP 414	4.54	-0.28*	0.08	1.12	2.67	-0.74**	0.55	1.60
VR 522	4.89	-0.13	0.02	1.83	4.62	0.45**	0.20	10.09
PL 406	5.27	1.25**	1.57	0.04	5.08	0.09	0.01	0.42
E 183	3.89	-0.15	0.02	0.05	7.01	1.20**	1.44	1.85
IS 268	4.33	-0.44**	0.20	0.41	3.66	0.83**	0.69	5.67
IS 261	4.00	-0.32*	0.10	0.06	4.66	0.50**	0.25	4.99
p=0.05 GCA line		0.11				0.10		
p=0.05 GCA tester		0.28				0.26		

Table 4.9c (*Cont'd.*)

Parental lines	Number of primary branches plant^{-1}							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	4.33	-0.03	0.00	18.03	4.40	0.07*	0.00	3.03
CMS4626A	4.38	0.14*	0.02	6.79	4.00	-0.18**	0.03	2.63
CMS463D13A	3.68	-0.11	0.01	12.82	4.10	0.11**	0.01	3.29
Testers								
AC 102	4.33	-0.56**	0.32	4.71	4.86	-0.70**	0.49	0.26
SL 475	4.01	1.33**	1.76	2.57	4.60	0.86**	0.74	0.21
PL 412	3.56	0.29	0.09	1.49	4.14	0.25**	0.06	0.83
IS 263	4.01	-1.04**	1.07	0.03	3.68	-0.54**	0.29	0.35
VR 523	5.01	-0.06	0.00	0.25	5.15	0.66**	0.43	0.98
DL 161	4.34	-0.23	0.05	0.39	4.50	-0.18*	0.03	0.00
IS 267	4.51	0.32	0.10	1.49	4.33	0.20*	0.04	0.43
YL 581	6.49	-0.43**	0.19	1.52	5.69	-0.31**	0.09	0.56
SL 473	3.84	-1.06**	1.13	0.63	3.96	-0.81**	0.65	0.02
IS 262	4.40	-1.30**	1.68	0.04	4.17	-0.79**	0.62	0.72
VR 521	6.34	1.35**	1.83	0.31	4.67	0.46**	0.21	0.44
FL 201	3.83	-0.69**	0.47	0.35	4.35	-0.05	0.00	0.16
PP 402	4.69	1.14**	1.29	5.38	4.04	0.13	0.02	0.34
C 142	5.32	-0.07	0.01	2.52	4.29	-0.29**	0.08	0.25
PP 414	4.33	-0.36*	0.13	1.21	3.85	-0.46**	0.21	0.22
VR 522	4.16	0.32	0.10	1.93	4.56	0.21*	0.04	0.14
PL 406	4.66	0.60**	0.36	5.86	5.00	0.65**	0.42	0.96
E 183	5.16	0.15	0.02	4.15	5.35	0.40**	0.16	0.28
IS 268	4.01	0.31	0.10	2.33	4.00	0.23**	0.05	1.12
IS 261	4.84	-0.01	0.00	0.47	4.50	0.06	0.00	0.67
p=0.05 GCA line		0.13				0.07		
p=0.05 GCA tester		0.32				0.17		

Table 4.9d: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for fruit weight (g) in 23 parental lines

Parental lines	Fruit weight (g)							
	E_1				E_2			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	2.82	-1.83**	3.33	18.80	2.73	-1.26**	1.58	21.32
CMS4626A	4.98	-0.36**	0.13	7.69	3.55	0.21**	0.05	9.47
CMS463D13A	6.05	2.18**	4.75	18.87	5.55	1.04**	1.09	12.64
Testers								
AC 102	4.96	-0.28	0.08	1.69	4.75	-1.15**	1.33	2.19
SL 475	6.39	0.65**	0.42	0.58	5.12	0.96**	0.92	4.92
PL 412	6.04	0.09	0.01	0.42	6.38	0.16	0.02	0.63
IS 263	5.59	-1.40**	1.97	0.83	2.53	-1.18**	1.39	0.10
VR 523	4.38	-0.07	0.00	0.41	3.78	-0.78**	0.61	1.35
DL 161	3.54	-1.73**	2.99	4.10	4.48	-1.12**	1.26	0.65
IS 267	6.29	0.25	0.06	1.43	4.76	-0.44**	0.19	0.67
YL 581	8.34	1.81**	3.27	4.76	7.93	1.45**	2.11	2.06
SL 473	3.99	-0.67**	0.44	1.52	3.21	-0.47**	0.22	0.25
IS 262	7.56	0.54**	0.29	0.06	4.93	-0.83**	0.70	0.03
VR 521	2.02	-2.33**	5.45	5.57	1.41	-2.90**	8.39	1.38
FL 201	12.81	2.10**	4.39	5.43	12.50	3.01**	9.07	11.82
PP 402	9.88	2.80**	7.85	9.05	8.93	3.06**	9.39	6.88
C 142	4.21	-0.23	0.05	1.03	3.48	-0.28*	0.08	0.16
PP 414	4.16	-1.94**	3.75	0.41	2.81	-1.12**	1.25	0.10
VR 522	6.89	0.83**	0.69	1.66	5.78	0.21	0.05	2.77
PL 406	5.99	0.69**	0.47	0.67	4.02	0.24	0.06	0.56
E 183	4.58	-2.23**	4.98	4.77	3.48	-2.40**	5.77	1.36
IS 268	7.39	1.01**	1.03	0.74	5.98	1.72**	2.96	1.42
IS 261	6.15	0.12	0.01	0.22	6.18	1.85**	3.41	4.14
p=0.05 GCA line		0.14				0.10		
p=0.05 GCA tester		0.36				0.26		

Table 4.9d (*Cont'd.*)

Parental lines	**Fruit weight (g)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	2.83	-0.80**	0.64	3.14	2.79	-1.29**	1.68	7.61
CMS4626A	3.92	0.25**	0.06	4.26	4.15	0.04	0.00	3.25
CMS463D13A	4.42	0.55**	0.30	2.82	5.34	1.26**	1.58	5.87
Testers								
AC 102	3.28	-0.94**	0.89	0.11	4.33	-0.79**	0.63	0.41
SL 475	5.02	0.64**	0.41	0.14	5.51	0.75**	0.56	0.50
PL 412	4.32	0.09	0.01	0.59	5.58	0.11	0.01	0.02
IS 263	3.62	-0.88**	0.78	0.01	3.91	-1.16**	1.34	0.08
VR 523	3.88	0.71**	0.50	0.65	4.01	-0.05	0.00	0.10
DL 161	3.42	-0.24*	0.06	0.21	3.81	-1.03**	1.07	0.75
IS 267	4.48	0.17	0.03	0.70	5.18	-0.01	0.00	0.28
YL 581	5.45	0.61**	0.37	0.71	7.24	1.29**	1.66	1.06
SL 473	3.82	0.26*	0.07	0.51	3.67	-0.29**	0.08	0.46
IS 262	4.05	-0.47**	0.22	0.82	5.51	-0.25**	0.06	0.06
VR 521	2.68	-1.11**	1.22	0.24	2.04	-2.11**	4.46	1.15
FL 201	7.25	0.94**	0.88	0.31	10.85	2.02**	4.06	3.49
PP 402	5.28	1.01**	1.01	0.59	8.03	2.29**	5.25	4.40
C 142	4.05	-0.08	0.01	0.07	3.91	-0.20*	0.04	0.05
PP 414	3.85	-0.85**	0.72	0.82	3.61	-1.30**	1.69	0.38
VR 522	4.28	0.24*	0.06	0.55	5.65	0.43**	0.18	0.58
PL 406	4.08	0.22	0.05	0.34	4.70	0.38**	0.15	0.07
E 183	3.65	-0.67**	0.45	0.42	3.90	-1.77**	3.13	1.66
IS 268	4.58	0.40**	0.16	1.88	5.98	1.04**	1.09	0.67
IS 261	4.12	-0.03	0.00	0.54	5.48	0.64**	0.41	0.57
p=0.05 GCA line		0.09				0.06		
p=0.05 GCA tester		0.23				0.17		

Table 4.9e: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for fruit length (cm) in 23 parental lines

Parental lines	Fruit length (cm)							
	E_1				E_2			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	**Mean**	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	4.89	-0.85**	0.72	4.84	4.70	-0.38**	0.14	2.59
CMS4626A	6.38	-0.02	0.00	6.52	5.02	-0.03	0.00	2.48
CMS463D13A	6.98	0.87**	0.75	4.86	6.65	0.41**	0.17	2.44
Testers								
AC 102	7.22	-0.59**	0.35	1.56	6.48	-0.86**	0.73	0.82
SL 475	9.57	1.23**	1.52	0.15	7.84	1.09**	1.19	0.31
PL 412	9.54	0.50*	0.25	0.78	7.16	0.41*	0.17	0.48
IS 263	9.40	-0.52*	0.27	0.63	5.86	-0.53**	0.28	0.41
VR 523	8.05	0.65**	0.42	0.06	6.93	0.00	0.00	0.52
DL 161	7.38	-0.66**	0.44	0.29	5.03	-0.88**	0.78	0.16
IS 267	8.51	0.54*	0.29	0.33	6.05	0.87**	0.75	0.08
YL 581	8.80	-0.32	0.10	0.94	7.70	0.92**	0.84	0.15
SL 473	7.07	-0.93**	0.86	2.50	6.03	-0.59**	0.34	0.05
IS 262	7.94	-0.02	0.00	0.11	5.83	-0.54**	0.30	0.65
VR 521	5.93	-1.58**	2.50	1.12	3.83	-0.21	0.04	0.06
FL 201	12.17	2.20**	4.85	0.20	10.67	1.21**	1.46	0.04
PP 402	6.44	0.38	0.14	1.95	5.97	0.15	0.02	0.43
C 142	7.68	0.21	0.04	1.13	5.13	0.12	0.01	0.36
PP 414	6.92	-1.01**	1.02	2.72	5.33	-0.46**	0.21	1.54
VR 522	8.07	-0.07	0.00	0.20	6.65	0.04	0.00	0.38
PL 406	8.12	0.31	0.10	0.10	5.39	-0.21	0.04	0.21
E 183	7.12	-1.70**	2.89	0.69	5.08	-1.34**	1.80	0.46
IS 268	7.85	0.15	0.02	0.62	5.63	-0.19	0.04	0.30
IS 261	8.55	1.23**	1.50	0.14	6.93	1.00**	1.00	0.09
p=0.05 GCA line		0.17				0.13		
p=0.05 GCA tester		0.43				0.33		

Table 4.9e (*Cont'd.*)

Parental lines	**Fruit length (cm)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	4.37	-0.63**	0.40	5.40	4.65	-0.62**	0.38	1.41
CMS4626A	5.45	0.25**	0.06	4.33	5.62	0.07	0.00	1.28
CMS463D13A	6.13	0.38**	0.15	5.41	6.59	0.55**	0.31	1.78
Testers								
AC 102	5.23	-0.77**	0.60	1.46	6.31	-0.74**	0.55	0.46
SL 475	7.15	1.08**	1.17	0.56	8.19	1.14**	1.29	0.00
PL 412	5.83	0.56**	0.31	1.83	7.51	0.49**	0.24	0.15
IS 263	4.61	-1.42**	2.02	0.07	6.62	-0.82**	0.68	0.25
VR 523	7.45	0.91**	0.83	0.07	7.48	0.52**	0.27	0.05
DL 161	7.05	-0.10	0.01	3.61	6.49	-0.55**	0.30	0.46
IS 267	5.42	-0.35*	0.12	0.32	6.66	0.35**	0.12	0.10
YL 581	6.86	1.02**	1.04	0.17	7.79	0.54**	0.29	0.13
SL 473	6.07	-0.21	0.04	0.03	6.39	-0.57**	0.33	0.21
IS 262	6.29	-0.65**	0.43	0.62	6.69	-0.41**	0.17	0.13
VR 521	4.78	-1.04**	1.07	0.45	4.85	-0.94**	0.89	0.09
FL 201	9.49	0.46**	0.21	0.23	10.77	1.29**	1.66	0.10
PP 402	5.90	0.30	0.09	0.30	6.10	0.28**	0.08	0.09
C 142	5.12	-0.28	0.08	0.53	5.97	0.02	0.00	0.23
PP 414	6.60	-0.37*	0.13	0.66	6.28	-0.61**	0.37	0.70
VR 522	5.51	0.65**	0.42	0.19	6.74	0.21*	0.04	0.24
PL 406	6.42	0.61**	0.38	0.47	6.64	0.24*	0.06	0.07
E 183	5.63	-0.59**	0.34	0.31	5.94	-1.21**	1.46	0.11
IS 268	5.71	-0.19	0.04	1.69	6.40	-0.08	0.01	0.56
IS 261	7.04	0.37*	0.14	1.55	7.51	0.87**	0.75	0.32
p=0.05 GCA line		0.12				0.08		
p=0.05 GCA tester		0.31				0.21		

Table 4.9f: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for fruit width (mm) in 23 parental lines

Parental lines	**Fruit width (mm)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	9.70	-1.30**	1.69	13.03	9.00	-0.81**	0.66	2.62
CMS4626A	10.71	0.16	0.03	5.75	10.25	0.02	0.00	4.45
CMS463D13A	11.53	1.14**	1.29	9.81	11.71	0.79**	0.63	2.64
Testers								
AC 102	13.57	0.21	0.04	2.94	10.47	-0.41	0.17	0.21
SL 475	12.95	0.67*	0.45	1.61	10.11	0.30	0.09	0.23
PL 412	10.44	-1.30**	1.69	0.00	10.53	0.07	0.01	0.02
IS 263	11.94	-1.83**	3.37	0.76	8.72	-0.31	0.10	1.01
VR 523	11.50	-0.42	0.17	0.11	10.02	-0.07	0.01	0.12
DL 161	10.55	-1.70**	2.88	2.88	10.22	0.04	0.00	1.07
IS 267	12.14	-0.60	0.36	0.38	9.94	0.67*	0.45	0.66
YL 581	15.38	2.26**	5.13	1.99	11.45	0.67*	0.44	0.37
SL 473	12.10	0.81*	0.66	0.25	9.70	0.26	0.07	1.58
IS 262	12.51	1.21**	1.46	0.35	9.70	-0.38	0.14	0.42
VR 521	8.26	-2.50**	6.26	1.82	6.92	-1.57**	2.45	0.40
FL 201	18.48	1.81**	3.29	2.86	13.16	0.96**	0.91	0.09
PP 402	16.34	2.56**	6.54	6.62	10.66	1.21**	1.47	0.59
C 142	11.58	0.54	0.29	0.41	9.64	0.18	0.03	0.22
PP 414	11.13	-0.96**	0.91	1.27	8.89	-0.59*	0.34	1.32
VR 522	13.31	0.35	0.12	0.10	8.88	-0.05	0.00	0.16
PL 406	13.43	0.41	0.17	0.15	9.94	-0.23	0.05	0.74
E 183	11.98	-2.42**	5.85	0.73	9.18	-1.24**	1.54	0.18
IS 268	13.59	1.34**	1.79	1.47	9.78	0.76**	0.58	0.17
IS 261	12.43	-0.46	0.21	1.88	10.25	-0.28	0.08	0.16
p=0.05 GCA line		0.26				0.22		
p=0.05 GCA tester		0.66				0.58		

Table 4.9f (*Cont'd.*)

Parental lines	Fruit width (mm)							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	7.95	-0.88**	0.77	5.42	8.88	-1.00**	0.99	3.86
CMS4626A	8.96	0.23*	0.05	4.54	9.97	0.14*	0.02	2.06
CMS463D13A	10.70	0.64**	0.41	2.69	11.31	0.86**	0.74	2.07
Testers								
AC 102	9.98	0.18	0.03	0.76	11.34	0.00	0.00	0.54
SL 475	9.91	0.03	0.00	0.02	10.99	0.33	0.11	0.17
PL 412	9.11	0.10	0.01	0.38	10.03	-0.38*	0.14	0.03
IS 263	7.92	-1.49**	2.23	0.11	9.52	-1.21**	1.47	0.35
VR 523	8.24	-0.28	0.08	0.57	9.92	-0.26	0.07	0.08
DL 161	9.06	-0.22	0.05	0.57	9.94	-0.63**	0.39	0.21
IS 267	10.85	0.26	0.07	0.82	10.98	0.11	0.01	0.06
YL 581	12.05	2.01**	4.02	0.13	12.96	1.64**	2.71	0.51
SL 473	9.62	0.45	0.21	0.81	10.48	0.51**	0.26	0.00
IS 262	8.66	-0.54*	0.30	0.41	10.29	0.10	0.01	0.29
VR 521	6.66	-1.76**	3.11	0.46	7.28	-1.94**	3.78	0.55
FL 201	12.93	1.11**	1.23	2.09	14.85	1.29**	1.67	0.85
PP 402	11.83	1.40**	1.96	2.26	12.94	1.72**	2.97	2.19
C 142	9.33	-0.35	0.12	0.10	10.18	0.12	0.02	0.16
PP 414	9.79	-0.43	0.18	0.42	9.94	-0.66**	0.43	0.84
VR 522	10.07	-0.16	0.03	0.44	10.75	0.05	0.00	0.18
PL 406	7.98	0.58*	0.33	0.31	10.45	0.25	0.06	0.07
E 183	8.73	-1.05**	1.11	1.43	9.96	-1.57**	2.47	0.60
IS 268	11.70	1.32**	1.75	0.48	11.69	1.14**	1.30	0.11
IS 261	8.99	-1.15**	1.32	0.06	10.55	-0.63**	0.39	0.23
p=0.05 GCA line		0.19				0.13		
p=0.05 GCA tester		0.48				0.34		

Table 4.9g: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for pericarp thickness (mm) in 23 parental lines

Parental lines	**Pericarp thickness (mm)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	0.80	-0.22**	0.05	0.33	0.84	-0.06**	0.00	0.17
CMS4626A	0.95	-0.07**	0.01	0.11	0.94	-0.05**	0.00	0.31
CMS463D13A	1.20	0.29**	0.08	0.36	1.10	0.11**	0.01	0.14
Testers								
AC 102	0.95	-0.15**	0.02	0.01	0.99	-0.15**	0.02	0.00
SL 475	1.31	0.25**	0.06	0.01	1.43	0.17**	0.03	0.04
PL 412	1.22	0.09*	0.01	0.02	1.12	0.00	0.00	0.01
IS 263	1.31	-0.15**	0.02	0.01	0.76	-0.12**	0.01	0.01
VR 523	1.02	0.08*	0.01	0.01	0.94	0.01	0.00	0.01
DL 161	0.89	-0.15**	0.02	0.04	0.98	-0.12**	0.01	0.02
IS 267	1.38	0.05	0.00	0.06	0.99	0.17**	0.03	0.03
YL 581	1.38	0.30**	0.09	0.03	1.50	0.30**	0.09	0.12
SL 473	0.78	-0.10**	0.01	0.02	0.91	0.06*	0.00	0.15
IS 262	1.48	-0.02	0.00	0.04	0.71	-0.26**	0.07	0.04
VR 521	0.71	-0.34**	0.11	0.08	0.61	-0.22**	0.05	0.00
FL 201	2.21	0.10**	0.01	0.13	1.84	0.49**	0.24	0.00
PP 402	2.15	0.45**	0.20	0.10	1.47	0.22**	0.05	0.02
C 142	1.12	0.05	0.00	0.04	0.71	-0.12**	0.01	0.02
PP 414	0.96	-0.13**	0.02	0.01	0.95	-0.18**	0.03	0.02
VR 522	0.99	0.00	0.00	0.00	0.84	-0.07*	0.00	0.01
PL 406	1.24	-0.03	0.00	0.03	0.68	-0.02	0.00	0.07
E 183	1.00	-0.31**	0.10	0.16	1.19	-0.22**	0.05	0.01
IS 268	1.59	0.14**	0.02	0.00	0.99	0.02	0.00	0.01
IS 261	1.32	-0.14**	0.02	0.01	0.91	0.04	0.00	0.01
p=0.05 GCA line		0.03				0.02		
p=0.05 GCA tester		0.07				0.06		

Table 4.9g (*Cont'd.*)

Parental lines	**Pericarp thickness (mm)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	0.49	-0.09**	0.01	0.24	0.71	-0.12**	0.01	0.11
CMS4626A	0.60	0.02*	0.00	0.11	0.83	-0.04**	0.00	0.05
CMS463D13A	0.70	0.07**	0.00	0.07	1.00	0.16**	0.02	0.06
Testers								
AC 102	0.71	-0.16**	0.03	0.01	0.88	-0.15**	0.02	0.00
SL 475	1.11	0.23**	0.05	0.03	1.28	0.22**	0.05	0.00
PL 412	0.61	-0.09**	0.01	0.01	0.98	0.00	0.00	0.01
IS 263	0.62	-0.18**	0.03	0.01	0.90	-0.15**	0.02	0.00
VR 523	1.02	0.21**	0.04	0.05	0.99	0.10**	0.01	0.01
DL 161	0.71	-0.04*	0.00	0.01	0.86	-0.11**	0.01	0.01
IS 267	1.01	0.01	0.00	0.00	1.13	0.08**	0.01	0.00
YL 581	1.12	0.27**	0.07	0.04	1.33	0.29**	0.08	0.04
SL 473	0.51	-0.20**	0.04	0.00	0.74	-0.08**	0.01	0.02
IS 262	0.91	-0.04	0.00	0.01	1.03	-0.11**	0.01	0.01
VR 521	0.50	-0.28**	0.08	0.01	0.61	-0.28**	0.08	0.01
FL 201	1.69	0.28**	0.08	0.06	1.92	0.29**	0.08	0.04
PP 402	1.04	0.16**	0.03	0.05	1.55	0.28**	0.08	0.02
C 142	0.73	-0.11**	0.01	0.00	0.85	-0.06**	0.00	0.00
PP 414	0.80	-0.13**	0.02	0.00	0.91	-0.15**	0.02	0.01
VR 522	0.76	-0.02	0.00	0.05	0.86	-0.03	0.00	0.00
PL 406	0.59	-0.04*	0.00	0.02	0.84	-0.03	0.00	0.00
E 183	0.60	-0.22**	0.05	0.00	0.93	-0.25**	0.06	0.03
IS 268	1.09	0.26**	0.07	0.02	1.22	0.14**	0.02	0.00
IS 261	0.87	0.12**	0.01	0.01	1.03	0.01	0.00	0.00
p=0.05 GCA (Line)		0.02				0.01		
p=0.05 GCA (Tester)		0.04				0.03		

Table 4.9h: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for number of fruits plant^{-1} in 23 parental lines

Parental lines	**Number of fruits plant^{-1}**							
	E$_1$				**E$_2$**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	277.88	15.94**	254.01	9208.33	233.63	12.94**	167.33	30729.03
CMS4626A	296.34	-1.28	1.65	8473.25	206.30	26.38**	695.86	34621.23
CMS463D13A	216.49	-14.65**	214.74	5206.89	178.25	-39.31**	1545.64	23804.15
Testers								
AC 102	208.34	-45.95**	2111.33	235.88	137.13	-59.71**	3565.73	4242.66
SL 475	259.84	-0.53	0.28	345.63	235.05	21.14**	446.87	1306.01
PL 412	303.10	59.01**	3482.21	4947.09	189.43	72.91**	5315.85	6605.01
IS 263	200.01	-14.76*	218.00	3159.99	200.68	8.31	69.10	11104.02
VR 523	232.69	7.84	61.44	236.12	204.19	-7.87	61.90	3032.25
DL 161	287.17	89.96**	8092.81	42.76	211.13	29.01**	841.56	1091.28
IS 267	245.16	20.42**	416.79	1189.47	190.71	44.01**	1936.98	3466.09
YL 581	194.87	-48.68**	2369.31	701.01	160.70	61.67**	3803.65	6641.11
SL 473	273.80	-17.22*	296.69	1314.99	208.37	-22.02**	484.94	3910.57
IS 262	253.91	30.35**	921.08	276.92	147.36	18.35*	336.81	9983.48
VR 521	237.70	-20.67**	427.21	937.02	253.71	3.44	11.86	8113.72
FL 201	147.92	-69.14**	4779.80	1370.58	109.52	-27.10**	734.41	1860.62
PP 402	150.07	-37.94**	1439.69	2428.24	93.32	-1.22	1.48	5096.93
C 142	260.73	75.40**	5685.82	650.02	185.71	26.97**	727.56	7750.50
PP 414	303.21	-7.83	61.25	594.42	171.27	-67.27**	4524.73	3664.70
VR 522	249.68	16.02*	256.56	1069.55	149.00	-11.24	126.32	4302.59
PL 406	239.11	21.05**	442.91	1843.42	159.02	-34.31**	1176.92	418.44
E 183	144.97	-81.07**	6572.21	774.63	177.16	-75.55**	5707.71	949.03
IS 268	231.18	38.22**	1460.41	342.49	152.58	23.89**	570.77	5137.87
IS 261	204.12	-14.47*	209.42	428.25	177.14	-3.44	11.81	477.51
p=0.05 GCA line		5.50				5.45		
p=0.05 GCA tester		14.20				14.07		

Table 4.9h (*Cont'd.*)

Parental lines	**Number of fruits plant^{-1}**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	
Lines								
CMS4611A	79.69	18.65**	347.79	23438.24	197.07	15.84**	250.93	9224.58
CMS4626A	84.21	-9.75**	95.14	17522.07	195.62	5.11**	26.15	7809.25
CMS463D13A	113.06	-8.89**	79.12	11154.25	169.27	-20.95**	439.09	5317.72
Testers								
AC 102	123.74	-7.71	59.46	4824.91	156.40	-37.79**	1428.18	2379.74
SL 475	152.29	78.51**	6164.20	15.61	215.73	33.04**	1091.76	362.43
PL 412	70.56	-29.88**	892.82	2383.88	187.70	34.01**	1156.91	617.48
IS 263	61.42	-57.97**	3360.69	26.67	154.04	-21.47**	461.16	291.69
VR 523	207.56	48.33**	2335.43	2711.56	214.81	16.10**	259.18	580.79
DL 161	184.90	106.01**	11237.22	2278.39	227.74	74.99**	5623.77	247.76
IS 267	61.54	-17.76**	315.49	3818.78	165.80	15.55**	241.95	1890.29
YL 581	82.46	-11.35**	128.88	114.27	146.01	0.55	0.30	934.39
SL 473	146.43	35.12**	1233.54	9286.11	209.53	-1.37	1.89	1741.87
IS 262	83.41	-18.13**	328.52	2069.94	161.56	10.19**	103.88	2377.54
VR 521	103.27	3.13	9.77	8.59	198.23	-4.70	22.09	483.52
FL 201	34.38	-72.00**	5184.50	1023.91	97.27	-56.08**	3144.95	158.13
PP 402	44.29	-38.79**	1504.53	393.70	95.89	-25.98**	675.12	1569.34
C 142	120.44	57.19**	3270.67	3851.02	188.96	53.19**	2829.09	3203.03
PP 414	62.15	-68.48**	4690.06	687.66	178.88	-47.86**	2290.47	496.79
VR 522	65.62	6.91	47.72	5467.38	154.76	3.90	15.17	3269.19
PL 406	58.30	-2.69	7.26	810.66	152.14	-5.32	28.28	346.41
E 183	84.06	-28.51**	812.86	941.13	135.40	-61.71**	3808.09	190.66
IS 268	76.75	15.40**	237.21	9506.10	153.51	25.84**	667.50	879.89
IS 261	89.55	2.69	7.24	1894.29	156.94	-5.07	25.73	330.64
p=0.05 GCA line		2.99				2.89		
p=0.05 GCA tester		7.73				7.46		

Table 4.9i: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for number of seed fruit^{-1} in 23 parental lines

Parental lines	Number of seed fruit^{-1}							
	E_1				E_2			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	51.83	-2.83**	8.01	571.57	40.53	-1.87**	3.48	579.36
CMS4626A	44.97	-1.11	1.22	700.69	37.53	-0.45	0.20	505.35
CMS463D13A	59.33	3.94**	15.49	365.21	53.07	2.31**	5.36	207.94
Testers								
AC 102	46.73	-5.07**	25.65	193.80	37.27	-6.07**	36.81	186.35
SL 475	64.73	20.96**	439.21	70.34	55.33	17.59**	309.35	23.08
PL 412	53.43	9.55**	91.13	26.00	46.93	14.44**	208.63	23.43
IS 263	47.83	-6.95**	48.36	171.56	40.57	-5.15**	26.47	150.54
VR 523	46.17	3.61*	13.05	3.64	38.07	5.60**	31.35	13.08
DL 161	49.13	-8.32**	69.23	40.54	39.43	-5.92**	35.08	18.10
IS 267	63.73	10.07**	101.37	23.86	53.67	12.84**	164.97	62.53
YL 581	31.43	-14.47**	209.24	83.13	22.07	-15.28**	233.43	63.93
SL 473	36.47	-4.26**	18.19	9.57	27.33	-4.40**	19.36	7.55
IS 262	38.67	-8.72**	76.05	5.41	33.33	-9.11**	83.02	0.19
VR 521	45.97	9.76**	95.20	34.79	39.53	7.99**	63.81	42.80
FL 201	26.67	-17.19**	295.40	205.42	20.83	-14.58**	212.53	64.24
PP 402	29.73	-12.06**	145.56	236.93	23.53	-10.07**	101.35	228.92
C 142	51.53	10.51**	110.52	77.24	46.80	9.60**	92.15	122.15
PP 414	31.73	-16.21**	262.75	39.41	22.07	-15.93**	253.89	30.07
VR 522	41.93	4.82**	23.27	41.78	30.53	0.79	0.62	69.86
PL 406	56.77	12.49**	156.01	12.73	45.33	11.82**	139.75	50.19
E 183	28.37	-22.00**	483.93	38.05	22.90	-20.88**	435.90	22.72
IS 268	59.77	11.73**	137.71	246.12	50.63	11.20**	125.43	92.85
IS 261	61.93	21.75**	472.89	77.15	55.43	15.51**	240.58	20.08
p=0.05 GCA line		1.14				0.92		
p=0.05 GCA tester		2.95				2.37		

Table 4.9i (*Cont'd.*)

Parental lines	Number of seed fruit^{-1}							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	**Mean**	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	35.70	-1.44**	2.06	136.96	42.69	-2.04**	4.18	355.03
CMS4626A	30.93	-0.90*	0.80	132.07	37.81	-0.82**	0.67	328.92
CMS463D13A	45.33	2.33**	5.43	176.44	52.58	2.86**	8.18	176.55
Testers								
AC 102	33.33	-7.63**	58.29	38.58	39.11	-6.26**	39.13	125.01
SL 475	48.53	15.61**	243.65	4.98	56.20	18.05**	325.86	18.60
PL 412	41.23	13.94**	194.40	16.01	47.20	12.64**	159.88	5.18
IS 263	36.17	-6.80**	46.26	12.90	41.52	-6.30**	39.69	93.16
VR 523	35.33	7.81**	60.99	1.59	39.86	5.67**	32.19	4.08
DL 161	31.77	1.52	2.31	49.00	40.11	-4.24**	17.99	23.81
IS 267	49.43	12.08**	145.83	2.43	55.61	11.66**	136.02	21.42
YL 581	16.80	-16.81**	282.67	7.41	23.43	-15.52**	240.83	40.99
SL 473	20.43	-7.54**	56.78	15.25	28.08	-5.40**	29.16	2.46
IS 262	24.83	-6.49**	42.13	2.37	32.28	-8.11**	65.73	1.62
VR 521	31.43	5.57**	30.97	57.95	38.98	7.77**	60.38	39.34
FL 201	15.13	-16.60**	275.62	1.95	20.88	-16.12**	259.93	62.02
PP 402	18.33	-11.25**	126.48	44.48	23.87	-11.13**	123.79	153.09
C 142	38.07	10.38**	107.66	13.90	45.47	10.16**	103.28	54.53
PP 414	16.83	-15.62**	244.11	23.27	23.54	-15.92**	253.52	30.54
VR 522	22.73	-1.15	1.31	66.60	31.73	1.49	2.22	47.35
PL 406	40.73	12.74**	162.38	1.94	47.61	12.35**	152.56	14.44
E 183	15.63	-16.98**	288.30	30.16	22.30	-19.95**	398.08	28.92
IS 268	43.07	11.39**	129.67	42.88	51.16	11.44**	130.89	84.24
IS 261	50.93	15.84**	250.99	11.81	56.10	17.70**	313.28	9.70
p=0.05 GCA line		0.80				0.59		
p=0.05 GCA tester		2.05				1.53		

Table 4.9j: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for 1000 seed weight (g) in 23 parental lines

Parental lines	1000 seed weight (g)							
	E_1				E_2			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	4.66	-0.21**	0.05	0.80	4.35	-0.20**	0.04	0.78
CMS4626A	4.75	-0.04	0.00	0.91	4.47	-0.05	0.00	0.73
CMS463D13A	4.89	0.26**	0.07	0.99	4.56	0.25**	0.06	0.89
Testers								
AC 102	3.68	-1.02**	1.05	0.02	3.36	-1.04**	1.09	0.00
SL 475	5.26	0.43**	0.18	0.28	4.97	0.42**	0.17	0.20
PL 412	4.98	-0.32**	0.11	0.04	4.76	-0.31*	0.10	0.04
IS 263	6.49	1.01**	1.02	0.04	6.19	1.05**	1.10	0.04
VR 523	5.49	0.26*	0.07	0.11	5.20	0.25*	0.06	0.07
DL 161	3.53	-1.27**	1.62	0.07	3.31	-1.30**	1.70	0.07
IS 267	5.47	0.16	0.02	0.12	5.18	0.21	0.04	0.10
YL 581	7.32	1.01**	1.01	0.01	6.99	1.02**	1.04	0.05
SL 473	5.64	0.22	0.05	0.09	5.37	0.22	0.05	0.06
IS 262	6.17	0.51**	0.26	0.12	5.88	0.62**	0.38	0.04
VR 521	3.21	-1.51**	2.27	0.22	2.89	-1.56**	2.43	0.17
FL 201	7.51	1.03**	1.06	0.07	7.05	1.02**	1.03	0.06
PP 402	5.78	0.66**	0.44	0.03	5.56	0.64**	0.41	0.05
C 142	3.89	-0.97**	0.93	0.29	3.56	-0.98**	0.95	0.22
PP 414	5.11	-0.06	0.00	0.13	4.85	-0.10	0.01	0.15
VR 522	5.14	0.30*	0.09	0.65	4.89	0.27*	0.07	0.65
PL 406	4.67	-0.47**	0.22	0.00	4.36	-0.45**	0.20	0.01
E 183	4.26	-1.02**	1.05	0.07	3.88	-1.06**	1.13	0.12
IS 268	5.46	0.27*	0.07	0.15	5.22	0.30*	0.09	0.12
IS 261	5.93	0.80**	0.64	0.19	5.69	0.80**	0.64	0.17
p=0.05 GCA line		0.09				0.09		
p=0.05 GCA tester		0.24				0.24		

Table 4.9j (*Cont'd.*)

Parental lines	1000 seed weight (g)							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	**Mean**	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	4.19	-0.21**	0.05	0.85	4.40	-0.21**	0.04	0.80
CMS4626A	4.27	-0.06	0.00	0.75	4.50	-0.05	0.00	0.77
CMS463D13A	4.34	0.27**	0.07	0.76	4.60	0.26**	0.07	0.84
Testers								
AC 102	3.11	-1.05**	1.10	0.00	3.39	-1.04**	1.08	0.00
SL 475	4.81	0.41**	0.17	0.14	5.02	0.42**	0.18	0.20
PL 412	4.60	-0.30*	0.09	0.06	4.78	-0.31**	0.10	0.05
IS 263	6.06	1.06**	1.13	0.04	6.25	1.04**	1.08	0.04
VR 523	4.99	0.17	0.03	0.06	5.23	0.22**	0.05	0.08
DL 161	3.08	-1.30**	1.69	0.09	3.31	-1.29**	1.67	0.07
IS 267	5.01	0.22	0.05	0.10	5.22	0.20**	0.04	0.11
YL 581	6.83	1.04**	1.08	0.05	7.05	1.02**	1.05	0.04
SL 473	5.13	0.25*	0.06	0.08	5.38	0.23**	0.05	0.07
IS 262	5.66	0.62**	0.39	0.05	5.91	0.58**	0.34	0.06
VR 521	2.71	-1.63**	2.66	0.14	2.94	-1.57**	2.45	0.18
FL 201	6.89	1.03**	1.06	0.03	7.15	1.02**	1.05	0.05
PP 402	5.36	0.68**	0.46	0.07	5.57	0.66**	0.44	0.05
C 142	3.39	-1.02**	1.03	0.18	3.62	-0.99**	0.97	0.22
PP 414	4.65	-0.14	0.02	0.16	4.87	-0.10	0.01	0.15
VR 522	4.65	0.28*	0.08	0.82	4.90	0.29**	0.08	0.70
PL 406	4.18	-0.47**	0.23	0.01	4.41	-0.46**	0.22	0.01
E 183	3.61	-1.14**	1.30	0.12	3.92	-1.08**	1.16	0.10
IS 268	5.03	0.47**	0.22	0.00	5.24	0.35**	0.12	0.06
IS 261	5.53	0.82**	0.67	0.16	5.72	0.80**	0.65	0.17
p=0.05 GCA line		0.09				0.05		
p=0.05 GCA tester		0.24				0.14		

Table 4.9k: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for total yield plant^{-1} (kg) in 23 parental lines

Parental lines	Total yield plant^{-1} (kg)							
	E$_1$				E$_2$			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	0.45	-0.10**	0.01	0.22	0.46	-0.11**	0.01	0.25
CMS4626A	0.50	-0.07**	0.005	0.16	0.45	0.07**	0.005	0.19
CMS463D13A	0.61	0.17**	0.03	0.26	0.47	0.04**	0.002	0.29
Testers								
AC 102	0.59	-0.19**	0.03	0.02	0.38	-0.29**	0.08	0.03
SL 475	0.94	0.05	0.002	0.01	0.73	0.25**	0.06	0.03
PL 412	1.07	0.13**	0.02	0.09	0.69	0.15**	0.02	0.04
IS 263	0.51	-0.24**	0.06	0.03	0.32	-0.01	0.000	0.07
VR 523	0.57	0.11**	0.01	0.01	0.45	0.00	0.000	0.08
DL 161	0.84	0.35**	0.12	0.01	0.52	-0.04*	0.002	0.06
IS 267	0.63	0.16**	0.03	0.09	0.44	0.15**	0.02	0.01
YL 581	0.54	-0.06**	0.004	0.01	0.51	0.29**	0.09	0.02
SL 473	0.67	-0.06**	0.004	0.03	0.45	-0.05**	0.002	0.05
IS 262	0.84	0.18**	0.03	0.04	0.32	-0.06**	0.004	0.04
VR 521	0.34	-0.40**	0.16	0.03	0.24	-0.32**	0.10	0.03
FL 201	0.68	-0.11**	0.01	0.02	0.39	0.23**	0.06	0.16
PP 402	0.51	0.11**	0.01	0.04	0.25	0.26**	0.07	0.03
C 142	0.76	0.28**	0.08	0.001	0.32	0.10**	0.01	0.01
PP 414	0.67	-0.23**	0.05	0.07	0.28	-0.28**	0.08	0.02
VR 522	0.85	0.08**	0.01	0.00	0.41	0.00	0.00	0.01
PL 406	0.85	0.06*	0.003	0.06	0.33	-0.13**	0.02	0.01
E 183	0.27	-0.47**	0.22	0.03	0.26	-0.39**	0.15	0.03
IS 268	0.71	0.36**	0.13	0.03	0.36	0.18**	0.03	0.01
IS 261	0.64	-0.10**	0.01	0.01	0.45	-0.03	0.001	0.002
p=0.05 GCA line		0.02				0.01		
p=0.05 GCA tester		0.05				0.03		

Table 4.9k (*Cont'd*)

Parental lines	**Total yield plant^{-1} (kg)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	0.19	-0.04**	0.002	0.11	0.37	-0.09**	0.01	0.06
CMS4626A	0.28	0.01	0.0001	0.06	0.41	0.003	0.00	0.05
CMS463D13A	0.39	0.04**	0.001	0.07	0.49	0.08**	0.01	0.09
Testers								
AC 102	0.28	-0.08**	0.01	0.02	0.42	-0.19**	0.03	0.02
SL 475	0.61	0.27**	0.07	0.0004	0.76	0.19**	0.04	0.0003
PL 412	0.23	-0.08**	0.01	0.002	0.67	0.07**	0.004	0.01
IS 263	0.16	-0.22**	0.05	0.002	0.33	-0.16**	0.02	0.001
VR 523	0.60	0.25**	0.06	0.01	0.54	0.12**	0.01	0.01
DL 161	0.45	0.23**	0.05	0.003	0.60	0.18**	0.03	0.01
IS 267	0.21	-0.05**	0.002	0.01	0.43	0.09**	0.01	0.01
YL 581	0.36	0.07**	0.005	0.01	0.47	0.10**	0.01	0.001
SL 473	0.41	0.08**	0.01	0.04	0.51	-0.01	0.0002	0.02
IS 262	0.26	-0.09**	0.01	0.02	0.47	0.01	0.0001	0.001
VR 521	0.17	-0.15**	0.02	0.01	0.25	-0.29**	0.08	0.02
FL 201	0.21	-0.12**	0.02	0.003	0.43	0.00	0.00	0.01
PP 402	0.19	0.03**	0.001	0.01	0.32	0.13**	0.02	0.01
C 142	0.37	0.11**	0.01	0.01	0.48	0.16**	0.03	0.002
PP 414	0.18	-0.23**	0.05	0.002	0.38	-0.25**	0.06	0.02
VR 522	0.22	0.04**	0.002	0.03	0.49	0.04**	0.002	0.002
PL 406	0.18	0.05**	0.003	0.01	0.45	-0.01	0.0001	0.02
E 183	0.22	-0.12**	0.01	0.02	0.25	-0.33**	0.11	0.02
IS 268	0.27	0.03*	0.001	0.02	0.45	0.19**	0.04	0.01
IS 261	0.28	-0.01	0.0002	0.01	0.46	-0.05**	0.002	0.001
p=0.05 GCA line		0.01				0.01		
p=0.05 GCA tester		0.02				0.02		

Table 4.9l: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for ascorbic acid (mg.100g^{-1}) in 23 parental lines

Parental lines	**Ascorbic acid (mg 100^{-1}g)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	86.33	-9.80**	96.06	2092.36	92.56	-2.94**	8.64	1455.60
CMS4626A	113.22	2.50**	6.26	1573.35	120.60	-1.84*	3.40	1693.34
CMS463D13A	125.51	7.30**	53.29	1113.92	129.70	4.78**	22.88	1126.73
Testers								
AC 102	168.68	23.07**	532.42	74.54	139.69	-8.93**	79.81	237.18
SL 475	131.54	1.89	3.58	3.20	180.76	33.31**	1109.73	191.54
PL 412	165.14	34.12**	1164.38	208.37	195.76	25.67**	658.87	211.08
IS 263	164.76	23.65**	559.10	319.47	177.51	17.85**	318.61	322.21
VR 523	152.26	15.12**	228.67	672.57	186.19	35.46**	1257.52	97.70
DL 161	132.26	-6.58**	43.29	172.71	142.93	-2.52	6.36	6.05
IS 267	179.04	26.54**	704.30	291.51	140.50	-9.86**	97.18	1.54
YL 581	69.34	-44.80**	2006.87	144.65	74.16	-49.98**	2497.66	292.34
SL 473	140.43	-6.99**	48.80	387.71	149.30	-9.60**	92.11	225.09
IS 262	143.76	-15.38**	236.66	32.83	151.34	-1.16	1.35	1249.28
VR 521	129.26	-3.65*	13.34	34.63	189.76	41.00**	1681.27	120.51
FL 201	89.14	-42.53**	1808.83	134.23	92.51	-47.58**	2263.73	118.61
PP 402	95.02	-34.56**	1194.49	120.56	101.59	-32.80**	1075.97	532.04
C 142	176.47	22.16**	490.95	1177.21	159.06	18.16**	329.69	75.59
PP 414	92.30	-45.51**	2071.09	6.44	95.79	-54.43**	2962.85	33.93
VR 522	147.11	-1.13	1.28	438.10	155.54	-1.73	3.00	281.37
PL 406	160.23	25.53**	651.65	18.11	161.29	26.22**	687.23	119.25
E 183	124.07	-31.62**	999.70	7.29	136.73	-31.03**	963.16	78.56
IS 268	182.00	47.82**	2286.93	62.38	169.23	16.46**	271.00	78.99
IS 261	171.46	12.85**	165.09	473.14	186.48	35.50**	1260.21	2.81
p=0.05 GCA line		1.30				1.46		
p=0.05 GCA tester		3.36				3.77		

Table 4.9l (*Cont'd.*)

Parental lines	Ascorbic acid (mg 100^{-1}g)							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	73.03	-7.92**	62.73	914.69	83.97	-6.89**	47.43	774.93
CMS4626A	99.57	4.08**	16.68	1132.14	111.13	1.58**	2.50	669.21
CMS463D13A	111.16	3.84**	14.71	1088.55	122.12	5.31**	28.16	692.01
Testers								
AC 102	144.14	13.84**	191.55	443.93	150.84	9.33**	86.99	4.99
SL 475	158.04	12.84**	164.93	581.40	156.78	16.02**	256.49	49.05
PL 412	152.55	28.34**	803.29	34.03	171.15	29.38**	863.06	79.05
IS 263	150.58	22.30**	497.25	41.69	164.28	21.26**	452.19	11.31
VR 523	137.86	11.34**	128.50	14.57	158.77	20.64**	425.99	64.54
DL 161	119.39	-7.40**	54.74	120.32	131.53	-5.50**	30.25	55.02
IS 267	112.81	-6.17**	38.12	77.30	144.12	3.50**	12.26	30.14
YL 581	56.21	-47.64**	2269.45	256.40	66.57	-47.47**	2253.51	220.40
SL 473	126.82	-7.31**	53.43	215.23	138.85	-7.96**	63.43	263.88
IS 262	125.71	-12.64**	159.79	149.87	140.27	-9.73**	94.65	271.79
VR 521	160.70	31.50**	992.05	1.36	159.91	22.95**	526.67	29.87
FL 201	76.31	-43.72**	1911.53	206.44	85.99	-44.61**	1990.05	127.86
PP 402	79.29	-37.60**	1414.00	326.54	91.97	-34.99**	1224.22	262.07
C 142	133.78	18.97**	359.74	96.56	156.44	19.76**	390.48	281.74
PP 414	77.32	-46.81**	2191.58	67.40	88.47	-48.92**	2393.02	18.95
VR 522	132.65	8.07**	65.14	165.65	145.10	1.74	3.01	279.39
PL 406	166.42	29.55**	873.34	64.18	162.65	27.10**	734.32	15.60
E 183	105.59	-28.60**	818.14	168.64	122.13	-30.42**	925.30	20.51
IS 268	149.58	26.45**	699.37	39.87	166.93	30.24**	914.65	32.00
IS 261	147.01	34.71**	1204.95	63.99	168.32	27.69**	766.56	17.99
p=0.05 GCA line		1.28				0.78		
p=0.05 GCA tester		3.32				2.03		

Table 4.9m: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for oleoresin content (%) in 23 parental lines

Parental lines	Oleoresin content (%)							
	E_1				E_2			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	Mean	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	9.73	-0.61**	0.38	11.71	9.29	0.08	0.01	10.59
CMS4626A	11.32	0.52**	0.27	25.17	10.13	-0.57**	0.33	22.96
CMS463D13A	10.93	0.10	0.01	30.12	11.68	0.49**	0.24	26.84
Testers								
AC 102	7.71	-2.08**	4.33	1.13	7.94	-3.65**	13.33	0.30
SL 475	11.78	4.12**	16.98	2.26	12.64	2.87**	8.24	0.91
PL 412	8.32	-0.56**	0.32	2.66	9.66	-0.23	0.05	10.95
IS 263	9.51	1.46**	2.15	12.26	9.03	-0.54**	0.29	0.03
VR 523	10.92	4.26**	18.11	1.75	14.66	4.71**	22.14	0.10
DL 161	12.11	2.75**	7.57	0.61	11.04	2.28**	5.20	16.41
IS 267	10.31	-0.59**	0.35	9.72	12.96	1.07**	1.14	1.42
YL 581	8.90	-2.15**	4.63	0.09	9.33	-2.01**	4.04	1.15
SL 473	9.49	-1.37**	1.88	0.48	10.02	-1.26**	1.59	2.94
IS 262	7.32	-2.12**	4.48	5.02	9.49	-1.80**	3.23	8.45
VR 521	10.96	1.22**	1.49	0.87	11.71	1.50**	2.25	6.54
FL 201	8.33	-1.89**	3.58	0.59	8.66	-2.23**	4.96	1.10
PP 402	10.96	0.71**	0.50	2.38	13.72	2.25**	5.05	1.14
C 142	11.30	3.05**	9.28	6.37	10.12	0.62**	0.39	2.15
PP 414	7.57	-3.06**	9.34	0.97	9.78	-3.24**	10.50	1.27
VR 522	7.75	-0.74**	0.55	8.42	10.98	0.55**	0.30	2.14
PL 406	11.32	2.42**	5.87	7.82	12.13	1.24**	1.54	0.26
E 183	7.86	-3.19**	10.14	0.13	7.12	-4.05**	16.44	0.49
IS 268	9.70	-1.54**	2.38	3.24	9.26	-1.03**	1.06	1.91
IS 261	10.69	-0.70**	0.48	0.21	13.40	2.96**	8.74	0.73
p=0.05 GCA line		0.15				0.15		
p=0.05 GCA tester		0.38				0.38		

Table 4.9m (*Cont'd.*)

Parental lines	**Oleoresin content (%)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	7.82	-0.66**	0.43	3.29	8.95	-0.40**	0.16	4.83
CMS4626A	8.94	0.19**	0.04	4.17	10.13	0.05	0.00	9.08
CMS463D13A	9.03	0.47**	0.22	6.49	10.55	0.35**	0.12	9.92
Testers								
AC 102	5.91	-2.03**	4.11	1.27	7.19	-2.59**	6.69	0.20
SL 475	9.01	2.08**	4.32	0.45	11.14	3.02**	9.14	0.10
PL 412	6.31	-0.57**	0.32	0.30	8.10	-0.45**	0.20	1.81
IS 263	7.75	-0.32*	0.10	2.34	8.76	0.20	0.04	2.55
VR 523	8.71	1.02**	1.03	1.30	11.43	3.33**	11.06	0.73
DL 161	9.30	1.92**	3.68	1.43	10.82	2.32**	5.37	3.99
IS 267	8.43	0.52**	0.27	0.04	10.57	0.33**	0.11	0.64
YL 581	6.95	-1.29**	1.66	0.18	8.39	-1.82**	3.30	0.27
SL 473	7.56	-1.05**	1.10	0.81	9.03	-1.23**	1.51	0.03
IS 262	5.42	-1.97**	3.89	0.36	7.41	-1.96**	3.85	3.65
VR 521	8.93	1.58**	2.48	1.33	10.53	1.43**	2.05	2.13
FL 201	7.02	-1.16**	1.34	0.23	8.00	-1.76**	3.09	0.58
PP 402	9.85	0.61**	0.37	0.36	11.51	1.19**	1.41	1.02
C 142	10.20	1.75**	3.06	0.06	10.54	1.81**	3.26	0.97
PP 414	5.49	-2.40**	5.75	0.04	7.61	-2.90**	8.40	0.29
VR 522	9.26	1.97**	3.86	0.75	9.33	0.59**	0.35	3.01
PL 406	7.59	0.39*	0.15	0.19	10.35	1.35**	1.83	0.69
E 183	5.73	-2.29**	5.25	0.41	6.90	-3.18**	10.09	0.23
IS 268	8.01	0.13	0.02	1.92	8.99	-0.82**	0.67	0.64
IS 261	9.01	1.13**	1.27	0.16	11.03	1.13**	1.27	0.31
p=0.05 GCA line		0.11				0.08		
p=0.05 GCA tester		0.30				0.21		

Table 4.9n: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for capsaicin content (%) in 23 parental lines

Parental lines	**Capsaicin content (%)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	0.49	-0.05**	0.003	0.06	0.52	-0.03**	0.0009	0.01
CMS4626A	0.61	0.04**	0.002	0.08	0.65	0.01**	0.0002	0.03
CMS463D13A	0.56	0.01**	0.0002	0.09	0.63	0.02**	0.0003	0.02
Testers								
AC 102	0.47	-0.10**	0.01	0.0002	0.53	-0.12**	0.02	0.0012
SL 475	0.86	0.25**	0.06	0.003	0.77	0.20**	0.04	0.0001
PL 412	0.42	-0.08**	0.01	0.001	0.41	-0.08**	0.01	0.0069
IS 263	0.76	0.16**	0.03	0.02	0.73	0.09**	0.01	0.0063
VR 523	0.56	0.10**	0.01	0.001	0.60	-0.01	0.00003	0.0030
DL 161	0.71	0.23**	0.05	0.01	0.85	0.27**	0.07	0.0003
IS 267	0.52	-0.03**	0.001	0.01	0.62	-0.03**	0.001	0.0029
YL 581	0.32	-0.22**	0.05	0.01	0.35	-0.19**	0.04	0.0016
SL 473	0.42	-0.13**	0.02	0.01	0.46	-0.10**	0.01	0.0008
IS 262	0.77	0.20**	0.04	0.0002	0.75	0.15**	0.02	0.0001
VR 521	0.48	0.01	0.00	0.02	0.61	0.02*	0.0003	0.0056
FL 201	0.33	-0.21**	0.04	0.01	0.34	-0.20**	0.04	0.0002
PP 402	0.33	-0.11**	0.01	0.01	0.39	-0.09**	0.01	0.0113
C 142	0.80	0.15**	0.02	0.02	0.84	0.21**	0.04	0.0091
PP 414	0.42	-0.05**	0.002	0.01	0.42	-0.14**	0.02	0.0013
VR 522	0.39	-0.13**	0.02	0.002	0.53	-0.04**	0.002	0.0065
PL 406	0.62	0.11**	0.01	0.03	0.57	0.04**	0.001	0.0033
E 183	0.34	-0.21**	0.04	0.01	0.37	-0.20**	0.04	0.0003
IS 268	0.63	0.05**	0.003	0.04	0.71	0.02*	0.000	0.0057
IS 261	0.52	0.00	0.00	0.02	0.84	0.24**	0.06	0.0007
p=0.05 GCA line		0.01				0.01		
p=0.05 GCA tester		0.01				0.02		

Table 4.9n (*Cont'd.*)

Parental lines	Capsaicin content (%)							
	E_3				Pooled			
	Mean	g_i	σ^2_{gi}	σ^2_{si}	**Mean**	g_i	σ^2_{gi}	σ^2_{si}
Lines								
CMS4611A	0.39	-0.06**	0.003	0.04	0.47	-0.05**	0.0023	0.02
CMS4626A	0.50	0.03**	0.001	0.03	0.59	0.03**	0.0007	0.02
CMS463D13A	0.51	0.03**	0.001	0.04	0.57	0.02**	0.0004	0.02
Testers								
AC 102	0.37	-0.09**	0.009	0.001	0.46	-0.11**	0.011	0.000
SL 475	0.52	0.13**	0.018	0.012	0.72	0.19**	0.037	0.001
PL 412	0.66	0.18**	0.032	0.006	0.50	0.01	0.000	0.004
IS 263	0.61	0.15**	0.021	0.009	0.70	0.13**	0.017	0.002
VR 523	0.78	0.18**	0.032	0.005	0.65	0.09**	0.008	0.001
DL 161	0.39	-0.06**	0.003	0.006	0.65	0.14**	0.021	0.001
IS 267	0.55	0.05**	0.002	0.003	0.56	0.00	0.000	0.005
YL 581	0.23	-0.19**	0.037	0.005	0.30	-0.20**	0.041	0.002
SL 473	0.32	-0.11**	0.013	0.008	0.40	-0.12**	0.013	0.004
IS 262	0.57	0.11**	0.011	0.020	0.70	0.15**	0.023	0.002
VR 521	0.64	0.13**	0.017	0.001	0.58	0.05**	0.003	0.002
FL 201	0.22	-0.18**	0.033	0.000	0.29	-0.20**	0.039	0.001
PP 402	0.24	-0.15**	0.022	0.002	0.32	-0.12**	0.013	0.003
C 142	0.41	0.02**	0.001	0.000	0.68	0.13**	0.016	0.000
PP 414	0.33	-0.12**	0.015	0.002	0.39	-0.10**	0.010	0.003
VR 522	0.57	0.06**	0.003	0.001	0.50	-0.04**	0.001	0.001
PL 406	0.65	0.13**	0.018	0.013	0.61	0.09**	0.009	0.007
E 183	0.26	-0.21**	0.045	0.009	0.32	-0.21**	0.043	0.003
IS 268	0.46	-0.01	0.0002	0.004	0.60	0.02**	0.000	0.004
IS 261	0.42	0.00	0.000	0.005	0.59	0.08**	0.006	0.005
p=0.05 GCA line		0.01				0.00		
p=0.05 GCA tester		0.02				0.01		

Table 4.9o: Mean, general combining ability (GCA) effects (g_i), GCA (σ^2_{gi}) and SCA variances (σ^2_{si}) for scoville heat units (SHU) in 23 parental lines

Parental lines	**Scoville heat units (SHU)**							
	E_1				**E_2**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	78506.66	-8671.11**	75188168.0	1594754048.0	82938.66	-4792.44**	22967522.0	310688832.0
CMS4626A	98346.66	6403.56**	41005524.0	1927236608.0	104613.34	2212.89**	4896877.5	801692672.0
CMS463D13A	89013.34	2267.56**	5141808.5	2177078784.0	100240.00	2579.56**	6654107.5	603310016.0
Testers								
AC 102	74826.66	-15853.33**	251328160.0	4487523.5	85264.00	-19810.58**	392459008.0	29626206.0
SL 475	137973.33	39577.78**	1566400512.0	78053576.0	122874.66	31261.42**	977276480.0	3233501.7
PL 412	66613.34	-12226.67**	149491392.0	23177514.0	66016.00	-12310.13**	151539392.0	176193536.0
IS 263	121973.34	26173.33**	685043392.0	421352224.0	117040.00	13965.42**	195033008.0	159734000.0
VR 523	90080.00	16342.22**	267068240.0	32822364.0	96698.66	-898.58	807442.0	76998768.0
DL 161	114080.00	36253.33**	1314304128.0	172018480.0	135690.67	42461.42**	1802972288.0	6481004.0
IS 267	82986.66	-4795.56**	22997354.0	318899232.0	99056.00	-4560.80**	20800894.0	72233160.0
YL 581	50720.00	-35444.45**	1256308736.0	164439360.0	55248.00	-31069.24**	965297920.0	41541216.0
SL 473	66613.34	-21044.45**	442868672.0	156448736.0	74032.00	-16029.24**	256936672.0	21364788.0
IS 262	123680.00	31897.78**	1017468224.0	4978664.0	120688.00	23330.76**	544324160.0	1688982.5
VR 521	76213.34	1053.33	1109511.2	479139648.0	98357.34	2740.53*	7510523.5	144377872.0
FL 201	52106.67	-32937.78**	1084897152.0	311280384.0	53978.67	-32720.80**	1070650816.0	6240985.0
PP 402	52533.33	-17791.11**	316523648.0	233983184.0	61930.67	-14258.58**	203307056.0	286758752.0
C 142	127200.00	23684.45**	560952960.0	394817184.0	134314.67	32809.87**	1076487424.0	231966112.0
PP 414	67413.34	-7266.67**	52804444.0	307116224.0	67098.66	-22384.80**	501079296.0	32677192.0
VR 522	63093.33	-20315.55**	412721760.0	48859908.0	84240.00	-6674.58**	44549988.0	166295136.0
PL 406	98453.34	17711.11**	313683456.0	833573632.0	91269.34	5892.53**	34721948.0	83532504.0
E 183	54666.67	-33880.00**	1147854336.0	139001872.0	59280.00	-32367.02**	1047624064.0	9011009.0
IS 268	100960.00	8680.00**	75342400.0	1062547456.0	113338.66	3003.64*	9021880.0	148020096.0
IS 261	83253.34	182.22	33204.9	512072256.0	134970.67	37618.75**	1415170688.0	17716646.0
p=0.05 GCA line		896.13				1001.36		
p=0.05 GCA tester		2313.80				2585.49		

Table 4.9o (*Cont'd.*)

Parental lines	**Scoville heat units (SHU)**							
	E_3				**Pooled**			
	Mean	**g_i**	**σ^2_{gi}**	**σ^2_{si}**	**Mean**	**g_i**	**σ^2_{gi}**	**σ^2_{si}**
Lines								
CMS4611A	63040.00	-9366.22**	87726128.0	946656576.0	74828.45	-7609.93**	57910972.0	409602240.0
CMS4626A	80533.34	4449.78**	19800522.0	860828800.0	94497.78	4355.41**	18969572.0	532038624.0
CMS463D13A	82026.66	4916.44**	24171424.0	1030710656.0	90426.66	3254.52**	10591891.0	413066176.0
Testers								
AC 102	58720.00	-15193.78**	230850864.0	14514635.0	72936.89	-16952.56**	287389376.0	86647.4
SL 475	82613.34	21357.33**	456135712.0	310801184.0	114487.11	30732.18**	944466752.0	31843232.0
PL 412	106293.34	28486.22**	811464896.0	158592864.0	79640.89	1316.47	1733104.1	95539768.0
IS 263	97920.00	23206.22**	538528768.0	237758288.0	112311.11	21114.99**	445842880.0	39918792.0
VR 523	124320.00	28735.11**	825706624.0	125517936.0	103699.55	14726.25**	216862496.0	19552968.0
DL 161	63040.00	-9416.00**	88661056.0	156443696.0	104270.22	23099.59**	533590880.0	37124932.0
IS 267	88640.00	7775.11**	60452356.0	76245056.0	90227.55	-527.08	277814.9	130818608.0
YL 581	36373.33	-30980.45**	959787968.0	122439408.0	47447.11	-32498.04**	1056122944.0	62870108.0
SL 473	50453.33	-18322.67**	335720096.0	205715728.0	63699.55	-18465.45**	340972896.0	108569424.0
IS 262	91786.66	17108.45**	292698912.0	520209312.0	112051.55	24112.33**	581404288.0	58340636.0
VR 521	103093.34	21019.55**	441821664.0	17494762.0	92554.66	8271.14**	68411768.0	43989916.0
FL 201	35093.33	-28971.55**	839350976.0	262262.5	47059.55	-31543.38**	994984640.0	28368406.0
PP 402	37813.33	-23549.33**	554571136.0	40187832.0	50759.11	-18533.01**	343472384.0	85691120.0
C 142	66293.34	3917.33**	15345500.0	721166.2	109269.34	20137.21**	405507424.0	3811117.0
PP 414	53386.67	-19282.67**	371821216.0	53051832.0	62632.89	-16311.38**	266061056.0	83333064.0
VR 522	91786.66	9410.67**	88560656.0	22965292.0	79706.66	-5859.82**	34337516.0	12829590.0
PL 406	103733.34	21392.89**	457655680.0	325376288.0	97818.66	14998.84**	224965344.0	185340080.0
E 183	40906.67	-33842.67**	1145326208.0	220131952.0	51617.78	-33363.23**	1113105152.0	88992896.0
IS 268	72960.00	-2358.22	5561212.0	110903184.0	95752.89	3108.47**	9662611.0	109711072.0
IS 261	66560.00	-491.56	241626.8	118863368.0	94928.00	12436.47**	154665872.0	127974672.0
p=0.05 GCA line		1084.64				589.22		
p=0.05 GCA tester		2800.52				1521.37		

*, significant at P=0.05; **, significant at P=0.01

4.3.4 Estimation of specific combining ability (SCA) effects of crosses

Specific combining ability effects are associated with dominance and non-allelic interaction effects. The effects are non-fixable and exploited through heterosis breeding. It denotes the high specific combining ability leading to the highest performance of some specific cross-combinations. The SCA effects of the 60 chilli crosses under three environments and pooled over the environments for 15 plant growth, yield and quality traits are given in Table 4.10a-f.

4.3.4.1 Plant height (cm)

Out of 60 crosses, thee crosses in E_1, eight crosses in E_2, five crosses in E_3 and six crosses over the three environments exhibited significant and positive SCA effects for plant height. Significant negative SCA effects for plant height were observed for one cross in E_1, for seven crosses in E_2, for six crosses in E_3 and for seven crosses over the three environments. The range of SCA effects varied from -11.54 in CMS4626A × IS 261 to 13.59 in CMS4611A × IS 261 under E_1, from -14.80 in CMS463D13A × C 142 to 15.41 in CMS463D13A × VR 521 under E_2, from -14.45 in CMS4611A × E 183 to 15.42 in CMS463D13A × E 183 under E_3 and from -8.18 in CMS4611A × E 183 to 9.39 in CMS463D13A × E 183, based on the pooled means (Table 4.10a).

The cross CMS4611A × IS 261 exhibited the highest SCA effects followed by CMS4611A × PL 412 and CMS4626A × PL 406 in E_1, the cross CMS463D13A × VR 521 followed by CMS4626A × IS 261 and CMS463D13A × DL 161 in E_2, the cross CMS463D13A × E 183 followed by CMS4611A × IS 261 and CMS4626A × VR 522 in E_3, and the cross CMS463D13A × E 183 followed by CMS463D13A × VR 521 and CMS4611A × IS 261 exhibited good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, two crosses namely CMS4611A × C 142 and CMS463D13A × VR 521 in E_2 and one cross namely CMS463D13A × VR 521 across the environments had both the parents with good GCA effects. This is suggested the involvement of additive gene effects for heterotic performance of these crosses. The heterotic performance of these crosses can also be exploited through pure line breeding. Two crosses namely CMS4611A × PL 412 and CMS4626A × PL 406 involved at least one parent with positive significant GCA effects in E_1, five crosses CMS4611A × VR 522, CMS4626A × IS 261, CMS4626A × PL 412, CMS463D13A × DL 161 and CMS463D13A × AC 102 in E_2, and four crosses CMS4611A × IS 261, CMS4611A × PP 402, CMS4626A × VR 522 and CMS463D13A × E 183 in E_3. Four crosses CMS4611A × IS 261, CMS4611A × PL 412, CMS463D13A × E 183 and CMS463D13A × DL 161 across the three environments have at least one parent with significant positive GCA effects. One cross in each environment namely CMS4611A × IS 261 in E_1, CMS4626A × PP 402 in E_2, CMS4611A × YL 581 in E_3, and one cross

CMS4626A × PP 402 over the three environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses. The genetic variation exhibited by these crosses can be exploited through heterosis breeding.

The significantly negative SCA effects was expressed by the cross CMS4626A × IS 261 in E_1, by CMS463D13A × C 142 followed by CMS4626A × DL 161, CMS463D13A × PL 412 and CMS4626A × AC 102 in E_2, and by CMS4611A × E 183 followed by CMS463D13A × IS 261, CMS4626A × PL 406 and CMS463D13A × PP 402 in E_3. The cross namely CMS4611A × E 183 exhibited highest significantly negative SCA effects for followed by CMS463D13A × IS 261, CMS463D13A × C 142 and CMS463D13A × PL 412 across the environments. Among the crosses showing significant negative SCA effects, one cross CMS4626A × IS 261 in E_1, two crosses CMS4626A × DL 161 and CMS4626A × AC 102 in E_2, one cross CMS4626A × YL 581 in E_3, and one cross CMS4626A × DL 161 based on the pooled means have both the parents with significantly negative GCA effects. These crosses are the potential source materials to derive true breeding lines with shorter plant stature from the segregating population. One cross CMS4626A × VR 521 in E_2, two crosses CMS4611A × E 183 and CMS4626A × PL 406 in E_3, and one cross CMS4611A × E 183 over the environments have at least one parent with significant and negative GCA effects. Four crosses namely CMS4611A × VR 521, CMS463D13A × C 142, CMS463D13A × PL 412 and CMS463D13A × PP 402 in E_2, three crosses CMS4611A × C 142, CMS463D13A × IS 261 and CMS463D13A × PP 402 in E_3, and five crosses CMS4611A × VR 521, CMS463D13A × IS 261, CMS463D13A × C 142, CMS463D13A × PL 412 and CMS463D13A × PP 402 pooled across the environments involved neither of the parents with significantly negative GCA effects. The contributions to the SCA effects of these crosses have come from the non-additive gene effects which can be exploited through heterosis breeding.

Earlier, Lohithaswa *et al* (2000) reported that the cross Pant C-1 × Pusa Jwala was the best specific combiner for plant height. High SCA effects for plant height was also observed by Patel *et al* (2004) in the cross ACMS-2 × RHRC-Pendent, by Saritha *et al* (2005) in RHRC-50-1 × Punjab Surkh and PMR-19 × PMR-21, by Prasath and Ponnuswami (2008) in Arka Abir × Co 4, Arka Lohit × S 1 and Co 4 × Arka Abir, by do Rego *et al* (2009) in CB 24 × CB 58, CB 56 × CB 58 and CB 04 × CB 44, by Hasanuzzaman *et al* (2012) in CCA 5 × CCA 11, CCA 15 × CCA 19 and CCA 5 × BARI Morich 1, by Rodrigues *et al* (2012) in UENF 1629 × UENF 1732, UENF 1624 × UENF 1639 and UENF 1624 × UENF 1629, and by Savitha *et al* (2013) in the crosses CA 27 × Kashi Anmol, CA 207 × CA 97 and CA 117 × CA 97.

4.3.4.2 Plant spread (cm)

The SCA effects for plant spread varied from -11.93 in the cross CMS463D13A × IS 261 to 9.45 in the cross CMS463D13A × VR 523 under E_1, from -10.88 in the cross CMS4611A × SL 475 to 10.17 in the cross CMS4611A × IS 268 under E_2, from -6.94 in the cross CMS463D13A × IS 263 to 5.42 in the cross CMS463D13A × VR 521 under E_3 and from -6.05 in the cross CMS4611A × VR 521 to 5.61 in the cross CMS463D13A × VR 521, based on the pooled means. Three crosses in E_1, nine crosses in E_2, three crosses in E_3 and four crosses over the three environments exhibited significant and positive SCA effects for plant spread. Five crosses in E_1, 12 crosses in E_2, six crosses in E_3 and five crosses over the three environments exhibited significantly negative SCA effects for plant spread and thus were adjudged as the poor specific combiners for plant spread (Table 4.10a).

The cross CMS463D13A × VR 523 followed by CMS4611A × YL 581 and CMS463D13A × IS 268 produced significantly positive SCA effects for plant spread under E_1, the cross CMS4611A × IS 268 followed by CMS463D13A × AC 102 and CMS4626A × VR 522 under E_2, the cross CMS463D13A × VR 521 followed by CMS4611A × SL 475 and CMS4611A × IS 263 under E_3, and the cross CMS463D13A × VR 521 followed by CMS463D13A × AC 102 and CMS4611A × YL 581 exhibited good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, one cross CMS463D13A × VR 523 in E_1 and one cross CMS4611A × PL 406 in E_2 had both the parents with good GCA effects. These crosses can be pursued further to develop true breeding lines with good plant spread. One cross has at least one parent with positively significant GCA effects in E_1, seven crosses in E_2, two crosses in E_3 and two crosses across the three environments and the remaining crosses have neither of the parents with positively significant GCA effects.

For smaller canopy diameter, the crosses CMS463D13A × IS 261, CMS4611A × VR 523, CMS463D13A × PL 412 and CMS463D13A × YL 581 registered significantly negative SCA values in E_1, the crosses CMS4611A × SL 475 CMS4626A × PL 406, CMS4626A × AC 102 and CMS463D13A × PP 402 in E_2, the crosses CMS463D13A × IS 263, CMS4611A × VR 521, CMS4626A × DL 161 and CMS4626A × SL 475 in E_3, and the crosses CMS4611A × VR 521, CMS463D13A × PL 412, CMS4626A × AC 102 and CMS4611A × VR 523 across the three environments. Only one cross namely CMS4626A × AC 102 in E_2 and pooled across the environments involved both the parents with significant negative GCA effects. The negative SCA effects of these crosses resulted from cumulative effects of additive genes which can be fixed in true breeding lines. Five crosses CMS4611A × VR 521, CMS4611A × PP 414, CMS4626A × PL 406, CMS4626A × IS 268 and CMS463D13A × IS 262 in E_2, one cross CMS4611A × SL 473 in E_3, and two crosses CMS4611A × VR 521 and CMS4626A ×

DL 161 across the environments involved at least one parent with negative significant GCA effects. Five crosses namely CMS4611A × VR 523, CMS4611A × IS 263, CMS463D13A × IS 261, CMS463D13A × PL 412 and CMS463D13A × YL 581 have neither of the parents with significantly negative GCA effects in E_1, six crosses CMS4611A × SL 475, CMS4611A × VR 522, CMS4611A × IS 261, CMS463D13A × PP 402, CMS463D13A × IS 267 and CMS463D13A × IS 268 in E_2, five crosses CMS4611A × VR 521, CMS4611A × C 142, CMS4626A × DL 161, CMS4626A × SL 475 and CMS463D13A × IS 263 in E_3, and two crosses CMS4611A × VR 523 and CMS463D13A × PL 412 across the environments. This suggested that non-additive gene effects were predominantly involved in the performance of these crosses which can be exploited through heterosis breeding.

do Rego *et al* (2009) reported that the crosses CB 04 × CB 24, CB 04 × CB 38, CB 24 × CB 58 and CB 24 × CB 56 had significant positive SCA effects for plant spread. Hasanuzzaman *et al* (2012) identified CCA 5 × CCA 11 and CCA 2 × BARI Morich 1, and Rodrigues *et al* (2012) identified UENF 1624 × UENF 1639, UENF 1629 × UENF 1732 and UENF 1616 × UENF 1624 with high SCA values for plant spread.

4.3.4.3 Number of primary branches plant^{-1}

Among the 60 crosses evaluated, seven crosses in E_1, 19 crosses in E_2, 15 crosses in E_3 and 17 crosses across the three environments exhibited significant positive SCA effects for number of primary branches plant^{-1}. Ten crosses were poor specific combiners for number of primary branches plant^{-1} in E_1, 18 crosses in E_2, 12 crosses in E_3 and 16 crosses over the three environments. The range of SCA effects varied from -1.15 in CMS4626A × IS 267 to 1.08 in CMS4626A × DL 161 under E_1, from -2.20 in CMS463D13A × VR 523 to 2.55 in CMS463D13A × VR 522 under E_2, from -1.97 in CMS4611A × PL 406 to 1.67 in CMS4611A × AC 102 under E_3 and from -0.81 in CMS463D13A × VR 523 to 0.84 in CMS463D13A × IS 268, based on the pooled means (Table 4.10a).

The cross CMS4626A × DL 161 exhibited the highest SCA effects followed by CMS4626A × VR 522 and CMS463D13A × IS 267 in E_1, the cross CMS463D13A × VR 522 followed by CMS4626A × IS 261 and CMS463D13A × SL 475 in E_2, the cross CMS4611A × AC 102 followed by CMS4611A × E 183 and CMS463D13A × PP 402 in E_3, and the cross CMS463D13A × IS 268 followed by CMS4611A × PL 412, CMS4626A × IS 262 and CMS463D13A × YL 581 exhibited good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, one cross CMS463D13A × IS 267 had both the parents with good GCA effects in E_1, three crosses CMS4611A × VR 523, CMS4611A × IS 268 and CMS4611A × FL 201 in E_2, and three crosses CMS4626A × SL 475, CMS4626A × PL 406 and CMS4626A × PP 402 in E_3. Eight crosses CMS4611A × PL 412, CMS4611A × VR 521, CMS4611A × VR 523, CMS4611A × E 183, CMS463D13A × IS 268,

CMS463D13A × IS 267, CMS463D13A × PL 406 and CMS463D13A × VR 522 exhibited significant positive GCA effects across the environments. Higher SCA effects of these crosses resulted from cumulative effects of additive genes which can be fixed in true breeding lines. Other crosses have either one parent with significant and desirable GCA values or both the parents were poor combiners. Earlier, Patel *et al* (2004) reported that the cross ACMS-1 × RHRC-Pendent was the best specific combiner for number of primary branches plant^{-1}. Saritha *et al* (2005) observed that the crosses AVRDC-95-06 × Byadgi Dabbi, PMR-14 × Arka Lohit and TIWARI × Arka Abir were the good specific combiners for number of primary branches plant^{-1}. Prasath and Ponnuswami (2008) identified the crosses S 1 × Bydagi Kaddi, Arka Lohit × MDU Y and Arka Lohit × Co 4 with significant positive SCA values.

4.3.4.4 Fruit weight (g)

For fruit weight, SCA effects were significant and positive in 13 crosses under E_1, 14 crosses under E_2, 11 crosses under E_3 and 15 crosses over the three environments. Significant negative SCA effects for fruit weight were observed for 14 crosses in E_1, for 14 crosses in E_2, for 12 crosses in E_3 and for 13 crosses over the three environments. The SCA effects ranged from -2.43 in CMS4611A × PP 402 to 1.89 in CMS463D13A × FL 201 under E_1, from -2.79 in CMS4611A × FL 201 to 1.79 in CMS4626A × PP 402 under E_2, from -0.82 in CMS4626A × IS 268 to 1.07 in CMS463D13A × IS 268 under E_3 and from -1.62 in CMS4611A × PP 402 to 1.28 in CMS4626A × PP 402 across the environments (Table 4.10b).

Top crosses exhibiting significantly positive SCA effects were CMS463D13A × FL 201, CMS463D13A × YL 581 and CMS4611A × DL 161 in E_1, CMS4626A × PP 402, CMS4611A × SL 475 and CMS463D13A × FL 201 in E_2, CMS463D13A × IS 268, CMS4611A × PP 414 and CMS4626A × VR 523 in E_3, and CMS4626A × PP 402, CMS463D13A × FL 201 and CMS463D13A × YL 581 across the environments. Five crosses CMS463D13A × FL 201, CMS463D13A × YL 581, CMS463D13A × PP 402, CMS463D13A × VR 522 and CMS463D13A × IS 268 in E_1, three crosses CMS4626A × PP 402, CMS4626A × FL 201 and CMS463D13A × FL 201 in E_2, five crosses CMS4626A × VR 523, CMS4626A × PP 402, CMS4626A × FL 201, CMS463D13A × IS 268 and CMS463D13A × SL 473 in E_3, and five crosses namely CMS463D13A × FL 201, CMS463D13A × YL 581, CMS463D13A × IS 268, CMS463D13A × VR 522 and CMS463D13A × PP 402 across the environments involved both the parents with significant and positive GCA effects. These crosses can be subjected to selection in segregating populations followed by inbreeding to develop recombinant inbred lines having higher fruit weight than the parental lines. Three crosses CMS4611A × PL 406, CMS4626A × PP 402 and CMS463D13A × IS 267 involved at least one parent with positive significant GCA effects in E_1, nine crosses CMS4611A × SL 475, CMS4611A × IS 261, CMS4611A × IS 268,

CMS4611A × YL 581, CMS4626A × VR 522, CMS463D13A × AC 102, CMS463D13A × VR 523, CMS463D13A × VR 522 and CMS463D13A × IS 267 in E_2, three crosses CMS4611A × VR 522, CMS4626A × IS 267 and CMS4626A × PL 412 in E_3, and four crosses CMS4611A × IS 261, CMS4611A × SL 475, CMS4626A × PP 402 and CMS463D13A × SL 473 across the three environments have at least one of the parents with positive significant GCA effects. Five crosses CMS4611A × DL 161, CMS4611A × E 183, CMS4611A × AC 102, CMS4611A × VR 521 and CMS4626A × VR 521 in E_1, two crosses CMS4611A × VR 521 and CMS4611A × E 183 in E_2, three crosses CMS4611A × PP 414, CMS4611A × IS 261 and CMS4611A × IS 262 in E_3, and six crosses CMS4611A × E 183, CMS4611A × DL 161, CMS4611A × VR 521, CMS4611A × PP 414, CMS4611A × AC 102 and CMS4626A × VR 521 over the three environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses which can be exploited through heterosis breeding.

Lohithaswa *et al* (2000) reported that the cross RHRC-16-5 × Arka lohit showed good SCA values for fruit weight followed by Chickballapur × X-235 and Chickballapur × RHRC-16-5. Geleta and Labuschagne (2006a) observed that the cross Kalocsai "M" Csereszyne × Pepper 1976 exhibited highest SCA effects followed by C00916 × PBC 142A, Szegedi 178 × Mareko Shote and Szegedi 178 × Pepper 1976. Good SCA effects for fruit weight was also observed by Prasath and Ponnuswami (2008) in the crosses MDU Y × Arka Abir, S 1 × Bydagi Kaddi and Arka Lohit × Bydagi Kaddi, by do Rego *et al* (2009) in CB 24 × CB 50, CB 44 × CB 56 and CB 04 × CB 24, by Hasanuzzaman *et al* (2012) in CCA 15 × CCA 19 and CCA 15 × BARI Morich 1, by Rodrigues *et al* (2012) in UENF 1616 × UENF 1732, UENF 1732 × UENF 1639 and UENF 1629 × UENF 1639, by do Nascimento *et al* (2014) in UFPB 132 × UFPB 134, and by Singh *et al* (2014) in SL 461 × EL 181, SL 461 × US 501, SL 461 × SD 463 and US 501 × SD 463.

4.3.4.5 Fruit length (cm)

The range of SCA effects for fruit length varied from -1.01 in the cross CMS4626A × AC 102 to 1.30 in the cross CMS4626A × PP 414 under E_1, from -0.66 in the cross CMS463D13A × AC 102 to 1.01 in the cross CMS4611A × PP 414 under E_2, from -1.10 in the cross CMS4611A × DL 161 to 1.49 in the cross CMS463D13A × DL 161 under E_3 and from -0.67 in the cross CMS463D13A × PP 414 to 0.56 in the cross CMS4611A × AC 102, based on the pooled means. Of the 60 crosses, five crosses in E_1, two crosses in E_2, nine crosses in E_3 and seven crosses across the three environments manifested significant and positive SCA effects. Five crosses were poor specific combiners for fruit length due to significant and negative SCA effects in E_1, two crosses in E_2, seven crosses in E_3 and six crosses over the three environments (Table 4.10b).

The highest SCA effects were expressed by the cross CMS4626A × PP 414 followed by CMS463D13A × SL 473 and CMS4626A × PP 402 in E_1, by CMS4611A × PP 414 followed by CMS4626A × AC 102 in E_2, by CMS463D13A × DL 161 followed by CMS4626A × PL 412 and CMS463D13A × IS 268 in E_3, and by CMS4611A × AC 102 followed by CMS463D13A × DL 161 and CMS463D13A × IS 268 across the three environments. The crosses showing significant positive SCA effects, two crosses CMS4626A × PL 412 and CMS4626A × IS 261 had both the parents with good GCA effects for fruit length in E_3. The two crosses can be used as potential source material to derive true breeding lines with longer fruits from the segregating population. One cross CMS463D13A × SL 473 have at least one parent with positive significant GCA effects in E_1, three crosses CMS4626A × PP 414, CMS463D13A × DL 161 and CMS463D13A × IS 268 in E_3, and four crosses CMS4626A × IS 261, CMS463D13A × DL 161, CMS463D13A × IS 268 and CMS463D13A × SL 473 across the three environments. Four crosses CMS4611A × C 142, CMS4626A × PP 414, CMS4626A × PP 402 and CMS4626A × VR 521 in E_1, two crosses CMS4611A × PP 414 and CMS4626A × AC 102 in E_2, four crosses CMS4611A × AC 102, CMS4611A × C 142, CMS4611A × IS 262 and CMS4611A × VR 521 in E_3 and three crosses CMS4611A × AC 102, CMS4611A × IS 263 and CMS4626A × PP 414 across the three environments have neither of the parents with positively significant GCA effects. Thus, the contributions to the mean performance in all these crosses come from the non-additive gene effects. The desirable effects depicted by these crosses can be exploited through heterosis breeding.

The crosses identified with significantly negative SCA effects for fruit length were CMS4626A × AC 102, CMS4611A × PP 402, CMS463D13A × PP 414 and CMS4611A × SL 473 in E_1, the crosses CMS463D13A × AC 102 and CMS463D13A × IS 262 in E_2, the crosses CMS4611A × DL 161, CMS4611A × IS 261, CMS4626A × IS 268 and CMS463D13A × PL 412 in E_3, and the crosses CMS463D13A × PP 414, CMS4626A × IS 268, CMS4611A × IS 261 and CMS4611A × DL 161 across the three environments. Among the crosses showing significantly negative SCA effects, one cross CMS4611A × SL 473 in E_1 and one cross CMS4611A × DL 161 over the three environments had both the parents with significantly negative GCA effects. These crosses are the potential source material to drive true breeding genotypes with small fruit from the segregating population. Three crosses CMS4611A × PP 402, CMS4626A × AC 102 and CMS463D13A × PP 414 in E_1, two crosses CMS463D13A × AC 102 and CMS463D13A × IS 262 in E_2, four crosses CMS4611A × DL 161, CMS4611A × IS 261, CMS4611A × PL 406 and CMS4626A × IS 262 in E_3, and three crosses CMS4611A × IS 261, CMS4611A × VR 522 and CMS463D13A × PP 414 based on pooled means have at least one of the parents with significantly negative GCA effects. One cross CMS4626A × YL 581 in E_1, three crosses CMS4626A × IS 268, CMS4626A × SL 475 and CMS463D13A × PL 412 in E_3, and two crosses CMS4626A × IS 268 and CMS463D13A × PP 415 over the three environments have neither of the parents with negatively significant GCA effects. Thus, the contributions to the mean performance in all these crosses come from the non-additive gene effects.

Patel *et al* (2004) identified ACMS-3 × SG-5 as good specific combiner for fruit length followed by ACMS-4 × ACS 2000-3 and ACMS-2 × RHRC-Pendent. Saritha *et al* (2005) identified the crosses namely AVRDC-95-06 × Arka Abhir, TIWARI × Byadgi Dabbi and PMR-14 × Byadgi Kaddi, Geleta and Labuschagne (2006a) identified Szegedi 178 × Bakko Local, Szegedi 178 × Mareko Shote and Mareko Shote × PBC 142A, do Rego *et al* (2009) identified CB 04 × CB 24, CB 04 × CB 58 and CB 38 × CB 50, Marchesan *et al* (2009) identified Quantum-R × HV-12, P36-R × HV-12 and Rubia-R × HV-12, Rodrigues *et al* (2012) identified UENF 1624 × UENF 1629 and UENF 1629 × UENF 1639, Savitha *et al* (2013) identified Sel. 1 × Kashi Anmol, 09CHIVAR03 × CA 97 and CA 27 × Kashi Anmol, Medeiros *et al* (2014) identified UENF 1616 × UENF 1629, UENF 1629 × UENF 1639 and UENF 1629 × UENF 1732, do Nascimento *et al* (2014) identified UFPB 77.2 × UFPB 132 and UFPB 01 × UFPB 137, Bhutia *et al* (2015) identified BCCH Sel-4 × AC-575, and Naresh *et al* (2016) identified IHR4507 × IHR3476, IHR3453 × IHR4507 and IHR4507 × IHR500 as good specific combiners for fruit length.

4.3.4.6 Fruit width (mm)

Only one cross in each E_1, E_2, E_3 and three crosses across the environments exhibited significant and positive SCA effects for fruit width. Four crosses in E_1, none in E_2, three crosses in E_3 and four crosses over the three environments showed significant negative SCA effects and thus were considered as the poor specific combiners for fruit width. The range of SCA effects varied from -2.10 in CMS4611A × PP 402 to 1.17 in CMS4611A × DL 161 under E_1, from -0.81 in CMS4626A × IS 263 to 1.01 in CMS4626A × SL 473 under E_2, from -1.21 in CMS4611A × PP 402 to 1.0 in CMS4626A × FL 201 under E_3 and from -1.17 in CMS4611A × PP 402 to 0.85 in CMS4626A × PP 402 over the three environments (Table 4.10b). Only one cross namely CMS4626A × FL 201 in E_3 and one cross CMS4626A × PP 402 across the environments had both the parents with good GCA effects. These crosses are potential source material to derive true breeding lines with thicker fruit from the segregating populations through simple selection scheme like the pedigree method. The remaining crosses *viz*., CMS4611A × DL 161 in E_1, CMS4626A × SL 473 in E_2, and CMS4611A × PP 414 and CMS4611A × VR 521 across the three environments have neither of the parents with positively significant GCA values. The contribution to the mean performance of these crosses comes from non-additive gene effects. Therefore, to improve fruit width in chilli the heterosis breeding would be a more appropriate approach.

Earlier, Prasath and Ponnuswami (2008) reported that the crosses MDU Y × Arka Abir, Arka Lohit × Bydagi Kaddi and Arka Lohit × Co 4 were the good specific combiners for fruit width. Marchesan *et al* (2009) reported that the cross P36-R × HV-12 was the good specific combiner for fruit width. Rodrigues *et al* (2012) identified the cross UENF 1732 × UENF 1639 with good SCA values followed by UENF 1616 × UENF 1624 and UENF 1616 × UENF 1732. Naresh *et al* (2016) found that the crosses IHR3849 × IHR2451, IHR4507 × IHR3476 and IHR4503 × IHR3476 expressed significantly positive SCA effects for fruit width in chilli.

4.3.4.7 Pericarp thickness (mm)

For pericarp thickness, the SCA effects were significant and positive in seven crosses under E_1, in five crosses under E_2, in 13 crosses under E_3 and in 10 crosses across the environments. Significantly negative SCA effects were observed for 10 crosses in E_1, for eight crosses in E_2, for nine crosses in E_3 and for nine crosses over the three environments. The SCA effects ranged from -0.27 in CMS463D13A × E 183 to 0.29 in CMS463D13A × FL 201 and CMS4611A × E 183 under E_1, from -0.23 in CMS4611A × SL 473 to 0.31 in CMS4626A × SL 473 under E_2, from -0.20 in CMS4611A × FL 201 to 0.19 in CMS4611A × VR 523 under E_3 and from -0.15 in CMS4611A × YL 581 to 0.14 in CMS4626A × YL 581 and CMS463D13A × FL 201, based on pooled means (Table 4.10c).

Top crosses producing significantly positive SCA effects were CMS463D13A × FL 201, CMS4611A × E 183 and CMS463D13A × IS 267 in E_1, CMS4626A × SL 473, CMS4626A × YL 581, CMS463D13A × IS 262 in E_2, CMS4611A × VR 523, CMS4611A × VR 522 and CMS4626A × FL 201 in E_3, and CMS4626A × YL 581, CMS463D13A × FL 201 and CMS4611A × E 183 across the environments. Only two crosses CMS463D13A × FL 201 and CMS463D13A × PP 402 in E_1, six crosses CMS4626A × FL 201, CMS4626A × SL 475, CMS4626A × PP 402, CMS463D13A × YL 581, CMS463D13A × IS 268 and CMS463D13A × FL 201 in E_3, and one cross CMS463D13A × FL 201 across the three environments had both the parents with good GCA effects. This suggested the involvement of additive gene effects for heterotic performance of these crosses which can be fixed through selection for obtaining chilli lines with thicker pericarp. One cross CMS463D13A × IS 267 in E_1, three crosses CMS4626A × SL 473, CMS4626A × YL 581 and CMS463D13A × IS 262 in E_2, three crosses CMS4611A × VR 523, CMS4626A × PL 406 and CMS463D13A × IS 262 in E_3, and four crosses CMS4611A × VR 523, CMS4626A × YL 581, CMS4626A × PP 402 and CMS463D13A × IS 262 across the three environments involved at least one of the parents with positive significant GCA effects. Four crosses namely CMS4611A × E 183, CMS4611A × DL 161, CMS4611A × VR 521 and CMS4626A × IS 262 in E_1, two crosses CMS4611A × PL 406 and CMS4611A × PP 414 in E_2, four crosses CMS4611A × VR 522, CMS4611A × IS 263, CMS4611A × PL 412 and CMS4611A × VR 521 in E_3, and five crosses CMS4611A × E 183, CMS4611A × PL 412, CMS4611A × VR 521, CMS4611A × PP 414 and CMS4626A × SL 473 across the three environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses which can be exploited through heterosis breeding.

The cross CMS463D13A × E 183 showed the highest significantly negative SCA effects for pericarp thickness followed by CMS4611A × PP 402, CMS463D13A × VR 521 and CMS4611A × FL 201 in E_1, the cross CMS4611A × SL 473 followed by CMS4626A × PL 406, CMS4626A × SL 475 and CMS4611A × YL 581 in E_2, the cross CMS4611A × FL 201 followed by CMS4611A × PP 402, CMS4626A × VR 522 and CMS4611A × YL 581 in E_3, and the cross CMS4611A × YL 581 followed by CMS4611A × FL 201, CMS463D13A × E 183 and CMS4611A × PP 402 across the environments. Among the crosses showing significantly negative SCA effects, only two crosses CMS4611A × C 142 and CMS4626A × IS 262 in E_2 and two crosses CMS4611A × SL 473 and CMS4611A × IS 262 based on pooled means have both the parents with significantly negative GCA effects. These crosses are the potential source materials to derive true breeding lines with thinner pericarp from the segregating population. Nine crosses CMS4611A × PP 402, CMS4611A × FL 201, CMS4611A × IS 262, CMS4611A × YL 581, CMS4611A × PL 406, CMS4626A × IS 267, CMS463D13A × E 183, CMS463D13A × VR 521 and CMS463D13A × DL 161 in E_1, four crosses CMS4611A × SL 473, CMS4611A × YL 581, CMS4626A × PL 406 and CMS4626A × SL 475 in E_2, six crosses CMS4611A × FL 201, CMS4611A × PP 402, CMS4611A × YL 581, CMS4611A × SL 475, CMS4611A × IS 268 and CMS463D13A × PL 406 in E_3, and six crosses CMS4611A × YL 581, CMS4611A × FL 201, CMS4611A × PP 402, CMS4626A × VR 523, CMS463D13A × E 183 and CMS463D13A × VR 521 across the environments have at least one of the parents with negatively significant GCA effects. One cross CMS463D13A × C 142 in E_1, two crosses CMS463D13A × IS 267 and CMS463D13A × YL 581 in E_2, three crosses CMS4626A × VR 522, CMS4626A × VR 523 and CMS4626A × VR 523 in E_3, and one cross CMS463D13A × PL 412 based on pooled means have neither of the parents with negative significant GCA effects. The contributions to the mean performance in all these crosses come from the non-additive gene effects.

Geleta and Labuschagne (2006a) reported that the crosses Kalocsai "M" Csereszyne × Pepper 1976 and Kalocsai "M" Csereszyne × Mareko Shote showed the good SCA effects for pericarp thickness. Pérez-Grajales *et al* (2009) identified Puebla × Peru and Huatusco ×

Chiapas as good specific combiners for pericarp thickness, do Rego *et al* (2009) identified CB 38 × CB 46, CB 04 × CB 46 and CB 50 × CB 56, and do Nascimento *et al* (2014) identified the crosses UFPB 77.1 × UFPB 134 and UFPB 134 × UFPB 137 with good SCA values.

4.3.4.8 Number of fruits plant^{-1}

Out of 60 crosses evaluated, six crosses manifested significant and positive SCA effects in E_1, 17 crosses in E_2, 15 crosses in E_3 and 16 crosses across the three environments. Six crosses were poor specific combiners for number of fruits plant^{-1} as indicated by their significantly negative SCA values in E_1, 18 crosses in E_2, 20 crosses in E_3 and 16 crosses over the three environments. The SCA effects ranged from -56.11 in the cross CMS4611A × PL 412 to 38.66 in the cross CMS4626A × PL 412 under E_1, from -80.86 in the cross CMS4611A × IS 263 to 81.42 in the cross CMS4626A × IS 262 under E_2, from -71.56 in the cross CMS4611A × IS 268 to 73.43 in the cross CMS4626A × SL 473 under E_3 and from -33.62 in the cross CMS4611A × SL 473 to 46.20 in the cross CMS4611A × C 142 across the three environments (Table 4.10c).

The cross CMS4626A × PL 412 followed by CMS4611A × IS 263 and CMS4626A × PL 406 were found to be good specific combiners in E_1, the cross CMS4626A × IS 262 followed by CMS4611A × VR 521 and CMS4611A × C 142 in E_2, and the cross CMS4626A × SL 473 followed by CMS4626A × IS 268 and CMS4611A × VR 522 in E_3. The cross CMS4611A × C 142 followed by CMS4611A × VR 522 and CMS463D13A × AC 102 exhibited the good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, one cross CMS4611A × VR 522 involved both the parents with significant positive GCA effects in E_1, six crosses CMS4611A × C 142, CMS4611A × IS 267, CMS4626A × IS 262, CMS4626A × YL 581, CMS4626A × PL 412 and CMS4626A × DL 161 in E_2, two crosses CMS4611A × C 142 and CMS4611A × DL 161 in E_3, and four crosses CMS4611A × C 142, CMS4611A × IS 267, CMS4626A × IS 262 and CMS4626A × PL 412 over the three environments. Therefore, these crosses are potential source material to derive true breeding lines with more number of fruits plant^{-1} from the segregating populations.

Four crosses CMS4611A × IS 263, CMS4611A × FL 201, CMS4626A × PL 412 and CMS4626A × PL 406 in E_1, seven crosses CMS4611A × VR 521, CMS4611A × VR 522, CMS4611A × PP 402, CMS4626A × IS 263, CMS4626A × PP 414, CMS463D13A × IS 268 and CMS463D13A × SL 475 in E_2, seven crosses CMS4611A × VR 522, CMS4611A × IS 267, CMS4611A × E 183, CMS4611A × PL 406, CMS4626A × SL 473, CMS4626A × IS 268 and CMS463D13A × VR 523 in E_3, and 10 crosses CMS4611A × VR 522, CMS4611A × VR 521, CMS4611A × PP 402, CMS4626A × YL 581, CMS4626A × SL 473, CMS4626A × PP 414, CMS4626A × IS 261, CMS463D13A × VR 523, CMS463D13A × IS 268 and CMS463D13A × SL 475 over the environments involved at least one parent with positive significant GCA values. One cross CMS4626A × SL 473 in E_1, four crosses CMS463D13A × AC 102, CMS463D13A × SL 473, CMS463D13A × VR 523 and CMS463D13A × FL 201 in E_2, six crosses CMS4626A × IS 261, CMS4626A × IS 262, CMS463D13A × AC 102, CMS463D13A × PL 412, CMS463D13A × FL 201 and CMS463D13A × PP 402 in E_3, and two crosses CMS463D13A × AC 102 and CMS463D13A × PP 402 across the three environments have neither of the parents with positively significant GCA effects. The contribution to the mean performance of these crosses has come from the non-additive gene effects. Heterosis breeding would be appropriate approach to exploit genetic variability for number of fruits plant^{-1} in these crosses.

Earlier, Lohithaswa *et al* (2000) identified the crosses Pant C-1 × Pusa Jwala, Pusa Lohit × Pant C-1 and Chickballapur × IHR 1822-1/3-1/5 as good specific combiners for number of fruits plant^{-1}. Good SCA effects for number of fruits plant^{-1} was observed by Patel *et al* (2004) in the crosses ACMS-4 × ACG-77, ACMS-2 × RHRC-Pendent and ACMS-2 × Pb. Guchhedar, by Saritha *et al* (2005) in PMR-14 × PMR-57 and AVRDC-95-06 × Byadgi Dabbi, by Pérez-Grajales *et al* (2009) in Zongolica × Puebla, Peru × Chiapas and Huatusco II × Puebla, by Rodrigues *et al* (2012) in UENF 1624 × UENF 1639 and UENF 1629 × UENF 1732, by Savitha *et al* (2013) in CA 117 × CA 97, CA 172 × Kashi Anmol and CA 197 × Kashi Anmol, by Medeiros *et al* (2014) in UENF 1624 × UENF 1624, UENF 1732 × UENF 1732 and UENF 1616 × UENF 1732, and by Rohini *et al* (2017b) in the crosses Arka Lohit × LCA334 and K 1 × LCA334.

4.3.4.9 Number of seed fruit^{-1}

The number of crosses showing significant and positive SCA values was seven in E_1, 11 in E_2, seven in E_3 and 14 across the three environments. Significant negative SCA effects for number of seed fruit^{-1} were observed for 11 crosses in E_1, for 11 crosses in E_2, for five crosses in E_3 and for 14 crosses over the three environments. The SCA effects varied from -11.54 in CMS4626A × IS 268 to 11.48 in CMS4626A × FL 201 under E_1, from -10.47 in CMS4611A × PP 402 to 11.13 in CMS4611A × AC 102 under E_2, from -4.94 in CMS4611A × PP 402 to 6.49 in CMS463D13A × VR 522 under E_3 and from -8.94 in CMS4611A × PP 402 to 9.08 in CMS4611A × AC 102 over the environments (Table 4.10c).

The cross CMS4626A × FL 201 exhibited the highest SCA effects for number of seed fruit^{-1} followed by CMS4611A × AC 102 and CMS463D13A × IS 268 in E_1, the cross CMS4611A × AC 102 followed by CMS4626A × PP 402 and CMS4611A × IS 263 in E_2, the cross CMS463D13A × VR 522 followed by CMS463D13A × VR 521 and CMS4611A × IS 268 in E_3, and the cross CMS4611A × AC 102 followed by CMS4626A × PP 402 and CMS4611A × IS 263 based on the pooled means. The cross CMS463D13A × IS 268 had both the parents with good GCA effects in E_1, the cross CMS463D13A × IS 267 in E_2, the cross

CMS463D13A × VR 521 in E_3, and the crosses CMS463D13A × VR 521 and CMS463D13A × IS 268 across the environments. This suggested the involvement of additive gene effects for heterotic performance of these crosses. The heterotic performance of these crosses can be exploited through pure line breeding. Two crosses CMS4626A × SL 475 and CMS4626A × C 142 involved at least one parent with positive significant GCA effects in E_1, four crosses CMS4611A × IS 268, CMS4626A × C 142, CMS4626A × PL 406 and CMS463D13A × VR 522 in E_2, two crosses CMS4611A × IS 268 and CMS463D13A × VR 522 in E_3, and five crosses CMS4611A × IS 268, CMS4626A × C 142, CMS4626A × PL 406, CMS4626A × SL 475 and CMS463D13A × VR 522 across the environments. Four crosses CMS4611A × AC 102, CMS4611A × IS 263, CMS4626A × FL 201 and CMS4626A × PP 402 in E_1, six crosses CMS4611A × AC 102, CMS4611A × IS 263, CMS4611A × YL 581, CMS4611A × PP 414, CMS4626A × PP 402 and CMS4626A × FL 201 in E_2, four crosses CMS4611A × AC 102, CMS4611A × PP 414, CMS4626A × DL 161 and CMS4626A × PP 402 in E_3, and seven crosses CMS4611A × AC 102, CMS4611A × IS 263, CMS4611A × PP 414, CMS4611A × YL 581, CMS4611A × E 183, CMS4626A × PP 402 and CMS4626A × FL 201 across the three environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses. The genetic variation exhibited by these crosses can be exploited through heterosis breeding.

Lohithaswa *et al* (2000) reported that the crosses PMR-14 × PMR-39, PMR-14 × Byadgi Kaddi and TIWARI × Byadgi Dabbi were good specific combiners for number of seed fruit^{-1}. Prasath and Ponnuswami (2008) found that the cross Arka Abir × Bydagi Kaddi had good SCA values followed by S 1 × Co 4 and Arka Lohit × MDU Y. Pérez-Grajales *et al* (2009) identified the crosses Puebla × Peru, Huatusco II × Peru and Puebla × Huatusco I as the good specific combiners, Hasanuzzaman *et al* (2012) identified BARI Morich 1 × CCA 19, CCA 15 × CCA 19 and CCA 2 × BARI Morich 1, and do Nascimento *et al* (2014) identified UFPB 01 × UFPB 77.2, UFPB 77.2 × UFPB 132 and UFPB 77.1 × UFPB 134 as good specific combiners for number of seed fruit^{-1}.

4.3.4.10 1000 seed weight (g)

The range of SCA effects for 1000 seed weight varied from -0.65 in CMS4611A × VR 522 to 0.43 in CMS4626A × VR 522 under E_1, from -0.65 in CMS4611A × VR 522 to 0.42 in CMS4626A × VR 522 under E_2, from -0.71 in CMS4611A × VR 522 to 0.52 in CMS4626A × VR 522 under E_3 and from -0.67 in CMS4611A × VR 522 to 0.46 in CMS4626A × VR 522, based on the pooled means (Table 4.10d). One cross in each E_1, E_2, E_3 and for six crosses across the three environments manifested significant and positive SCA effects. Significant negative SCA effects were observed for one cross in each E_1, E_2 and E_3

and six crosses over the three environments and were adjudged as poor specific combiners for 1000 seed weight.

Among the crosses showing significant positive SCA effects, only one cross, CMS463D13A × SL 475 had both the parents with good GCA effects across the environments. Thus, there is an ample scope of developing true breeding lines with higher seed weight from the segregating populations generated from this cross. The crosses CMS4626A × VR 522 in E_1, CMS4626A × VR 522 in E_2, CMS4626A × VR 522 in E_3, and CMS4626A × VR 522, CMS463D13A × C 142 and CMS463D13A × VR 521 across the three environments have one of the parents with significant positive GCA values. The crosses CMS4611A × PP 414 and CMS4611A × E 183 across the environments have both the parents with poor GCA effects. Thus, the contribution to the mean performance of these crosses has come from the non-additive gene effects. Therefore, for obtaining superior lines with higher seed weight, one will have to go for hybrid development rather than true breeding lines. Kaur *et al* (2017) reported the highest significant positive SCA effects for seed weight in the cross MS 341 × PP 403 followed by the cross SD 463 × PP 403.

4.3.4.11 Total yield plant^{-1} (kg)

Out of 60 crosses evaluated, 12 crosses in E_1, 18 crosses in E_2, 17 crosses in E_3 and 13 crosses over the three environments exhibited significant and positive SCA effects. Twelve crosses were poor specific combiners in E_1, 20 crosses in E_2, 16 crosses in E_3 and 13 crosses over the three environments. The SCA effects ranged from -0.23 in the cross CMS4611A × PL 412 to 0.23 in the cross CMS463D13A × IS 267 under E_1, from -0.32 in the cross CMS4611A × FL 201 to 0.22 in the cross CMS463D13A × VR 523 under E_2, from -0.14 in the cross CMS4611A × SL 473 to 0.14 in the cross CMS4626A × SL 473 under E_3 and from -0.11 in the cross CMS463D13A × PP 414 and CMS4626A × AC 102 to 0.12 in the cross CMS4611A × E 183, based on the pooled means (Table 4.10d).

The cross CMS463D13A × IS 267 exhibited the highest SCA effects for followed by CMS4626A × PL 412 and CMS4611A × PP 414 in E_1, the cross CMS463D13A × VR 523 followed by CMS4626A × DL 161 and CMS463D13A × FL 201 in E_2, and the cross CMS4626A × SL 473 followed by CMS4611A × VR 522 and CMS463D13A × AC 102 in E_3. The cross CMS4611A × E 183 followed by CMS463D13A × AC 102, CMS4611A × VR 521 and CMS463D13A × SL 473 exhibited the good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, four crosses CMS463D13A × IS 267, CMS463D13A × PP 402, CMS463D13A × IS 262 and CMS463D13A × IS 268 had both the parents with good GCA effects in E_1, five crosses CMS4626A × FL 201, CMS4626A × PL 412, CMS463D13A × FL 201, CMS463D13A × SL 475 and CMS463D13A × IS 268 in E_2, and four crosses CMS463D13A × YL 581, CMS463D13A × C 142, CMS463D13A × IS

268 and CMS463D13A × PP 402 in E_3. Four crosses CMS463D13A × IS 268, CMS463D13A × PP 402, CMS463D13A × IS 267 and CMS463D13A × VR 523 with good SCA effects across the environments had both the parents with good GCA effects. The heterotic performance of these crosses can also be exploited through the pure line breeding.

Three crosses CMS4626A × PL 412, CMS4626A × PL 406 and CMS463D13A × SL 473 involved at least one parent with positive significant GCA effects in E_1, 11 crosses CMS4611A × PP 402, CMS4611A × PL 412, CMS4611A × C 142, CMS4626A × DL 161, CMS4626A × IS 262, CMS4626A × IS 263, CMS4626A × PP 414, CMS463D13A × VR 523, CMS463D13A × SL 473, CMS463D13A × AC 102 and CMS463D13A × IS 263 in E_2, seven crosses CMS4611A × VR 522, CMS4611A × DL 161, CMS4611A × VR 523, CMS4626A × SL 473, CMS4626A × PL 406, CMS4626A × IS 268 and CMS463D13A × AC 102 in E_3, and five crosses CMS4626A × PL 412, CMS4626A × DL 161, CMS463D13A × AC 102, CMS463D13A × SL 473 and CMS463D13A × FL 201 across the three environments have at least one of the parents with positive significant GCA effects. Five crosses CMS4611A × PP 414, CMS4611A × E 183, CMS4611A × IS 263, CMS4611A × VR 521 and CMS4611A × FL 201 in E_1, two crosses CMS4611A × VR 521 and CMS4611A × E 183 in E_2, six crosses CMS4611A × IS 262, CMS4611A × IS 267, CMS4611A × E 183, CMS4611A × VR 521, CMS4611A × IS 263 and CMS4626A × IS 261 in E_3, and four crosses CMS4611A × E 183, CMS4611A × VR 521, CMS4611A × PP 414 and CMS4626A × PL 406 over the three environments have neither of the parents with positively significant GCA effects. The non-additive genetic variation exhibited by these crosses can be exploited through heterosis breeding.

Earlier, Saritha *et al* (2005) reported that the crosses PMR-14 × PMR-57 and AVRDC-95-06 × Byadgi Dabbi exhibited good SCA effects for total yield plant^{-1}. Geleta and Labuschagne (2006a) identified Mareko Shote × Pepper 1976 to be the good specific combiner for total yield plant^{-1} followed by Mareko Shote × C00916 and Kalocsai "M" Cseresznye × C00916. Pérez-Grajales *et al* (2009) reported that the cross Zongolica × Puebla had highest SCA effects followed by Huatusco II × Puebla and Puebla × Huatusco I. do Rego *et al* (2009) reported that the crosses CB 04 × CB 24, CB 24 × CB 50 and CB 46 × CB 50 were good specific combiners for yield. Rodrigues *et al* (2012) identified the cross UENF 1629 × UENF 1732 as the best specific combiner followed by UENF 1624 × UENF 1639 and UENF 1616 × UENF 1732. Good SCA effects for total yield plant^{-1} was reported by Medeiros *et al* (2014) in the crosses UENF 1639 × UENF 1732, UENF 1616 × UENF 1732 and UENF 1616 × UENF 1624, by do Nascimento *et al* (2014) in UFPB 01 × UFPB 132, by Singh *et al* (2014) in CC 141 × VR 521, by Bhutia *et al* (2015) in BCCH Sel-4 × AC-575, by Naresh *et al* (2016) in IHR3849 × IHR3448 and IHR3453 × IHR4507, and by Rohini *et al* (2017b) in the crosses Arka Lohit × LCA334 and K1 × LCA334.

4.3.4.12 Ascorbic acid (mg.100g^{-1})

Out of 60 crosses, 14 crosses in E_1, 12 crosses in E_2, 13 crosses in E_3 and 12 crosses over the three environments exhibited significant and positive SCA effects for ascorbic acid. Significant negative SCA effects for ascorbic acid were observed for 14 crosses in E_1, for 14 crosses in E_2, for 13 crosses in E_3 and for 16 crosses over the three environments. The range of SCA effects varied from -17.74 in CMS4611A × IS 261 to 27.86 in CMS4611A × C 142 under E_1, from -18.44 in CMS4611A × PP 402 to 28.85 in CMS4626A × IS 262 under E_2, from -15.54 in CMS4611A × SL 475 to 18.24 in CMS4626A × SL 475 under E_3 and from -11.32 in CMS4611A × YL 581 to 13.37 in CMS4626A × VR 522, based on the pooled means (Table 4.10d).

The cross CMS4611A × C 142 exhibited the highest SCA effects for ascorbic acid followed by CMS4626A × VR 523 and CMS4626A × VR 522 in E_1, the cross CMS4626A × IS 262 followed by CMS4626A × VR 522 and CMS463D13A × PP 402 in E_2, the cross CMS4626A × SL 475 followed by CMS4626A × AC 102 and CMS463D13A × PP 402 in E_3, and the cross CMS4626A × VR 522 followed by CMS4626A × IS 262 and CMS4611A × C 142 exhibited good SCA effects based on the pooled means. Seven crosses CMS4626A × VR 523, CMS4626A × IS 263, CMS4626A × IS 261, CMS463D13A × IS 267, CMS463D13A × IS 261, CMS463D13A × PL 412 and CMS463D13A × AC 102 involved both the parents with significant and positive GCA effects for ascorbic acid in E_1, two crosses CMS463D13A × IS 263 and CMS463D13A × VR 523 in E_2, three crosses CMS4626A × SL 475, CMS4626A × AC 102 and CMS4626A × VR 522 in E_3. Two crosses namely CMS4626A × SL 475 and CMS4626A × VR 523 across the environments involved both the parents with good GCA effects for ascorbic acid, indicating the predominant role of additive gene effects. From the hybrid populations derived from these crosses, there are possibilities of developing true breeding lines rich in ascorbic acid content.

Five crosses CMS4611A × C 142, CMS4626A × VR 522, CMS463D13A × PP 402, CMS463D13A × FL 201 and CMS463D13A × YL 581 involved at least one parent with positive significant GCA effects in E_1, six crosses CMS4611A × SL 475, CMS4611A × PL 412, CMS4611A × VR 521, CMS463D13A × PP 402, CMS463D13A × YL 581 and CMS463D13A × FL 201 in E_2, six crosses CMS4611A × IS 261, CMS4626A × IS 262, CMS463D13A × PP 402, CMS463D13A × YL 581, CMS463D13A × FL 201 and CMS463D13A × E 183 in E_3, and eight crosses CMS4611A × C 142, CMS4611A × PL 412, CMS4611A × IS 268, CMS4626A × VR 522, CMS4626A × IS 262, CMS463D13A × PP 402, CMS463D13A × YL 581 and CMS463D13A × FL 201 across the three environments. Two crosses CMS4611A × SL 473 and CMS4611A × DL 161 in E_1, three crosses CMS4611A × AC 102, CMS4626A × IS 262 and CMS4626A × VR 522 in E_2, four crosses CMS4611A × SL 473, CMS4611A × DL 161, CMS4611A × IS 267 and CMS4611A × PP

414 in E_3, and two crosses CMS4611A × SL 473 and CMS4611A × DL 161 across the three environments have neither of the parents with positively significant GCA effects. The non-additive gene effects played predominant role in their expression and is worthwhile for exploitation through heterosis breeding.

Good SCA values for ascorbic acid content were recorded by Geleta and Labuschagne (2006b) in the crosses Kalocsai ‘M’ Cseresznye × Bakko Local, Kalocsai ‘M’ Cseresznye × Szegedi 178, Mareko Shote × Pepper 1976 and C00916 × PBC 142A, by Savitha *et al* (2013) in CA 172 × Kashi Anmol, CA 71 × Kashi Anmol and CA 192 × CA 97, by do Nascimento *et al* (2014) in UFPB 77.1 × UFPB 77.2, UFPB 01 × UFPB 77.2 and UFPB 132 × UFPB 134, and by Rohini *et al* (2017b) in the crosses LCA334 × Pusa Jwala, K 1 × LCA334 and Arka Lohit × LCA334.

4.3.4.13 Oleoresin content (%)

The number of crosses showing significant and positive SCA values was 13 in E_1, 11 in E_2, 9 in E_3 and 15 across the three environments. Significant negative SCA effects for oleoresin content were observed for 15 crosses in E_1, for 14 crosses in E_2, for seven crosses in E_3 and for 18 crosses over the three environments. The SCA effects varied from -2.27 (CMS463D13A × PL 406) to 2.83 (CMS463D13A × IS 263) in E_1, from -2.86 (CMS4626A × DL 161) to 2.87 (CMS463D13A × DL 161) in E_2, from -0.95 (CMS4626A × IS 263) to 1.18 (CMS463D13A × IS 263) in E_3 and from -1.38 (CMS4626A × DL 161) to 1.56 (CMS4626A × IS 262) over the environments (Table 4.10e).

The cross CMS463D13A × IS 263 exhibited the highest SCA effects for oleoresin content followed by CMS463D13A × IS 267 and CMS4626A × VR 522 in E_1, the cross CMS463D13A × DL 161 followed by CMS4626A × IS 262 and CMS463D13A × VR 521 in E_2, the cross CMS463D13A × IS 263 followed by CMS4611A × IS 268 and CMS463D13A × DL 161 in E_3, and the cross CMS4626A × IS 262 followed by CMS463D13A × DL 161 and CMS4626A × VR 522 expressed good SCA effects based on the pooled means. Among the crosses showing significant positive SCA effects, four crosses CMS4626A × SL 475, CMS4626A × C 142, CMS4626A × PL 406 and CMS4626A × PP 402 had both the parents with good GCA effects for oleoresin content in E_1, two crosses CMS463D13A × DL 161 and CMS463D13A × VR 521 in E_2, five crosses CMS4626A × VR 522, CMS463D13A × DL 161, CMS463D13A × VR 523, CMS463D13A × VR 521 and CMS463D13A × SL 475 in E_3. Four crosses CMS463D13A × DL 161, CMS463D13A × VR 521, CMS463D13A × IS 267 and CMS463D13A × VR 523 had both the parents with good GCA effects across the environments. These crosses could serve as a source material to derive true breeding lines with high oleoresin content from the segregating progeny. Six crosses CMS4611A × PL 406, CMS4611A × C 142, CMS4626A × VR 522, CMS4626A × IS 262, CMS463D13A × IS 263 and CMS463D13A × VR 521 involved at least one parent with positive significant GCA effects in E_1, four crosses CMS4611A × C 142, CMS4626A × VR 522, CMS4626A × IS 267 and CMS463D13A × SL 473 in E_2, two crosses CMS4626A × SL 473 and CMS463D13A × IS 263 in E_3, and six crosses CMS4611A × C 142, CMS4611A × IS 261, CMS4611A × PL 406, CMS4626A × VR 522, CMS4626A × PP 402 and CMS463D13A × IS 263 across the three environments. Three crosses CMS4611A × PL 412, CMS463D13A × IS 267 and CMS463D13A × IS 268 in E_1, five crosses CMS4611A × PL 412, CMS4611A × PP 414, CMS4626A × IS 262, CMS4626A × PL 412 and CMS4626A × FL 201 in E_2, two crosses CMS4611A × IS 268 and CMS4611A × AC 102 in E_3, and five crosses CMS4611A × PL 412, CMS4611A × IS 268, CMS4611A × PP 414, CMS4626A × IS 262 and CMS4626A × FL 201 over the three environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses which can be exploited through heterosis breeding.

Saritha *et al* (2005) reported that the cross AVRDC-95-06 × Byadgi Kaddi exhibited the highest SCA values followed by TIWARI × Arka Abhir and TIWARI × Arka Lohit. Prasath and Ponnuswami (2008) found that the crosses Bydagi Kaddi × Co 4, Arka Lohit × S 1 and Arka Lohit × Arka Abir were good specific combiners for oleoresin content. Savitha *et al* (2013) recorded the highest SCA effects by the cross CA 192 × CA 97 followed by CA 117 × Kashi Anmol and CA 72 × CA 97. Rohini *et al* (2017b) identified K1 × LCA625 as the best cross for oleoresin content followed by LCA334 × Pusa Jwala and Arka Lohit × PKM1.

4.3.4.14 Capsaicin content (%)

The SCA effects for capsaicin content varied between -0.13 in the cross CMS463D13A × PL 406 to 0.16 in the cross CMS463D13A × IS 268 under E_1, from -0.07 in the cross CMS4626A × C 142 to 0.08 in the cross CMS4626A × PP 402 under E_2, from -0.10 in the cross CMS4611A × IS 262 to 0.10 in the cross CMS463D13A × IS 262 under E_3 and from -0.06 in the cross CMS463D13A × PL 406 to 0.06 in the cross CMS4626A × PL 406, based on the pooled means. Twenty crosses in E_1, 12 crosses in E_2, 15 crosses in E_3 and 18 crosses over the three environments exhibited significant and positive SCA effects for capsaicin content. Eighteen crosses in E_1, 11 crosses in E_2, 16 crosses in E_3 and 20 crosses over the three environments exhibited significantly negative SCA effects and thus were adjudged as the poor specific combiners (Table 4.10e).

The cross CMS463D13A × IS 268 followed by CMS4626A × PL 406 and CMS4626A × VR 521 produced significantly positive SCA effects for capsaicin content under E_1, the cross CMS4626A × PP 402 followed by CMS463D13A × C 142 and CMS4626A × VR 522 under E_2, the cross CMS463D13A × IS 262 followed by CMS463D13A × SL 475 and CMS4626A × IS 263 under E_3, and the cross CMS4626A × PL

406 followed by CMS4626A × IS 267 and CMS4611A × SL 473 exhibited good SCA effects based on the pooled means. Six crosses CMS4626A × PL 406, CMS4626A × C 142, CMS4626A × IS 263, CMS463D13A × IS 268, CMS463D13A × IS 263 and CMS463D13A × VR 523 had both the parents with good GCA effects for capsaicin content in E_1, four crosses CMS4626A × IS 268, CMS463D13A × C 142, CMS463D13A × VR 521 and CMS463D13A × PL 406 in E_2, seven crosses CMS4626A × IS 263, CMS4626A × PL 406, CMS4626A × IS 267, CMS4626A × VR 523, CMS463D13A × IS 262, CMS463D13A × SL 475 and CMS463D13A × PL 412 in E_3, and eight crosses CMS4626A × PL 406, CMS4626A × IS 263, CMS4626A × VR 521, CMS463D13A × IS 268, CMS463D13A × IS 261, CMS463D13A × IS 262, CMS463D13A × SL 475 and CMS463D13A × DL 161 across the three environments. This suggested the involvement of additive gene effects in heterotic performance of these crosses. The hybrid populations derived from these crosses can be pursued further to recover transgressive segregants with high pungency.

Eight crosses CMS4611A × DL 161, CMS4611A × SL 475, CMS4626A × VR 521, CMS4626A × IS 267, CMS4626A × PP 414, CMS463D13A × IS 261, CMS463D13A × FL 201 and CMS463D13A × PP 402 involved at least one parent with positive significant GCA effects in E_1, six crosses CMS4611A × IS 263, CMS4626A × PP 402, CMS4626A × VR 522, CMS4626A × IS 267, CMS4626A × VR 523 and CMS463D13A × PL 412 in E_2, four crosses CMS4611A × PL 412, CMS4626A × YL 581, CMS4626A × PP 402 and CMS463D13A × DL 161 in E_3, and five crosses CMS4611A × IS 261, CMS4626A × IS 267, CMS4626A × PP 402, CMS463D13A × PL 412 and CMS463D13A × FL 201 across the three environments. Six crosses CMS4611A × YL 581, CMS4611A × SL 473, CMS4611A × E 183, CMS4611A × PP 414, CMS4611A × VR 522 and CMS4611A × IS 261 in E_1, two crosses CMS4611A × YL 581 and CMS4611A × PP 414 in E_2, four crosses CMS4611A × E 183, CMS4611A × SL 473, CMS4611A × IS 268 and CMS4611A × IS 261 in E_3, and five crosses CMS4611A × SL 473, CMS4611A × E 183, CMS4611A × YL 581, CMS4611A × PP 414 and CMS4611A × PL 412 over the environments have neither of the parents with positively significant GCA effects. This suggested that the non-additive gene effects were predominantly involved in superior performance of these crosses which can be exploited through heterosis breeding.

The cross CMS463D13A × PL 406 expressed the highest significant negative SCA effects followed by CMS4611A × IS 268, CMS4626A × IS 261 and CMS4611A × IS 263 in E_1, the cross CMS4626A × C 142 followed by CMS463D13A × PP 402, CMS4626A × PL 412 and CMS4611A × IS 268 in E_2, the cross CMS4611A × IS 262 followed by CMS463D13A × PL 406, CMS4626A × PL 412 and CMS4611A × SL 475 in E_3, and the cross CMS463D13A × PL 406 followed by CMS4626A × IS 261, CMS4626A × PL 412 and CMS463D13A × PP 414 across the three environments.

Earlier, Lohithaswa *et al* (2000) identified Pant C-1 × Pusa Jwala, X-235 × Pusa Jwala and PMR-57 × Arka Lohit, Zewdie and Bosland (2001) identified NMCA80004 × NMCA80058, NMCA80058 × NMCA80062 and NMCA80004 × NMCA80062, Saritha *et al* (2005) identified PMR-14 × Byadgi Dabbi, RHRC-50-1 × Punjab Surkh and AVRDC-95-06 × Punjab Surkh, Sánchez-Sánchez *et al* (2010) identified Huatusco × Zongolica, Puebla × Tacámbaro and Tacámbaro × Perú, Savitha *et al* (2013) identified CA 192 × CA 97, CA 71 × Kashi Anmol and CA 207 × CA 97, and Rohini *et al* (2017b) identified LCA334 × PKM1, K 1 × PKM1 and K 1 × LCA334 crosses with high SCA effects for capsaicin content.

4.3.4.15 Scoville heat units (SHU)

The SCA effects for SHU varied from -21236.45 in the cross CMS463D13A × PL 406 to 24968.0 in the cross CMS463D13A × IS 268 under E_1, from -10689.33 in the cross CMS4626A × C 142 to 13099.11 in the cross CMS4626A × PP 402 under E_2, from -15700.44 in the cross CMS4611A × IS 262 to 16523.55 in the cross CMS463D13A × IS 262 under E_3 and from -9155.56 in the cross CMS463D13A × PL 406 to 10036.89 in the cross CMS4626A × PL 406, based on the pooled means. Twenty crosses in E_1, 12 crosses in E_2, 15 crosses in E_3 and 18 crosses over the three environments exhibited significant and positive SCA effects for SHU. Eighteen crosses in E_1, 11 crosses in E_2, 16 crosses in E_3 and 20 crosses over the three environments exhibited significant negative SCA effects for SHU and thus were adjudged as the poor specific combiners (Table 4.10f).

The cross CMS463D13A × IS 268 followed by CMS4626A × PL 406 and CMS4626A × VR 521 produced significantly positive SCA effects in E_1, the cross CMS4626A × PP 402 followed by CMS463D13A × C 142 and CMS4626A × VR 522 in E_2, the cross CMS463D13A × IS 262 followed by CMS463D13A × SL 475 and CMS4626A × IS 263 in E_3, and the cross CMS4626A × PL 406 followed by CMS4626A × IS 267 and CMS4611A × SL 473 exhibited good SCA effects based on the pooled means. Six crosses CMS4626A × PL 406, CMS4626A × C 142, CMS4626A × IS 263, CMS463D13A × IS 268, CMS463D13A × IS 263 and CMS463D13A × VR 523 had both the parents with good GCA effects for SHU in E_1, four crosses CMS4626A × IS 268, CMS463D13A × C 142, CMS463D13A × VR 521 and CMS463D13A × PL 406 in E_2, seven crosses CMS4626A × IS 263, CMS4626A × PL 406, CMS4626A × IS 267, CMS4626A × VR 523, CMS463D13A × IS 262, CMS463D13A × SL 475 and CMS463D13A × PL 412 in E_3, and eight crosses CMS4626A × PL 406, CMS4626A × IS 263, CMS4626A × VR 521, CMS463D13A × IS 268, CMS463D13A × IS 261, CMS463D13A × IS 262, CMS463D13A × SL 475 and

CMS463D13A × DL 161 across the three environments. These crosses can serve as a source material to derive true breeding lines with high SHU from the segregating populations.

Eight crosses CMS4611A × DL 161, CMS4611A × SL 475, CMS4626A × VR 521, CMS4626A × IS 267, CMS4626A × PP 414, CMS463D13A × IS 261, CMS463D13A × FL 201 and CMS463D13A × PP 402 involved at least one parent with positive significant GCA effects in E_1, six crosses CMS4611A × IS 263, CMS4626A × PP 402, CMS4626A × VR 522, CMS4626A × IS 267, CMS4626A × VR 523 and CMS463D13A × PL 412 in E_2, four crosses CMS4611A × PL 412, CMS4626A × YL 581, CMS4626A × PP 402 and CMS463D13A × DL 161 in E_3, and five crosses CMS4611A × IS 261, CMS4626A × IS 267, CMS4626A × PP 402, CMS463D13A × PL 412 and CMS463D13A × FL 201 across the three environments. Six crosses CMS4611A × YL 581, CMS4611A × SL 473, CMS4611A × E 183, CMS4611A × PP 414, CMS4611A × VR 522 and CMS4611A × IS 261 in E_1, two crosses CMS4611A × YL 581 and CMS4611A × PP 414 in E_2, four crosses CMS4611A × E 183, CMS4611A × SL 473, CMS4611A × IS 268 and CMS4611A × IS 261 in E_3, and five crosses CMS4611A × SL 473, CMS4611A × E 183, CMS4611A × YL 581, CMS4611A × PP 414 and CMS4611A × PL 412 over the environments have neither of the parents with positively significant GCA effects. The contributions to the SCA effects of these crosses have come from the non-additive gene effects. The desirable effects exhibited by these crosses can be exploited through heterosis breeding. Naresh *et al* (2016) reported that the cross IHR3849 × IHR4503 showed the highest SCA effects for capsaicin followed by IHR3448 × IHR4516.

The cross CMS463D13A × PL 406 showed the highest significant negative SCA effects followed by CMS4611A × IS 268, CMS4626A × IS 261 and CMS4611A × IS 263 in E_1, the cross CMS4626A × C 142 followed by CMS463D13A × PP 402, CMS4626A × PL 412 and CMS4611A × IS 268 in E_2, and the cross CMS4611A × IS 262 followed by CMS463D13A × PL 406, CMS4626A × PL 412 and CMS4611A × SL 475 in E_3. The cross CMS463D13A × PL 406 followed by CMS4626A × IS 261, CMS4626A × PL 412 and CMS463D13A × PP 414 exhibited significant negative SCA effects based on pooled means.

Among the crosses showing significantly negative SCA effects, two crosses CMS4611A × PP 402 and CMS4611A × IS 267 in E_1 and one cross CMS4611A × PP 402 across the three environments had both the parents with negatively significant GCA effects. These crosses can be pursued further to develop true breeding lines with mildly pungency. Nine crosses CMS4611A × IS 268, CMS4611A × IS 263, CMS4611A × VR 521, CMS4626A × FL 201, CMS4626A × E 183, CMS4626A × YL 581, CMS4626A × SL 473, CMS463D13A × PP 414 and CMS463D13A × IS 267 have at least one of the parents with significantly negative GCA effects in E_1, six crosses CMS4611A × IS 268, CMS4611A × PL

406, CMS4626A × PL 412, CMS463D13A × PP 402, CMS463D13A × VR 522 and CMS463D13A × IS 267 in E_2, eleven crosses CMS4611A × IS 262, CMS4611A × SL 475, CMS4611A × VR 523, CMS4611A × IS 263, CMS4626A × DL 161, CMS4626A × E 183, CMS4626A × SL 473, CMS463D13A × YL 581, CMS463D13A × SL 473, CMS463D13A × PP 414 and CMS463D13A × E 183 in E_3, and thirteen crosses CMS4611A × IS 268, CMS4611A × VR 521, CMS4611A × IS 262, CMS4611A × IS 263, CMS4611A × IS 267, CMS4611A × VR 523, CMS4626A × E 183, CMS4626A × SL 473, CMS4626A × FL 201, CMS463D13A × PP 414, CMS463D13A × YL 581, CMS463D13A × SL 473 and CMS463D13A × VR 522 across the three environments. Seven crosses CMS4626A × IS 261, CMS4626A × DL 161, CMS4626A × SL 475, CMS4626A × IS 268, CMS463D13A × PL 406, CMS463D13A × C 142 and CMS463D13A × VR 521 in E_1, five crosses CMS4626A × C 142, CMS4626A × VR 521, CMS4626A × IS 263, CMS463D13A × VR 523 and CMS463D13A × IS 263 in E_2, five crosses CMS4626A × PL 412, CMS4626A × IS 261, CMS4626A × IS 268, CMS463D13A × PL 406 and CMS463D13A × IS 263 in E_3, and six crosses CMS4626A × IS 261, CMS4626A × PL 412, CMS4626A × DL 161, CMS4626A × SL 475, CMS463D13A × PL 406 and CMS463D13A × IS 267 based on pooled means have neither of the parents with negatively significant GCA effects. The contribution to the mean performance of these crosses has come from non-additive gene effects. Thus, for obtaining lines with mildly pungency, one will have to go for F_1 hybrids rather than true breeding lines.

On basis of the SCA estimates over the environments, crosses have been identified for early, main and late season cultivation with pungent and non-pungent fruits. Further, crosses have been identified for exploitation through pure line breeding or heterosis breeding. Total yield plant^{-1} is the most important economic trait which deserves highest consideration in any crop improvement program. Therefore, all crosses identified for further use have high SCA estimates for total yield plant^{-1}. Apart from high SCA effects for total yield plant^{-1} in E_1, the cross CMS463D13A × IS 268 also expressed significant positive SCA effects for fruit weight, number of seed fruit^{-1}, capsaicin content and SHU values; CMS463D13A × PP 402 for fruit weight and pericarp thickness; and the cross CMS463D13A × IS 267 was good specific combiner for number of primary branches palnt^{-1} and ascorbic acid. These crosses can be pursued further to develop high yielding true breeding lines for cultivation in the early season. The crosses CMS4611A × PP 414, CMS4611A × E 183 and CMS463D13A × PP 402 also expressed significant SCA effects for capsaicin content and SHU values. These crosses have been identified for production of pungent chilli. The cross CMS463D13A × IS 267 showed significant positive SCA effects for oleoresin content and significantly negative SCA effects for capsaicin and SHU. These crosses have been identified for oleoresin extraction, used in food industry as natural colorant. The cross CMS4611A × IS 263 expressed significantly positive SCA effects for number of seed fruit^{-1} and negatively significant SCA effects for capsaicin content and SHU. The cross is identified for paprika production and fresh consumption. In these crosses, the contribution to the mean performance comes primarily from the non-additive gene effects. Heterosis breeding would be the appropriate approach to exploit high SCA effects attributed to the non-additive gene action.

In E_2, the crosses CMS463D13A × FL 201 and CMS4626A × FL 201 had good SCA effects for fruit weight and the cross CMS4626A × PL 412 was found to be good specific combiner for number of fruits plant^{-1}. Both the traits are important to enhance fruit yield. High SCA performance of these crosses is attributed to the additive gene effects and are, therefore, potential source material to derive true breeding lines with high yield potential. Apart from the high SCA effects for total yield plant^{-1}, the crosses CMS463D13A × VR 523, CMS463D13A × AC 102 and CMS4611A × VR 521 were regarded as good specific combiners for fruit weight and number of fruits plant^{-1}; CMS4611A × PP 402, CMS4626A × IS 263, CMS4626A × DL 161, CMS4626A × PP 414, CMS463D13A × SL 475, CMS463D13A × SL 473 and CMS463D13A × IS 268 for number of fruits plant^{-1}; and CMS4626A × FL 201 for number of seed fruit^{-1}. These crosses are identified for dry chilli production in main-season. The crosses CMS4611A × C 142, CMS4626A × FL 201, CMS463D13A × SL 473, CMS4626A × IS 262 and CMS4626A × PL 412 were found to be good specific combiners for oleoresin content, and are identified for oleoresin extraction. The crosses CMS4626A × IS 263, CMS4626A × PL 412, CMS463D13A × IS 263 and CMS463D13A × VR 523 were identified with low pungency for fresh consumption and paprika production. Superior SCA performance of these crosses was attributed to the non-additive gene effects. Heterosis breeding would be an appropriate approach to exploit non-additive gene effected exhibited by these crosses.

In late season planted (E_3) crop, the high SCA performance for total yield plant^{-1} in the crosses CMS463D13A × IS 268 and CMS463D13A × YL 581 was contributed by the additive gene effects. These crosses are recommended to be pursued further to develop high yielding true breeding lines for late season cultivation. The cross CMS4611A × E 183 and CMS4626A × PL 406 exhibited good SCA effects for capsaicin content and SHU, and are identified for cultivation of highly pungent chilli. On the basis of high SCA effects, the crosses CMS4611A × IS 267, CMS463D13A × PP 402, CMS4611A × VR 522, CMS4611A × E 183, CMS4626A × IS 268, CMS4626A × IS 261 and CMS463D13A × AC 102 have been identified for total yield plant^{-1} and number of fruits plant^{-1}; the crosses CMS4611A × IS 262, CMS4611A × VR 521 and CMS463D13A × IS 268 for long fruits; the crosses CMS4611A × IS 262, CMS4611A × IS 263, CMS4611A × VR 523, CMS4626A × IS 261, CMS4626A × IS

268, CMS4626A × SL 473 and CMS463D13A × YL 581 for low pungency; and the crosses CMS4611A × DL 161 and CMS4626A × IS 268 for short fruits. The contribution to the high SCA performance of these crosses has come from the non-additive gene effects. Heterosis breeding would be the appropriate approach to exploit non-additive gene effects.

On basis of the performance across the environments, the cross CMS463D13A × IS 268 was identified with significant SCA estimates for total yield plant^{-1}, number of primary branches plant^{-1}, fruit weight, number of seed fruit^{-1}, capsaicin content and SHU. The cross may be pursued further to recover true breeding lines with high yield and pungent fruits for cultivation across the environments. Two crosses CMS463D13A × VR 523 and CMS463D13A × IS 267 have been identified for high oleoresin content. Higher SCA effects of these crosses have resulted from cumulative effects of additive genes which can be fixed in true breeding lines rich in oleoresin content. Along with total yield plant^{-1}, the crosses CMS4611A × PP 414, CMS4611A × E 183 and CMS463D13A × FL 201 also expressed good SCA effects for capsaicin content and SHU. The high SCA effects of these crosses were attributed to the non-additive gene effects. The genetic variation exhibited by these crosses can be exploited through heterosis breeding for the development of high yielding pungent cultivars. The cross CMS4611A × VR 521 showed significantly positive SCA effects for fruit weight, fruit width, pericarp thickness and number of fruits plant^{-1} and significant negative SCA effects for oleoresin content, capsaicin content and SHU. The cross is identified for paprika production and fresh consumption. The cross CMS463D13A × IS 268 expressed high SCA estimates for number of fruits plant^{-1} and has been identified for the development of long fruit types. The crosses CMS4626A × PL 412, CMS463D13A × IS 267 and CMS463D13A × SL 473 exhibited negatively significant SCA effects for capsaicin content and SHU. Hence, these crosses can be utilized for breeding high yielding chilli with mildly pungent fruits.

The critical examination of the results would reveal that the crosses exhibiting good SCA effects for various plant growth, yield and quality traits involved all possible combinations between parents with good, average and poor general combining ability. This indicated that the GCA, in general, had no bearing on the SCA effects of the crosses. This was evident from cross CMS4611A × E 183, which showed highest SCA for total yield plant^{-1} based on pooled means but involved poor × poor GCA parents. The superior SCA performance of such crosses could be attributed to the dominance × dominance and the higher order non-allelic gene interactions producing non-fixable effects. Contrary to this, the cross CMS463D13A × DL 161 exhibited significant negative SCA effects for total yield plant^{-1}, even though both of the parents had high GCA values.

Table 4.10a: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for plant growth traits evaluated over environments

Crosses	Plant height (cm)				Plant spread (cm)				Number of primary branches plant^{-1}			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	-2.62	-0.78	-3.42	-2.27	4.64	-1.07	-2.78	0.26	0.34	-0.82**	1.67**	0.40*
CMS4611A × SL 475	5.39	-3.71	-1.02	0.22	3.93	-10.88**	5.09*	-0.62	0.19	-0.99**	0.30	-0.17
CMS4611A × PL 412	9.92*	1.65	4.33	5.30*	4.95	4.20	-1.27	2.63	0.01	1.18**	0.97**	0.72**
CMS4611A × IS 263	-3.77	0.79	2.62	-0.12	-6.36*	-3.51	4.90*	-1.65	0.44	0.87**	0.12	0.48**
CMS4611A × VR 523	-5.33	-5.60	3.62	-2.44	-9.16**	-0.70	-1.05	-3.64*	0.43	1.15**	-0.32	0.42**
CMS4611A × DL 161	3.61	0.49	-3.02	0.36	1.28	2.74	1.42	1.81	-0.78**	0.39	0.25	-0.05
CMS4611A × IS 267	3.30	6.83	-3.00	2.38	4.28	5.62*	-2.90	2.34	0.28	-1.09**	-0.68*	-0.50**
CMS4611A × YL 581	-0.11	-1.61	8.85**	2.38	8.89**	-1.35	3.50	3.68*	-0.24	0.24	-0.56*	-0.19
CMS4611A × SL 473	-6.86	3.59	-5.30	-2.86	0.60	2.71	-4.67*	-0.45	0.29	-0.30	-0.11	-0.04
CMS4611A × IS 262	-0.49	0.65	1.29	0.48	-3.10	3.17	3.69	1.25	0.08	-0.19	0.08	-0.01
CMS4611A × VR 521	-5.97	-7.12*	-2.23	-5.11*	-4.81	-7.25**	-6.10**	-6.05**	0.44	0.60**	0.43	0.49**
CMS4611A × FL 201	-1.12	-3.11	-1.00	-1.74	0.55	-1.90	2.35	0.33	-0.76**	0.77**	0.48	0.16
CMS4611A × PP 402	-6.74	-1.31	9.08**	0.34	-5.03	3.95	1.59	0.17	0.34	0.15	-1.86**	-0.46**
CMS4611A × C 142	6.89	8.69*	-6.06*	3.17	-1.11	-0.27	-4.84*	-2.07	-0.18	0.33	0.20	0.11
CMS4611A × PP 414	6.57	4.42	-5.52	1.82	0.95	-4.77*	-1.60	-1.81	-0.30	0.89**	-0.34	0.08
CMS4611A × VR 522	-2.09	8.45*	-4.04	0.77	-1.01	-6.30**	2.17	-1.71	0.10	-1.70**	1.13**	-0.15
CMS4611A × PL 406	-5.80	-4.72	4.28	-2.08	-3.61	7.28**	0.03	1.24	-0.04	-0.39	-1.97**	-0.80**
CMS4611A × E 183	-7.35	-2.74	-14.45**	-8.18**	2.41	3.50	-2.57	1.11	0.09	-0.81**	1.66**	0.31*
CMS4611A × IS 268	-1.01	2.09	3.60	1.56	-4.35	10.17**	1.27	2.36	-0.52*	0.87**	-1.05**	-0.23
CMS4611A × IS 261	13.59**	-6.94	11.39**	6.01**	6.06	-5.34*	1.76	0.82	-0.20	-1.15**	-0.39	-0.58**
CMS4626A × AC 102	2.59	-8.53*	0.33	-1.87	-3.76	-8.85**	-0.57	-4.39**	-0.64**	0.00	-0.32	-0.32*

Crosses	**Plant height (cm)**				**Plant spread (cm)**				**Number of primary branches plant^{-1}**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS4626A × SL 475	2.60	1.44	2.71	2.25	-4.48	6.35**	-4.91*	-1.01	0.60*	-0.43	0.95**	0.38*
CMS4626A × PL 412	-6.05	9.13*	-0.94	0.71	3.09	-1.76	4.03	1.79	0.36	-0.24	-0.69*	-0.19
CMS4626A × IS 263	3.59	-5.34	2.09	0.11	4.69	-2.27	2.04	1.49	-0.50*	-0.46*	-0.01	-0.32*
CMS4626A × VR 523	3.29	3.50	1.23	2.67	-0.29	3.19	1.73	1.54	-0.27	1.05**	0.38	0.39*
CMS4626A × DL 161	-2.61	-11.80**	-1.60	-5.33*	-0.69	-3.32	-5.10*	-3.03*	1.08**	-0.43	-0.51	0.05
CMS4626A × IS 267	1.99	-0.92	-1.02	0.02	-5.42	-0.36	2.23	-1.19	-1.15**	0.43	0.97**	0.08
CMS4626A × YL 581	-1.66	2.57	-6.21*	-1.77	-2.49	0.48	-2.04	-1.35	-0.28	-0.50*	-0.44	-0.41**
CMS4626A × SL 473	-1.10	-2.30	2.30	-0.37	-2.41	-2.42	2.22	-0.87	0.02	0.23	-0.50	-0.08
CMS4626A × IS 262	0.68	0.92	-1.76	-0.06	3.63	2.27	-3.54	0.79	0.75**	0.98**	0.08	0.60**
CMS4626A × VR 521	-2.02	-8.29*	-1.24	-3.85	0.93	-0.29	0.68	0.44	-0.41	-0.85**	-0.09	-0.45**
CMS4626A × FL 201	1.75	-2.61	-0.30	-0.39	0.87	-0.34	-2.60	-0.69	0.46	-1.25**	-0.20	-0.33*
CMS4626A × PP 402	8.33	9.14*	-2.73	4.91*	0.89	3.91	-1.02	1.26	-0.37	0.76**	0.64*	0.34*
CMS4626A × C 142	-1.38	6.10	5.48	3.40	0.43	2.07	4.25	2.25	-0.28	0.12	1.01**	0.28
CMS4626A × PP 414	-0.66	-2.93	2.12	-0.49	4.37	5.42*	-0.17	3.21*	-0.55*	0.01	-0.55	-0.36*
CMS4626A × VR 522	-3.53	-3.53	9.23**	0.72	-1.68	8.89**	1.81	3.01	0.90**	-0.85**	-0.51	-0.15
CMS4626A × PL 406	9.75*	4.87	-7.26*	2.45	1.53	-8.89**	0.81	-2.18	-0.12	0.50*	0.85**	0.41**
CMS4626A × E183	-0.65	-2.02	-0.97	-1.21	-1.77	-0.77	1.11	-0.47	0.09	1.06**	-0.85**	0.10
CMS4626A × IS 268	-3.37	-3.15	-4.50	-3.67	-3.29	-5.21*	2.16	-2.11	0.19	-1.94**	-0.05	-0.60**
CMS4626A × IS 261	-11.54*	13.75***	3.04	1.75	5.87	1.89	-3.13	1.54	0.10	1.80**	-0.16	0.58**
CMS463D13A × AC 102	0.02	9.31**	3.10	4.14	-0.88	9.92**	3.35	4.13**	0.30	0.82**	-1.35**	-0.08
CMS463D13A × SL 475	-7.99	2.27	-1.69	-2.47	0.55	4.53	-0.19	1.63	-0.79**	1.41**	-1.25**	-0.21
CMS463D13A × PL 412	-3.87	-10.78**	-3.39	-6.01**	-8.04*	-2.45	-2.77	-4.42**	-0.37	-0.94**	-0.28	-0.53**

Crosses	**Plant height (cm)**				**Plant spread (cm)**				**Number of primary branches plant^{-1}**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS463D13A × IS 263	0.18	4.55	-4.71	0.01	1.67	5.78*	-6.94**	0.17	0.06	-0.42	-0.11	-0.16
CMS463D13A × VR 523	2.04	2.11	-4.85	-0.23	9.45**	-2.49	-0.68	2.09	-0.16	-2.20**	-0.06	-0.81**
CMS463D13A × DL 161	-1.01	11.31**	4.62	4.97*	-0.58	0.58	3.68	1.23	-0.30	0.03	0.26	0.00
CMS463D13A × IS 267	-5.28	-5.91	4.02	-2.39	1.14	-5.26*	0.67	-1.15	0.87**	0.66**	-0.29	0.41**
CMS463D13A × YL 581	1.77	-0.96	-2.64	-0.61	-6.39*	0.87	-1.46	-2.33	0.52*	0.27	1.01**	0.60**
CMS463D13A × SL 473	7.96	-1.28	3.00	3.22	1.81	-0.29	2.45	1.33	-0.30	0.07	0.61*	0.12
CMS463D13A × IS 262	-0.19	-1.57	0.48	-0.43	-0.54	-5.44*	-0.15	-2.04	-0.82**	-0.80**	-0.16	-0.59**
CMS463D13A × VR 521	7.99	15.41**	3.48	8.96**	3.89	7.53**	5.42*	5.61**	-0.04	0.25	-0.33	-0.04
CMS463D13A × FL 201	-0.63	5.73	1.30	2.13	-1.43	2.24	0.25	0.36	0.30	0.49*	-0.28	0.17
CMS463D13A × PP 402	-1.58	-7.83*	-6.35*	-5.26*	4.14	-7.86**	-0.57	-1.43	0.03	-0.91**	1.23**	0.12
CMS463D13A × C 142	-5.51	-14.80**	0.58	-6.58**	0.68	-1.79	0.58	-0.18	0.46	-0.44	-1.21**	-0.40*
CMS463D13A × PP 414	-5.91	-1.49	3.39	-1.34	-5.32	-0.65	1.77	-1.40	0.85**	-0.90**	0.89**	0.28
CMS463D13A × VR 522	5.63	-4.93	-5.20	-1.50	2.69	-2.59	-3.99	-1.29	-1.01**	2.55**	-0.62*	0.31*
CMS463D13A × PL 406	-3.95	-0.15	2.98	-0.37	2.08	1.61	-0.84	0.95	0.15	-0.11	1.12**	0.39*
CMS463D13A × E 183	8.00	4.76	15.42**	9.39**	-0.64	-2.74	1.46	-0.64	-0.18	-0.25	-0.81**	-0.41**
CMS463D13A × IS 268	4.38	1.06	0.90	2.11	7.64*	-4.96*	-3.43	-0.25	0.33	1.07**	1.11**	0.84**
CMS463D13A × IS 261	-2.05	-6.81	-14.42**	-7.76**	-11.93**	3.45	1.38	-2.37	0.09	-0.66**	0.55	-0.01
LSD at *p*=0.05	8.97	6.98	5.87	4.43	6.17	4.63	4.49	3.03	0.48	0.45	0.56	0.30
LSD at *p*=0.01	11.86	9.23	7.76	5.84	8.15	6.12	5.94	3.99	0.63	0.59	0.74	0.40

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.10b: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for fruit weight (g), fruit length (cm) and fruit width (mm) evaluated over environments

Crosses	Fruit weight (g)				Fruit length (cm)				Fruit width (mm)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	1.05**	0.04	0.21	0.43**	0.65	0.03	0.99**	0.56**	0.60	-0.24	0.70	0.35
CMS4611A × SL 475	-0.43	1.72**	-0.13	0.39**	0.13	-0.38	0.35	0.03	0.56	0.35	-0.11	0.26
CMS4611A × PL 412	0.31	0.28	-0.44*	0.05	0.02	0.01	-0.47	-0.15	0.04	0.05	0.02	0.03
CMS4611A × IS 263	0.18	0.21	0.07	0.15	0.64	0.33	0.19	0.39*	-0.15	0.31	0.27	0.14
CMS4611A × VR 523	0.32	-0.44	-0.29	-0.14	-0.07	-0.55	0.21	-0.14	0.23	-0.15	-0.25	-0.06
CMS4611A × DL 161	1.62**	0.25	0.16	0.68**	-0.35	0.28	-1.10**	-0.39*	1.17*	-0.64	0.30	0.28
CMS4611A × IS 267	-0.94**	-0.26	-0.07	-0.42**	-0.46	0.11	0.10	-0.08	0.00	0.24	-0.69	-0.15
CMS4611A × YL 581	-0.95**	0.78**	-0.69**	-0.29	0.40	-0.02	0.16	0.18	-1.10	-0.35	-0.29	-0.58
CMS4611A × SL 473	0.38	-0.38	0.16	0.05	-0.86*	0.16	0.04	-0.22	0.13	-0.63	0.61	0.04
CMS4611A × IS 262	-0.16	-0.06	0.52*	0.10	-0.02	0.06	0.57*	0.20	-0.36	0.22	0.10	-0.02
CMS4611A × VR 521	0.76*	0.65**	0.16	0.52**	-0.39	0.19	0.55*	0.12	0.83	0.44	0.52	0.60*
CMS4611A × FL 201	-1.16**	-2.79**	-0.36	-1.43**	-0.19	-0.12	-0.37	-0.23	-1.27*	0.07	-1.04*	-0.75*
CMS4611A × PP 402	-2.43**	-1.91**	-0.52*	-1.62**	-1.00**	0.51	0.30	-0.06	-2.10**	-0.20	-1.21**	-1.17**
CMS4611A × C 142	0.62	-0.28	-0.13	0.07	0.80*	-0.43	0.57*	0.31	0.41	-0.06	-0.10	0.08
CMS4611A × PP 414	0.53	0.25	0.73**	0.50**	-0.34	1.01**	-0.08	0.20	0.74	0.89	0.51	0.71*
CMS4611A × VR 522	-1.01**	-1.36**	0.58**	-0.60**	-0.28	-0.50	-0.35	-0.38*	0.06	-0.06	-0.36	-0.12
CMS4611A × PL 406	0.65*	0.43	-0.47*	0.20	0.21	-0.31	-0.54*	-0.21	-0.30	-0.11	-0.13	-0.18
CMS4611A × E 183	1.54**	0.56*	0.19	0.76**	0.65	-0.06	0.21	0.27	0.27	0.35	0.60	0.41
CMS4611A × IS 268	-0.50	0.88**	-0.25	0.04	0.51	-0.18	-0.30	0.01	-0.86	-0.26	0.37	-0.25
CMS4611A × IS 261	-0.38	1.43**	0.60**	0.55**	-0.07	-0.14	-1.01**	-0.40*	1.10	-0.20	0.19	0.37
CMS4626A × AC 102	-0.39	-1.06**	0.04	-0.47**	-1.01**	0.63*	-0.53	-0.30	-1.40*	-0.13	-0.26	-0.59*

Crosses	Fruit weight (g)				Fruit length (cm)				Fruit width (mm)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4626A × SL 475	0.60	-0.37	0.30	0.18	0.19	0.40	-0.61*	-0.01	0.48	-0.34	0.01	0.05
CMS4626A × PL 412	0.21	-0.65**	0.60**	0.06	-0.63	0.49	1.10**	0.32	-0.01	-0.12	0.43	0.10
CMS4626A × IS 263	0.54	-0.24	-0.05	0.08	-0.41	-0.52	-0.02	-0.31	-0.53	-0.81	-0.06	-0.47
CMS4626A × VR 523	-0.52	-0.51*	0.66**	-0.12	-0.13	0.10	-0.09	-0.04	-0.01	-0.12	-0.36	-0.16
CMS4626A × DL 161	-0.51	0.40	-0.37	-0.16	-0.05	0.00	-0.39	-0.15	0.05	0.80	-0.61	0.08
CMS4626A × IS 267	0.24	-0.40	0.63**	0.15	0.15	-0.23	-0.44	-0.17	-0.43	0.41	0.58	0.18
CMS4626A × YL 581	-0.82*	-1.15**	0.36	-0.54**	-0.79*	-0.26	0.18	-0.29	0.25	0.48	0.18	0.30
CMS4626A × SL 473	-1.00**	0.05	-0.56**	-0.50**	-0.41	-0.16	0.09	-0.16	-0.40	1.01*	-0.66	-0.01
CMS4626A × IS 262	-0.04	0.14	-0.72**	-0.20	0.24	0.54	-0.54*	0.08	-0.09	-0.53	-0.50	-0.37
CMS4626A × VR 521	1.15**	0.28	-0.40*	0.35*	0.86*	-0.14	-0.32	0.13	0.22	-0.45	-0.43	-0.22
CMS4626A × FL 201	-0.73*	1.09**	0.43*	0.26	0.37	-0.02	0.29	0.21	0.17	-0.24	1.00*	0.31
CMS4626A × PP 402	1.50**	1.79**	0.56**	1.28**	0.98*	-0.40	0.14	0.24	1.13	0.62	0.80	0.85**
CMS4626A × C 142	0.17	0.28	-0.09	0.12	-0.12	0.42	-0.13	0.05	0.07	0.35	0.26	0.23
CMS4626A × PP 414	-0.28	-0.08	-0.29	-0.21	1.30**	-0.51	0.61*	0.47*	0.10	-0.18	-0.40	-0.16
CMS4626A × VR 522	0.24	0.65**	-0.44*	0.15	-0.06	0.16	0.14	0.08	-0.25	-0.25	-0.17	-0.22
CMS4626A × PL 406	-0.45	0.17	0.18	-0.04	0.01	-0.04	0.38	0.12	0.07	-0.55	0.44	-0.01
CMS4626A × E183	0.02	0.38	0.34	0.24	-0.17	-0.45	0.24	-0.13	0.42	-0.15	0.37	0.21
CMS4626A × IS 268	-0.18	-0.79**	-0.82**	-0.60**	-0.60	-0.26	-0.73**	-0.53**	0.86	0.31	-0.56	0.20
CMS4626A × IS 261	0.25	0.01	-0.35	-0.03	0.29	0.25	0.64*	0.39*	-0.72	-0.12	-0.07	-0.30
CMS463D13A × AC 102	-0.66*	1.03**	-0.25	0.04	0.35	-0.66*	-0.46	-0.25	0.80	0.37	-0.44	0.24
CMS463D13A × SL 475	-0.18	-1.35**	-0.18	-0.57**	-0.32	-0.03	0.26	-0.03	-1.03	-0.01	0.10	-0.32
CMS463D13A × PL 412	-0.52	0.37	-0.16	-0.11	0.61	-0.49	-0.63*	-0.17	-0.02	0.07	-0.44	-0.13
CMS463D13A × IS 263	-0.71*	0.03	-0.01	-0.23	-0.23	0.19	-0.18	-0.07	0.68	0.50	-0.20	0.33

Crosses	**Fruit weight (g)**				**Fruit length (cm)**				**Fruit width (mm)**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS463D13A × VR 523	0.19	0.95**	-0.37	0.26	0.20	0.45	-0.12	0.18	-0.23	0.28	0.61	0.22
CMS463D13A × DL 161	-1.11**	-0.65**	0.21	-0.52**	0.40	-0.28	1.49**	0.54**	-1.23*	-0.16	0.32	-0.36
CMS463D13A × IS 267	0.70*	0.66**	-0.55**	0.27	0.31	0.12	0.34	0.26	0.44	-0.65	0.11	-0.03
CMS463D13A × YL 581	1.78**	0.37	0.33	0.83**	0.39	0.29	-0.34	0.11	0.85	-0.13	0.11	0.28
CMS463D13A × SL 473	0.62	0.32	0.41*	0.45**	1.27**	-0.01	-0.13	0.38*	0.26	-0.38	0.04	-0.02
CMS463D13A × IS 262	0.20	-0.08	0.20	0.11	-0.22	-0.60*	-0.02	-0.28	0.45	0.31	0.40	0.39
CMS463D13A × VR 521	-1.91**	-0.93**	0.24	-0.87**	-0.48	-0.06	-0.22	-0.25	-1.05	0.01	-0.09	-0.38
CMS463D13A × FL 201	1.89**	1.69**	-0.07	1.17**	-0.18	0.14	0.08	0.02	1.10	0.17	0.03	0.44
CMS463D13A × PP 402	0.93**	0.12	-0.04	0.34*	0.02	-0.11	-0.44	-0.17	0.97	-0.41	0.41	0.32
CMS463D13A × C 142	-0.79*	0.00	0.22	-0.19	-0.68	0.02	-0.44	-0.37*	-0.48	-0.30	-0.16	-0.31
CMS463D13A × PP 414	-0.25	-0.17	-0.45*	-0.29	-0.96*	-0.50	-0.53	-0.67**	-0.84	-0.71	-0.11	-0.55
CMS463D13A × VR 522	0.77*	0.71**	-0.14	0.45**	0.34	0.34	0.21	0.30	0.18	0.31	0.53	0.34
CMS463D13A × PL 406	-0.20	-0.59*	0.30	-0.17	-0.22	0.34	0.16	0.09	0.23	0.66	-0.32	0.19
CMS463D13A × E 183	-1.55**	-0.95**	-0.53**	-1.01**	-0.48	0.51	-0.46	-0.14	-0.69	-0.20	-0.97*	-0.62*
CMS463D13A × IS 268	0.68*	-0.09	1.07**	0.55**	0.09	0.44	1.03**	0.52**	0.00	-0.04	0.19	0.05
CMS463D13A × IS 261	0.13	-1.44**	-0.25	-0.52**	-0.22	-0.11	0.37	0.01	-0.39	0.32	-0.12	-0.06
LSD at *p*=0.05	0.63	0.45	0.40	0.29	0.74	0.57	0.54	0.36	1.15	1.00	0.83	0.58
LSD at *p*=0.01	0.84	0.60	0.52	0.38	0.98	0.75	0.71	0.47	1.51	1.32	1.10	0.77

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.10c: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for pericarp thickness (mm), number of fruits plant^{-1} and number of seed fruit^{-1} evaluated over environments

Crosses	Pericarp thickness (mm)				Number of fruits plant^{-1}				Number of seed fruit^{-1}			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	-0.04	-0.01	0.07	0.01	-10.45	-14.70	-31.44**	-18.86**	11.35**	11.13**	4.75**	9.08**
CMS4611A × SL 475	0.08	0.07	-0.14**	0.00	-13.46	-25.20*	-2.95	-13.87*	-5.24*	-3.72	-0.36	-3.11*
CMS4611A × PL 412	0.10	0.06	0.09*	0.08**	-56.11**	20.76	-12.63	-15.99*	3.47	-1.68	-3.23	-0.48
CMS4611A × IS 263	-0.03	0.06	0.10**	0.04	35.32**	-80.86**	3.75	-13.93*	9.24**	8.74**	2.61	6.87**
CMS4611A × VR 523	0.07	0.01	0.19**	0.09**	-5.42	-40.69**	12.42	-11.23	1.37	2.60	-0.16	1.27
CMS4611A × DL 161	0.17**	-0.07	0.07	0.06	-0.58	-7.30	38.91**	10.34	4.41	3.39	-0.21	2.53
CMS4611A × IS 267	-0.06	0.06	0.05	0.02	0.41	47.54**	50.04**	32.66**	-3.98	-6.28**	-0.73	-3.66**
CMS4611A × YL 581	-0.14*	-0.16**	-0.16**	-0.15**	-17.49	-7.52	5.91	-6.37	2.58	5.11*	1.26	2.98*
CMS4611A × SL 473	-0.09	-0.23**	0.02	-0.10**	-24.89*	-14.79	-61.19**	-33.62**	-1.82	-2.23	0.55	-1.17
CMS4611A × IS 262	-0.15*	0.00	-0.05	-0.07*	6.59	-45.20**	9.26	-9.79	-1.29	0.28	-1.00	-0.67
CMS4611A × VR 521	0.15*	-0.01	0.08*	0.07*	-21.34	73.36**	0.91	17.64**	-2.04	1.31	-3.25	-1.33
CMS4611A × FL 201	-0.17**	-0.03	-0.20**	-0.13**	25.05*	-26.61*	-22.92**	-8.16	-3.79	-2.32	-0.79	-2.30
CMS4611A × PP 402	-0.25**	0.10	-0.18**	-0.11**	20.25	36.65**	-14.52*	14.13*	-11.41**	-10.47**	-4.94**	-8.94**
CMS4611A × C 142	0.06	-0.11*	-0.02	-0.02	20.67	69.24**	48.69**	46.20**	-6.59*	-8.30**	-2.56	-5.82**
CMS4611A × PP 414	0.08	0.10*	0.01	0.07*	19.45	-29.51*	-21.40**	-10.49	5.10	4.47*	3.94*	4.50**
CMS4611A × VR 522	-0.02	-0.07	0.16**	0.02	25.44*	53.44**	59.10**	45.99**	-5.20*	-5.92**	-1.94	-4.36**
CMS4611A × PL 406	-0.12*	0.13*	-0.04	-0.01	-0.01	-16.37	18.71**	0.78	-2.57	-2.16	-0.93	-1.89
CMS4611A × E 183	0.29**	0.07	0.03	0.13**	-18.68	17.70	24.25**	7.76	3.52	2.81	1.69	2.67*
CMS4611A × IS 268	0.02	0.07	-0.12**	-0.01	0.16	-0.75	-71.56**	-24.05**	0.95	4.37*	5.32**	3.55**
CMS4611A × IS 261	0.03	-0.06	0.06	0.01	15.12	-9.20	-33.35**	-9.14	1.94	-1.11	0.00	0.28

Crosses	**Pericarp thickness (mm)**				**Number of fruits plant^{-1}**				**Number of seed fruit^{-1}**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS4626A × AC 102	-0.04	0.02	-0.01	-0.01	-0.77	-36.92**	-25.16**	-20.95**	-5.17*	-5.08*	-0.83	-3.69**
CMS4626A × SL 475	-0.08	-0.17**	0.11**	-0.04	0.66	-0.70	2.61	0.86	6.44*	0.79	1.73	2.99*
CMS4626A × PL 412	-0.01	0.02	-0.02	0.00	38.66**	44.20**	-26.43**	18.81**	0.25	3.94	1.20	1.79
CMS4626A × IS 263	-0.04	-0.09	-0.03	-0.05	-43.04**	65.89**	-0.21	7.54	-9.28**	-8.61**	-2.46	-6.78**
CMS4626A × VR 523	-0.05	-0.08	-0.10**	-0.08**	12.51	3.78	-41.43**	-8.38	-0.05	-0.08	0.96	0.28
CMS4626A × DL 161	-0.04	0.10	-0.06	0.00	-4.31	26.14*	-17.52*	1.44	0.18	-1.03	5.05**	1.40
CMS4626A × IS 267	-0.14*	0.09	-0.02	-0.03	-24.59	-29.92*	-30.61**	-28.37**	1.79	1.84	-0.54	1.03
CMS4626A × YL 581	0.07	0.28**	0.07	0.14**	19.75	61.02**	-8.52	24.08**	-7.34**	-6.07**	-2.22	-5.21**
CMS4626A × SL 473	-0.01	0.31**	-0.05	0.08**	26.33*	-34.93**	73.43**	21.61**	2.43	0.95	-2.99	0.13
CMS4626A × IS 262	0.14*	-0.15**	-0.04	-0.02	7.00	81.42**	26.53**	38.31**	1.85	0.06	1.16	1.02
CMS4626A × VR 521	0.07	-0.01	-0.02	0.01	-0.59	-32.15*	-2.37	-11.71	-2.76	-5.14*	-2.96	-3.62**
CMS4626A × FL 201	-0.12	-0.02	0.13**	0.00	2.13	-6.67	0.60	-1.31	11.48**	6.46**	1.11	6.35**
CMS4626A × PP 402	0.06	0.00	0.11**	0.06*	-40.23**	-57.58**	1.03	-32.26**	10.26**	10.92**	4.45*	8.54**
CMS4626A × C 142	0.10	0.03	-0.03	0.03	-8.16	-51.33**	-12.21	-23.90**	5.75*	7.22**	-0.14	4.28**
CMS4626A × PP 414	-0.05	-0.06	0.00	-0.04	-6.06	49.09**	11.34	18.12**	-3.03	-2.52	-2.10	-2.55
CMS4626A × VR 522	0.02	-0.01	-0.17**	-0.05	-19.76	-29.84*	-40.25**	-29.95**	1.84	0.03	-4.55*	-0.89
CMS4626A × PL 406	0.11	-0.21**	0.12**	0.01	30.36*	5.30	2.60	12.75	2.47	5.73**	1.03	3.08*
CMS4626A × E183	-0.01	-0.03	0.02	-0.01	-1.86	-24.33	-6.70	-10.96	1.36	0.93	2.75	1.68
CMS4626A × IS 268	-0.01	0.00	0.03	0.01	13.01	-50.31**	65.98**	9.56	-11.54**	-7.85**	-3.08	-7.49**
CMS4626A × IS 261	0.03	-0.02	-0.05	-0.01	-1.03	17.84	27.30**	14.70*	-6.95**	-2.46	2.43	-2.33
CMS463D13A × AC 102	0.08	-0.01	-0.05	0.00	11.23	51.61**	56.60**	39.81**	-6.18*	-6.05**	-3.92*	-5.38**
CMS463D13A × SL 475	0.00	0.09	0.03	0.04	12.80	25.89*	0.34	13.01*	-1.20	2.93	-1.36	0.12

Crosses	**Pericarp thickness (mm)**				**Number of fruits plant^{-1}**				**Number of seed fruit^{-1}**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS463D13A × PL 412	-0.10	-0.08	-0.07	-0.08**	17.45	-64.96**	39.06**	-2.82	-3.72	-2.26	2.04	-1.32
CMS463D13A × IS 263	0.07	0.03	-0.07	0.01	7.72	14.97	-3.54	6.38	0.04	-0.14	-0.15	-0.08
CMS463D13A × VR 523	-0.03	0.08	-0.09*	-0.01	-7.09	36.91**	29.00**	19.61**	-1.32	-2.51	-0.80	-1.55
CMS463D13A × DL 161	-0.12*	-0.03	-0.01	-0.06	4.89	-18.84	-21.38**	-11.78	-4.59	-2.36	-4.84**	-3.93**
CMS463D13A × IS 267	0.20**	-0.15**	-0.03	0.01	24.18	-17.63	-19.43**	-4.29	2.19	4.44*	1.27	2.63
CMS463D13A × YL 581	0.07	-0.12*	0.09*	0.01	-2.26	-53.49**	2.60	-17.72**	4.75	0.96	0.96	2.22
CMS463D13A × SL 473	0.11	-0.08	0.03	0.02	-1.44	49.72**	-12.24	12.01	-0.61	1.29	2.45	1.04
CMS463D13A × IS 262	0.01	0.14**	0.09*	0.08**	-13.59	-36.22**	-35.78**	-28.53**	-0.56	-0.34	-0.16	-0.35
CMS463D13A × VR 521	-0.22**	0.02	-0.06	-0.08**	21.93	-41.21**	1.46	-5.94	4.80	3.83	6.21**	4.95**
CMS463D13A × FL 201	0.29**	0.05	0.07*	0.14**	-27.18*	33.28**	22.32**	9.47	-7.69**	-4.14*	-0.32	-4.05**
CMS463D13A × PP 402	0.18**	-0.10	0.07	0.05	19.98	20.93	13.49*	18.13**	1.15	-0.45	0.49	0.40
CMS463D13A × C 142	-0.16**	0.08	0.05	-0.01	-12.51	-17.91	-36.48**	-22.30**	0.84	1.09	2.70	1.54
CMS463D13A × PP 414	-0.04	-0.04	-0.01	-0.03	-13.39	-19.58	10.06	-7.64	-2.07	-1.95	-1.83	-1.95
CMS463D13A × VR 522	0.00	0.07	0.01	0.03	-5.68	-23.59	-18.85**	-16.04*	3.36	5.90**	6.49**	5.25**
CMS463D13A × PL 406	0.01	0.09	-0.07*	0.01	-30.35*	11.06	-21.30**	-13.53*	0.10	-3.57	-0.10	-1.19
CMS463D13A × E 183	-0.27**	-0.04	-0.05	-0.12**	20.54	6.63	-17.55*	3.21	-4.88	-3.74	-4.44*	-4.35**
CMS463D13A × IS 268	-0.01	-0.07	0.09*	0.00	-13.16	51.05**	5.58	14.49*	10.59**	3.49	-2.24	3.94**
CMS463D13A × IS 261	-0.06	0.08	-0.01	0.00	-14.09	-8.64	6.05	-5.56	5.01	3.57	-2.43	2.05
LSD at *p*=0.05	0.12	0.10	0.07	0.06	24.59	24.37	13.39	12.92	5.12	4.11	3.56	2.65
LSD at *p*=0.01	0.16	0.14	0.10	0.08	32.52	32.23	17.71	17.01	6.76	5.43	4.70	3.48

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.10d: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for 1000 seed weight (g), total yield plant^{-1} (kg) and ascorbic acid (mg 100^{-1}g) evaluated over environments

Crosses	1000 seed weight (g)				Total yield plant^{-1} (kg)				Ascorbic acid (mg 100^{-1}g)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	0.02	-0.02	0.01	0.00	0.06	0.01	-0.06**	0.00	-6.13*	9.47**	-2.09	0.41
CMS4611A × SL 475	0.13	0.06	0.09	0.09	0.01	-0.05	0.01	-0.01	0.04	9.83**	-15.54**	-1.89
CMS4611A × PL 412	0.15	0.15	0.19	0.17	-0.23**	0.09**	-0.02	-0.05**	2.64	9.43**	3.39	5.15**
CMS4611A × IS 263	-0.12	-0.09	-0.09	-0.10	0.14**	-0.21**	0.04*	-0.01	-11.94**	6.05	4.25	-0.55
CMS4611A × VR 523	-0.24	-0.16	-0.13	-0.18	-0.07	-0.16**	0.04*	-0.06**	-16.10**	-4.60	2.87	-5.94**
CMS4611A × DL 161	-0.18	-0.15	-0.15	-0.16	0.00	-0.03	0.05*	0.01	10.55**	-1.30	8.79**	6.01**
CMS4611A × IS 267	0.15	0.13	0.11	0.13	-0.04	0.04	0.08**	0.03	-1.27	-0.95	7.11*	1.63
CMS4611A × YL 581	0.01	0.01	-0.01	0.00	-0.07	0.06	-0.06**	-0.02	-9.13**	-13.74**	-11.08**	-11.32**
CMS4611A × SL 473	-0.09	-0.08	-0.11	-0.09	-0.08	-0.01	-0.14**	-0.08**	15.73**	10.27**	10.66**	12.22**
CMS4611A × IS 262	-0.01	-0.05	-0.08	-0.05	-0.14**	0.02	0.12**	0.00	3.39	-13.89**	-3.18	-4.56*
CMS4611A × VR 521	-0.05	-0.05	-0.04	-0.05	0.13**	0.13**	0.05**	0.10**	2.34	7.50*	0.61	3.48
CMS4611A × FL 201	0.06	0.01	0.01	0.03	0.11**	-0.32**	-0.04*	-0.08**	-0.50	-7.53*	-2.38	-3.47
CMS4611A × PP 402	-0.01	0.03	0.03	0.02	-0.01	0.12**	-0.07**	0.01	-5.61	-18.44**	-8.20**	-10.75**
CMS4611A × C 142	-0.01	-0.01	0.03	0.00	0.00	0.08**	-0.01	0.02	27.86**	6.10	5.13	13.03**
CMS4611A × PP 414	0.29	0.30	0.30	0.30*	0.18**	0.02	0.03	0.08**	0.27	-1.86	5.80*	1.40
CMS4611A × VR 522	-0.65**	-0.65**	-0.71**	-0.67**	-0.04	0.02	0.13**	0.04	-4.68	-2.89	-5.42	-4.33*
CMS4611A × PL 406	-0.01	-0.07	0.01	-0.02	0.05	0.03	-0.03	0.01	3.46	6.30	-6.11*	1.22
CMS4611A × E 183	0.20	0.27	0.28	0.25*	0.15**	0.13**	0.08**	0.12**	1.74	-7.05*	-3.21	-2.84
CMS4611A × IS 268	0.09	0.13	0.04	0.09	-0.13**	0.03	-0.11**	-0.07**	5.08	6.37	2.13	4.53*
CMS4611A × IS 261	0.25	0.24	0.23	0.24	-0.01	0.00	-0.07**	-0.03	-17.74**	0.92	6.48*	-3.45

Crosses	**1000 seed weight (g)**				**Total yield plant^{-1} (kg)**				**Ascorbic acid (mg 100^{-1}g)**			
	E$_1$	**E$_2$**	**E$_3$**	**Pooled**	**E$_1$**	**E$_2$**	**E$_3$**	**Pooled**	**E$_1$**	**E$_2$**	**E$_3$**	**Pooled**
CMS4626A × AC 102	0.07	0.04	0.00	0.04	-0.12**	-0.14**	-0.07**	-0.11**	0.06	-11.90**	15.83**	1.33
CMS4626A × SL 475	-0.42	-0.34	-0.30	-0.35**	0.08	-0.10**	0.01	0.00	-1.29	-0.09	18.24**	5.62**
CMS4626A × PL 412	-0.07	-0.01	-0.02	-0.03	0.19**	0.07*	-0.01	0.08**	-11.27**	-10.95**	1.20	-7.01**
CMS4626A × IS 263	0.16	0.16	0.17	0.16	-0.10*	0.10**	-0.03	-0.01	13.24**	-14.59**	-4.82	-2.06
CMS4626A × VR 523	0.22	0.20	0.19	0.21	0.06	-0.07*	0.02	0.01	19.96**	-3.44	-0.39	5.38**
CMS4626A × DL 161	-0.02	-0.05	-0.10	-0.05	0.07	0.19**	-0.03	0.08**	-3.60	-0.68	-2.91	-2.39
CMS4626A × IS 267	0.12	0.13	0.15	0.13	-0.19**	-0.07*	-0.01	-0.09**	-11.39**	0.79	-2.70	-4.43*
CMS4626A × YL 581	-0.08	-0.17	-0.16	-0.14	0.04	0.05	-0.02	0.03	1.44	4.73	-0.47	1.90
CMS4626A × SL 473	-0.16	-0.12	-0.11	-0.13	-0.06	-0.15**	0.14**	-0.02	-4.97	0.65	-0.59	-1.64
CMS4626A × IS 262	0.25	0.16	0.18	0.20	0.00	0.12**	-0.04*	0.03	1.10	28.85**	9.80**	13.25**
CMS4626A × VR 521	-0.30	-0.26	-0.24	-0.27*	-0.01	-0.01	0.02	0.00	2.46	0.50	-0.94	0.67
CMS4626A × FL 201	-0.22	-0.18	-0.12	-0.17	-0.03	0.14**	0.00	0.04	-7.93**	-0.34	-8.76**	-5.68**
CMS4626A × PP 402	0.12	0.14	0.17	0.14	-0.14**	-0.11**	0.04	-0.07**	-3.25	5.92	-6.53*	-1.29
CMS4626A × C 142	-0.37	-0.33	-0.31	-0.34**	0.03	-0.07*	-0.05**	-0.03	-16.50**	-6.20	-7.91**	-10.20**
CMS4626A × PP 414	-0.08	-0.06	-0.04	-0.06	0.02	0.10**	0.00	0.04	-1.91	-2.87	-5.81*	-3.53*
CMS4626A × VR 522	0.43*	0.42*	0.52*	0.46**	0.00	0.04	-0.13**	-0.03	16.58**	13.04**	10.51**	13.37**
CMS4626A × PL 406	0.05	0.08	0.06	0.06	0.14**	0.05	0.06**	0.08**	-2.00	-8.61*	1.03	-3.19
CMS4626A × E183	-0.03	-0.07	-0.08	-0.06	-0.04	-0.03	0.02	-0.02	0.30	4.95	-7.15*	-0.63
CMS4626A × IS 268	0.22	0.15	-0.05	0.11	0.01	-0.10**	0.05*	-0.01	0.90	-0.18	-5.13	-1.47
CMS4626A × IS 261	0.09	0.08	0.09	0.09	0.06	-0.03	0.04*	0.02	8.09**	0.42	-2.51	2.00
CMS463D13A × AC 102	-0.10	-0.02	-0.01	-0.04	0.07	0.12**	0.13**	0.11**	6.08*	2.43	-13.74**	-1.74
CMS463D13A × SL 475	0.29	0.28	0.21	0.26*	-0.09*	0.15**	-0.02	0.01	1.24	-9.74**	-2.69	-3.73*

Crosses	**1000 seed weight (g)**				**Total yield plant^{-1} (kg)**				**Ascorbic acid (mg 100^{-1}g)**			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
CMS463D13A × PL 412	-0.09	-0.14	-0.17	-0.13	0.04	-0.16**	0.04	-0.03	8.63**	1.52	-4.59	1.85
CMS463D13A × IS 263	-0.04	-0.07	-0.08	-0.06	-0.04	0.11**	-0.01	0.02	-1.30	8.53*	0.57	2.60
CMS463D13A × VR 523	0.02	-0.04	-0.07	-0.03	0.00	0.22**	-0.06**	0.05**	-3.86	8.04*	-2.48	0.57
CMS463D13A × DL 161	0.19	0.20	0.25	0.21	-0.07	-0.16**	-0.02	-0.08**	-6.96*	1.98	-5.88*	-3.62*
CMS463D13A × IS 267	-0.28	-0.26	-0.26	-0.27*	0.23**	0.02	-0.08**	0.06**	12.66**	0.16	-4.41	2.80
CMS463D13A × YL 581	0.07	0.15	0.17	0.13	0.02	-0.11**	0.08**	0.00	7.69**	9.01**	11.55**	9.42**
CMS463D13A × SL 473	0.24	0.20	0.23	0.22	0.14**	0.16**	0.00	0.10**	-10.75**	-10.92**	-10.07**	-10.58**
CMS463D13A × IS 262	-0.24	-0.11	-0.10	-0.15	0.14**	-0.14**	-0.07**	-0.02	-4.49	-14.96**	-6.62*	-8.69**
CMS463D13A × VR 521	0.36	0.31	0.29	0.32*	-0.12**	-0.12**	-0.07**	-0.10**	-4.80	-8.00*	0.33	-4.16*
CMS463D13A × FL 201	0.15	0.17	0.11	0.15	-0.08	0.18**	0.04	0.04*	8.43**	7.86*	11.14**	9.14**
CMS463D13A × PP 402	-0.11	-0.17	-0.20	-0.16	0.15**	-0.01	0.04*	0.06**	8.86**	12.52**	14.72**	12.04**
CMS463D13A × C 142	0.39	0.33	0.28	0.33**	-0.03	-0.01	0.07**	0.01	-11.36**	0.10	2.78	-2.82
CMS463D13A × PP 414	-0.21	-0.24	-0.26	-0.24	-0.19**	-0.12**	-0.03	-0.11**	1.65	4.72	0.01	2.13
CMS463D13A × VR 522	0.22	0.22	0.19	0.21	0.04	-0.06*	0.00	-0.01	-11.89**	-10.15**	-5.09	-9.04**
CMS463D13A × PL 406	-0.04	-0.01	-0.07	-0.04	-0.19**	-0.08*	-0.03	-0.10**	-1.46	2.32	5.08	1.98
CMS463D13A × E 183	-0.17	-0.20	-0.20	-0.19	-0.11*	-0.10**	-0.09**	-0.10**	-2.04	2.10	10.36**	3.47
CMS463D13A × IS 268	-0.31	-0.28	0.01	-0.19	0.12**	0.06*	0.06**	0.08**	-5.98*	-6.19	3.00	-3.06
CMS463D13A × IS 261	-0.35	-0.32	-0.32	-0.33**	-0.05	0.03	0.03	0.00	9.64**	-1.34	-3.97	1.45
LSD at *p*=0.05	0.42	0.41	0.42	0.24	0.08	0.06	0.04	0.04	5.81	6.53	5.75	3.51
LSD at *p*=0.01	0.56	0.55	0.56	0.32	0.11	0.08	0.05	0.05	7.68	8.63	7.60	4.62

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.10e: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for oleoresin content (%) and capsaicin content (%) evaluated over environments

Crosses	Oleoresin content (%)				Capsaicin content (%)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	0.29	-0.45	0.92**	0.25	-0.01	0.01	0.00	0.00
CMS4611A × SL 475	-0.62	0.16	-0.28	-0.25	0.04**	0.00	-0.06**	-0.01
CMS4611A × PL 412	0.97**	1.65**	0.27	0.96**	0.02	0.01	0.03*	0.02**
CMS4611A × IS 263	-1.78**	0.14	-0.23	-0.62**	-0.10**	0.06**	-0.04**	-0.03**
CMS4611A × VR 523	0.55	-0.17	0.00	0.13	-0.01	0.00	-0.06**	-0.02**
CMS4611A × DL 161	0.08	-0.02	-0.25	-0.06	0.06**	-0.01	-0.01	0.01
CMS4611A × IS 267	-0.50	-0.39	0.05	-0.28	-0.06**	-0.01	-0.02	-0.03**
CMS4611A × YL 581	0.13	0.64	-0.16	0.20	0.06**	0.03*	0.02	0.04**
CMS4611A × SL 473	0.56	-0.71*	0.09	-0.02	0.06**	0.02	0.07**	0.05**
CMS4611A × IS 262	-0.67*	-1.11**	-0.25	-0.68**	0.00	0.00	-0.10**	-0.03**
CMS4611A × VR 521	-0.02	-1.15**	-0.82**	-0.67**	-0.07**	-0.01	-0.02	-0.03**
CMS4611A × FL 201	-0.12	-0.16	0.02	-0.09	0.00	-0.01	0.00	0.00
CMS4611A × PP 402	-1.20**	-0.85*	-0.20	-0.75**	-0.07**	-0.02	-0.02	-0.04**
CMS4611A × C 142	1.04**	1.08**	-0.15	0.65**	0.02	0.00	0.00	0.00
CMS4611A × PP 414	0.07	0.90**	0.15	0.37*	0.05**	0.03*	0.01	0.03**
CMS4611A × VR 522	-1.08**	-0.68*	-0.22	-0.66**	0.04**	-0.02	0.01	0.01
CMS4611A × PL 406	1.33**	0.09	-0.27	0.38*	0.01	-0.03*	0.01	-0.01
CMS4611A × E 183	0.28	-0.20	-0.03	0.02	0.06**	0.01	0.08**	0.05**
CMS4611A × IS 268	0.33	0.59	1.05**	0.66**	-0.13**	-0.05**	0.05**	-0.04**
CMS4611A × IS 261	0.38	0.63	0.33	0.45*	0.03*	-0.01	0.04**	0.02*

Crosses	**Oleoresin content (%)**				**Capsaicin content (%)**			
	E$_1$	**E$_2$**	**E$_3$**	**Pooled**	**E$_1$**	**E$_2$**	**E$_3$**	**Pooled**
CMS4626A × AC 102	-0.85*	0.18	-0.38	-0.35	0.01	-0.03	0.02	0.00
CMS4626A × SL 475	1.23**	-0.74*	-0.27	0.07	-0.04**	0.01	-0.03	-0.02*
CMS4626A × PL 412	-1.28**	1.03**	0.18	-0.02	-0.02	-0.06**	-0.06**	-0.05**
CMS4626A × IS 263	-1.04**	-0.04	-0.95**	-0.68**	0.04**	-0.04*	0.08**	0.03**
CMS4626A × VR 523	-1.08**	-0.09	-0.81**	-0.66**	-0.02	0.04**	0.03*	0.02
CMS4626A × DL 161	-0.59	-2.86**	-0.69**	-1.38**	-0.05**	0.01	-0.05**	-0.03**
CMS4626A × IS 267	-1.91**	0.96**	-0.17	-0.37*	0.09**	0.04**	0.04**	0.06**
CMS4626A × YL 581	-0.25	-0.84*	-0.18	-0.42*	-0.04**	-0.02	0.04*	-0.01
CMS4626A × SL 473	-0.26	-0.69*	0.59*	-0.12	-0.04**	-0.01	-0.03*	-0.03**
CMS4626A × IS 262	1.81**	2.37**	0.49	1.56**	-0.01	0.01	-0.01	0.00
CMS4626A × VR 521	-0.65	-0.94**	0.02	-0.52**	0.11**	-0.05**	0.00	0.02**
CMS4626A × FL 201	0.59	0.81*	0.33	0.58**	-0.08**	0.01	0.00	-0.02**
CMS4626A × PP 402	0.94**	0.60	0.49	0.68**	0.02	0.08**	0.03*	0.04**
CMS4626A × C 142	1.03**	-0.99**	0.19	0.08	0.08**	-0.07**	0.00	0.01
CMS4626A × PP 414	0.66	-0.61	-0.01	0.01	0.04**	-0.02	0.02	0.01
CMS4626A × VR 522	2.37**	1.19**	0.69**	1.42**	-0.01	0.06**	-0.02	0.01
CMS4626A × PL 406	0.94**	-0.40	0.34	0.30	0.12**	-0.01	0.08**	0.06**
CMS4626A × E183	-0.04	0.56	0.47	0.33	-0.05**	-0.02	-0.04**	-0.04**
CMS4626A × IS 268	-1.40**	0.54	-0.15	-0.34	-0.03*	0.06**	-0.04**	-0.01
CMS4626A × IS 261	-0.20	-0.07	-0.17	-0.15	-0.11**	-0.01	-0.05**	-0.06**
CMS463D13A × AC 102	0.56	0.27	-0.53*	0.10	0.00	0.02	-0.02	0.00
CMS463D13A × SL 475	-0.61	0.58	0.55*	0.17	0.00	-0.01	0.09**	0.03**

Crosses	Oleoresin content (%)				Capsaicin content (%)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
CMS463D13A × PL 412	0.31	-2.68**	-0.44	-0.94**	0.00	0.05**	0.03*	0.03**
CMS463D13A × IS 263	2.83**	-0.10	1.18**	1.30**	0.06**	-0.03*	-0.03*	0.00
CMS463D13A × VR 523	0.53	0.25	0.81**	0.53**	0.03*	-0.04**	0.03	0.01
CMS463D13A × DL 161	0.51	2.87**	0.94**	1.44**	-0.01	0.00	0.06**	0.02*
CMS463D13A × IS 267	2.41**	-0.58	0.11	0.65**	-0.04**	-0.03*	-0.03	-0.03**
CMS463D13A × YL 581	0.12	0.20	0.34	0.22	-0.02	-0.02	-0.05**	-0.03**
CMS463D13A × SL 473	-0.30	1.40**	-0.68*	0.14	-0.02	-0.01	-0.04**	-0.02**
CMS463D13A × IS 262	-1.14**	-1.26**	-0.24	-0.88**	0.01	-0.01	0.10**	0.04**
CMS463D13A × VR 521	0.67*	2.08**	0.81**	1.19**	-0.04**	0.06**	0.02	0.01
CMS463D13A × FL 201	-0.47	-0.65	-0.35	-0.49**	0.08**	-0.01	0.00	0.03**
CMS463D13A × PP 402	0.26	0.24	-0.29	0.07	0.06**	-0.07**	-0.01	-0.01
CMS463D13A × C 142	-2.06**	-0.09	-0.04	-0.73**	-0.10**	0.07**	0.00	-0.01
CMS463D13A × PP 414	-0.73*	-0.29	-0.14	-0.38*	-0.09**	-0.01	-0.04*	-0.05**
CMS463D13A × VR 522	-1.28**	-0.50	-0.47	-0.75**	-0.02	-0.04**	0.01	-0.02*
CMS463D13A × PL 406	-2.27**	0.31	-0.07	-0.68**	-0.13**	0.04**	-0.08**	-0.06**
CMS463D13A × E 183	-0.23	-0.36	-0.44	-0.34	-0.01	0.01	-0.03*	-0.01
CMS463D13A × IS 268	1.08**	-1.13**	-0.90**	-0.32	0.16**	0.00	-0.01	0.05**
CMS463D13A × IS 261	-0.18	-0.57	-0.16	-0.30	0.08**	0.02	0.01	0.04**
LSD at *p*=0.05	0.66	0.66	0.51	0.36	0.03	0.03	0.03	0.02
LSD at *p*=0.01	0.87	0.87	0.68	0.48	0.03	0.04	0.04	0.02

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.10f: Specific combining ability (SCA) effects exhibited by 60 crosses of chilli for Scoville heat units (SHU) evaluated over environments

Crosses	Scoville heat units (SHU)			
	E_1	E_2	E_3	Pooled
CMS4611A × AC 102	-1693.33	1528.44	228.44	21.19
CMS4611A × SL 475	5968.89**	-98.22	-9602.67**	-1244.00
CMS4611A × PL 412	3426.67	2049.33	5295.11*	3590.37**
CMS4611A × IS 263	-16626.67**	10296.44**	-7184.89**	-4505.04**
CMS4611A × VR 523	-822.22	-471.56	-9140.44**	-3478.07**
CMS4611A × DL 161	9986.67**	-1948.89	-1229.33	2269.48
CMS4611A × IS 267	-8804.44**	-942.67	-2740.44	-4162.52**
CMS4611A × YL 581	10324.44**	5261.78*	2521.78	6036.00**
CMS4611A × SL 473	10057.78**	3773.78	11677.33**	8502.96**
CMS4611A × IS 262	262.22	136.44	-15700.44**	-5100.59**
CMS4611A × VR 521	-10760.00**	-2014.67	-3131.56	-5302.07**
CMS4611A × FL 201	-502.22	-910.67	-180.44	-531.11
CMS4611A × PP 402	-11915.56**	-2716.89	-3469.33	-6033.93**
CMS4611A × C 142	2715.56	-158.67	-269.33	762.52
CMS4611A × PP 414	7853.33**	4614.67*	2397.33	4955.11**
CMS4611A × VR 522	5648.89**	-3431.56	2237.33	1484.89
CMS4611A × PL 406	1755.56	-5588.00*	1188.44	-881.33
CMS4611A × E 183	8920.00**	1023.56	12050.67**	7331.41**
CMS4611A × IS 268	-20466.67**	-8325.78**	7926.22**	-6955.41**
CMS4611A × IS 261	4671.11*	-2076.89	7126.22**	3240.15*

Crosses	**Scoville heat units (SHU)**			
	E_1	**E_2**	**E_3**	**Pooled**
CMS4626A × AC 102	1152.00	-4378.22	2572.44	-217.93
CMS4626A × SL 475	-6492.44**	1317.78	-4485.33	-3220.00*
CMS4626A × PL 412	-3381.33	-10241.33**	-10280.89**	-7967.85**
CMS4626A × IS 263	6485.33**	-5743.56*	12545.78**	4429.19**
CMS4626A × VR 523	-3576.89	6427.11**	4883.56*	2577.93
CMS4626A × DL 161	-8341.33**	1600.44	-8165.33**	-4968.74**
CMS4626A × IS 267	14467.56**	6425.33**	7070.22**	9321.04**
CMS4626A × YL 581	-6670.22**	-2554.22	6252.44*	-990.67
CMS4626A × SL 473	-6563.56**	-1850.22	-5072.00*	-4495.26**
CMS4626A × IS 262	-1692.44	843.11	-823.11	-557.48
CMS4626A × VR 521	17738.67**	-7308.00**	385.78	3605.48**
CMS4626A × FL 201	-12216.89**	2036.00	-236.44	-3472.44**
CMS4626A × PP 402	2716.44	13099.11**	5061.33*	6958.96**
CMS4626A × C 142	12494.22**	-10689.33**	688.00	830.96
CMS4626A × PP 414	6432.00**	-2913.33	3514.67	2344.44
CMS4626A × VR 522	-2119.11	10336.44**	-3898.67	1439.56
CMS4626A × PL 406	19480.89**	-1489.33	12119.11**	10036.89**
CMS4626A × E183	-7594.67**	-2440.44	-7098.67**	-5711.26**
CMS4626A × IS 268	-4501.33*	8855.56**	-6849.78**	-831.85
CMS4626A × IS 261	-17816.89**	-1332.89	-8183.11**	-9110.96**
CMS463D13A × AC 102	541.33	2849.78	-2800.89	196.74

Crosses	**Scoville heat units (SHU)**			
	E_1	**E_2**	**E_3**	**Pooled**
CMS463D13A × SL 475	523.56	-1219.56	14088.00**	4464.00**
CMS463D13A × PL 412	-45.33	8192.00**	4985.78*	4377.48**
CMS463D13A × IS 263	10141.33**	-4552.89*	-5360.89*	75.85
CMS463D13A × VR 523	4399.11*	-5955.56**	4256.89	900.15
CMS463D13A × DL 161	-1645.33	348.44	9394.67**	2699.26*
CMS463D13A × IS 267	-5663.11**	-5482.67*	-4329.78	-5158.52**
CMS463D13A × YL 581	-3654.22	-2707.56	-8774.22**	-5045.33**
CMS463D13A × SL 473	-3494.22	-1923.56	-6605.33**	-4007.70**
CMS463D13A × IS 262	1430.22	-979.56	16523.55**	5658.07**
CMS463D13A × VR 521	-6978.67**	9322.67**	2745.78	1696.59
CMS463D13A × FL 201	12719.11**	-1125.33	416.89	4003.56**
CMS463D13A × PP 402	9199.11**	-10382.22**	-1592.00	-925.04
CMS463D13A × C 142	-15209.78**	10848.00**	-418.67	-1593.48
CMS463D13A × PP 414	-14285.33**	-1701.33	-5912.00*	-7299.56**
CMS463D13A × VR 522	-3529.78	-6904.89**	1661.33	-2924.44*
CMS463D13A × PL 406	-21236.45**	7077.33**	-13307.56**	-9155.56**
CMS463D13A × E 183	-1325.33	1416.89	-4952.00*	-1620.15
CMS463D13A × IS 268	24968.00**	-529.78	-1076.44	7787.26**
CMS463D13A × IS 261	13145.78**	3409.78	1056.89	5870.81**
LSD at *p*=0.05	4007.61	4478.20	4850.64	2635.09
LSD at *p*=0.01	5298.51	5920.68	6413.09	3469.98

*, significant at *p*=0.05; **, significant at *p*=0.01

4.4 Estimation of components of genetic variance

The results pertaining to the components of genetic variance for plant growth, yield and quality traits over three environments and pooled across the environments are presented in Table 4.11. The estimates revealed that both the additive and the non-additive genetic variation were important for the traits studied suggesting that genetic improvement of chilli for the traits under evaluation could be achieved both by hybrid development and pure line breeding.

The magnitude of additive variance (σ^2A) was more than non-additive variance (σ^2D) for all the traits evaluated except number of primary branches plant^{-1} in E_2, E_3 and across the three environments, and for plant height, plant spread and number of fruits plant^{-1} in E_3, where non-additive gene effects predominated in the expression of these traits. The ratio σ^2D/ σ^2A was <1 for most of the traits evaluated except for number of primary branches plant^{-1} in E_2, E_3 and when pooled across the environments; and for plant height, plant spread and number of fruits plant^{-1} in E_3. Different gene expression in the three environments for plant height, plant spread, number of primary branches plant^{-1} and number of fruits plant^{-1} indicated the need for environment specific breeding for these traits. Therefore, heterosis breeding would be useful plant breeding tool for improving plant height, plant spread, number of primary branches plant^{-1} and number of fruits plant^{-1}. Reciprocal recurrent selection at early stages or pure line breeding would be the best breeding approach for yield improvement in chilli. The predominant role of additive genes for fruit weight was reported by Ben-Chaim and Paran (2000), Farag and Khalil (2007), Prasath and Ponnuswami (2008), Rodrigues *et al* (2012) and Medeiros *et al* (2014); for fruit length by Ben-Chaim and Paran (2000), do Rego *et al* (2009), Pérez-Grajales *et al* (2009) and Medeiros *et al* (2014); for fruit width by Ben-Chaim and Paran (2000), Sousa and Maluf (2003), Anand and Subbaraman (2006) and Medeiros *et al* (2014); for pericarp thickness by Ben-Chaim and Paran (2000), Rodrigues *et al* (2012) and Bento *et al* (2016); and for total yield plant^{-1} by Geleta *et al* (2004). Predominant role of non-additive gene effects for plant height was reported by Shukla *et al* (1999) and do Rego *et al* (2009); for plant spread by Singh *et al* (2014); for number of primary branches plant^{-1} by Bhutia *et al* (2015) and for number of fruits plant^{-1} by Shukla *et al* (1999).

The relative magnitude and importance of additive and non-additive variances in the genetic control of various traits were further revealed by the predictability ratio. The predictability ratios of ≥0.80 in the pooled analysis highlighted the predominant role of additive gene effects for plant height, plant spread, fruit weight, fruit length, fruit width, pericarp thickness, 1000 seed weight, ascorbic acid, capsaicin content and SHU. The predictability ratio was between 0.51 and 0.79 for number of fruits plant^{-1}, number of seed fruit^{-1}, total yield plant^{-1} and oleoresin content indicating the importance of both the additive and the non-additive gene action. The predictability ratio was <0.50 for number of primary branches plant^{-1} indicating the importance of non-additive gene effects in inheritance of this trait.

Genetic improvement of any crop plant depends on the magnitude of heritability of the economic traits because it determines the response to selection (Dudley and Moll 1969). Heritability estimates vary not only with the environment but also with the nature of the test population. The estimates of heritability in the narrow sense (h^2ns) for different traits were found to range between 0.51 for number of primary branches plant^{-1} to 0.86 for fruit weight under E_1; from 0.21 for primary branches plant^{-1} to 0.82 for fruit width under E_2; from 0.13 for number of primary branches plant^{-1} to 0.82 for 1000 seed weight under $E_{3.}$ Across the environments, h^2(ns) ranged between 0.06 for number of primary branches plant^{-1} to 0.95 for 1000 seed weight. The pooled analysis revealed that the h^2(ns) was low for number of primary branches plant^{-1} and number of fruits plant^{-1}. The selection would be considerably difficult or virtually impractical for a trait with low heritability due to the masking effect of the environment on the genotypic effects. Genetic improvement of these traits would require growing of large populations over locations and years to reliably make selection on phenotypic basis. The h^2ns was moderate for plant height, plant spread, fruit length, pericarp thickness, total yield plant^{-1}, oleoresin content, capsaicin content and SHU. High h^2ns was observed for fruit weight, fruit width, number of seed fruit^{-1}, 1000 seed weight and ascorbic acid. The selection would fairly be easy in highly heritable traits because there would be a close correspondence between genotype and phenotype owing to a relatively smaller contribution of environment to the phenotype. The high h^2ns was observed in fruit width by Hasanuzzaman *et al* (2012) and for fruit weight by Ben-Chaim and Paran (2000) and Hasanuzzaman *et al* (2012).

Table 4.11: Estimates of components of genetic variances of plant growth, yield and quality traits in chilli over environments

Genetic components	**Plant height (cm)**	**Plant spread (cm)**	**Number of primary branches plant^{-1}**	**Fruit weight (g)**	**Fruit length (cm)**	**Fruit width (mm)**	**Pericarp thickness (mm)**	**Number of fruits plant^{-1}**
E_1								
σ^2A	204.89	80.64	0.38	7.65	1.50	3.13	0.13	921.88
σ^2D	20.62	19.16	0.31	1.09	0.29	0.42	0.02	448.09
σ^2D/σ^2A	0.10	0.24	0.82	0.14	0.19	0.13	0.15	0.49
Predictability ratio	0.91	0.81	0.56	0.88	0.84	0.88	0.88	0.67
h^2_{ns} (%)	0.83	0.73	0.51	0.86	0.77	0.80	0.85	0.60
E_2								
σ^2A	52.25	36.09	0.35	3.03	0.40	1.20	0.03	2486.45
σ^2D	47.21	29.84	1.25	1.09	0.11	0.00	0.01	2194.67
σ^2D/σ^2A	0.90	0.83	3.57	0.36	0.28	0.00	0.33	0.88
Predictability ratio	0.53	0.55	0.22	0.74	0.78	1.00	0.66	0.53
h^2_{ns} (%)	0.46	0.50	0.21	0.72	0.66	0.82	0.61	0.51
E_3								
σ^2A	24.16	5.71	0.16	0.97	0.64	1.30	0.02	1020.30
σ^2D	35.10	8.21	0.91	0.23	0.32	0.16	0.01	1325.69
σ^2D/σ^2A	1.45	1.44	5.69	0.24	0.50	0.12	0.50	1.30
Predictability ratio	0.41	0.41	0.15	0.81	0.66	0.89	0.67	0.43
h^2_{ns} (%)	0.35	0.29	0.13	0.78	0.61	0.79	0.64	0.42
Pooled								
σ^2A	66.84	27.96	0.10	3.18	0.73	1.75	0.04	943.07
σ^2D	14.63	5.15	0.21	0.42	0.08	0.12	0.01	545.05
σ^2D/σ^2A	0.22	0.18	2.10	0.13	0.11	0.07	0.25	0.58
Predictability ratio	0.82	0.84	0.33	0.88	0.90	0.94	0.90	0.63
h^2_{ns} (%)	0.43	0.37	0.06	0.60	0.58	0.78	0.51	0.27

Table 4.11 (*Cont'd.*)

Genetic components	**Number of seed fruit^{-1}**	**1000 seed weight (g)**	**Total yield plant^{-1} (kg)**	**Ascorbic acid (mg 100^{-1} g)**	**Oleoresin content (%)**	**Capsaicin content (%)**	**Scoville heat units (SHU)**
E_1							
σ^2A	65.29	0.26	0.05	342.66	1.98	0.01	254991840.00
σ^2D	36.41	0.03	0.02	117.17	1.65	0.006	145879904.00
σ^2D/ σ^2A	0.56	0.12	0.40	0.34	0.83	0.60	0.57
Predictability ratio	0.64	0.91	0.77	0.75	0.55	0.64	0.64
h^2_{ns} (%)	0.60	0.78	0.74	0.73	0.52	0.62	0.62
E_2							
σ^2A	45.75	0.26	0.03	270.36	2.00	0.01	176278720.00
σ^2D	29.71	0.02	0.02	101.66	1.48	0.002	40035860.00
σ^2D/ σ^2A	0.65	0.08	0.67	0.38	0.74	0.20	0.23
Predictability ratio	0.61	0.93	0.60	0.73	0.57	0.81	0.81
h^2_{ns} (%)	0.57	0.80	0.59	0.70	0.55	0.79	0.79
E_3							
σ^2A	44.42	0.29	0.008	284.83	1.19	0.01	230459616.00
σ^2D	8.50	0.02	0.006	74.09	0.30	0.003	68689456.00
σ^2D/ σ^2A	0.19	0.07	0.75	0.26	0.25	0.30	0.30
Predictability ratio	0.84	0.95	0.59	0.79	0.80	0.77	0.77
h^2_{ns} (%)	0.79	0.82	0.57	0.77	0.76	0.75	0.75
Pooled							
σ^2A	50.61	0.27	0.02	265.16	1.25	0.007	185917872.00
σ^2D	20.83	0.05	0.005	53.03	0.59	0.001	33854964.00
σ^2D/ σ^2A	0.41	0.19	0.25	0.20	0.47	0.14	0.18
Predictability ratio	0.71	0.85	0.79	0.83	0.68	0.85	0.85
h^2_{ns} (%)	0.63	0.95	0.37	0.60	0.36	0.53	0.53

4.5 Estimation of heterosis

The commercial exploitation of the phenomenon of heterosis is one of the most important contributions to plant breeding. The extent of heterotic response of the F_1 hybrid largely depends on the breeding value and genetic diversity of the parents included in the cross and on the environmental conditions under which the hybrid is grown (Geleta and Labuschagne 2004b). Heterosis is often depicted as mid-parent heterosis by comparing the trait value of the cross to mean of the parents. In agricultural context, the F_1 hybrid must express heterosis over better parent (H_{BP}) to be commercially useful and thus, H_{BP} must be determined (Meyer *et al* 2004).

In the current study, different proportions of crosses with negative to positive heterosis were obtained for various traits and suggested the potential of heterosis breeding in chilli. However, high heterosis does not necessarily mean that the hybrid is superior to the presently grown commercial cultivars or hybrids. Therefore, it is imperative to compare the performance of newly developed F_1 hybrids with the commercial cultivar(s). From the plant breeding point of view standard heterosis is of practical significance (Young and Virmani 1990 and Geleta and Labuschagne 2004b). In this study, to estimate the standard heterosis the crosses were compared with the early maturing hybrid Soldier in E_1 and with the high yielding hybrid CH-27 in E_2, E_3 and pooled across the three environments. Mean performance and heterosis over mid-parent, better parent and standard checks expressed by the crosses for plant growth, yield and quality trait is presented in Table 4.12a-o.

4.5.1 Plant height (cm)

In chilli, plant height is one of the most important agronomic traits from productivity and crop management point of view. Taller plants have more number of fruits resulting in higher fruit yield. Therefore, plant height can be useful to select for high yielding genotypes (do Rego *et al* 2009). The crosses means for plant height ranged from 69.60 cm in the cross CMS4626A × IS 261 to 132.82 cm in the cross CMS463D13A × IS 268 with an average of 99.19 cm under E_1, from 43.47 cm in the cross CMS4626A × AC 102 to 105.83 cm in the cross CMS4611A × IS 268 with a mean value of 79.84 cm under E_2, from 43.36 cm in the cross CMS4611A × E 183 to 85.49 cm in the cross CMS4611A × IS 261 with an average of 63.0 cm under E_3. Across the environments, plant height ranged from 56.30 cm in the cross CMS4626A × AC 102 to 104.24 cm in the cross CMS463D13A × IS 268 with an overall mean of 80.67 cm (Table 4.12a). Out of 60 crosses evaluated, 26 and three crosses in E_1, 14 and nine in E_2, 21 and two in E_3 and 31 and four when pooled across the environments expressed significant positive and negative heterosis over their respective better parent, respectively.

Over the standard checks CH-27 and Soldier, two and 30, 27 and two crosses in E_1, none and 42, 15 and 11 in E_2, one and 36, 17 and eight in E_3, one and 42, 30 and nine crosses pooled across the three environments exhibited significant positive and negative heterosis, respectively. The extent of heterosis over better parent ranged from -27.05 in the cross CMS4626A × IS 261 to 51.81% in the cross CMS4626A × PP 402 under E_1, from -33.22 in the cross CMS4626A × AC 102 to 40.76% in the cross CMS463D13A × IS 268 under E_2, from -34.67 in the cross CMS4611A × E 183 to 57.18% in the cross CMS4611A × IS 261 under E_3 and from -14.37 in the cross CMS4626A × IS 262 to 36.67% in the cross CMS463D13A × IS 268 across the three environments. The range of heterosis over superior check Soldier varied from -19.72 in the cross CMS4626A × IS 261 to 53.20% in the cross CMS463D13A × IS 268 under E_1. Over the superior check CH-27, the heterosis ranged from -54.94 in the cross CMS4626A × AC 102 to 9.70% in the cross CMS4611A × IS 268 under E_2, from -40.41 in the cross CMS4611A × E 183 to 17.50% in the cross CMS4611A × IS 261 under E_3 and from -39.75 in the cross CMS4626A × AC 102 to 11.56% in the cross CMS463D13A × IS 268 when pooled across the three environments.

The cross CMS4626A × PP 402 exhibited highest significant positive heterosis over better parent for plant height followed by CMS4611A × IS 268, CMS463D13A × IS 268 and CMS4611A × SL 475 in E_1, the cross CMS463D13A × IS 268 followed by CMS4626A × SL 475, CMS463D13A × VR 521 and CMS4626A × IS 261 in E_2, the cross CMS4611A × IS 261 followed by CMS4626A × VR 522, CMS4611A × PP 402 and CMS4626A × IS 261 in E_3, and the cross CMS463D13A × IS 268 showed maximum heterosis based on pooled means followed by CMS4626A × PP 402, CMS4611A × IS 268 and CMS463D13A × VR 521. The cross CMS463D13A × IS 268 performed significantly better than the superior check Soldier followed by CMS463D13A × VR 521, CMS4611A × PL 412 and CMS463D13A × E 183 in E_1. Over the superior check CH-27, the cross CMS4611A × IS 261 performed significantly better in E_3 and the cross CMS463D13A × IS 268 across the three environments. However, none of the crosses was superior to the standard check CH-27 in E_2.

Shorter plant height is positively associated with early fruit yield in chilli. Such genotypes can fit well in multiple cropping systems and can escape adverse climatic conditions due to shorter life span. Based on *per se* performance and standard heterosis the cross-combinations CMS4626A × IS 261, CMS4626A × DL 161, CMS4626A × FL 201 and CMS4626A × SL 473 were identified with shorter plant height in E_1, the crosses CMS4626A × AC 102, CMS4626A × DL 161, CMS4611A × AC 102 and CMS4626A × FL 201 in E_2, the crosses CMS4611A × E 183, CMS4626A × YL 581, CMS4626A × AC 102 and CMS4611A × AC 102 in E_3, and the crosses CMS4626A × AC 102, CMS4626A × DL 161, CMS4611A × AC 102 and CMS4626A × FL 201 based on pooled means.

Earlier, Shankarnag *et al* (2006) reported that the crosses L3 × T15, L1 × T17 and L1 × L14 exhibited significant positive standard heterosis for plant height. Marame *et al* (2009) found that the heterosis for plant height over mid-parent ranged from -40.8 in ICPN9#16 × PBC 731 to 25.65% in ICPN10#5 × PBC 731, from -47.7 in PBC 602 × Marekoshote to 18.24% in PBC 223 × PBC 580 over better parent and from -63.07 in ICPN9#16 × PBC 731 to 7.29% in PBC 580 × Marekoshote over the standard check. Heterosis over better parent was also reported by Tembhurne and Rao (2012) and Singh *et al* (2014). Bhutia *et al* (2015) observed that the heterosis over the better parent ranged from -39.54 in BCC-1 × Kashi Anmol to 2.08% in BCCH Sel-4 × Chaitali.

4.5.2 Plant spread (cm)

The plant canopy width contributes directly to the total yield (Singh *et al* 2014). The trait is also important to determine the plant spacing (do Rego *et al* 2009). Plant spread of the crosses varied from 51.07 cm in CMS4626A × VR 522 to 91.20 cm in CMS463D13A × VR 523 with an average of 67.92 cm under E_1, from 36.94 cm in CMS4626A × AC 102 to 75.37 cm in CMS463D13A × SL 475 with a mean value of 54.96 cm under E_2, from 35.42 cm in CMS4611A × E 183 to 59.82 cm in CMS4611A × SL 475 with an average of 45.45 cm under E_3 and from 45.68 cm in CMS4626A × AC 102 to 68.56 cm in CMS463D13A × SL 475 with an overall mean of 56.11 cm when pooled across the environments (Table 4.12b). Out of 60 crosses, 30, eight and 43 crosses in E_1; 15, eight and 16 in E_2; 16, 26 and four in E_3; and 38, 16 and 28 crosses across the three environments expressed significant positive heterosis over the respective better parent and standard checks, CH-27 and Soldier, respectively. One, 13 and none of the cross-combinations in E_1; seven, 22 and 12 in E_2; none, none and 22 in E_3; and none, 11 and four crosses showed significant negative heterosis based on pooled means over the respective better parent and standard checks, CH-27 and Soldier, respectively.

The magnitude of heterosis over better parent ranged from -16.74 in CMS4626A × VR 522 to 45.28% in CMS463D13A × VR 523 under E_1, from -32.75 in CMS4626A × AC 102 to 40.20% in CMS463D13A × SL 475 under E_2, from -12.80 in CMS4611A × PP 414 to 41.03% in CMS4626A × IS 267 under E_3 and from -8.38 in CMS4626A × AC 102 to 28.04% in CMS463D13A × VR 523, when pooled across the environments. The range of heterosis over Soldier under E_1 varied from -3.55 in CMS4626A × VR 522 to 72.26% in CMS463D13A × VR 523. Over CH-27, the heterosis varied from -35.55 in CMS4626A × AC 102 to 31.48% in CMS463D13A × SL 475 under E_2, from -10.65 in CMS4611A × E 183 to 50.90% in CMS4611A × SL 475 under E_3 and from -16.70 in CMS4626A × AC 102 to 25.02% in CMS463D13A × SL 475 over the environments.

The cross CMS463D13A × VR 523 followed by CMS4611A × YL 581, CMS4611A × PL 412 and CMS463D13A × IS 268 in E_1, CMS463D13A × SL 475 followed by CMS463D13A × IS 261, CMS4626A × SL 475 and CMS4611A × PL 406 in E_2, CMS4626A

× IS 267 followed by CMS4626A × VR 522, CMS4626A × IS 263 and CMS4611A × IS 263 in E_3, and CMS463D13A × VR 523 followed by CMS463D13A × SL 475, CMS463D13A × PL 406 and CMS4611A × PL 412 across the three environments showed significant positive heterosis over better parent. The cross CMS463D13A × VR 523 exhibited the highest significant positive heterosis over superior check Soldier followed by CMS463D13A × IS 268, CMS463D13A × PL 406 and CMS4611A × IS 261 in E_1, the cross CMS463D13A × SL 475 showed the maximum heterosis over superior check CH-27 followed by CMS463D13A × IS 261, CMS4626A × SL 475 and CMS4611A × PL 406 in E_2, CMS4611A × SL 475 followed by CMS463D13A × IS 261, CMS4611A × IS 261 and CMS463D13A × SL 475 in E_3, and CMS463D13A × SL 475, CMS463D13A × VR 523, CMS4611A × IS 261 and CMS463D13A × IS 261 expressed significant positive heterosis over superior check CH-27 across the three environments.

The crosses with smaller canopy width allow less spacing, high density planting and facilitate better land use and increase productivity per unit area. Based on *per se* performance and standard heterosis, the crosses CMS4626A × VR 522, CMS4626A × IS 267, CMS4626A × PP 402 and CMS4626A × SL 473 are identified to breed for genotypes with shorter canopy width in E_1, the crosses CMS4626A × AC 102, CMS4626A × E 183, CMS4611A × VR 521 and CMS4626A × YL 581 in E_2, the crosses CMS4611A × E 183, CMS4611A × PP 414, CMS4626A × IS 262 and CMS4611A × SL 473 in E_3, and the crosses CMS4626A × AC 102, CMS4626A × E 183, CMS4626A × IS 262 and CMS4611A × VR 521 across the three environments.

Standard heterosis for plant spread up to 72.1% has been observed by Shankarnag *et al* (2006). Marame *et al* (2009) reported the range of mid-parent heterosis from -19.1 in PBC 972 × ICPN10#5 to 32.22% in ICPN9#16 × Bakolocal, from -32.50 in ICPN9#16 × PBC 731 to 24.84% in PBC 223 × PBC 731 over better parent and from -45.67 in ICPN9#16 × PBC 731 to 21.22% in PBC 580 × Marekoshote over the standard check. Singh *et al* (2014) observed highest heterosis of 20.66% over better parent in the cross EL 181 × US 501.

4.5.3 Number of primary branches plant^{-1}

The crosses means for number of primary branches plant^{-1} ranged from 3.33 in CMS4626A × AC 102 to 6.96 in CMS463D13A × IS 267 with overall mean value of 4.80 under E_1, from 3.74 in CMS463D13A × IS 262 to 9.32 in CMS4611A × VR 523 with overall mean value of 5.67 under E_2 and from 3.56 in CMS463D13A × AC 102 to 8.00 in CMS4626A × SL 475 with overall mean of 5.58 under E_3. Over the three environments, number of primary branches plant^{-1} varied from 4.08 in CMS463D13A × IS 262 to 6.53 in CMS463D13A × IS 268 with overall mean of 5.35 (Table 4.12c). Range of heterosis over the better parent varied from -21.76 in CMS4626A × PP 414 to 47.75% in CMS463D13A × C 142 under E_1, from -32.90 in CMS4611A × AC 102 to 85.47% in CMS463D13A × VR 522 under E_2, from -29.79 in CMS4611A × YL 581 to 82.76% in CMS4626A × SL 475 under E_3 and from -21.61 in CMS4626A × YL 581 to 59.39% in CMS463D13A × IS 268 across the three environments. Of the 60 crosses, 26 and five crosses in E_1, 25 and 11 in E_2, 28 and three in E_3 and 43 and three across the three environments expressed significant positive and negative heterosis over their respective better parent, respectively. The extent of heterosis over superior checks ranged from 0.0 in CMS4626A × AC 102 to 108.66% in CMS463D13A × IS 267 under E_1 (over Sildier), from -34.18 in CMS463D13A × IS 262 to 63.88% in CMS4611A × VR 523 under E_2 (over CH-27), from -7.52 in CMS463D13A × AC 102 to 108.10% in CMS4626A × SL 475 under E_3 (over CH-27) and from -12.06 in CMS463D13A × IS 262 to 40.81% in CMS463D13A × IS 268 across the three environments (over CH-27). Eighteen and three, 53 and none in E_1, 17 and 24, 28 and three in E_2, 48 and none, 15 and 21 in E_3, 41 and two, 41 and two crosses over the three environments exhibited significant positive and negative heterosis over the standard checks, CH-27, and Soldier, respectively.

The cross-combination CMS463D13A × C 142 showed highest significant positive better parent heterosis followed by CMS463D13A × IS 267, CMS463D13A × YL 581 and CMS4626A × IS 262 in E_1, the cross CMS463D13A × VR 522 followed by CMS4626A × IS 261, CMS463D13A × IS 268 and CMS463D13A × SL 475 in E_2, the cross CMS4626A × SL 475 followed by CMS463D13A × IS 268, CMS463D13A × PP 402 and CMS4611A × SL 475 in E_3, and the cross CMS463D13A × IS 268 followed by CMS4611A × PL 412, CMS463D13A × IS 267 and CMS4626A × PP 402 across the three environments. The cross CMS463D13A × IS 267 exhibited highest significant positive heterosis over superior check Soldier followed by CMS463D13A × PL 406, CMS4611A × PL 406 and CMS463D13A × C 142 in E_1, the cross CMS4611A × VR 523 followed by CMS4626A × VR 523, CMS463D13A × VR 522 and CMS463D13A × SL 475 in E_2 (over CH-27), the cross CMS4626A × SL 475 followed by CMS463D13A × PP 402, CMS4626A × PP 402 and CMS4611A × E 183 in E_3 (over CH-27), and the cross CMS463D13A × IS 268 followed by CMS4611A × VR 523, CMS463D13A × PL 406 and CMS4626A × SL 475 when pooled across the three environments (over CH-27). Heterosis over better parent and standard check for number of primary branches plant^{-1} was also reported by Marame *et al* (2009) and Tembhurne and Rao (2012).

4.5.4 *Fruit weight (g)*

Fruit weight is considered as an independent variable that contributes directly towards total yield of chilli and has a key role in acceptance of the produce by the consumer. Among the 60 crosses, the maximum fruit weight was recorded by CMS463D13A × FL 201 (12.38 g) in E_1, by CMS463D13A × FL 201 (10.65 g) in E_2, by CMS463D13A × IS 268 (6.42 g) in E_3 and by CMS463D13A × FL 201 (9.62 g) when means were pooled over the environments. The minimum fruit weight was observed in CMS4611A × VR 521 under E_1 (2.82 g), E_2 (1.40 g), E_3 (2.65 g) and based on pooled means (2.29 g). The overall means of fruit weight was 6.21 g in E_1, 4.91 g in E_2, 4.40 g in E_3 and 5.17 g across the environments (Table 4.12d). Extent of heterosis over better parent varied from -58.42 in CMS4611A × FL 201 to 48.46% in CMS463D13A × IS 267 under E_1, from -69.02 in CMS4611A × FL 201 to 44.18% in CMS4626A × C 142 under E_2, from -42.30 in CMS4611A × FL 201 to 53.62% in CMS4626A × VR 523 under E_3 and from -58.90 in CMS4611A × FL 201 to 34.16% in CMS463D13A × IS 268 when pooled across the environments. Over the superior check Soldier, the heterosis ranged from -14.47 in CMS4611A × VR 521 to 275.81% in CMS463D13A × FL 201 under E_1. Over the superior check CH-27, the heterosis varied from -63.49 in CMS4611A × VR 521 to 177.19% in CMS463D13A × FL 201 under E_2, from -29.58 in CMS4611A × VR 521 to 70.50% in CMS463D13A × IS 268 under E_3 and from -39.29 in CMS4611A × VR 521 to 154.90% in CMS463D13A × FL 201 over the three environments.

Of the 60 crosses evaluated, 14 and 20 in E_1, nine and 23 in E_2, 13 and 17 in E_3 and 18 and 25 across the three environments showed significant positive and negative heterosis over the better parent, respectively. Over the standard checks, 46 and 49 in E_1, 33 and 42 in E_2, 27 and 39 in E_3 and 39 and 48 crosses over the environments exhibited significant positive heterosis, respectively, while none of the cross in E_1, 17 and six in E_2, five and two in E_3 and four and one cross across the three environments showed significant negative heterosis over CH-27 and Soldier, respectively.

The better parent heterosis was high and positively significant in the cross CMS463D13A × IS 267 followed by CMS463D13A × PL 406, CMS463D13A × VR 522 and CMS463D13A × YL 581 in E_1, in the cross CMS4626A × C 142 followed by CMS4626A × PL 406, CMS4626A × SL 473 and CMS463D13A × IS 268 in E_2, in the cross CMS4626A × VR 523 followed by CMS463D13A × IS 268, CMS463D13A × SL 473 and CMS4626A × PL 412 in E_3, and in the cross CMS463D13A × IS 268 based on pooled means, followed by CMS463D13A × VR 522, CMS463D13A × IS 267 and CMS463D13A × PL 406. Over the superior check Soldier in E_1, the cross CMS463D13A × FL 201 exhibited the highest significant positive heterosis. This was followed by CMS463D13A × PP 402, CMS463D13A × YL 581 and CMS4626A × PP 402. Over the superior check CH-27, CMS463D13A × FL 201 expressed the highest significant positive heterosis followed by CMS4626A × PP 402, CMS4626A × FL 201 and CMS463D13A × PP 402 in E_2, CMS463D13A × IS 268 followed by CMS4626A × PP 402, CMS4626A × FL 201 and CMS4626A × VR 523 in E_3, and CMS463D13A × FL 201 followed by CMS463D13A × PP 402, CMS4626A × PP 402 and CMS463D13A × YL 581 over the three environments.

Standard heterosis for fruit weight up to 381.6% has been reported by Geleta and Labuschagne (2004b). Marame *et al* (2009) have reported mid-parent heterosis in the range of -32.94 in the cross PBC 223 × Marekofana to 74.29% in the cross PBC 602 × Bakolocal, better parent heterosis from -38.19 in the cross PBC 580 × Marekofana to 50.29%in the cross PBC 223 × Marekofana, standard heterosis from -50.22 in the cross PBC 223 × Marekofana to 1.31% in the cross ICPN10#5 × Marekoshote. IPB C2 × IPB C15 and IPB C15 × IPB C19 were identified as the most promising crosses for fruit weight over the better parent by Sitaresmi *et al* (2010), cross JNA1 × LCA960 by Tembhurne and Rao (2012), the crosses SP15 × SP5, PapP27 × PapP67 and SP15 × SP55 by Butcher *et al* (2013), the cross LS 2-2 × W 5-15 by Khalil and Hatem (2014) and the crosses CC 141 × VR 521, CC 141 × SL 462 and CC 141 × DL 161 by Singh *et al* (2014).

4.5.5 Fruit length (cm)

Fruit length is of the utmost importance in chilli that is destined for fresh consumption. According to Klieber (2001) and Lannes *et al* (2007) the smaller fruits are more suitable for the production of dehydrated products, since they contain up to 3.5-fold more dry matter content than large fruited genotypes. Higher content of dry matter means higher processed product yield. The fruit length of 60 crosses varied from 5.75 cm in the cross CMS4611A × VR 521 to 11.46 cm in the cross CMS463D13A × FL 201 with a mean value of 8.57 cm under E_1, from 4.76 cm in the cross CMS4626A × E 183 to 8.34 cm in the cross CMS463D13A × FL 201 with a mean value of 6.58 cm under E_2 and from 4.55 cm in the cross CMS4611A × IS 263 to 8.31 cm in the cross CMS4626A × PL 412 with a mean value of 6.40 cm under E_3. Across the three environments, fruit length varied from 5.62 cm in the cross CMS4611A × DL 161 and CMS4611A × E 183 to 9.04 cm in the cross CMS463D13A × FL 201 with an overall mean of 7.18 cm (Table 4.12e). Of the 60 crosses, 17 and seven crosses in E_1, 11 and 10 in E_2, 12 and nine in E_3 and 25 and eight across the three environments showed significant positive and negative heterosis over their respective better parent, respectively.

Over the standard checks, CH-27 and Soldier, 38 and one, 37 and two crosses in E_1, 22 and three, eight and 18 in E_2, 26 and two, 22 and 10 in E_3 and 37 and four, 28 and seven crosses based on pooled means exhibited significant positive and negative heterosis, respectively. The extent of heterosis over better parent ranged from -20.0 in CMS4611A × FL 201 to 53.70% in CMS4626A × PP 402 under E_1, from -31.74 in CMS4611A × FL 201 to 38.04% in CMS4626A × C 142 under E_2, from -38.26 in CMS4611A × FL 201 to 42.46% in

CMS4626A × PL 412 under E_3 and from -29.24 in CMS4611A × FL 201 to 27.18% in CMS4626A × PP 402 when pooled across the environments. The range of heterosis over superior checks varied from -19.38 in CMS4611A × VR 521 to 60.58% in CMS463D13A × FL 201 under E_1 (over Soldier), from -23.49 in CMS4626A × E 183 to 34.16% in CMS463D13A × FL 201 under E_2 (over CH-27), from -20.93 in CMS4611A × IS 263 to 44.52% in CMS4626A × PL 412 under E_3 (over CH-27) and from -10.42 in CMS4611A × DL 161 and CMS4611A × E 183 to 44.04% in CMS463D13A × FL 201 when means were pooled across the three environments (over CH-27).

The maximum significant and positive better parent heterosis for fruit length was expressed by the cross CMS4626A × PP 402 followed by CMS463D13A × PP 402, CMS463D13A × SL 473 and CMS4626A × PP 414 in E_1, by the cross CMS4626A × C 142 followed by CMS4611A × VR 521, CMS4611A × PP 414 and CMS4626A × VR 521 in E_2, by the cross CMS4626A × PL 412 followed by CMS4626A × VR 522, CMS463D13A × VR 522 and CMS463D13A × IS 268 in E_3, and by the cross CMS4626A × PP 402 followed by CMS463D13A × IS 267, CMS463D13A × IS 268 and CMS4626A × C 142 across the three environments. The cross CMS463D13A × FL 201 exhibited the highest significant positive heterosis over the superior check Soldier followed by CMS4626A × FL 201, CMS463D13A × PL 412 and CMS463D13A × IS 261 in E_1. Over the standard check CH-27, the cross CMS463D13A × FL 201 followed by CMS463D13A × YL 581, CMS463D13A × SL 475 and CMS4626A × SL 475 expressed the highest standard heterosis in E_2, the cross CMS4626A × PL 412 followed by CMS463D13A × DL 161, CMS463D13A × SL 475 and CMS4626A × YL 581 in E_3, and the cross CMS463D13A × FL 201 followed by CMS463D13A × SL 475, CMS4626A × FL 201 and CMS463D13A × IS 261 across the three environments.

Based on *per se* performance and standard heterosis, the crosses namely CMS4611A × VR 521 and CMS4611A × SL 473 were identified as promising to develop chilli cultivars with small fruit size in E_1, the crosses CMS4626A × E 183, CMS4611A × E 183 and CMS4611A × AC 102 in E_2, the crosses CMS4611A × IS 263 and CMS4611A × DL 161 in E_3, and the crosses CMS4611A × DL 161, CMS4611A × E 183, CMS4611A × VR 521 and CMS4611A × SL 473 based on the pooled means. These crosses could be useful for processing by the spice pepper industry for the production of dehydrated products.

Geleta and Labuschagne (2006a) stated that the medium sized fruits are more preferred to the long fruits. Medium fruits remain intact in storage than longer fruits, which tend to break at the distal ends (Weiss 2002). Similarly, for vegetable and paprika production also medium sized fleshy fruits are required (Geleta and Labuschagne 2006a). The crosses CMS4626A × PL 412, CMS4626A × VR 522, CMS4626A × C 142, CMS463D13A × IS 263 and CMS4611A × C 142 were identified with medium fruit length under E_1, the crosses CMS4626A × AC 102, CMS463D13A × SL 473, CMS4626A × IS 262, CMS4611A × PL 412 and CMS4626A × VR 523 under E_2, the crosses CMS4626A × E 183, CMS4611A × PP 402, CMS463D13A × SL 473, CMS4626A × SL 473 and CMS463D13A × PP 402 under E_3, and the crosses CMS4611A × IS 261, CMS463D13A × IS 262, CMS4626A × PP 414, CMS4611A × YL 581 and CMS4626A × C 142 when pooled across the environments.

Geleta and Labuschagne (2004b) identified Szegedi 178 × Bakko Local, Szegedi 178 × Mareko Shote, Szegedi 178 × Pepper 1976 and Bakko Local × Pepper 1976 as the most promising crosses for fruit length. Prasath and Ponnuswami (2008) reported that the magnitude of better parent heterosis varied from -20.59 to 39.85%. Marame *et al* (2009) found that the heterosis for fruit length over better parent ranged from -23.8 in PBC 602 × PBC 535 to 26.59% in PBC 223 × Bakolocal and from -13.26 in ICPN9#16 × PBC 731 to 51.36% in PBC 972 × Marekoshote over standard check. Butcher *et al* (2013) reported that the crosses SP15 × SP128, SP79 × SP2, SP15 × SP5 and SP15 × SP57 expressed 24.49, 23.74, 21.84 and 21.21% better parent heterosis, respectively. Bhutia *et al* (2015) found that two crosses expressed significant positive heterosis and the range of heterosis over the better parent varied between -64.66 to 6.14%. Naresh *et al* (2016) found that highest positive heterosis of 31.36 and 33.33% over better parent and standard check, respectively in the two crosses IHR 3453 × IHR 4507 and IHR 4507 × IHR 3476.

4.5.6 Fruit width (mm)

For fruit width, the lowest and the highest mean values were recorded by the cross-CMS4611A × E 183 (9.65 mm) and CMS463D13A × PP 402 (17.76 mm) with an average of 13.10 mm under E_1, by CMS4626A × VR 521 (8.76 mm) and CMS463D13A × FL 201 (12.68 mm) with a mean value of 10.75 mm under E_2, by CMS4611A × VR 521 (7.79 mm) and CMS463D13A × YL 581 (12.68 mm) with an average of 9.92 mm under E_3 and by CMS4611A × VR 521 (8.91 mm) and CMS463D13A × PP 402 (14.16 mm) with an overall mean of 11.26 mm when pooled across the environments (Table 4.12f). Out of the 60 crosses, 11, 13 and 47 crosses in E_1; four, none and 25 crosses in E_2; three, seven and 23 in E_3 and 18, 12 and 43 crosses across the three environments expressed significant and positive heterosis over better parent and standard checks, CH-27 and Soldier, respectively. Better parent heterosis was ranged from -33.25 in the cross CMS4611A × FL 201 to 27.10% in the cross CMS463D13A × IS 262 under E_1, from -16.64 in the cross CMS4611A × FL 201 to 18.17% in the cross CMS4626A × PP 402 under E_2, from -29.53 in the cross CMS4611A × FL 201 to 24.74% in the cross CMS4626A × PL 406 under E_3 and from -27.27 in the cross CMS4611A × FL 201 to 15.36% in the cross CMS4626A × C 142 when pooled across the environments. Over the standard checks CH-27 and Soldier, the respective heterosis varied from -25.37 in the cross CMS4611A × E 183 to 37.31% in the cross CMS463D13A × PP 402 and from -3.24 in the cross CMS4611A × E 183 to 78.03% in the cross CMS463D13A × PP 402 under E_1, from -23.11 in the cross CMS4626A × VR 521 to 11.32% in the cross CMS463D13A × FL 201 and from -11.47 in the cross CMS4626A × VR 521 to 28.17% in the cross CMS463D13A × FL 201 under E_2, from -25.42 in the cross CMS4611A × VR 521 to 21.30% in the cross CMS463D13A × YL 581 and from -13.8 in the cross CMS4611A × VR 521 to 40.2% in the cross CMS463D13A × YL 581 under E_3, from -23.11 in the cross CMS4611A × VR 521 to 22.15% in the cross CMS463D13A × PP 402 and from -7.51 in the cross CMS4611A × VR 521 to 46.93% in the cross CMS463D13A × PP 402 across the three environments.

The best combinations for fruit width over their respective better parent were CMS463D13A × IS 262 followed by CMS463D13A × SL 473, CMS463D13A × C 142 and CMS4626A × C 142 in E_1, CMS4626A × PP 402 followed by CMS4626A × SL 473, CMS4626A × IS 267 and CMS4626A × IS 268 in E_2, CMS4626A × PL 406 followed by CMS4611A × PL 406 and CMS4626A × PL 412 in E_3, and CMS4626A × C 142 followed by CMS463D13A × IS 268, CMS4626A × SL 473 and CMS463D13A × SL 473 when means were pooled across the three environments. The cross CMS463D13A × PP 402 exhibited maximum significant positive heterosis over superior check Soldier followed by CMS463D13A × YL 581, CMS463D13A × FL 201 and CMS4626A × PP 402 in E_1, the cross CMS463D13A × YL 581 followed by CMS463D13A × PP 402, CMS4626A × PP 402 and CMS4626A × YL 581 in E_3 and the cross CMS463D13A × PP 402 followed by CMS463D13A × YL 581, CMS4626A × PP 402 and CMS463D13A × FL 201 showed desirable significant positive heterosis over superior check, CH-27 across the three environments. None of the crosses showed significant positive heterosis over the superior check CH-27 in E_2.

Fruits that express larger width will more than likely have more potential to produce fruits with higher weight and thicker pericarp. Ben-Chaim and Paran (2000) reported highly positive genetic association of fruit weight with fruit width and pericarp thickness. In the current study, the crosses which showed larger fruit width also have higher fruit weight and pericarp thickness. These associated traits are especially important for producers who continually strive for an opportunity to more accurately increase their profitability margin using cultivars that have a greater capacity to produce larger characteristics and hence more yield.

Tembhurne and Rao (2012) observed that the range of heterosis for fruit width varied from -54.05 to -1.42% over better parent and from -49.51 to 28.74% over standard check. The cross JNA1 × LCA960 expressed highest standard heterosis. Butcher *et al* (2013) identified the crosses PapP27 × PapP67, SP5 × SP73 and SP5 × SP71 as most promising. Singh *et al* (2014) reported that only one cross namely EL 181 × PA 401 recorded significant positive better parent heterosis. Naresh *et al* (2016) observed that the crosses IHR4507 × IHR3476, IHR 4503 × IHR 3476, IHR 4506 × IHR 3476, IHR3453 × IHR 3476 and IHR 4516 × IHR 3476 exhibited standard heterosis of 165.0, 143.57, 133.93, 102.86 and 102.86%, respectively for fruit width.

4.5.7 Pericarp thickness (mm)

A thick pericarp is vital for green chilli and chilli paste and fruits with thicker pericarp are more resistant to damage during postharvest handling and subsequent transportation. Such fruits have a fresher appearance compared to fruits with thinner pericarp (Lannes *et al* 2007). Lannes *et al* (2007) reported that the pericarp thickness was negatively associated with the content of soluble solids present in the pulp in ripened fruits, while soluble solids content and dry matter content was highly correlated. Hence, fruits with thinner pericarp are more suitable for processing, due to their higher content of soluble solids and the reduced energy inputs required dehydrating them for paprika production. Thinner pericarp can also be used effectively as an indirect selection criterion to improve the dry matter content in chilli (do Rego *et al* 2009).

The cross means for pericarp thickness ranged from 0.84 mm in CMS4611A × SL 473 to 2.17 mm in CMS463D13A × PP 402 with a mean value of 1.25 mm under E_1, from 0.63 mm in the cross CMS4626A × IS 262 to 1.75 mm in the cross CMS463D13A × FL 201 with an average of 1.10 mm under E_2, and from 0.50 mm in CMS4611A × VR 521 to 1.23 mm in CMS4626A × FL 201 and CMS463D13A × YL 581 with a mean value of 0.80 mm under E_3. Across the three environments, pericarp thickness varied from 0.72 mm in CMS4611A × VR 521 to 1.63 mm in CMS463D13A × FL 201 with an overall mean of 1.05 mm (Table 4.12g). The extent of heterosis over better parent ranged from -56.51 in CMS4611A × FL 201 to 38.29% in CMS463D13A × YL 581 under E_1, from -33.63 in CMS4626A × E 183 to 50.35% in CMS4626A × SL 473 under E_2, from -53.59 in CMS4611A × FL 201 to 50.11% in CMS4626A × PL 406 under E_3 and from -43.53 in CMS4611A × FL 201 to 28.87% in CMS463D13A × VR 523 when pooled across the three environments. Of the 60 crosses evaluated, 14 and 19 crosses in E_1, seven and 10 in E_2, seven and 18 in E_3 and 17 and 20 across the three environments showed significant positive and negative heterosis over their respective better parent. Over the standard checks CH-27 and Soldier, 19 and 20, 41 and none of the cross in E_1, eight and 29, 38 and one in E_2, 13 and 29, 26 and eight in E_3, 15 and 24, 44 and none of the crosses over the three environments exhibited significant positive and negative heterosis. The range of heterosis over superior check Soldier varied from -0.56 in CMS4611A × SL 473 to 157.61% in CMS463D13A × PP 402 under E_1. Heterosis over CH-27 varied from -47.35 in CMS4626A × IS 262 to 44.80% in CMS463D13A × FL 201under E_2, from -40.33 in CMS4611A × VR 521 to 46.22% in CMS463D13A × YL 581 under E_3 and from -33.59 in CMS4611A × VR 521 to 50.97% in CMS463D13A × FL 201 across the three environments.

Under E_1, the cross CMS463D13A × YL 581 showed the highest significant positive heterosis over the better parent for pericarp thickness. This was followed by CMS463D13A × SL 475, CMS463D13A × VR 523 and CMS463D13A × IS 267. Under E_2, the cross CMS4626A × SL 473 followed by CMS4611A × PL 406, CMS4626A × IS 267 and CMS4611A × IS 267; under E_3 the cross CMS4626A × PL 406 followed by CMS4611A × PL 412, CMS463D13A × DL 161 and CMS463D13A × VR 522, and across the three environments the cross CMS463D13A × VR 523 followed by CMS4626A × SL 473, CMS463D13A × VR 522 and CMS463D13A × IS 261 exhibited significant positive better parent heterosis. The cross CMS463D13A × PP 402 expressed the maximum significant positive heterosis over superior check Soldier followed by CMS463D13A × FL 201, CMS463D13A × YL 581 and CMS463D13A × SL 475 in E_1. The crosses CMS463D13A × FL 201, CMS4626A × YL 581, CMS4626A × FL 201 and CMS4611A × FL 201 in E_2, CMS463D13A × YL 581, CMS4626A × FL 201, CMS463D13A × FL 201 and CMS463D13A × IS 268 in E_3, and CMS463D13A × FL 201, CMS463D13A × PP 402, CMS463D13A × YL 581 and CMS463D13A × SL 475 when means were pooled across the three environments exhibited significantly positive heterosis over CH-27. These crosses are suitable for local market, for processing chilli into paste and are also suitable for long distance transportation and export. Fruits with thicker pericarp are more appropriate for fresh consumption due to higher resistance of the pericarp to the wounding, firmness, and freshness aspect of the fruits.

Based on *per se* performance and standard heterosis, the crosses namely CMS4611A × SL 473, CMS4611A × AC 102, CMS4611A × IS 263, CMS4611A × VR 521 and CMS4611A × VR 522 in E_1, CMS4626A × IS 262, CMS4611A × IS 262, CMS4626A × E 183 and CMS4611A × VR 521 in E_2, CMS4611A × VR 521, CMS4626A × VR 521, CMS4611A × E 183, CMS463D13A × VR 521 in E_3, and CMS4611A × VR 521, CMS4626A × VR 521, CMS4611A × SL 473 and CMS4611A × IS 262 when pooled across the three environments, were identified with thinner pericarp, and are suitable for processing into chilli powder.

The crosses CMS4611A × VR 549, CMS4611A × VR 550, CMS4611A × VR 551, CMS4611A × VR 552 and CMS4611A × VR 553 in E_1, CMS4626A × IS 261, CMS4626A × PL 412, CMS4626A × IS 268, CMS463D13A × IS 262, CMS4611A × PL 412 and

CMS463D13A × IS 263 in E_2, CMS4611A × IS 267, CMS4611A × FL 201, CMS4611A × SL 475, CMS463D13A × C 142, CMS4626A × IS 267 and CMS463D13A × DL 161 in E_3, and CMS4611A × IS 267, CMS463D13A × PP 414, CMS4626A × VR 523, CMS463D13A × DL 161 and CMS4611A × IS 268 based on pooled means were identified with medium pericarp thickness. Pérez-Grajales *et al* (2009) observed that the better parent heterosis for pericarp thickness ranged from -17.0 in Zongolica × Huatusco I to 9.0% in Huatusco II × Peru. Butcher *et al* (2013) reported that the best cross for pericarp thickness was SP5 × SP73 with expressed heterosis of 16.67%. Singh *et al* (2014) recorded a range of heterosis from -37.98 in US 501 × PS 403 to 14.39% in SL 462 × DL 161 over better parent.

4.5.8 Number of fruits plant^{-1}

Number of fruits plant^{-1} is the most important primary component of total yield in chilli. Heterosis for total yield has principally been attributed to heterosis for number of fruits plant^{-1}. Thus, it is imperative to increase fruit number coupled with acceptable fruit weight to enhance yield and adoption of chilli genotypes. For number of fruits plant^{-1}, the cross means varied from 156.46 in CMS463D13A × FL 201 to 379.43 in CMS4611A × C 142 with an average of 267.43 under E_1, from 117.66 in CMS463D13A × PP 414 to 392.89 in CMS4626A × YL 581 with a mean value of 243.82 under E_2, from 59.45 in CMS4626A × FL 201 to 304.17 in CMS4611A × DL 161 with an average of 140.61 under E_3. Across the three environments, number of fruits plant^{-1} varied from 137.83 in CMS463D13A × E 183 to 332.52 in CMS4611A × C 142 with an overall mean of 217.28 (Table 4.12h). Twelve and 18 crosses in E_1, 25 and eight crosses in E_2, 33 and eight crosses in E_3 and 32 and 10 crosses across the three environments showed significant positive and negative heterosis over their respective better parent. Four and 37, seven and 27 crosses in E_1, 22 and eight, 13 and 25 in E_2, 16 and 29, 14 and 35 in E_3, and 15 and 28, 10 and 29 crosses over the three environments exhibited significant positive and negative heterosis over the standard checks, CH-27 and Soldier, respectively. The extent of heterosis over better parent ranged from -38.17 in CMS4626A × E 183 to 36.54% in CMS4611A × C 142 under E_1, from -34.28 in CMS463D13A × VR 521 to 90.44% in CMS4626A × YL 581 under E_2, from -37.91 in CMS463D13A × IS 263 to 182.68% in CMS4611A × VR 522 under E_3 and from -23.46 in CMS4626A × E 183 to 68.73% in CMS4611A × C 142 across the environments.

The range of better parent heterosis manifested in the crosses was high, indicating the prevalence of dominant gene action for the trait and its exploitation through heterosis breeding. The range of heterosis over Soldier in E_1 varied from -46.16 in CMS463D13A × FL 201 to 30.57% in CMS4611A × C 142. Over CH-27, the heterosis varied from -45.67 in CMS463D13A × PP 414 to 81.41% in CMS4626A × YL 581 under E_2, from -60.41 in

CMS4626A × FL 201 to 102.57% in CMS4611A × DL 161 under E_3 and from -39.29 in CMS463D13A × E 183 to 46.47% in CMS4611A × C 142 across the three environments.

On the basis of better parent heterosis, the promising crosses identified were CMS4611A × C 142, CMS4611A × DL 161, CMS463D13A × IS 267 and CMS463D13A × C 142 in E_1, CMS4626A × YL 581, CMS4626A × PL 412, CMS4626A × IS 262 and CMS4626A × IS 263 in E_2,CMS4611A × VR 522, CMS4626A × IS 268, CMS4611A × IS 267 and CMS4611A × C 142 in E_3, and CMS4611A × C 142, CMS4611A × VR 522, CMS4611A × IS 267 and CMS4626A × PL 412 based on the pooled means. Over the superior check Soldier in E_1, CMS4611A × C 142 exhibited the highest significant positive heterosis. This was followed by CMS4611A × DL 161, CMS4626A × PL 412 and CMS4626A × DL 161. Over the superior check CH-27, CMS4626A × YL 581 expressed the maximum significant positive heterosis followed by CMS4626A × PL 412, CMS4626A × IS 262 and CMS4611A × C 142 in E_2, CMS4611A × DL 161 followed by CMS4611A × C 142, CMS4626A × SL 473 and CMS4611A × SL 475 in E_3, and CMS4611A × C 142 followed by CMS4611A × DL 161, CMS4626A × DL 161 and CMS4611A × VR 522 across the three environments. Significant and positive heterosis for number of fruits plant^{-1} has also been reported by Geleta and Labuschagne (2004b), Prasath and Ponnuswami (2008), Marame *et al* (2009), Pérez-Grajales *et al* (2009), Sitaresmi *et al* (2010), Shrestha *et al* (2011), Tembhurne and Rao (2012), Chaudhary *et al* (2013) and Khalil and Hatem (2014). Heterosis ranging from -44.77 in the cross BCCH Sel-4 × BCC-1 to 0.29% in the cross BCCH Sel-4 × AC-575 has been observed by Bhutia *et al* (2015).

4.5.9 Number of seed fruit^{-1}

Seed number is one of the most important criteria in the eyes of breeders and producers of hybrid seed. The less seeded fruits are normally soft with poor shelf-life and transportability besides negatively correlated with pungency. The number of seed fruit^{-1} varied from 36.37 in CMS4611A × PP 402 to 93.37 in CMS463D13A × IS 261 with an average of 62.68 under E_1, from 30.33 in CMS4611A × PP 402 to 75.57 in CMS463D13A × SL 475 with a mean value of 52.73 under E_2, from 24.13 in CMS4626A × YL 581 to 62.37 in CMS463D13A × PL 412 with an average of 44.06 under E_3 and from 31.04 in CMS4611A × PP 402 to 75.77 in CMS463D13A × IS 261 with an overall mean of 53.16 across the three environments (Table 4.12i). Among the 60 crosses evaluated, 34, 12 and 52 crosses in E_1; 32, eight and 51 in E_2; 32, none and 52 crosses in E_3 and 37, 12 and 53 crosses over the three environments showed significant positive heterosis over their respective better parent and standard checks, CH-27 and Soldier, respectively. The appreciable amount of better parent heterosis found suggested the involvement of dominant genes in expression of the trait and the possibility of increasing number of seed fruit^{-1}through heterosis breeding.

The range of heterosis over their respective better parent varied from -33.03 in the cross CMS463D13A × E 183 to 51.74% in the cross CMS4626A × VR 522 under E_1, from -42.65 in the cross CMS463D13A × E 183 to 54.04% in the cross CMS4626A × PL 406 under E_2, from -44.93 in the cross CMS463D13A × E 183 to 56.56% in the cross CMS4626A × DL 161 under E_3 and from -39.69 in the cross CMS463D13A × E 183 to 46.87% in the cross CMS4626A × C 142 across the environments. Over the superior check Soldier in E_1, the heterosis ranged from -1.09 in the cross CMS4611A × PP 402 to 153.94% in the cross CMS463D13A × IS 261. Over the superior check CH-27, the heterosis varied from -51.65 in the cross CMS4611A × PP 402 to 20.46% in the cross CMS463D13A × SL 475 under E_2, from -58.77 in the cross CMS4626A × YL 581 to 6.55% in the cross CMS463D13A × PL 412 under E_3 and from -50.90 in the cross CMS4611A × PP 402 to 19.82% in the cross CMS463D13A × IS 261 across the three environments.

The highest significant positive heterosis over the better parent was exhibited by the cross CMS4626A × VR 522 followed by CMS4626A × C 142, CMS463D13A × IS 261 and CMS4626A × VR 521 in E_1, by CMS4626A × PL 406 followed by CMS4626A × VR 523, CMS4626A × PL 412 and CMS4611A × VR 521 in E_2, by CMS4626A × DL 161 followed by CMS4626A × VR 523, CMS4626A × VR 521 and CMS4626A × PL 412 in E_3, and across the three environments the crosses CMS4626A × C 142, CMS4626A × VR 523, CMS4626A × VR 521 and CMS4626A × PL 406 showed significant positive better parent heterosis. In E_1, the cross CMS463D13A × IS 261 expressed the maximum significant positive heterosis over superior check Soldier. This was followed by CMS4626A × SL 475, CMS463D13A × IS 268 and CMS463D13A × SL 475. Over the superior check CH-27, the cross CMS463D13A × SL 475 followed by CMS463D13A × IS 261, CMS463D13A × IS 267, CMS4626A × SL 475 and CMS4626A × PL 412 performed significantly better in E_2 and the cross CMS463D13A × IS 261 followed by CMS463D13A × SL 475, CMS4626A × SL 475 and CMS463D13A × IS 268 over the three environments. None of the crosses was superior to CH-27 in E_3.

Better parent heterosis up to 87.65% has been reported by Prasath and Ponnuswami (2008). The range varied from -28.0 in the cross Zongolica × Huatusco I to 22.0% in the cross Puebla × Peru (Pérez-Grajales *et al* 2009). Tembhurne and Rao (2012) recorded heterosis over better parent with a range from -68.98 to 40.68% and the most heterotic cross-combination was JNA1 × BVC-37. Singh *et al* (2014) observed that the extent of heterosis over better parent varied from -80.70 to 89.94%. Eighteen crosses showed significant positive better parent heterosis, out of which SL 462 × PP 402 exhibited the highest heterosis. Bhutia *et al* (2015) found that the heterosis for number of seed fruit^{-1} over their respective better parent varied between -40.0 in the cross BCC-1 × AC-575 to 7.24% in the cross BCCH Sel-4 × AC-575.

4.5.10 1000 seed weight (g)

The cross means for 1000 seed weight varied from 3.59 g to 6.88 g with a mean value of 5.44 g under E_1, from 3.29 g to 6.60 g with an average of 5.17 g under E_2, from 3.04 g to 6.46 g with a mean value of 4.98 g under E_3 and from 3.31 g to 6.63 g with an overall mean of 5.20 g over the three environments. The cross CMS463D13A × FL 201 expressed the highest mean value in E_1, CMS463D13A × FL 201 in E_2, CMS463D13A × YL 581 in E_3 and the cross CMS463D13A × FL 201 expressed the highest mean value when means were pooled across the environments (Table 4.12j). Out of the 60 crosses, three crosses in E_1, three in E_2, four in E_3 and 12 over the three environments registered positive significant heterosis over the better parent. On the other hand, two and 35 crosses in E_1, two and 37 in E_2, two and 36 in E_3 and four and 41 across the three environments showed significant positive heterosis over the standard checks, CH-27 and Soldier, respectively. The extent of heterosis over better parent ranged from -24.40 in CMS4626A × VR 521 to 21.98% in CMS463D13A × SL 475 under E_1, from -26.38 in CMS4626A × VR 521 to 22.92% in CMS463D13A × SL 475 under E_2, from -28.78 in CMS4626A × VR 521 to 23.07% in CMS4626A × VR 522 under E_3 and from -26.44 in CMS4626A × VR 521 to 22.30% in CMS463D13A × SL 475 across the environments. The range of heterosis over superior check Soldier in E_1 varied from -25.03 in CMS4626A × VR 521 to 43.60% in CMS463D13A × FL 201. Over CH-27, the range varied from -43.83 in CMS4626A × VR 521 to 12.62% in CMS463D13A × FL 201 under E_2, from -46.73 in CMS4626A × VR 521 to 13.13% in CMS463D13A × YL 581 under E_3 and from -43.87 in CMS4626A × VR 521 to 12.38% in CMS463D13A × FL 201 across the three environments.

The maximum better parent heterosis for 1000 seed weight was exhibited by the cross CMS463D13A × SL 475 followed by CMS463D13A × VR 522 and CMS4626A × VR 522 in E_1, by CMS463D13A × SL 475 followed by CMS463D13A × VR 522 and CMS4626A × VR 522 in E_2, by CMS4626A × VR 522 followed by CMS463D13A × VR 522, CMS463D13A × SL 475 and CMS463D13A × IS 268 in E_3, and by the cross CMS463D13A × SL 475 followed by CMS463D13A × VR 522, CMS4626A × VR 522 and CMS463D13A × SL 473 across the three environments. In E_1, the cross CMS463D13A × FL 201 exhibited significant positive heterosis over superior check Soldier. This was followed by CMS463D13A × YL 581, CMS463D13A × IS 263 and CMS4626A × IS 263. The cross CMS463D13A × FL 201 followed by CMS463D13A × YL 581 in E_2, the cross CMS463D13A × YL 581 followed by CMS463D13A × FL 201 in E_3, and the cross CMS463D13A × FL 201 followed by

CMS463D13A × YL 581, CMS463D13A × IS 263 and CMS4626A × IS 263 across the three environments exhibited significantly positive heterosis over CH-27.

Tembhurne and Rao (2012) observed that the extent of heterosis for 1000 seed weight ranged from -45.65 to 60.88% over the better parent and from -38.90 to 39.62% over the standard check. Twenty six crosses expressed significant positive heterosis over standard check, out of which ACA1 × GUK2 depicted the highest heterosis. Bhutia *et al* (2015) reported that the heterosis for seed weight over their better parent varied from -36.36 to 2.68%.

4.5.11 Total yield plant^{-1} (kg)

Total yield plant^{-1} is one of the most important breeding goals in any crop improvement program. Total yield heterosis is a variable parameter and depends not only on the parental combinations but also on the environmental conditions (Geleta and Labuschagne 2004a). The total yield plant^{-1} of 60 crosses varied from 0.34 kg in CMS4626A × E 183 to 1.57 kg in CMS463D13A × IS 268 with a mean value of 0.92 kg under E_1, from 0.21 kg in CMS463D13A × E 183 to 1.12 kg in CMS463D13A × FL 201 with an average of 0.66 kg under E_2 and from 0.17 kg in CMS4611A × PP 414 and CMS4626A × IS 263 to 0.70 kg in CMS463D13A × SL 475 and CMS4626A × SL 475 with a mean value of 0.41 kg under E_3. Across the three environments, total yield plant^{-1} varied from 0.32 kg in CMS463D13A × E 183 and CMS4626A × E 183 to 1.02 kg in CMS463D13A × IS 268 with an overall mean of 0.66 kg (Table 4.12k). Of the 60 crosses, 34 and two crosses in E_1, 35 and 10 crosses in E_2, 31 and 10 crosses in E_3 and 44 and five crosses across the three environments showed significant positive and negative heterosis over their respective better parent. The appreciable amount of better parent heterosis found suggested the involvement of dominance gene effects and the possibility of improving total yield of chilli through heterosis breeding. Over the standard checks CH-27 and Soldier, 15 and 22 crosses in E_1, 15 and 15 in E_2, 16 and 17 in E_3 and 14 and 22 crosses over the three environments exhibited significant positive heterosis, respectively.

The extent of heterosis over the better parent ranged from -32.62 in the cross CMS4611A × PL 412 to 135.43% in the cross CMS463D13A × IS 267 in E_1, from -55.76 in the cross CMS463D13 × E 183 to 147.61% in the cross CMS4626A × FL 201 in E_2, from -50.26 in the cross CMS463D13A × PP 414 to 150.70% in the cross CMS4611A × VR 522 in E_3 and from -34.96 in the cross CMS463D13A × E 183 to 108.72% in the cross CMS463D13A × IS 268 based on the pooled mean. In E_1, the range of heterosis over the superior check Soldier varied from -60.54 in the cross CMS4626A × E 183 to 80.18% in the cross CMS463D13A × IS 268. Over the superior check CH-27, the range varied from -72.78

in the cross CMS463D13A × E 183 to 45.52% in the cross CMS463D13A × FL 201 in E_2, from -63.32 in the cross CMS4611A × PP 414 to 49.05% in the cross CMS463D13A × SL 475 in E_3 and from -57.20 in the cross CMS463D13A × E 183 to 37.33% in the cross CMS463D13A × IS 268 when means were pooled across the three environments.

The promising crosses identified based on their respective better parent heterosis were CMS463D13A × IS 267, CMS463D13A × PP 402, CMS463D13A × IS 268 and CMS463D13A × VR 523 in E_1, CMS4626A × FL 201, CMS463D13A × FL 201, CMS4626A × YL 581 and CMS463D13A × PP 402 in E_2, CMS4611A × VR 522, CMS4611A × PL 406, CMS4626A × PL 406 and CMS4611A × IS 267 in E_3, and CMS463D13A × IS 268, CMS4611A × PP 402, CMS463D13A × PP 402 and CMS463D13A × C 142 when means were pooled across the three environments. The cross CMS463D13A × IS 268 exhibited highest significant positive heterosis over superior check Soldier followed by CMS463D13A × IS 267, CMS463D13A × IS 262 and CMS463D13A × DL 161 in E_1. The crosses CMS463D13A × FL 201, CMS4626A × FL 201, CMS463D13A × SL 475 and CMS4626A × YL 581 in E_2, CMS463D13A × SL 475, CMS4626A × SL 475, CMS4626A × VR 523 and CMS463D13A × DL 161 in E_3, and CMS463D13A × IS 268, CMS463D13A × SL 475, CMS463D13A × PP 402 and CMS4626A × DL 161 across the three environments performed significantly better than superior check CH-27. This suggests that hybrids will be the better option for developing chilli cultivars with higher yield.

Earlier, Milerue and Nikornpun (2000), Geleta and Labuschagne (2004b), Khalil *et al* (2004), Patel *et al* (2004) and Prasath and Ponnuswami (2008) reported significant positive better parent heterois for total yield plant^{-1}. Marame *et al* (2009) recorded the extent of better parent heterosis for total yield plant^{-1}from -52.67 in Marekofana × Marekoshote to 161.79% in PBC 602 × ICPN9#16, hetersis over standard check from -52.67 in Marekofana × Marekoshote to 92.05% in PBC 223 × Marekoshote. The crosses Zongolica× Puebla, Huatusco II × Puebla and Puebla × Huatusco I were identified as promising by Pérez-Grajales *et al* (2009), the crosses SP12 × SP38, 5AVS7 × SP32 and 5AVS7 × SP45 by Shrestha *et al* (2011); and the crosses LS 2-2 × W 5-15, W 5-15 × B 23-5 and LS 2-2 × B 16-10 by Khalil and Hatem (2014). Singh *et al* (2014) reported the heterosis over better parent in 66 crosses with a range from -71.82 to 331.11%. The most heterotic combination was reported to be CC 141 × VR 521 followed by SL 462 × PA 401, PP 402 × VR 521, SL 462 × VR 521 and MS 341 × PP 402. Bhutia *et al* (2015) found that the heterosis over better parent varied between -49.45 in BCC-1 × Kashi Anmol to 71.06% in BCCH Sel -4 × AC-575. Naresh *et al* (2016) identified IHR 3849 × IHR 3448 with expressed heterosis of 291.47% over better parent as the best cross. Other promising crosses included IHR 3453 × IHR 3448, IHR 3448 × IHR 2451, IHR 3448 × IHR 4516 and IHR 3849 × IHR 4516.

4.5.12 Ascorbic acid (mg.100g^{-1})

A chilli fruit from green to red succulent stage contains enough ascorbic acid or vitamin C to meet or exceed the adult recommended daily allowance (National Research Council 1989). The amount of vitamin C obtained from one medium-sized chilli fruit is six times as much as that of an orange (Geleta and Labuschagne 2006b). Ascorbic acid, as an antioxidant, reportedly decreases the risk of arteriosclerosis, cardiovascular diseases and some forms of cancer (Harris 1996).

The ascorbic acid content of crosses varied from 82.46 mg.100g^{-1} in CMS4611A × YL 581 to 197.41 mg.100g^{-1} in CMS4626A × IS 268 with an average of 146.19 mg.100g^{-1} under E_1, from 90.70 mg.100g^{-1} in CMS4611A × YL 581 to 205.64 mg.100g^{-1} in CMS463D13A × VR 523 with a mean value of 157.35 mg.100g^{-1} under E_2, from 67.30 mg.100g^{-1} in CMS4611A × YL 581 to 172.41 mg.100g^{-1} in CMS4611A × PL 406 with an average of 133.94 mg.100g^{-1} under E_3 and from 80.15 mg.100g^{-1} in CMS4611A × YL 581 to 182.36 mg.100g^{-1} in CMS463D13A × PL 412 with an overall mean of 145.83 mg.100g^{-1} over the three environments (Table 4.12l). For ascorbic acid content, 17, 27 and 45 crosses in E_1; 18, 30 and 47 in E_2; 23, 29 and 40 in E_3 and 27, 34 and 47 crosses based on pooled means showed significant positive heterosis over the respective better parent and standard checks, CH-27 and Soldier, respectively. The magnitude of heterosis over better parent ranged from -23.31 in CMS4611A × IS 261 to 20.69% in CMS4626A × VR 523 under E_1, from -18.57 in CMS4626A × PP 414 to 21.05% in CMS4626A × IS 262 under E_2, from -21.97 in CMS4611A × SL 475 to 19.25% in CMS463D13A × C 142 under E_3 and from -14.56 in CMS463D13A × PP 414 to 12.0% in CMS4626A × VR 522 across the three environments. The range of heterosis over superior check Soldier in E_1 varied from -29.88 in CMS4611A × YL 581 to 67.88% in CMS4626A × IS 268. Over the superior check CH-27, range of heterosis varied from -38.35 in CMS4611A × YL 581 to 39.79% in CMS463D13A × VR 523 under E_2, from -48.38 in CMS4611A × YL 581 to 32.24% in CMS463D13A × PL 406 under E_3 and from -42.54 in CMS4611A × YL 581 to 30.7% in CMS463D13A × PL 412 over the environments.

The outstanding crosses over their respective better parents were CMS4626A × VR 523, CMS463D13A × SL 475, CMS463D13A × PL 412 and CMS4626A × VR 521 in E_1, CMS4626A × IS 262, CMS463D13A × PL 406, CMS4611A × PL 406 and CMS463D13A × C 142 in E_2, CMS463D13A × C 142, CMS4626A × VR 522, CMS4626A × AC 102 and CMS4626A × IS 261 in E_3, and CMS4626A × VR 522, CMS463D13A × PL 406, CMS4611A × C 142 and CMS463D13A × IS 267 across the three environments. In E_1, the cross CMS4626A × IS 268 exhibited the highest significant positive heterosis over the superior check Soldier. This was followed by CMS463D13A × PL 412, CMS463D13A × IS 268 and CMS463D13A × IS 267. Over CH-27, the crosses CMS463D13A × VR 523, CMS4611A × VR 521, CMS4611A × SL 475 and CMS4626A × VR 521 expressed significantly positive heterosis in E_2, CMS463D13A × PL 406, CMS4626A × IS 261, CMS463D13A × VR 521 and CMS4626A × SL 475 in E_3, and CMS463D13A × PL 412, CMS463D13A × IS 261, CMS463D13A × PL 406 and CMS463D13A × IS 268 over the three environments.

Based on *per se* performance and standard heterosis, the ascorbic acid content in E_2 was higher than in E_1 and E_3. The determination of ascorbic acid content at different maturity stages can be a reason for differences in ascorbic acid content between the environments. The ascorbic acid content of chilli pepper fruit increases upon maturation (Howard *et al* 1994, Simonne *et al* 1997, Markus *et al* 1999, Howard *et al* 2000, Marin *et al* 2004 and Topuz and Ozdemir 2007). The amount and intensity of light during the growing season have also been described to have a definite influence increasing the ascorbic acid formed (Somers and Beeson 1948, Lee and Kader 2000 and Marin *et al* 2004). In general, lower the light intensity during growth, the lower the ascorbic acid content (Harris 1975), whereas ascorbic acid content is increases with increased in light intensity (Howard *et al* 2000) and sunshine (Somers and Beeson 1948). The outside fruit exposed to maximum sunlight contain higher amount of ascorbic acid than inside and shaded fruit on the same plant (Somers and Beeson 1948). Therefore, the lower ascorbic acid in the fruits in E_1 and E_3 might be due to poor light intensity and sunshine hours than E_2. The average weekly sunshine hours during E_1, E_2 and E_3 were 6.76, 7.83 and 7.67 h, respectively.

Geleta and Labuschagne (2004b) reported that crosses Kalocsai ‘‘M’’ Cseresznye × Bakko Local, Kalocsai ‘‘M’’ Cseresznye × Mareko Shote, Bakko Local × Mareko Shote, Mareko Shote × PBC 142A, Mareko Shote × Pepper 1976, PBC 142A × Pepper 1976 and C00916 × PBC 142A were rich in ascorbic acid. Butcher *et al* (2013) reported that the cross SP41 × SP95 displayed maximum positive better parent heterosis of 75.91% followed by SP16 × SP73 (56.01%) and PapP27 × PapP67 (48.19%). Khalil and Hatem (2014) identified Big Dipper × B 16-10 and Big Dipper × LS 2-2 as the most promising crosses for ascorbic acid over better parent. Bhutia *et al* (2015) observed that heterosis over better parent for ascorbic acid varied from -69.44 in BCC-1 × AC-575 to 28.93% in BCCH Sel-4 × Chaitali.

4.5.13 Oleoresin content (%)

Oleoresin refers to the fractionated components that constitute the color and flavor (pungency, aroma and related sensory factors) and truly recreate upon dilution of the sensory qualities of the original fresh material. Oleoresin of red pepper is a source of both color and pungency, essentially used in canned meats, sausages, in some snacks and in a dispersed form in some drinks such as ginger ale and orange juice (Singh *et al* 2010 and Singh *et al* 2015). In comparison with whole dry chilli and chilli powder, chilli oleoresin has many advantages, such as uniform quality, easier to handle, more stable colour retention, improved shelf-life, less contamination by microorganisms and reduced transportation costs. Therefore, oleoresin is gaining in importance from an export point of view (Singh and Hundal 2001).

For oleoresin content (%), the cross means varied from 8.06 in CMS463D13A × PP 414 to 17.61 in CMS4626A × SL 475 with an average of 11.74 under E_1, from 8.44 in CMS4626A × PP 414 to 18.50 in CMS463D13A × DL 161 with a mean value of 12.86 under E_2, from 6.25 in CMS4611A × E 183 to 12.56 in CMS463D13A × DL 161 with an average of 9.23 under E_3. Across the three environments, oleoresin content varied from 7.72 in CMS4611A × E 183 to 15.49 in CMS463D13A × VR 523 with an overall mean of 11.28 (Table 4.12m). Twenty five and fifteen crosses in E_1, 38 and 9 crosses in E_2, 25 and 16 crosses in E_3 and 36 and 12 crosses across the three environments showed significant positive and negative heterosis over their respective better parent. Twenty nine and 25 in E_1, 21 and 35 in E_2, 26 and 35 in E_3 and 30 and 36 based on pooled means exhibited significant positive heterosis over the standard checks, CH-27 and Soldier, respectively. The extent of better parent heterosis ranged from -26.29 in the cross CMS463D13A × PP 414 to 52.15% in the cross CMS463D13A × VR 523 under E_1, from -23.52 in the cross CMS463D13A × E 183 to 58.42% in the cross CMS463D13A × DL 161 under E_2, from -22.82 in the cross CMS463D13A × E 183 to 36.52% in the cross CMS463D13A × SL 475 under E_3 and from -23.12 in the cross CMS463D13A × E 183 to 42.26% in the cross CMS463D13A × DL 161 when means were pooled across the three environments. In E_1, the range of standard heterosis over the superior check Soldier varied from -24.82 in the cross CMS463D13A × PP 414 to 64.32% in the cross CMS4626A × SL 475. Over the superior check CH-27, the standard heterosis ranged from -34.95 in the cross CMS4626A × PP 414 to 42.66% in the cross CMS463D13A × DL 161 under E_2, from -30.42 in the cross CMS4611A × E 183 to 39.76% in the cross CMS463D13A × DL 161 under E_3 and from -28.23 in the cross CMS4611A × E 183 to 43.95% in the cross CMS463D13A × VR 523 across the three environments.

Among the 60 crosses, the cross CMS463D13A × VR 523 registered the highest significant positive heterosis over better parent followed by CMS4626A × SL 475, CMS463D13A × IS 263 and CMS4611A × VR 523 in E_1, CMS463D13A × DL 161 followed by CMS4611A × PL 412, CMS4611A × C 142 and CMS463D13A × VR 521 in E_2, CMS463D13A × SL 475 followed by CMS463D13A × DL 161, CMS463D13A × VR 521 and CMS4626A × VR 522 in E_3, and CMS463D13A × DL 161 followed by CMS463D13A × VR 523, CMS463D13A × VR 521 and CMS463D13A × SL 475 based on the pooled mean. In E_1, the cross CMS4626A × SL 475 exhibited the highest significant positive heterosis over superior check Soldier. This was followed by the crosses CMS463D13A × VR 523, CMS4626A × C 142 and CMS463D13A × IS 263. Over the superior check CH-27, the cross CMS463D13A × DL 161 followed by CMS463D13A × VR 523, CMS4611A × VR 523 and CMS463D13A × VR 521 showed maximum significant positive heterosis in E_2, CMS463D13A × DL 161 followed by CMS463D13A × SL 475, CMS463D13A × VR 521 and CMS4626A × VR 522 in E_3, and CMS463D13A × VR 523 followed by CMS463D13A × DL 161, CMS463D13A × SL 475 and CMS4626A × SL 475 across the three environments.

4.5.14 Capsaicin content (%)

The cross means for capsaicin content varied from 0.39 to 0.92% with a mean value of 0.65% under E_1, from 0.45 to 0.98% with an average of 0.69% under E_2, from 0.30 to 0.79% with a mean value of 0.54% under E_3 and from 0.38 to 0.87% with an overall mean of 0.63% over the three environments. The cross CMS4626A × PL 406 expressed the highest mean value for capsaicin content in E_1, CMS463D13A × C 142 and CMS4626A × DL 161 in E_2, CMS463D13A × SL 475 and CMS4626A × IS 263 in E_3 and CMS463D13A × SL 475 across the three environments (Table 4.12n). Out of the 60 crosses, 27 and 18 crosses in E_1, 28 and 15 in E_2, 20 and 19 in E_3 and 34 and 17 over the three environments registered positive and negative significant heterosis over the respective better parent. Over the standard check CH-27, 29 and 21 crosses in E_1, 19 and 33 in E_2, 29 and 21 in E_3 and 30 and 24 across the three environments showed significant positive and negative heterosis. Over the standard check Soldier, 25 and 25 crosses in E_1, 26 and 23 in E_2, 27 and 22 in E_3 and 31 and 23 over the environments exhibited significant positive and negative heterosis.

The extent of heterosis over better parent ranged from -33.89 in CMS4626A × FL 201 to 49.67% in CMS4626A × PL 406 under E_1, from -25.52 in CMS4626A × E 183 to 25.74% in CMS463D13A × PL 406 under E_2, from -37.48 in CMS4626A × E 183 to 53.97% in CMS463D13A × SL 475 under E_3 and from -30.52 in CMS4626A × E 183 to 32.64% in CMS4626A × PL 406 across the environments. In E_1, the range of heterosis over superior check Soldier varied from -38.35 in CMS4611A × FL 201 to 47.36% in CMS4626A × PL 406. Over the superior check CH-27, the standard heterosis ranged from -38.63 in CMS4611A × FL 201 to 33.45% in CMS463D13A × C 142 under E_2, from -41.09 in CMS4611A × FL 201 to 55.07% in CMS463D13A × SL 475 under E_3 and from -37.78 in CMS4611A × FL 201 to 42.3% in CMS463D13A × SL 475 across the three environments.

The maximum better parent heterosis for capsaicin content was expressed by the cross CMS4626A × PL 406 followed by CMS463D13A × VR 523, CMS463D13A × IS 268 and CMS463D13A × IS 261 in E_1, by CMS463D13A × PL 406 followed by CMS463D13A × VR 521, CMS4626A × SL 475 and CMS463D13A × C 142 in E_2, by CMS463D13A × SL

475 followed by CMS463D13A × IS 262, CMS4626A × SL 475 and CMS4626A × IS 263 in E_3, and by the cross-combination CMS4626A × PL 406 followed by CMS463D13A × IS 261, CMS463D13A × DL 161 and CMS4626A × VR 521 across the three environments. In E_1, the cross CMS4626A × PL 406 exhibited the highest significant positive heterosis over superior check Soldier followed by CMS4626A × C 142, CMS463D13A × SL 475 and CMS4626A × SL 475. Over the superior check CH-27, the cross CMS463D13A × C 142 followed by CMS4626A × DL 161, CMS463D13A × DL 161 and CMS463D13A × IS 261 depicted the highest significant positive heterosis in E_2, CMS463D13A × SL 475 followed by CMS4626A × IS 263, CMS463D13A × IS 262 and CMS463D13A × PL 412 in E_3, and CMS463D13A × SL 475 followed by CMS463D13A × IS 262, CMS4626A × SL 475 and CMS4626A × IS 263 when means were pooled across the three environments.

The crosses KY 1-1 × Nhum Khiew Maejo, CF 21789 × Nhurn Khiew and KY 1-1 × Nhum Khiew were identified as most promising for capsaicin content by Milerue and Nikornpun (2000), and NMCA80004 × NMCA80058 and NMCA80058 × NMCA80062 by Zewdie and Bosland (2001). Prasath and Ponnuswami (2008) observed that the better parent heterosis varied from -53.57 to 202.38%. Butcher *et al* (2013) observed that the magnitude of better parent heterosis varied from -72.98 to 814.95%. The cross SP16 × SP15 showed the highest heterosis followed by SP16 × SP57, SP50 × SP16 and SP50 × SP15. Bhutia *et al* (2015) reported that heterosis over the better parent ranged from -31.43 in the crosses BCC-1 × Kashi Anmol and BCC -1 × Chaitali to 46.67% in the cross AC-575 × Chaitali.

4.5.15 Scoville heat units (SHU)

Chilli is valued in the world market for its pungency, color and aroma (Zewdie and Bosland 2001). Pungency is caused by the presence of alkaloid compounds, named capsaicinoids (Nelson and Dawson 1923 and Suzuki and Iwai 1984). Till date, more than 20 capsaicinoids are found in chilli (Bosland and Votava 1999, Zewdie and Bosland 2001 and Islam *et al* 2015). Capsaicinoids are unique to the *Capsicum* genus and are produced in glands on the placenta of the fruit (Blum *et al* 2003 and Cruz-Pérez *et al* 2007). They are colorless, flavorless and odorless non-nutrient compounds. Capsaicin (*trans*-8-methyl-*N*-vanillyl-6-nonenamide), a major alkaloid compound among the capsaicinoids and characterized by acrid and burning sensation. It is widely used in the food, medicine, spice and pharmaceutical industries. Capsaicin is known to kill some types of cancer cells (Min *et al* 2004) and counter-irritant against pain (Sicuteri *et al* 1990), provide relief in arthritis and respiratory ailments (Mazzone and Geraghty 1999). Capsaicin and dihydrocapsaicin represent about 90% of the total capsaicinoid content in most cultivated peppers (Suzuki *et al* 1980, Govindarajan and Sathyanarayana 1991, Ben-Chaim *et al* 2006 and Monforte-Gonzalez *et al* 2010), with capsaicin accounting for ~71% of the total capsaicinoids in most of the pungent cultivars (Othman *et al* 2011).

The specific pungency levels must be maintained for food manufacturers to reliably label food products as mild, medium and hot. Because industrials needs for chilli pungency varies from low or non-pungent paprika for color to very pungent for pharmaceutical purposes. Therefore, cultivars must have a pungency level within a specific range to have commercial value (Zewdie and Bosland 2000). Chilli pungency is measured in Scoville heat units (SHU) (Scoville 1912). The use of the SHU parameter is the recommended method for pepper evaluation as it provides a better indicator of the pungency levels (Othman *et al* 2011).

The cross means for SHU varied from 61653.33 to 147360.0 with a mean value of 103764.44 in E_1, from 72090.67 to 156789.33 with an average of 110514.58 in E_2, from 48320.0 to 127200.0 with a mean value of 86838.22 in E_3 and from 60688.0 to 138823.11 with an overall mean of 100372.42 over the three environments. Cross CMS4626A × PL 406 expressed the highest mean value for SHU in E_1, CMS4626A × DL 161 in E_2, CMS463D13A × SL 475 in E_3 and CMS463D13A × SL 475 across the environments (Table 4.12o). Out of the 60 crosses, 27 and 18 crosses in E_1, 28 and 15 in E_2, 20 and 19 in E_3 and 34 and 17 over the three environments registered positive and negative significant heterosis over the respective better parent. Over the standard check CH-27, 29 and 21 crosses in E_1, 19 and 33 in E_2, 29 and 21 in E_3 and 30 and 24 across the three environments showed significant positive and negative heterosis. Over the standard check Soldier, 25 and 25 crosses in E_1, 26 and 23 in E_2, 27 and 22 in E_3 and 31 and 23 over the environments exhibited significant positive and negative heterosis.

The extent of better parent heterosis ranged from -33.89 in the cross CMS4626A × FL 201 to 49.67% in the cross CMS4626A × PL 406 under E_1, from -25.52 in the cross CMS4626A × E 183 to 25.76% in the cross CMS463D13A × PL 406 under E_2, from -37.48 in the cross CMS4626A × E 183 to 53.97% in the cross CMS463D13A × SL 475 under E_3 and from -30.52 in the cross CMS4626A × E 183 to 32.66% in the cross CMS4626A × PL 406 based on the pooled mean. In E_1, the range of heterosis over superior check Soldier varied from -38.35 in the cross CMS4611A × FL 201 to 47.36% in the cross CMS4626A × PL 406. Over the superior check CH-27, the standard heterosis ranged from -38.63 in the cross CMS4611A × FL 201 to 33.45% in the cross CMS463D13A × C 142 under E_2, from -41.09 in the cross CMS4611A × FL 201 to 55.07% in the cross CMS463D13A × SL 475 under E_3 and from -37.78 in the cross CMS4611A × FL 201 to 42.3% in the cross CMS463D13A × SL 475 when the means were pooled across the three environments.

The maximum significant and positive better parent heterosis for SHU was exhibited by the cross CMS4626A × PL 406 followed by CMS463D13A × VR 523, CMS463D13A × IS 268 and CMS463D13A × IS 261 in E_1, by CMS463D13A × PL 406 followed by CMS463D13A × VR 521, CMS4626A × SL 475 and CMS463D13A × C 142 in E_2, by CMS463D13A × SL 475 followed by CMS463D13A × IS 262, CMS4626A × SL 475 and CMS4626A × IS 263 in E_3, and by the cross CMS4626A × PL 406 followed by CMS463D13A × IS 261, CMS463D13A × DL 161 and CMS4626A × VR 521 across the three environments. In E_1, the cross CMS4626A × PL 406 exhibited the highest significant positive heterosis over the superior check Soldier followed by CMS4626A × C 142, CMS463D13A × SL 475 and CMS4626A × SL 475. Over the superior check CH-27, the cross CMS463D13A × C 142 followed by CMS4626A × DL 161, CMS463D13A × DL 161 and CMS463D13A × IS 261 expressed the maximum significant positive heterosis in E_2, the cross CMS463D13A × SL 475 followed by CMS4626A × IS 263, CMS463D13A × IS 262 and CMS463D13A × PL 412 in E_3, and the cross CMS463D13A × SL 475, followed by CMS463D13A × IS 262, CMS4626A × SL 475 and CMS4626A × IS 263 performed significantly better across the three environments.

Prasath and Ponnuswami (2008) stated that the market for less pungent paprika types has been growing steadily and mainly utilized as natural food colorant or to provide flavoring in the form of oleoresin. But the paprika types are not suitable for all the chilli growing areas in India and this necessitated the development of less pungent paprika type chilli hybrids to tap the paprika oleoresin market. Based on *per se* performance and standard heterosis, the crosses namely CMS4611A × FL 201, CMS4626A × FL 201, CMS4611A × PP 402 and CMS463D13A × YL 581 were identified as mildly pungent as they had significantly negative standard heterosis over the superior check with lowest mean values for SHU in E_1, the crosses CMS4611A × FL 201, CMS4611A × E 183, CMS4626A × E 183 and CMS4626A × YL 581 in E_2, the crosses CMS4611A × FL 201, CMS4611A × YL 581, CMS4626A × E 183 and CMS4611A × PP 402 in E_3, and the crosses CMS4611A × FL 201, CMS4626A × E 183, CMS463D13A × YL 581 and CMS4611A × YL 581 when means were pooled across the three environments. The promising crosses having moderately pungency were CMS463D13A × VR 521, CMS463D13A × PL 406, CMS4611A × IS 263, CMS4626A × PP 414 and CMS4611A × VR 523 in E_1, the crosses CMS4626A × VR 521, CMS463D13A × PL 412, CMS4626A × PP 402, CMS4626A × IS 267 and CMS463D13A × IS 268 in E_2, the crosses CMS4611A × IS 268, CMS4611A × IS 261, CMS463D13A × IS 268, CMS4611A × VR 522 and CMS4611A × SL 475 in E_3, and the crosses CMS463D13A × IS 267, CMS4626A × PL

412, CMS4626A × VR 522, CMS4611A × VR 523 and CMS4611A × PL 406 based on pooled means.

In the current study, based on *per se* performance and standard heterosis, the SHU in E_2 was higher than in E_1 and E_3. The lower SHU in the fruits of the tested crosses grown in E_1 and E_3 might be a result of the poor light intensity and soil fertility than E_2. Lesser sunshine hours during fruit maturity period could be attributed to the lower SHU in E_1 and E_3. The average weekly sunshine hours during E_1, E_2 and E_3 were 6.76, 7.83 and 7.67 h, respectively. Iwai *et al* (1979) also reported that light exposure could be an important factor in the formation and accumulation of capsaicin in chilli. The determination of SHU at different maturity stages could be another reason for differences in SHU between the environments. Othman *et al* (2011) stated that the amount of capsaicin in a given variety can vary depending on the light intensity and temperature at which the plant is grown, the age of the fruit and the position of the fruit on the plant. Pungency also increases with water stress (drought or flooding) (Bosland and Votava 1999 and Sung *et al* 2005) and soil fertility imbalances (Johnson and Decoteau 1996, Medina-Lara *et al* 2008 and Monforte-Gonzalez *et al* 2010). Medina-Lara *et al* (2008) reported that nitrogen fertilizer significantly increased plant growth and fruit yield while maintaining high levels of capsaicin. Gurung *et al* (2011) observed that capsaicinoids content was higher in the fruits of the crop that grown at high potassium content sites.

Cruz-Pérez *et al* (2007) reported that the crosses Puebla × Huatusco, Puebla × Chiapas and Puebla × Zongolica were most promising for SHU value. These crosses expressed heterosis to the tune of 225%, 190.32% and 88.38% over their respective better parent after 94 days of development after flowering. Naresh *et al* (2016) observed that the range of heterosis for SHU varied from -88.89 in IHR 4503 × IHR 3476 to 278.35% in IHR 4506 × IHR 3476 over better parent and from -95.18 in IHR3453 × IHR 3476 to 118.72% in IHR3849 × IHR4503 over standard check. Of the 45 F_1 hybrids evaluated, only six crosses namely, IHR4506 × IHR3476, IHR3849 × IHR4506, IHR3453 × IHR4506, IHR3849 × IHR3476, IHR3849 × IHR4516 and IHR3849 × IHR3453 showed significant positive better parent heterosis.

In the present study, the highest mean better parent heterosis was exhibited for total yield plant^{-1} (32.96%) followed by number of seed fruit^{-1} (14.19%), plant spread (13.37%), number of primary branched plant^{-1} (13.01%), plant height (12.23%), oleoresin content (6.96%) and fruit length (6.2) in E_1, for total yield plant^{-1} (35.1%) followed by number of fruit plant^{-1} (15.09%), number of seed fruit^{-1} (13.52%), oleoresin content (12.46%), number of primary branched plant^{-1} (11.43%) and plant spread (3.4%) in E_2, for number of fruit plant^{-1} (28.38%) followed by total yield plant^{-1} (20.98%), number of primary branched plant^{-1} (20.28%), plant height (10.89%) and plant spread (10.52%) in E_3, and for total yield plant^{-1} (35.29%) followed by number of primary branched plant^{-1} (17.96%), number of seed fruit^{-1} (12.46%), number of fruit plant^{-1} (11.43%) and plant spread (10.4%) across the environments. The appreciable amount of better parent heterosis found suggested the involvement of dominance gene effects and the possibility of improving total yield of chilli through heterosis breeding. Based on mid-parent heterosis, the partial dominance, complete dominance and over-dominance was recorded for different studied traits under three environments.

The promising crosses were identified based on their *per se* performance and standard heterosis over the environments for early, main and late season cultivation with pungent and non-pungent fruits (Table 4.13a-d). Total yield plant^{-1} is one of the most important breeding goals in any crop improvement program. The breeding goal is to develop a cultivar or hybrid that performs better than the commercial cultivar. The crosses which expressed 20% standard heterosis or more are identified as promising. Therefore, all the identified crosses have high *per se* performance and heterosis over standard checks, CH-27 and Soldier. Besides high *per se* performance and significant positive standard heterosis over the superior check Soldier for total yield plant^{-1} in early season planted (E_1) crop, the crosses CMS463D13A × IS 268, CMS463D13A × C 142, CMS463D13A × IS 262, CMS4626A × C 142, CMS4626A × PL 406, CMS463D13A × VR 523, CMS4611A × C 142, CMS463D13A × SL 475, CMS4626A × IS 262 and CMS4626A × VR 523 were identified as promising for fruit weight, fruit length, fruit width, pericarp thickness and number of seed fruit^{-1}. These crosses also expressed superior fruit quality traits like ascorbic acid, capsaicin content and SHU, and identified for early maturity high pungency segment. These crosses also showed significantly positive standard heterosis for oleoresin content except CMS463D13A × IS 262 and CMS463D13A × IS 268. Due to thick pericarp, these crosses are suitable for local market for processing chilli into paste and are also suitable for long distance transportation and export. The crosses namely CMS463D13A × VR 522, CMS463D13A × SL 473, CMS463D13A × PL 412, CMS463D13A × YL 581 and CMS4611A × IS 268 expressed significantly positive standard heterosis for plant height, plant spread, fruit weight, fruit length, fruit width, pericarp thickness, number of seed fruit^{-1} and significant negative standard heterosis for capsaicin content and SHU. These crosses have been identified for non-pungent paprika production used in food industry and for fresh consumption. The crosses CMS463D13A × DL 161, CMS4626A × DL 161 and CMS4611A × DL 161 were identified as promising for number of fruits palnt^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU. These crosses are identified for pungent oleoresin extraction, used as a source of both colour and pungency in canned meats, sandwich spreads, sausages, soups and in dispersed form in some drinks such as ginger ale and orange juice and also used for pharmaceutical purpose.

In main season planted (E_2) crop, the crosses CMS463D13A × SL 475 and CMS4626A × SL 475 were found to be superior over the standard check CH-27 in respect of total yield plant^{-1}, plant spread, number of primary branches plant^{-1}, fruit weight, fruit length, number of fruits plant^{-1}, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU. These crosses can be utilized in spice and pharmaceutical industries and markets where consumers prefer chillies that are more pungent. The crosses CMS463D13A × PP 402, CMS463D13A × VR 523 and CMS4611A × PP 402 have shown significantly positive standard heterosis for total yield plant^{-1}, fruit weight and oleoresin content and significant negative standard heterosis for plant height, capsaicin content and SHU. These crosses are identified as promising with shorter plant stature and high yield, and for extraction of non-pungent oleoresin used as a source of red colour and flavour in various processed products where pungency is not desired like lunchmeats, sausages, cheeses and other dairy products, soups, sauces and snacks such as potato chips. The crosses CMS463D13A × FL 201, CMS4626A × FL 201, CMS4626A × YL 581, CMS4611A × YL 581 and CMS463D13A × YL 581 exhibited significantly positive standard heterosis for total yield plant^{-1}, fruit weight and fruit length and significant negative standard heterosis for plant height, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU. These crosses have been identified for production of mildly-pungent chillies.

In E_3, along with total yield plant^{-1}, the crosses CMS463D13A × SL 475, CMS4626A × SL 475, CMS463D13A × DL 161 and CMS463D13A × VR 523 registered significantly positive standard heterosis over superior check CH-27 for plant spread, number of primary branches plant^{-1}, fruit weight, fruit length, number of fruits plant^{-1}, oleoresin content, capsaicin content and SHU. These crosses are identified for the development of pungent and long fruit types in chilli for late season cultivation. The crosses namely CMS4611A × DL 161 and CMS4626A × DL 161 showed significantly positive standard heterosis for number of primary branches plant^{-1}, number of fruits plant^{-1} and oleoresin content and significant negative standard heterosis for plant height, pericarp thickness, number of seed fruit^{-1}, 1000 seed weight, capsaicin content and SHU. These crosses will be better option for developing chilli cultivars with shorter plant stature and for non-pungent oleoresin extraction. These crosses would also be useful where chillies are marketed for processing into powder. A chilli with thin pericarp is desirable for quick drying. The crosses CMS4626A × SL 473, CMS463D13A × YL 581 and CMS463D13A × SL 473 have been identified for the development of high yielding non-pungent chilli cultivars.

Evaluation over environments is important to identify stable genotypes. Stability of the genotypes is defined as the consistent performance across different environments for a given trait. Pooled across the three environments, the cross CMS463D13A × IS 268 had significantly positive standard heterosis over superior check CH-27 for total yield plant^{-1}, plant height, plant spread, number of primary branches plant^{-1}, fruit weight, fruit length, fruit width, pericarp thickness, number of seed fruit^{-1}, ascorbic acid, capsaicin content and SHU. Apart from significant positive standard heterosis for total yield plant^{-1}, the crosses namely CMS463D13A × SL 475, CMS463D13A × C 142, CMS463D13A × VR 523, CMS4626A × SL 475, CMS463D13A × DL 161 and CMS4626A × C 142 also expressed standard heterosis for fruit weight, fruit length, oleoresin content, capsaicin content and SHU. These crosses are identified for development of chilli cultivars with high yield and pungent fruits for cultivation across the environments. The crosses CMS463D13A × YL 581 and CMS463D13A × SL 473 have shown significantly positive standard heterosis for fruit weight, fruit length and fruit width and significant negative standard heterosis for plant height, ascorbic acid, capsaicin content and SHU. These crosses are identified as smaller plant stature with mildly pungent fruits for fresh consumption. The cross CMS4626A × DL 161 exhibited significant positive standard heterosis for number of fruits plant^{-1}, oleoresin content, capsaicin content and SHU and significantly negative standard heterosis for plant height, plant spread, pericarp thickness, number of seed fruit^{-1} and 1000 seed weight. This cross is identified with small stature, compact canopy and pungent fruits with thin pericarp. Such plant types are of immense agronomic use for multiple cropping systems and industrial uses such as processing for powder making. The cross CMS463D13A × PP 402 expressed significantly positive standard heterosis for number of primary branched palnt^{-1}, fruit weight, fruit length, fruit width, pericarp thickness and oleoresin content and significant negative standard heterosis for plant height, number of fruits plant^{-1}, number of seed fruit^{-1}, ascorbic acid, capsaicin content and SHU, and is identified for oleoresin extraction, used as a coloring agent and flavour additive in processed products.

Table 4.12a: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for plant height (cm) evaluated over environments

Crosses	**Plant height (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	82.39	17.44*	12.65	-25.84**	-4.97	56.70	-18.66**	-32.98**	-41.23**	-27.60**
CMS4611A × SL 475	102.31	35.58**	31.54**	-7.91	18.01*	89.72	21.99**	6.05	-7.00	14.57*
CMS4611A × PL 412	120.74	43.87**	27.49**	8.68	39.26**	100.38	17.52**	16.41**	4.05	28.18**
CMS4611A × IS 263	87.57	17.09*	14.57	-21.17**	1.01	78.83	6.33	-6.82	-18.29**	0.67
CMS4611A × VR 523	94.04	28.59**	28.58**	-15.35**	8.47	73.17	-2.75	-13.51*	-24.16**	-6.57
CMS4611A × DL 161	87.14	23.02**	19.14*	-21.56**	0.51	66.02	-5.27	-21.96**	-31.57**	-15.69*
CMS4611A × IS 267	113.10	38.38**	25.21**	1.80	30.45**	92.56	16.30**	9.40	-4.07	18.19**
CMS4611A × YL 581	94.10	28.37**	28.08**	-15.30**	8.54	63.92	-5.06	-24.45**	-33.75**	-18.38**
CMS4611A × SL 473	78.54	3.54	-0.04	-29.31**	-9.41	80.49	0.47	-4.86	-16.57**	2.78
CMS4611A × IS 262	91.88	-0.76	-17.99**	-17.29**	5.98	78.29	-1.73	-7.46	-18.85**	-0.03
CMS4611A × VR 521	97.64	17.96**	5.66	-12.11*	12.62	79.03	3.61	-6.58	-18.08**	0.92
CMS4611A × FL 201	80.06	24.78**	9.46	-27.94**	-7.66	64.58	-7.69	-23.67**	-33.06**	-17.54**
CMS4611A × PP 402	91.40	33.12**	24.96**	-17.73**	5.42	80.87	6.08	-4.41	-16.18**	3.26
CMS4611A × C 142	115.05	29.02**	9.36	3.56	32.70**	100.30	19.89**	18.55**	3.96	28.07**
CMS4611A × PP 414	112.25	34.09**	19.06**	1.04	29.47**	87.53	7.43	3.47	-9.27	11.78
CMS4611A × VR 522	91.61	22.76**	20.37*	-17.54**	5.66	91.00	18.88**	7.57	-5.68	16.20*
CMS4611A × PL 406	105.33	28.78**	16.46*	-5.19	21.49**	82.76	2.90	-2.18	-14.22**	5.68
CMS4611A × E 183	93.01	17.09*	8.48	-16.28**	7.28	74.70	-9.95	-11.70*	-22.57**	-4.61
CMS4611A × IS 268	115.24	46.93**	37.64**	3.73	32.92**	105.83	32.70**	25.10**	9.70	35.14**
CMS4611A × IS 261	102.77	21.95**	7.72	-7.49	18.54*	82.47	3.09	-2.52	-14.52**	5.31

Crosses	**Plant height (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	79.55	20.53*	18.44	-28.39**	-8.24	43.47	-27.50**	-33.22**	-54.94**	-44.49**
CMS4626A × SL 475	91.47	28.28**	17.60*	-17.66**	5.51	89.38	40.10**	37.32**	-7.36	14.13*
CMS4626A × PL 412	96.72	21.26**	2.13	-12.94*	11.56	102.37	35.30**	18.71**	6.11	30.72**
CMS4626A × IS 263	86.88	23.00**	13.67	-21.79**	0.21	67.22	4.41	3.28	-30.32**	-14.16*
CMS4626A × VR 523	94.61	37.17**	29.40**	-14.84*	9.13	76.78	17.25*	16.55*	-20.42**	-1.96
CMS4626A × DL 161	72.87	9.28	6.33	-34.41**	-15.95*	48.25	-19.51**	-25.87**	-49.99**	-38.39**
CMS4626A × IS 267	103.74	33.72**	14.85*	-6.62	19.66**	79.31	13.58*	6.36	-17.79**	1.28
CMS4626A × YL 581	84.50	22.19**	15.01	-23.94**	-2.54	62.61	8.75	-3.81	-35.10**	-20.05**
CMS4626A × SL 473	76.25	6.35	-2.95	-31.36**	-12.05	69.11	-1.77	-8.61	-28.37**	-11.75
CMS4626A × IS 262	84.99	-3.89	-24.14**	-23.49**	-1.96	73.07	4.52	-2.22	-24.26**	-6.69
CMS4626A × VR 521	93.54	18.98**	1.23	-15.80**	7.90	72.37	8.78	6.49	-24.99**	-7.59
CMS4626A × FL 201	74.88	24.79**	15.49	-32.60**	-13.63	59.59	-1.01	-8.45	-38.23**	-23.91**
CMS4626A × PP 402	98.42	52.57**	51.81**	-11.41	13.52	85.83	29.12**	26.47**	-11.03*	9.61
CMS4626A × C 142	98.73	16.13*	-6.15	-11.13	13.88	92.22	24.79**	11.49	-4.41	17.76**
CMS4626A × PP 414	96.97	21.88**	2.85	-12.72*	11.85	74.70	4.15	-4.67	-22.57**	-4.61
CMS4626A × VR 522	82.12	16.53*	7.90	-26.08**	-5.28	73.53	10.09	7.35	-23.78**	-6.10
CMS4626A × PL 406	112.83	45.32**	24.74**	1.56	30.14**	86.85	22.91**	13.92*	-9.98	10.91
CMS4626A × E 183	91.66	21.76**	6.91	-17.49**	5.73	69.92	-4.48	-14.01*	-27.53**	-10.71
CMS4626A × IS 268	104.83	41.13**	25.21**	-5.64	20.92**	95.11	35.87**	26.97**	-1.42	21.45**
CMS4626A × IS 261	69.60	-13.13	-27.05**	-37.35**	-19.72**	97.67	39.05**	29.55**	1.23	24.72**
CMS463D13A × AC 102	97.23	17.33*	-1.36	-12.48*	12.15	67.43	4.09	-9.77	-30.11**	-13.90*
CMS463D13A × SL 475	101.13	14.69*	2.59	-8.97	16.64*	96.33	40.39**	28.90**	-0.15	23.01**

Crosses	**Plant height (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	119.15	23.30**	20.88**	7.26	37.44**	88.59	10.07	2.73	-8.18	13.12*
CMS463D13A × IS 263	103.72	18.53**	5.22	-6.64	19.63**	83.23	20.27**	11.37	-13.73**	6.28
CMS463D13A × VR 523	113.61	32.35**	15.26*	2.27	31.05**	81.51	15.94*	9.07	-15.51**	4.08
CMS463D13A × DL 161	94.72	13.37*	-3.91	-14.74*	9.25	77.48	19.63**	3.67	-19.69**	-1.06
CMS463D13A × IS 267	116.72	23.58**	18.41**	5.06	34.63**	80.44	7.76	7.64	-16.62**	2.72
CMS463D13A × YL 581	108.18	25.76**	9.75	-2.62	24.78**	65.20	4.50	-12.76	-32.42**	-16.74**
CMS463D13A × SL 473	105.55	19.18**	7.09	-4.99	21.75**	76.26	1.43	0.84	-20.96**	-2.62
CMS463D13A × IS 262	104.38	-0.88	-6.84	-6.05	20.39**	76.71	2.65	2.65	-20.49**	-2.04
CMS463D13A × VR 521	123.80	29.65**	25.60**	11.44*	42.80**	102.19	43.23**	36.74**	5.92	30.49**
CMS463D13A × FL 201	92.75	20.65**	-5.91	-16.51**	6.98	74.06	13.89*	-0.91	-23.24**	-5.43
CMS463D13A × PP 402	108.76	33.65**	10.33	-2.10	25.45**	74.98	5.16	0.33	-22.29**	-4.26
CMS463D13A × C 142	114.85	12.72*	9.17	3.38	32.48**	77.44	-1.63	-6.37	-19.73**	-1.11
CMS463D13A × PP 414	111.97	16.12**	13.60*	0.79	29.15**	82.26	7.46	4.98	-14.74**	5.04
CMS463D13A × VR 522	111.53	27.70**	13.15*	0.39	28.64**	78.26	9.27	4.71	-18.89**	-0.07
CMS463D13A × PL 406	119.38	26.32**	21.12**	7.46	37.70**	87.96	16.52**	15.36*	-8.83	12.32
CMS463D13A × E 183	120.56	30.83**	22.31**	8.52	39.06**	82.83	6.16	1.87	-14.15**	5.77
CMS463D13A × IS 268	132.82	45.72**	34.75**	19.56**	53.20**	105.44	40.93**	40.76**	9.29	34.65**
CMS463D13A × IS 261	99.33	2.41	0.77	-10.59	14.57	83.23	10.89	10.41	-13.73**	6.28
LSD at p=0.05		10.99	12.69	12.69	12.69		8.55	9.88	9.88	9.88
LSD at p=0.01		14.53	16.78	16.78	16.78		11.31	13.06	13.06	13.06

Table 4.12a (*Cont'd.*)

Crosses	Plant height (cm)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	46.27	-3.96	-14.93	-36.41**	-24.76**	61.78	-1.43	-12.62**	-33.88**	-18.16**
CMS4611A × SL 475	73.45	31.51**	28.14**	0.96	19.46**	88.49	29.59**	25.15**	-5.30	17.21**
CMS4611A × PL 412	68.81	25.84**	25.16**	-5.42	11.91	96.64	29.42**	22.90**	3.43	28.01**
CMS4611A × IS 263	61.91	20.35**	13.83	-14.91*	0.69	76.11	13.95**	7.63	-18.55**	0.80
CMS4611A × VR 523	70.43	29.83**	29.50**	-3.19	14.55*	79.21	17.28**	12.03**	-15.23**	4.92
CMS4611A × DL 161	51.22	-0.27	-5.82	-29.60**	-16.70*	68.13	6.51	-3.65	-27.09**	-9.76*
CMS4611A × IS 267	65.77	14.16*	8.11	-9.61	6.96	90.47	23.98**	20.24**	-3.18	19.83**
CMS4611A × YL 581	64.82	26.81**	19.18*	-10.90	5.42	74.28	16.22**	5.05	-20.51**	-1.61
CMS4611A × SL 473	55.76	0.64	-1.16	-23.37**	-9.32	71.59	1.62	1.25	-23.38**	-5.17
CMS4611A × IS 262	56.60	3.00	1.96	-22.21**	-7.95	75.59	-0.19	-6.40	-19.11**	0.12
CMS4611A × VR 521	66.42	19.68**	17.33*	-8.70	8.02	81.03	13.30**	12.04**	-13.28**	7.33
CMS4611A × FL 201	57.02	23.69**	4.84	-21.63**	-7.27	67.22	11.90*	-4.94	-28.07**	-10.97**
CMS4611A × PP 402	77.70	48.05**	42.86**	6.80	26.36**	83.32	26.64**	17.84**	-10.83**	10.36*
CMS4611A × C 142	65.66	7.18	-3.62	-9.76	6.78	93.67	20.04**	9.75**	0.24	24.06**
CMS4611A × PP 414	58.28	-3.55	-12.31	-19.90**	-5.22	86.02	14.38**	7.93*	-7.94*	13.93**
CMS4611A × VR 522	63.83	22.48**	17.37*	-12.26*	3.81	82.15	21.23**	16.17**	-12.09**	8.80*
CMS4611A × PL 406	73.84	32.38**	29.15**	1.50	20.09**	87.31	20.15**	17.00**	-6.56	15.64**
CMS4611A × E 183	43.36	-28.19**	-34.67**	-40.41**	-29.49**	70.36	-5.25	-9.57*	-24.71**	-6.81
CMS4611A × IS 268	76.51	30.36**	21.45**	5.16	24.43**	99.19	37.21**	34.27**	6.16	31.39**
CMS4611A × IS 261	85.49	59.45**	57.18**	17.50**	39.03**	90.24	24.25**	21.06**	-3.42	19.53**
CMS4626A × AC 102	45.88	3.65	-1.48	-36.94**	-25.39**	56.30	-0.77	-4.30	-39.75**	-25.43**

Crosses	**Plant height (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × SL 475	73.06	40.64**	27.45**	0.41	18.81**	84.63	35.75**	28.49**	-9.43**	12.10**
CMS4626A × PL 412	59.40	16.99*	8.04	-18.36**	-3.40	86.16	25.36**	9.57*	-7.79*	14.13**
CMS4626A × IS 263	57.24	20.43**	18.03*	-21.32**	-6.90	70.45	15.78**	12.05*	-24.61**	-6.69
CMS4626A × VR 523	63.91	26.96**	18.11*	-12.16*	3.94	78.43	27.33**	21.85**	-16.06**	3.89
CMS4626A × DL 161	48.50	2.21	0.34	-33.34**	-21.12**	56.54	-2.56	-3.89	-39.49**	-25.11**
CMS4626A × IS 267	63.61	18.46**	4.57	-12.57*	3.45	82.22	22.65**	9.28*	-12.01**	8.90*
CMS4626A × YL 581	45.62	-3.36	-4.65	-37.30**	-25.81**	64.24	10.81*	9.20	-31.25**	-14.91**
CMS4626A × SL 473	59.22	15.02*	4.98	-18.60**	-3.69	68.19	5.70	-2.86	-27.02**	-9.68*
CMS4626A × IS 262	49.41	-3.19	-10.99	-32.09**	-19.64**	69.16	-0.91	-14.37**	-25.99**	-8.40*
CMS4626A × VR 521	63.28	22.66**	11.78	-13.03*	2.91	76.40	16.50**	5.63	-18.24**	1.19
CMS4626A × FL 201	53.58	27.00**	15.06	-26.36**	-12.87	62.68	15.80**	6.55	-32.92**	-16.98**
CMS4626A × PP 402	61.74	27.12**	22.08**	-15.13**	0.42	82.00	37.00**	34.70**	-12.25**	8.61*
CMS4626A × C 142	73.06	27.40**	7.24	0.41	18.81**	88.00	22.08**	3.11	-5.82	16.56**
CMS4626A × PP 414	61.78	9.32	-7.04	-15.09*	0.47	77.81	12.35**	-2.36	-16.72**	3.07
CMS4626A × VR 522	72.97	51.37**	46.39**	0.29	18.67**	76.21	23.27**	17.57**	-18.45**	0.94
CMS4626A × PL 406	58.17	12.13	1.73	-20.05**	-5.40	85.95	28.81**	15.18**	-8.02*	13.84**
CMS4626A × E 183	52.70	-6.67	-20.59**	-27.57**	-14.29*	71.43	4.55	-8.20*	-23.56**	-5.39
CMS4626A × IS 268	64.28	17.33*	2.03	-11.65*	4.54	88.07	32.73**	19.21**	-5.75	16.66**
CMS4626A × IS 261	73.00	46.87**	38.14**	0.34	18.72**	80.09	20.10**	7.44	-14.29**	6.08
CMS463D13A × AC 102	53.44	9.66	-3.74	-26.54**	-13.08	72.70	11.06**	-4.69	-22.20**	-3.71
CMS463D13A × SL 475	73.44	30.17**	28.13**	0.95	19.44**	90.30	27.06**	18.39**	-3.36	19.61**
CMS463D13A × PL 412	61.74	11.75	11.21	-15.13**	0.42	89.83	15.97**	14.23**	-3.87	18.98**

Crosses	Plant height (cm)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS463D13A × IS 263	55.24	6.22	-0.50	-24.07**	-10.16	80.73	16.04**	5.84	-13.60**	6.93
CMS463D13A × VR 523	62.62	14.24*	12.79	-13.93*	1.84	85.91	22.17**	12.64**	-8.06*	13.80**
CMS463D13A × DL 161	59.51	14.60*	7.18	-18.20**	-3.22	77.24	15.71**	1.26	-17.34**	2.30
CMS463D13A × IS 267	73.44	26.24**	20.73**	0.95	19.44**	90.20	19.07**	18.26**	-3.47	19.47**
CMS463D13A × YL 581	53.99	4.46	-2.76	-25.79**	-12.20	75.79	13.63**	-0.63	-18.89**	0.39
CMS463D13A × SL 473	64.71	15.63*	14.71	-11.06	5.24	82.17	12.20**	7.73	-12.06**	8.84*
CMS463D13A × IS 262	56.44	1.67	1.66	-22.42**	-8.20	79.18	0.84	-1.96	-15.27**	4.87
CMS463D13A × VR 521	72.79	29.83**	28.58**	0.05	18.38**	99.59	34.04**	30.57**	6.58	31.91**
CMS463D13A × FL 201	59.98	28.52**	8.03	-17.56**	-2.46	75.59	20.27**	-0.89	-19.10**	0.13
CMS463D13A × PP 402	62.92	18.61**	13.33	-13.52*	2.33	82.22	19.90**	7.79	-12.01**	8.90*
CMS463D13A × C 142	72.94	17.99**	7.08	0.26	18.63**	88.41	9.41**	3.59	-5.38	17.11**
CMS463D13A × PP 414	67.84	11.24	2.09	-6.75	10.34	87.36	12.02**	9.61*	-6.51	15.71**
CMS463D13A × VR 522	63.33	20.21**	14.07	-12.95*	3.00	84.37	19.60**	10.62*	-9.71**	11.75**
CMS463D13A × PL 406	73.20	29.90**	28.02**	0.61	19.05**	93.51	23.94**	22.60**	0.08	23.86**
CMS463D13A × E 183	73.88	21.22**	11.32	1.54	20.15**	92.42	19.97**	18.79**	-1.09	22.42**
CMS463D13A × IS 268	74.47	25.66**	18.20**	2.35	21.11**	104.24	38.85**	36.67**	11.56**	38.07**
CMS463D13A × IS 261	60.33	11.35	8.67	-17.07**	-1.88	80.96	7.37*	6.15	-13.35**	7.24
LSD at p=0.05		7.19	8.30	8.30	8.30		5.43	6.27	6.27	6.27
LSD at p=0.01		9.51	10.98	10.98	10.98		7.15	8.26	8.26	8.26

*, significant at p=0.05; **, significant at p=0.01

Table 4.12b: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for plant spread (cm) evaluated over environments**

Crosses	Plant spread (cm)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	74.88	32.39**	31.75**	10.84	41.43**	50.72	-7.93	-8.20	-11.51*	-5.44
CMS4611A × SL 475	71.12	17.61**	10.94	5.28	34.33**	58.47	7.69	5.81	2.00	8.99
CMS4611A × PL 412	78.00	43.57**	37.24**	15.46*	47.32**	58.30	5.94	5.51	1.71	8.68
CMS4611A × IS 263	65.49	11.84	8.64	-3.06	23.69**	54.68	7.84	-1.05	-4.61	1.93
CMS4611A × VR 523	65.72	12.93	10.33	-2.71	24.13**	61.80	14.44**	11.84	7.81	15.21*
CMS4611A × DL 161	68.78	22.89**	21.02**	1.81	29.91**	58.77	4.88	3.45	2.52	9.55
CMS4611A × IS 267	69.94	28.45**	23.07**	3.54	32.11**	61.82	39.82**	11.88*	7.85	15.25*
CMS4611A × YL 581	78.17	45.67**	37.54**	15.71*	47.64**	46.84	9.55	-15.22*	-18.28**	-12.67*
CMS4611A × SL 473	65.67	10.84	6.51	-2.80	24.03**	60.37	11.57*	9.25	5.31	12.54*
CMS4611A × IS 262	56.50	-1.07	-1.55	-16.37*	6.72	54.44	5.26	-1.47	-5.02	1.50
CMS4611A × VR 521	57.62	0.31	-0.75	-14.70*	8.84	41.88	-10.38	-24.21**	-26.94**	-21.93**
CMS4611A × FL 201	63.82	17.42*	12.30	-5.53	20.55*	52.43	12.09	-5.11	-8.53	-2.25
CMS4611A × PP 402	56.61	3.29	-0.39	-16.20*	6.93	59.79	18.88**	8.20	4.30	11.46
CMS4611A × C 142	70.50	24.42**	24.05**	4.36	33.16**	53.99	1.43	-2.29	-5.82	0.65
CMS4611A × PP 414	68.56	29.98**	20.63**	1.48	29.49**	46.77	4.36	-15.36*	-18.41**	-12.82*
CMS4611A × VR 522	58.10	-1.66	-5.27	-14.00*	9.74	57.91	2.29	-0.10	1.03	7.96
CMS4611A × PL 406	69.00	11.54	3.16	2.14	30.33**	68.72	36.34**	24.37**	19.89**	28.11**
CMS4611A × E 183	69.04	32.50**	21.49**	2.20	30.41**	51.32	1.04	-7.12	-10.47	-4.32
CMS4611A × IS 268	66.34	30.83**	16.74*	-1.79	25.31**	67.83	48.76**	22.76**	18.34**	26.46**
CMS4611A × IS 261	81.22	25.87**	12.46*	20.23**	53.41**	62.40	13.60*	12.93*	8.86	16.33**

Crosses	**Plant spread (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	60.11	11.44	6.80	-11.02	13.54	36.94	-26.49**	-32.75**	-35.55**	-31.13**
CMS4626A × SL 475	56.35	-2.61	-12.11	-16.59*	6.43	69.70	40.95**	30.71**	21.59**	29.94**
CMS4626A × PL 412	69.78	34.94**	34.65**	3.29	31.79**	46.33	-7.68	-15.45*	-19.17**	-13.62*
CMS4626A × IS 263	70.17	25.44**	16.41*	3.87	32.54**	49.91	8.83	8.16	-12.93*	-6.96
CMS4626A × VR 523	68.22	22.74**	14.53	0.99	28.86**	59.68	21.39**	13.14*	4.11	11.25
CMS4626A × DL 161	60.44	13.30	9.70	-10.53	14.17	46.71	-8.76	-17.77**	-18.51**	-12.92*
CMS4626A × IS 267	53.88	3.94	3.46	-20.25**	1.76	49.83	26.55**	9.34	-13.06*	-7.10
CMS4626A × YL 581	60.42	18.37*	17.10*	-10.56	14.13	42.67	12.51	-6.39	-25.57**	-20.46**
CMS4626A × SL 473	56.29	-0.60	-8.70	-16.68*	6.32	49.23	-0.07	-7.03	-14.11*	-8.22
CMS4626A × IS 262	56.87	4.35	-0.91	-15.82*	7.41	47.54	1.41	-1.34	-17.06**	-11.37
CMS4626A × VR 521	57.00	3.96	-1.82	-15.63*	7.66	42.83	2.25	-6.02	-25.28**	-20.15**
CMS4626A × FL 201	57.78	11.67	11.37	-14.47*	9.13	47.99	14.43*	5.29	-16.28**	-10.54
CMS4626A × PP 402	56.17	7.62	6.42	-16.86*	6.09	53.75	18.24**	17.93*	-6.23	0.20
CMS4626A × C 142	65.68	21.53**	16.27*	-2.78	24.05**	50.32	4.00	-1.71	-12.21*	-6.19
CMS4626A × PP 414	65.61	30.89**	27.15**	-2.88	23.92**	50.96	27.48**	11.80	-11.11	-5.01
CMS4626A × VR 522	51.07	-9.56	-16.74*	-24.41**	-3.55	67.10	29.61**	15.75**	17.06**	25.09**
CMS4626A × PL 406	67.78	14.40*	1.33	0.33	28.02**	46.54	2.15	2.12	-18.80**	-13.23*
CMS4626A × E 183	58.50	18.20*	13.37	-13.41*	10.49	41.04	-10.69	-11.42	-28.40**	-23.48**
CMS4626A × IS 268	61.05	26.93**	18.31*	-9.64	15.30	46.44	13.95*	1.90	-18.98**	-13.42*
CMS4626A × IS 261	74.67	20.60**	3.38	10.53	41.03**	63.63	27.04**	16.54**	11.01	18.63**
CMS463D13A × AC 102	76.23	28.05**	21.43**	12.84	43.99**	63.20	16.30**	15.05*	10.26	17.82**
CMS463D13A × SL 475	74.61	17.60**	16.38*	10.44	40.92**	75.37	40.77**	40.20**	31.48**	40.50**

Crosses	**Plant spread (cm)**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	H_{BP}	**CH-27**	**Soldier**		H_{MP}	H_{BP}	**CH-27**	**Soldier**
CMS463D13A × PL 412	71.89	25.46**	14.51*	6.41	35.78**	53.14	-2.11	-3.04	-7.30	-0.94
CMS463D13A × IS 263	80.38	30.65**	28.04**	18.99**	51.83**	65.45	31.02**	21.75**	14.17*	22.01**
CMS463D13A × VR 523	91.20	49.09**	45.28**	35.01**	72.26**	61.49	15.47**	14.38*	7.27	14.63*
CMS463D13A × DL 161	73.79	25.20**	17.54*	9.23	39.37**	58.09	5.08	2.26	1.35	8.30
CMS463D13A × IS 267	73.67	28.29**	17.35*	9.05	39.15**	52.42	20.60**	-2.48	-8.55	-2.27
CMS463D13A × YL 581	69.76	23.18**	11.12	3.26	31.76**	50.55	20.31**	-5.97	-11.82*	-5.77
CMS463D13A × SL 473	73.75	18.54**	17.48*	9.17	39.30**	58.85	10.30	9.48	2.67	9.72
CMS463D13A × IS 262	65.93	9.73	5.02	-2.41	24.53**	47.32	-7.17	-11.97	-17.45**	-11.78
CMS463D13A × VR 521	73.19	21.15**	16.59*	8.35	38.25**	58.14	26.46**	8.16	1.43	8.39
CMS463D13A × FL 201	68.71	19.86**	9.46	1.71	29.78**	58.06	26.13**	7.99	1.28	8.23
CMS463D13A × PP 402	72.66	25.75**	15.74*	7.55	37.23**	49.47	-0.16	-7.98	-13.70*	-7.78
CMS463D13A × C 142	79.16	32.74**	26.09**	17.17**	49.51**	53.95	2.81	0.36	-5.88	0.58
CMS463D13A × PP 414	69.16	24.13**	10.17	2.37	30.63**	52.38	18.87**	-2.57	-8.63	-2.36
CMS463D13A × VR 522	68.68	10.67	9.39	1.66	29.71**	63.11	12.98*	8.87	10.10	17.65**
CMS463D13A × PL 406	81.56	25.81**	21.94**	20.74**	54.06**	64.53	29.96**	20.05**	12.58*	20.30**
CMS463D13A × E 183	72.86	32.28**	16.07*	7.86	37.62**	46.57	-6.95	-13.38*	-18.76**	-13.19*
CMS463D13A × IS 268	85.20	58.72**	35.72**	26.13**	60.93**	54.18	20.80**	0.78	-5.48	1.00
CMS463D13A × IS 261	70.11	3.86	-2.93	3.78	32.42**	72.68	34.15**	33.11**	26.79**	35.49**
LSD at p=0.05		7.55	8.72	8.72	8.72		5.67	6.54	6.54	6.54
LSD at p=0.01		9.99	11.53	11.53	11.53		7.49	8.65	8.65	8.65

Table 4.12b (*Cont'd.*)

Crosses	**Plant spread (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	38.04	-0.85	-0.90	-4.04	-22.90**	54.55	9.08*	8.75*	-0.53	4.95
CMS4611A × SL 475	59.82	40.94**	28.65**	50.90**	21.23**	63.14	20.49**	15.54**	15.13**	21.47**
CMS4611A × PL 412	45.86	12.42	6.17	15.67	-7.07	60.72	21.32**	21.05**	10.72**	16.82**
CMS4611A × IS 263	49.51	36.25**	28.97**	24.89**	0.34	56.56	16.54**	12.76**	3.13	8.82*
CMS4611A × VR 523	46.93	12.84	4.76	18.38*	-4.89	58.15	13.43**	11.04**	6.04	11.88**
CMS4611A × DL 161	47.67	19.36**	14.92	20.23*	-3.40	58.40	15.32**	14.23**	6.50	12.36**
CMS4611A × IS 267	43.69	20.41**	13.81	10.20	-11.46	58.49	30.01**	16.60**	6.65	12.52**
CMS4611A × YL 581	46.18	20.97**	20.29*	16.48*	-6.42	57.06	27.19**	13.76**	4.05	9.79*
CMS4611A × SL 473	37.56	-4.78	-7.25	-5.27	-23.89**	54.53	7.07	5.47	-0.57	4.91
CMS4611A × IS 262	44.51	13.73	11.59	12.27	-9.80	51.82	5.06	3.31	-5.51	-0.31
CMS4611A × VR 521	41.93	2.76	-2.98	5.77	-15.02*	47.14	-2.45	-6.01	-14.03**	-9.30*
CMS4611A × FL 201	44.76	34.07**	16.58*	12.89	-9.30	53.67	19.70**	7.00	-2.13	3.26
CMS4611A × PP 402	43.28	25.18**	12.74	9.16	-12.29	53.23	14.32**	6.11	-2.94	2.40
CMS4611A × C 142	42.89	1.77	-6.56	8.18	-13.08*	55.79	10.09**	8.98*	1.74	7.34
CMS4611A × PP 414	37.01	-8.43	-12.80	-6.64	-24.99**	50.78	10.41*	1.23	-7.41	-2.31
CMS4611A × VR 522	49.48	35.23**	28.89**	24.80**	0.27	55.16	8.67*	7.40	0.59	6.13
CMS4611A × PL 406	49.88	15.31*	3.65	25.81**	1.08	62.53	20.63**	16.84**	14.03**	20.31**
CMS4611A × E 183	35.42	-10.27	-12.68	-10.65	-28.21**	51.93	9.41*	3.53	-5.31	-0.09
CMS4611A × IS 268	42.80	21.80**	11.49	7.96	-13.26*	58.99	34.64**	17.61**	7.57	13.50**
CMS4611A × IS 261	55.83	30.18**	17.82**	40.83**	13.15*	66.49	22.86**	14.49**	21.23**	27.91**

Crosses	**Plant spread (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	39.99	9.89	4.26	0.87	-18.96**	45.68	-2.52	-8.38	-16.70**	-12.11**
CMS4626A × SL 475	49.56	22.48**	6.57	25.00**	0.43	58.53	18.84**	7.12	6.73	12.62**
CMS4626A × PL 412	50.89	31.14**	17.83*	28.36**	3.13	55.67	18.69**	11.47**	1.51	7.10
CMS4626A × IS 263	46.38	34.99**	34.73**	16.98*	-6.01	55.49	22.26**	18.30**	1.18	6.75
CMS4626A × VR 523	49.46	24.85**	10.39	24.75**	0.23	59.12	22.86**	12.88**	7.80	13.74**
CMS4626A × DL 161	40.89	7.74	-1.42	3.14	-17.14**	49.35	3.90	-3.48	-10.02*	-5.06
CMS4626A × IS 267	48.54	41.53**	41.03**	22.45**	-1.62	50.75	21.31**	15.70**	-7.46	-2.36
CMS4626A × YL 581	40.38	11.58	6.38	1.85	-18.17**	47.82	14.63**	9.02	-12.80**	-7.99
CMS4626A × SL 473	44.18	17.95*	9.11	11.43	-10.47	49.90	4.43	-3.48	-9.01*	-4.00
CMS4626A × IS 262	37.01	-0.39	-7.21	-6.64	-24.99**	47.14	2.08	-2.78	-14.04**	-9.30*
CMS4626A × VR 521	48.44	24.79**	12.08	22.20**	-1.82	49.43	9.40*	6.31	-9.87*	-4.91
CMS4626A × FL 201	39.54	25.94**	14.88	-0.25	-19.86**	48.44	16.18**	10.42*	-11.68**	-6.81
CMS4626A × PP 402	40.40	23.97**	17.37	1.91	-18.13**	50.10	15.42**	14.22**	-8.64*	-3.60
CMS4626A × C 142	51.71	28.76**	12.66	30.44**	4.80	55.90	17.61**	9.19*	1.94	7.55
CMS4626A × PP 414	38.18	-0.66	-10.05	-3.70	-22.63**	51.58	20.39**	17.59**	-5.94	-0.76
CMS4626A × VR 522	48.86	41.18**	40.43**	23.23**	-0.99	55.67	16.93**	8.39*	1.52	7.11
CMS4626A × PL 406	50.39	22.09**	4.71	27.10**	2.12	54.90	12.75**	2.58	0.11	5.63
CMS4626A × E 183	38.84	3.60	-4.24	-2.02	-21.28**	46.13	4.10	3.05	-15.88**	-11.25**
CMS4626A × IS 268	43.42	30.97**	26.15**	9.53	-12.00	50.30	23.69**	14.68**	-8.27*	-3.22
CMS4626A × IS 261	50.68	23.89**	6.94	27.83**	2.70	62.99	23.59**	8.48*	14.86**	21.19**
CMS463D13A × AC 102	45.34	17.02*	15.84	14.38	-8.11	61.59	21.07**	18.69**	12.31**	18.50**
CMS463D13A × SL 475	55.71	30.10**	19.81**	40.53**	12.90*	68.56	28.71**	25.47**	25.02**	31.91**

Crosses	**Plant spread (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	45.52	10.58	5.40	14.83	-7.75	56.85	11.65**	9.55*	3.66	9.37*
CMS463D13A × IS 263	38.83	5.77	-0.79	-2.05	-21.30**	61.55	24.61**	18.62**	12.24**	18.43**
CMS463D13A × VR 523	48.48	15.50*	8.21	22.28**	-1.76	67.06	28.63**	28.04**	22.28**	29.01**
CMS463D13A × DL 161	51.10	26.76**	23.20**	28.89**	3.56	60.99	18.41**	17.54**	11.22**	17.35**
CMS463D13A × IS 267	48.42	32.08**	23.70**	22.14**	-1.87	58.17	26.87**	12.10**	6.07	11.92**
CMS463D13A × YL 581	42.39	9.96	8.29	6.92	-14.10*	54.23	18.59**	4.51	-1.11	4.34
CMS463D13A × SL 473	45.84	15.14*	13.23	15.64	-7.09	59.48	14.84**	14.63**	8.47*	14.44**
CMS463D13A × IS 262	41.83	5.86	4.88	5.52	-15.22*	51.69	3.00	-0.38	-5.74	-0.54
CMS463D13A × VR 521	54.62	32.63**	26.37**	37.78**	10.69	61.99	26.01**	19.45**	13.03**	19.26**
CMS463D13A × FL 201	43.83	29.83**	11.98	10.57	-11.17	56.87	24.42**	9.59*	3.70	9.41*
CMS463D13A × PP 402	42.29	21.00**	8.03	6.67	-14.30*	54.80	15.56**	5.61	-0.07	5.44
CMS463D13A × C 142	49.48	16.36*	7.79	24.80**	0.27	60.86	18.08**	17.28**	10.98**	17.09**
CMS463D13A × PP 414	41.54	1.84	-2.12	4.79	-15.81*	54.36	16.01**	4.76	-0.88	4.59
CMS463D13A × VR 522	44.49	20.35**	13.65	12.22	-9.84	58.76	13.81**	13.23**	7.14	13.05**
CMS463D13A × PL 406	50.17	14.97*	4.25	26.54**	1.67	65.42	24.12**	22.23**	19.29**	25.87**
CMS463D13A × E 183	40.62	1.92	0.14	2.47	-17.68**	53.35	10.39**	2.81	-2.72	2.64
CMS463D13A × IS 268	39.27	10.56	0.31	-0.95	-20.42**	59.55	33.27**	14.75**	8.59*	14.57**
CMS463D13A × IS 261	56.62	30.87**	19.48**	42.82**	14.75*	66.47	20.89**	14.46**	21.20**	27.88**
LSD at *p*=0.05		5.50	6.35	6.35	6.35		3.72	4.29	4.29	4.29
LSD at *p*=0.01		7.28	8.40	8.40	8.40		4.89	5.65	5.65	5.65

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.12c: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for number of primary branches plant^{-1} evaluated over environments**

Crosses	Number of primary branches plant^{-1}									
	E$_1$					E$_2$				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	4.67	20.00**	10.53	6.60	40.00**	4.03	-28.68**	-32.90**	-29.09**	-17.87**
CMS4611A × SL 475	4.78	19.45**	7.51	9.14	43.34**	6.39	20.06**	19.58**	12.32*	30.10**
CMS4611A × PL 412	5.00	23.45**	10.02	14.21	49.99**	7.36	52.70**	38.78**	29.30**	49.77**
CMS4611A × IS 263	4.84	34.16**	32.13**	10.67	45.34**	6.60	52.33**	24.54**	16.03**	34.39**
CMS4611A × VR 523	5.00	36.36**	32.36**	14.22	50.00**	9.32	55.81**	39.84**	63.88**	89.82**
CMS4611A × DL 161	4.33	4.00	-9.31	-1.01	30.00**	5.69	17.70**	7.34	0.01	15.84*
CMS4611A × IS 267	5.83	38.88**	20.40**	33.24**	74.99**	4.36	-2.49	-17.82**	-23.43**	-11.31
CMS4611A × YL 581	4.56	17.15*	7.90	4.07	36.67**	5.67	-2.77	-10.84*	-0.39	15.37*
CMS4611A × SL 473	4.67	28.44**	25.75**	6.60	40.00**	4.68	-2.72	-11.72	-17.75**	-4.73
CMS4611A × IS 262	4.84	32.12**	28.23**	10.67	45.34**	4.69	-2.62	-11.53	-17.57**	-4.53
CMS4611A × VR 521	5.38	42.35**	34.44**	22.84**	61.33**	6.39	42.25**	20.49**	12.25*	30.02**
CMS4611A × FL 201	3.96	-5.82	-18.35*	-9.64	18.67	7.31	51.10**	37.95**	28.53**	48.87**
CMS4611A × PP 402	4.78	36.50**	34.37**	9.14	43.33**	5.69	22.60**	7.34	0.01	15.84*
CMS4611A × C 142	4.67	37.71**	31.25**	6.60	40.00**	5.39	11.88*	1.67	-5.27	9.72
CMS4611A × PP 414	4.16	2.60	-8.56	-5.08	24.66*	6.12	53.54**	15.50*	7.61	24.65**
CMS4611A × VR 522	4.71	11.58	-3.63	7.61	41.33**	4.72	-4.81	-10.90	-16.99**	-3.85
CMS4611A × PL 406	5.96	35.01**	13.08*	36.05**	78.67**	5.67	9.22	6.92	-0.38	15.39*
CMS4611A × E 183	4.68	25.66**	20.28*	6.85	40.33**	6.36	3.25	-9.35*	11.73*	29.41**
CMS4611A × IS 268	3.78	-4.23	-12.82	-13.71	13.33	7.67	71.22**	44.66**	34.78**	56.11**
CMS4611A × IS 261	4.22	11.77	5.56	-3.55	26.67*	5.32	6.91	0.42	-6.45	8.36

Crosses	**Number of primary branches plant^{-1}**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	3.33	-14.28	-21.05*	-23.86**	0.00	4.30	-14.56**	-28.47**	-24.41**	-12.45
CMS4626A × SL 475	4.84	21.11**	9.00	10.66	45.33**	6.39	35.96**	19.56**	12.31*	30.08**
CMS4626A × PL 412	5.00	23.45**	10.02	14.21	49.99**	5.38	28.23**	24.10**	-5.46	9.50
CMS4626A × IS 263	3.56	-1.54	-3.03	-18.78*	6.67	4.71	26.98**	16.20*	-17.18**	-4.07
CMS4626A × VR 523	3.96	7.88	4.71	-9.64	18.67	8.67	61.68**	30.01**	52.36**	76.47**
CMS4626A × DL 161	5.84	40.26**	22.32**	33.50**	75.33**	4.31	2.39	-1.27	-24.21**	-12.22
CMS4626A × IS 267	4.04	-3.71	-16.52*	-7.61	21.33*	5.32	38.47**	31.28**	-6.43	8.38
CMS4626A × YL 581	4.17	7.14	-1.31	-4.82	25.00*	4.37	-16.11**	-31.29**	-23.24**	-11.09
CMS4626A × SL 473	4.04	11.31	8.98	-7.61	21.33*	4.64	10.92	7.52	-18.35**	-5.43
CMS4626A × IS 262	5.17	40.91**	36.77**	18.03*	55.01**	5.30	26.43**	22.41**	-6.83	7.92
CMS4626A × VR 521	4.18	10.59	4.45	-4.56	25.34*	4.38	13.24	7.98	-23.04**	-10.86
CMS4626A × FL 201	4.82	14.80*	-0.47	10.15	44.66**	4.73	12.27	8.12	-16.79**	-3.62
CMS4626A × PP 402	3.72	6.35	4.69	-14.97	11.67	5.73	42.71**	41.41**	0.79	16.74*
CMS4626A × C 142	4.22	24.59**	18.74	-3.56	26.66*	4.62	10.22	6.68	-18.75**	-5.88
CMS4626A × PP 414	3.56	-12.21	-21.76**	-18.78*	6.67	4.68	39.04**	15.37	-17.77**	-4.75
CMS4626A × VR 522	5.16	22.10**	5.45	17.76*	54.66**	5.01	15.44*	8.35	-11.97*	1.97
CMS4626A × PL 406	5.52	25.18**	4.85	26.14**	65.66**	6.00	31.41**	18.18**	5.47	22.17**
CMS4626A × E 183	4.33	16.41*	11.43	-1.01	30.00**	7.67	38.63**	9.40*	34.84**	56.18**
CMS4626A × IS 268	4.13	4.80	-4.61	-5.57	24.01*	4.30	11.54	6.06	-24.41**	-12.44
CMS4626A × IS 261	4.17	10.29	4.17	-4.82	25.00*	7.71	77.07**	65.64**	35.56**	57.01**
CMS463D13A × AC 102	5.16	26.09**	22.11**	17.77*	54.67**	5.34	0.22	-11.09*	-6.04	8.83
CMS463D13A × SL 475	4.33	3.17	-2.50	-1.01	30.00**	8.46	69.13**	58.25**	48.64**	72.17**

Crosses	**Number of primary branches plant^{-1}**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	5.16	21.31**	13.45	17.77*	54.67**	4.91	9.27	5.49	-13.67*	0.00
CMS463D13A × IS 263	5.00	31.20**	26.41**	14.22	50.01**	4.98	24.11**	6.92	-12.49*	1.36
CMS463D13A × VR 523	4.94	27.87**	24.99**	12.94	48.33**	5.64	-0.29	-15.33**	-0.77	14.93*
CMS463D13A × DL 161	5.36	22.63**	12.08	22.33**	60.65**	5.00	10.81	7.38	-12.12*	1.79
CMS463D13A × IS 267	6.96	58.07**	43.57**	58.88**	108.66**	5.78	39.42**	24.11**	1.57	17.65**
CMS463D13A × YL 581	5.84	42.93**	38.43**	33.50**	75.33**	5.37	-2.52	-15.56**	-5.66	9.27
CMS463D13A × SL 473	4.61	20.29**	16.57	5.33	38.33**	4.71	4.98	1.20	-17.18**	-4.07
CMS463D13A × IS 262	4.48	15.80*	13.20	2.28	34.33**	3.74	-16.65**	-19.57**	-34.18**	-23.76**
CMS463D13A × VR 521	5.43	36.58**	35.82**	24.11**	62.99**	5.70	36.89**	22.51**	0.26	16.13*
CMS463D13A × FL 201	5.54	26.00**	14.44*	26.65**	66.33**	6.70	48.34**	43.91**	17.78**	36.42**
CMS463D13A × PP 402	5.00	35.23**	26.49**	14.29	50.10**	4.30	-0.42	-7.63	-24.41**	-12.44
CMS463D13A × C 142	5.84	62.86**	47.75**	33.51**	75.34**	4.29	-4.57	-7.88	-24.61**	-12.67
CMS463D13A × PP 414	5.84	37.51**	28.61**	33.50**	75.33**	4.00	9.16	-14.07*	-29.67**	-18.54**
CMS463D13A × VR 522	4.13	-6.52	-15.44*	-5.57	24.01*	8.63	86.14**	85.47**	51.79**	75.82**
CMS463D13A × PL 406	6.68	44.82**	26.79**	52.54**	100.33**	5.61	15.32**	10.53	-1.35	14.26*
CMS463D13A × E 183	4.94	26.03**	24.97**	12.92	48.30**	6.59	12.96**	-6.02	15.83**	34.17**
CMS463D13A × IS 268	5.16	24.39**	18.97*	17.76*	54.66**	7.54	81.53**	62.04**	32.61**	53.60**
CMS463D13A × IS 261	5.04	26.81**	26.11**	15.23	51.33**	5.48	17.74**	17.74*	-3.64	11.61
LSD at p=0.05		0.59	0.68	0.68	0.68		0.55	0.63	0.63	0.63
LSD at p=0.01		0.77	0.89	0.89	0.89		0.72	0.84	0.84	0.84

Table 4.12c (*Cont'd.*)

Crosses	Number of primary branches plant^{-1}									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	6.66	53.59**	53.58**	73.12**	16.76*	5.12	10.65**	5.42	10.39*	10.12*
CMS4611A × SL 475	7.18	72.04**	65.65**	86.72**	25.93**	6.11	35.95**	32.95**	31.88**	31.56**
CMS4611A × PL 412	6.81	72.68**	57.18**	77.17**	19.49**	6.39	49.61**	45.32**	37.78**	37.44**
CMS4611A × IS 263	4.63	11.05	6.92	20.52	-18.72**	5.36	32.70**	21.91**	15.58**	15.30**
CMS4611A × VR 523	5.17	10.58	3.10	34.39**	-9.36	6.50	36.07**	26.10**	40.10**	39.76**
CMS4611A × DL 161	5.57	28.29**	28.13**	44.79**	-2.35	5.20	16.87**	15.57**	12.06*	11.79*
CMS4611A × IS 267	5.19	17.33*	15.02	34.97**	-8.97	5.13	17.48**	16.59**	10.54*	10.27*
CMS4611A × YL 581	4.56	-15.81*	-29.79**	18.50	-20.08**	4.93	-2.31	-13.41**	6.23	5.97
CMS4611A × SL 473	4.38	7.07	1.03	13.88	-23.19**	4.57	9.51*	4.05	-1.34	-1.58
CMS4611A × IS 262	4.33	-0.76	-1.52	12.72	-23.98**	4.62	7.93	5.14	-0.31	-0.56
CMS4611A × VR 521	7.33	37.35**	15.58*	90.76**	28.65**	6.37	40.36**	36.19**	37.28**	36.95**
CMS4611A × FL 201	5.34	30.89**	23.34*	39.03**	-6.23	5.54	26.59**	25.95**	19.42**	19.13**
CMS4611A × PP 402	4.82	6.90	2.85	25.44*	-15.40*	5.10	20.85**	15.92**	9.91*	9.64*
CMS4611A × C 142	5.68	17.60*	6.68	47.69**	-0.39	5.24	20.72**	19.29**	13.10**	12.82**
CMS4611A × PP 414	4.84	11.79	11.78	26.01*	-15.01*	5.04	22.24**	14.65**	8.70	8.44
CMS4611A × VR 522	7.00	64.91**	61.53**	82.08**	22.80**	5.48	22.38**	20.24**	18.13**	17.84**
CMS4611A × PL 406	4.18	-7.05	-10.26	8.67	-26.71**	5.27	12.11**	5.34	13.58**	13.31**
CMS4611A × E 183	7.37	55.27**	42.88**	91.62**	29.24**	6.13	25.83**	14.60**	32.27**	31.95**
CMS4611A × IS 268	4.81	15.31	11.02	25.15*	-15.60*	5.42	29.07**	23.25**	16.86**	16.57**
CMS4611A × IS 261	5.16	12.35	6.43	34.11**	-9.55	4.90	10.16*	8.89	5.67	5.42

Crosses	**Number of primary branches plant^{-1}**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	4.83	10.98	10.42	25.73*	-15.20*	4.16	-6.10	-14.41**	-10.38*	-10.60*
CMS4626A × SL 475	8.00	90.74**	82.76**	108.10**	40.35**	6.41	49.17**	39.38**	38.26**	37.92**
CMS4626A × PL 412	5.32	34.19**	21.59*	38.45**	-6.63	5.23	28.58**	26.27**	12.86**	12.59**
CMS4626A × IS 263	4.68	11.53	6.86	21.68*	-17.94*	4.31	12.41*	7.98	-6.94	-7.17
CMS4626A × VR 523	6.03	28.53**	20.40*	56.94**	5.85	6.22	35.96**	20.71**	34.11**	33.79**
CMS4626A × DL 161	4.98	14.14	13.71	29.48**	-12.67	5.04	18.80**	12.19*	8.79	8.52
CMS4626A × IS 267	7.01	57.76**	55.42**	82.37**	23.00**	5.46	31.15**	26.09**	17.74**	17.45**
CMS4626A × YL 581	4.84	-10.84	-25.35**	26.01*	-15.01*	4.46	-7.91*	-21.61**	-3.83	-4.07
CMS4626A × SL 473	4.16	1.09	-5.06	8.10	-27.09**	4.28	7.65	7.15	-7.66	-7.89
CMS4626A × IS 262	4.50	2.54	2.27	17.06	-21.05**	4.99	22.20**	19.66**	7.60	7.33
CMS4626A × VR 521	6.98	30.16**	9.98	81.51**	22.42**	5.18	19.44**	10.78*	11.67*	11.40*
CMS4626A × FL 201	4.83	17.72*	10.41	25.72*	-15.21*	4.80	14.91**	10.21*	3.44	3.18
CMS4626A × PP 402	7.49	65.21**	59.73**	94.81**	31.39**	5.65	40.61**	39.88**	21.81**	21.52**
CMS4626A × C 142	6.66	37.23**	25.05**	73.12**	16.76*	5.17	24.67**	20.36**	11.42*	11.15*
CMS4626A × PP 414	4.81	10.46	9.91	25.15*	-15.60*	4.35	10.83*	8.82	-6.23	-6.45
CMS4626A × VR 522	5.52	29.43**	26.16**	43.65**	-3.12	5.23	22.29**	14.78**	12.76**	12.49**
CMS4626A × PL 406	7.17	58.69**	53.95**	86.43**	25.74**	6.23	38.51**	24.60**	34.35**	34.02**
CMS4626A × E 183	5.02	5.37	-2.59	30.64**	-11.89	5.68	21.43**	6.04	22.40**	22.10**
CMS4626A × IS 268	5.98	42.52**	36.56**	55.49**	4.87	4.80	20.16**	20.09**	3.60	3.35
CMS4626A × IS 261	5.56	20.49**	14.68	44.52**	-2.53	5.81	36.80**	29.14**	25.33**	25.02**
CMS463D13A × AC 102	3.56	-11.24	-17.95	-7.52	-37.63**	4.69	4.68	-3.50	1.04	0.80
CMS463D13A × SL 475	5.54	44.22**	38.23**	44.22**	-2.73	6.11	40.55**	32.86**	31.79**	31.47**

Crosses	**Number of primary branches plant^{-1}**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	5.49	51.78**	49.25**	42.78**	-3.70	5.19	25.85**	25.12**	11.83*	11.56*
CMS463D13A × IS 263	4.32	12.43	7.75	12.43	-24.18**	4.77	22.58**	16.37**	2.80	2.55
CMS463D13A × VR 523	5.34	23.03**	6.66	39.03**	-6.23	5.31	14.86**	3.10	14.54**	14.26**
CMS463D13A × DL 161	5.50	37.12**	26.60**	43.07**	-3.51	5.28	23.00**	17.53**	13.97**	13.69**
CMS463D13A × IS 267	5.50	34.33**	21.92*	43.07**	-3.51	6.08	44.26**	40.38**	31.08**	30.76**
CMS463D13A × YL 581	6.04	18.90**	-6.85	57.23**	6.04	5.75	17.56**	1.11	24.04**	23.74**
CMS463D13A × SL 473	5.01	33.23**	30.34**	30.34**	-12.09	4.78	18.63**	16.63**	3.04	2.78
CMS463D13A × IS 262	4.01	-0.69	-8.84	4.34	-29.63**	4.08	-1.33	-2.20	-12.06*	-12.27**
CMS463D13A × VR 521	6.49	29.49**	2.27	68.79**	13.84	5.88	33.98**	25.69**	26.71**	26.40**
CMS463D13A × FL 201	4.50	19.82*	17.39	17.06	-21.05**	5.58	32.13**	28.25**	20.37**	20.08**
CMS463D13A × PP 402	7.83	87.25**	67.06**	103.75**	37.42**	5.71	40.45**	39.45**	23.19**	22.89**
CMS463D13A × C 142	4.19	-6.91	-21.29**	8.97	-26.51**	4.77	13.82**	11.22*	2.96	2.71
CMS463D13A × PP 414	6.00	49.80**	38.46**	56.08**	5.27	5.28	32.92**	28.94**	13.91**	13.63**
CMS463D13A × VR 522	5.17	31.91**	24.33*	34.40**	-9.36	5.98	38.20**	31.24**	28.93**	28.62**
CMS463D13A × PL 406	7.19	72.54**	54.43**	87.00**	26.12**	6.49	42.76**	29.86**	40.03**	39.68**
CMS463D13A × E 183	4.81	8.93	-6.69	25.15*	-15.60*	5.45	15.32**	1.79	17.49**	17.20**
CMS463D13A × IS 268	6.89	79.19**	71.74**	79.19**	20.85**	6.53	61.29**	59.39**	40.81**	40.47**
CMS463D13A × IS 261	6.01	41.07**	24.08**	56.36**	5.46	5.51	28.25**	22.49**	18.88**	18.59**
LSD at p=0.05		0.69	0.79	0.79	0.79		0.37	0.43	0.43	0.43
LSD at p=0.01		0.91	1.05	1.05	1.05		0.49	0.56	0.56	0.56

*, significant at p=0.05; **, significant at p=0.01

Table 4.12d: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for fruit weight (g) evaluated over environments

Crosses	Fruit weight (g)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	5.16	32.68**	4.03	39.17**	56.78**	2.53	-32.35**	-46.77**	-34.17**	-19.77
CMS4611A × SL 475	4.61	0.07	-27.89**	24.26*	39.98**	6.33	61.27**	23.55**	64.70**	100.74**
CMS4611A × PL 412	4.79	8.09	-20.74**	29.11*	45.45**	4.08	-10.29	-35.96**	6.24	29.49**
CMS4611A × IS 263	3.16	-24.88**	-43.50**	-14.82	-4.05	2.68	1.90	-1.83	-30.36**	-15.12
CMS4611A × VR 523	4.65	29.13**	6.17	25.25*	41.09**	2.42	-25.47**	-35.83**	-36.95**	-23.15*
CMS4611A × DL 161	4.28	34.49**	20.81	15.27	29.86*	2.77	-23.00**	-38.05**	-27.84**	-12.05
CMS4611A × IS 267	3.70	-18.87*	-41.26**	-0.36	12.25	2.95	-21.07**	-37.91**	-23.16**	-6.34
CMS4611A × YL 581	5.24	-6.06	-37.16**	41.33**	59.21**	5.88	10.33	-25.86**	52.91**	86.36**
CMS4611A × SL 473	4.10	20.45	2.75	10.60	24.60	2.80	-5.62	-12.68	-27.15**	-11.21
CMS4611A × IS 262	4.77	-8.16	-36.95**	28.48*	44.74**	2.75	-28.14**	-44.18**	-28.45**	-12.79
CMS4611A × VR 521	2.82	16.31	-0.12	-24.08	-14.47	1.40	-32.10*	-48.53**	-63.49**	-55.50**
CMS4611A × FL 201	5.33	-31.84**	-58.42**	43.58**	61.74**	3.87	-49.14**	-69.02**	0.78	22.83*
CMS4611A × PP 402	4.76	-25.07**	-51.84**	28.21*	44.43**	4.80	-17.62**	-46.23**	24.89**	52.22**
CMS4611A × C 142	4.78	35.83**	13.37	28.75*	45.04**	3.08	-0.59	-11.31	-19.77*	-2.22
CMS4611A × PP 414	2.98	-14.71	-28.45**	-19.77	-9.62	2.78	0.36	-1.07	-27.75**	-11.95
CMS4611A × VR 522	4.21	-13.32	-38.93**	13.48	27.83*	2.50	-41.12**	-56.66**	-34.87**	-20.61*
CMS4611A × PL 406	5.73	29.95**	-4.45	54.36**	73.89**	4.32	28.03**	7.47	12.32	36.89**
CMS4611A × E 183	3.69	-0.14	-19.30	-0.45	12.15	1.81	-41.64**	-47.94**	-52.91**	-42.60**
CMS4611A × IS 268	4.90	-3.98	-33.68**	32.17**	48.89**	6.25	43.62**	4.57	62.62**	98.20**
CMS4611A × IS 261	4.13	-8.02	-32.94**	11.23	25.30	6.93	55.60**	12.14*	80.23**	119.66**

Crosses	**Fruit weight (g)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	5.19	4.36	4.22	39.80**	57.49**	2.90	-30.10**	-38.92**	-24.46**	-7.93
CMS4626A × SL 475	7.11	25.07**	11.21	91.64**	115.89**	5.71	31.54**	11.39	48.48**	80.97**
CMS4626A × PL 412	6.16	11.80	1.93	66.04**	87.04**	4.63	-6.75	-27.39**	20.47*	46.83**
CMS4626A × IS 263	4.99	-5.52	-10.73	34.59**	51.62**	3.70	21.82*	4.22	-3.64	17.44
CMS4626A × VR 523	5.28	12.83	6.03	42.23**	60.22**	3.83	4.50	1.41	-0.35	21.46*
CMS4626A × DL 161	3.62	-14.99	-27.26**	-2.43	9.92	4.40	9.59	-1.71	14.48	39.53**
CMS4626A × IS 267	6.34	12.57	0.79	70.98**	92.61**	4.28	3.01	-10.02	11.36	35.73**
CMS4626A × YL 581	6.84	2.75	-17.98**	84.46**	107.79**	5.42	-5.52	-31.58**	41.11**	71.99**
CMS4626A × SL 473	4.20	-6.43	-15.67	13.12	27.43*	4.71	39.25**	32.46**	22.46**	49.26**
CMS4626A × IS 262	6.36	1.46	-15.87**	71.43**	93.12**	4.43	4.48	-10.08	15.26	40.49**
CMS4626A × VR 521	4.68	33.62**	-6.03	26.06*	42.00**	2.50	0.94	-29.55**	-34.87**	-20.61*
CMS4626A × FL 201	7.23	-18.74**	-43.59**	94.79**	119.43**	9.23	14.93**	-26.21**	140.07**	192.60**
CMS4626A × PP 402	10.16	36.85**	2.90	173.94**	208.60**	9.98	59.88**	11.76**	159.58**	216.38**
CMS4626A × C 142	5.79	26.08**	16.41	56.15**	75.91**	5.12	45.76**	44.18**	33.30**	62.47**
CMS4626A × PP 414	3.64	-20.25*	-26.79**	-1.80	10.63	3.93	23.48**	10.51	2.17	24.52*
CMS4626A × VR 522	6.93	16.71*	0.48	86.70**	110.32**	5.98	28.19**	3.52	55.59**	89.64**
CMS4626A × PL 406	6.09	11.09	1.67	64.24**	85.02**	5.53	46.01**	37.59**	43.80**	75.26**
CMS4626A × E 183	3.64	-23.73**	-26.79**	-1.80	10.63	3.10	-11.81	-12.76	-19.34*	-1.69
CMS4626A × IS 268	6.69	8.22	-9.47	80.41**	103.24**	6.05	26.90**	1.17	57.33**	91.75**
CMS4626A × IS 261	6.23	11.89	1.19	67.83**	89.07**	6.98	43.41**	12.95*	81.53**	121.25**
CMS463D13A × AC 102	7.46	35.43**	23.24**	101.08**	126.52**	5.82	13.04*	4.92	51.52**	84.67**
CMS463D13A × SL 475	8.87	42.47**	38.69**	138.99**	169.23**	5.56	4.25	0.24	44.75**	76.43**

Crosses	**Fruit weight (g)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	7.96	31.61**	31.50**	114.56**	141.70**	6.47	8.55	1.52	68.43**	105.29**
CMS463D13A × IS 263	6.28	7.78	3.69	69.18**	90.59**	4.80	18.86**	-13.51*	24.89**	52.22**
CMS463D13A × VR 523	8.52	63.37**	40.75**	129.65**	158.70**	6.12	31.17**	10.21	59.15**	93.97**
CMS463D13A × DL 161	5.56	15.91	-8.15	49.87**	68.83**	4.17	-16.76**	-24.80**	8.59	32.35**
CMS463D13A × IS 267	9.34	51.35**	48.46**	151.84**	183.70**	6.18	19.86**	11.29	60.71**	95.88**
CMS463D13A × YL 581	11.98	66.47**	43.63**	223.00**	263.87**	7.78	15.41**	-1.89	102.34**	146.62**
CMS463D13A × SL 473	8.34	66.09**	37.83**	124.89**	153.34**	5.81	32.62**	4.62	51.08**	84.14**
CMS463D13A × IS 262	9.13	34.08**	20.72**	146.00**	177.13**	5.03	-3.91	-9.31	30.96**	59.62**
CMS463D13A × VR 521	4.15	2.68	-31.50**	11.77	25.91	2.12	-39.05**	-61.80**	-44.84**	-32.77**
CMS463D13A × FL 201	12.38	31.22**	-3.38	233.60**	275.81**	10.65	18.02**	-14.80**	177.19**	237.84**
CMS463D13A × PP 402	12.13	52.25**	22.78**	226.86**	268.22**	9.13	26.18**	2.32	137.64**	189.64**
CMS463D13A × C 142	7.38	43.70**	21.86**	98.83**	123.99**	5.67	25.70**	2.22	47.61**	79.92**
CMS463D13A × PP 414	6.21	21.61**	2.59	67.39**	88.56**	4.66	11.61	-15.98**	21.34*	47.89**
CMS463D13A × VR 522	9.99	54.38**	44.97**	169.36**	203.44**	6.88	21.42**	19.04**	78.92**	118.08**
CMS463D13A × PL 406	8.88	47.37**	46.64**	139.26**	169.53**	5.60	17.00**	0.84	45.62**	77.48**
CMS463D13A × E 183	4.61	-13.26	-23.84**	24.26*	39.98**	2.60	-42.32**	-53.09**	-32.26**	-17.44
CMS463D13A × IS 268	10.09	50.02**	36.43**	171.88**	206.28**	7.58	31.58**	26.88**	97.31**	140.49**
CMS463D13A × IS 261	8.64	41.62**	40.47**	132.97**	162.45**	6.35	8.36	2.86	65.31**	101.48**
LSD at p=0.05		0.77	0.89	0.89	0.89		0.55	0.64	0.64	0.64
LSD at p=0.01		1.02	1.18	1.18	1.18		0.73	0.84	0.84	0.84

Table 4.12d (*Cont'd.*)

Crosses	Fruit weight (g)									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	2.87	-6.27	-12.69	-23.83**	-15.27	3.52	-1.22	-18.77**	-6.69	7.43
CMS4611A × SL 475	4.12	4.88	-17.94**	9.39	21.67*	5.02	20.87**	-8.93*	33.05**	53.17**
CMS4611A × PL 412	3.25	-9.09	-24.71**	-13.64	-3.94	4.04	-3.46	-27.56**	7.13	23.33**
CMS4611A × IS 263	2.78	-13.70	-23.04**	-26.04**	-17.73*	2.87	-14.30**	-26.55**	-23.83**	-12.31
CMS4611A × VR 523	4.02	19.60**	3.43	6.73	18.72*	3.70	8.60	-7.89	-2.03	12.78*
CMS4611A × DL 161	3.52	12.53	2.93	-6.55	3.94	3.52	6.66	-7.58	-6.63	7.49
CMS4611A × IS 267	3.70	1.14	-17.47**	-1.68	9.36	3.45	-13.44**	-33.37**	-8.54	5.29
CMS4611A × YL 581	3.52	-15.09*	-35.47**	-6.55	3.94	4.88	-2.75	-32.61**	29.34**	48.90**
CMS4611A × SL 473	4.02	20.80**	5.24	6.73	18.72*	3.64	12.60*	-0.88	-3.51	11.09
CMS4611A × IS 262	3.65	6.05	-9.88	-3.01	7.88	3.72	-10.37*	-32.47**	-1.33	13.60*
CMS4611A × VR 521	2.65	-3.93	-6.47	-29.58**	-21.67*	2.29	-5.20	-18.02*	-39.29**	-30.11**
CMS4611A × FL 201	4.18	-17.02**	-42.30**	11.16	23.65**	4.46	-34.63**	-58.90**	18.26**	36.15**
CMS4611A × PP 402	4.08	0.62	-22.71**	8.50	20.69*	4.55	-15.98**	-43.37**	20.53**	38.76**
CMS4611A × C 142	3.38	-1.69	-16.46*	-10.10	0.00	3.75	11.76*	-4.23	-0.65	14.38*
CMS4611A × PP 414	3.48	4.24	-9.52	-7.44	2.96	3.08	-3.77	-14.61*	-18.38**	-6.04
CMS4611A × VR 522	4.42	24.12**	3.11	17.36*	30.54**	3.71	-12.13**	-34.35**	-1.65	13.22*
CMS4611A × PL 406	3.35	-3.13	-17.96*	-10.98	-0.99	4.46	19.19**	-4.97	18.35**	36.25**
CMS4611A × E 183	3.12	-3.86	-14.61	-17.18*	-7.88	2.87	-14.16**	-26.35**	-23.83**	-12.31
CMS4611A × IS 268	3.75	1.12	-18.18**	-0.35	10.84	4.97	13.19**	-16.99**	31.69**	51.61**
CMS4611A × IS 261	4.17	19.90**	1.21	10.72	23.15**	5.07	22.61**	-7.46	34.49**	54.83**

Crosses	Fruit weight (g)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4626A × AC 102	3.75	4.17	-4.26	-0.35	10.84	3.95	-6.94	-8.92	4.62	20.45**
CMS4626A × SL 475	5.60	25.37**	11.63*	48.80**	65.52**	6.14	27.10**	11.39**	62.74**	87.35**
CMS4626A × PL 412	5.35	29.96**	23.94**	42.16**	58.13**	5.38	10.61**	-3.57	42.62**	64.19**
CMS4626A × IS 263	3.72	-1.33	-5.11	-1.24	9.85	4.14	2.66	-0.27	9.69	26.28**
CMS4626A × VR 523	6.02	54.27**	53.62**	59.88**	77.83**	5.04	23.54**	21.51**	33.64**	53.85**
CMS4626A × DL 161	4.03	10.00	2.98	7.17	19.21*	4.02	0.95	-3.16	6.51	22.62**
CMS4626A × IS 267	5.45	29.76**	21.56**	44.82**	61.08**	5.36	14.89**	3.48	42.03**	63.51**
CMS4626A × YL 581	5.62	19.93**	3.06	49.25**	66.01**	5.96	4.68	-17.66**	58.03**	81.93**
CMS4626A × SL 473	4.35	12.50	11.06	15.59*	28.57**	4.42	12.97**	6.48	17.11**	34.83**
CMS4626A × IS 262	3.47	-12.97*	-14.40*	-7.88	2.46	4.75	-1.62	-13.79**	25.98**	45.03**
CMS4626A × VR 521	3.15	-4.55	-19.57**	-16.30*	-6.90	3.44	11.31	-17.01**	-8.72	5.09
CMS4626A × FL 201	6.02	7.76	-17.01**	59.88**	77.83**	7.49	-0.16	-31.00**	98.56**	128.59**
CMS4626A × PP 402	6.22	35.14**	17.67**	65.19**	83.74**	8.79	44.29**	9.42**	132.90**	168.12**
CMS4626A × C 142	4.48	12.55*	10.70	19.13*	32.51**	5.13	27.34**	23.73**	36.08**	56.66**
CMS4626A × PP 414	3.52	-9.44	-10.21	-6.55	3.94	3.70	-4.69	-10.93*	-2.03	12.78*
CMS4626A × VR 522	4.45	8.54	3.89	18.25*	31.53**	5.79	18.07**	2.38	53.37**	76.57**
CMS4626A × PL 406	5.05	26.25**	23.67**	34.19**	49.26**	5.56	25.62**	18.28**	47.30**	69.58**
CMS4626A × E 183	4.32	14.10*	10.21	14.70	27.59**	3.69	-8.41	-11.14*	-2.27	12.51
CMS4626A × IS 268	4.23	-0.39	-7.64	12.49	25.12**	5.66	11.67**	-5.46	49.99**	72.67**
CMS4626A × IS 261	4.27	6.22	3.64	13.37	26.11**	5.82	20.93**	6.22	54.37**	77.72**
CMS463D13A × AC 102	3.75	-2.60	-15.09*	-0.35	10.84	5.68	17.39**	6.33	50.52**	73.28**
CMS463D13A × SL 475	5.42	14.84**	7.97	43.93**	60.10**	6.62	21.93**	20.04**	75.38**	101.90**

Crosses	Fruit weight (g)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS463D13A × PL 412	4.88	11.83*	10.57	29.76**	44.33**	6.44	17.94**	15.42**	70.69**	96.51**
CMS463D13A × IS 263	4.05	0.83	-8.30	7.62	19.70*	5.04	8.99*	-5.58	33.67**	53.88**
CMS463D13A × VR 523	5.28	27.31**	19.62**	40.39**	56.16**	6.64	42.00**	24.34**	76.02**	102.64**
CMS463D13A × DL 161	4.92	25.53**	11.32	30.65**	45.32**	4.88	6.73	-8.55*	29.46**	49.03**
CMS463D13A × IS 267	4.57	2.62	1.86	21.35**	34.98**	6.70	27.32**	25.38**	77.50**	104.34**
CMS463D13A × YL 581	5.88	19.26**	7.95	56.33**	73.89**	8.55	35.89**	18.06**	126.60**	160.87**
CMS463D13A × SL 473	5.62	36.44**	27.17**	49.25**	66.01**	6.59	46.22**	23.39**	74.67**	101.09**
CMS463D13A × IS 262	4.68	10.63	6.04	24.45**	38.42**	6.28	15.76**	13.95**	66.51**	91.69**
CMS463D13A × VR 521	4.08	15.02*	-7.55	8.50	20.69*	3.45	-6.48	-35.39**	-8.54	5.29
CMS463D13A × FL 201	5.82	-0.29	-19.77**	54.56**	71.92**	9.62	18.75**	-11.41**	154.90**	193.46**
CMS463D13A × PP 402	5.92	21.99**	11.99*	57.22**	74.88**	9.06	35.52**	12.83**	140.15**	176.47**
CMS463D13A × C 142	5.08	20.08**	15.09*	35.08**	50.25**	6.04	30.64**	13.19**	60.24**	84.47**
CMS463D13A × PP 414	3.65	-11.69	-17.36**	-3.01	7.88	4.84	8.24*	-9.34*	28.34**	47.74**
CMS463D13A × VR 522	5.05	16.09**	14.34*	34.19**	49.26**	7.31	32.96**	29.30**	93.70**	122.99**
CMS463D13A × PL 406	5.47	28.63**	23.77**	45.26**	61.58**	6.65	32.43**	24.47**	76.20**	102.85**
CMS463D13A × E 183	3.75	-7.02	-15.09*	-0.35	10.84	3.65	-20.91**	-31.56**	-3.12	11.53
CMS463D13A × IS 268	6.42	42.59**	40.00**	70.50**	89.66**	8.03	41.80**	34.16**	112.84**	145.03**
CMS463D13A × IS 261	4.67	9.38	5.66	24.00**	37.93**	6.55	21.13**	19.56**	73.76**	100.03**
LSD at *p*=0.05		0.49	0.56	0.56	0.56		0.36	0.41	0.41	0.41
LSD at *p*=0.01		0.64	0.74	0.74	0.74		0.47	0.54	0.54	0.54

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.12e: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for fruit length (cm) evaluated over environments**

Crosses	**Fruit length (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	7.78	28.49**	7.81	13.30	9.01	5.37	-4.02	-17.22**	-13.67*	-19.94**
CMS4611A × SL 475	9.08	25.60**	-5.09	32.28**	27.28**	6.91	10.29	-11.78*	11.21	3.13
CMS4611A × PL 412	8.24	14.25*	-13.56*	20.05*	15.51*	6.61	11.49	-7.68	6.38	-1.34
CMS4611A × IS 263	7.84	9.77	-16.53**	14.22	9.90	5.99	13.55*	2.33	-3.59	-10.59
CMS4611A × VR 523	8.29	28.18**	3.07	20.78**	16.21*	5.65	-2.87	-18.48**	-9.17	-15.76*
CMS4611A × DL 161	6.71	9.32	-9.08	-2.33	-6.03	5.60	15.00*	11.19	-9.97	-16.51**
CMS4611A × IS 267	7.80	16.41*	-8.34	13.64	9.34	7.18	33.52**	18.62**	15.44*	7.06
CMS4611A × YL 581	7.81	14.05*	-11.25	13.69	9.39	7.09	14.27*	-8.01	13.99*	5.72
CMS4611A × SL 473	5.94	-0.78	-16.07*	-13.54	-16.81*	5.77	7.61	-4.26	-7.13	-13.87*
CMS4611A × IS 262	7.68	19.66**	-3.32	11.84	7.61	5.71	8.49	-2.00	-8.15	-14.82*
CMS4611A × VR 521	5.75	6.28	-3.03	-16.21*	-19.38*	6.18	44.77**	31.42**	-0.64	-7.86
CMS4611A × FL 201	9.73	14.11**	-20.00**	41.75**	36.38**	7.28	-5.23	-31.74**	17.16**	8.65
CMS4611A × PP 402	7.10	25.20**	10.14	3.35	-0.56	6.85	28.46**	14.80*	10.24	2.24
CMS4611A × C 142	8.73	38.96**	13.76*	27.18**	22.37**	5.88	19.67**	14.69	-5.42	-12.28*
CMS4611A × PP 414	6.37	7.93	-7.86	-7.18	-10.70	6.75	34.60**	26.64**	8.58	0.70
CMS4611A × VR 522	7.37	13.73	-8.67	7.38	3.32	5.74	1.20	-13.63*	-7.61	-14.32*
CMS4611A × PL 406	8.24	26.66**	1.48	20.05*	15.51*	5.68	12.55	5.32	-8.63	-15.27*
CMS4611A × E 183	6.67	11.10	-6.27	-2.82	-6.49	4.79	-1.94	-5.58	-22.90**	-28.49**
CMS4611A × IS 268	8.38	31.43**	6.66	21.99**	17.38*	5.83	12.77	3.43	-6.27	-13.08*
CMS4611A × IS 261	8.88	32.03**	3.78	29.27**	24.38**	7.06	21.41**	1.88	13.57*	5.32

Crosses	**Fruit length (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	6.95	2.25	-3.65	1.26	-2.57	6.31	9.73	-2.62	1.55	-5.82
CMS4626A × SL 475	9.97	24.99**	4.18	45.19**	39.70**	8.04	25.04**	2.59	29.33**	19.94**
CMS4626A × PL 412	8.42	5.78	-11.71*	22.62**	17.98*	7.44	22.10**	3.86	19.68**	10.99
CMS4626A × IS 263	7.63	-3.30	-18.80**	11.12	6.91	5.49	0.98	-6.20	-11.64	-18.05**
CMS4626A × VR 523	9.07	25.66**	12.68	32.04**	27.04**	6.64	11.19	-4.09	6.86	-0.90
CMS4626A × DL 161	7.84	13.91*	6.24	14.13	9.81	5.66	12.63	12.52	-8.90	-15.51*
CMS4626A × IS 267	9.24	24.10**	8.57	34.61**	29.52**	7.18	29.68**	18.68**	15.50*	7.11
CMS4626A × YL 581	7.45	-1.89	-15.35*	8.45	4.34	7.19	13.04*	-6.62	15.71*	7.31
CMS4626A × SL 473	7.21	7.21	1.98	5.05	1.07	5.80	4.95	-3.81	-6.70	-13.48*
CMS4626A × IS 262	8.78	22.52**	10.49	27.82**	22.98**	6.54	20.49**	12.19	5.15	-2.49
CMS4626A × VR 521	7.84	27.25**	22.77**	14.13	9.81	6.20	39.93**	23.36**	-0.32	-7.56
CMS4626A × FL 201	11.12	19.93**	-8.58	61.99**	55.86**	7.73	-1.44	-27.52**	24.40**	15.37*
CMS4626A × PP 402	9.90	54.42**	53.70**	44.22**	38.77**	6.30	14.55*	5.47	1.29	-6.07
CMS4626A × C 142	8.64	22.85**	12.51	25.78**	21.02**	7.08	39.44**	38.04**	13.83*	5.57
CMS4626A × PP 414	8.84	32.98**	27.86**	28.79**	23.91**	5.58	7.73	4.63	-10.29	-16.81**
CMS4626A × VR 522	8.42	16.53*	4.34	22.67**	18.03*	6.74	15.53*	1.40	8.47	0.60
CMS4626A × PL 406	8.87	22.29**	9.19	29.17**	24.29**	6.30	20.90**	16.75*	1.29	-6.07
CMS4626A × E 183	6.68	-1.06	-6.18	-2.72	-6.40	4.76	-5.81	-6.30	-23.49**	-29.04**
CMS4626A × IS 268	8.10	13.84*	3.18	18.01*	13.55	6.09	14.23*	8.05	-2.09	-9.20
CMS4626A × IS 261	10.07	34.84**	17.73**	46.65**	41.10**	7.79	30.40**	12.46*	25.36**	16.26**
CMS463D13A × AC 102	9.20	29.59**	27.44**	33.93**	28.87**	5.48	-16.62**	-17.69**	-11.90	-18.30**
CMS463D13A × SL 475	10.35	25.10**	8.15	50.73**	45.03**	8.05	11.16*	2.76	29.54**	20.14**

Crosses	**Fruit length (cm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	10.55	27.82**	10.66	53.69**	47.87**	6.91	-0.02	-3.58	11.10	3.03
CMS463D13A × IS 263	8.69	6.15	-7.52	26.55**	21.77**	6.65	6.31	-0.05	6.97	-0.80
CMS463D13A × VR 523	10.29	36.94**	27.84**	49.81**	44.14**	7.44	9.62	7.46	19.73**	11.04
CMS463D13A × DL 161	9.17	27.82**	24.36**	33.59**	28.54**	5.82	-0.34	-12.47*	-6.33	-13.13*
CMS463D13A × IS 267	10.29	32.82**	20.83**	49.81**	44.14**	7.97	25.53**	19.84**	28.26**	18.95**
CMS463D13A × YL 581	9.51	20.58**	8.11	38.50**	33.26**	8.19	14.14**	6.36	31.80**	22.23**
CMS463D13A × SL 473	9.77	39.12**	38.17**	42.33**	36.95**	6.40	0.87	-3.86	2.90	-4.57
CMS463D13A × IS 262	9.19	23.24**	15.74*	33.88**	28.82**	5.85	-6.30	-12.12*	-5.95	-12.78*
CMS463D13A × VR 521	7.38	14.33*	5.78	7.48	3.41	6.72	28.23**	1.05	8.15	0.30
CMS463D13A × FL 201	11.46	19.73**	-5.81	66.89**	60.58**	8.34	-3.71	-21.84**	34.16**	24.42**
CMS463D13A × PP 402	9.84	46.60**	40.99**	43.25**	37.83**	7.03	11.43*	5.71	13.14*	4.92
CMS463D13A × C 142	8.96	22.34**	16.76*	30.53**	25.60**	7.13	21.00**	7.11	14.64*	6.32
CMS463D13A × PP 414	7.47	7.53	7.07	8.79	4.67	6.03	0.58	-9.42	-3.06	-10.09
CMS463D13A × VR 522	9.71	28.99**	20.23**	41.36**	36.01**	7.37	10.80*	10.77	18.55**	9.95
CMS463D13A × PL 406	9.52	26.14**	17.23**	38.69**	33.44**	7.12	18.26**	7.06	14.58*	6.27
CMS463D13A × E 183	7.25	2.91	1.87	5.63	1.63	6.16	4.97	-7.46	-0.97	-8.16
CMS463D13A × IS 268	9.68	30.55**	23.26**	40.97**	35.64**	7.24	17.85**	8.82	16.46*	8.01
CMS463D13A × IS 261	10.44	34.45**	22.06**	52.04**	46.29**	7.88	15.98**	13.66*	26.70**	17.50**
LSD at p=0.05		0.91	1.05	1.05	1.05		0.70	0.81	0.81	0.81
LSD at p=0.01		1.20	1.39	1.39	1.39		0.92	1.07	1.07	1.07

Table 4.12e (*Cont'd.*)

Crosses	**Fruit length (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	5.99	24.77**	14.47	4.12	-2.07	6.38	16.35**	1.07	1.59	-4.11
CMS4611A × SL 475	7.20	25.09**	0.75	25.28**	17.83**	7.73	20.47**	-5.52	23.19**	16.27**
CMS4611A × PL 412	5.86	14.90*	0.46	1.91	-4.14	6.91	13.54**	-8.06*	10.00*	3.83
CMS4611A × IS 263	4.55	1.26	-1.45	-20.93**	-25.63**	6.13	8.69*	-7.47	-2.39	-7.87*
CMS4611A × VR 523	6.90	16.75**	-7.42	20.00**	12.87*	6.95	14.55**	-7.07*	10.65**	4.44
CMS4611A × DL 161	4.57	-20.00**	-35.22**	-20.58**	-25.30**	5.62	0.96	-13.31**	-10.42*	-15.45**
CMS4611A × IS 267	5.52	12.91	1.97	-3.94	-9.65	6.83	20.82**	2.62	8.87*	2.76
CMS4611A × YL 581	6.96	23.93**	1.41	20.99**	13.79*	7.28	17.10**	-6.46	16.02**	9.51*
CMS4611A × SL 473	5.61	7.48	-7.58	-2.49	-8.29	5.77	4.54	-9.67*	-8.05*	-13.21**
CMS4611A × IS 262	5.69	6.73	-9.59	-1.10	-6.98	6.36	12.15**	-4.90	1.29	-4.39
CMS4611A × VR 521	5.28	15.57*	10.61	-8.12	-13.58*	5.74	20.78**	18.36**	-8.60*	-13.73**
CMS4611A × FL 201	5.86	-15.45**	-38.26**	1.86	-4.20	7.62	-1.16	-29.24**	21.45**	14.63**
CMS4611A × PP 402	6.37	24.16**	8.02	10.84	4.25	6.77	25.95**	10.98**	7.91	1.85
CMS4611A × C 142	6.06	27.83**	18.42*	5.45	-0.82	6.89	29.70**	15.36**	9.79*	3.63
CMS4611A × PP 414	5.33	-2.77	-19.20**	-7.30	-12.81*	6.15	12.51**	-2.07	-2.02	-7.52
CMS4611A × VR 522	6.07	22.98**	10.22	5.62	-0.65	6.40	12.24**	-5.16	1.89	-3.83
CMS4611A × PL 406	5.84	8.38	-8.94	1.62	-4.42	6.59	16.64**	-0.84	4.96	-0.94
CMS4611A × E 183	5.40	8.14	-3.97	-6.03	-11.61	5.62	6.16	-5.35	-10.42*	-15.45**
CMS4611A × IS 268	5.28	4.83	-7.53	-8.12	-13.58*	6.50	17.53**	1.49	3.47	-2.34
CMS4611A × IS 261	5.14	-9.79	-26.91**	-10.55	-15.87*	7.03	15.57**	-6.39	11.93**	5.65

Crosses	**Fruit length (cm)**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	5.35	0.16	-1.84	-7.01	-12.54*	6.20	4.03	-1.67	-1.17	-6.72
CMS4626A × SL 475	7.12	13.10*	-0.37	23.88**	16.52*	8.38	21.39**	2.35	33.45**	25.96**
CMS4626A × PL 412	8.31	47.34**	42.46**	44.52**	35.93**	8.06	22.73**	7.26*	28.34**	21.13**
CMS4626A × IS 263	5.21	3.64	-4.28	-9.33	-14.72*	6.11	-0.13	-7.70*	-2.64	-8.10*
CMS4626A × VR 523	7.47	15.81**	0.22	29.91**	22.19**	7.73	18.02**	3.36	23.08**	16.17**
CMS4626A × DL 161	6.16	-1.47	-12.67*	7.07	0.71	6.55	8.26*	1.01	4.37	-1.49
CMS4626A × IS 267	5.86	7.82	7.53	1.86	-4.20	7.43	20.98**	11.51**	18.30**	11.66**
CMS4626A × YL 581	7.85	27.52**	14.38*	36.46**	28.35**	7.50	11.84**	-3.74	19.40**	12.70**
CMS4626A × SL 473	6.54	13.55*	7.75	13.68*	6.92	6.52	8.54*	1.98	3.81	-2.02
CMS4626A × IS 262	5.45	-7.07	-13.30*	-5.16	-10.80	6.92	12.52**	3.52	10.27*	4.08
CMS4626A × VR 521	5.29	3.49	-2.88	-8.00	-13.47*	6.44	23.09**	14.66**	2.60	-3.16
CMS4626A × FL 201	7.40	-0.94	-22.03**	28.64**	20.99**	8.75	6.77*	-18.78**	39.40**	31.57**
CMS4626A × PP 402	7.09	24.97**	20.17**	23.30**	15.98*	7.76	32.45**	27.18**	23.66**	16.72**
CMS4626A × C 142	6.24	18.04**	14.50*	8.46	2.02	7.32	26.23**	22.47**	16.55**	10.01**
CMS4626A × PP 414	6.90	14.53*	4.55	19.94**	12.81*	7.11	19.43**	13.13**	13.19**	6.83
CMS4626A × VR 522	7.44	35.75**	34.97**	29.33**	21.65**	7.53	21.89**	11.71**	20.02**	13.28**
CMS4626A × PL 406	7.65	28.91**	19.17**	32.99**	25.08**	7.60	24.03**	14.45**	21.13**	14.33**
CMS4626A × E 183	6.31	13.91*	12.09	9.68	3.16	5.91	2.34	-0.45	-5.79	-11.08**
CMS4626A × IS 268	5.72	2.57	0.18	-0.46	-6.38	6.64	10.47**	3.72	5.73	-0.20
CMS4626A × IS 261	7.66	22.78**	8.91	33.28**	25.35**	8.51	29.66**	13.35**	35.54**	27.93**
CMS463D13A × AC 102	5.56	-2.14	-9.30	-3.36	-9.11	6.74	4.58	2.40	7.42	1.39
CMS463D13A × SL 475	8.13	22.52**	13.75*	41.45**	33.04**	8.85	19.77**	8.06*	40.90**	32.99**

Crosses	**Fruit length (cm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	6.71	12.26*	9.58	16.75*	9.81	8.06	14.32**	7.28*	28.35**	21.15**
CMS463D13A × IS 263	5.19	-3.41	-15.34*	-9.80	-15.16*	6.84	3.61	3.32	8.99*	2.87
CMS463D13A × VR 523	7.58	11.63*	1.70	31.83**	23.99**	8.44	20.00**	12.86**	34.39**	26.85**
CMS463D13A × DL 161	8.18	24.11**	15.98**	42.20**	33.75**	7.72	18.18**	17.29**	23.04**	16.14**
CMS463D13A × IS 267	6.78	17.41**	10.61	17.86**	10.85	8.35	26.01**	25.31**	32.94**	25.48**
CMS463D13A × YL 581	7.46	14.94**	8.79	29.80**	22.08**	8.39	16.74**	7.73*	33.63**	26.13**
CMS463D13A × SL 473	6.45	5.80	5.28	12.17	5.51	7.54	16.22**	14.49**	20.11**	13.36**
CMS463D13A × IS 262	6.11	-1.64	-2.91	6.20	-0.11	7.05	6.22	5.42	12.28**	5.98
CMS463D13A × VR 521	5.53	1.38	-9.79	-3.88	-9.60	6.54	14.46**	-0.64	4.23	-1.62
CMS463D13A × FL 201	7.33	-6.15	-22.77**	27.42**	19.85**	9.04	4.17	-16.08**	44.04**	35.95**
CMS463D13A × PP 402	6.64	10.48	8.43	15.54*	8.67	7.84	23.53**	19.01**	24.85**	17.84**
CMS463D13A × C 142	6.07	7.94	-0.92	5.57	-0.71	7.39	17.62**	12.16**	17.66**	11.06**
CMS463D13A × PP 414	5.89	-7.47	-10.76	2.38	-3.71	6.46	0.43	-1.89	2.92	-2.86
CMS463D13A × VR 522	7.65	31.48**	24.86**	33.04**	25.14**	8.24	23.66**	22.21**	31.29**	23.92**
CMS463D13A × PL 406	7.56	20.49**	17.77**	31.42**	23.61**	8.07	21.96**	21.42**	28.51**	21.30**
CMS463D13A × E 183	5.74	-2.27	-6.26	-0.12	-6.05	6.38	1.93	-3.05	1.70	-4.01
CMS463D13A × IS 268	7.62	28.77**	24.43**	32.58**	24.70**	8.18	26.00**	24.23**	30.32**	23.00**
CMS463D13A × IS 261	7.53	14.36**	6.96	30.90**	23.12**	8.61	22.26**	14.76**	37.22**	29.52**
LSD at *p*=0.05		0.66	0.76	0.76	0.76		0.44	0.50	0.50	0.50
LSD at *p*=0.01		0.88	1.01	1.01	1.01		0.57	0.66	0.66	0.66

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.12f: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for fruit width (mm) evaluated over environments

Crosses	Fruit width (mm)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	12.61	8.34	-7.08	-2.54	26.37**	9.29	-4.51	-11.22	-18.40**	-6.06
CMS4611A × SL 475	13.03	15.00*	0.58	0.72	30.59**	10.59	10.87	4.77	-7.00	7.07
CMS4611A × PL 412	10.54	4.58	0.87	-18.54**	5.61	10.06	3.08	-4.41	-11.64	1.73
CMS4611A × IS 263	9.81	-9.32	-17.80*	-24.13**	-1.62	9.94	12.29	10.53	-12.68*	0.53
CMS4611A × VR 523	11.61	9.53	0.96	-10.20	16.43*	9.72	2.22	-2.99	-14.67*	-1.76
CMS4611A × DL 161	11.27	11.34	6.88	-12.84*	13.01	9.34	-2.76	-8.60	-17.94**	-5.53
CMS4611A × IS 267	11.20	2.51	-7.77	-13.44*	12.23	10.86	14.67*	9.21	-4.65	9.78
CMS4611A × YL 581	12.96	3.36	-15.72**	0.23	29.95**	10.26	0.34	-10.42	-9.91	3.73
CMS4611A × SL 473	12.75	16.91*	5.32	-1.44	27.79**	9.57	2.38	-1.36	-15.94*	-3.22
CMS4611A × IS 262	12.65	13.86*	1.10	-2.23	26.77**	9.78	4.65	0.84	-14.08*	-1.08
CMS4611A × VR 521	10.12	12.70	4.32	-21.73**	1.48	8.82	10.81	-1.95	-22.54**	-10.82
CMS4611A × FL 201	12.34	-12.46*	-33.25**	-4.61	23.68**	10.97	-0.99	-16.64**	-3.69	10.88
CMS4611A × PP 402	12.26	-5.87	-24.98**	-5.23	22.87**	10.95	11.42	2.71	-3.82	10.74
CMS4611A × C 142	12.75	19.81**	10.10	-1.42	27.81**	10.06	7.99	4.38	-11.64	1.74
CMS4611A × PP 414	11.58	11.19	4.04	-10.43	16.13	10.25	14.55*	13.88	-10.03	3.58
CMS4611A × VR 522	12.21	6.13	-8.23	-5.60	22.40**	9.84	10.04	9.34	-13.63*	-0.56
CMS4611A × PL 406	11.91	2.93	-11.37	-7.93	19.38*	9.61	1.48	-3.33	-15.63*	-2.87
CMS4611A × E 183	9.65	-10.98	-19.44**	-25.37**	-3.24	9.05	-0.37	-1.35	-20.51**	-8.48
CMS4611A × IS 268	12.28	5.43	-9.64	-5.07	23.08**	10.44	11.26	6.82	-8.29	5.59
CMS4611A × IS 261	12.45	12.49	0.16	-3.76	24.78**	9.47	-1.63	-7.65	-16.88**	-4.30

Crosses	**Fruit width (mm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	12.08	-0.52	-10.99	-6.64	21.05*	10.24	-1.16	-2.19	-10.10	3.50
CMS4626A × SL 475	14.41	21.80**	11.27	11.42	44.46**	10.73	5.47	4.75	-5.74	8.53
CMS4626A × PL 412	11.95	12.97	11.57	-7.61	19.79*	10.73	3.27	1.91	-5.80	8.45
CMS4626A × IS 263	10.90	-3.78	-8.73	-15.75*	9.24	9.65	1.74	-5.86	-15.29*	-2.47
CMS4626A × VR 523	12.84	15.58*	11.60	-0.74	28.70**	10.57	4.35	3.17	-7.16	6.89
CMS4626A × DL 161	11.62	9.30	8.46	-10.18	16.46*	11.61	13.40*	13.27	1.93	17.35*
CMS4626A × IS 267	12.23	7.03	0.74	-5.46	22.58**	11.86	17.45**	15.71*	4.12	19.88**
CMS4626A × YL 581	15.77	20.90**	2.55	21.95**	58.12**	11.92	9.84	4.06	4.66	20.49**
CMS4626A × SL 473	13.67	19.88**	12.99	5.73	37.09**	12.05	20.79**	17.58*	5.81	21.82**
CMS4626A × IS 262	14.37	23.82**	14.92*	11.14	44.10**	9.87	-1.09	-3.71	-13.36*	-0.25
CMS4626A × VR 521	10.98	15.74*	2.50	-15.12*	10.06	8.76	1.98	-14.55*	-23.11**	-11.47
CMS4626A × FL 201	15.25	4.45	-17.51**	17.88**	52.84**	11.49	-1.84	-12.70*	0.87	16.14*
CMS4626A × PP 402	16.95	25.33**	3.74	31.05**	69.92**	12.60	20.52**	18.17**	10.66	27.40**
CMS4626A × C 142	13.87	24.49**	19.81**	7.27	39.09**	11.30	13.66*	10.30	-0.75	14.27*
CMS4626A × PP 414	12.41	13.57*	11.41	-4.09	24.36**	10.01	4.62	-2.30	-12.09	1.22
CMS4626A × VR 522	13.36	11.27	0.42	3.31	33.94**	10.47	9.48	2.19	-8.04	5.87
CMS4626A × PL 406	13.74	13.84*	2.30	6.27	37.78**	10.00	-0.96	-2.46	-12.22	1.06
CMS4626A × E 183	11.26	-0.75	-6.01	-12.94*	12.88	9.38	-3.40	-8.44	-17.61**	-5.15
CMS4626A × IS 268	15.45	27.20**	13.74*	19.49**	54.92**	11.84	18.27**	15.56*	3.99	19.72**
CMS4626A × IS 261	12.09	4.47	-2.74	-6.55	21.16*	10.37	1.22	1.21	-8.91	4.88
CMS463D13A × AC 102	15.24	21.48**	12.37*	17.87**	52.83**	11.51	3.81	-1.69	1.07	16.36*
CMS463D13A × SL 475	13.87	13.33*	7.12	7.27	39.08**	11.84	8.53	1.11	3.95	19.68**

Crosses	**Fruit width (mm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	12.91	17.53**	11.98	-0.15	29.46**	11.69	5.14	-0.17	2.64	18.17*
CMS463D13A × IS 263	13.08	11.45	9.55	1.13	31.12**	11.73	14.89*	0.21	3.03	18.62*
CMS463D13A × VR 523	13.59	18.00**	17.85*	5.08	36.25**	11.75	8.17	0.37	3.18	18.80*
CMS463D13A × DL 161	11.31	2.45	-1.93	-12.55*	13.38	11.43	4.23	-2.38	0.36	15.55*
CMS463D13A × IS 267	14.08	18.93**	15.96*	8.83	41.11**	11.57	6.84	-1.21	1.56	16.93*
CMS463D13A × YL 581	17.35	28.94**	12.81*	34.15**	73.93**	12.08	4.33	3.20	6.09	22.15**
CMS463D13A × SL 473	15.31	29.58**	26.53**	18.40**	53.52**	11.43	6.78	-2.35	0.39	15.58*
CMS463D13A × IS 262	15.90	32.26**	27.10**	22.92**	59.37**	11.48	7.28	-1.91	0.85	16.11*
CMS463D13A × VR 521	10.69	8.00	-7.32	-17.36**	7.15	9.99	7.20	-14.70*	-12.31	0.96
CMS463D13A × FL 201	17.15	14.27**	-7.21	32.59**	71.91**	12.68	1.97	-3.65	11.32	28.17**
CMS463D13A × PP 402	17.76	27.43**	8.69	37.31**	78.03**	12.35	10.39	5.48	8.44	24.84**
CMS463D13A × C 142	14.29	23.68**	23.43**	10.51	43.29**	11.43	7.07	-2.39	0.35	15.54*
CMS463D13A × PP 414	12.44	9.75	7.85	-3.83	24.69**	10.25	-0.48	-12.44*	-9.99	3.63
CMS463D13A × VR 522	14.77	18.91**	10.99	14.18*	48.04**	11.81	14.72*	0.88	3.71	19.40**
CMS463D13A × PL 406	14.87	19.13**	10.69	14.98*	49.09**	11.97	10.64	2.28	5.15	21.06**
CMS463D13A × E 183	11.12	-5.39	-7.16	-14.01*	11.50	10.11	-3.19	-13.65*	-11.23	2.20
CMS463D13A × IS 268	15.57	23.98**	14.61*	20.40**	56.11**	12.27	14.17*	4.76	7.70	24.00**
CMS463D13A × IS 261	13.39	11.81*	7.79	3.56	34.28**	11.59	5.57	-1.01	1.77	17.17*
LSD at p=0.05		1.40	1.62	1.62	1.62		1.22	1.41	1.41	1.41
LSD at p=0.01		1.85	2.14	2.14	2.14		1.62	1.87	1.87	1.87

Table 4.12f (*Cont’d.*)

Crosses	**Fruit width (mm)**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	9.93	10.74	-0.54	-5.02	9.78	10.61	4.93	-6.43	-8.48*	10.09*
CMS4611A × SL 475	8.96	0.26	-9.68	-14.32*	-0.97	10.86	9.26*	-1.22	-6.33	12.67**
CMS4611A × PL 412	9.16	7.38	0.55	-12.38*	1.28	9.92	4.91	-1.08	-14.43**	2.93
CMS4611A × IS 263	7.81	-1.53	-1.72	-25.26**	-13.61*	9.19	-0.15	-3.51	-20.72**	-4.64
CMS4611A × VR 523	8.50	5.01	3.13	-18.65**	-5.98	9.94	5.77	0.23	-14.20**	3.20
CMS4611A × DL 161	9.12	7.22	0.66	-12.76*	0.83	9.91	5.30	-0.32	-14.49**	2.86
CMS4611A × IS 267	8.61	-8.35	-20.61**	-17.58**	-4.74	10.22	2.95	-6.87	-11.80**	6.09
CMS4611A × YL 581	10.75	7.51	-10.80*	2.87	18.90**	11.32	3.68	-12.63**	-2.30	17.52**
CMS4611A × SL 473	10.11	15.04*	5.04	-3.30	11.77	10.81	11.67**	3.17	-6.75	12.17**
CMS4611A × IS 262	8.59	3.48	-0.76	-17.79**	-4.98	10.34	7.87*	0.50	-10.79**	7.31
CMS4611A × VR 521	7.79	6.69	-1.94	-25.42**	-13.80*	8.91	10.27*	0.34	-23.11**	-7.51
CMS4611A × FL 201	9.11	-12.73*	-29.53**	-12.85*	0.73	10.80	-8.97**	-27.27**	-6.79	12.12**
CMS4611A × PP 402	9.23	-6.61	-21.92**	-11.65*	2.12	10.81	-0.90	-16.45**	-6.70	12.23**
CMS4611A × C 142	8.59	-0.53	-7.88	-17.79**	-4.98	10.47	9.81*	2.80	-9.69**	8.63*
CMS4611A × PP 414	9.12	2.82	-6.84	-12.75*	0.84	10.32	9.62*	3.80	-11.00**	7.05
CMS4611A × VR 522	8.52	-5.47	-15.44**	-18.51**	-5.81	10.19	3.77	-5.26	-12.11**	5.72
CMS4611A × PL 406	9.49	19.14**	18.89*	-9.20	4.95	10.34	6.91	-1.12	-10.83**	7.25
CMS4611A × E 183	8.58	2.88	-1.75	-17.89**	-5.09	9.10	-3.48	-8.72*	-21.53**	-5.61
CMS4611A × IS 268	10.73	9.24	-8.28	2.69	18.69**	11.15	8.42*	-4.59	-3.79	15.72**
CMS4611A × IS 261	8.09	-4.50	-10.01	-22.62**	-10.57	10.00	2.89	-5.25	-13.73**	3.77

Crosses	**Fruit width (mm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	10.07	6.37	0.91	-3.63	11.38	10.79	1.32	-4.79	-6.87	12.02**
CMS4626A × SL 475	10.19	8.02	2.80	-2.48	12.71	11.78	12.38**	7.17	1.62	22.24**
CMS4626A × PL 412	10.68	18.21**	17.23**	2.16	18.08**	11.12	11.19**	10.89**	-4.08	15.38**
CMS4626A × IS 263	8.59	1.86	-4.04	-17.77**	-4.95	9.71	-0.36	-2.60	-16.20**	0.79
CMS4626A × VR 523	9.51	10.58	6.19	-9.00	5.18	10.97	10.33**	10.05*	-5.33	13.88**
CMS4626A × DL 161	9.32	3.42	2.84	-10.87	3.02	10.85	8.93*	8.77*	-6.42	12.56**
CMS4626A × IS 267	10.99	10.99*	1.31	5.17	21.55**	11.69	11.63**	6.51	0.87	21.33**
CMS4626A × YL 581	12.34	17.46**	2.37	18.06**	36.46**	13.34	16.36**	2.94	15.12**	38.47**
CMS4626A × SL 473	9.95	7.10	3.40	-4.81	10.02	11.89	16.31**	13.50**	2.59	23.40**
CMS4626A × IS 262	9.11	3.46	1.73	-12.82*	0.77	11.12	9.74**	8.05*	-4.08	15.37**
CMS4626A × VR 521	7.96	1.95	-11.11	-23.82**	-11.95	9.23	7.02	-7.41	-20.35**	-4.19
CMS4626A × FL 201	12.26	12.09*	-5.12	17.33**	35.62**	13.00	4.72	-12.49**	12.15**	34.89**
CMS4626A × PP 402	12.35	18.86**	4.43	18.18**	36.59**	13.97	21.91**	7.91*	20.50**	44.95**
CMS4626A × C 142	10.06	10.07	7.89	-3.72	11.28	11.75	16.57**	15.36**	1.34	21.90**
CMS4626A × PP 414	9.33	-0.47	-4.70	-10.75	3.16	10.58	6.30	6.12	-8.71*	9.81*
CMS4626A × VR 522	9.82	3.20	-2.52	-6.06	8.58	11.22	8.25*	4.32	-3.22	16.41**
CMS4626A × PL 406	11.17	31.91**	24.74**	6.90	23.55**	11.64	13.96**	11.34**	0.40	20.77**
CMS4626A × E 183	9.47	7.09	5.76	-9.36	4.76	10.04	0.71	0.67	-13.39**	4.17
CMS4626A × IS 268	10.92	5.70	-6.69	4.46	20.74**	12.74	17.62**	8.98*	9.89**	32.18**
CMS4626A × IS 261	8.93	-0.42	-0.59	-14.52*	-1.21	10.46	1.96	-0.85	-9.72**	8.59*
CMS463D13A × AC 102	10.30	-0.37	-3.73	-1.41	13.95*	12.35	9.06**	8.95*	6.57	28.19**
CMS463D13A × SL 475	10.68	3.63	-0.19	2.22	18.15**	12.13	8.78**	7.22	4.66	25.90**

Crosses	**Fruit width (mm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	10.22	3.15	-4.54	-2.24	13.00*	11.61	8.77*	2.58	0.14	20.45**
CMS463D13A × IS 263	8.87	-4.75	-17.15**	-15.15**	-1.93	11.23	7.75*	-0.78	-3.14	16.50**
CMS463D13A × VR 523	10.89	14.97**	1.76	4.22	20.45**	12.08	13.75**	6.75	4.20	25.34**
CMS463D13A × DL 161	10.66	7.84	-0.45	1.96	17.84**	11.13	4.73	-1.62	-3.96	15.52**
CMS463D13A × IS 267	10.94	1.52	0.83	4.67	20.98**	12.19	9.40**	7.77*	5.20	26.54**
CMS463D13A × YL 581	12.68	11.42*	5.18	21.30**	40.20**	14.04	15.64**	8.29*	21.10**	45.66**
CMS463D13A × SL 473	11.06	8.83	3.33	5.82	22.31**	12.60	15.66**	11.38**	8.72*	30.77**
CMS463D13A × IS 262	10.42	7.60	-2.68	-0.34	15.19*	12.60	16.64**	11.36**	8.70*	30.75**
CMS463D13A × VR 521	8.71	0.27	-18.66**	-16.70**	-3.72	9.79	5.33	-13.44**	-15.51**	1.63
CMS463D13A × FL 201	11.70	-0.94	-9.45*	11.98*	29.43**	13.84	5.80*	-6.81*	19.43**	43.66**
CMS463D13A × PP 402	12.37	9.79*	4.58	18.34**	36.78**	14.16	16.73**	9.39**	22.15**	46.93**
CMS463D13A × C 142	10.06	0.41	-6.05	-3.78	11.21	11.93	10.95**	5.40	2.89	23.76**
CMS463D13A × PP 414	10.03	-2.12	-6.31	-4.05	10.90	10.91	2.63	-3.61	-5.91	13.17**
CMS463D13A × VR 522	10.93	5.21	2.11	4.57	20.87**	12.50	13.31**	10.50**	7.86*	29.74**
CMS463D13A × PL 406	10.82	15.80**	1.08	3.52	19.65**	12.55	15.36**	10.96**	8.32*	30.29**
CMS463D13A × E 183	8.54	-12.14*	-20.22**	-18.30**	-5.57	9.92	-6.73*	-12.29**	-14.39**	2.98
CMS463D13A × IS 268	12.07	7.77	3.17	15.51**	33.50**	13.30	15.66**	13.82**	14.77**	38.05**
CMS463D13A × IS 261	9.29	-5.63	-13.20*	-11.11	2.75	11.43	4.49	0.98	-1.43	18.56**
LSD at p=0.05		1.02	1.17	1.17	1.17		0.72	0.83	0.83	0.83
LSD at p=0.01		1.34	1.55	1.55	1.55		0.94	1.09	1.09	1.09

*, significant at p=0.05; **, significant at p=0.01

Table 4.12g: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for pericarp thickness (mm) evaluated over environments**

Crosses	**Pericarp thickness (mm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	0.85	-3.35	-10.81	-29.00**	0.75	0.87	-4.71	-12.05	-27.52**	1.79
CMS4611A × SL 475	1.37	29.12**	4.04	14.53*	62.53**	1.28	13.37*	-9.89	6.55	49.63**
CMS4611A × PL 412	1.23	21.46**	0.82	2.79	45.88**	1.09	11.81	-2.06	-9.18	27.53**
CMS4611A × IS 263	0.85	-19.75**	-35.25**	-28.97**	0.79	0.98	21.98**	16.34	-18.89**	13.90
CMS4611A × VR 523	1.18	29.64**	15.80	-0.89	40.64**	1.05	17.90*	11.44	-12.75*	22.52**
CMS4611A × DL 161	1.04	22.86**	16.69	-12.69	23.91*	0.85	-6.22	-12.71	-29.37**	-0.82
CMS4611A × IS 267	1.02	-6.63	-26.24**	-14.39*	21.49*	1.27	38.36**	27.80**	5.14	47.65**
CMS4611A × YL 581	1.20	9.70	-13.24*	0.36	42.43**	1.18	0.71	-21.47**	-2.16	37.40**
CMS4611A × SL 473	0.84	5.44	4.11	-29.92**	-0.56	0.87	-0.25	-4.13	-27.52**	1.79
CMS4611A × IS 262	0.86	-24.36**	-41.67**	-27.61**	2.74	0.78	-0.13	-7.70	-35.65**	-9.63
CMS4611A × VR 521	0.85	11.80	5.56	-28.95**	0.83	0.80	10.88	-4.56	-33.46**	-6.56
CMS4611A × FL 201	0.96	-36.19**	-56.51**	-19.39**	14.39	1.50	11.63*	-18.71**	24.20**	74.41**
CMS4611A × PP 402	1.23	-16.54**	-42.69**	3.32	46.63**	1.36	17.79**	-7.49	13.00*	58.68**
CMS4611A × C 142	1.15	19.30*	2.32	-3.72	36.64**	0.80	3.83	-4.28	-33.27**	-6.29
CMS4611A × PP 414	0.99	11.81	2.64	-17.35*	17.29	0.96	7.40	1.01	-20.08**	12.23
CMS4611A × VR 522	1.01	12.29	1.79	-15.73*	19.59	0.91	7.80	7.70	-24.92**	5.44
CMS4611A × PL 406	0.88	-13.42	-28.69**	-25.85**	5.23	1.15	50.66**	36.61**	-4.76	33.75**
CMS4611A × E 183	1.01	11.91	0.93	-15.48*	19.94	0.89	-12.77*	-25.60**	-26.52**	3.18
CMS4611A × IS 268	1.18	-0.82	-25.29**	-0.73	40.88**	1.13	23.22**	13.82	-6.36	31.50**
CMS4611A × IS 261	0.92	-12.95	-29.96**	-22.60**	9.83	1.02	16.23*	11.84	-15.65*	18.45*

Crosses	**Pericarp thickness (mm)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	0.98	3.76	3.72	-17.44*	17.17	0.91	-5.55	-8.12	-24.28**	6.33
CMS4626A × SL 475	1.35	19.20**	2.66	13.02	60.39**	1.05	-11.05*	-26.22**	-12.75*	22.52**
CMS4626A × PL 412	1.26	16.50*	3.70	5.73	50.04**	1.06	3.48	-4.77	-11.70	24.00**
CMS4626A × IS 263	0.98	-12.98*	-24.94**	-17.66*	16.85	0.83	-2.00	-11.21	-30.81**	-2.83
CMS4626A × VR 523	1.21	22.71**	18.38*	1.31	43.77**	0.97	2.99	2.76	-19.55**	12.97
CMS4626A × DL 161	0.98	6.03	2.88	-18.16*	16.14	1.03	7.28	5.30	-14.80*	19.65*
CMS4626A × IS 267	1.08	-7.36	-21.93**	-9.39	28.59**	1.30	34.68**	31.13**	7.88	51.50**
CMS4626A × YL 581	1.55	32.96**	12.20	29.78**	84.18**	1.62	32.98**	8.08	34.65**	89.09**
CMS4626A × SL 473	1.06	22.46**	11.73	-11.12	26.13*	1.41	52.63**	50.35**	17.17**	64.54**
CMS4626A × IS 262	1.29	6.38	-12.72*	8.33	53.73**	0.63	-23.18**	-32.43**	-47.35**	-26.06**
CMS4626A × VR 521	0.91	8.96	-4.57	-24.08**	7.73	0.81	5.02	-13.59	-32.66**	-5.44
CMS4626A × FL 201	1.16	-26.52**	-47.49**	-2.68	38.10**	1.51	8.50	-18.08**	25.17**	75.77**
CMS4626A × PP 402	1.69	8.84	-21.57**	41.41**	100.67**	1.27	5.29	-13.76**	5.34	47.92**
CMS4626A × C 142	1.33	27.95**	18.05*	11.09	57.65**	0.96	15.87*	1.67	-20.77**	11.26
CMS4626A × PP 414	1.00	4.38	3.75	-16.46*	18.56	0.80	-15.02*	-15.66*	-33.27**	-6.29
CMS4626A × VR 522	1.20	23.89**	21.46*	0.56	42.70**	0.97	9.34	3.48	-19.36**	13.24
CMS4626A × PL 406	1.26	15.36*	1.80	5.87	50.24**	0.81	0.06	-13.56	-32.63**	-5.40
CMS4626A × E 183	0.85	-12.63	-14.81	-28.67**	1.23	0.79	-25.81**	-33.63**	-34.46**	-7.96
CMS4626A × IS 268	1.31	3.12	-17.58**	9.53	55.43**	1.07	10.58	7.66	-11.42	24.39**
CMS4626A × IS 261	1.07	-5.62	-18.84**	-10.31	27.28**	1.06	15.13*	13.27	-11.73	23.96**
CMS463D13A × AC 102	1.47	36.49**	22.15**	23.11**	74.70**	1.04	-0.37	-5.26	-13.41*	21.59*
CMS463D13A × SL 475	1.79	42.10**	36.09**	49.82**	112.61**	1.47	16.74**	3.48	22.37**	71.84**

Crosses	Pericarp thickness (mm)									
	E$_1$					E$_2$				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H$_{MP}$	***H$_{BP}$***	**CH-27**	**Soldier**		***H$_{MP}$***	***H$_{BP}$***	**CH-27**	**Soldier**
CMS463D13A × PL 412	1.53	26.46**	25.73**	28.19**	81.92**	1.13	2.25	1.52	-5.86	32.19**
CMS463D13A × IS 263	1.45	15.70**	11.00	21.77**	72.80**	1.11	19.47**	1.09	-7.61	29.75**
CMS463D13A × VR 523	1.59	42.79**	32.02**	33.05**	88.82**	1.30	26.83**	17.73**	7.61	51.11**
CMS463D13A × DL 161	1.26	20.51**	4.99	5.81	50.16**	1.06	2.07	-3.78	-12.06*	23.50**
CMS463D13A × IS 267	1.78	37.95**	28.86**	49.57**	112.25**	1.23	17.23**	11.38	1.80	42.95**
CMS463D13A × YL 581	1.91	47.80**	38.29**	59.96**	127.00**	1.38	6.27	-7.88	14.77*	61.17**
CMS463D13A × SL 473	1.54	55.50**	28.36**	29.37**	83.58**	1.19	18.30**	8.08	-1.22	38.72**
CMS463D13A × IS 262	1.53	13.98*	3.26	28.16**	81.88**	1.09	19.91**	-1.24	-9.73	26.76**
CMS463D13A × VR 521	0.98	2.63	-18.24*	-17.60*	16.93	1.01	17.80*	-8.68	-16.54**	17.20*
CMS463D13A × FL 201	1.93	12.91**	-12.84**	61.53**	129.22**	1.75	18.60**	-5.23	44.80**	103.34**
CMS463D13A × PP 402	2.17	29.17**	0.68	81.53**	157.61**	1.33	3.52	-9.51	10.54	55.22**
CMS463D13A × C 142	1.43	23.21**	19.13**	20.06**	70.38**	1.18	29.82**	6.69	-2.49	36.93**
CMS463D13A × PP 414	1.37	26.92**	14.17*	15.06*	63.28**	0.99	-3.24	-9.74	-17.51**	15.84
CMS463D13A × VR 522	1.54	40.30**	27.78**	28.78**	82.75**	1.21	25.13**	10.20	0.72	41.44**
CMS463D13A × PL 406	1.52	24.41**	22.49**	27.38**	80.77**	1.28	43.02**	15.89*	5.92	48.74**
CMS463D13A × E 183	0.96	-13.20	-20.54**	-19.92**	13.64	0.95	-17.45**	-20.53**	-21.52**	10.21
CMS463D13A × IS 268	1.66	19.31**	4.90	39.40**	97.82**	1.16	10.51	4.99	-4.04	34.76**
CMS463D13A × IS 261	1.34	6.56	1.87	12.57	59.75**	1.34	32.82**	21.21**	10.79	55.57**
LSD at *p*=0.05		0.15	0.17	0.17	0.17		0.13	0.14	0.14	0.14
LSD at *p*=0.01		0.19	0.22	0.22	0.22		0.17	0.19	0.19	0.19

Table 4.12g (*Cont'd.*)

Crosses	**Pericarp thickness (mm)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	0.61	2.50	-13.63	-27.09**	-11.43	0.78	-2.40	-12.03*	-27.95**	-2.41
CMS4611A × SL 475	0.80	-0.65	-28.58**	-5.61	14.65	1.15	15.19**	-10.55**	6.32	44.02**
CMS4611A × PL 412	0.71	29.74**	16.88*	-15.66*	2.45	1.01	19.53**	3.05	-6.46	26.70**
CMS4611A × IS 263	0.63	13.55	1.68	-25.62**	-9.65	0.82	1.76	-8.78	-24.35**	2.47
CMS4611A × VR 523	1.11	47.24**	8.96	31.32**	59.51**	1.11	30.72**	12.09**	3.07	39.62**
CMS4611A × DL 161	0.74	23.19**	4.10	-12.73*	6.00	0.88	11.72*	2.10	-18.90**	9.85
CMS4611A × IS 267	0.77	3.18	-23.57**	-8.19	11.53	1.02	10.97**	-9.63**	-5.51	27.98**
CMS4611A × YL 581	0.82	2.47	-26.37**	-2.53	18.40*	1.07	4.37	-19.99**	-1.33	33.65**
CMS4611A × SL 473	0.53	6.62	3.82	-36.62**	-23.01**	0.75	3.42	1.60	-30.77**	-6.23
CMS4611A × IS 262	0.62	-10.95	-31.52**	-26.37**	-10.57	0.75	-13.59**	-27.10**	-30.28**	-5.56
CMS4611A × VR 521	0.50	2.13	1.14	-40.33**	-27.52**	0.72	9.05	1.02	-33.59**	-10.04
CMS4611A × FL 201	0.79	-27.94**	-53.59**	-6.80	13.21	1.08	-17.62**	-43.53**	0.09	35.58**
CMS4611A × PP 402	0.70	-8.35	-32.63**	-17.12**	0.67	1.10	-3.01	-29.33**	1.60	37.62**
CMS4611A × C 142	0.58	-4.50	-20.27**	-31.12**	-16.33*	0.84	8.02	-1.03	-21.83**	5.88
CMS4611A × PP 414	0.59	-9.09	-26.94**	-30.41**	-15.47*	0.85	4.61	-6.67	-21.76**	5.98
CMS4611A × VR 522	0.85	36.05**	11.85	0.43	22.00**	0.92	16.96**	6.72	-14.94**	15.21**
CMS4611A × PL 406	0.62	15.44	5.30	-26.10**	-10.23	0.89	14.30**	5.55	-18.07**	10.98*
CMS4611A × E 183	0.52	-3.75	-12.60	-38.04**	-24.74**	0.81	-1.74	-13.30**	-25.45**	0.98
CMS4611A × IS 268	0.85	7.90	-21.90**	0.95	22.62**	1.05	9.15*	-13.71**	-2.39	32.22**
CMS4611A × IS 261	0.89	31.73**	2.84	5.97	28.72**	0.94	8.41*	-8.48*	-12.59**	18.40**

Crosses	Pericarp thickness (mm)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4626A × AC 102	0.64	-1.50	-9.41	-23.53**	-7.11	0.85	-1.08	-4.23	-21.57**	6.24
CMS4626A × SL 475	1.16	35.61**	4.16	37.64**	67.20**	1.19	12.34**	-7.59*	9.84*	48.78**
CMS4626A × PL 412	0.71	17.61*	16.55	-15.90*	2.16	1.01	11.82**	3.14	-6.38	26.81**
CMS4626A × IS 263	0.61	0.33	-1.24	-27.76**	-12.25	0.81	-6.24	-9.77*	-25.17**	1.35
CMS4626A × VR 523	0.93	14.96**	-8.73	10.00	33.62**	1.04	13.63**	4.19	-4.19	29.78**
CMS4626A × DL 161	0.72	10.43	1.89	-14.59*	3.75	0.91	7.63	5.77	-15.98**	13.80**
CMS4626A × IS 267	0.81	0.33	-20.24**	-4.19	16.38*	1.06	8.57*	-5.90	-1.61	33.26**
CMS4626A × YL 581	1.16	35.29**	3.85	37.49**	67.00**	1.44	33.58**	8.32**	33.60**	80.96**
CMS4626A × SL 473	0.58	3.72	-3.46	-31.59**	-16.91*	1.02	29.92**	22.68**	-5.92	27.43**
CMS4626A × IS 262	0.74	-1.35	-18.17**	-12.02	6.87	0.89	-4.45	-13.91**	-17.67**	11.52*
CMS4626A × VR 521	0.52	-5.54	-13.45	-38.67**	-25.50**	0.74	3.86	-10.11*	-31.07**	-6.63
CMS4626A × FL 201	1.23	7.29	-27.43**	45.75**	77.04**	1.30	-5.28*	-32.15**	20.27**	62.91**
CMS4626A × PP 402	1.09	33.80**	5.43	29.70**	57.54**	1.35	13.35**	-13.10**	24.95**	69.24**
CMS4626A × C 142	0.68	2.84	-6.41	-19.14**	-1.78	0.99	17.41**	15.70**	-8.62*	23.78**
CMS4626A × PP 414	0.69	-1.36	-13.99*	-18.07**	-0.48	0.83	-4.22	-8.30	-23.13**	4.12
CMS4626A × VR 522	0.63	-7.21	-17.00*	-25.46**	-9.46	0.93	10.48*	8.39	-13.62**	17.01**
CMS4626A × PL 406	0.90	50.83**	50.11**	6.37	29.20**	0.99	18.83**	18.11**	-8.32*	24.18**
CMS4626A × E 183	0.63	4.83	4.80	-25.70**	-9.75	0.76	-14.00**	-18.65**	-30.05**	-5.25
CMS4626A × IS 268	1.10	30.76**	1.22	30.84**	58.93**	1.16	13.04**	-5.16	7.28	45.31**
CMS4626A × IS 261	0.89	21.69**	2.69	5.81	28.53**	1.01	8.43*	-2.26	-6.64	26.45**
CMS463D13A × AC 102	0.65	-7.46	-8.20	-22.50**	-5.86	1.06	11.88**	5.37	-2.33	32.29**
CMS463D13A × SL 475	1.13	24.64**	1.50	34.12**	62.92**	1.46	28.13**	14.02**	35.53**	83.58**

Crosses	Pericarp thickness (mm)									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS463D13A × PL 412	0.71	8.61	1.48	-15.70*	2.40	1.12	13.50**	12.33**	4.11	41.02**
CMS463D13A × IS 263	0.62	-5.39	-11.04	-26.10**	-10.23	1.06	12.06**	6.16	-1.60	33.28**
CMS463D13A × VR 523	0.99	15.05**	-2.82	17.12**	42.27**	1.29	29.38**	28.87**	19.45**	61.79**
CMS463D13A × DL 161	0.81	15.61*	15.09*	-3.52	17.20*	1.05	12.41**	4.37	-3.26	31.03**
CMS463D13A × IS 267	0.85	-0.45	-15.80**	1.15	22.86**	1.29	20.88**	14.02**	19.21**	61.47**
CMS463D13A × YL 581	1.23	35.73**	10.45*	46.22**	77.62**	1.51	29.23**	13.17**	39.58**	89.07**
CMS463D13A × SL 473	0.71	16.27*	0.86	-16.21**	1.78	1.15	31.99**	14.51**	6.14	43.77**
CMS463D13A × IS 262	0.92	14.81**	1.77	9.41	32.90**	1.18	15.96**	14.17**	9.19*	47.90**
CMS463D13A × VR 521	0.53	-11.27	-24.13**	-36.97**	-23.44**	0.84	4.55	-16.11**	-22.24**	5.32
CMS463D13A × FL 201	1.22	2.03	-27.88**	44.84**	75.94**	1.63	11.85**	-14.83**	50.97**	104.49**
CMS463D13A × PP 402	1.10	26.71**	6.14	30.57**	58.60**	1.53	20.00**	-1.32	41.88**	92.17**
CMS463D13A × C 142	0.80	12.60*	10.43	-4.59	15.90*	1.14	22.64**	13.57**	5.27	42.58**
CMS463D13A × PP 414	0.72	-4.04	-10.17	-14.43*	3.94	1.03	7.95*	2.80	-4.72	29.06**
CMS463D13A × VR 522	0.86	18.53**	14.09*	2.45	24.45**	1.20	29.36**	20.29**	11.50**	51.02**
CMS463D13A × PL 406	0.75	16.46*	7.43	-10.76	8.41	1.18	28.57**	18.12**	9.48*	48.29**
CMS463D13A × E 183	0.60	-8.01	-14.75*	-29.18**	-13.98	0.83	-13.72**	-16.84**	-22.92**	4.40
CMS463D13A × IS 268	1.21	35.72**	11.47*	44.09**	75.02**	1.34	20.95**	10.03**	24.47**	68.59**
CMS463D13A × IS 261	0.98	25.13**	13.01*	16.45**	41.45**	1.22	19.99**	18.22**	12.92**	52.95**
LSD at p=0.05		0.09	0.10	0.10	0.10		0.07	0.08	0.08	0.08
LSD at p=0.01		0.12	0.14	0.14	0.14		0.09	0.11	0.11	0.11

*, significant at p=0.05; **, significant at p=0.01

Table 4.12h: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for number of fruits plant^{-1} evaluated over environments**

Crosses	Number of fruits plant^{-1}									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	226.96	-6.64	-18.32**	-27.79**	-21.90**	182.35	-1.64	-21.95**	-15.81	-28.55**
CMS4611A × SL 475	269.37	0.19	-3.06	-14.30*	-7.31	252.70	7.83	7.51	16.68*	-0.98
CMS4611A × PL 412	286.27	-1.45	-5.55	-8.92	-1.49	350.43	65.66**	49.99**	61.80**	37.31**
CMS4611A × IS 263	303.92	27.19**	9.37	-3.31	4.58	184.21	-15.17*	-21.15**	-14.95	-27.82**
CMS4611A × VR 523	285.78	11.94*	2.84	-9.08	-1.66	208.20	-4.89	-10.88	-3.87	-18.42**
CMS4611A × DL 161	372.74	31.93**	29.80**	18.59**	28.26**	278.47	25.22**	19.19*	28.58**	9.12
CMS4611A × IS 267	304.19	16.31**	9.46	-3.22	4.67	348.31	64.16**	49.09**	60.83**	36.48**
CMS4611A × YL 581	217.20	-8.11	-21.84**	-30.90**	-25.26**	310.91	57.69**	33.08**	43.56**	21.83**
CMS4611A × SL 473	241.25	-12.54*	-13.18*	-23.25**	-16.99**	219.95	-0.48	-5.86	1.56	-13.81*
CMS4611A × IS 262	320.30	20.46**	15.27*	1.90	10.22	229.91	20.69*	-1.59	6.16	-9.91
CMS4611A × VR 521	241.35	-6.38	-13.15*	-23.21**	-16.95**	333.56	36.89**	31.48**	54.02**	30.70**
CMS4611A × FL 201	239.27	12.39	-13.89*	-23.88**	-17.66**	203.04	18.34*	-13.09	-6.25	-20.44**
CMS4611A × PP 402	265.67	24.16**	-4.39	-15.48**	-8.58	292.19	78.74**	25.07**	34.91**	14.49*
CMS4611A × C 142	379.43	40.89**	36.54**	20.72**	30.57**	352.97	68.35**	51.08**	62.98**	38.31**
CMS4611A × PP 414	294.99	1.53	-2.71	-6.15	1.51	159.98	-20.98**	-31.52**	-26.13**	-37.31**
CMS4611A × VR 522	324.82	23.14**	16.89**	3.34	11.77	298.95	56.26**	27.96**	38.04**	17.14*
CMS4611A × PL 406	304.40	17.76**	9.54	-3.16	4.75	206.08	4.97	-11.79	-4.85	-19.25**
CMS4611A × E 183	183.61	-13.16	-33.93**	-41.58**	-36.82**	198.91	-3.16	-14.86*	-8.16	-22.06**
CMS4611A × IS 268	321.73	26.40**	15.78*	2.36	10.71	279.90	44.95**	19.80**	29.24**	9.68
CMS4611A × IS 261	284.02	17.85**	2.21	-9.64	-2.27	244.12	18.86*	4.49	12.72	-4.34

Crosses	**Number of fruits plant^{-1}**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	219.42	-13.05*	-25.96**	-30.19**	-24.50**	173.57	1.08	-15.87	-19.86*	-31.99**
CMS4626A × SL 475	266.27	-4.25	-10.15	-15.29**	-8.37	290.64	31.70**	23.65**	34.20**	13.89*
CMS4626A × PL 412	363.81	21.38**	20.03**	15.75**	25.19**	387.31	95.74**	87.74**	78.83**	51.76**
CMS4626A × IS 263	208.33	-16.05**	-29.70**	-33.72**	-28.31**	344.40	69.25**	66.94**	59.02**	34.95**
CMS4626A × VR 523	286.49	8.31	-3.32	-8.85	-1.42	266.11	29.65**	28.99**	22.87**	4.27
CMS4626A × DL 161	351.80	20.58**	18.71**	11.92*	21.06**	325.35	55.88**	54.10**	50.22**	27.49**
CMS4626A × IS 267	261.97	-3.24	-11.60	-16.65**	-9.85	284.29	43.22**	37.80**	31.27**	11.40
CMS4626A × YL 581	237.22	-3.42	-19.95**	-24.53**	-18.37**	392.89	114.11**	90.44**	81.41**	53.95**
CMS4626A × SL 473	275.25	-3.45	-7.12	-12.43*	-5.29	213.25	2.85	2.34	-1.54	-16.44*
CMS4626A × IS 262	303.49	10.31	2.41	-3.45	4.43	369.97	109.22**	79.33**	70.83**	44.97**
CMS4626A × VR 521	244.88	-8.29	-17.36**	-22.09**	-15.73*	241.49	4.99	-4.81	11.50	-5.37
CMS4626A × FL 201	199.14	-10.35	-32.80**	-36.64**	-31.48**	236.43	49.72**	14.60	9.17	-7.36
CMS4626A × PP 402	187.97	-15.79*	-36.57**	-40.20**	-35.32**	211.40	41.11**	2.47	-2.39	-17.16*
CMS4626A × C 142	333.39	19.69**	12.50*	6.07	14.72*	245.84	25.42**	19.17*	13.51	-3.67
CMS4626A × PP 414	252.26	-15.85**	-16.80**	-19.74**	-13.20*	252.03	33.50**	22.16**	16.37*	-1.24
CMS4626A × VR 522	262.40	-3.89	-11.45	-16.52**	-9.71	229.12	28.97**	11.06	5.79	-10.22
CMS4626A × PL 406	317.55	18.61**	7.16	1.03	9.27	241.20	32.05**	16.91*	11.37	-5.49
CMS4626A × E 183	183.21	-16.97*	-38.17**	-41.71**	-36.95**	170.32	-11.17	-17.44*	-21.36**	-33.26**
CMS4626A × IS 268	317.37	20.32**	7.09	0.97	9.21	243.79	35.86**	18.17*	12.56	-4.47
CMS4626A × IS 261	250.64	0.16	-15.42*	-20.26**	-13.75*	284.60	48.45**	37.95**	31.41**	11.52
CMS463D13A × AC 102	218.05	2.65	0.72	-30.63**	-24.97**	196.41	24.55*	10.18	-9.31	-23.04**
CMS463D13A × SL 475	265.05	11.29	2.00	-15.67**	-8.79	251.54	21.72**	7.01	16.14*	-1.44

Crosses	**Number of fruits plant^{-1}**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	329.23	26.73**	8.62	4.74	13.29*	212.45	15.56	12.15	-1.90	-16.75*
CMS463D13A × IS 263	245.73	18.00*	13.51	-21.82**	-15.44*	227.79	20.23*	13.51	5.18	-10.74
CMS463D13A × VR 523	253.52	12.88	8.95	-19.34**	-12.76*	233.55	22.14**	14.38	7.84	-8.48
CMS463D13A × DL 161	347.62	38.04**	21.05**	10.59	19.62**	214.68	10.27	1.68	-0.88	-15.88*
CMS463D13A × IS 267	297.37	28.83**	21.30**	-5.39	2.33	230.89	25.16**	21.07*	6.61	-9.53
CMS463D13A × YL 581	201.84	-1.87	-6.77	-35.79**	-30.55**	212.69	25.50**	19.32	-1.80	-16.66*
CMS463D13A × SL 473	234.11	-4.50	-14.50*	-25.52**	-19.44**	232.20	20.12*	11.44	7.22	-9.01
CMS463D13A × IS 262	269.54	14.60*	6.16	-14.25*	-7.25	186.64	14.64	4.71	-13.82	-26.86**
CMS463D13A × VR 521	254.04	11.86	6.87	-19.18**	-12.58*	166.75	-22.80**	-34.28**	-23.01**	-34.66**
CMS463D13A × FL 201	156.46	-14.13	-27.73**	-50.22**	-46.16**	210.69	46.43**	18.20	-2.72	-17.44*
CMS463D13A × PP 402	234.81	28.12**	8.46	-25.30**	-19.20**	224.22	65.12**	25.79**	3.53	-12.14
CMS463D13A × C 142	315.67	32.29**	21.07**	0.43	8.62	213.57	17.36*	15.00	-1.39	-16.31*
CMS463D13A × PP 414	231.55	-10.89	-23.63**	-26.33**	-20.32**	117.66	-32.68**	-33.99**	-45.67**	-53.90**
CMS463D13A × VR 522	263.11	12.88	5.38	-16.29**	-9.46	169.67	3.70	-4.81	-21.66**	-33.51**
CMS463D13A × PL 406	243.46	6.88	1.82	-22.54**	-16.22**	181.26	7.49	1.69	-16.30*	-28.97**
CMS463D13A × E 183	192.25	6.37	-11.20	-38.84**	-33.85**	135.59	-23.70**	-23.94*	-37.40**	-46.87**
CMS463D13A × IS 268	277.82	24.12**	20.18**	-11.61*	-4.40	279.45	68.94**	56.77**	29.03**	9.50
CMS463D13A × IS 261	224.21	6.61	3.57	-28.67**	-22.85**	192.43	8.29	7.95	-11.15	-24.60**
LSD at p=0.05		30.12	34.78	34.78	34.78		29.85	34.47	34.47	34.47
LSD at p=0.01		39.82	45.98	45.98	45.98		39.47	45.57	45.57	45.57

Table 4.12h (*Cont'd.*)

Crosses	Number of fruits plant^{-1}									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	120.10	18.08*	-2.93	-20.01**	-24.82**	176.47	-0.15	-10.45*	-22.27**	-24.97**
CMS4611A × SL 475	234.82	102.45**	54.20**	56.39**	46.98**	252.30	22.24**	16.95**	11.14**	7.27
CMS4611A × PL 412	116.74	55.41**	46.50**	-22.25**	-26.93**	251.15	30.55**	27.44**	10.63**	6.78
CMS4611A × IS 263	105.04	48.88**	31.81**	-30.05**	-34.25**	197.72	12.63**	0.33	-12.90**	-15.93**
CMS4611A × VR 523	220.01	53.19**	6.00	46.52**	37.71**	238.00	15.57**	10.79*	4.84	1.19
CMS4611A × DL 161	304.17	129.92**	64.51**	102.57**	90.39**	318.46	49.93**	39.84**	40.28**	35.40**
CMS4611A × IS 267	191.54	171.25**	140.36**	27.56**	19.89**	281.34	55.07**	42.77**	23.93**	19.62**
CMS4611A × YL 581	153.82	89.73**	86.55**	2.44	-3.72	227.31	32.51**	15.35**	0.13	-3.35
CMS4611A × SL 473	133.19	17.81*	-9.04	-11.30	-16.63**	198.13	-2.54	-5.44	-12.73**	-15.76**
CMS4611A × IS 262	150.39	84.41**	80.30**	0.16	-5.87	233.53	30.24**	18.50**	2.87	-0.71
CMS4611A × VR 521	163.29	78.50**	58.12**	8.75	2.21	246.07	24.50**	24.13**	8.39*	4.62
CMS4611A × FL 201	64.33	12.80	-19.27	-57.16**	-59.73**	168.88	14.75**	-14.30**	-25.61**	-28.19**
CMS4611A × PP 402	105.95	70.92**	32.96**	-29.44**	-33.68**	221.27	51.06**	12.28**	-2.53	-5.92
CMS4611A × C 142	265.14	164.97**	120.14**	76.58**	65.96**	332.52	72.27**	68.73**	46.47**	41.38**
CMS4611A × PP 414	69.37	-2.18	-12.94	-53.80**	-56.58**	174.78	-7.02	-11.31*	-23.01**	-25.69**
CMS4611A × VR 522	225.26	210.06**	182.68**	50.02**	40.99**	283.01	60.88**	43.61**	24.67**	20.33**
CMS4611A × PL 406	175.27	154.04**	119.95**	16.73**	9.71	228.58	30.91**	15.99**	0.69	-2.81
CMS4611A × E 183	155.00	89.32**	84.40**	3.23	-2.98	179.17	7.78	-9.08	-21.08**	-23.82**
CMS4611A × IS 268	103.10	31.80**	29.38*	-31.34**	-35.47**	234.91	34.01**	19.20**	3.48	-0.12
CMS4611A × IS 261	128.59	51.97**	43.60**	-14.36*	-19.51**	218.91	23.68**	11.08*	-3.57	-6.92

Crosses	**Number of fruits plant^{-1}**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	97.98	-5.76	-20.81**	-34.74**	-38.67**	163.66	-7.02	-16.34**	-27.91**	-30.41**
CMS4626A × SL 475	211.97	79.26**	39.19**	41.17**	32.68**	256.30	24.61**	18.81**	12.90**	8.97*
CMS4626A × PL 412	74.54	-3.67	-11.48	-50.36**	-53.34**	275.22	43.60**	40.69**	21.23**	17.02**
CMS4626A × IS 263	72.67	-0.20	-13.70	-51.60**	-54.52**	208.47	19.24**	6.57	-8.17*	-11.36**
CMS4626A × VR 523	137.75	-5.57	-33.63**	-8.26	-13.78*	230.12	12.13**	7.12	1.37	-2.16
CMS4626A × DL 161	219.33	63.01**	18.62**	46.07**	37.29**	298.83	41.17**	31.22**	31.63**	27.06**
CMS4626A × IS 267	82.48	13.18	-2.05	-45.07**	-48.37**	209.58	15.98**	7.14	-7.68	-10.89**
CMS4626A × YL 581	110.98	33.18**	31.80**	-26.09**	-30.53**	247.03	44.62**	26.28**	8.82*	5.03
CMS4626A × SL 473	239.41	107.61**	63.50**	59.44**	49.85**	242.63	19.78**	15.80**	6.88	3.16
CMS4626A × IS 262	139.26	66.16**	65.37**	-7.26	-12.84*	270.90	51.69**	38.49**	19.33**	15.18**
CMS4626A × VR 521	131.61	40.39**	27.43**	-12.35	-17.62**	205.99	4.61	3.92	-9.26*	-12.41**
CMS4626A × FL 201	59.45	0.27	-29.40*	-60.41**	-62.79**	165.01	12.67*	-15.65**	-27.32**	-29.84**
CMS4626A × PP 402	93.09	44.89**	10.55	-38.00**	-41.73**	164.15	12.62*	-16.08**	-27.69**	-30.20**
CMS4626A × C 142	175.83	71.84**	45.99**	17.10**	10.06	251.69	30.89**	28.66**	10.87**	7.01
CMS4626A × PP 414	73.71	0.72	-12.47	-50.91**	-53.87**	192.66	2.89	-1.51	-15.13**	-18.08**
CMS4626A × VR 522	97.51	30.17**	15.80	-35.06**	-38.96**	196.35	12.08**	0.37	-13.51**	-16.52**
CMS4626A × PL 406	130.76	83.50**	55.28**	-12.92*	-18.16**	229.84	32.18**	17.49**	1.24	-2.28
CMS4626A × E 183	95.64	13.67	13.57	-36.31**	-40.14**	149.72	-9.54	-23.46**	-34.05**	-36.34**
CMS4626A × IS 268	212.24	163.72**	152.04**	41.35**	32.84**	257.80	47.68**	31.79**	13.56**	9.61*
CMS4626A × IS 261	160.84	85.14**	79.61**	7.12	0.68	232.03	31.63**	18.61**	2.21	-1.35
CMS463D13A × AC 102	180.60	52.54**	45.96**	20.28**	13.04*	198.35	21.81**	17.18**	-12.63**	-15.66**
CMS463D13A × SL 475	210.56	58.70**	38.27**	40.23**	31.80**	242.38	25.91**	12.36**	6.77	3.06

Crosses	**Number of fruits plant^{-1}**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	140.89	53.46**	24.62**	-6.17	-11.81	227.53	27.48**	21.22**	0.22	-3.26
CMS463D13A × IS 263	70.20	-19.53*	-37.91**	-53.25**	-56.06**	181.24	12.12*	7.07	-20.16**	-22.94**
CMS463D13A × VR 523	209.04	30.40**	0.71	39.22**	30.84**	232.04	20.83**	8.02	2.21	-1.34
CMS463D13A × DL 161	216.33	45.21**	17.00**	44.07**	35.41**	259.54	30.75**	13.97**	14.33**	10.35**
CMS463D13A × IS 267	94.52	8.27	-16.40	-37.05**	-40.84**	207.59	23.91**	22.64**	-8.56*	-11.73**
CMS463D13A × YL 581	122.96	25.78**	8.76	-18.11**	-23.04**	179.16	13.65**	5.84	-21.08**	-23.82**
CMS463D13A × SL 473	154.59	19.15**	5.58	2.96	-3.24	206.97	9.28*	-1.22	-8.83*	-12.00**
CMS463D13A × IS 262	77.80	-20.80*	-31.19**	-48.18**	-51.30**	177.99	7.60	5.15	-21.59**	-24.32**
CMS463D13A × VR 521	136.30	26.01**	20.55*	-9.23	-14.69*	185.69	1.06	-6.32	-18.20**	-21.05**
CMS463D13A × FL 201	82.03	11.27	-27.45**	-45.37**	-48.66**	149.73	12.35*	-11.55*	-34.05**	-36.34**
CMS463D13A × PP 402	106.41	35.25**	-5.88	-29.13**	-33.39**	188.48	42.16**	11.35*	-16.98**	-19.86**
CMS463D13A × C 142	152.42	30.55**	26.55**	1.51	-4.60	227.22	26.86**	20.25**	0.09	-3.39
CMS463D13A × PP 414	73.29	-16.34	-35.18**	-51.19**	-54.13**	140.83	-19.09**	-21.27**	-37.96**	-40.12**
CMS463D13A × VR 522	119.77	34.06**	5.93	-20.23**	-25.03**	184.19	13.68**	8.81	-18.87**	-21.69**
CMS463D13A × PL 406	107.71	25.71**	-4.73	-28.26**	-32.58**	177.48	10.44*	4.85	-21.82**	-24.54**
CMS463D13A × E 183	85.65	-13.10	-24.24**	-42.96**	-46.39**	137.83	-9.52	-18.57**	-39.29**	-41.40**
CMS463D13A × IS 268	152.69	60.89**	35.05**	1.69	-4.43	236.66	46.64**	39.81**	4.25	0.62
CMS463D13A × IS 261	140.45	38.64**	24.23**	-6.46	-12.09*	185.70	13.85**	9.71	-18.20**	-21.04**
LSD at p=0.05		16.40	18.94	18.94	18.94		15.82	18.27	18.27	18.27
LSD at p=0.01		21.69	25.04	25.04	25.04		20.84	24.06	24.06	24.06

*, significant at p=0.05; **, significant at p=0.01

Table 4.12i: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for number of seed fruit^{-1} evaluated over environments

Crosses	Number of seed fruit^{-1}									
	E$_1$					E$_2$				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	66.13	34.19**	27.59**	-3.36	79.87**	55.93	43.79**	37.99**	-10.84*	77.75**
CMS4611A × SL 475	75.57	29.65**	16.74**	10.42	105.53**	64.73	35.05**	16.99**	3.19	105.72**
CMS4611A × PL 412	72.87	38.44**	36.37**	6.48	98.19**	63.63	45.50**	35.58**	1.43	102.22**
CMS4611A × IS 263	62.13	24.68**	19.87**	-9.21	68.99**	54.47	34.32**	34.26**	-13.18**	73.09**
CMS4611A × VR 523	64.83	32.31**	25.08**	-5.26	76.34**	59.07	50.30**	45.72**	-5.84	87.71**
CMS4611A × DL 161	55.93	10.80	7.91	-18.27**	52.13**	48.33	20.88**	19.24**	-22.95**	53.60**
CMS4611A × IS 267	65.93	14.10*	3.45	-3.65	79.33**	57.43	21.94**	7.02	-8.45	82.52**
CMS4611A × YL 581	47.97	15.21*	-7.46	-29.91**	30.46**	40.70	30.03**	0.41	-35.12**	29.34**
CMS4611A × SL 473	53.77	21.78**	3.73	-21.43**	46.24**	44.23	30.35**	9.13	-29.49**	40.57**
CMS4611A × IS 262	49.83	10.13	-3.86	-27.18**	35.54**	42.03	13.81*	3.70	-33.00**	33.58**
CMS4611A × VR 521	67.57	38.17**	30.35**	-1.27	83.77**	60.17	50.29**	48.44**	-4.09	91.21**
CMS4611A × FL 201	38.87	-0.98	-25.02**	-43.21**	5.71	33.97	10.70	-16.20*	-45.86**	7.94
CMS4611A × PP 402	36.37	-10.83	-29.84**	-46.86**	-1.09	30.33	-5.31	-25.16**	-51.65**	-3.60
CMS4611A × C 142	63.77	23.38**	23.02**	-6.82	73.44**	52.17	19.47**	11.47	-16.84**	65.78**
CMS4611A × PP 414	48.73	16.63*	-5.98	-28.79**	32.55**	39.40	25.88**	-2.80	-37.19**	25.21**
CMS4611A × VR 522	59.47	26.84**	14.73*	-13.10*	61.74**	45.73	28.71**	12.83	-27.10**	45.34**
CMS4611A × PL 406	69.77	28.48**	22.90**	1.95	89.76**	60.53	40.99**	33.53**	-3.51	92.37**
CMS4611A × E 183	41.37	3.16	-20.19**	-39.55**	12.51	32.80	3.42	-19.08**	-47.72**	4.24
CMS4611A × IS 268	72.53	29.99**	21.36**	5.99	97.28**	66.43	45.74**	31.20**	5.90	111.12**
CMS4611A × IS 261	83.53	46.85**	34.88**	22.07**	127.20**	65.27	36.02**	17.74**	4.04	107.42**

Crosses	Number of seed fruit^{-1}									
	E$_1$					E$_2$				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4626A × AC 102	51.33	11.96	9.84	-24.99**	39.62**	41.13	9.98	9.59	-34.43**	30.72**
CMS4626A × SL 475	88.97	62.20**	37.44**	30.00**	141.98**	70.67	52.19**	27.71**	12.65**	124.58**
CMS4626A × PL 412	71.37	45.05**	33.56**	4.29	94.11**	70.67	67.32**	50.57**	12.65**	124.58**
CMS4626A × IS 263	45.33	-2.30	-5.23	-33.76**	23.30*	38.53	-1.32	-5.01	-38.58**	22.46*
CMS4626A × VR 523	65.13	42.94**	41.08**	-4.82	77.15**	57.80	52.91**	51.84**	-7.86	83.69**
CMS4626A × DL 161	53.43	13.57*	8.75	-21.92**	45.33**	45.33	17.80**	14.96*	-27.74**	44.07**
CMS4626A × IS 267	73.43	35.11**	15.22**	7.31	99.73**	66.97	46.86**	24.78**	6.75	112.82**
CMS4626A × YL 581	39.77	4.10	-11.56	-41.89**	8.16	30.93	3.80	-17.58*	-50.69**	-1.69
CMS4626A × SL 473	59.73	46.70**	32.84**	-12.71*	62.47**	48.83	50.57**	30.11**	-22.16**	55.19**
CMS4626A × IS 262	54.70	30.81**	21.65**	-20.07**	48.78**	43.23	22.01**	15.19	-31.08**	37.39**
CMS4626A × VR 521	68.57	50.81**	49.17**	0.19	86.49**	55.13	43.08**	39.46**	-12.11*	75.21**
CMS4626A × FL 201	55.87	55.98**	24.24**	-18.36**	51.95**	44.17	51.34**	17.67*	-29.60**	40.36**
CMS4626A × PP 402	59.77	60.02**	32.91**	-12.66*	62.56**	53.13	74.02**	41.56**	-15.30**	68.86**
CMS4626A × C 142	77.83	61.31**	51.03**	13.74*	111.70**	69.10	63.87**	47.65**	10.15*	119.60**
CMS4626A × PP 414	42.33	10.39	-5.86	-38.14**	15.14	33.83	13.53	-9.86	-46.07**	7.52
CMS4626A × VR 522	68.23	57.04**	51.74**	-0.29	85.58**	53.10	56.02**	41.47**	-15.36**	68.75**
CMS4626A × PL 406	76.53	50.46**	34.82**	11.84*	108.16**	69.83	68.54**	54.04**	11.32*	121.93**
CMS4626A × E 183	40.93	11.64	-8.97	-40.19**	11.33	32.33	7.00	-13.85	-48.46**	2.75
CMS4626A × IS 268	61.77	17.95**	3.35	-9.74	68.00**	55.63	26.20**	9.87	-11.32*	76.80**
CMS4626A × IS 261	76.37	42.87**	23.30**	11.59*	107.71**	65.33	40.55**	17.86**	4.14	107.63**
CMS463D13A × AC 102	55.37	4.40	-6.69	-19.09**	50.59**	42.93	-4.94	-19.10**	-31.56**	36.44**
CMS463D13A × SL 475	86.37	39.23**	33.42**	26.21**	134.90**	75.57	39.42**	36.57**	20.46**	140.15**

Crosses	**Number of seed fruit^{-1}**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	72.43	28.47**	22.08**	5.85	97.01**	67.23	34.47**	26.70**	7.17	113.67**
CMS463D13A × IS 263	59.70	11.42	0.62	-12.76*	62.38**	49.77	6.30	-6.22	-20.67**	58.16**
CMS463D13A × VR 523	68.90	30.62**	16.12*	0.68	87.40**	58.13	27.58**	9.55	-7.33	84.75**
CMS463D13A × DL 161	53.70	-0.98	-9.49	-21.53**	46.06**	46.77	1.12	-11.87*	-25.45**	48.62**
CMS463D13A × IS 267	78.87	28.17**	23.74**	15.25**	114.51**	72.33	35.54**	34.78**	15.30**	129.87**
CMS463D13A × YL 581	56.90	25.38**	-4.10	-16.85**	54.76**	40.73	8.43	-23.24**	-35.07**	29.45**
CMS463D13A × SL 473	61.73	28.88**	4.04	-9.79	67.91**	51.93	29.19**	-2.14	-17.22**	65.04**
CMS463D13A × IS 262	57.33	17.01**	-3.37	-16.22**	55.94**	45.60	5.56	-14.07*	-27.31**	44.92**
CMS463D13A × VR 521	81.17	54.16**	36.80**	18.61**	120.76**	66.87	44.42**	26.01**	6.59	112.50**
CMS463D13A × FL 201	41.73	-2.95	-29.66**	-39.02**	13.51	36.33	-1.67	-31.53**	-42.08**	15.47
CMS463D13A × PP 402	55.70	25.07**	-6.12	-18.61**	51.50**	44.53	16.28*	-16.08**	-29.01**	41.53**
CMS463D13A × C 142	77.97	40.65**	31.40**	13.93*	112.06**	65.73	31.64**	23.87**	4.78	108.90**
CMS463D13A × PP 414	48.33	6.15	-18.54**	-29.37**	31.46**	37.17	-1.06	-29.96**	-40.75**	18.11
CMS463D13A × VR 522	74.80	47.73**	26.07**	9.30	103.45**	61.73	47.69**	16.33**	-1.59	96.19**
CMS463D13A × PL 406	79.20	36.43**	33.48**	15.73**	115.41**	63.30	28.66**	19.28**	0.90	101.17**
CMS463D13A × E 183	39.73	-9.39	-33.03**	-41.94**	8.07	30.43	-19.88**	-42.65**	-51.49**	-3.28
CMS463D13A × IS 268	88.93	49.34**	48.80**	29.96**	141.89**	69.73	34.49**	31.41**	11.16*	121.61**
CMS463D13A × IS 261	93.37	53.99**	50.75**	36.43**	153.94**	74.13	36.65**	33.73**	18.17**	135.59**
LSD at *p*=0.05		6.27	7.24	7.24	7.24		5.03	5.81	5.81	5.81
LSD at *p*=0.01		8.29	9.57	9.57	9.57		6.66	7.68	7.68	7.68

Table 4.12i (*Cont'd.*)

Crosses	**Number of seed fruit^{-1}**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	H_{BP}	**CH-27**	**Soldier**		H_{MP}	H_{BP}	**CH-27**	**Soldier**
CMS4611A × AC 102	39.73	15.11*	11.30	-32.12**	71.76**	53.93	31.87**	26.34**	-14.71**	77.09**
CMS4611A × SL 475	57.87	37.40**	19.23**	-1.14	150.14**	66.06	33.60**	17.54**	4.46	116.89**
CMS4611A × PL 412	53.33	38.65**	29.35**	-8.88*	130.55**	63.28	40.79**	34.06**	0.07	107.77**
CMS4611A × IS 263	38.43	6.96	6.27	-34.34**	66.14**	51.68	22.73**	21.06**	-18.27**	69.68**
CMS4611A × VR 523	50.27	41.53**	40.80**	-14.12**	117.29**	58.06	40.66**	36.00**	-8.19**	90.62**
CMS4611A × DL 161	43.93	30.24**	23.06**	-24.94**	89.91**	49.40	19.32**	15.72**	-21.88**	62.20**
CMS4611A × IS 267	53.97	26.78**	9.17	-7.80	133.29**	59.11	20.27**	6.29	-6.52*	94.09**
CMS4611A × YL 581	27.07	3.11	-24.18**	-53.76**	17.00	38.58	16.69**	-9.63*	-38.99**	26.67**
CMS4611A × SL 473	35.63	26.96**	-0.19	-39.12**	54.03**	44.54	25.89**	4.35	-29.56**	46.26**
CMS4611A × IS 262	35.13	16.08*	-1.59	-39.98**	51.87**	42.33	12.94**	-0.83	-33.05**	39.00**
CMS4611A × VR 521	44.93	33.86**	25.86**	-23.23**	94.24**	57.56	40.95**	34.83**	-8.98**	88.98**
CMS4611A × FL 201	25.23	-0.72	-29.32**	-56.89**	9.08	32.69	2.85	-23.43**	-48.30**	7.33
CMS4611A × PP 402	26.43	-2.16	-25.96**	-54.84**	14.27	31.04	-6.71	-27.28**	-50.90**	1.93
CMS4611A × C 142	50.43	36.74**	32.49**	-13.84**	118.01**	55.46	25.81**	21.97**	-12.30**	82.09**
CMS4611A × PP 414	30.93	17.77*	-13.35	-47.15**	33.72**	39.69	19.85**	-7.03	-37.23**	30.32**
CMS4611A × VR 522	39.53	35.31**	10.74	-32.46**	70.89**	48.24	29.65**	13.01**	-23.70**	58.41**
CMS4611A × PL 406	54.43	42.43**	33.63**	-7.00	135.30**	61.58	36.38**	29.33**	-2.62	102.19**
CMS4611A × E 183	27.33	6.49	-23.44**	-53.30**	18.16	33.83	4.12	-20.74**	-46.49**	11.09
CMS4611A × IS 268	59.33	50.66**	37.77**	1.37	156.48**	66.10	40.87**	29.21**	4.53	117.04**
CMS4611A × IS 261	58.47	34.97**	14.79**	-0.11	152.74**	69.09	39.87**	23.15**	9.26**	126.85**

Crosses	**Number of seed fruit^{-1}**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	34.70	7.99	4.10	-40.72**	50.00**	42.39	10.21*	8.38	-32.96**	39.18**
CMS4626A × SL 475	60.50	52.27**	24.66**	3.36	161.53**	73.38	56.10**	30.57**	16.04**	140.93**
CMS4626A × PL 412	58.30	61.57**	41.39**	-0.40	152.02**	66.78	57.10**	41.48**	5.61	119.26**
CMS4626A × IS 263	33.90	1.04	-6.27	-42.08**	46.54**	39.26	-1.04	-5.46	-37.92**	28.89**
CMS4626A × VR 523	51.93	56.74**	46.98**	-11.28*	124.50**	58.29	50.10**	46.25**	-7.82**	91.39**
CMS4626A × DL 161	49.73	58.64**	56.56**	-15.03**	114.99**	49.50	27.05**	23.41**	-21.72**	62.53**
CMS4626A × IS 267	54.70	36.13**	10.65*	-6.55	136.46**	65.03	39.22**	16.94**	2.85	113.54**
CMS4626A × YL 581	24.13	1.12	-21.98**	-58.77**	4.32	31.61	3.23	-16.40**	-50.01**	3.79
CMS4626A × SL 473	32.63	27.06**	5.50	-44.25**	41.07**	47.07	42.87**	24.48**	-25.57**	54.54**
CMS4626A × IS 262	37.83	35.68**	22.31**	-35.36**	63.54**	45.26	29.14**	19.69**	-28.43**	48.60**
CMS4626A × VR 521	45.77	46.77**	45.60**	-21.81**	97.84**	56.49	47.13**	44.93**	-10.67**	85.48**
CMS4626A × FL 201	27.67	20.12*	-10.56	-52.73**	19.60	42.57	45.06**	12.58*	-32.68**	39.77**
CMS4626A × PP 402	36.37	47.63**	17.56*	-37.87**	57.20**	49.76	61.34**	31.59**	-21.31**	63.37**
CMS4626A × C 142	53.40	54.78**	40.28**	-8.77*	130.84**	66.78	60.37**	46.87**	5.61	119.26**
CMS4626A × PP 414	25.43	6.49	-17.78*	-56.55**	9.94	33.87	10.39	-10.43*	-46.44**	11.20
CMS4626A × VR 522	37.47	39.63**	21.12*	-35.99**	61.96**	52.93	52.23**	39.99**	-16.29**	73.81**
CMS4626A × PL 406	56.93	58.88**	39.77**	-2.73	146.11**	67.77	58.66**	42.33**	7.17*	122.51**
CMS4626A × E 183	28.93	24.27*	-6.47	-50.57**	25.07*	34.07	13.35*	-9.90*	-46.13**	11.86
CMS4626A × IS 268	51.47	39.10**	19.50**	-12.07**	122.48**	56.29	26.54**	10.03**	-10.98**	84.82**
CMS4626A × IS 261	61.43	50.08**	20.62**	4.95	165.56**	67.71	44.20**	20.70**	7.08*	122.33**
CMS463D13A × AC 102	34.83	-11.44*	-23.16**	-40.49**	50.58**	44.38	-3.20	-15.60**	-29.82**	45.71**
CMS463D13A × SL 475	60.63	29.19**	24.93**	3.59	162.10**	74.19	36.40**	32.01**	17.33**	143.60**

Crosses	**Number of seed fruit^{-1}**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	62.37	44.09**	37.57**	6.55	169.60**	67.34	34.99**	28.09**	6.50*	121.12**
CMS463D13A × IS 263	39.43	-3.23	-13.01*	-32.63**	70.46**	49.63	5.49	-5.60	-21.51**	62.97**
CMS463D13A × VR 523	53.40	32.40**	17.79**	-8.77*	130.84**	60.14	30.14**	14.39**	-4.88	97.48**
CMS463D13A × DL 161	43.07	11.72*	-5.00	-26.42**	86.17**	47.84	3.24	-9.00*	-24.34**	57.10**
CMS463D13A × IS 267	59.73	26.06**	20.84**	2.05	158.21**	70.31	29.98**	26.43**	11.19**	130.86**
CMS463D13A × YL 581	30.53	-1.72	-32.65**	-47.84**	31.99**	42.72	12.41**	-18.74**	-32.44**	40.28**
CMS463D13A × SL 473	41.30	25.60**	-8.90	-29.44**	78.53**	51.66	28.09**	-1.75	-18.31**	69.61**
CMS463D13A × IS 262	39.73	13.25*	-12.35*	-32.12**	71.76**	47.56	12.09**	-9.55**	-24.79**	56.15**
CMS463D13A × VR 521	58.17	51.54**	28.31**	-0.63	151.44**	68.73	50.15**	30.73**	8.70**	125.68**
CMS463D13A × FL 201	29.47	-2.54	-35.00**	-49.66**	27.38*	35.84	-2.41	-31.83**	-43.31**	17.69**
CMS463D13A × PP 402	35.63	11.94	-21.40**	-39.12**	54.03**	45.29	18.49**	-13.86**	-28.38**	48.70**
CMS463D13A × C 142	59.47	42.61**	31.18**	1.59	157.06**	67.72	38.15**	28.80**	7.10*	122.36**
CMS463D13A × PP 414	28.93	-6.92	-36.18**	-50.57**	25.07*	38.14	0.22	-27.45**	-39.68**	25.25**
CMS463D13A × VR 522	51.73	52.01**	14.12*	-11.62**	123.63**	62.76	48.87**	19.36**	-0.76	106.06**
CMS463D13A × PL 406	59.03	37.18**	30.22**	0.85	155.19**	67.18	34.10**	27.77**	6.24*	120.58**
CMS463D13A × E 183	24.97	-18.10*	-44.93**	-57.35**	7.93	31.71	-15.30**	-39.69**	-49.85**	4.12
CMS463D13A × IS 268	55.53	25.64**	22.50**	-5.13	140.06**	71.40	37.66**	35.80**	12.92**	134.44**
CMS463D13A × IS 261	59.80	24.24**	17.41**	2.16	158.50**	75.77	39.43**	35.06**	19.82**	148.78**
LSD at *p*=0.05		4.36	5.03	5.03	5.03		3.24	3.74	3.74	3.74
LSD at *p*=0.01		5.76	6.65	6.65	6.65		4.27	4.93	4.93	4.93

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.12j: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for 1000 seed weight (g) evaluated over environments

Crosses	1000 seed weight (g)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	4.23	1.44	-9.22	-30.75**	-11.68	3.90	1.17	-10.34	-33.43**	-12.35
CMS4611A × SL 475	5.79	16.72**	10.07	-5.23	20.86**	5.44	16.73**	9.45	-7.16	22.23**
CMS4611A × PL 412	5.06	4.98	1.61	-17.18**	5.63	4.81	5.59	1.05	-17.91**	8.08
CMS4611A × IS 263	6.12	9.77*	-5.70	0.16	27.75**	5.93	12.39*	-4.31	1.08	33.08**
CMS4611A × VR 523	5.25	3.31	-4.49	-14.18**	9.46	5.05	5.76	-2.88	-13.81**	13.47*
CMS4611A × DL 161	3.79	-7.60	-18.80**	-38.06**	-21.00**	3.51	-8.35	-19.30**	-40.08**	-21.11**
CMS4611A × IS 267	5.54	9.37	1.28	-9.32	15.65*	5.31	11.43*	2.51	-9.38	19.31**
CMS4611A × YL 581	6.25	4.34	-14.61**	2.29	30.46**	6.00	5.82	-14.16**	2.39	34.81**
CMS4611A × SL 473	5.36	4.08	-4.96	-12.27*	11.89	5.12	5.28	-4.71	-12.68*	14.97*
CMS4611A × IS 262	5.73	5.81	-7.13	-6.22	19.61**	5.54	8.17	-5.89	-5.57	24.33**
CMS4611A × VR 521	3.67	-6.73	-21.23**	-39.91**	-23.37**	3.36	-7.18	-22.74**	-42.64**	-24.48**
CMS4611A × FL 201	6.32	3.86	-15.84**	3.44	31.92**	5.99	5.12	-14.99**	2.22	34.58**
CMS4611A × PP 402	5.88	12.64*	1.73	-3.76	22.74**	5.64	13.82**	1.44	-3.75	26.72**
CMS4611A × C 142	4.25	-0.58	-8.79	-30.43**	-11.27	3.99	0.80	-8.35	-31.95**	-10.40
CMS4611A × PP 414	5.46	11.63*	6.71	-10.74*	13.84*	5.17	12.38*	6.59	-11.77*	16.17*
CMS4611A × VR 522	4.89	-0.27	-4.93	-20.01**	2.02	4.59	-0.65	-6.13	-21.66**	3.14
CMS4611A × PL 406	4.75	1.75	1.64	-22.30**	-0.90	4.45	2.18	2.06	-24.05**	0.00
CMS4611A × E 183	4.41	-1.12	-5.36	-27.81**	-7.93	4.18	1.42	-4.06	-28.77**	-6.21
CMS4611A × IS 268	5.59	10.47*	2.38	-8.51	16.69**	5.39	12.63*	3.25	-8.02	21.11**
CMS4611A × IS 261	6.28	18.59**	5.90	2.78	31.08**	6.01	19.64**	5.56	2.50	34.96**

Crosses	**1000 seed weight (g)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	4.45	5.49	-6.38	-27.21**	-7.16	4.12	5.06	-7.97	-29.79**	-7.56
CMS4626A × SL 475	5.41	8.09	2.85	-11.45*	12.93*	5.19	9.95	4.42	-11.43*	16.62*
CMS4626A × PL 412	5.01	2.91	0.54	-18.05**	4.52	4.79	3.79	0.63	-18.25**	7.63
CMS4626A × IS 263	6.57	16.89**	1.23	7.52	37.13**	6.32	18.56**	2.10	7.85	41.99**
CMS4626A × VR 523	5.88	14.83**	7.10	-3.76	22.74**	5.57	15.05**	6.98	-5.06	25.00**
CMS4626A × DL 161	4.11	-0.72	-13.46*	-32.72**	-14.19*	3.76	-3.34	-15.87*	-35.82**	-15.49*
CMS4626A × IS 267	5.68	11.15*	3.84	-7.03	18.57**	5.46	13.08*	5.34	-6.88	22.60**
CMS4626A × YL 581	6.33	4.78	-13.61**	3.49	31.99**	5.97	4.19	-14.59**	1.88	34.13**
CMS4626A × SL 473	5.47	5.16	-3.13	-10.58*	14.05*	5.22	6.03	-2.85	-10.97*	17.22*
CMS4626A × IS 262	6.15	12.63**	-0.32	0.65	28.37**	5.89	13.81**	0.17	0.51	32.34**
CMS4626A × VR 521	3.59	-9.79	-24.40**	-41.22**	-25.03**	3.29	-10.59	-26.38**	-43.83**	-26.05**
CMS4626A × FL 201	6.21	1.30	-17.30**	1.64	29.62**	5.95	3.33	-15.56**	1.53	33.68**
CMS4626A × PP 402	6.18	17.37**	6.92	1.15	29.00**	5.90	17.57**	6.05	0.63	32.49**
CMS4626A × C 142	4.06	-6.01	-14.52*	-33.53**	-15.23*	3.81	-5.10	-14.75*	-34.96**	-14.37*
CMS4626A × PP 414	5.26	6.69	2.93	-13.90**	9.81	4.96	6.29	2.13	-15.46**	11.30
CMS4626A × VR 522	6.13	23.95**	19.25**	0.33	27.96**	5.81	24.13**	18.80**	-0.85	30.54**
CMS4626A × PL 406	4.98	5.73	4.84	-18.48**	3.96	4.75	7.51	6.18	-18.99**	6.66
CMS4626A × E 183	4.35	-3.59	-8.56	-28.90**	-9.32	3.99	-4.59	-10.88	-32.01**	-10.48
CMS4626A × IS 268	5.89	15.37**	7.87	-3.60	22.95**	5.56	14.75**	6.51	-5.12	24.93**
CMS4626A × IS 261	6.29	17.78**	6.07	2.94	31.29**	5.99	17.90**	5.27	2.22	34.58**
CMS463D13A × AC 102	4.58	6.80	-6.40	-25.08**	-4.45	4.35	9.84	-4.60	-25.75**	-2.25
CMS463D13A × SL 475	6.42	26.42**	21.98**	5.02	33.94**	6.11	28.21**	22.92**	4.26	37.28**

Crosses	**1000 seed weight (g)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	5.29	7.12	6.15	-13.47**	10.36	4.96	6.43	4.20	-15.35**	11.45
CMS463D13A × IS 263	6.67	17.21**	2.77	9.16	39.22**	6.39	18.87**	3.23	9.04	43.56**
CMS463D13A × VR 523	5.98	15.08**	8.80	-2.24	24.69**	5.62	15.15**	8.07	-4.09	26.27**
CMS463D13A × DL 161	4.62	9.73	-5.52	-24.37**	-3.55	4.32	9.61	-5.41	-26.38**	-3.07
CMS463D13A × IS 267	5.58	7.72	2.01	-8.67	16.48**	5.36	10.05	3.47	-8.53	20.43**
CMS463D13A × YL 581	6.78	10.94*	-7.46	10.85*	41.38**	6.59	14.10**	-5.72	12.45*	48.05**
CMS463D13A × SL 473	6.17	17.05**	9.27	0.87	28.65**	5.84	17.48**	8.62	-0.45	31.06**
CMS463D13A × IS 262	5.97	7.83	-3.35	-2.40	24.48**	5.92	13.40**	0.68	1.02	33.01**
CMS463D13A × VR 521	4.55	12.34	-6.95	-25.52**	-5.01	4.17	11.76	-8.69	-28.94**	-6.44
CMS463D13A × FL 201	6.88	10.96*	-8.39*	12.60*	43.60**	6.60	13.72**	-6.34	12.62*	48.28**
CMS463D13A × PP 402	6.25	17.14**	8.13	2.29	30.46**	5.88	16.19**	5.75	0.34	32.11**
CMS463D13A × C 142	5.12	16.62**	4.70	-16.19**	6.88	4.77	17.47**	4.60	-18.59**	7.19
CMS463D13A × PP 414	5.43	8.46	6.13	-11.23*	13.21*	5.08	7.96	4.74	-13.30**	14.15*
CMS463D13A × VR 522	6.23	24.08**	21.06**	1.85	29.90**	5.91	25.06**	20.84**	0.85	32.78**
CMS463D13A × PL 406	5.19	8.57	6.13	-15.05**	8.34	4.95	10.98	8.55	-15.52**	11.23
CMS463D13A × E 183	4.51	-1.49	-7.83	-26.23**	-5.91	4.15	-1.66	-8.98	-29.16**	-6.74
CMS463D13A × IS 268	5.66	9.37	3.66	-7.36	18.15**	5.43	11.04*	4.02	-7.33	22.01**
CMS463D13A × IS 261	6.15	13.67**	3.71	0.65	28.37**	5.89	14.92**	3.51	0.51	32.34**
LSD at p=0.05		0.52	0.60	0.60	0.60		0.51	0.58	0.58	0.58
LSD at p=0.01		0.68	0.79	0.79	0.79		0.67	0.77	0.77	0.77

Table 4.12j (*Cont'd.*)

Crosses	1000 seed weight (g)									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	3.72	1.92	-11.21	-34.83**	-11.98	3.95	1.50	-10.22*	-32.96**	-12.00**
CMS4611A × SL 475	5.26	16.88**	9.35	-7.88	24.43**	5.50	16.77**	9.63**	-6.73*	22.43**
CMS4611A × PL 412	4.65	5.88	1.23	-18.55**	10.01	4.84	5.47	1.30	-17.86**	7.82*
CMS4611A × IS 263	5.74	12.07*	-5.17	0.53	35.78**	5.93	11.37**	-5.07	0.58	32.03**
CMS4611A × VR 523	4.81	4.79	-3.54	-15.81**	13.71	5.04	4.59	-3.66	-14.58**	12.12**
CMS4611A × DL 161	3.31	-8.89	-20.99**	-42.01**	-21.67**	3.54	-8.26*	-19.66**	-40.00**	-21.25**
CMS4611A × IS 267	5.09	10.64	1.60	-10.85*	20.41**	5.32	10.46**	1.79	-9.84**	18.35**
CMS4611A × YL 581	5.79	5.08	-15.22**	1.40	36.96**	6.02	5.06	-14.66**	2.04	33.94**
CMS4611A × SL 473	4.90	5.08	-4.55	-14.24**	15.84*	5.13	4.79	-4.75	-13.04**	14.15**
CMS4611A × IS 262	5.30	7.54	-6.42	-7.23	25.30**	5.52	7.15*	-6.49*	-6.33*	22.95**
CMS4611A × VR 521	3.09	-10.52	-26.31**	-45.92**	-26.95**	3.38	-8.06	-23.34**	-42.75**	-24.86**
CMS4611A × FL 201	5.80	4.72	-15.77**	1.58	37.19**	6.04	4.55	-15.54**	2.43	34.45**
CMS4611A × PP 402	5.47	14.54**	2.05	-4.20	29.39**	5.67	13.64**	1.74	-3.90	26.14**
CMS4611A × C 142	3.77	-0.53	-10.02	-33.96**	-10.80	4.01	-0.11	-9.03*	-32.07**	-10.83**
CMS4611A × PP 414	4.92	11.30	5.80	-13.83*	16.39*	5.18	11.77**	6.38	-12.08**	15.41**
CMS4611A × VR 522	4.33	-2.03	-6.88	-24.15**	2.44	4.61	-0.96	-5.95	-21.90**	2.52
CMS4611A × PL 406	4.30	2.75	2.62	-24.68**	1.73	4.50	2.21	2.17	-23.65**	0.22
CMS4611A × E 183	3.90	-0.09	-7.00	-31.74**	-7.80	4.16	0.04	-5.45	-29.40**	-7.32
CMS4611A × IS 268	5.27	14.39*	4.91	-7.70	24.67**	5.42	12.44**	3.48	-8.08**	20.65**
CMS4611A × IS 261	5.81	19.47**	5.00	1.69	37.35**	6.03	19.22**	5.50	2.34	34.33**

Crosses	1000 seed weight (g)									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4626A × AC 102	3.87	4.87	-9.36	-32.21**	-8.43	4.15	5.16	-7.85*	-29.68**	-7.69*
CMS4626A × SL 475	5.03	10.79	4.57	-11.90*	18.99**	5.21	9.56**	3.92	-11.59**	16.05**
CMS4626A × PL 412	4.60	3.72	0.07	-19.49**	8.75	4.80	3.46	0.42	-18.58**	6.88
CMS4626A × IS 263	6.15	19.14**	1.60	7.70	45.47**	6.35	18.16**	1.64	7.69**	41.36**
CMS4626A × VR 523	5.28	14.11*	5.95	-7.53	24.90**	5.58	14.68**	6.70*	-5.41	24.17**
CMS4626A × DL 161	3.52	-4.17	-17.55*	-38.33**	-16.71*	3.80	-2.68	-15.56**	-35.56**	-15.41**
CMS4626A × IS 267	5.28	13.78*	5.39	-7.53	24.90**	5.48	12.63**	4.83	-7.14*	21.89**
CMS4626A × YL 581	5.80	4.44	-15.12**	1.52	37.12**	6.03	4.47	-14.42**	2.32	34.31**
CMS4626A × SL 473	5.05	7.44	-1.56	-11.55*	19.46**	5.25	6.17*	-2.54	-11.02**	16.79**
CMS4626A × IS 262	5.72	15.20**	1.06	0.18	35.30**	5.92	13.84**	0.28	0.45	31.86**
CMS4626A × VR 521	3.04	-12.88	-28.78**	-46.73**	-28.05**	3.31	-11.02**	-26.44**	-43.87**	-26.32**
CMS4626A × FL 201	5.82	4.33	-15.48**	1.93	37.67**	6.00	2.94	-16.14**	1.70	33.49**
CMS4626A × PP 402	5.76	19.61**	7.46	0.88	36.25**	5.95	18.15**	6.80*	0.89	32.43**
CMS4626A × C 142	3.59	-6.26	-15.91*	-37.11**	-15.05*	3.82	-5.79	-15.04**	-35.16**	-14.89**
CMS4626A × PP 414	4.73	6.05	1.72	-17.15**	11.90	4.98	6.35	2.28	-15.47**	10.96**
CMS4626A × VR 522	5.73	28.30**	23.07**	0.23	35.38**	5.89	25.39**	20.31**	-0.09	31.14**
CMS4626A × PL 406	4.50	6.50	5.38	-21.18**	6.46	4.75	6.56	5.46	-19.52**	5.64
CMS4626A × E 183	3.70	-6.09	-13.34	-35.18**	-12.45	4.01	-4.70	-10.84**	-31.96**	-10.69**
CMS4626A × IS 268	5.34	14.91**	6.30	-6.48	26.32**	5.60	15.02**	6.92*	-5.03	24.66**
CMS4626A × IS 261	5.82	18.76**	5.24	1.93	37.67**	6.04	18.13**	5.54	2.37	34.38**
CMS463D13A × AC 102	4.19	12.47	-3.45	-26.60**	-0.87	4.38	9.57*	-4.88	-25.80**	-2.60
CMS463D13A × SL 475	5.87	28.29**	22.02**	2.80	38.85**	6.14	27.60**	22.30**	4.05	36.58**

Crosses	**1000 seed weight (g)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	4.79	7.08	4.13	-16.22**	13.16	5.01	6.88*	4.86	-14.98**	11.60**
CMS463D13A × IS 263	6.23	19.87**	2.92	9.10	47.36**	6.43	18.61**	2.97	9.10**	43.21**
CMS463D13A × VR 523	5.36	14.83**	7.42	-6.24	26.64**	5.65	15.03**	8.12*	-4.15	25.82**
CMS463D13A × DL 161	4.20	13.16	-3.30	-26.49**	-0.71	4.38	10.76**	-4.78	-25.72**	-2.50
CMS463D13A × IS 267	5.21	11.44*	3.99	-8.75	23.25**	5.39	9.67**	3.13	-8.65**	19.91**
CMS463D13A × YL 581	6.46	15.66**	-5.41	13.13*	52.80**	6.61	13.50**	-6.23*	12.12**	47.17**
CMS463D13A × SL 473	5.73	20.86**	11.56	0.23	35.38**	5.91	18.40**	9.78**	0.23	31.56**
CMS463D13A × IS 262	5.77	15.39**	1.94	1.05	36.49**	5.89	12.08**	-0.32	-0.15	31.07**
CMS463D13A × VR 521	3.91	10.72	-10.05	-31.62**	-7.64	4.21	11.64**	-8.50*	-28.62**	-6.31
CMS463D13A × FL 201	6.39	13.83**	-7.21	11.90*	51.14**	6.63	12.78**	-7.33**	12.38**	47.51**
CMS463D13A × PP 402	5.73	18.13**	6.90	0.35	35.54**	5.96	17.14**	6.94*	1.02	32.60**
CMS463D13A × C 142	4.52	16.76*	3.99	-20.95**	6.78	4.80	16.94**	4.44	-18.52**	6.95
CMS463D13A × PP 414	4.85	7.89	4.30	-15.05**	14.74*	5.12	8.12*	5.08	-13.15**	14.00**
CMS463D13A × VR 522	5.72	27.23**	22.99**	0.18	35.30**	5.95	25.40**	21.60**	0.98	32.55**
CMS463D13A × PL 406	4.70	10.32	8.29	-17.68**	11.19	4.95	9.92**	7.61*	-16.05**	10.19**
CMS463D13A × E 183	3.91	-1.72	-9.98	-31.56**	-7.57	4.19	-1.62	-8.89*	-28.92**	-6.70
CMS463D13A × IS 268	5.73	22.23**	13.93*	0.23	35.38**	5.61	14.00**	7.06*	-4.90	24.83**
CMS463D13A × IS 261	5.75	16.50**	3.98	0.70	36.01**	5.93	14.99**	3.73	0.62	32.08**
LSD at p=0.05		0.52	0.60	0.60	0.60		0.30	0.34	0.34	0.34
LSD at p=0.01		0.69	0.79	0.79	0.79		0.39	0.45	0.45	0.45

*, significant at p=0.05; **, significant at p=0.01

Table 4.12k: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for total yield plant^{-1} (g) evaluated over environments**

Crosses	Total yield plant^{-1} (kg)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	0.69	32.38**	16.95	-29.90**	-20.51**	0.27	-35.12**	-40.82**	-64.70**	-63.81**
CMS4611A × SL 475	0.88	26.04**	-6.47	-11.20	0.69	0.74	24.63**	1.23	-3.30	-0.89
CMS4611A × PL 412	0.72	-5.36	-32.62**	-26.93**	-17.15*	0.78	36.58**	13.45*	2.35	4.90
CMS4611A × IS 263	0.72	49.65**	41.26**	-26.86**	-17.07*	0.32	-16.68	-29.37**	-57.87**	-56.82**
CMS4611A × VR 523	0.86	69.16**	52.14**	-12.45*	-0.73	0.39	-15.02	-15.67	-49.70**	-48.44**
CMS4611A × DL 161	1.17	81.79**	40.14**	18.90**	34.83**	0.48	-2.35	-8.21	-37.78**	-36.23**
CMS4611A × IS 267	0.94	73.69**	49.39**	-4.66	8.11	0.74	64.25**	61.73**	-3.52	-1.11
CMS4611A × YL 581	0.69	38.93**	27.94*	-30.14**	-20.78**	0.89	85.42**	76.28**	16.65**	19.56**
CMS4611A × SL 473	0.68	20.40*	0.89	-31.39**	-22.20**	0.48	6.09	5.32	-37.17**	-35.61**
CMS4611A × IS 262	0.86	33.30**	2.57	-12.52*	-0.80	0.50	29.16**	9.91	-34.43**	-32.80**
CMS4611A × VR 521	0.55	37.40**	20.85	-44.45**	-37.01**	0.36	2.40	-22.38*	-53.70**	-52.54**
CMS4611A × FL 201	0.83	45.72**	21.36*	-16.20**	-4.98	0.46	8.35	0.29	-40.17**	-38.68**
CMS4611A × PP 402	0.92	92.84**	83.05**	-6.34	6.20	0.92	159.04**	100.51**	19.61**	22.59**
CMS4611A × C 142	1.10	82.23**	45.69**	11.81	26.79**	0.72	85.15**	58.09**	-5.70	-3.34
CMS4611A × PP 414	0.77	36.20**	14.15	-22.41**	-12.02	0.29	-22.72*	-37.54**	-62.74**	-61.81**
CMS4611A × VR 522	0.85	31.05**	0.59	-13.60*	-2.03	0.57	31.85**	25.07**	-25.39**	-23.53**
CMS4611A × PL 406	0.93	42.05**	9.04	-6.34	6.20	0.44	11.01	-4.08	-42.78**	-41.35**
CMS4611A × E 183	0.50	37.82**	9.84	-49.51**	-42.75**	0.28	-22.10*	-38.48**	-63.30**	-62.39**
CMS4611A × IS 268	1.05	79.09**	46.56**	5.80	19.98**	0.76	86.69**	66.69**	-0.57	1.92
CMS4611A × IS 261	0.72	30.58**	11.34	-27.44**	-17.72*	0.51	13.05	11.73	-33.35**	-31.68**

Crosses	**Total yield plant^{-1} (kg)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	0.55	-0.12	-7.55	-44.58**	-37.16**	0.30	-26.29**	-31.99**	-60.43**	-59.45**
CMS4626A × SL 475	0.98	35.45**	4.12	-1.15	12.09	0.88	48.63**	19.57**	14.22*	17.07**
CMS4626A × PL 412	1.17	48.57**	9.24	18.46**	34.33**	0.95	66.66**	37.06**	23.65**	26.74**
CMS4626A × IS 263	0.51	1.05	0.33	-48.06**	-41.10**	0.82	115.36**	84.45**	7.30	9.98
CMS4626A × VR 523	1.03	91.54**	80.70**	3.98	17.91*	0.66	46.60**	45.89**	-14.30*	-12.17*
CMS4626A × DL 161	1.27	89.42**	51.67**	28.69**	45.92**	0.88	81.36**	68.51**	14.22*	17.07**
CMS4626A × IS 267	0.83	46.05**	31.41**	-16.13**	-4.90	0.81	82.83**	82.29**	6.04	8.69
CMS4626A × YL 581	0.83	59.74**	54.51**	-15.63*	-4.32	1.07	124.97**	111.37**	39.87**	43.36**
CMS4626A × SL 473	0.73	24.98**	9.38	-25.62**	-15.65*	0.53	18.66*	18.05	-30.61**	-28.88**
CMS4626A × IS 262	1.03	53.21**	22.44**	4.42	18.41**	0.79	106.26**	77.35**	3.17	5.75
CMS4626A × VR 521	0.45	4.87	-11.71	-54.94**	-48.91**	0.40	15.93	-11.36	-48.43**	-47.15**
CMS4626A × FL 201	0.71	20.35*	4.64	-27.74**	-18.06**	1.10	164.41**	147.61**	44.04**	47.64**
CMS4626A × PP 402	0.82	62.55**	62.34**	-16.94**	-5.82	0.88	151.29**	96.26**	14.17*	17.02**
CMS4626A × C 142	1.17	84.94**	53.96**	18.16**	33.98**	0.75	95.41**	68.61**	-1.91	0.53
CMS4626A × PP 414	0.63	8.05	-5.41	-35.71**	-27.10**	0.54	48.81**	21.45*	-29.35**	-27.58**
CMS4626A × VR 522	0.93	37.89**	9.90	-5.60	7.04	0.77	79.68**	72.50**	0.35	2.85
CMS4626A × PL 406	1.05	55.68**	24.09**	6.58	20.86**	0.65	65.77**	44.77**	-15.78**	-13.68*
CMS4626A × E 183	0.34	-11.16	-31.81**	-65.20**	-60.54**	0.30	-14.77	-32.06**	-60.48**	-59.49**
CMS4626A × IS 268	1.22	100.93**	71.48**	23.79**	40.38**	0.81	101.74**	82.14**	5.96	8.60
CMS4626A × IS 261	0.81	41.50**	26.15**	-17.79**	-6.77	0.67	49.44**	49.33**	-13.00*	-10.83
CMS463D13A × AC 102	0.97	61.74**	60.00**	-1.99	11.14	0.53	25.53**	12.93	-30.52**	-28.79**
CMS463D13A × SL 475	1.05	35.74**	11.66	6.01	20.21**	1.09	81.51**	49.20**	42.52**	46.08**

Crosses	**Total yield plant^{-1} (kg)**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	1.26	50.68**	17.90**	27.84**	44.97**	0.69	18.22**	-0.58	-10.30	-8.07
CMS463D13A × IS 263	0.81	45.48**	34.21**	-17.79**	-6.77	0.80	103.38**	70.25**	4.74	7.35
CMS463D13A × VR 523	1.20	104.20**	98.02**	21.30**	37.54**	0.92	99.35**	94.84**	19.87**	22.86**
CMS463D13A × DL 161	1.37	89.47**	63.13**	38.41**	56.95**	0.50	1.08	-3.59	-34.65**	-33.02**
CMS463D13A × IS 267	1.48	140.26**	135.43**	50.25**	70.38**	0.88	91.40**	85.65**	14.22*	17.07**
CMS463D13A × YL 581	1.05	83.34**	73.39**	6.21	20.44**	0.89	81.00**	74.64**	15.57**	18.45**
CMS463D13A × SL 473	1.16	81.72**	72.70**	17.45**	33.18**	0.81	76.29**	72.37**	6.04	8.69
CMS463D13A × IS 262	1.41	95.12**	67.63**	42.96**	62.11**	0.50	25.99**	5.87	-34.87**	-33.24**
CMS463D13A × VR 521	0.56	18.78	-6.78	-42.90**	-35.25**	0.26	-26.52*	-44.88**	-66.09**	-65.24**
CMS463D13A × FL 201	0.90	39.39**	31.52**	-9.18	2.99	1.12	159.16**	136.54**	45.52**	49.15**
CMS463D13A × PP 402	1.35	143.47**	123.42**	36.85**	55.19**	0.95	162.76**	101.20**	23.78**	26.87**
CMS463D13A × C 142	1.35	97.65**	77.70**	36.38**	54.65**	0.79	99.08**	67.84**	3.26	5.84
CMS463D13A × PP 414	0.66	3.37	-1.74	-33.21**	-24.26**	0.30	-19.86*	-35.97**	-60.61**	-59.63**
CMS463D13A × VR 522	1.21	65.83**	42.04**	22.00**	38.35**	0.65	46.33**	36.82**	-15.83**	-13.73*
CMS463D13A × PL 406	0.96	31.70**	12.81	-3.10	9.87	0.49	21.96*	4.03	-36.00**	-34.40**
CMS463D13A × E 183	0.51	16.92	-15.48	-48.23**	-41.29**	0.21	-43.35**	-55.76**	-72.78**	-72.10**
CMS463D13A × IS 268	1.57	138.14**	120.10**	58.89**	80.18**	0.95	128.08**	100.92**	23.61**	26.69**
CMS463D13A × IS 261	0.94	50.19**	45.68**	-5.06	7.65	0.70	51.87**	47.84**	-9.04	-6.77
LSD at p=0.05		0.10	0.12	0.12	0.12		0.07	0.08	0.08	0.08
LSD at p=0.01		0.14	0.16	0.16	0.16		0.10	0.11	0.11	0.11

Table 4.12k (*Cont'd.*)

Crosses	**Total yield plant^{-1} (kg)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	0.22	-4.63	-20.17*	-52.72**	-51.52**	0.40	1.02	-4.99	-46.72**	-42.95**
CMS4611A × SL 475	0.65	61.20**	5.32	37.10**	40.58**	0.75	33.88**	-0.83	1.75	8.95*
CMS4611A × PL 412	0.26	24.61*	12.38	-44.17**	-42.75**	0.59	14.29**	-11.38**	-20.50**	-14.88**
CMS4611A × IS 263	0.19	6.99	-1.06	-60.49**	-59.49**	0.41	17.92*	12.00	-44.67**	-40.76**
CMS4611A × VR 523	0.65	65.09**	8.44	38.02**	41.52**	0.63	39.87**	17.44**	-14.59**	-8.55*
CMS4611A × DL 161	0.64	100.10**	41.89**	35.48**	38.91**	0.76	57.54**	26.68**	2.89	10.17*
CMS4611A × IS 267	0.40	99.01**	86.94**	-15.05**	-12.90*	0.69	74.40**	61.65**	-6.47	0.14
CMS4611A × YL 581	0.38	35.87**	3.12	-20.49**	-18.48**	0.65	56.12**	38.93**	-11.98**	-5.76
CMS4611A × SL 473	0.30	0.50	-26.63**	-36.33**	-34.71**	0.49	10.95*	-4.70	-34.43**	-29.79**
CMS4611A × IS 262	0.40	78.03**	54.08**	-15.83**	-13.70*	0.59	39.94**	24.11**	-20.77**	-15.17**
CMS4611A × VR 521	0.27	48.43**	42.12**	-43.25**	-41.81**	0.39	26.45**	6.52	-47.38**	-43.66**
CMS4611A × FL 201	0.20	1.83	-4.07	-56.68**	-55.58**	0.50	25.06**	16.07*	-33.03**	-28.30**
CMS4611A × PP 402	0.32	70.95**	70.05**	-31.38**	-29.64**	0.72	111.70**	96.94**	-2.71	4.17
CMS4611A × C 142	0.46	65.83**	25.39**	-2.26	0.22	0.76	79.55**	57.89**	2.80	10.07*
CMS4611A × PP 414	0.17	-5.03	-8.14	-63.32**	-62.39**	0.41	9.91	8.47	-44.97**	-41.08**
CMS4611A × VR 522	0.54	167.27**	150.70**	14.28*	17.17**	0.65	52.67**	33.30**	-11.76**	-5.52
CMS4611A × PL 406	0.39	109.54**	106.02**	-17.74**	-15.65**	0.58	42.24**	28.48**	-21.31**	-15.74**
CMS4611A × E 183	0.32	57.76**	45.80**	-31.38**	-29.64**	0.37	18.91*	0.36	-50.42**	-46.91**
CMS4611A × IS 268	0.28	22.69*	3.66	-40.00**	-38.48**	0.70	70.99**	55.38**	-6.09	0.55
CMS4611A × IS 261	0.28	20.49*	0.96	-40.35**	-38.84**	0.50	22.25**	10.23	-32.21**	-27.42**

Crosses	**Total yield plant^{-1} (kg)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	0.27	-3.72	-4.18	-43.25**	-41.81**	0.37	-9.63	-10.41	-49.76**	-46.21**
CMS4626A × SL 475	0.70	56.66**	13.63**	47.92**	51.67**	0.85	45.25**	11.63**	14.54**	22.64**
CMS4626A × PL 412	0.32	26.29**	16.63	-31.59**	-29.86**	0.81	51.42**	22.22**	9.64*	17.40**
CMS4626A × IS 263	0.17	-20.46	-37.23**	-63.18**	-62.25**	0.50	36.22**	23.04**	-32.20**	-27.40**
CMS4626A × VR 523	0.69	57.20**	14.83**	46.15**	49.86**	0.79	66.80**	46.59**	6.62	14.16**
CMS4626A × DL 161	0.62	69.92**	37.16**	30.95**	34.28**	0.92	82.18**	52.89**	24.18**	32.96**
CMS4626A × IS 267	0.36	48.68**	31.93**	-22.61**	-20.65**	0.67	59.57**	55.77**	-9.87**	-3.50
CMS4626A × YL 581	0.47	46.17**	28.69**	-0.78	1.74	0.79	80.03**	68.31**	6.63	14.17**
CMS4626A × SL 473	0.63	83.77**	53.99**	33.64**	37.03**	0.63	37.55**	23.85**	-14.78**	-8.75*
CMS4626A × IS 262	0.29	8.30	4.58	-38.66**	-37.10**	0.70	59.51**	48.60**	-5.14	1.57
CMS4626A × VR 521	0.28	26.65*	2.77	-39.72**	-38.19**	0.37	13.62	-8.32	-49.48**	-45.90**
CMS4626A × FL 201	0.30	21.03*	7.11	-37.17**	-35.58**	0.70	68.41**	64.62**	-5.02	1.70
CMS4626A × PP 402	0.49	108.14**	75.66**	3.04	5.65	0.73	100.80**	77.85**	-1.99	4.94
CMS4626A × C 142	0.47	46.61**	28.47**	0.14	2.68	0.80	78.72**	65.00**	7.43*	15.02**
CMS4626A × PP 414	0.19	-16.94	-32.05**	-60.14**	-59.13**	0.45	15.85*	11.25	-38.69**	-34.36**
CMS4626A × VR 522	0.33	33.83**	18.92**	-30.25**	-28.48**	0.68	50.40**	37.80**	-8.78*	-2.32
CMS4626A × PL 406	0.53	132.41**	92.65**	13.00*	15.87**	0.74	72.30**	63.67**	0.24	7.33
CMS4626A × E 183	0.31	26.07**	13.61	-33.36**	-31.67**	0.32	-3.09	-21.66**	-56.83**	-53.78**
CMS4626A × IS 268	0.49	79.75**	78.55**	4.73	7.39	0.84	96.66**	87.98**	13.61**	21.65**
CMS4626A × IS 261	0.45	61.10**	60.53**	-5.16	-2.75	0.64	48.43**	40.71**	-13.46**	-7.34
CMS463D13A × AC 102	0.49	48.25**	27.49**	4.88	7.54	0.67	47.09**	36.23**	-10.36**	-4.02
CMS463D13A × SL 475	0.70	40.32**	14.50**	49.05**	52.83**	0.95	51.66**	24.46**	27.70**	36.73**

Crosses	**Total yield plant^{-1} (kg)**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	0.40	29.83**	4.12	-14.35*	-12.17*	0.78	36.02**	17.89**	5.77	13.24**
CMS463D13A × IS 263	0.21	-21.65*	-44.67**	-54.49**	-53.33**	0.61	49.12**	24.92**	-17.80**	-11.99**
CMS463D13A × VR 523	0.63	28.43**	5.72	34.56**	37.97**	0.92	78.47**	69.96**	23.61**	32.36**
CMS463D13A × DL 161	0.66	57.06**	46.19**	39.58**	43.12**	0.84	54.39**	39.73**	13.49**	21.52**
CMS463D13A × IS 267	0.32	7.58	-16.49*	-31.31**	-29.57**	0.89	94.99**	83.23**	20.56**	29.08**
CMS463D13A × YL 581	0.60	58.94**	53.95**	26.64**	29.86**	0.84	76.16**	72.89**	13.76**	21.81**
CMS463D13A × SL 473	0.53	32.36**	28.91**	11.87*	14.71*	0.83	66.92**	63.26**	12.34**	20.28**
CMS463D13A × IS 262	0.29	-10.07	-25.17**	-38.45**	-36.88**	0.73	52.59**	50.32**	-1.09	5.90
CMS463D13A × VR 521	0.23	-17.91*	-40.72**	-51.24**	-50.00**	0.35	-4.95	-28.04**	-52.65**	-49.30**
CMS463D13A × FL 201	0.36	20.02*	-7.04	-23.53**	-21.59**	0.79	72.67**	62.04**	6.62	14.16**
CMS463D13A × PP 402	0.52	79.14**	33.51**	9.82	12.61*	0.94	133.82**	92.44**	26.62**	35.58**
CMS463D13A × C 142	0.62	64.18**	59.88**	31.52**	34.86**	0.92	89.36**	88.37**	23.94**	32.71**
CMS463D13A × PP 414	0.19	-31.56**	-50.26**	-59.08**	-58.04**	0.38	-10.97*	-21.17**	-48.13**	-44.46**
CMS463D13A × VR 522	0.49	61.19**	25.26**	3.04	5.65	0.78	59.02**	58.54**	4.96	12.38**
CMS463D13A × PL 406	0.47	64.68**	20.96**	-0.49	2.03	0.64	35.57**	30.88**	-13.88**	-7.79
CMS463D13A × E 183	0.23	-23.72**	-40.03**	-50.67**	-49.42**	0.32	-14.23*	-34.96**	-57.20**	-54.18**
CMS463D13A × IS 268	0.54	63.39**	39.18**	14.49*	17.39**	1.02	117.58**	108.72**	37.33**	47.04**
CMS463D13A × IS 261	0.47	40.10**	20.36**	-0.99	1.52	0.70	48.36**	43.51**	-5.57	1.11
LSD at p=0.05		0.05	0.05	0.05	0.05		0.05	0.05	0.05	0.05
LSD at p=0.01		0.06	0.07	0.07	0.07		0.06	0.07	0.07	0.07

*, significant at p=0.05; **, significant at p=0.01

Table 4.12l: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for ascorbic acid (mg.100g^{-1}) evaluated over environments**

Crosses	**Ascorbic acid (mg.100g^{-1})**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	153.33	20.25**	-9.10**	8.75**	30.39**	154.95	33.44**	10.92**	5.33	27.19**
CMS4611A × SL 475	138.32	26.97**	5.15	-1.89	17.63**	197.56	44.57**	9.30**	34.29**	62.17**
CMS4611A × PL 412	173.15	37.71**	4.85	22.81**	47.25**	189.51	31.46**	-3.20	28.82**	55.56**
CMS4611A × IS 263	148.09	17.96**	-10.12**	5.04	25.94**	178.31	32.05**	0.45	21.21**	46.37**
CMS4611A × VR 523	135.40	13.50**	-11.07**	-3.96	15.15**	185.28	32.93**	-0.49	25.94**	52.09**
CMS4611A × DL 161	140.36	28.42**	6.12	-0.45	19.36**	150.59	27.90**	5.36	2.37	23.62**
CMS4611A × IS 267	161.65	21.83**	-9.71**	14.66**	37.47**	143.61	23.24**	2.21	-2.38	17.88**
CMS4611A × YL 581	82.46	5.94	-4.49	-41.52**	-29.88**	90.70	8.81	-2.01	-38.35**	-25.55**
CMS4611A × SL 473	145.13	28.00**	3.34	2.93	23.42**	155.09	28.24**	3.87	5.42	27.31**
CMS4611A × IS 262	124.39	8.13*	-13.47**	-11.77**	5.79	139.36	14.28**	-7.92*	-5.27	14.40**
CMS4611A × VR 521	135.08	25.31**	4.50	-4.19	14.87**	202.92	43.75**	6.93**	37.93**	66.57**
CMS4611A × FL 201	93.36	6.41	4.73	-33.78**	-20.61**	99.31	7.32	7.30	-32.50**	-18.48**
CMS4611A × PP 402	96.22	6.11	1.26	-31.76**	-18.18**	103.17	6.28	1.55	-29.87**	-15.31**
CMS4611A × C 142	186.40	41.86**	5.63*	32.21**	58.52**	178.67	42.01**	12.32**	21.45**	46.66**
CMS4611A × PP 414	91.14	2.05	-1.25	-35.35**	-22.49**	98.13	4.20	2.43	-33.30**	-19.45**
CMS4611A × VR 522	130.57	11.87**	-11.24**	-7.39*	11.04**	149.79	20.76**	-3.69	1.82	22.96**
CMS4611A × PL 406	165.37	34.14**	3.21	17.29**	40.64**	186.93	47.28**	15.90**	27.07**	53.44**
CMS4611A × E 183	106.51	1.25	-14.15**	-24.46**	-9.42**	116.33	1.47	-14.92**	-20.92**	-4.51
CMS4611A × IS 268	189.29	41.09**	4.01	34.26**	60.97**	177.25	35.42**	4.74	20.49**	45.50**
CMS4611A × IS 261	131.50	2.02	-23.31**	-6.73*	11.83**	190.83	36.78**	2.33	29.72**	56.64**

Crosses	**Ascorbic acid (mg.100g^{-1})**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	171.82	21.90**	1.86	21.87**	46.12**	134.68	3.48	-3.59	-8.45**	10.55**
CMS4626A × SL 475	149.29	21.99**	13.50**	5.89*	26.96**	188.73	25.25**	4.41	28.29**	54.92**
CMS4626A × PL 412	171.54	23.25**	3.88	21.67**	45.88**	170.23	7.61**	-13.04**	15.71**	39.73**
CMS4626A × IS 263	185.57	33.51**	12.63**	31.62**	57.81**	158.77	6.52*	-10.56**	7.93*	30.33**
CMS4626A × VR 523	183.77	38.44**	20.69**	30.34**	56.28**	187.53	22.25**	0.72	27.47**	53.93**
CMS4626A × DL 161	138.51	12.85**	4.73	-1.76	17.79**	152.31	15.59**	6.56*	3.53	25.03**
CMS4626A × IS 267	163.84	12.12**	-8.49**	16.21**	39.33**	146.44	12.17**	4.23	-0.46	20.21**
CMS4626A × YL 581	105.33	15.39**	-6.97	-25.29**	-10.43**	110.26	13.23**	-8.57*	-25.05**	-9.49*
CMS4626A × SL 473	136.73	7.81**	-2.64	-3.02	16.28**	146.56	8.60**	-1.84	-0.38	20.30**
CMS4626A × IS 262	134.40	4.60	-6.51*	-4.67	14.30**	183.20	34.73**	21.05**	24.53**	50.38**
CMS4626A × VR 521	147.50	21.65**	14.11**	4.61	25.43**	197.01	26.96**	3.82	33.92**	61.72**
CMS4626A × FL 201	98.23	-2.92	-13.25**	-30.33**	-16.47**	107.59	0.97	-10.79**	-26.86**	-11.68**
CMS4626A × PP 402	110.87	6.49	-2.08	-21.36**	-5.71	128.63	15.78**	6.65	-12.57**	5.59
CMS4626A × C 142	154.35	6.56**	-12.54**	9.47**	31.26**	167.47	19.76**	5.28	13.84**	37.47**
CMS4626A × PP 414	101.27	-1.45	-10.56**	-28.17**	-13.88**	98.21	-9.23*	-18.57**	-33.24**	-19.38**
CMS4626A × VR 522	164.13	26.09**	11.57**	16.41**	39.58**	166.81	20.82**	7.25*	13.39**	36.93**
CMS4626A × PL 406	172.21	25.95**	7.48**	22.15**	46.45**	173.11	22.82**	7.33*	17.67**	42.10**
CMS4626A × E 183	117.37	-1.07	-5.40	-16.75**	-0.19	129.42	0.58	-5.35	-12.03**	6.24
CMS4626A × IS 268	197.41	33.74**	8.47**	40.01**	67.88**	171.79	18.55**	1.52	16.78**	41.02**
CMS4626A × IS 261	169.63	19.17**	-1.07	20.31**	44.26**	191.43	24.68**	2.65	30.13**	57.14**
CMS463D13A × AC 102	182.64	24.16**	8.28**	29.54**	55.32**	155.63	15.55**	11.41**	5.79	27.75**
CMS463D13A × SL 475	156.62	21.86**	19.07**	11.09**	33.19**	185.71	19.64**	2.74	26.24**	52.44**

Crosses	**Ascorbic acid (mg.100g^{-1})**									
	E$_1$					**E$_2$**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	196.24	35.03**	18.83**	39.18**	66.88**	189.33	16.34**	-3.29	28.70**	55.41**
CMS463D13A × IS 263	175.84	21.15**	6.72**	24.72**	49.53**	188.52	22.73**	6.20*	28.15**	54.75**
CMS463D13A × VR 523	164.75	18.62**	8.20**	16.85**	40.11**	205.64	30.20**	10.45**	39.79**	68.80**
CMS463D13A × DL 161	139.95	8.59**	5.81	-0.74	19.02**	161.59	18.54**	13.05**	9.84**	32.64**
CMS463D13A × IS 267	192.68	26.54**	7.62**	36.66**	63.86**	152.43	12.83**	8.49*	3.62	25.13**
CMS463D13A × YL 581	116.38	19.46**	-7.27*	-17.45**	-1.03	121.17	18.88**	-6.58	-17.63**	-0.54
CMS463D13A × SL 473	135.75	2.09	-3.34	-3.72	15.44**	141.62	1.52	-5.15	-3.73	16.25**
CMS463D13A × IS 262	133.62	-0.76	-7.06*	-5.23	13.63**	146.01	3.91	-3.52	-0.75	19.86**
CMS463D13A × VR 521	145.03	13.85**	12.20**	2.87	23.34**	195.14	22.17**	2.84	32.65**	60.18**
CMS463D13A × FL 201	119.39	11.24**	-4.88	-15.32**	1.53	122.42	10.18**	-5.61	-16.78**	0.49
CMS463D13A × PP 402	127.79	15.89**	1.81	-9.36**	8.67*	141.86	22.66**	9.37*	-3.57	16.45**
CMS463D13A × C 142	164.29	8.81**	-6.90**	16.52**	39.71**	180.39	24.94**	13.41**	22.62**	48.08**
CMS463D13A × PP 414	109.62	0.66	-12.66**	-22.25**	-6.77	112.42	-0.29	-13.32**	-23.58**	-7.71*
CMS463D13A × VR 522	140.46	3.05	-4.52	-0.37	19.45**	150.25	5.35	-3.40	2.13	23.34**
CMS463D13A × PL 406	177.56	24.28**	10.81**	25.94**	51.00**	190.67	31.05**	18.21**	29.61**	56.51**
CMS463D13A × E 183	119.83	-3.98	-4.53	-15.01**	1.90	133.20	-0.01	-2.58	-9.45**	9.34*
CMS463D13A × IS 268	195.33	27.04**	7.33**	38.54**	66.11**	172.41	15.35**	1.88	17.19**	41.52**
CMS463D13A × IS 261	175.98	18.52**	2.64	24.82**	49.66**	196.30	24.17**	5.26*	33.43**	61.13**
LSD at *p*=0.05		7.12	8.22	8.22	8.22		7.99	9.23	9.23	9.23
LSD at *p*=0.01		9.41	10.87	10.87	10.87		10.57	12.20	12.20	12.20

Table 4.12l (*Cont'd.*)

Crosses	Ascorbic acid (mg.100g^{-1})									
	E_3					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	137.77	26.88**	-4.42	5.67	17.58**	148.68	26.64**	-1.43	6.59**	25.09**
CMS4611A × SL 475	123.32	6.74*	-21.97**	-5.41	5.25	153.07	27.16**	-2.37	9.73**	28.78**
CMS4611A × PL 412	157.76	39.87**	3.41	21.00**	34.64**	173.47	35.99**	1.36	24.36**	45.95**
CMS4611A × IS 263	152.58	36.47**	1.33	17.03**	30.22**	159.66	28.63**	-2.81	14.46**	34.33**
CMS4611A × VR 523	140.23	32.99**	1.72	7.56*	19.69**	153.64	26.58**	-3.23*	10.14**	29.26**
CMS4611A × DL 161	127.42	32.44**	6.73	-2.27	8.75*	139.46	29.43**	6.03**	-0.03	17.33**
CMS4611A × IS 267	126.96	36.63**	12.54**	-2.62	8.36*	144.07	26.33**	-0.03	3.28	21.21**
CMS4611A × YL 581	67.30	4.15	-7.85	-48.38**	-42.56**	80.15	6.48*	-4.55	-42.54**	-32.57**
CMS4611A × SL 473	129.37	29.46**	2.01	-0.77	10.42**	143.19	28.53**	3.13	2.65	20.47**
CMS4611A × IS 262	110.21	10.90**	-12.33**	-15.47**	-5.94	124.65	11.18**	-11.13**	-10.64**	4.87*
CMS4611A × VR 521	158.13	35.31**	-1.60	21.28**	34.96**	165.37	35.62**	3.42*	18.55**	39.13**
CMS4611A × FL 201	79.93	7.04	4.74	-38.70**	-31.78**	90.86	6.92**	5.67	-34.86**	-23.55**
CMS4611A × PP 402	80.22	5.33	1.18	-38.47**	-31.53**	93.20	5.95*	1.34	-33.18**	-21.59**
CMS4611A × C 142	150.12	45.17**	12.21**	15.14**	28.12**	171.73	42.86**	9.77**	23.11**	44.48**
CMS4611A × PP 414	85.01	13.08**	9.94	-34.80**	-27.45**	91.43	6.04*	3.34	-34.46**	-23.08**
CMS4611A × VR 522	128.68	25.12**	-2.99	-1.30	9.82**	136.35	19.04**	-6.03**	-2.25	14.71**
CMS4611A × PL 406	149.47	24.84**	-10.19**	14.64**	27.57**	167.26	35.64**	2.83	19.90**	40.72**
CMS4611A × E 183	94.21	5.49	-10.77**	-27.74**	-19.59**	105.68	2.56	-13.47**	-24.24**	-11.08**
CMS4611A × IS 268	154.60	38.89**	3.35	18.58**	31.95**	173.71	38.47**	4.06**	24.53**	46.15**
CMS4611A × IS 261	167.21	51.98**	13.74**	28.25**	42.71**	163.18	29.36**	-3.05*	16.98**	37.29**

Crosses	**Ascorbic acid (mg.100g^{-1})**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	167.70	37.63**	16.35**	28.63**	43.13**	158.07	20.68**	4.79**	13.31**	32.99**
CMS4626A × SL 475	169.11	31.29**	7.00**	29.71**	44.33**	169.04	26.19**	7.82**	21.18**	42.22**
CMS4626A × PL 412	167.57	32.93**	9.85**	28.53**	43.02**	169.78	20.29**	-0.80	21.71**	42.84**
CMS4626A × IS 263	155.50	24.33**	3.27	19.27**	32.72**	166.62	20.99**	1.42	19.44**	40.18**
CMS4626A × VR 523	148.97	25.49**	8.06**	14.26**	27.15**	173.42	28.51**	9.23**	24.32**	45.91**
CMS4626A × DL 161	127.72	16.66**	6.98*	-2.04	9.00*	139.51	14.99**	6.07**	0.02	17.38**
CMS4626A × IS 267	129.16	21.63**	14.49**	-0.94	10.23**	146.48	14.77**	1.64	5.01**	23.24**
CMS4626A × YL 581	89.92	15.45**	-9.69*	-31.03**	-23.25**	101.84	14.62**	-8.36**	-26.99**	-14.32**
CMS4626A × SL 473	130.13	14.96**	2.61	-0.19	11.06**	137.81	10.25**	-0.75	-1.21	15.94**
CMS4626A × IS 262	135.18	20.01**	7.53*	3.69	15.38**	150.93	20.07**	7.60**	8.20**	26.98**
CMS4626A × VR 521	168.59	29.55**	4.91	29.31**	43.89**	171.03	26.20**	6.96**	22.61**	43.89**
CMS4626A × FL 201	85.55	-2.72	-14.08**	-34.38**	-26.99**	97.12	-1.46	-12.61**	-30.37**	-18.29**
CMS4626A × PP 402	93.90	5.00	-5.69	-27.98**	-19.86**	111.13	9.44**	0.00	-20.33**	-6.50**
CMS4626A × C 142	149.09	27.78**	11.44**	14.35**	27.24**	156.97	17.33**	0.34	12.53**	32.06**
CMS4626A × PP 414	85.40	-3.44	-14.22**	-34.49**	-27.11**	94.96	-4.85*	-14.55**	-31.92**	-20.11**
CMS4626A × VR 522	156.61	34.88**	18.06**	20.12**	33.66**	162.52	26.85**	12.00**	16.51**	36.73**
CMS4626A × PL 406	168.61	26.78**	1.32	29.33**	43.91**	171.31	25.15**	5.33**	22.81**	44.13**
CMS4626A × E 183	102.28	-0.29	-3.13	-21.55**	-12.71**	116.36	-0.24	-4.73*	-16.59**	-2.11
CMS4626A × IS 268	159.34	27.91**	6.53*	22.22**	36.00**	176.18	26.72**	5.54**	26.30**	48.23**
CMS4626A × IS 261	170.23	38.08**	15.80**	30.57**	45.29**	177.10	26.75**	5.22**	26.96**	49.00**
CMS463D13A × AC 102	137.88	8.01**	-4.34	5.76	17.68**	158.72	16.29**	5.23**	13.78**	33.53**
CMS463D13A × SL 475	147.93	9.90**	-6.40*	13.46**	26.26**	163.42	17.19**	4.24**	17.15**	37.49**

Crosses	Ascorbic acid (mg.100g^{-1})									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	H_{BP}	**CH-27**	**Soldier**		H_{MP}	H_{BP}	**CH-27**	**Soldier**
CMS463D13A × PL 412	161.53	22.51**	5.89*	23.89**	37.86**	182.36	24.36**	6.55**	30.73**	53.43**
CMS463D13A × IS 263	160.65	22.76**	6.69*	23.22**	37.11**	175.00	22.21**	6.53**	25.46**	47.23**
CMS463D13A × VR 523	146.63	17.77**	6.36*	12.47**	25.15**	172.34	22.71**	8.55**	23.55**	45.00**
CMS463D13A × DL 161	124.50	8.01*	4.29	-4.50	6.26	142.01	11.98**	7.97**	1.81	19.48**
CMS463D13A × IS 267	127.19	13.58**	12.75**	-2.44	8.56*	157.44	18.27**	9.24**	12.86**	32.46**
CMS463D13A × YL 581	101.69	21.52**	-8.52*	-22.00**	-13.21**	113.08	19.86**	-7.40**	-18.93**	-4.86*
CMS463D13A × SL 473	120.40	1.19	-5.06	-7.65*	2.76	132.59	1.61	-4.51*	-4.95**	11.55**
CMS463D13A × IS 262	118.52	0.07	-5.72	-9.09**	1.16	132.72	1.16	-5.39**	-4.86**	11.66**
CMS463D13A × VR 521	169.61	24.78**	5.54*	30.09**	44.76**	169.93	20.50**	6.27**	21.82**	42.96**
CMS463D13A × FL 201	105.20	12.23**	-5.36	-19.31**	-10.22**	115.67	11.16**	-5.29*	-17.08**	-2.69
CMS463D13A × PP 402	114.90	20.66**	3.36	-11.87**	-1.93	128.18	19.75**	4.96*	-8.11**	7.84**
CMS463D13A × C 142	159.53	30.26**	19.25**	22.36**	36.16**	168.07	20.67**	7.44**	20.49**	41.40**
CMS463D13A × PP 414	90.98	-3.46	-18.16**	-30.22**	-22.35**	104.34	-0.91	-14.56**	-25.20**	-12.21**
CMS463D13A × VR 522	140.76	15.47**	6.12	7.97*	20.14**	143.83	7.65**	-0.88	3.11	21.00**
CMS463D13A × PL 406	172.41	24.22**	3.60	32.24**	47.15**	180.21	26.57**	10.80**	29.19**	51.62**
CMS463D13A × E 183	119.53	10.30**	7.53*	-8.32**	2.02	124.19	1.69	1.69	-10.97**	4.48*
CMS463D13A × IS 268	167.23	28.27**	11.80**	28.27**	42.73**	178.32	23.38**	6.82**	27.84**	50.03**
CMS463D13A × IS 261	168.52	30.55**	14.63**	29.26**	43.83**	180.27	24.13**	7.10**	29.23**	51.66**
LSD at p=0.05		7.04	8.13	8.13	8.13		4.30	4.96	4.96	4.96
LSD at p=0.01		9.30	10.74	10.74	10.74		5.66	6.54	6.54	6.54

*, significant at p=0.05; **, significant at p=0.01

Table 4.12m: Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for oleoresin content (%) evaluated over environments

Crosses	Oleoresin content (%)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	9.34	7.19	-3.94	-9.43*	-12.81**	8.84	2.65	-4.77	-31.82**	-22.65**
CMS4611A × SL 475	14.63	36.06**	24.19**	41.84**	36.55**	15.97	45.66**	26.35**	23.10**	39.65**
CMS4611A × PL 412	11.54	27.87**	18.64**	11.86*	7.68	14.36	51.65**	48.74**	10.74**	25.63**
CMS4611A × IS 263	10.81	12.40**	11.17*	4.81	0.90	12.54	36.90**	35.03**	-3.32	9.68*
CMS4611A × VR 523	15.94	54.40**	45.98**	54.47**	48.71**	17.48	45.97**	19.21**	34.77**	52.89**
CMS4611A × DL 161	13.96	27.87**	15.27**	35.35**	30.30**	15.20	49.61**	37.75**	17.22**	32.97**
CMS4611A × IS 267	10.04	0.20	-2.62	-2.71	-6.35	13.62	22.43**	5.07	5.01	19.13**
CMS4611A × YL 581	9.11	-2.24	-6.37	-11.73*	-15.02**	11.57	24.28**	24.02**	-10.82**	1.17
CMS4611A × SL 473	10.32	7.42	6.13	0.06	-3.67	10.97	13.60**	9.45*	-15.45**	-4.08
CMS4611A × IS 262	8.35	-2.01	-14.15**	-19.06**	-22.08**	10.03	6.89	5.76	-22.64**	-12.24**
CMS4611A × VR 521	12.33	19.16**	12.44**	19.48**	15.02**	13.29	26.61**	13.53**	2.47	16.24**
CMS4611A × FL 201	9.12	1.00	-6.27	-11.63*	-14.93**	10.55	17.59**	13.60**	-18.66**	-7.73
CMS4611A × PP 402	10.64	2.90	-2.89	3.17	-0.68	14.34	24.66**	4.52	10.56**	25.42**
CMS4611A × C 142	15.21	44.73**	34.67**	47.46**	41.96**	14.64	50.94**	44.74**	12.90**	28.08**
CMS4611A × PP 414	8.15	-5.78	-16.24**	-21.03**	-23.98**	10.60	11.21**	8.42	-18.27**	-7.29
CMS4611A × VR 522	9.31	6.56	-4.28	-9.76*	-13.13**	12.80	26.37**	16.64**	-1.29	11.98**
CMS4611A × PL 406	14.88	41.45**	31.52**	44.26**	38.88**	14.27	33.24**	17.61**	10.02**	24.81**
CMS4611A × E 183	8.22	-6.50	-15.46**	-20.29**	-23.27**	8.69	5.87	-6.46	-33.02**	-24.02**
CMS4611A × IS 268	9.92	2.08	1.95	-3.88	-7.47	12.50	34.86**	34.64**	-3.60	9.36*
CMS4611A × IS 261	10.81	5.94	1.19	4.81	0.90	16.53	45.72**	23.36**	27.45**	44.58**

Crosses	**Oleoresin content (%)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	9.33	-1.96	-17.61**	-9.60*	-12.97**	8.82	-2.43	-12.96**	-32.02**	-22.89**
CMS4626A × SL 475	17.61	52.45**	49.45**	70.69**	64.32**	14.42	26.68**	14.11**	11.18**	26.12**
CMS4626A × PL 412	10.42	6.13	-7.92	1.03	-2.74	13.09	32.35**	29.25**	0.95	14.52**
CMS4626A × IS 263	12.68	21.76**	12.04**	22.94**	18.35**	11.71	22.21**	15.60**	-9.71**	2.42
CMS4626A × VR 523	15.44	38.84**	36.37**	49.63**	44.04**	16.91	36.41**	15.32**	30.38**	47.90**
CMS4626A × DL 161	14.42	23.10**	19.07**	39.81**	34.59**	11.71	10.68**	6.13	-9.69**	2.45
CMS4626A × IS 267	9.76	-9.77*	-13.81**	-5.43	-8.96*	14.32	24.02**	10.47**	10.41**	25.25**
CMS4626A × YL 581	9.86	-2.49	-12.90**	-4.43	-7.99	9.44	-2.96	-6.81	-27.22**	-17.43**
CMS4626A × SL 473	10.63	2.11	-6.12	3.00	-0.84	10.34	2.63	2.07	-20.28**	-9.56*
CMS4626A × IS 262	11.95	28.28**	5.59	15.86**	11.54**	12.86	31.15**	26.98**	-0.82	12.51**
CMS4626A × VR 521	12.83	15.18**	13.37**	24.39**	19.75**	12.85	17.72**	9.79*	-0.90	12.42**
CMS4626A × FL 201	10.96	11.61**	-3.15	6.27	2.30	10.87	15.76**	7.34	-16.17**	-4.90
CMS4626A × PP 402	13.91	24.84**	22.85**	34.80**	29.77**	15.14	26.96**	10.35**	16.73**	32.42**
CMS4626A × C 142	16.33	44.44**	44.29**	58.32**	52.41**	11.93	17.81**	17.74**	-8.04*	4.31
CMS4626A × PP 414	9.86	4.45	-12.87**	-4.39	-7.96	8.44	-15.24**	-16.72**	-34.95**	-26.21**
CMS4626A × VR 522	13.89	45.70**	22.70**	34.64**	29.61**	14.03	32.91**	27.79**	8.15*	22.68**
CMS4626A × PL 406	15.63	38.09**	38.07**	51.50**	45.85**	13.13	17.95**	8.21*	1.23	14.84**
CMS4626A × E 183	9.03	-5.82	-20.20**	-12.44**	-15.71**	8.80	1.97	-13.16**	-32.18**	-23.06**
CMS4626A × IS 268	9.31	-11.40**	-17.73**	-9.73*	-13.09**	11.80	21.73**	16.49**	-9.02*	3.21
CMS4626A × IS 261	11.36	3.27	0.38	10.15*	6.03	15.18	29.03**	13.28**	17.04**	32.77**
CMS463D13A × AC 102	10.32	10.79*	-5.55	0.06	-3.67	9.97	1.58	-14.67**	-23.16**	-12.83**
CMS463D13A × SL 475	15.35	35.19**	30.30**	48.82**	43.27**	16.80	38.20**	32.97**	29.56**	46.97**

Crosses	Oleoresin content (%)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS463D13A × PL 412	11.59	20.36**	6.01	12.31**	8.12	10.45	-2.08	-10.56**	-19.46**	-8.63*
CMS463D13A × IS 263	16.13	57.83**	47.61**	56.38**	50.54**	12.71	22.76**	8.85*	-1.98	11.20**
CMS463D13A × VR 523	16.63	52.24**	52.15**	61.20**	55.18**	18.31	38.99**	24.85**	41.15**	60.12**
CMS463D13A × DL 161	15.10	31.09**	24.68**	46.40**	40.93**	18.50	62.91**	58.42**	42.66**	61.84**
CMS463D13A × IS 267	13.66	28.65**	24.98**	32.41**	27.47**	13.84	12.30**	6.74	6.68	21.02**
CMS463D13A × YL 581	9.81	-1.04	-10.22*	-4.88	-8.43	11.54	9.87*	-1.20	-11.03**	0.93
CMS463D13A × SL 473	10.17	-0.44	-6.98	-1.45	-5.13	13.49	24.33**	15.50**	4.01	17.99**
CMS463D13A × IS 262	8.58	-5.92	-21.47**	-16.80**	-19.91**	10.29	-2.77	-11.90**	-20.66**	-10.00*
CMS463D13A × VR 521	13.73	25.46**	25.27**	33.12**	28.15**	16.93	44.81**	44.65**	30.56**	48.10**
CMS463D13A × FL 201	9.48	-1.54	-13.27**	-8.11	-11.54**	10.48	3.03	-10.30*	-19.22**	-8.37*
CMS463D13A × PP 402	12.81	17.01**	16.85**	24.14**	19.50**	15.84	24.72**	15.45**	22.13**	38.54**
CMS463D13A × C 142	12.83	15.42**	13.54**	24.33**	19.69**	13.88	27.36**	18.84**	7.02	21.40**
CMS463D13A × PP 414	8.06	-12.89**	-26.29**	-21.91**	-24.82**	9.82	-8.44*	-15.90**	-24.26**	-14.08**
CMS463D13A × VR 522	9.82	5.16	-10.16*	-4.81	-8.37	13.39	18.23**	14.67**	3.26	17.14**
CMS463D13A × PL 406	11.99	7.82*	5.98	16.25**	11.91**	14.90	25.14**	22.80**	14.88**	30.32**
CMS463D13A × E 183	8.42	-10.36*	-22.93**	-18.35**	-21.40**	8.93	-4.98	-23.52**	-31.12**	-21.87**
CMS463D13A × IS 268	11.37	10.24*	4.06	10.24*	6.13	11.19	6.93	-4.17	-13.70**	-2.10
CMS463D13A × IS 261	10.97	1.50	0.37	6.33	2.36	15.74	25.49**	17.44**	21.33**	37.64**
LSD at p=0.05		0.81	0.93	0.93	0.93		0.80	0.93	0.93	0.93
LSD at p=0.01		1.07	1.23	1.23	1.23		1.06	1.23	1.23	1.23

Table 4.12m (*Cont'd.*)

Crosses	**Oleoresin content (%)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	7.46	8.64	-4.64	-16.99**	-8.39	8.55	5.99*	-4.43	-20.53**	-15.34**
CMS4611A × SL 475	10.37	23.14**	15.01**	15.36**	27.30**	13.66	35.94**	22.53**	26.94**	35.23**
CMS4611A × PL 412	8.27	17.00**	5.71	-7.97	1.56	11.39	33.67**	27.34**	5.89*	12.81**
CMS4611A × IS 263	8.02	3.06	2.56	-10.72**	-1.47	10.46	18.11**	16.92**	-2.78	3.58
CMS4611A × VR 523	9.59	15.94**	10.02*	6.68	17.72**	14.33	40.69**	25.40**	33.25**	41.96**
CMS4611A × DL 161	10.24	19.54**	10.03*	13.91**	25.71**	13.13	32.92**	21.42**	22.09**	30.07**
CMS4611A × IS 267	9.15	12.57**	8.54	1.78	12.32**	10.93	12.08**	3.49	1.64	8.29**
CMS4611A × YL 581	7.13	-3.50	-8.90	-20.70**	-12.48**	9.27	6.90**	3.59	-13.86**	-8.23**
CMS4611A × SL 473	7.61	-1.13	-2.77	-15.36**	-6.59	9.63	7.20**	6.72*	-10.46**	-4.61
CMS4611A × IS 262	6.35	-4.13	-18.88**	-29.38**	-22.06**	8.24	0.82	-7.85**	-23.37**	-18.36**
CMS4611A × VR 521	9.32	11.28**	4.37	3.75	14.49**	11.65	19.58**	10.56**	8.26**	15.34**
CMS4611A × FL 201	7.43	0.16	-4.99	-17.28**	-8.72	9.03	6.61*	0.98	-16.03**	-10.54**
CMS4611A × PP 402	8.98	1.64	-8.83*	-0.04	10.32*	11.32	10.69**	-1.64	5.25*	12.13**
CMS4611A × C 142	10.17	12.85**	-0.29	13.17**	24.89**	13.34	36.96**	26.61**	24.02**	32.13**
CMS4611A × PP 414	6.32	-5.06	-19.22**	-29.67**	-22.39**	8.36	0.93	-6.60*	-22.33**	-17.25**
CMS4611A × VR 522	10.32	20.84**	11.49**	14.84**	26.73**	10.81	18.33**	15.92**	0.50	7.06**
CMS4611A × PL 406	8.69	12.80**	11.12*	-3.26	6.75	12.62	30.78**	21.93**	17.27**	24.93**
CMS4611A × E 183	6.25	-7.70	-20.07**	-30.42**	-23.21**	7.72	-2.57	-13.69**	-28.23**	-23.54**
CMS4611A × IS 268	9.74	23.07**	21.64**	8.42*	19.65**	10.72	19.55**	19.26**	-0.34	6.17*
CMS4611A × IS 261	10.03	19.14**	11.28**	11.61**	23.17**	12.46	24.71**	12.91**	15.80**	23.37**

Crosses	**Oleoresin content (%)**									
	E$_3$					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	H_{BP}	**CH-27**	**Soldier**		H_{MP}	H_{BP}	**CH-27**	**Soldier**
CMS4626A × AC 102	7.01	-5.57	-21.56**	-22.00**	-13.92**	8.38	-3.16	-17.22**	-22.06**	-16.97**
CMS4626A × SL 475	11.23	25.13**	24.59**	24.96**	37.90**	14.42	35.57**	29.39**	34.04**	42.80**
CMS4626A × PL 412	9.03	18.38**	1.01	0.45	10.85*	10.85	19.03**	7.10**	0.84	7.43**
CMS4626A × IS 263	8.15	-2.30	-8.80*	-9.31*	0.08	10.85	14.83**	7.10**	0.84	7.43**
CMS4626A × VR 523	9.63	9.12*	7.76	7.16	18.26**	13.99	29.80**	22.40**	30.07**	38.57**
CMS4626A × DL 161	10.65	16.78**	14.48**	18.51**	30.78**	12.26	17.08**	13.35**	13.98**	21.43**
CMS4626A × IS 267	9.77	12.57**	9.36*	8.75*	20.02**	11.28	9.05**	6.79**	4.89*	11.74**
CMS4626A × YL 581	7.95	0.10	-11.04**	-11.54**	-2.37	9.08	-1.91	-10.32**	-15.56**	-10.05**
CMS4626A × SL 473	8.96	8.61*	0.26	-0.30	10.03*	9.98	4.16	-1.51	-7.27**	-1.21
CMS4626A × IS 262	7.94	10.59*	-11.19**	-11.68**	-2.54	10.92	24.52**	7.79**	1.49	8.12**
CMS4626A × VR 521	11.01	23.26**	23.24**	22.55**	35.24**	12.23	18.41**	16.13**	13.72**	21.15**
CMS4626A × FL 201	8.59	7.67	-3.88	-4.41	5.49	10.14	11.88**	0.13	-5.72*	0.44
CMS4626A × PP 402	10.52	11.94**	6.73	17.03**	29.14**	13.19	21.88**	14.57**	22.59**	30.60**
CMS4626A × C 142	11.36	18.76**	11.41**	26.45**	39.54**	13.21	27.82**	25.34**	22.77**	30.80**
CMS4626A × PP 414	7.01	-2.77	-21.52**	-21.96**	-13.88**	8.44	-4.87	-16.70**	-21.57**	-16.44**
CMS4626A × VR 522	12.08	32.76**	30.46**	34.38**	48.30**	13.33	37.04**	31.61**	23.92**	32.02**
CMS4626A × PL 406	10.15	22.83**	13.58**	12.95**	24.64**	12.97	26.69**	25.35**	20.56**	28.44**
CMS4626A × E 183	7.60	3.61	-14.99**	-15.47**	-6.71	8.48	-0.48	-16.32**	-21.21**	-16.07**
CMS4626A × IS 268	9.40	10.90**	5.15	4.56	15.39**	10.17	6.39**	0.41	-5.46*	0.72
CMS4626A × IS 261	10.38	15.62**	15.13**	15.47**	27.43**	12.31	16.31**	11.54**	14.40**	21.88**
CMS463D13A × AC 102	7.14	-4.45	-20.95**	-20.60**	-12.37**	9.14	3.11	-13.31**	-15.02**	-9.47**
CMS463D13A × SL 475	12.32	36.62**	36.52**	37.13**	51.33**	14.83	36.71**	33.04**	37.82**	46.83**

Crosses	**Oleoresin content (%)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	8.68	13.21**	-3.80	-3.38	6.63	10.24	9.84**	-2.91	-4.82*	1.40
CMS463D13A × IS 263	10.55	25.83**	16.91**	17.43**	29.59**	13.13	36.03**	24.54**	22.08**	30.06**
CMS463D13A × VR 523	11.52	29.88**	27.62**	28.19**	41.47**	15.49	40.93**	35.47**	43.95**	53.36**
CMS463D13A × DL 161	12.56	37.04**	35.01**	39.76**	54.24**	15.39	44.07**	42.26**	43.05**	52.40**
CMS463D13A × IS 267	10.33	18.37**	14.44**	14.95**	26.85**	12.61	19.45**	19.34**	17.21**	24.87**
CMS463D13A × YL 581	8.75	9.56*	-3.06	-2.63	7.45	10.03	5.97*	-4.85	-6.72**	-0.63
CMS463D13A × SL 473	7.97	-3.92	-11.71**	-11.31**	-2.13	10.54	7.73**	-0.03	-2.00	4.40
CMS463D13A × IS 262	7.49	3.67	-17.06**	-16.69**	-8.06	8.79	-2.11	-16.68**	-18.32**	-12.98**
CMS463D13A × VR 521	12.08	34.48**	33.79**	34.38**	48.30**	14.25	35.18**	35.11**	32.44**	41.10**
CMS463D13A × FL 201	8.19	2.08	-9.27*	-8.86*	0.57	9.38	1.17	-11.03**	-12.79**	-7.09**
CMS463D13A × PP 402	10.01	6.04	1.59	11.39**	22.92**	12.89	16.84**	11.94**	19.78**	27.61**
CMS463D13A × C 142	11.41	18.65**	11.83**	26.93**	40.07**	12.70	20.52**	20.47**	18.10**	25.81**
CMS463D13A × PP 414	7.16	-1.31	-20.64**	-20.29**	-12.03**	8.35	-8.05**	-20.84**	-22.40**	-17.33**
CMS463D13A × VR 522	11.19	22.37**	20.85**	24.48**	37.37**	11.47	15.40**	8.73**	6.59**	13.56**
CMS463D13A × PL 406	10.01	20.52**	10.93**	11.42**	22.96**	12.30	17.77**	16.66**	14.36**	21.83**
CMS463D13A × E 183	6.97	-5.56	-22.82**	-22.48**	-14.45**	8.11	-7.07**	-23.12**	-24.63**	-19.71**
CMS463D13A × IS 268	8.92	4.75	-1.14	-0.70	9.58*	10.50	7.46**	-0.46	-2.43	3.95
CMS463D13A × IS 261	10.66	18.22**	18.13**	18.66**	30.95**	12.46	15.45**	12.90**	15.79**	23.36**
LSD at p=0.05		0.63	0.72	0.72	0.72		0.44	0.51	0.51	0.51
LSD at p=0.01		0.83	0.96	0.96	0.96		0.58	0.67	0.67	0.67

*, significant at p=0.05; **, significant at p=0.01

Table 4.12n: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for capsaicin content (%) evaluated over environments**

Crosses	Capsaicin content (%)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	0.48	1.15	-1.22	-16.72**	-22.45**	0.55	3.99	2.56	-25.56**	-17.30**
CMS4611A × SL 475	0.88	29.93**	1.93	51.03**	40.64**	0.86	33.04**	11.41**	16.52**	29.45**
CMS4611A × PL 412	0.54	18.93**	9.92**	-7.33*	-13.71**	0.60	28.18**	15.11**	-18.75**	-9.73**
CMS4611A × IS 263	0.65	4.39	-14.21**	12.37**	4.64	0.81	30.03**	11.07**	10.67**	22.95**
CMS4611A × VR 523	0.69	31.22**	22.79**	18.79**	10.61**	0.65	16.21**	7.94*	-11.17**	-1.31
CMS4611A × DL 161	0.88	46.77**	23.89**	51.78**	41.33**	0.91	33.79**	7.78**	24.47**	38.28**
CMS4611A × IS 267	0.51	0.92	-1.80	-12.49**	-18.51**	0.63	10.20**	1.24	-14.66**	-5.19
CMS4611A × YL 581	0.44	8.30*	-10.87**	-24.86**	-30.03**	0.50	15.63**	-3.67	-32.00**	-24.46**
CMS4611A × SL 473	0.53	15.91**	7.13	-9.68**	-15.89**	0.58	19.09**	12.73**	-20.43**	-11.60**
CMS4611A × IS 262	0.80	25.88**	2.89	36.66**	27.25**	0.81	26.84**	6.98**	9.94**	22.14**
CMS4611A × VR 521	0.53	10.38**	8.76*	-8.30**	-14.61**	0.67	17.45**	8.24*	-9.40**	0.66
CMS4611A × FL 201	0.39	-5.59	-21.47**	-33.79**	-38.35**	0.45	5.34	-13.05**	-38.63**	-31.82**
CMS4611A × PP 402	0.41	-0.20	-16.71**	-29.78**	-34.61**	0.55	22.53**	7.01	-24.47**	-16.09**
CMS4611A × C 142	0.76	18.12**	-4.49*	30.47**	21.49**	0.86	27.39**	3.02	17.79**	30.86**
CMS4611A × PP 414	0.60	31.14**	21.87**	2.75	-4.32	0.55	17.24**	6.05	-25.15**	-16.84**
CMS4611A × VR 522	0.50	13.60**	2.45	-13.63**	-19.57**	0.60	14.42**	13.55**	-18.61**	-9.58**
CMS4611A × PL 406	0.72	29.48**	16.36**	23.02**	14.56**	0.66	21.70**	16.12**	-9.76**	0.25
CMS4611A × E 183	0.44	5.33	-10.67**	-24.68**	-29.87**	0.47	4.61	-10.29**	-36.68**	-29.65**
CMS4611A × IS 268	0.52	-7.16*	-17.49**	-10.54**	-16.69**	0.63	2.39	-11.34**	-14.48**	-4.99
CMS4611A × IS 261	0.62	23.57**	20.05**	7.33*	-0.05	0.88	29.66**	4.66	20.25**	33.59**

Crosses	Capsaicin content (%)									
	E_1					E_2				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4626A × AC 102	0.60	10.26**	-2.93	2.52	-4.53	0.55	-6.79*	-15.44**	-24.65**	-16.29**
CMS4626A × SL 475	0.90	21.24**	3.83	53.84**	43.25**	0.91	27.77**	18.32**	23.74**	37.47**
CMS4626A × PL 412	0.59	14.65**	-3.85	1.55	-5.44	0.56	5.65	-13.86**	-23.24**	-14.73**
CMS4626A × IS 263	0.89	29.65**	17.10**	53.38**	42.83**	0.76	9.09**	3.33	2.95	14.37**
CMS4626A × VR 523	0.77	30.48**	25.00**	32.02**	22.93**	0.74	17.43**	12.94**	0.64	11.80**
CMS4626A × DL 161	0.86	30.00**	21.04**	48.28**	38.08**	0.98	30.46**	15.57**	33.45**	48.26**
CMS4626A × IS 267	0.75	32.18**	21.85**	28.69**	19.84**	0.72	12.57**	9.53**	-2.41	8.42**
CMS4626A × YL 581	0.43	-8.69*	-30.80**	-26.92**	-31.95**	0.49	-1.03	-24.40**	-32.64**	-25.16**
CMS4626A × SL 473	0.52	0.10	-16.05**	-11.34**	-17.44**	0.59	6.15*	-9.37**	-19.25**	-10.29**
CMS4626A × IS 262	0.88	26.45**	13.50**	50.74**	40.37**	0.86	21.50**	13.43**	16.57**	29.50**
CMS4626A × VR 521	0.81	47.75**	31.13**	38.49**	28.96**	0.68	6.59**	3.36	-7.90**	2.32
CMS4626A × FL 201	0.41	-13.58**	-33.89**	-30.18**	-34.99**	0.51	3.39	-21.65**	-30.19**	-22.44**
CMS4626A × PP 402	0.59	26.05**	-3.31	2.12	-4.91	0.70	33.99**	6.62*	-4.99	5.55
CMS4626A × C 142	0.91	29.77**	15.05**	57.16**	46.35**	0.84	12.81**	0.36	14.75**	27.48**
CMS4626A × PP 414	0.68	31.92**	11.17**	17.41**	9.33**	0.55	1.77	-16.51**	-25.60**	-17.35**
CMS4626A × VR 522	0.55	8.69**	-10.79**	-5.78	-12.27**	0.73	23.26**	11.21**	-0.91	10.09**
CMS4626A × PL 406	0.92	49.76**	49.67**	58.25**	47.36**	0.73	19.51**	11.87**	-0.32	10.74**
CMS4626A × E 183	0.43	-10.21**	-30.15**	-26.23**	-31.31**	0.49	-4.91	-25.52**	-33.64**	-26.27**
CMS4626A × IS 268	0.71	14.74**	13.26**	22.79**	14.35**	0.78	14.29**	9.93**	6.04*	17.80**
CMS4626A × IS 261	0.58	1.91	-5.91*	-0.63	-7.47*	0.93	24.34**	10.39**	26.83**	40.90**
CMS463D13A × AC 102	0.57	10.74**	1.92	-2.58	-9.28**	0.60	3.65	-4.10	-18.16**	-9.08**
CMS463D13A × SL 475	0.91	28.76**	5.91**	56.93**	46.13**	0.89	28.25**	16.45**	21.79**	35.30**

Crosses	**Capsaicin content (%)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	0.59	20.49**	5.33	0.69	-6.24*	0.68	31.05**	8.67**	-7.26**	3.03
CMS463D13A × IS 263	0.89	34.93**	16.70**	52.86**	42.35**	0.77	12.79**	4.69	4.31	15.89**
CMS463D13A × VR 523	0.79	41.57**	40.73**	36.14**	26.77**	0.66	7.88**	5.96	-9.58**	0.45
CMS463D13A × DL 161	0.88	38.50**	23.28**	51.03**	40.64**	0.97	32.19**	14.94**	32.73**	47.45**
CMS463D13A × IS 267	0.60	11.13**	7.37*	2.63	-4.43	0.64	3.40	2.77	-12.30**	-2.57
CMS463D13A × YL 581	0.42	-4.20	-24.81**	-28.12**	-33.07**	0.50	1.99	-20.90**	-32.50**	-25.01**
CMS463D13A × SL 473	0.51	4.73	-8.45**	-12.49**	-18.51**	0.60	9.21**	-5.05	-18.97**	-9.98**
CMS463D13A × IS 262	0.87	31.04**	12.68**	49.66**	39.36**	0.85	22.59**	12.19**	15.30**	28.09**
CMS463D13A × VR 521	0.63	21.17**	12.46**	7.50*	0.11	0.78	26.05**	24.84**	6.54*	18.36**
CMS463D13A × FL 201	0.54	21.62**	-3.59	-7.85*	-14.19**	0.50	2.84	-20.90**	-32.50**	-25.01**
CMS463D13A × PP 402	0.61	37.68**	9.47**	4.64	-2.56	0.55	9.04**	-11.81**	-24.74**	-16.39**
CMS463D13A × C 142	0.72	5.92*	-9.98**	22.97**	14.51**	0.98	33.67**	16.71**	33.45**	48.26**
CMS463D13A × PP 414	0.53	8.01*	-5.09	-9.28**	-15.52**	0.56	6.37	-11.22**	-24.24**	-15.83**
CMS463D13A × VR 522	0.51	8.06*	-7.67*	-11.74**	-17.81**	0.62	7.89**	-0.74	-15.30**	-5.90
CMS463D13A × PL 406	0.64	9.36**	4.12	10.08**	2.51	0.79	31.63**	25.74**	7.31**	19.21**
CMS463D13A × E 183	0.44	-1.41	-20.43**	-23.94**	-29.17**	0.51	3.01	-18.03**	-30.05**	-22.29**
CMS463D13A × IS 268	0.87	47.05**	38.35**	50.00**	39.68**	0.72	8.16**	1.93	-1.68	9.23**
CMS463D13A × IS 261	0.75	38.58**	34.09**	28.18**	19.36**	0.96	31.04**	14.18**	31.18**	45.74**
LSD at p=0.05		0.03	0.04	0.04	0.04		0.03	0.04	0.04	0.04
LSD at p=0.01		0.04	0.05	0.05	0.05		0.05	0.05	0.05	0.05

Table 4.12n (*Cont'd.*)

Crosses	**Capsaicin content (%)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4611A × AC 102	0.39	2.67	-0.85	-23.80**	-25.11**	0.47	2.65	1.35	-22.25**	-21.34**
CMS4611A × SL 475	0.56	22.52**	8.01	8.78*	6.90	0.76	29.16**	6.79**	25.33**	26.81**
CMS4611A × PL 412	0.70	31.40**	4.67	35.63**	33.29**	0.61	26.46**	22.63**	0.13	1.31
CMS4611A × IS 263	0.58	16.17**	-4.52	13.98**	12.01**	0.68	16.90**	-2.61	12.14**	13.46**
CMS4611A × VR 523	0.61	3.62	-21.92**	18.34**	16.29**	0.65	16.53**	0.31	6.63**	7.89**
CMS4611A × DL 161	0.42	6.01	6.01	-18.53**	-19.94**	0.74	31.92**	13.30**	21.10**	22.53**
CMS4611A × IS 267	0.52	8.79*	-6.92	0.59	-1.15	0.55	6.74**	-2.36	-9.70**	-8.63**
CMS4611A × YL 581	0.31	-1.39	-22.25**	-40.25**	-41.28**	0.41	8.43**	-11.40**	-32.04**	-31.24**
CMS4611A × SL 473	0.44	24.81**	12.35*	-13.65**	-15.14**	0.52	19.54**	10.67**	-15.11**	-14.11**
CMS4611A × IS 262	0.49	1.89	-14.06**	-3.84	-5.50	0.70	19.60**	-0.27	14.58**	15.93**
CMS4611A × VR 521	0.60	14.80**	-7.50*	16.25**	14.25**	0.60	14.39**	3.44	-1.86	-0.70
CMS4611A × FL 201	0.30	-1.52	-23.35**	-41.09**	-42.11**	0.38	-0.41	-18.89**	-37.78**	-37.05**
CMS4611A × PP 402	0.32	0.05	-19.97**	-38.49**	-39.55**	0.43	8.61**	-8.86**	-30.09**	-29.26**
CMS4611A × C 142	0.51	25.44**	22.37**	-1.11	-2.81	0.71	23.48**	4.02*	16.53**	17.91**
CMS4611A × PP 414	0.38	4.08	-3.89	-26.14**	-27.41**	0.51	18.44**	8.79**	-16.55**	-15.56**
CMS4611A × VR 522	0.56	15.12**	-2.91	8.65*	6.77	0.55	14.40**	10.91**	-9.39**	-8.32**
CMS4611A × PL 406	0.63	19.99**	-3.55	21.98**	19.87**	0.67	23.81**	9.25**	9.57**	10.86**
CMS4611A × E 183	0.35	7.13	-11.68*	-32.12**	-33.29**	0.42	5.55*	-10.81**	-31.58**	-30.78**
CMS4611A × IS 268	0.52	22.12**	13.82**	1.24	-0.51	0.56	4.28*	-7.11**	-8.82**	-7.74**
CMS4611A × IS 261	0.53	29.79**	26.36**	2.54	0.77	0.68	27.76**	14.23**	11.17**	12.48**

Crosses	**Capsaicin content (%)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	0.49	12.98**	-2.32	-4.10	-5.75	0.55	4.56*	-7.37**	-10.24**	-9.18**
CMS4626A × SL 475	0.68	32.59**	30.92**	31.86**	29.58**	0.83	26.56**	15.53**	35.59**	37.19**
CMS4626A × PL 412	0.68	17.21**	3.01	33.49**	31.18**	0.61	12.63**	3.76	0.55	1.73
CMS4626A × IS 263	0.79	42.38**	29.74**	54.88**	52.20**	0.81	25.96**	15.99**	33.55**	35.13**
CMS4626A × VR 523	0.78	21.95**	0.47	52.28**	49.65**	0.76	23.12**	17.68**	25.10**	26.57**
CMS4626A × DL 161	0.46	2.67	-8.48	-10.14*	-11.69**	0.77	23.61**	17.83**	25.95**	27.44**
CMS4626A × IS 267	0.66	25.47**	19.74**	29.39**	27.16**	0.71	22.92**	20.12**	16.40**	17.78**
CMS4626A × YL 581	0.42	13.87**	-17.35**	-18.86**	-20.26**	0.45	0.38	-24.62**	-26.95**	-26.09**
CMS4626A × SL 473	0.42	3.66	-15.70**	-17.23**	-18.66**	0.51	3.36	-13.49**	-16.17**	-15.18**
CMS4626A × IS 262	0.67	24.85**	17.20**	31.14**	28.88**	0.80	24.21**	14.48**	31.53**	33.08**
CMS4626A × VR 521	0.70	22.74**	9.31**	37.39**	35.02**	0.73	24.68**	23.38**	19.56**	20.97**
CMS4626A × FL 201	0.39	7.38	-22.91**	-24.32**	-25.62**	0.44	-1.53	-26.26**	-28.54**	-27.70**
CMS4626A × PP 402	0.46	23.03**	-9.60*	-11.25**	-12.78**	0.58	28.27**	-1.43	-4.48*	-3.36
CMS4626A × C 142	0.60	30.62**	19.07**	16.91**	14.89**	0.79	23.34**	15.02**	28.85**	30.37**
CMS4626A × PP 414	0.47	12.78**	-6.23	-7.93	-9.52*	0.57	15.50**	-3.99*	-6.96**	-5.86**
CMS4626A × VR 522	0.60	12.35**	5.46	18.01**	15.97**	0.63	15.16**	6.13**	2.84	4.06*
CMS4626A × PL 406	0.78	35.46**	20.31**	52.15**	49.52**	0.81	34.92**	32.64**	33.02**	34.59**
CMS4626A × E 183	0.31	-17.08**	-37.48**	-38.62**	-39.68**	0.41	-10.13**	-30.52**	-32.68**	-31.88**
CMS4626A × IS 268	0.51	6.95	1.92	0.07	-1.66	0.67	12.47**	11.75**	9.70**	10.99**
CMS4626A × IS 261	0.52	12.33**	2.58	0.72	-1.02	0.68	14.07**	13.82**	10.77**	12.08**
CMS463D13A × AC 102	0.46	4.81	-10.08*	-10.08*	-11.63**	0.54	6.35**	-3.93	-10.93**	-9.88**
CMS463D13A × SL 475	0.79	54.52**	53.97**	55.07**	52.40**	0.87	35.47**	21.24**	42.30**	43.98**

Crosses	Capsaicin content (%)									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS463D13A × PL 412	0.78	32.99**	17.81**	52.67**	50.03**	0.68	28.55**	20.88**	12.06**	13.39**
CMS463D13A × IS 263	0.68	21.81**	11.93**	33.62**	31.31**	0.78	23.14**	11.14**	27.98**	29.49**
CMS463D13A × VR 523	0.78	20.91**	0.34	52.08**	49.46**	0.75	22.86**	15.00**	22.25**	23.70**
CMS463D13A × DL 161	0.57	26.47**	11.83**	11.83**	9.90*	0.81	32.96**	24.14**	32.70**	34.26**
CMS463D13A × IS 267	0.60	11.56**	7.40	16.06**	14.06**	0.61	8.42**	8.30**	0.40	1.59
CMS463D13A × YL 581	0.32	-12.16*	-36.61**	-36.61**	-37.70**	0.41	-4.15	-26.93**	-32.26**	-31.46**
CMS463D13A × SL 473	0.42	0.89	-18.53**	-18.53**	-19.94**	0.51	5.32*	-10.24**	-16.79**	-15.80**
CMS463D13A × IS 262	0.78	44.28**	36.61**	52.86**	50.22**	0.83	31.75**	19.04**	36.76**	38.37**
CMS463D13A × VR 521	0.72	24.81**	12.05**	40.83**	38.40**	0.71	24.16**	22.74**	16.46**	17.83**
CMS463D13A × FL 201	0.40	7.92	-22.95**	-22.95**	-24.28**	0.48	10.71**	-15.84**	-21.98**	-21.06**
CMS463D13A × PP 402	0.42	11.17*	-18.79**	-18.79**	-20.19**	0.53	19.21**	-6.94**	-13.72**	-12.71**
CMS463D13A × C 142	0.60	28.44**	16.12**	16.12**	14.12**	0.76	22.36**	11.81**	25.26**	26.74**
CMS463D13A × PP 414	0.42	-1.69	-18.86**	-18.86**	-20.26**	0.50	4.55*	-11.52**	-17.97**	-17.00**
CMS463D13A × VR 522	0.64	18.32**	12.03**	25.36**	23.19**	0.59	11.49**	4.88*	-2.77	-1.62
CMS463D13A × PL 406	0.62	7.49*	-3.75	21.72**	19.62**	0.68	16.30**	11.90**	12.23**	13.55**
CMS463D13A × E 183	0.33	-13.84**	-35.44**	-35.44**	-36.55**	0.43	-3.34	-24.08**	-29.62**	-28.78**
CMS463D13A × IS 268	0.55	13.97**	7.67	7.67	5.81	0.72	23.00**	19.59**	17.39**	18.77**
CMS463D13A × IS 261	0.58	24.26**	12.55**	12.55**	10.61*	0.76	31.56**	28.45**	25.00**	26.48**
LSD at *p*=0.05		0.04	0.04	0.04	0.04		0.02	0.02	0.02	0.02
LSD at *p*=0.01		0.05	0.06	0.06	0.06		0.03	0.03	0.03	0.03

*, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.12o: **Mean and heterosis (%) over mid parent (H_{MP}), better parent (H_{BP}) and standard checks (CH-27 and Soldier) exhibited by 60 crosses of chilli for scoville heat units evaluated over environments**

Crosses	Scoville Heat Units (SHU)									
	E$_1$					E$_2$				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	77546.67	1.15	-1.22	-16.72**	-22.45**	87440.00	3.97	2.55	-25.57**	-17.31**
CMS4611A × SL 475	140640.00	29.93**	1.93	51.03**	40.64**	136885.33	33.02**	11.40**	16.52**	29.46**
CMS4611A × PL 412	86293.33	18.93**	9.92**	-7.33*	-13.71**	95461.33	28.18**	15.10**	-18.74**	-9.72**
CMS4611A × IS 263	104640.00	4.39	-14.21**	12.37**	4.64	129984.00	30.00**	11.06**	10.65**	22.93**
CMS4611A × VR 523	110613.33	31.22**	22.79**	18.79**	10.61**	104352.00	16.18**	7.91*	-11.17**	-1.31
CMS4611A × DL 161	141333.33	46.77**	23.89**	51.78**	41.33**	146234.67	33.77**	7.77**	24.48**	38.30**
CMS4611A × IS 267	81493.33	0.92	-1.80	-12.49**	-18.51**	100218.67	10.13**	1.17	-14.69**	-5.22
CMS4611A × YL 581	69973.33	8.30*	-10.87**	-24.86**	-30.03**	79914.67	15.66**	-3.65	-31.97**	-24.42**
CMS4611A × SL 473	84106.67	15.91**	7.13	-9.68**	-15.89**	93466.67	19.09**	12.69**	-20.44**	-11.61**
CMS4611A × IS 262	127253.33	25.88**	2.89	36.66**	27.25**	129189.33	26.89**	7.04**	9.97**	22.18**
CMS4611A × VR 521	85386.67	10.38**	8.76*	-8.30**	-14.61**	106448.00	17.43**	8.23*	-9.39**	0.67
CMS4611A × FL 201	61653.33	-5.59	-21.47**	-33.79**	-38.35**	72090.67	5.31	-13.08**	-38.63**	-31.82**
CMS4611A × PP 402	65386.67	-0.20	-16.71**	-29.78**	-34.61**	88746.67	22.52**	7.00	-24.46**	-16.07**
CMS4611A × C 142	121493.33	18.12**	-4.49*	30.47**	21.49**	138373.33	27.38**	3.02	17.79**	30.86**
CMS4611A × PP 414	95680.00	31.14**	21.88**	2.75	-4.32	87952.00	17.24**	6.04	-25.13**	-16.82**
CMS4611A × VR 522	80426.67	13.60**	2.45	-13.63**	-19.57**	95616.00	14.39**	13.50**	-18.61**	-9.57**
CMS4611A × PL 406	114560.00	29.48**	16.36**	23.02**	14.56**	106026.67	21.72**	16.17**	-9.75**	0.27
CMS4611A × E 183	70133.33	5.33	-10.67**	-24.68**	-29.87**	74378.67	4.60	-10.32**	-36.69**	-29.66**
CMS4611A × IS 268	83306.67	-7.16*	-17.49**	-10.54**	-16.69**	100400.00	2.30	-11.42**	-14.54**	-5.05
CMS4611A × IS 261	99946.67	23.57**	20.05**	7.33*	-0.05	141264.00	29.65**	4.66	20.25**	33.60**

Crosses	**Scoville Heat Units (SHU)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	95466.67	10.26**	-2.93	2.52	-4.53	88538.67	-6.74*	-15.37**	-24.63**	-16.27**
CMS4626A × SL 475	143253.33	21.24**	3.83	53.84**	43.25**	145306.67	27.75**	18.26**	23.69**	37.42**
CMS4626A × PL 412	94560.00	14.65**	-3.85	1.55	-5.44	90176.00	5.70	-13.80**	-23.24**	-14.72**
CMS4626A × IS 263	142826.67	29.65**	17.10**	53.38**	42.83**	120949.33	9.13**	3.34	2.96	14.39**
CMS4626A × VR 523	122933.33	30.48**	25.00**	32.02**	22.93**	118256.00	17.49**	13.04**	0.66	11.84**
CMS4626A × DL 161	138080.00	30.00**	21.04**	48.28**	38.08**	156789.33	30.49**	15.55**	33.46**	48.28**
CMS4626A × IS 267	119840.00	32.18**	21.85**	28.69**	19.84**	114592.00	12.53**	9.54**	-2.46	8.37**
CMS4626A × YL 581	68053.33	-8.69*	-30.80**	-26.92**	-31.95**	79104.00	-1.03	-24.38**	-32.66**	-25.19**
CMS4626A × SL 473	82560.00	0.10	-16.05**	-11.34**	-17.44**	94848.00	6.19*	-9.33**	-19.26**	-10.30**
CMS4626A × IS 262	140373.33	26.45**	13.50**	50.74**	40.37**	136901.33	21.53**	13.43**	16.53**	29.47**
CMS4626A × VR 521	128960.00	47.75**	31.13**	38.49**	28.96**	108160.00	6.58*	3.39	-7.93**	2.29
CMS4626A × FL 201	65013.33	-13.58**	-33.89**	-30.18**	-34.99**	82042.67	3.46	-21.58**	-30.16**	-22.41**
CMS4626A × PP 402	95093.33	26.05**	-3.31	2.12	-4.91	111568.00	33.98**	6.65*	-5.03	5.51
CMS4626A × C 142	146346.67	29.77**	15.05**	57.16**	46.35**	134848.00	12.88**	0.40	14.79**	27.53**
CMS4626A × PP 414	109333.33	31.92**	11.17**	17.41**	9.33**	87429.33	1.83	-16.43**	-25.58**	-17.32**
CMS4626A × VR 522	87733.33	8.69**	-10.79**	-5.78	-12.27**	116389.33	23.26**	11.26**	-0.93	10.07**
CMS4626A × PL 406	147360.00	49.76**	49.67**	58.25**	47.36**	117130.67	19.59**	11.97**	-0.30	10.77**
CMS4626A × E 183	68693.33	-10.21**	-30.15**	-26.23**	-31.31**	77920.00	-4.91	-25.52**	-33.67**	-26.31**
CMS4626A × IS 268	114346.67	14.74**	13.26**	22.79**	14.35**	124586.67	14.32**	9.92**	6.05*	17.83**
CMS4626A × IS 261	92533.33	1.91	-5.91*	-0.63	-7.47*	149013.33	24.39**	10.40**	26.84**	40.93**
CMS463D13A × AC 102	90720.00	10.74**	1.92	-2.58	-9.28**	96133.33	3.65	-4.10	-18.17**	-9.08**
CMS463D13A × SL 475	146133.33	28.76**	5.91**	56.93**	46.13**	143136.00	28.31**	16.49**	21.84**	35.37**

Crosses	**Scoville Heat Units (SHU)**									
	E_1					**E_2**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	93760.00	20.49**	5.33	0.69	-6.24*	108976.00	31.09**	8.72**	-7.24**	3.06
CMS463D13A × IS 263	142346.67	34.93**	16.70**	52.86**	42.35**	122506.67	12.76**	4.67	4.28	15.86**
CMS463D13A × VR 523	126773.33	41.57**	40.73**	36.14**	26.77**	106240.00	7.89**	5.99	-9.57**	0.47
CMS463D13A × DL 161	140640.00	38.50**	23.28**	51.03**	40.64**	155904.00	32.16**	14.90**	32.71**	47.44**
CMS463D13A × IS 267	95573.33	11.13**	7.37*	2.63	-4.43	103050.67	3.41	2.80	-12.28**	-2.54
CMS463D13A × YL 581	66933.33	-4.20	-24.81**	-28.12**	-33.07**	79317.33	2.02	-20.87**	-32.48**	-24.99**
CMS463D13A × SL 473	81493.33	4.73	-8.45**	-12.49**	-18.51**	95141.33	9.19**	-5.09	-19.01**	-10.02**
CMS463D13A × IS 262	139360.00	31.04**	12.68**	49.66**	39.36**	135445.33	22.61**	12.23**	15.29**	28.09**
CMS463D13A × VR 521	100106.67	21.17**	12.46**	7.50*	0.11	125157.33	26.04**	24.86**	6.54*	18.36**
CMS463D13A × FL 201	85813.33	21.62**	-3.59	-7.85*	-14.19**	79248.00	2.77	-20.94**	-32.54**	-25.05**
CMS463D13A × PP 402	97440.00	37.68**	9.47**	4.64	-2.56	88453.33	9.09**	-11.76**	-24.71**	-16.35**
CMS463D13A × C 142	114506.67	5.92*	-9.98**	22.97**	14.51**	156752.00	33.66**	16.71**	33.43**	48.24**
CMS463D13A × PP 414	84480.00	8.01*	-5.09	-9.28**	-15.52**	89008.00	6.38	-11.21**	-24.23**	-15.82**
CMS463D13A × VR 522	82186.67	8.06*	-7.67*	-11.74**	-17.81**	99514.67	7.89**	-0.72	-15.29**	-5.89
CMS463D13A × PL 406	102506.67	9.36**	4.12	10.08**	2.51	126064.00	31.65**	25.76**	7.31**	19.22**
CMS463D13A × E 183	70826.67	-1.41	-20.43**	-23.94**	-29.17**	82144.00	2.99	-18.05**	-30.08**	-22.31**
CMS463D13A × IS 268	139680.00	47.05**	38.35**	50.00**	39.68**	115568.00	8.22**	1.97	-1.63	9.30**
CMS463D13A × IS 261	119360.00	38.58**	34.09**	28.18**	19.36**	154122.67	31.05**	14.19**	31.19**	45.76**
LSD at *p*=0.05		4908.31	5667.62	5667.62	5667.62		5484.65	6333.13	6333.13	6333.13
LSD at *p*=0.01		6489.32	7493.22	7493.22	7493.22		7251.32	8373.10	8373.10	8373.10

Table 4.12o (*Cont'd.*)

Crosses	Scoville Heat Units (SHU)									
	E$_3$					Pooled				
	Mean	Heterosis (%) over				Mean	Heterosis (%) over			
		H_{MP}	H_{BP}	CH-27	Soldier		H_{MP}	H_{BP}	CH-27	Soldier
CMS4611A × AC 102	62506.67	2.67	-0.85	-23.80**	-25.11**	75831.11	2.64	1.34	-22.26**	-21.34**
CMS4611A × SL 475	89226.67	22.52**	8.01	8.78*	6.90	122250.67	29.15**	6.78**	25.33**	26.81**
CMS4611A × PL 412	111253.33	31.40**	4.67	35.63**	33.29**	97669.33	26.46**	22.64**	0.13	1.31
CMS4611A × IS 263	93493.33	16.17**	-4.52	13.98**	12.01**	109372.44	16.89**	-2.62	12.13**	13.45**
CMS4611A × VR 523	97066.67	3.62	-21.92**	18.34**	16.29**	104010.67	16.52**	0.30	6.63**	7.89**
CMS4611A × DL 161	66826.67	6.01	6.01	-18.53**	-19.94**	118131.56	31.92**	13.29**	21.11**	22.54**
CMS4611A × IS 267	82506.67	8.79*	-6.92	0.59	-1.15	88072.89	6.72**	-2.39	-9.71**	-8.64**
CMS4611A × YL 581	49013.33	-1.39	-22.25**	-40.25**	-41.28**	66300.44	8.44**	-11.40**	-32.03**	-31.22**
CMS4611A × SL 473	70826.67	24.81**	12.35*	-13.65**	-15.14**	82800.00	19.54**	10.65**	-15.11**	-14.11**
CMS4611A × IS 262	78880.00	1.89	-14.06**	-3.84	-5.50	111774.22	19.62**	-0.25	14.59**	15.95**
CMS4611A × VR 521	95360.00	14.80**	-7.50*	16.25**	14.25**	95731.56	14.39**	3.43	-1.86	-0.70
CMS4611A × FL 201	48320.00	-1.52	-23.35**	-41.09**	-42.11**	60688.00	-0.42	-18.90**	-37.78**	-37.05**
CMS4611A × PP 402	50453.33	0.05	-19.97**	-38.49**	-39.55**	68195.56	8.60**	-8.86**	-30.09**	-29.26**
CMS4611A × C 142	81120.00	25.44**	22.37**	-1.11	-2.81	113662.22	23.48**	4.02*	16.53**	17.90**
CMS4611A × PP 414	60586.67	4.08	-3.89	-26.14**	-27.41**	81406.22	18.44**	8.79**	-16.54**	-15.56**
CMS4611A × VR 522	89120.00	15.12**	-2.91	8.65*	6.77	88387.56	14.39**	10.89**	-9.38**	-8.31**
CMS4611A × PL 406	100053.33	19.99**	-3.55	21.98**	19.87**	106880.00	23.81**	9.26**	9.57**	10.87**
CMS4611A × E 183	55680.00	7.13	-11.68*	-32.12**	-33.29**	66730.67	5.55*	-10.82**	-31.59**	-30.78**
CMS4611A × IS 268	83040.00	22.12**	13.82**	1.24	-0.51	88915.56	4.25*	-7.14**	-8.84**	-7.77**
CMS4611A × IS 261	84106.67	29.79**	26.36**	2.54	0.77	108439.11	27.76**	14.23**	11.17**	12.49**

Crosses	**Scoville Heat Units (SHU)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS4626A × AC 102	78666.67	12.98**	-2.32	-4.10	-5.75	87557.33	4.59*	-7.34**	-10.24**	-9.17**
CMS4626A × SL 475	108160.00	32.59**	30.92**	31.86**	29.58**	132240.00	26.55**	15.51**	35.57**	37.18**
CMS4626A × PL 412	109493.33	17.21**	3.01	33.49**	31.18**	98076.44	12.64**	3.79	0.55	1.74
CMS4626A × IS 263	127040.00	42.38**	29.74**	54.88**	52.20**	130272.00	25.98**	15.99**	33.56**	35.13**
CMS4626A × VR 523	124906.67	21.95**	0.47	52.28**	49.65**	122032.00	23.14**	17.68**	25.11**	26.59**
CMS4626A × DL 161	73706.67	2.67	-8.48	-10.14*	-11.69**	122858.67	23.62**	17.83**	25.96**	27.44**
CMS4626A × IS 267	106133.33	25.47**	19.74**	29.39**	27.16**	113521.78	22.91**	20.13**	16.38**	17.76**
CMS4626A × YL 581	66560.00	13.87**	-17.35**	-18.86**	-20.26**	71239.11	0.38	-24.61**	-26.97**	-26.10**
CMS4626A × SL 473	67893.33	3.66	-15.70**	-17.23**	-18.66**	81767.11	3.37	-13.47**	-16.17**	-15.18**
CMS4626A × IS 262	107573.33	24.85**	17.20**	31.14**	28.88**	128282.67	24.22**	14.49**	31.52**	33.07**
CMS4626A × VR 521	112693.33	22.74**	9.31**	37.39**	35.02**	116604.44	24.68**	23.39**	19.54**	20.96**
CMS4626A × FL 201	62080.00	7.38	-22.91**	-24.32**	-25.62**	69712.00	-1.51	-26.23**	-28.53**	-27.69**
CMS4626A × PP 402	72800.00	23.03**	-9.60*	-11.25**	-12.78**	93153.78	28.26**	-1.42	-4.50*	-3.37
CMS4626A × C 142	95893.33	30.62**	19.07**	16.91**	14.89**	125696.00	23.37**	15.03**	28.86**	30.39**
CMS4626A × PP 414	75520.00	12.78**	-6.23	-7.93	-9.52*	90760.89	15.52**	-3.95*	-6.95**	-5.85**
CMS4626A × VR 522	96800.00	12.35**	5.46	18.01**	15.97**	100307.56	15.16**	6.15**	2.84	4.05*
CMS4626A × PL 406	124800.00	35.46**	20.31**	52.15**	49.52**	129763.56	34.95**	32.66**	33.03**	34.61**
CMS4626A × E 183	50346.67	-17.08**	-37.48**	-38.62**	-39.68**	65653.33	-10.14**	-30.52**	-32.69**	-31.90**
CMS4626A × IS 268	82080.00	6.95	1.92	0.07	-1.66	107004.44	12.49**	11.75**	9.70**	11.00**
CMS4626A × IS 261	82613.33	12.33**	2.58	0.72	-1.02	108053.33	14.09**	13.83**	10.78**	12.09**
CMS463D13A × AC 102	73760.00	4.81	-10.08*	-10.08*	-11.63**	86871.11	6.35**	-3.93	-10.94**	-9.89**
CMS463D13A × SL 475	127200.00	54.52**	53.97**	55.07**	52.40**	138823.11	35.49**	21.26**	42.32**	44.00**

Crosses	**Scoville Heat Units (SHU)**									
	E_3					**Pooled**				
	Mean	**Heterosis (%) over**				**Mean**	**Heterosis (%) over**			
		H_{MP}	**H_{BP}**	**CH-27**	**Soldier**		**H_{MP}**	**H_{BP}**	**CH-27**	**Soldier**
CMS463D13A × PL 412	125226.67	32.99**	17.81**	52.67**	50.03**	109320.89	28.56**	20.89**	12.08**	13.40**
CMS463D13A × IS 263	109600.00	21.81**	11.93**	33.62**	31.31**	124817.78	23.13**	11.14**	27.96**	29.48**
CMS463D13A × VR 523	124746.67	20.91**	0.34	52.08**	49.46**	119253.33	22.86**	15.00**	22.26**	23.70**
CMS463D13A × DL 161	91733.33	26.47**	11.83**	11.83**	9.90*	129425.78	32.95**	24.13**	32.69**	34.26**
CMS463D13A × IS 267	95200.00	11.56**	7.40	16.06**	14.06**	97941.33	8.43**	8.31**	0.41	1.60
CMS463D13A × YL 581	52000.00	-12.16*	-36.61**	-36.61**	-37.70**	66083.56	-4.14	-26.92**	-32.25**	-31.45**
CMS463D13A × SL 473	66826.67	0.89	-18.53**	-18.53**	-19.94**	81153.78	5.31*	-10.25**	-16.80**	-15.82**
CMS463D13A × IS 262	125386.67	44.28**	36.61**	52.86**	50.22**	133397.33	31.76**	19.05**	36.76**	38.38**
CMS463D13A × VR 521	115520.00	24.81**	12.05**	40.83**	38.40**	113594.67	24.16**	22.73**	16.46**	17.83**
CMS463D13A × FL 201	63200.00	7.92	-22.95**	-22.95**	-24.28**	76087.11	10.68**	-15.86**	-22.00**	-21.07**
CMS463D13A × PP 402	66613.33	11.17*	-18.79**	-18.79**	-20.19**	84168.89	19.23**	-6.92**	-13.71**	-12.69**
CMS463D13A × C 142	95253.33	28.44**	16.12**	16.12**	14.12**	122170.67	22.36**	11.81**	25.25**	26.73**
CMS463D13A × PP 414	66560.00	-1.69	-18.86**	-18.86**	-20.26**	80016.00	4.56*	-11.51**	-17.97**	-17.00**
CMS463D13A × VR 522	102826.67	18.32**	12.03**	25.36**	23.19**	94842.67	11.49**	4.88*	-2.77	-1.62
CMS463D13A × PL 406	99840.00	7.49*	-3.75	21.72**	19.62**	109470.22	16.31**	11.91**	12.23**	13.56**
CMS463D13A × E 183	52960.00	-13.84**	-35.44**	-35.44**	-36.55**	68643.56	-3.35	-24.09**	-29.63**	-28.79**
CMS463D13A × IS 268	88320.00	13.97**	7.67	7.67	5.81	114522.67	23.02**	19.60**	17.41**	18.80**
CMS463D13A × IS 261	92320.00	24.26**	12.55**	12.55**	10.61*	121934.22	31.57**	28.45**	25.01**	26.49**
LSD at p=0.05		5940.80	6859.85	6859.85	6859.85		3227.31	3726.57	3726.57	3726.57
LSD at p=0.01		7854.39	9069.47	9069.47	9069.47		4249.84	4907.29	4907.29	4907.29

*, significant at p=0.05; **, significant at p=0.01

Table 4.13a: Selected crosses based on total yield heterosis over superior check Soldier, their corresponding SCA effects and GCA of parents in E$_1$

Crosses	Total yield plant^{-1} (kg)			Plant height (cm)			Plant spread (cm)			Number of primary branches plant^{-1}		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × DL 161	34.83**	0	P × G	0.51	3.61	A × P	29.91**	1.28	A × A	30.00**	-0.78**	A × G
CMS4611A × C 142	26.79**	0	P × G	32.70**	6.89	A × G	33.16**	-1.11	A × G	40.00**	-0.18	A × A
CMS4611A × IS 268	19.98**	-0.13**	P × G	32.92**	-1.01	A × G	25.31**	-4.35	A × A	13.33	-0.52*	A × P
CMS4626A × PL 412	34.33**	0.19**	P × G	11.56	-6.05	P × G	31.79**	3.09	P × G	49.99**	0.36	P × A
CMS4626A × VR 523	17.91*	0.06	P × G	9.13	3.29	P × A	28.86**	-0.29	P × G	18.67	-0.27	P × A
CMS4626A × DL 161	45.92**	0.07	P × G	-15.95*	-2.61	P × P	14.17	-0.69	P × A	75.33**	1.08**	P × G
CMS4626A × IS 262	18.41**	0	P × G	-1.96	0.68	P × P	7.41	3.63	P × P	55.01**	0.75**	P × A
CMS4626A × C 142	33.98**	0.03	P × G	13.88	-1.38	P × G	24.05**	0.43	P × G	26.66*	-0.28	P × A
CMS4626A × PL 406	20.86**	0.14**	P × G	30.14**	9.75*	P × G	28.02**	1.53	P × G	65.66**	-0.12	P × G
CMS4626A × IS 268	40.38**	0.01	P × G	20.92**	-3.37	P × G	15.3	-3.29	P × A	24.01*	0.19	P × P
CMS463D13A × SL 475	20.21**	-0.09*	G × A	16.64*	-7.99	G × A	40.92**	0.55	G × A	30.00**	-0.79**	G × A
CMS463D13A × PL 412	44.97**	0.04	G × G	37.44**	-3.87	G × G	35.78**	-8.04*	G × G	54.67**	-0.37	G × A
CMS463D13A × VR 523	37.54**	0	G × G	31.05**	2.04	G × A	72.26**	9.45**	G × G	48.33**	-0.16	G × A
CMS463D13A × DL 161	56.95**	-0.07	G × G	9.25	-1.01	G × P	39.37**	-0.58	G × A	60.65**	-0.3	G × G
CMS463D13A × IS 267	70.38**	0.23**	G × G	34.63**	-5.28	G × G	39.15**	1.14	G × A	108.66**	0.87**	G × G
CMS463D13A × YL 581	20.44**	0.02	G × P	24.78**	1.77	G × A	31.76**	-6.39*	G × A	75.33**	0.52*	G × A
CMS463D13A × SL 473	33.18**	0.14**	G × P	21.75**	7.96	G × P	39.30**	1.81	G × A	38.33**	-0.3	G × P
CMS463D13A × IS 262	62.11**	0.14**	G × G	20.39**	-0.19	G × P	24.53**	-0.54	G × P	34.33**	-0.82**	G × A
CMS463D13A × PP 402	55.19**	0.15**	G × G	25.45**	-1.58	G × A	37.23**	4.14	G × P	50.10**	0.03	G × P
CMS463D13A × C 142	54.65**	-0.03	G × G	32.48**	-5.51	G × G	49.51**	0.68	G × G	75.34**	0.46	G × A
CMS463D13A × VR 522	38.35**	0.04	G × G	28.64**	5.63	G × A	29.71**	2.69	G × P	24.01*	-1.01**	G × A
CMS463D13A × IS 268	80.18**	0.12**	G × G	53.20**	4.38	G × G	60.93**	7.64*	G × A	54.66**	0.33	G × P

Table 4.13a (*Cont'd.*)

Crosses	Fruit weight (g)			Fruit length (cm)			Fruit width (mm)			Pericarp thickness (mm)		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × DL 161	29.86*	1.62**	P × P	-6.03	-0.35	P × P	13.01	1.17*	P × P	23.91*	0.17**	P × P
CMS4611A × C 142	45.04**	0.62	P × A	22.37**	0.80*	P × A	27.81**	0.41	P × A	36.64**	0.06	P × A
CMS4611A × IS 268	48.89**	-0.5	P × G	17.38*	0.51	P × A	23.08**	-0.86	P × G	40.88**	0.02	P × G
CMS4626A × PL 412	87.04**	0.21	P × A	17.98*	-0.63	A × G	19.79*	-0.01	A × P	50.04**	-0.01	P × G
CMS4626A × VR 523	60.22**	-0.52	P × A	27.04**	-0.13	A × G	28.70**	-0.01	A × A	43.77**	-0.05	P × G
CMS4626A × DL 161	9.92	-0.51	P × P	9.81	-0.05	A × P	16.46*	0.05	A × P	16.14	-0.04	P × P
CMS4626A × IS 262	93.12**	-0.04	P × G	22.98**	0.24	A × A	44.10**	-0.09	A × G	53.73**	0.14*	P × A
CMS4626A × C 142	75.91**	0.17	P × A	21.02**	-0.12	A × A	39.09**	0.07	A × A	57.65**	0.1	P × A
CMS4626A × PL 406	85.02**	-0.45	P × G	24.29**	0.01	A × A	37.78**	0.07	A × A	50.24**	0.11	P × A
CMS4626A × IS 268	103.24**	-0.18	P × G	13.55	-0.6	A × A	54.92**	0.86	A × G	55.43**	-0.01	P × G
CMS463D13A × SL 475	169.23**	-0.18	G × G	45.03**	-0.32	G × G	39.08**	-1.03	G × G	112.61**	0	G × G
CMS463D13A × PL 412	141.70**	-0.52	G × A	47.87**	0.61	G × G	29.46**	-0.02	G × P	81.92**	-0.1	G × G
CMS463D13A × VR 523	158.70**	0.19	G × A	44.14**	0.2	G × G	36.25**	-0.23	G × A	88.82**	-0.03	G × G
CMS463D13A × DL 161	68.83**	-1.11**	G × P	28.54**	0.4	G × P	13.38	-1.23*	G × P	50.16**	-0.12*	G × P
CMS463D13A × IS 267	183.70**	0.70*	G × A	44.14**	0.31	G × G	41.11**	0.44	G × A	112.25**	0.20**	G × A
CMS463D13A × YL 581	263.87**	1.78**	G × G	33.26**	0.39	G × A	73.93**	0.85	G × G	127.00**	0.07	G × G
CMS463D13A × SL 473	153.34**	0.62	G × P	36.95**	1.27**	G × P	53.52**	0.26	G × G	83.58**	0.11	G × P
CMS463D13A × IS 262	177.13**	0.2	G × G	28.82**	-0.22	G × A	59.37**	0.45	G × G	81.88**	0.01	G × A
CMS463D13A × PP 402	268.22**	0.93**	G × G	37.83**	0.02	G × A	78.03**	0.97	G × G	157.61**	0.18**	G × G
CMS463D13A × C 142	123.99**	-0.79*	G × A	25.60**	-0.68	G × A	43.29**	-0.48	G × A	70.38**	-0.16**	G × A
CMS463D13A × VR 522	203.44**	0.77*	G × G	36.01**	0.34	G × A	48.04**	0.18	G × A	82.75**	0	G × A
CMS463D13A × IS 268	206.28**	0.68*	G × G	35.64**	0.09	G × A	56.11**	0	G × G	97.82**	-0.01	G × G

Table 4.13a (*Cont'd.*)

Crosses	**Number of fruits plant^{-1}**			**Number of seed fruit^{-1}**			**1000 seed weight (g)**			**Ascorbic acid (mg.100g^{-1})**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × DL 161	28.26**	-0.58	G × G	52.13**	4.41	P × P	-21.00**	-0.18	P × P	19.36**	10.55**	P × P
CMS4611A × C 142	30.57**	20.67	G × G	73.44**	-6.59*	P × G	-11.27	-0.01	P × P	58.52**	27.86**	P × G
CMS4611A × IS 268	10.71	0.16	G × G	97.28**	0.95	P × G	16.69**	0.09	P × G	60.97**	5.08	P × G
CMS4626A × PL 412	25.19**	38.66**	A × G	94.11**	0.25	A × G	4.52	-0.07	A × P	45.88**	-11.27**	G × G
CMS4626A × VR 523	-1.42	12.51	A × A	77.15**	-0.05	A × G	22.74**	0.22	A × G	56.28**	19.96**	G × G
CMS4626A × DL 161	21.06**	-4.31	A × G	45.33**	0.18	A × P	-14.19*	-0.02	A × P	17.79**	-3.6	G × P
CMS4626A × IS 262	4.43	7	A × G	48.78**	1.85	A × P	28.37**	0.25	A × G	14.30**	1.1	G × P
CMS4626A × C 142	14.72*	-8.16	A × G	111.70**	5.75*	A × G	-15.23*	-0.37	A × P	31.26**	-16.50**	G × G
CMS4626A × PL 406	9.27	30.36*	A × G	108.16**	2.47	A × G	3.96	0.05	A × P	46.45**	-2	G × G
CMS4626A × IS 268	9.21	13.01	A × G	68.00**	-11.54**	A × G	22.95**	0.22	A × G	67.88**	0.9	G × G
CMS463D13A × SL 475	-8.79	12.8	P × A	134.90**	-1.2	G × G	33.94**	0.29	G × G	33.19**	1.24	G × A
CMS463D13A × PL 412	13.29*	17.45	P × G	97.01**	-3.72	G × G	10.36	-0.09	G × P	66.88**	8.63**	G × G
CMS463D13A × VR 523	-12.76*	-7.09	P × A	87.40**	-1.32	G × G	24.69**	0.02	G × G	40.11**	-3.86	G × G
CMS463D13A × DL 161	19.62**	4.89	P × G	46.06**	-4.59	G × P	-3.55	0.19	G × P	19.02**	-6.96*	G × P
CMS463D13A × IS 267	2.33	24.18	P × G	114.51**	2.19	G × G	16.48**	-0.28	G × A	63.86**	12.66**	G × G
CMS463D13A × YL 581	-30.55**	-2.26	P × P	54.76**	4.75	G × P	41.38**	0.07	G × G	-1.03	7.69**	G × P
CMS463D13A × SL 473	-19.44**	-1.44	P × P	67.91**	-0.61	G × P	28.65**	0.24	G × A	15.44**	-10.75**	G × P
CMS463D13A × IS 262	-7.25	-13.59	P × G	55.94**	-0.56	G × P	24.48**	-0.24	G × G	13.63**	-4.49	G × P
CMS463D13A × PP 402	-19.20**	19.98	P × P	51.50**	1.15	G × P	30.46**	-0.11	G × G	8.67*	8.86**	G × P
CMS463D13A × C 142	8.62	-12.51	P × G	112.06**	0.84	G × G	6.88	0.39	G × P	39.71**	-11.36**	G × G
CMS463D13A × VR 522	-20.32**	-5.68	P × G	103.45**	3.36	G × G	29.90**	0.22	G × G	19.45**	-11.89**	G × A
CMS463D13A × IS 268	-4.4	-13.16	P × G	141.89**	10.59**	G × G	18.15**	-0.31	G × G	66.11**	-5.98*	G × G

Table 4.13a (*Cont'd.*)

Crosses	Oleoresin content (%)			Capsaicin content (%)			Scoville Heat Units (SHU)		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × DL 161	30.30**	0.08	P × G	41.33**	0.06**	P × G	41.33**	9986.67**	P × G
CMS4611A × C 142	41.96**	1.04**	P × G	21.49**	0.02	P × G	21.49**	2715.56	P × G
CMS4611A × IS 268	-7.47	0.33	P × P	-16.69**	-0.13**	P × G	-16.69**	-20466.67**	P × G
CMS4626A × PL 412	-2.74	-1.28**	G × P	-5.44	-0.02	G × P	-5.44	-3381.33	G × P
CMS4626A × VR 523	44.04**	-1.08**	G × G	22.93**	-0.02	G × G	22.93**	-3576.89	G × G
CMS4626A × DL 161	34.59**	-0.59	G × G	38.08**	-0.05**	G × G	38.08**	-8341.33**	G × G
CMS4626A × IS 262	11.54**	1.81**	G × P	40.37**	-0.01	G × G	40.37**	-1692.44	G × G
CMS4626A × C 142	52.41**	1.03**	G × G	46.35**	0.08**	G × G	46.35**	12494.22**	G × G
CMS4626A × PL 406	45.85**	0.94**	G × G	47.36**	0.12**	G × G	47.36**	19480.89**	G × G
CMS4626A × IS 268	-13.09**	-1.40**	G × P	14.35**	-0.03*	G × G	14.35**	-4501.33*	G × G
CMS463D13A × SL 475	43.27**	-0.61	A × G	46.13**	0	G × G	46.13**	523.56	G × G
CMS463D13A × PL 412	8.12	0.31	A × P	-6.24*	0	G × P	-6.24*	-45.33	G × P
CMS463D13A × VR 523	55.18**	0.53	A × G	26.77**	0.03*	G × G	26.77**	4399.11*	G × G
CMS463D13A × DL 161	40.93**	0.51	A × G	40.64**	-0.01	G × G	40.64**	-1645.33	G × G
CMS463D13A × IS 267	27.47**	2.41**	A × P	-4.43	-0.04**	G × P	-4.43	-5663.11**	G × P
CMS463D13A × YL 581	-8.43	0.12	A × P	-33.07**	-0.02	G × P	-33.07**	-3654.22	G × P
CMS463D13A × SL 473	-5.13	-0.3	A × P	-18.51**	-0.02	G × P	-18.51**	-3494.22	G × P
CMS463D13A × IS 262	-19.91**	-1.14**	A × P	39.36**	0.01	G × G	39.36**	1430.22	G × G
CMS463D13A × PP 402	19.50**	0.26	A × G	-2.56	0.06**	G × P	-2.56	9199.11**	G × P
CMS463D13A × C 142	19.69**	-2.06**	A × G	14.51**	-0.10**	G × G	14.51**	-15209.78**	G × G
CMS463D13A × VR 522	-8.37	-1.28**	A × P	-17.81**	-0.02	G × P	-17.81**	-3529.78	G × P
CMS463D13A × IS 268	6.13	1.08**	A × P	39.68**	0.16**	G × G	39.68**	24968.00**	G × G

Where, G- Good, A- Average, P- Poor; *, significant at p=0.05; **, significant at p=0.01

Table 4.13b: Selected crosses based on total yield heterosis over superior check CH-27, their corresponding SCA effects and GCA of parents in E_2

Crosses	**Total yield plant^{-1} (kg)**			**Plant height (cm)**			**Plant spread (cm)**			**Number of primary branches plant^{-1}**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × YL 581	16.65**	0.06	P × G	-33.75**	-1.61	G × P	-18.28**	-1.35	G × P	-0.39	0.24	G × P
CMS4611A × PP 402	19.61**	0.12**	P × G	-16.18**	-1.31	G × A	4.3	3.95	G × A	0.01	0.15	G × P
CMS4626A × SL 475	14.22*	-0.10**	G × G	-7.36	1.44	P × G	21.59*	6.35**	P × G	12.31*	-0.43	P × G
CMS4626A × PL 412	23.65**	0.07*	G × G	6.11	9.13*	P × G	-19.17**	-1.76	P × A	-5.46	-0.24	P × A
CMS4626A × DL 161	14.22*	0.19**	G × P	-49.99**	-11.80**	P × P	-18.51**	-3.32	P × A	-24.21**	-0.43	P × P
CMS4626A × YL 581	39.87**	0.05	G × G	-35.10**	2.57	P × P	-25.57*	0.48	P × P	-23.24**	-0.50*	P × P
CMS4626A × FL 201	44.04**	0.14**	G × G	-38.23**	-2.61	P × P	-16.28**	-0.34	P × A	-16.79**	-1.25**	P × G
CMS4626A × PP 402	14.17*	-0.11**	G × G	-11.03*	9.14*	P × A	-6.23	3.91	P × A	0.79	0.76**	P × P
CMS463D13A × SL 475	42.52**	0.15**	G × G	-0.15	2.27	G × G	31.48**	4.53	G × G	48.64**	1.41**	A × G
CMS463D13A × VR 523	19.87**	0.22**	G × A	-15.51**	2.11	G × A	7.27	-2.49	G × G	-0.77	-2.20**	A × G
CMS463D13A × IS 267	14.22*	0.02	G × G	-16.62**	-5.91	G × G	-8.55	-5.26*	G × A	1.57	0.66**	A × P
CMS463D13A × YL 581	15.57**	-0.11**	G × G	-32.42**	-0.96	G × P	-11.82*	0.87	G × P	-5.66	0.27	A × P
CMS463D13A × FL 201	45.52**	0.18**	G × G	-23.24**	5.73	G × P	1.28	2.24	G × A	17.78**	0.49*	A × G
CMS463D13A × PP 402	23.78**	-0.01	G × G	-22.29**	-7.83*	G × A	-13.70*	-7.86**	G × A	-24.41**	-0.91**	A × P
CMS463D13A × IS 268	23.61**	0.06*	G × G	9.29	1.06	G × G	-5.48	-4.96*	G × A	32.61**	1.07**	A × G

Table 4.13b (*Cont'd.*)

Crosses	Fruit weight (g)			Fruit length (cm)			Fruit width (mm)			Pericarp thickness (mm)		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × YL 581	52.91**	0.78**	P × G	13.99*	-0.02	P × G	-9.91	-0.35	P × G	-2.16	-0.16**	P × G
CMS4611A × PP 402	24.89**	-1.91**	P × G	10.24	0.51	P × A	-3.82	-0.2	P × G	13.00*	0.1	P × G
CMS4626A × SL 475	48.48**	-0.37	G × G	29.33**	0.4	A × G	-5.74	-0.34	A × A	-12.75*	-0.17**	P × G
CMS4626A × PL 412	20.47*	-0.65**	G × A	19.68**	0.49	A × G	-5.8	-0.12	A × A	-11.7	0.02	P × A
CMS4626A × DL 161	14.48	0.4	G × P	-8.9	0	A × P	1.93	0.8	A × A	-14.80*	0.1	P × P
CMS4626A × YL 581	41.11**	-1.15**	G × G	15.71*	-0.26	A × G	4.66	0.48	A × G	34.65**	0.28**	P × G
CMS4626A × FL 201	140.07**	1.09**	G × G	24.40**	-0.02	A × G	0.87	-0.24	A × G	25.17**	-0.02	P × G
CMS4626A × PP 402	159.58**	1.79**	G × G	1.29	-0.4	A × A	10.66	0.62	A × G	5.34	0	P × G
CMS463D13A × SL 475	44.75**	-1.35**	G × G	29.54**	-0.03	G × G	3.95	-0.01	G × A	22.37**	0.09	G × G
CMS463D13A × VR 523	59.15**	0.95**	G × P	19.73**	0.45	G × A	3.18	0.28	G × A	7.61	0.08	G × A
CMS463D13A × IS 267	60.71**	0.66**	G × P	28.26**	0.12	G × G	1.56	-0.65	G × G	1.8	-0.15**	G × G
CMS463D13A × YL 581	102.34**	0.37	G × G	31.80**	0.29	G × G	6.09	-0.13	G × G	14.77*	-0.12*	G × G
CMS463D13A × FL 201	177.19**	1.69**	G × G	34.16**	0.14	G × G	11.32	0.17	G × G	44.80**	0.05	G × G
CMS463D13A × PP 402	137.64**	0.12	G × G	13.14*	-0.11	G × A	8.44	-0.41	G × G	10.54	-0.1	G × G
CMS463D13A × IS 268	97.31**	-0.09	G × G	16.46*	0.44	G × A	7.7	-0.04	G × G	-4.04	-0.07	G × A

Table 4.13b (*Cont'd.*)

Crosses	**Number of fruits plant^{-1}**			**Number of seed fruit^{-1}**			**1000 seed weight (g)**			**Ascorbic acid (mg.100g^{-1})**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × YL 581	43.56**	-7.52	G × G	-35.12**	5.11*	P × P	2.39	0.01	P × G	-38.35**	-13.74**	P × P
CMS4611A × PP 402	34.91**	36.65**	G × A	-51.65**	-10.47**	P × P	-3.75	0.03	P × G	-29.87**	-18.44**	P × P
CMS4626A × SL 475	34.20**	-0.7	G × G	12.65**	0.79	A × G	-11.43*	-0.34	A × G	28.29**	-0.09	P × G
CMS4626A × PL 412	78.83**	44.20**	G × G	12.65**	3.94	A × G	-18.25**	-0.01	A × P	15.71**	-10.95**	P × G
CMS4626A × DL 161	50.22**	26.14*	G × G	-27.74**	-1.03	A × P	-35.82**	-0.05	A × P	3.53	-0.68	P × A
CMS4626A × YL 581	81.41**	61.02**	G × G	-50.69**	-6.07**	A × P	1.88	-0.17	A × G	-25.05**	4.73	P × P
CMS4626A × FL 201	9.17	-6.67	G × P	-29.60**	6.46**	A × P	1.53	-0.18	A × G	-26.86**	-0.34	P × P
CMS4626A × PP 402	-2.39	-57.58**	G × A	-15.30**	10.92**	A × P	0.63	0.14	A × G	-12.57**	5.92	P × P
CMS463D13A × SL 475	16.14*	25.89*	P × G	20.46**	2.93	G × G	4.26	0.28	G × G	26.24**	-9.74**	G × G
CMS463D13A × VR 523	7.84	36.91**	P × A	-7.33	-2.51	G × G	-4.09	-0.04	G × G	39.79**	8.04*	G × G
CMS463D13A × IS 267	6.61	-17.63	P × G	15.30**	4.44*	G × G	-8.53	-0.26	G × A	3.62	0.16	G × P
CMS463D13A × YL 581	-1.8	-53.49**	P × G	-35.07**	0.96	G × P	12.45*	0.15	G × G	-17.63**	9.01**	G × P
CMS463D13A × FL 201	-2.72	33.28**	P × P	-42.08**	-4.14*	G × P	12.62*	0.17	G × G	-16.78**	7.86*	G × P
CMS463D13A × PP 402	3.53	20.93	P × A	-29.01**	-0.45	G × P	0.34	-0.17	G × G	-3.57	12.52**	G × P
CMS463D13A × IS 268	29.03**	51.05**	P × G	11.16*	3.49	G × G	-7.33	-0.28	G × G	17.19**	-6.19	G × G

Table 4.13b (*Cont'd.*)

Crosses	**Oleoresin content (%)**			**Capsaicin content (%)**			**Scoville Heat Units (SHU)**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × YL 581	-10.82**	0.64	A × P	-32.00**	0.03*	P × P	-31.97**	5261.78*	P × P
CMS4611A × PP 402	10.56**	-0.85*	A × G	-24.47**	-0.02	P × P	-24.46**	-2716.89	P × P
CMS4626A × SL 475	11.18**	-0.74*	P × G	23.74**	0.01	G × G	23.69**	1317.78	G × G
CMS4626A × PL 412	0.95	1.03**	P × A	-23.24**	-0.06**	G × P	-23.24**	-10241.33**	G × P
CMS4626A × DL 161	-9.69**	-2.86**	P × G	33.45**	0.01	G × G	33.46**	1600.44	G × G
CMS4626A × YL 581	-27.22**	-0.84*	P × P	-32.64**	-0.02	G × P	-32.66**	-2554.22	G × P
CMS4626A × FL 201	-16.17**	0.81*	P × P	-30.19**	0.01	G × P	-30.16**	2036	G × P
CMS4626A × PP 402	16.73**	0.6	P × G	-4.99	0.08**	G × P	-5.03	13099.11**	G × P
CMS463D13A × SL 475	29.56**	0.58	G × G	21.79**	-0.01	G × G	21.84**	-1219.56	G × G
CMS463D13A × VR 523	41.15**	0.25	G × G	-9.58**	-0.04**	G × A	-9.57**	-5955.56**	G × A
CMS463D13A × IS 267	6.68	-0.58	G × G	-12.30**	-0.03*	G × P	-12.28**	-5482.67*	G × P
CMS463D13A × YL 581	-11.03**	0.2	G × P	-32.50**	-0.02	G × P	-32.48**	-2707.56	G × P
CMS463D13A × FL 201	-19.22**	-0.65	G × P	-32.50**	-0.01	G × P	-32.54**	-1125.33	G × P
CMS463D13A × PP 402	22.13**	0.24	G × G	-24.74**	-0.07**	G × P	-24.71**	-10382.22**	G × P
CMS463D13A × IS 268	-13.70**	-1.13**	G × P	-1.68	0	G × G	-1.63	-529.78	G × G

Where, G- Good, A- Average, P- Poor; *, significant at p=0.05; **, significant at p=0.01

Table 4.13c: Selected crosses based on total yield heterosis over superior check CH-27, their corresponding SCA effects and GCA of parents in E_3

Crosses	Total yield plant^{-1} (kg)			Plant height (cm)			Plant spread (cm)			Number of primary branches plant^{-1}		
	Hsc	SCA	GCA	*Hsc*	SCA	GCA	*Hsc*	SCA	GCA	*Hsc*	SCA	GCA
CMS4611A × SL 475	37.1**	0.01	P × G	0.96	-1.02	A × G	50.90**	5.09*	A × G	86.72**	0.3	A × G
CMS4611A × VR 523	38.02**	0.04*	P × G	-3.19	3.62	A × A	18.38*	-1.05	A × G	34.39**	-0.32	A × A
CMS4611A × DL 161	35.48**	0.05*	P × G	-29.60**	-3.02	A × P	20.23*	1.42	A × A	44.79**	0.25	A × A
CMS4611A × VR 522	14.28*	0.13**	P × G	-12.26*	-4.04	A × G	24.80**	2.17	A × A	82.08**	1.13**	A × A
CMS4626A × SL 475	47.92**	0.01	A × G	0.41	2.71	P × G	25.00**	-4.91*	A × G	108.10**	0.95**	G × G
CMS4626A × VR 523	46.15**	0.02	A × G	-12.16*	1.23	P × A	24.75**	1.73	A × G	56.94**	0.38	G × A
CMS4626A × DL 161	30.95**	-0.03	A × G	-33.34**	-1.6	P × P	3.14	-5.10*	A × A	29.48**	-0.51	G × A
CMS4626A × SL 473	33.64**	0.14**	A × G	-18.60**	2.3	P × A	11.43	2.22	A × P	8.1	-0.5	G × P
CMS4626A × PL 406	13*	0.06**	A × G	-20.05**	-7.26*	P × G	27.10**	0.81	A × G	86.43**	0.85**	G × G
CMS463D13A × SL 475	49.05**	-0.02	G × G	0.95	-1.69	G × G	40.53**	-0.19	A × G	44.22**	-1.25**	A × G
CMS463D13A × VR 523	34.56**	-0.06**	G × G	-13.93*	-4.85	G × A	22.28**	-0.68	A × G	39.03**	-0.06	A × A
CMS463D13A × DL 161	39.58**	-0.02	G × G	-18.20**	4.62	G × P	28.89**	3.68	A × A	43.07**	0.26	A × A
CMS463D13A × YL 581	26.64**	0.08**	G × G	-25.79**	-2.64	G × P	6.92	-1.46	A × A	57.23**	1.01**	A × P
CMS463D13A × SL 473	11.87*	0	G × G	-11.06	3	G × A	15.64	2.45	A × P	30.34**	0.61*	A × P
CMS463D13A × C 142	31.52**	0.07**	G × G	0.26	0.58	G × G	24.80**	0.58	A × A	8.97	-1.21**	A × A
CMS463D13A × IS 268	14.49*	0.06**	G × G	2.35	0.9	G × G	-0.95	-3.43	A × P	79.19**	1.11**	A × A

Table 4.13c (*Cont'd.*)

Crosses	Fruit weight (g)			Fruit length (cm)			Fruit width (mm)			Pericarp thickness (mm)		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × SL 475	9.39	-0.13	P × G	25.28**	0.35	P × G	-14.32*	-0.11	P × A	-5.61	-0.14**	P × G
CMS4611A × VR 523	6.73	-0.29	P × G	20.00**	0.21	P × G	-18.65**	-0.25	P × A	31.32**	0.19**	P × G
CMS4611A × DL 161	-6.55	0.16	P × P	-20.58**	-1.10**	P × A	-12.76*	0.3	P × A	-12.73*	0.07	P × P
CMS4611A × VR 522	17.36*	0.58**	P × G	5.62	-0.35	P × G	-18.51**	-0.36	P × A	0.43	0.16**	P × A
CMS4626A × SL 475	48.80**	0.3	G × G	23.88**	-0.61*	G × G	-2.48	0.01	G × A	37.64**	0.11**	G × G
CMS4626A × VR 523	59.88**	0.66**	G × G	29.91**	-0.09	G × G	-9	-0.36	G × A	10	-0.10**	G × G
CMS4626A × DL 161	7.17	-0.37	G × P	7.07	-0.39	G × A	-10.87	-0.61	G × A	-14.59*	-0.06	G × P
CMS4626A × SL 473	15.59*	-0.56**	G × G	13.68*	0.09	G × A	-4.81	-0.66	G × A	-31.59**	-0.05	G × P
CMS4626A × PL 406	34.19**	0.18	G × A	32.99**	0.38	G × G	6.9	0.44	G × G	6.37	0.12**	G × P
CMS463D13A × SL 475	43.93**	-0.18	G × G	41.45**	0.26	G × G	2.22	0.1	G × A	34.12**	0.03	G × G
CMS463D13A × VR 523	40.39**	-0.37	G × G	31.83**	-0.12	G × G	4.22	0.61	G × A	17.12**	-0.09*	G × G
CMS463D13A × DL 161	30.65**	0.21	G × P	42.20**	1.49**	G × A	1.96	0.32	G × A	-3.52	-0.01	G × P
CMS463D13A × YL 581	56.33**	0.33	G × G	29.80**	-0.34	G × G	21.30**	0.11	G × G	46.22**	0.09*	G × G
CMS463D13A × SL 473	49.25**	0.41*	G × G	12.17	-0.13	G × A	5.82	0.04	G × A	-16.21**	0.03	G × P
CMS463D13A × C 142	35.08**	0.22	G × A	5.57	-0.44	G × A	-3.78	-0.16	G × A	-4.59	0.05	G × P
CMS463D13A × IS 268	70.50**	1.07**	G × G	32.58**	1.03**	G × A	15.51**	0.19	G × G	44.09**	0.09*	G × G

Table 4.13c (*Cont'd.*)

Crosses	**Number of fruits plant^{-1}**			**Number of seed fruit^{-1}**			**1000 seed weight (g)**			**Ascorbic acid (mg.100g^{-1})**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × SL 475	56.39**	-2.95	G × G	-1.14	-0.36	P × G	-7.88	0.09	P × G	-5.41	-15.54**	P × G
CMS4611A × VR 523	46.52**	12.42	G × G	-14.12**	-0.16	P × G	-15.81**	-0.13	P × A	7.56*	2.87	P × G
CMS4611A × DL 161	102.57**	38.91**	G × G	-24.94**	-0.21	P × A	-42.01**	-0.15	P × P	-2.27	8.79**	P × P
CMS4611A × VR 522	50.02**	59.10**	G × A	-32.46**	-1.94	P × A	-24.15**	-0.71**	P × G	-1.3	-5.42	P × G
CMS4626A × SL 475	41.17**	2.61	P × G	3.36	1.73	P × G	-11.90*	-0.3	A × G	29.71**	18.24**	G × G
CMS4626A × VR 523	-8.26	-41.43**	P × G	-11.28*	0.96	P × G	-7.53	0.19	A × A	4.26**	-0.39	G × G
CMS4626A × DL 161	46.07**	-17.52*	P × G	-15.03**	5.05**	P × A	-38.33**	-0.1	A × P	-2.04	-2.91	G × P
CMS4626A × SL 473	59.44**	73.43**	P × G	-44.25**	-2.99	P × P	-11.55*	-0.11	A × G	-0.19	-0.59	G × P
CMS4626A × PL 406	-12.92*	2.6	P × A	-2.73	1.03	P × G	-21.18**	0.06	A × P	29.33**	1.03	G × G
CMS463D13A × SL 475	40.23**	0.34	P × G	3.59	-1.36	G × G	2.8	0.21	G × G	13.46**	-2.69	G × G
CMS463D13A × VR 523	39.22**	29.00**	P × G	-8.77*	-0.8	G × G	-6.24	-0.07	G × A	12.47**	-2.48	G × G
CMS463D13A × DL 161	44.07**	-21.38**	P × G	-26.42**	-4.84**	G × A	-26.49**	0.25	G × P	-4.5	-5.88*	G × P
CMS463D13A × YL 581	-18.11**	2.6	P × P	-47.84**	0.96	G × P	13.13*	0.17	G × G	-22.00**	11.55**	G × P
CMS463D13A × SL 473	2.96	-12.24	P × G	-29.44**	2.45	G × P	0.23	0.23	G × G	-7.65*	-10.07**	G × P
CMS463D13A × C 142	1.51	-36.48**	P × G	1.59	2.7	G × G	-20.95**	0.28	G × P	22.36**	2.78	G × G
CMS463D13A × IS 268	1.69	5.58	P × G	-5.13	-2.24	G × G	0.23	0.01	G × G	28.27**	3	G × G

Table 4.13c (*Cont'd.*)

Crosses	**Oleoresin content (%)**			**Capsaicin content (%)**			**Scoville Heat Units (SHU)**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4611A × SL 475	15.36**	-0.28	P × G	8.78*	-0.06**	P × G	8.78*	-9602.67**	P × G
CMS4611A × VR 523	6.68	0	P × G	18.34**	-0.06**	P × G	18.34**	-9140.44**	P × G
CMS4611A × DL 161	13.91**	-0.25	P × G	-18.53**	-0.01	P × P	-18.53**	-1229.33	P × P
CMS4611A × VR 522	14.84**	-0.22	P × G	8.65*	0.01	P × G	8.65*	2237.33	P × G
CMS4626A × SL 475	24.96**	-0.27	G × G	31.86**	-0.03	G × G	31.86**	-4485.33	G × G
CMS4626A × VR 523	7.16	-0.81**	G × G	52.28**	0.03*	G × G	52.28**	4883.56*	G × G
CMS4626A × DL 161	18.51**	-0.69**	G × G	-10.14*	-0.05**	G × P	-10.14*	-8165.33**	G × P
CMS4626A × SL 473	-0.3	0.59*	G × P	-17.23**	-0.03*	G × P	-17.23**	-5072.00*	G × P
CMS4626A × PL 406	12.95**	0.34	G × G	52.15**	0.08**	G × G	52.15**	12119.11**	G × G
CMS463D13A × SL 475	37.13**	0.55*	G × G	55.07**	0.09**	G × G	55.07**	14088.00**	G × G
CMS463D13A × VR 523	28.19**	0.81**	G × G	52.08**	0.03	G × G	52.08**	4256.89	G × G
CMS463D13A × DL 161	39.76**	0.94**	G × G	11.83**	0.06**	G × P	11.83**	9394.67**	G × P
CMS463D13A × YL 581	-2.63	0.34	G × P	-36.61**	-0.05**	G × P	-36.61**	-8774.22**	G × P
CMS463D13A × SL 473	-11.31**	-0.68*	G × P	-18.53**	-0.04**	G × P	-18.53**	-6605.33**	G × P
CMS463D13A × C 142	26.93**	-0.04	G × G	16.12**	0	G × G	16.12**	-418.67	G × G
CMS463D13A × IS 268	-0.7	-0.90**	G × A	7.67	-0.01	G × A	7.67	-1076.44	G × A

Where, G- Good, A- Average, P- Poor; *, significant at *p*=0.05; **, significant at *p*=0.01

Table 4.13d: Selected crosses based on total yield heterosis over superior check CH-27, their corresponding SCA effects and GCA of parents over the environments

Crosses	Total yield plant^{-1} (kg)			Plant height (cm)			Plant spread (cm)			Number of primary branches plant^{-1}		
	Hsc	SCA	GCA	*Hsc*	SCA	GCA	*Hsc*	SCA	GCA	*Hsc*	SCA	GCA
CMS4626A × SL 475	14.54**	0	A × G	-9.43**	2.25	P × G	6.73	-1.01	P × G	38.26**	0.38*	P × G
CMS4626A × PL 412	9.64*	0.08**	A × G	-7.79*	0.71	P × G	1.51	1.79	P × A	12.86**	-0.19	P × G
CMS4626A × DL 161	24.18**	0.08**	A × G	-39.49**	-5.33*	P × P	-10.02*	-3.03*	P × A	8.79	0.05	P × P
CMS4626A × C 142	7.43*	-0.03	A × G	-5.82	3.4	P × G	1.94	2.25	P × A	11.42*	0.28	P × P
CMS4626A × IS 268	13.61**	-0.01	A × G	-5.75	-3.67	P × G	-8.27*	-2.11	P × A	3.6	-0.60**	P × G
CMS463D13A × SL 475	27.7**	0.01	G × G	-3.36	-2.47	G × G	25.02**	1.63	G × G	31.79**	-0.21	G × G
CMS463D13A × VR 523	23.61**	0.05**	G × G	-8.06*	-0.23	G × A	22.28**	2.09	G × G	14.54**	-0.81**	G × G
CMS463D13A × DL 161	13.49**	-0.08**	G × G	-17.34**	4.97*	G × P	11.22**	1.23	G × A	13.97**	0	G × P
CMS463D13A × IS 267	20.56**	0.06**	G × G	-3.47	-2.39	G × G	6.07	-1.15	G × A	31.08**	0.41**	G × G
CMS463D13A × YL 581	13.76**	0	G × G	-18.89**	-0.61	G × P	-1.11	-2.33	G × P	24.04**	0.60**	G × P
CMS463D13A × SL 473	12.34**	0.10**	G × A	-12.06**	3.22	G × P	8.47*	1.33	G × A	3.04	0.12	G × P
CMS463D13A × PP 402	26.62**	0.06**	G × G	-12.01**	-5.26*	G × A	-0.07	-1.43	G × P	23.19**	0.12	G × A
CMS463D13A × C 142	23.94**	0.01	G × G	-5.38	-6.58**	G × G	10.98**	-0.18	G × A	2.96	-0.40*	G × P
CMS463D13A × IS 268	37.33**	0.08**	G × G	11.56**	2.11	G × G	8.59*	-0.25	G × A	40.81**	0.84**	G × G

Table 4.13d (*Cont'd.*)

Crosses	**Fruit weight (g)**			**Fruit length (cm)**			**Fruit width (mm)**			**Pericarp thickness (mm)**		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4626A × SL 475	62.74**	0.18	A × G	33.45**	-0.01	A × G	1.62	0.05	G × A	9.84*	-0.04	P × G
CMS4626A × PL 412	42.62**	0.06	A × A	28.34**	0.32	A × G	-4.08	0.1	G × P	-6.38	0	P × A
CMS4626A × DL 161	6.51	-0.16	A × P	4.37	-0.15	A × P	-6.42	0.08	G × P	-15.98**	0	P × P
CMS4626A × C 142	36.08**	0.12	A × P	16.55**	0.05	A × A	1.34	0.23	G × A	-8.62*	0.03	P × P
CMS4626A × IS 268	49.99**	-0.60**	A × G	5.73	-0.53**	A × A	9.89**	0.2	G × G	7.28	0.01	P × G
CMS463D13A × SL 475	75.38**	-0.57**	G × G	40.90**	-0.03	G × G	4.66	-0.32	G × A	35.53**	0.04	G × G
CMS463D13A × VR 523	76.02**	0.26	G × A	34.39**	0.18	G × G	4.2	0.22	G × A	19.45**	-0.01	G × G
CMS463D13A × DL 161	29.46**	-0.52**	G × P	23.04**	0.54**	G × P	-3.96	-0.36	G × P	-3.26	-0.06	G × P
CMS463D13A × IS 267	77.50**	0.27	G × A	32.94**	0.26	G × G	5.2	-0.03	G × A	19.21**	0.01	G × G
CMS463D13A × YL 581	126.60**	0.83**	G × G	33.63**	0.11	G × G	21.10**	0.28	G × G	39.58**	0.01	G × G
CMS463D13A × SL 473	74.67**	0.45**	G × P	20.11**	0.38*	G × P	8.72*	-0.02	G × G	6.14	0.02	G × P
CMS463D13A × PP 402	140.15**	0.34*	G × G	24.85**	-0.17	G × G	22.15**	0.32	G × G	41.88**	0.05	G × G
CMS463D13A × C 142	60.24**	-0.19	G × P	17.66**	-0.37*	G × A	2.89	-0.31	G × A	5.27	-0.01	G × P
CMS463D13A × IS 268	112.84**	0.55**	G × G	30.32**	0.52**	G × A	14.77**	0.05	G × G	24.47**	0	G × G

Table 4.13d (*Cont'd.*)

Crosses	Number of fruits plant^{-1}			Number of seed fruit^{-1}			1000 seed weight (g)			Ascorbic acid (mg.100g^{-1})		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4626A × SL 475	12.90**	0.86	G × G	16.04**	2.99*	P × G	-11.59**	-0.35**	A × G	21.18**	5.62**	G × G
CMS4626A × PL 412	21.23**	18.81**	G × G	5.61	1.79	P × G	-18.58**	-0.03	A × P	21.71**	-7.01**	G × G
CMS4626A × DL 161	31.63**	1.44	G × G	-21.72**	1.4	P × P	-35.56**	-0.05	A × P	0.02	-2.39	G × P
CMS4626A × C 142	10.87**	-23.90**	G × G	5.61	4.28**	P × G	-35.16**	-0.34**	A × P	12.53**	-10.20**	G × G
CMS4626A × IS 268	13.56**	9.56	G × G	-10.98**	-7.49**	P × G	-5.03	0.11	A × G	26.30**	-1.47	G × G
CMS463D13A × SL 475	6.77	13.01*	P × G	17.33**	0.12	G × G	4.05	0.26*	G × G	17.15**	-3.73*	G × G
CMS463D13A × VR 523	2.21	19.61**	P × G	-4.88	-1.55	G × G	-4.15	-0.03	G × G	23.55**	0.57	G × G
CMS463D13A × DL 161	14.33**	-11.78	P × G	-24.34**	-3.93**	G × P	-25.72**	0.21	G × P	1.81	-3.62*	G × P
CMS463D13A × IS 267	-8.56*	-4.29	P × G	11.19**	2.63	G × G	-8.65**	-0.27*	G × G	12.86**	2.8	G × G
CMS463D13A × YL 581	-21.08**	-17.72**	P × A	-32.44**	2.22	G × P	12.12**	0.13	G × G	-18.93**	9.42**	G × P
CMS463D13A × SL 473	-8.83*	12.01	P × A	-18.31**	1.04	G × P	0.23	0.22	G × G	-4.95**	-10.58**	G × P
CMS463D13A × PP 402	-16.98**	18.13**	P × P	-28.38**	0.4	G × P	1.02	-0.16	G × G	-8.11**	12.04**	G × P
CMS463D13A × C 142	0.09	-22.30*	P × G	7.10*	1.54	G × G	-18.52**	0.33**	G × P	20.49**	-2.82	G × G
CMS463D13A × IS 268	4.25	14.49*	P × G	12.92**	3.94**	G × G	-4.9	-0.19	G × G	27.84**	-3.06	G × G

Table 4.13d (*Cont'd.*)

Crosses	Oleoresin content (%)			Capsaicin content (%)			Scoville Heat Units (SHU)		
	Hsc	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**	***Hsc***	**SCA**	**GCA**
CMS4626A × SL 475	34.04**	0.07	A × G	35.59**	-0.02*	G × G	35.57**	-3220.00*	G × G
CMS4626A × PL 412	0.84	-0.02	A × P	0.55	-0.05**	G × A	0.55	-7967.85**	G × A
CMS4626A × DL 161	13.98**	-1.38**	A × G	25.95**	-0.03**	G × G	25.96**	-4968.74**	G × G
CMS4626A × C 142	22.77**	0.08	A × G	28.85**	0.01	G × G	28.86**	830.96	G × G
CMS4626A × IS 268	-5.46*	-0.34	A × P	9.70**	-0.01	G × G	9.70**	-831.85	G × G
CMS463D13A × SL 475	37.82**	0.17	G × G	42.30**	0.03**	G × G	42.32**	4464.00**	G × G
CMS463D13A × VR 523	43.95**	0.53**	G × G	22.25**	0.01	G × G	22.26**	900.15	G × G
CMS463D13A × DL 161	43.05**	1.44**	G × G	32.70**	0.02*	G × G	32.69**	2699.26*	G × G
CMS463D13A × IS 267	17.21**	0.65**	G × G	0.4	-0.03**	G × A	0.41	-5158.52**	G × A
CMS463D13A × YL 581	-6.72**	0.22	G × P	-32.26**	-0.03**	G × P	-32.25**	-5045.33**	G × P
CMS463D13A × SL 473	-2	0.14	G × P	-16.79**	-0.02**	G × P	-16.80**	-4007.70**	G × P
CMS463D13A × PP 402	19.78**	0.07	G × G	-13.72**	-0.01	G × P	-13.71**	-925.04	G × P
CMS463D13A × C 142	18.10**	-0.73**	G × G	25.26**	-0.01	G × G	25.25**	-1593.48	G × G
CMS463D13A × IS 268	-2.43	-0.32	G × P	17.39**	0.05**	G × G	17.41**	7787.26**	G × G

Where, G- Good, A- Average, P- Poor; *, significant at *p*=0.05; **, significant at *p*=0.01

CHAPTER V

SUMMARY

Chilli (*Capsicum annuum* L., 2n=2x=24) belongs to the family Solanaceae and is native to Central and South America. Mexico is the major center of diversity of chilli. It is an important spice-cum-vegetable crop in many parts of the world and is valued for its sensory attributes of colour, pungency and flavour. In the recent years, hybrid cultivars of chilli have become very popular with the growers. Hybrid seed in chilli is produced both manually and by exploiting the male sterility. Both the cytoplasmic male sterility (CMS) and the genetic male sterility (GMS) are available in chilli. The CMS in chilli could be sensitive to temperature variations and fertility often is partially restored when temperature drops below 25º/17ºC day/night. However, commercial hybrid seed production demands that the CMS is highly stable to ensure genetic purity of F_1 seed. Stable CMS lines could be established by growing single plant progeny, retaining only those maintainer genotypes producing 100% male sterility, and by screening under the environmental conditions that ensures selection for the highest level of male sterility. The present investigation was carried out at the Department of Vegetable Science, Punjab Agricultural University, Ludhiana (India) with the following objectives;

i. To study stability of the newly developed CMS lines
ii. To check the genetic similarity between A and B- lines
iii. To estimate combining ability effects of parental lines and hybrids for important horticultural traits
iv. To identify promising hybrid combinations for commercial exploitation

A total of 17 CMS A-lines with different genetic backgrounds were evaluated under the low (E_1 and E_3) and the high (E_2 and E_4) temperature environments during 2014-15 and 2015-16. Observations were recorded on pollen sterility (%), pollen release score (0-2), fruit setting (%) and number of seed fruit^{-1} under the caged conditions. The analysis of variance (ANOVA) revealed that the mean squares (MS) due to genotypes and the environments were significant at p=0.01 for all the male sterility associated traits, suggesting that both the genetic factors and the temperature influenced performance of the CMS lines. Further, the lines responded differently to the change in temperature condition as indicated by the genotype × environment interaction. Ten lines namely 'CMS4611A', 'CMS4614A', 'CMS4622A', 'CMS4624A', 'CMS4626A', 'CMS46213A', 'CMS463D2A', 'CMS463D13A', 'CMS463D14A' and 'CMS463L5A' expressed 100% pollen sterility and recorded 'zero' pollen release score across the environments. Pollen sterility of the CMS lines was further confirmed by their inability to set fruit and bear seed under the caged conditions. The lines did not set any fruit irrespective of the environmental conditions. The lines have been regarded as temperature stable as the four environments represented the varied temperature conditions ranging from 24.1 °C/ 12.1 °C to 41.1 °C/ 28.5 °C day/ night.

As per the pollen viability and the pollen release score tests, two lines 'CMS46214A' and 'CMS463L3A' were regarded as partially male sterile during the first year of evaluation and completely male sterile in the second year of evaluation. Five lines namely 'CMS46113A', 'CMS4623A', 'CMS4627A', 'CMS463L9A' and 'CMS463L11A' were unstable under both the low and the high temperature regimes. Fruit setting of partially male sterile lines varied from 1.33% in 'CMS4627A' under E_2 to 9.31% in 'CMS463L11A' under E_4 and the number of seed fruit^{-1} ranged from 1.15 in 'CMS4627A' under E_2 to 17.4 in 'CMS46113A' under E_4. Under the low temperature environments, the periodic observations on pollen viability indicated that these lines were partially male sterile during the initial few weeks of screening when the corresponding day/ night temperature was relatively low (<26°C/ 14°C). As the temperature approached 32°C/ 23°C day/ night, these lines behaved as complete male sterile. Under high temperature regime also, these lines showed partial sterility during the initial stages of screening, though the level of fertility was much lower than under the low temperature regime. It is, therefore, speculated that the partial sterility of these lines is primarily due to the presence of modifier gene(s). Activity of these gene(s) slows down with the rise in temperature and stops at advanced stage of plant growth. The yearly means indicated that these lines could be stabilized by 1-2 additional cycles of backcrossing and selection.

To assess suitability of the CMS lines in hybrid breeding programs, the lines were evaluated for fruit setting ability and for important fruit traits under the open pollination conditions. Pooled across the environments, the range of fruit setting varied from 18.09 in 'CMS4614A' to 42.22% in 'CMS463D13A', the number of fruits plant^{-1} ranged from 47.0 in 'CMS463L9A' to 118.2 in 'CMS463D13A' and number of seed fruit^{-1} varied from 27.5 in 'CMS4624A' to 67.98 in 'CMS463D13A', indicating that female fertility of the CMS lines is normal. The lines possessed though the varied but the commercially acceptable fruit traits and provide a wider choice of a female parent for the development of commercial hybrids. Their tolerance to temperature variations would ensure genetic purity of the F_1 seed even under the uncertain temperature conditions.

The genetic similarity index of the three selected CMS A- and their corresponding CMS B- lines was assessed by the SSR marker analysis. The marker analysis showed that out of the 120 markers screened, 84 markers (70%) were amplified in 'CMS4611A', 90 markers (75%) in 'CMS4626A' and 88 markers (73.3%) in 'CMD463D13A'. Based on the proportion of amplified monomorphic and polymorphic bands, the genome recovery of the recurrent parent in 'CMS4611A', 'CMS4626A' and 'CMS463D13A' was estimated to be 98.8, 98.9 and

96.6%, respectively. The lines are, therefore, genetically stable and are ready for utilization in hybrid breeding programs.

For combining ability analysis three CMS lines and 20 potential restorer lines selected based on the *per se* performance were crossed in a Line × tester mating design to produce 60 crosses. A total of 85 genotypes including 60 crosses, 23 parental lines and two standard checks CH-27 and Soldier were evaluated for 15 plant growth, yield and quality traits. The experiment was conducted in a randomized complete block design with three replications over three environments *viz*. the early season (E_1), the main season (E_2) and the late season (E_3). The MS values due to the genotypes and the environments were significant at p=0.01 for all the traits evaluated over the three environments. The MS due to the genotype × environment interaction effects were non-significant for 1000 seed weight and were significant for rest of the traits. Due to significance of the environment and the genotype × environment interaction effects, promising crosses have been identified for each season. Further the crosses have been identified for pungent, mildly pungent or non-pungent types and for oleoresin extraction. Based on GCA effects of the parents involved, crosses have been identified to be pursued further through pure line breeding or to be exploited through heterosis breeding.

The ANOVA for combining ability showed that the MS values due to parents, testers and crosses for all traits over the three environments and when pooled across the environments were significant at p=0.01. The pooled ANOVA showed that the GCA effects for lines were significant for all the traits except number of primary branches plant^{-1}. The effects due to GCA testers and SCA crosses were significant for all the plant growth, yield and quality traits indicating that both the additive and the non-additive gene effects were involved in genetic control of these traits. These findings were further substantiated by the estimates of the genetic components of variation. Therefore, genetic improvement of chilli could be achieved both by pure line breeding and hybrid development. Among lines, CMS463D13A was the best general combiner for most of the traits except number of fruits plant^{-1} in E_1, E_2, E_3 and across the three environments, number of primary branches plant^{-1} in E_2 and E_3, total yield plant^{-1} in E_2, ascorbic acid in E_3, oleoresin content in E_1, capsaicin content and SHU in E_1 and across the environments. The line CMS4611A exhibited significantly negative GCA effects for fruit length, pericarp thickness, capsaicin content and SHU across the environments.

Among the testers, IS 268 was the best general combiner for total yield plant^{-1} in E_1; PP 402 for fruit weight in E_1, E_2 and E_3 and for pericarp thickness in E_1; FL 201 for fruit length in E_1 and E_2 and for pericarp thickness in E_2 and E_3; DL 161 for number of fruits plant^{-1} in E_1 and E_3 and for capsaicin content and SHU in E_2; SL 475 for fruit length, total yield plant^{-1} and oleoresin content in E_3 and for capsaicin content and SHU in E_1; YL 581 for total yield plant^{-1} in E_2; VR 523 for oleoresin content in E_1 and E_2 and for capsaicin content and SHU in E_3; and PL 412 for number of fruits plant^{-1} in E_2. Tester E 183 showed highly significant and negative GCA estimates for fruit length in E_1 and E_2, for capsaicin content and SHU in E_2 and E_3; IS 262 for pericarp thickness in E_2; IS 263 for fruit length in E_3; VR 521 for pericarp thickness in E_1 and E_3; YL 581 for capsaicin content and SHU in E_1, and FL 201 showed highly significant negative GCA values for capsaicin content and SHU in E_2. To breed for genotypes suitable for early season cultivation (E_1), the parental lines CMS463D13A, IS 268, DL 161, C 142, IS 262, VR 523 and PL 406 could be involved in hybridization to develop genotypes with high yield and highly pungent fruits. For mid-season planting (E_2), CMS463D13A, SL 475, IS 268 and C 142 were identified to breed for pungent chilli, and PP 402 and IS 267 were identified to breed for mildly-pungent genotypes suitable for oleoresin extraction. For late season planting (E_3), CMS463D13A, SL 475, VR 523, C 142, PL 406 and VR 522 were identified as potential parents to breed for genotypes with high yield and pungent fruits; and DL 161 and PP 402 were identified to breed for genotypes suitable for extraction of mildly pungent oleoresin.

Pooled across the environments, tester SL 475 showed the highest GCA effects for total yield plant^{-1}, capsaicin content and SHU. Therefore, SL 475 can be used in hybrid breeding program to generate high yielding recombinants with pungent fruits. IS 268 was the best general combiner for total yield plant^{-1}; PP 402 for fruit weight; FL 201 and YL 581 for pericarp thickness and FL 201 for fruit length. DL 161 had the best GCA values for number of fruits plant^{-1} and VR 523 for oleoresin content. E 183 exhibited highly significant and negative GCA effects for fruit length, capsaicin content and SHU. The parents SL 475, DL 161, C 142 and VR 523 were identified to develop the genotypes with high yield and pungent fruits. PP 402 and VR 522 can be utilized to breed the genotypes with mildly pungent fruits suitable for colour extraction for use by the food industry as a natural food colorant, and for the development of genotypes for fresh consumption.

The crosses identified on basis of the SCA effects included CMS463D13A × PP 402, CMS463D13A × IS 268 and CMS4611A × E 183 for total yield plant^{-1}, fruit weight, capsaicin content and SHU in E_1; CMS463D13A × SL 473, CMS4626A × IS 262, CMS4611A × C 142 and CMS4626A × PL 412 for total yield plant^{-1}, number of fruits plant^{-1} and oleoresin content, and CMS463D13A × VR 523, CMS463D13A × FL 201 and CMS4611A × VR 521 for total yield plant^{-1}, fruit weight, number of fruits plant^{-1} and ascorbic acid content in E_2; CMS4611A × E 183 and CMS4626A × PL 406 for total yield plant^{-1}, capsaicin content and SHU; and CMS4611A × VR 522, CMS4626A × IS 268, CMS4626A × IS 261, CMS463D13A × AC 102, CMS4626A × SL 473, CMS463D13A × PP 402, CMS4611A × IS 267 and CMS4611A × DL 161 for total yield plant^{-1} and number of fruits plant^{-1} in E_3. Pooled across the environments, the crosses CMS4611A × E 183, CMS463D13A × IS 268, CMS4611A × PP 414 and CMS463D13A × FL 201 were regarded as good specific combiners for total yield plant^{-1}, fruit weight, capsaicin content and SHU.

Out of the 60 crosses evaluated, the number of crosses expressing ≥20% better parent overall heterosis was the highest for total yield plant^{-1} (40) followed by number of primary branches plant^{-1} (28), number of seed fruit^{-1} (28), oleoresin content (17) and number of fruits plant^{-1} (16). Pooled across the environments, the maximum standard heterosis in the desired direction was observed for fruit weight (154.90%), followed by number of fruits plant^{-1} (46.47%), oleoresin content (43.95%), capsaicin content and SHU (42.32%), and total yield plant^{-1} (37.33%). The yield enhancement in crosses is due to the cumulative effect of both the yield contributing traits viz. the number of fruits plant^{-1} and fruit weight. For enhancement of yield and quality traits such as capsaicin, oleoresin and SHU, heterosis breeding would be the more effective approach than pure line breeding.

Yield is the most important economic trait for any commercial crop. On basis of the heterosis performance, the hybrids identified for the three planting seasons for different purposes also expressed significant heterosis for yield. The highest heterosis over BP for plant height was expressed by the cross CMS4626A × PP 402 (51.81%) in E_1, by CMS463D13A × IS 268 in E_2 (40.76%) and across the environments (36.67%) and by CMS4611A × IS 261 (57.18%) in E_3; for fruit weight by CMS463D13A × IS 267 (48.46%) in E_1, by CMS4626A × C 142 (44.18%) in E_2, by CMS4626A × VR 523 (53.62%) in E_3 and by CMS463D13A × IS 268 (34.16%) across the environments; for fruit length by CMS4626A × PP 402 (53.70%) in E_1, by CMS4626A × C 142 (38.04%) in E_2, by CMS4626A × PL 412 (42.46%) in E_3 and by CMS4626A × PP 402 (27.18%) across the environments; for number of fruits plant^{-1} by CMS4611A × C 142 in E_1 (36.54%) and across the environments (68.73%), by CMS4626A × YL 581 (90.44%) in E_2 and by CMS4611A × VR 522 (182.68%) in E_3; for total yield plant^{-1} by CMS463D13A × IS 267 (135.43%) in E_1, by CMS4626A × FL 201 (147.61%) in E_2, by CMS4611A × VR 522 (150.70%) in E_3 and by CMS463D13A × IS 268 (108.72%) based on the pooled means; for oleoresin content by CMS463D13A × VR 523 (52.15%) in E_1, by CMS463D13A × DL 161 in E_2 (58.42%) and across the environments (42.26%) and by CMS463D13A × SL 475 (36.52%) in E_3, and for capsaicin content and SHU by CMS4626A × PL 406 in E_1 (49.67%) and across the environments (32.64%), by CMS463D13A × PL 406 (25.74%) in E_2, by CMS463D13A × SL 475 (53.97%) in E_3.

In the early season (E_1), significant heterosis over the superior check Soldier was exhibited by the crosses CMS463D13A × IS 268, CMS463D13A × C 142, CMS463D13A × IS 262, CMS4626A × C 142, CMS4626A × PL 406, CMS463D13A × VR 523, CMS4611A ×

C 142, CMS463D13A × SL 475, CMS4626A × IS 262 and CMS4626A × VR 523 for total yield plant^{-1}, fruit weight, fruit length, fruit width, pericarp thickness, number of seed fruit^{-1}, ascorbic acid, capsaicin content and SHU. The crosses CMS463D13A × VR 522, CMS463D13A × SL 473, CMS463D13A × PL 412, CMS463D13A × YL 581 and CMS4611A × IS 268 depicted significant and positive heterosis for fruit weight, fruit length, fruit width, pericarp thickness, number of seed fruit^{-1} and significantly negative heterosis for capsaicin content and SHU. In the main-season (E_2), the crosses CMS463D13A × SL 475 and CMS4626A × SL 475 performed significantly better over the superior check CH-27 for total yield plant^{-1}, fruit weight, fruit length, number of fruits plant^{-1}, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU. The crosses CMS463D13A × FL 201, CMS4626A × FL 201, CMS4626A × YL 581, CMS4611A × YL 581 and CMS463D13A × YL 581 have shown significantly positive heterosis for total yield plant^{-1}, fruit weight and fruit length and significant negative heterosis for plant height, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU.

In the late season (E_3), the crosses CMS463D13A × SL 475, CMS4626A × SL 475, CMS463D13A × DL 161 and CMS463D13A × VR 523 performed significantly better than the superior check CH-27 for total yield plant^{-1}, fruit weight, fruit length, number of fruits plant^{-1}, oleoresin content, capsaicin content and SHU. The crosses CMS4611A × DL 161 and CMS4626A × DL 161 expressed significantly positive heterosis for total yield plant^{-1}, number of fruits plant^{-1} and oleoresin content and significant negative heterosis for plant height, pericarp thickness, number of seed fruit^{-1}, 1000 seed weight, capsaicin content and SHU. Pooled across the environments, the crosses CMS463D13A × SL 475, CMS463D13A × C 142, CMS463D13A × VR 523, CMS4626A × SL 475, CMS463D13A × DL 161 and CMS4626A × C 142 performed significantly better than CH-27 for total yield plant^{-1}, fruit weight, fruit length, oleoresin content, capsaicin content and SHU. The crosses CMS463D13A × YL 581 and CMS463D13A × SL 473 showed significantly positive heterosis for fruit weight, fruit length and fruit width and significant negative heterosis for plant height, ascorbic acid, capsaicin content and SHU. The identified crosses are recommended for multi-location testing.

The crosses viz. CMS463D13A × IS 268, CMS463D13A × C 142, CMS463D13A × IS 262, CMS463D13A × DL 161 and CMS463D13A × VR 523 identified as promising for total yield plant^{-1}, capsaicin content and SHU in E_1, CMS463D13A × IS 268, CMS463D13A × SL 475 and CMS4626A × SL 475 for total yield plant^{-1}, fruit weight, capsaicin content and SHU in E_2, CMS463D13A × C 142, CMS463D13A × SL 475 and CMS463D13A × VR 523 for total yield plant^{-1}, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU in E_3, and CMS463D13A × IS 268, CMS463D13A × C 142, CMS463D13A × VR 523 and CMS463D13A × SL 475 for total yield plant^{-1}, number of seed fruit^{-1}, ascorbic acid, oleoresin content, capsaicin content and SHU across the environments involved good × good GCA parents. These crosses can be pursued further to recover potential transgressive segregants through pure line breeding.

CMS463D13A × C 142 CMS463D13A × DL 161

CMS463D13A × IS 261 CMS463D13A × IS 267

Plate 4.3a: View of some identified promising crosses of chilli

CMS463D13A × IS 268

CMS463D13A × PP 402

CMS463D13A × SL 475

CMS463D13A × VR 523

Plate 4.3b: View of some identified promising crosses of chilli

CMS463D13A × YL 581

CMS4611A × PP 402

CMS4626A × DL 161

CMS4626A × IS 267

Plate 4.3c: View of some identified promising crosses of chilli

CMS4626A × IS 268

CMS4626A × PP 402

CMS4626A × SL 475

CMS4626A × YL 581

Plate 4.3d: View of some identified promising crosses of chilli

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APPENDIX I

List of SSR primer pairs used in the present study to check genetic similarity between CMS A- and B-lines

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
1	AA840689	GACAACATAGGCGGACCTTTGG	TGCTTTAGGTCTACGTCCTTGCAC	267	3
2	AA840692	TGGAAGTGATTACTGGAAACCATGC	GGGGTTTAGTCATGGAATCTTTTGC	202	3
3	asu 7	GTGTCTTCCCTCCTTCACAGTGCTC	TCTCTCTGTTTCTTATGTTTTGCGG	-	6
4	BD 76366	AAAACTCCAAACTACCCCTGG	TTAAGCGTAGCGCTTGTGTG	330	2
5	BM 59622	CGTCTTTCACTTGTCTTTTGTTC	AGTGGGTTCACTGACTTGGG	90	3
6	BM 061910	ATTGTGATAGCAACCCCTGG	CACAGATGAGGGCACAAATG	292	3
7	BM 64867	TCTGGGAATTTTGGAACTGC	TCCAGTTTTGATCATCTCCAAC	138	2
8	BM 67271	GTATGCTGCAACCATCGTTG	ATTGGTTTGGGAGACACAGC	202	8
9	CA 514621	GTCGAACAAAATGGGGTTTG	GCTGGAGAGTGCTGGTGG	216	2
10	CA 515275	CTCTGCCCTCCTCAACCC	AAAATATGGTCGGAGATCCG	100	12
11	CA 515649	TCTCCAATTTCCATTCGGAG	TAATCGCATTTGCGAACTTG	190	2
12	CA 516334	ACCCACCTTCATCAACAACC	ATTTGTGGCTTTTCGAAACG	248	6
13	CA 516439	GACAGTCTTTCAAGAACTAGAGAGAG	TGGAGCAAACACAGCAGAAC	158	10
14	CA 517699	ACGCCAAGAAAATCATCTCC	CCATTGCTGAAGAAAATGGG	147	3
15	CA 523558	AATCCTCCAAATCCACCCTC	ATTCGATTGCTTGCTCCTTG	176	6
16	CA 526211	TTGGGGACTTCACGTCTCTC	TTGATGATAAATCCTCCCCC	175	8
17	CA 847460	ACGAGGCGCCCTCTCTC	GAGTCCAAACTGAAGCTGCC	178	8
18	CAMS-024	TGTTGAGGCTTGGGAAAAAC	CAAGATAATGGGTAGAAAGGCAAC	219	8
19	CAMS-065	CCAGTCTCATCCAGCAGACA	CATATGCTGCTCCTGCATTC	213	2
20	CAMS-072	CCCGCGAAATCAAGGTAAT	AAAGCTATTGCTACTGGGTTCG	153	5
21	CAMS-090	TCGCTCAAAGCACATCAAAG	CTTGATTGTTCTTCCACTGCTG	243	8
22	CAMS-095	CGCTAGCATGACACTCAAGG	AAACGGCAAGGCTACACATC	228	5

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
23	CAMS-122	CATCCACGTGCATAGTCAGG	TTCTAAGTGTTGAAATTATGGATTT	178	5
24	CAMS-163	TCCATATAGCCCGTGTGTGA	GCGTGGGAATACAATGCTAGA	250	5
25	CAMS-177	ATTCTCTACCCCTGCCTGTG	CTCAGGAGATGTCCCACGAT	229	2
26	CAMS-190	TTTCTGCAGTGTTACCAATATTTCA	CCCATGGGTCCTACCTCAG	212	5
27	CAMS-199	CCCTACCTCGGCATGTGATA	TGCATTGCATGGGGATATAA	188	5
28	CAMS-207-2	CTCACGAGCCACTTGAACAC	GCCTTGTTTCCTATCCCAAC	243	5
29	CAMS-301	CTGTCCATGCTTGTGATGCT	TGATTTGTGCCTCGTTTGAG	180	8
30	CAMS-309	GAAAATCGACCCGTTTTGAA	TCAATTCGGACAAAATTAGCAA	235	9
31	CAMS-311	GGTGCGCTAGAGATGGAGAG	TTTGAGTGTTCGGGACTGGT	234	6
32	CAMS-330	GGCTACCGCCTTCTGACTTA	TTCGTATCTGGGGTGTCAAA	208	4
33	CAMS-336	GGTGGAAACTTGCTTGGAGA	CCCAGAACCATCCACCTACT	157	3
34	CAMS-340	TTTATGCCCATTCACAAAATAA	GGACGAATTCACCGAGTGC	250	10
35	CAMS-361	TTGGTGTGGTTAGGGGAGAG	GGCGTTCGAACTTGTGAAAT	207	4
36	CAMS-373	GGTTGATGGTCCATGTTCAA	CCTCCTACCCTATCCCCAAG	230	12
37	CAMS-405	TTCTTGGGTCCCACACTTTC	AGGTTGAAAGGAGGGCAATA	241	11
38	CAMS-420	CAGCGTTCTATCGTCTCAAATG	TTGACAAACCAGAAATTGATCG	200	5
39	CAMS-456	ATGGAGCTGGGGCTAAAAAT	GCTCAGCAAATTGAGGAGAAG	153	1
40	CAMS-460	CCTTTCACTTCAGCCCACAT	ACCATCCGCTAAGACGAGAA	215	7
41	CAMS-492	GTTCAAACACTTCCCCCTCA	TGTCATCGTTGGTCGTTACC	250	12
42	CAMS493	TCGATGACGAAAAAGTGTGAA	AGGGCAAAAGACCCATTCTT	223-225	8
43	CAMS-494	GGTAGGTGAGGACCCACAGA	AACTATACCCCCGCTGCTCT	247	4
44	CAMS-606	GACTAGTCCCCGTTCAACCA	TTTGCGAGAAGATGCTTCAG	208	7
45	CAMS-647	CGGATTCGGTTGAGTCGATA	GTGCTTTGGTTCGGTCTTTC	221	3
46	CAMS-655-2	CCTTGCTGCTACCTATTGAAGA	TCCAATCGTCGATATGTTTGTT	224	4
47	CAMS-668-2	ATCGTCCATTTGTGGGAAAA	TGTGGTCGGAAATAGGAAGAA	158	10

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
48	CAMS-679	TTTGCATGTTTTACCCATTCC	ATGTGAAACACATAGGTAGCACTGA	200	1
49	CAMS-826	CTTGATCTCAAGAACCAGCTACAA	TGTACATTGAAGACACGGAAGAA	244	8
50	CAMS-838	CCAGGATGGTGTTAAGGGTTT	GTCGCATCAATGAGCATAGG	229	6
51	CAMS-844	GCAAAGAAAAAGAAAAGCCTGA	CTGCAACTGCTGCTTCATTC	223	1
52	CAMS-855	AAGTGTCAAGGAAGGGGACA	CCTAACCACCCCCAAAAGTT	243	8
53	CAMS-876	TGTGTCTGAAGCGGAACAAA	AAGCAGTGAGCGACGAAGA	243	9
54	CAMS-880	GAGCCAAGAAAAAGGTGGAA	CAACTCATCGTTCAACAACACA	237	6
55	GPMS 93	ATCCTTGGCGTATTTTGCAC	TTCACTTTGCACACAGGCTT	202-268	3
56	GPMS 100	TCCATACGGTTGGAGGAGAG	ACTATGCTCTGCTGTGCCCT	141-169	2
57	GPMS 103	TGGCAGTTGCAATATCAATCTC	AAACCTTGTCACGCATCCAT	134-149	7
58	GPMS 109	ATCTATGCATGCCATCACCG	TGGGCTAAAGGCCATGTTAC	165-183	10
59	GPMS 156	GATATAGAACCACACAAGACTGGG	TATGGCTCTTGCGGGAATAC	228-232	10
60	GPMS 159	AAGAACATGAGGAACTTTAACCATG	TTCACCCTTCTCCGACTCC	281-317	10
61	GPMS 164	AATGAAATCAATCGGGCTTG	ACCTCGCACCAATTCTTTTG	230-259	12
62	GPMS 169	TCGAACAAATGGGTCATGTG	GATGAGGGTCCTGTGCTACC	176-220	2
63	GPMS 171	TCCACCACAATATTTCGAAGG	TGGCTGTCCAACACTGTGAG	288-346	9
64	GPMS 183	GAGCTTCATAGATGATATGCAAGAG	TCCCAAGCTAACCCATTTACTG	195-227	12
65	GPMS 187	TTTAGAATCCTCACCACGGG	TCAATGCACAAACTTTAATTTGC	219-246	6
66	GPMS 191	AGGTCAGCGACGGCAAC	ATTTTAGGAGCCGACCTTCC	261-286	1
67	Hpms 1–139	CCAACAGTAGGACCCGAAAATCC	ATGAAGGCTACTGCTGCGATCC	299	1
68	Hpms 1–148	GGCGGAGAAGAACTAGACGATTAGC	CCACCCAATCCACATAGACG	197	1
69	Hpms 1–155	ACGAGGCCCAAGCTGTTATGTC	TTGTCCCGACTCTCCATTGACC	207	1
70	Hpms 1-165	GGCTATTTCCGACAAACCCTCAG	CCATTGGTGTTTTCACTGTTGTG	213	4
71	Hpms 1–172	GGGTTTGCATGATCTAAGCATTTT	CGCTGGAATGCATTGTCAAAGA	344	11
72	Hpms 1–173	TGCTGGGAAAGATCTCAAAAGG	ATCAAGGAAGCAAACCAATGC	163	3

S. No.	Marker	Forward sequence	Reverse sequence	Fragment size (bp)	Linkage group
73	Hpms 1–227	CGTGGCTTCAAGTATGGACTGC	GGGGCGGAACTTTTCTTATCC	237	7
74	Hpms 1–274	TCCCAGACCCCTCGTGATAG	TCCTGCTCCTTCCACAACTG	174	7
75	Hpms 1–281	TGAGGCAGTGGTATGGTCTGC	CCCGAGTTCGTCTGCCAATAG	132	1
76	Hpms 2–2h	GCAAGGATGCTTAGTTGGGTGTC	TCCCAAAATTACCTTGCAGCAC	146	11
77	Hpms 2–13	TCACCTCATAAGGGCTTATCAATC	TCCTTAACCTTACGAAACCTTGG	259	1
78	Hpms 2–21	TTTTTCAATTGATGCATGACCGATA	CATGTCATTTTGTCATTGATTTGG	295	10
79	Hpms 2–23	CCCTCGGCTCAGGATAAATACC	CCCCAGACTCCCACTTTGTG	126	5
80	Hpms 2–24	TCGTATTGGCTTGTGATTTACCG	TTGAATCGAATACCCGCAGGAG	205	9
81	HpmsAT2–20	TGCACTGTCTTGTGTTAAAATGACG	AAAATTGCACAAATATGGCTGCTG	148	6
82	HpmsE003	TTTCTGCAATTCCCCTTGTTCA	CAGCAGAGCCTTCAGTAGCAGC	164	2
83	HpmsE006	GCTGACCGTTTTCGTTTTGGG	CAAAATTCAACCGCACCAACA	243	4
84	HpmsE012	AAACGCTGAAAAAGGCGTTGAC	TGCACCAACTTCTTCCATGCAC	208	11
85	HpmsE020	CCCCCGAGAGGAACAGAATCAT	TTCCATTTTGGTCCAGCTACCA	200	7
86	HpmsE024	CGAGCCTAACCACCCAAATCAG	AAGGGAACGGAGGGACGACTAC	212	12
87	HpmsE025	TGAGCATCCCGTTATCTCAAATCA	CCCAATTCTTCAGGCAATCTCC	213	9
88	HpmsE031	CCCTAAATCAACCCCAAATTCAA	CCCCCATTACCTGACTGCAAAA	167	10
89	HpmsE049	CACTCCAACAGCAGCAGCAAAC	CCTTGCCGATGTTGAAGCTTTT	247	4
90	HpmsE050	CCCCACCTTCCATCATCAGCTA	TGGTAATTCTGCGGTCGATTCC	247	3
91	HpmsE051	TGGCCAGCTTCACACAGAGGTA	TGTCACAATATTGGAGGCCAGAA	262	9
92	HpmsE054	GCCACCCCTCACCTCTCTCTCT	GTTGTTCGCTGGGCTCTTTCTC	219	12
93	HpmsE056	TCCGATTCAATCACTCCCAACA	GTATCGGCAATACGGGCAGAAG	214	1
94	HpmsE061	CCCAAGAAAGAAGTTGGGAATGG	TTCGACGAGCTTGGAAGGTGAT	249	11
95	HpmsE064	CCCTCCTTTTACCTCGTCAAAAA	ATGCCAAGGAGCAATGAGAACC	221	12
96	HpmsE065	TGAAATAGGCCAATCCCTTTGC	ATTCCCTGGGATTCCTGCATTA	199	10
97	HpmsE068	TGTTCCTTTTGTTGTTACCTTTTG	CGTCTAGGAATGGAAGAAGAGC	232	7

S. No.	**Marker**	**Forward sequence**	**Reverse sequence**	**Fragment size (bp)**	**Linkage group**
98	HpmsE071	CCCCTTCTCCTCCCTCATAAGC	TTCCATGATGTTACCGGAGCAA	188	4
99	HpmsE082	TTTTTCCCACTTTGCCCTTTCC	CAACCCAAGAAAACCCATTGGA	232	9
100	HpmsE084	GCCAGAAGATCCATACTCTCATCA	GGAATGAGCAAAAACAAGAGTCC	220	9
101	HpmsE092	CTCTGGCCCTTTTGTTCTTTCTTG	ACGCCTATTGCGAATTTCAGGA	180	11
102	HpmsE094	CCAGTTGAGAGCTGCTGCAAAA	CACCAACAAAACAAAGGCCACA	241	12
103	HpmsE095	TGCTTAAACCCACTTGCGTCTTG	TCTGCACAGCACAAGACATTCG	184	7
104	HpmsE096	CGGGTCAAACAAAAACCGAAGT	GCTTGTGGTTGAGCTCGCTCTT	237	10
105	HpmsE103	ATTGTGACCCGACTCCTCCAT	TGCTAATGGTGCTAATGCGGTA	177	7
106	HpmsE105	CAACCAAATTGAAACCCCTCCA	CGTCCACCTAATAATGCGACCA	238	12
107	HpmsE113	CCCTAAAGCTCGAGAAATTGAAGC	GAATGCTGTTGCTGGGGTTGTT	225	6
108	HpmsE114	GGTGAGGGAGGTGTGAGCAAA	GATCCACATACGCCATCACTGC	190	7
109	HpmsE116	CATCTCTCCGTTGAATCTATTTCC	ACGGTCATCCATTAGAACCGTA	189	5
110	HpmsE120	GGGGGAGGAAGAGAAGAAGTCG	CCGGACTTTACGAGCACAACCT	209	6
111	HpmsE124	TCGTTAGCAGCAACAACAACAA	CTGCTTCCTGTACATGGCTGTC	227	11
112	HpmsE125	AGGGAGTTCACGCCATTTTTGA	GCGATAACCCACCGGAGAAAAT	204	11
113	HpmsE132	ACATCCACAGCAAAAGGAAAAA	GTGGAAAGTTTGGTGGATCAGA	197	11
114	HpmsE140	GGCTCTGCCTCTCGTCTCCTC	AGGATCAGAAGCAGCGCATTTC	225	4
115	HpmsE141	TCCCAACAACTCAAATGGCTTC	TGGAGGTGCCCTTCTGGTAAAG	206	2
116	HpmsE143	CCATTCAGCTAGGGTTCAGTCCA	CGACCAAATCGAATCTTCGTGA	107	9
117	HpmsE145	TGAGGGTATTTTCGTCATTTCAC	GAAAGCGGAAAACATTAAGAGTCA	222	8
118	HpmsE146	CCCTTCTTCCTTTCCACCATCA	AGGCGTGAAAGGGTTA TGAGGA	227	4
119	HpmsE149	CGGAAACTAAACACACTTTCTCTC	GACTGGACGCCAGTTTGATT	198	11
120	HpmsE150	CCCTCTTCCCCGACTCTCTCTT	AAGCCAATGACTGCATGACCAC	219	9

APPENDIX II

Mean weekly agro-meteorological data recorded during the early crop season (E_1)

Period	Min.T (°C)	Max.T (°C)	RH (%)	Rainfall (mm)	Sunshine hrs.
Oct 29-Nov 4	14.4	27.8	68	0	3.8
Nov 5-11	14.8	26.8	65	0	3.1
Nov 12-18	12.5	28	59	0	7.1
Nov 19-25	9.9	27	61	0	7.4
Nov 26-Dec 2	11.4	24.7	71	0	1.4
Dec 3-9	10	23.8	72	0	3.7
Dec 10-16	7	20.1	68	1.7	5.2
Dec 17-23	4.9	20.4	67	0	6
Dec 24-31	5.3	20.4	65	0	7.5
Jan 1-7	7.3	21.1	72	0	2.9
Jan 8-14	7.9	19.1	77	16	3.4
Jan 15-21	8	13	86	0	0.2
Jan 22-28	5.2	14.1	82	0.4	2.9
Jan 29-Feb 4	7.6	20.5	73	3	6.4
Feb 5-11	8.2	21.4	69	0.8	6.5
Feb 12-18	7.5	22.1	65	0.6	7.8
Feb 19-25	11.7	24.2	73	7.4	8.1
Feb 26-Mar 4	12.9	28.1	68	0	7.9
Mar 5-11	14.5	26.7	68	23	7.8
Mar 12-18	14.2	24.2	73	14.9	6.5
Mar 19-25	14.5	29.8	60	3.2	8.8
Mar 26-Apr 1	16	31.7	59	0	9.5
Apr 2-8	20.1	34.3	50	0	6.3
Apr 9-15	18	35.1	44	0.4	10.2
Apr 16-22	22.3	38.9	40	2.6	10.2
Apr 23-29	18.1	37.8	33	0	12.1
Apr 30-May 6	22.4	39.2	36	2.4	6.6
May 7-13	25.5	39.1	43	1.2	7.6
May 14-20	25	42.6	37	0	12
May 21-27	25.3	39.3	47	5.8	9.8
May 28-Jun 3	25.4	39.1	44	14.8	10.9
Jun 4-10	28.5	41.1	42	3.2	10.5
Jun 11-17	28.1	39.1	50	0	6.5
Jun 18-24	28.9	37.3	66	22.6	6.4
Jun 25-Jul 1	29.2	36.2	64	52.4	5.2
Jul 2-8	26.1	33.6	75	48.8	6.1
Jul 9-15	28.4	33.4	76	54.8	5.8
Average	16.14	29.22	61.30	7.57	6.76

Mean weekly agro-meteorological data recorded during the main crop season (E_2)

Period	Min.T (°C)	Max.T (°C)	RH (%)	Rainfall (mm)	Sunshine hrs.
Feb 19-25	11.7	24.2	73	7.4	8.1
Feb 26-Mar 4	12.9	28.1	68	0	7.9
Mar 5-11	14.5	26.7	68	23	7.8
Mar 12-18	14.2	24.2	73	14.9	6.5
Mar 19-25	14.5	29.8	60	3.2	8.8
Mar 26-Apr 1	16	31.7	59	0	9.5
Apr 2-8	20.1	34.3	50	0	6.3
Apr 9-15	18	35.1	44	0.4	10.2
Apr 16-22	22.3	38.9	40	2.6	10.2
Apr 23-29	18.1	37.8	33	0	12.1
Apr 30-May 6	22.4	39.2	36	2.4	6.6
May 7-13	25.5	39.1	43	1.2	7.6
May 14-20	25	42.6	37	0	12
May 21-27	25.3	39.3	47	5.8	9.8
May 28-Jun 3	25.4	39.1	44	14.8	10.9
Jun 4-10	28.5	41.1	42	3.2	10.5
Jun 11-17	28.1	39.1	50	0	6.5
Jun 18-24	28.9	37.3	66	22.6	6.4
Jun 25-Jul 1	29.2	36.2	64	52.4	5.2
Jul 2-8	26.1	33.6	75	48.8	6.1
Jul 9-15	28.4	33.4	76	54.8	5.8
Jul 16-22	27.6	34.9	73	31.5	7.3
Jul 23-29	27	32.3	80	77.8	4.5
Jul 30-5	27.3	34.5	70	1.4	6.7
Aug 6-12	26.9	32.2	75	8	3.3
Aug 13-19	26.4	34.4	73	27.4	6.9
Average	22.70	34.58	58.42	15.52	7.83

Mean weekly agro-meteorological data recorded during the main crop season (E_3)

Period	**Min.T (°C)**	**Max.T (°C)**	**RH (%)**	**Rainfall (mm)**	**Sunshine hrs.**
Apr 2-8	20.1	34.3	50	0	6.3
Apr 9-15	18	35.1	44	0.4	10.2
Apr 16-22	22.3	38.9	40	2.6	10.2
Apr 23-29	18.1	37.8	33	0	12.1
Apr 30-May 6	22.4	39.2	36	2.4	6.6
May 7-13	25.5	39.1	43	1.2	7.6
May 14-20	25	42.6	37	0	12
May 21-27	25.3	39.3	47	5.8	9.8
May 28-Jun 3	25.4	39.1	44	14.8	10.9
Jun 4-10	28.5	41.1	42	3.2	10.5
Jun 11-17	28.1	39.1	50	0	6.5
Jun 18-24	28.9	37.3	66	22.6	6.4
Jun 25-Jul 1	29.2	36.2	64	52.4	5.2
Jul 2-8	26.1	33.6	75	48.8	6.1
Jul 9-15	28.4	33.4	76	54.8	5.8
Jul 16-22	27.6	34.9	73	31.5	7.3
Jul 23-29	27	32.3	80	77.8	4.5
Jul 30-5	27.3	34.5	70	1.4	6.7
Aug 6-12	26.9	32.2	75	8	3.3
Aug 13-19	26.4	34.4	73	27.4	6.9
Aug 20-26	24.9	33.1	77	45.2	6.2
Average	25.30	36.55	56.90	19.06	7.67

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