GENETIC ANALYSIS FOR YIELD, QUALITY TRAITS AND PLANT IDEOTYPE IN CHILLI (*Capsicum annuum* L.)

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BY

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M.Sc., (Hort.)

THESIS SUBMITTED TO Dr. Y. S. R. HORTICULTURAL UNIVERSITY IN PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE AWARD OF THE DEGREE OF

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March, 2016

DECLARATION

I, **Ms. JANAKI MARADANA**, hereby declare that the thesis entitled "**GENETIC ANALYSIS FOR YIELD, QUALITY TRAITS AND PLANT IDEOTYPE IN CHILLI (*Capsicum annuum* L.)**" submitted to the Dr. Y.S.R. Horticultural University, Venkataramannagudem, for the degree of Doctor of Philosophy in Horticulture (Vegetable Science) is the result of original research work done by me. I declare that no material contained in the thesis has been published earlier in any manner.

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CERTIFICATE

Miss. JANAKI MARADANA has satisfactorily prosecuted the course of research and the thesis entitled "**GENETIC ANALYSIS FOR YIELD, QUALITY TRAITS AND PLANT IDEOTYPE IN CHILLI (*Capsicum annuum* L.)**" submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination**.**

I certify that neither the thesis nor its part there of has been previously submitted by her for a degree of any university.

Place: Venkataramannagudem **(J. DILIP BABU)**

Date: **Chairman**

CERTIFICATE

This is to certify that the thesis entitled "**GENETIC ANALYSIS FOR YIELD, QUALITY TRAITS AND PLANT IDEOTYPE IN CHILLI (*Capsicum annuum* L.)**" submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Horticulture (Vegetable Science) of Dr. Y.S.R. Horticultural University, Venkataramannagudem, is a record of the bonafide research work carried out by **Miss. JANAKI MARADANA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of investigation have been duly acknowledged by the author of the thesis.

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Date: ***(JANAKI MARADANA)***

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	per cent
/	:	or
&	:	and
^{0}	:	degrees
^{0}C	:	degree Celsius
=	:	equal to
–	:	average
:	:	colon
“ ”	:	quotation marks
√	:	square root of
χ^2	:	Chi-square
∑	:	Summation of the data
σ^2	:	Variance
A	:	Absorbance
AH	:	Average Heterosis
ANOVA	:	Analysis of variance
A.P.	:	Andhra Pradesh
ASTA	:	American Spice Trade Association
BC_1	:	Back cross generation derived from crossing F_1 with P_1
BC_2	:	Back cross generation derived from crossing F_1 with P_2
BP	:	Better Parent
C.	:	Capsicum
CD	:	Critical Difference
cm	:	centimetre
Contd...	:	Continued
Cov	:	Covariance
C^R	:	Red Carotenoids
C^Y	:	Yellow Carotenoids

d	:	Additive gene effect
d.f.	:	degrees of freedom
Dr.Y.S.R.H.U.	:	Dr. Y S R Horticultural University
Dept.	:	Department
E	:	Expected frequency
EC	:	Electrical Conductivity
E-W	:	East – West
et al.	:	and others
etc.	:	and so on
F	:	Females
F_1	:	First generation
F_2	:	Second generation
F_3	:	Third generation
Fig.	:	Figure
FS	:	Full sibs
g	:	gram
g/plant	:	gram per plant
GCA / *gca*	:	General Combining Ability
GPB	:	Genetics and Plant Breeding
GMA	:	Generation Mean Analysis
h	:	Dominance gene effect
ha	:	hectare
ha^{-1}	:	per hectare
HB	:	Heterobeltiosis
HC & RI	:	Horticultural College and Research Institute
HRS	:	Horticultural Research Station
hr	:	hour
HS	:	Half sibs
i	:	Additive x Additive epistasis
i.e.	:	that is

j	:	Additive x Dominance epistasis
Kg	:	kilogram
kg ha^{-1}	:	kilogram per hectare
L.	:	Linnaeus
l	:	Dominance x Dominance epistasis
L	:	Lines
LCA	:	Lam Capsicum Annuum
L x T	:	Line x Tester
M	:	males
M	:	metre
m	:	mean
M_1	:	Mean sum of squares due to females
M_2	:	Mean sum of squares due to males
M_3	:	Mean sum of squares due to hybrids
M_4	:	Mean sum of squares due to error
mg	:	milligram
µg	:	microgram
µg/ml	:	microgram per millilitre
mg/100g	:	milligram per 100 grams
min	:	minutes
ml	:	millilitre
m. mhos/cm	:	millimhos per centimetre
mm	:	millimetre
MP	:	Mid Parent
MSS	:	Mean Sum of Squares
N-S	:	North – South
n	:	Basic chromosome number
n	:	Number of treatments
NaOH	:	Sodium hydroxide
NHB	:	National Horticulture Board

nm	:	nanometre
No.	:	Number
NPK	:	Nitrogen, Phosphorus, Potassium
O	:	Observed frequency
Ph	:	Puissance de hydrogen
P_1	:	First parent
P_2	:	Second parent
r	:	Number of replications
RBD	:	Randomised Block Design
RH	:	Relative Humidity
rpm	:	rotations per minute
SCA / *sca*	:	Specific Combining Ability
SC	:	Standard Check
SE	:	Standard Error
S.Em	:	Standard Error mean
SH	:	Standard Heterosis
S.No.	:	Serial number
t	:	treatments
t	:	testers
t	:	tonne
t/ha	:	tonne per hectare
USA	:	United States of America
UV	:	Ultra Violet
V	:	Volume
V	:	Variance
Viz.	:	Namely
V.R.Gudem	:	Venkataramannagudem
W	:	Weight

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ABSTRACT

The present investigation entitled "Genetic analysis for yield, quality traits and plant ideotype in chilli (*Capsicum annuum* L.)" was undertaken at Horticultural Research Station, Lam farm, Guntur, Andhra Pradesh during *kharif*, 2013-14 and 2014-15 to estimate the heterosis, combining ability, gene action employing line x tester mating design and to study the nature and magnitude of gene effects using generation mean analysis for nineteen yield, yield components and quality traits. For line x tester analysis, the planting material consisted of nine lines (LCA 504, LCA 615, LCA 446, LCA 466, LCA 442, LCA 654, LCA 607, LCA 655 and LCA 355), six testers (G4, LCA 678, LCA 453, LCA 703-2, LCA 705-2 and LCA 315), the resultant 54 F_1 hybrids and two commercial checks *i.e.* Indam-5 and Tejaswini which were grown in RBD design whereas for generation mean analysis, the planting material consisted of four crosses (F_1s - F_1s of LCA 710 x HC-28, LCA 712 x HC-28, LCA 712 x LCA 710 and LCA 764 x LCA 315), their P_1's, P_2's, F_2's, BC_1's and BC_2's. Among these four crosses, the cross LCA 712 x HC-28 was selected to study the inheritance pattern of fruit bearing habit and fruit position whereas the cross LCA 712 x LCA 710 was selected to study the inheritance pattern of branching habit.

The heterosis of the F_1 hybrids resulted from line x tester analysis revealed that five crosses *viz.*, LCA 607 x LCA 703-2, LCA 655 x LCA 703-2, LCA 655 x LCA 315, LCA 446 x 703-2 and LCA 466 x LCA 705-2 were the most promising crosses over the both commercial checks *viz.*, Indam 5 and Tejaswini for yield and other important yield components.

The analysis of variance for combining ability revealed significant differences due to parents and crosses for all the characters whereas the significant differences due to parents *vs* hybrids were observed for only fourteen characters indicating that the existence of wide variability in the material studied and the good scope for identifying promising parents and hybrid combinations. The contribution due to Line x Tester interactions was the highest for total variance followed by lines and testers.

The ratio of *gca* to *sca* variance was less than unity for thirteen characters and indicated the predominance of non additive gene action and improvement of these traits can be made through heterosis breeding. The additive gene action was predominant for characters *viz.* plant height, no. of primary branches, fruit length, fruit diameter, average dry fruit weight and seed weight due to higher *gca* variances than *sca* variances and in which case the improvement can be made through simple selection.

The lines LCA 442, LCA 654 and LCA 655 and the testers LCA 703-2 and LCA 453 recording significant positive *gca* effects were found to be promising general combiners for yield, yield components and quality traits. In respect of *sca* effects, nine crosses *viz*., LCA 466 x LCA 705-2, LCA 607 x LCA 703-2, LCA 355 x LCA 678, LCA 504 x LCA 705-2, LCA 446 x LCA 703-2, LCA 615 x LCA 453, LCA 442 x LCA 453, LCA 607 x G4 and LCA 654 x LCA 678 were identified as promising specific combiners for fruit yield, yield components and quality traits.

Based on the studies of line x tester analysis, it was concluded that three hybrids *viz*., LCA 607 x LCA 703-2, LCA 446 X LCA 703-2 and LCA 466 X LCA 705-2 were most promising with desirable *sca* effects, heterosis and *per se* performance for fruit yield and other desirable traits. These hybrids may be further tested over locations and seasons and recommended for commercial release.

With respect to generation mean analysis, the significance of one or more scales in one or more crosses was observed for all the characters indicating that the role of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) type of gene interactions in the inheritance of all characters.

From the point of view, gene effects either additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions or all were found to be significant in one or more crosses indicating that in all the four crosses, the characters were governed by all or either additive, non-additive and epistatic interactions. This suggested that these four crosses can be improved by either pedigree method of selection, heterosis breeding and reciprocal recurrent selection.

In general, duplicate epistasis for many traits in four crosses was found and this will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistatic effects and these crosses can be improved by delayed

selection or selection after biparental intermating. The complementary epistasis was also found for some characters in all four crosses which favours the heterosis and such crosses can be exploited effectively through pedigree method of selection.

From the studies of generation mean analysis, it can be concluded that all the characters in one or more crosses are controlled by either additive, dominant and epistatic interactions or all gene effects. The crosses, in which the characters governed by additive, additive x additive and complementary epistasis can be improved effectively by pedigree method of selection whereas the crosses, in which the characters controlled by dominant, dominant x dominant and duplicate epistasis could be exploited effectively by heterosis breeding or reciprocal recurrent selection or full sib selection or delayed selection.

From the chi-square analysis, it was concluded that the nature of solitary fruit bearing habit and pendent fruit position were monogenic and dominant whereas the nature of the branching habit was digenic and governed by two gene pairs with specific dominant and recessive epistasis.

Chapter I

INTRODUCTION

Chilli (*Capsicum annuum* L.) is one of the most important commercial crops of India. It belongs to the genus *Capsicum* under the family Solanaceae *(2n = 24)*. In India, only two species *viz*., *Capsicum annuum* L. and *Capsicum frutescence* L. are well known and most of the cultivated varieties belong to *Capsicum annuum*. This cultivated species has its unique place in the diet as a vegetable cum spice crop (Gadagimath, 1992). The primary centre of origin of chilli is said to be Mexico with secondary centre in Guatemala and Bulgaria (Salvador, 2002). It was introduced in Europe by Columbus in 15th century and spread to rest of the globe along the spice trading routes to Africa, India, China and Japan. Chilli was introduced in India by the Portuguese from Brazil in the middle of 17th century.

Chilli has diverse uses as spice, condiment, culinary supplement, medicine, vegetable and ornamental plant. It is an indispensable spice due to its pungency, taste, appealing colour and flavour. Chilli comprises wide spectrum of chemicals including steam-volatile oil, fatty oils, capsaicinoids, carotenoids, vitamins, protein, fiber and mineral elements (Bosland and Votava, 2000). In India, it is an important ingredient in daily cuisine and is also used in the preparation of pickles, chutneys, sauces *etc.* The alkaloid capsaicin responsible for its pungency has diverse prophylactic and therapeutic uses in Allopathic and Ayurvedic medicine (Sumathy and Mathew, 1984). Besides being rich in vitamins (Hosamani, 1993), the fruits are good source of oleoresin which has varied uses in processed food and beverage industries for colour distribution.

India is the largest producer (1.492 million tonnes from 0.775 million hectares), consumer and exporter of chilli in the world (National Horticulture Board (NHB, 2014)) with productivity of 1.9 metric t/ha. Andhra Pradesh is the leading producer and exporter of the chilli with an annual production of 0.60 million tonnes from 0.13 million ha (NHB, 2014) followed by Telangana, Karnataka, West Bengal

and Madhya Pradesh *etc*. In Andhra Pradesh, Guntur, Prakasam, Kurnool, Krishna, Kadapa and West Godavari are the major chilli growing districts.

Even though India ranks first in area and production of chilli, its productivity is very low as compared to other countries like Japan (3.6 t/ha) and Korea (2 t/ha), USA and Indonesia (Patil *et al.,* 2012). The low productivity in India is mainly due to lack of superior genotypes/varieties with acceptable quality traits, with resistance to pests and diseases and presence of only a limited number of improved varieties and hybrids. One of the options to achieve quantum jump in yield is heterosis breeding.

Heterosis refers to the superiority/inferiority of the F_1 hybrid over the mean parental value (mid parent heterosis) or the better parent (heterobeltiosis) or the best commercial variety (standard heterosis). The term heterosis was coined by Shull (1908) to describe the stimulation resulting from increased heterozygosity. The popularity of F_1 hybrid cultivars is due to their vigour, high productivity, uniformity, improved quality, built in resistance, environmental adaptations, stress tolerance and good horticultural traits including earliness and long shelf life and therefore giving constant stable high yield (Sood and Kumar 2010). Heterosis breeding is a quick and convenient way of combining desirable characters and has assumed greater significance in the production of F_1 hybrids (Ramesh *et al.*, 2013). East and Hays (1912) were the first to advocate heterosis breeding as an alternative crop improvement strategy. The negative heterosis has been reported to be important for dwarfness and earliness whereas positive heterosis for commercially important attributes (Kalloo, 1988).

The knowledge of the relative importance of additive and non-additive gene action is essential to a plant breeder for the development of an efficient hybridization programme (Dudley and Moll, 1969). In any hybridization programme, proper choice of parents based on their combining ability is a prerequisite to gain better heterotic effects.

Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its crosses. The concept of combining ability was originally developed in maize by Richey and Meyar (1925). Sprauge and Tatum (1942) have defined the terms ‘general combining ability’ (GCA) and ‘specific combining ability’ (SCA) as a measure of gene action while working with maize. Combing ability analysis is a common tool used in breeding programme for testing the performance of parents in hybrid combinations, for characterizing the nature and magnitude of gene action involved in the expression of quantitative traits and also to identify the best parent(s) and hybrid(s) for further exploitation. Griffing (1956), showed the relationship between GCA and SCA variances. The GCA variance is due to additive whereas SCA variance is due to non-additive gene action. Hence, both act as an important diagnostic tool in selection of suitable parents. Top crossing, line x tester, diallel and partial diallel crossing techniques are used to study the combining ability. But a more precise estimate of GCA, SCA and other parameters can be estimated from Line x tester (L x T) mating design (Kempthorne, 1957).

In order to improve any particular trait, it is essential to know the kind of gene action (additive, dominance or epistasis) involved in the expression of the trait to adopt appropriate breeding procedure for the genetic improvement of various quantitative characters. Line x Tester (L x T) analysis is used to select the parents based on their combining ability but fails to detect the epistasis, which remains the most complex problem and on which it is extremely difficult to obtain reliable results. The inherent drawback of L x T design is that, it estimates additive and dominance components of gene action only and information on epistasis cannot be estimated which is an integral component of genetic architecture of population. So, information on the presence of type of epistatic genetic effects in the inheritance of various traits is important for adopting suitable breeding procedures to improve the traits. Generation mean analysis (Hayman, 1958) gives a comprehensive picture of gene action controlling the trait. It is relatively a simple first degree statistically analyzed technique to know the predominant genetic effects that are responsible in

effecting the variation of character. In this area of generation mean analysis in chilli, very little work has been reported from India and abroad.

By these breeding methods, the productivity can be increased through the improvement of yield attributing characters. Further, identification of ideotypes amenable for mechanical harvesting will be an added advantage since 20 per cent of cost of production in chilli accounted for harvesting alone (Dhamayanthi and Reddy, 2003). The genotypes with cluster fruit bearing habit and upright fruit position are suitable for mechanical harvesting as the fruits are borne mainly in the periphery (Dhamayanthi and Reddy, 2001) and the compact plant types enable closer spacing leading to higher yield per unit area (Thomas and Peter, 1986). But the problems associated with mechanical harvesting of peppers include difficulty in separating fruit from the plant, non-uniform maturity, breakage of branches and uprooting of plants by the action of the harvester (McCammon and Honma, 1984). Plant breeders have been charged with the responsibility of attempting to breed a plant adaptable to the harvester. This would require a plant archetype exhibiting concentrated fruit set, uniform maturity and with fruit set high off the ground. It also should possess the necessary horticultural characteristics and resistance to diseases and insects (McCammon and Honma, 1984).

Understanding of the inheritance of yield, yield component traits, quality traits and plant archetype in advance would be important to maximize the use of genetic potential in an effective breeding program. Considering the importance of chilli and in view of the above mentioned constraints, the present study was carried out with the following objectives.

Objectives of the Investigation:

1) To estimate the heterosis for yield and quality traits in chilli.
2) To estimate the general combining ability (gca) of parents and specific combining ability (sca) of the crosses for yield and quality traits in chilli.
3) To study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and plant ideotype in chilli.

Chapter II

REVIEW OF LITERATURE

The knowledge of genetic architecture and inheritance pattern of yield and yield components is very essential from the breeder's point of view to plan efficient breeding programmes adopting suitable breeding methods for genetic improvement of crops. Therefore, an attempt has been made to compile and present the available literature pertaining to morphological characterization, heterosis, combining ability and gene action. The available literature has been reviewed and presented under following heads.

2.1 MORPHOLOGICAL CHARACTERIZATION

Genetic cataloguing based on standard descriptors helps to easily describe the morphological features of a genotype and thus helps exchange of information about new genotypes. Characterization and evaluation of germplasm are prerequisite for the utilization of available diversity in crop improvement programme. Desirable parental combinations provide the basis for selection in the follow up hybrid breeding process for exploitation of heterosis (Thul *et al.*, 2009).

Sreelathakumary (2000) reported high variability for morphological characters in *C. annumm* and Manju and Sreelathakumary (2002) reported that 90% had green leaf colour and 87.55% had sparse leaf pubescence in case of *Capsicum chinense* germplam.

Pradheep and Veeraragavathatham (2006) reported that most of the genotypes showed green coloured fruits at mature stage than other colours.

Chattopadhyay *et al.* (2011) recorded sixteen morphological characters in accordance with the standard descriptors and reported that intermediate plant growth habit (53% genotypes), dense branching habit (41%), medium-sized leaves (74%), pigmentation at nodes (present - 88%) in the genotypes, lanceolate shaped-leaves ((82%), green leaf color (77%), flower per axil (1flower/axil - 100%), blue anther color (32%), entire and intermediate type calyx margins (38% and 38% respectively), long fruit shape (80%), pendant fruit position (91%), the pointed fruit shape at blossom-end (65%), green immature fruit color (85%), red ripe fruit color (62%) and obtuse fruit shape at the pedicel attachment (85%) were predominant than others.

Five lines (Kashi Anmol, Pant C-1, Japani Longi, Kashi Sinduri and Pusa Jwala) and five testers (R-Line, VR-339, AKC-89/38, DC-16 and Punjab Lal) of chilli were crossed in line x tester mating design to derive 25 F1 hybrids and observed green coloured fruits in majority of the crosses followed by light green colour and dark purple coloured fruits (Chaudhary *et al.,* 2013)

Datta and Das (2013) collected fifty three chilli genotypes and characterized for 20 characters and reported that green stem colour, intermediate plant growth habit, dense branching habit, small leaf size, lanceolate leaf shape, entire leaf margin, green leaf colour, sparse leaf pubescence, without pigment at node (83.02 %), single flower per axil (86.79 %), white corolla colour (100 %), pale blue anther colour, intermediate calyx margin, green fruit colour at intermediate stage, triangular fruit shape, pendent fruit position, hard fruit adherence to the calyx, acute fruit shape at pedicel attachment, pointed blossom end and semi wrinkled fruit surface were predominant than others. The genotypes upon cataloguing showed distinct variations with respect to vegetative, inflorescence and fruit characters.

Janaki (2013) evaluated sixty three genotypes for three morphological characters and reported three traits *viz.*, solitary fruit per axil (82.53%), pendent fruit position (85.71%) and green fruit colour at mature stage (74.60%) were predominant than others.

Three morphological parameters were studied in thirty F_1 hybrids evolved from six lines and five testers and reported predominance of absence of pigmentation at node, green fruit colour at mature stage and red ripe fruits (Rekha, 2015).

2.4 GENERATION MEAN ANALYSIS (GMA)

Gene action refers to the behaviour or mode of expression of genes in a genetic population. Knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also in the choice of appropriate procedures for the genetic improvement of various quantitative characters. Hence, insight into the nature of gene action involved in the expression of various quantitative characters is essential to a plant breeder starting a judicious breeding programme. Basic requirement in adopting a suitable breeding method is a sound understanding of the genetic behaviour. Therefore, success in development of genotypes with desired characters depends on the knowledge of genetic architecture of the traits and their inheritance pattern in different genetic backgrounds.

Gene action may be additive (includes additive x additive type) and / or non-additive (consist of dominance, additive x dominance and dominance x dominance type of epistatic components). Earlier epistatic factors were neglected, now researchers found its importance in governing the polygenic trait inheritance and started exploiting the digenic interactions in the crops.

In order to improve any particular character, it is essential to know the kind of gene action involved *i.e.*, additive, dominance or epistasis present in the population. But the Line x Tester mating design estimates only additive and dominance components of gene action and information on epistasis cannot be

estimated which is an integral component of genetic architecture of population. So, information on the presence of type of epistatic gene effects in the inheritance of traits is important for adopting suitable breeding procedures to improve the traits. Generation mean analysis (Hayman, 1958) gives a comprehensive picture of gene action controlling the trait. It is relatively a simple first degree statistically analyzed technique to know the predominant genetic effects that are responsible in effecting the variation of character.

The concept of generation mean analysis was developed by Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation. Analysis of this technique is based on five (P_1, P_2, F_1, F_2, F_3) or six (P_1, P_2, F_1, F_2, BC_1, BC_2) different generations of a cross. The mean values over replications are used for the estimation of gene effects. Owing to presence of six generations in each cross, Hayman's (1958) six parameter model (when presence of epistasis) or Jinks and Jones (1958) three parameter model (when absence of epistasis) were followed to estimate the gene effects.

2.4.1 Yield and Quality traits

Ribeiro and Costa (1990) studied the inheritance of capsaicin content in *C. chinense* and reported that the capsaicin content showed predominance of additive gene effects.

Nazzer *et al*. (1992) studied inheritance of red and purple fruit colour in six generations of two crosses. F_1 mean values indicated partial dominance of bright red over light red colour and purple fruit colour over green. Additive and additive x additive components were found to be significant with higher magnitude of additive components indicating the importance of additive gene action in the inheritance of these quality traits.

Ahmed *et al.* (1993) studied inheritance of earliness in six generations of three crosses and reported dominance of earliness over late maturity. Both additive

and non-additive gene effects were noted and thus recommended recurrent selection as an option for breeding for improvement of this trait.

Jadhav and Dhumal (1994) revealed the importance of additive gene effects for fruit length, dominance gene effect for yield and fruits per plant and both additive and dominance gene effects for plant height and fruit width in chilli. Thus, they suggested heterosis breeding or reciprocal recurrent selection for improvement of these traits.

Khereba *et al.* (1995) studied genetics of bell pepper for fruit length, diameter, pericarp thickness and locules in the cross Fimento x Pip and reported that these traits were governed by multiple gene effects. Partial dominanace was found towards the longer, wider and thicker fleshed fruits.

Murthy and Deshpande (1997) studied the six generations of four crosses of chilli and observed three types of gene action *viz.*, additive, dominance and interaction components in the inheritance of fruit number, length, width and yield. They attributed this to differences in magnitude of the gene effects and genetic background of the parents and further suggested the exploitation of heterosis breeding, pedigree breeding and selection of desirable transgressive segregants for varietal improvement.

Sarma and Talukdar (1998) evaluated six generations of chilli intervarietal crosses for plant height, fruits per plant, fruit length, fruit diameter and fruit yield per plant and observed that dominance and dominance × dominance interaction prevailed in the inheritance of these traits.

Bal and Singh (1999) studied nature and magnitude of gene effects on fruit length and breadth among ten crosses of capsicum and reported that digenic interactions together with additive and dominance effects influenced the inheritance of fruit length and breadth with predominance of additive effects. Further, dominance and dominance × dominance components had opposite signs in most of the crosses indicated the presence of duplicate type of epistasis.

Jagadeesh (2000) analysed nine crosses through generation mean analysis for 15 characters to understand the nature and magnitude of gene effects and indicated that the growth related traits were under the control dominance and additive x additive type of gene interaction whereas fruit related traits were under the control of additive, additive x additive type of gene interaction.

Zewdie and Bosland (2000) studied capsaicinoid inheritance in an interspecific hybridization of *Capsicum annuum* x *C. chinense* through generation mean analysis and observed significant additive, dominance, and interaction effects for capsaicin, dihydrocapsaicin and isomer of dihydrocapsaicin.

Kumar (2002) studied six generations derived from crossing of one common parent with each of six parents to find out the nature and magnitude of gene effects for yield and quality traits. He detected epistasis for all the characters except for early and total yield, capsaicin content and dry matter content in one or more crosses and also reported higher magnitude of additive component than dominance component for all the traits except for early yield. The duplicate type of epistasis was observed for most of the crosses except for early and total yield in one and two crosses, respectively.

Khalil *et al.* (2004) studied inheritance of yield and contributing traits in pepper and reported that both additive and non-additive gene effects were involved in the inheritance of early and total fruit yield. The additive gene effects were more important in the genetic mechanism for total yield and average fruit weight whereas for early yield non-additive effects played the main role.

Ajith and Anju (2005) reported that additive, dominance and all the three types of interactions were found to be significant for fruit yield per plant. But only additive and dominance x dominance effects were in the positive direction. The highest magnitude was possessed by dominance x dominance effect.

Dhall and Hundal (2005a) studied the nature and magnitude of gene effects in six crosses of chilli through six parameter generation mean analysis and shown that

capsaicin content of red ripe fruits is controlled by both additive and non additive gene effects but additive effects with partial dominance has more influence on the inheritance of this quality characters and improvement can be made through selection. They (2005b) also have reported that mean of all the crosses surpassed both of their corresponding parental means suggesting over dominance for both early and total yield whereas for colouring matter of red ripe fruits and total chlorophyll content of green fruits, means were higher than mid-parental means suggesting partial dominance for these traits.

Singh and Chaudhary (2005b) studying generation mean analysis in capsicum and concluded the importance of both additive and dominant type of gene effects for most of the plant and fruit characters. Among the epistatic components, additive × additive type of epistasis was more prevalent than dominance × dominance type of epistasis for most of the traits.

Dhall and Hundal (2006) reported higher magnitude of epistasis and dominance effects than that of additive effects for fruit weight and fruit number in all the crosses except 'PBC 830' **x** 'Punjab Lal' for fruit weight and concluded that both traits are controlled by both additive and non additive gene effects. However, the additive effects had more influence on their inheritance and hence selection can be used for improving these traits.

Kamboj *et al.* (2006) conducted an experiment for the genetic study of ascorbic acid content in green and red ripe fresh fruits of chilli using generation mean analysis of eight crosses *viz.*, Utkal Ragini x KDCS-810, HC-28 x LCA-334, HC-28 x LCA-206, HC-28 x Utkal Ragini, DC-24 x KDCS-810, DC-24 x DC-16, DC-16 x HC-28 and DC-16 x LCA-334 and revealed that both additive (d) and dominance (h) gene effects were equally important for genetic control of ascorbic acid content in fresh green and red ripe chilli fruits.

Patel *et al.* (2006) studied the genetic analysis for the yield and yield components of six generations of 6 crosses of *C. annuum* and indicated that intra-

and inter-allelic interaction was significant for green fruit yield and most of the yield components along with the marginal influence of additive gene effect on these traits.

Dhall and Hundal (2007) reported epistasis for all crosses (except in PBC 830 x Punjab Lal) with higher magnitude of dominance effects than that of additive effects. They concluded that early and total yield are controlled by both additive and non additive gene effects but dominance effects has more influence on the inheritance of these characters and selection for improvement should be effective in later generations.

Studies on the gene effects in chilli through generation mean analysis for six characters revealed additive gene effects (d) were important for the expression of plant height, plant spread, fruits per plant and dried red fruit yield per plant. However, dominance gene effects (h) were found predominant for the control of branches per plant and fresh red fruit yield per plant. Digenic interaction as well as duplicate epistasis also displayed their significance in the inheritance of characters studied (Kamboj *et al.*, 2007)

Somashekhar *et al.* (2008) estimated gene effects for fruit yield and its components in chilli using generation mean analysis of 5 crosses and reported greater magnitude of dominance (h) gene effect than that of additive gene effect in three crosses. However, the additive x additive (i) component was more predominant than other types of interactions.

Jabeen *et al.* (2009) reported that both additive and non-additive components were played a vital role in the inheritance of yield and yield components in chilli. However, non additive gene actions were predominant for days to first fruit set, days to first ripening, branch number, fruit width, plant height, plant spread and fruit yield. Among interallelic interactions, the dominance x dominance type of interactions was more frequent as compared to additive x additive and additive x dominance type of interactions.

Marame *et al.* (2009) worked out gene effects for fruits per plant and fruit weight by using five crosses in chilli and observed presence of significant gene interactions which indicated a polygenic inheritance of the fruit traits and the possibility of pyramiding favourable alleles in the required directions at different levels of progeny generations. Heterosis, backcrossing, multiple crossing and pedigree breeding methods with recurrent selection were recommended to facilitate simultaneous exploitation of the genetic components and gene effects obtained.

Anandhi and Khader (2011) studied gene actions for yield and it's component characters through generation mean analysis and reported that the additive (*d*) component was significant for all the traits studied. But wherever dominance gene effects were significant, the dominance (*h*) values were higher than the additive (*d*) values. Dominance (*h*) and dominance x dominance (*l*) effects were also in the same direction, suggesting complementary-type epistasis. The dominance x dominance (*l*) interaction was predominant and significant levels of all types of gene actions (additive, dominance and epistasis) were observed for yield.

Hasanuzzaman and Golam (2011) reported the presence of digenic epistasis for days to flowering, fruit length, fruit width, fruit weight, fruits per plant, plant height and yield per plant in chilli. Further analysis of generation means indicated that fruits and yield per plant were controlled by additive, dominance and epistatic gene action. Presence of complementary gene action and prevalence of the high magnitude of non-additive gene effects were found in most of the traits. They suggested the utilization of heterosis breeding to be more feasible option for majority of traits.

Kamboj *et al.* (2011) studied eight crosses of chilli to observe the genetic control for days taken to flowering, fruit set and fruit ripening through generation mean analysis and revealed that the additive gene action (d) to be more important over the dominance gene action (h). Besides this, epistasis gene interactions were also present in the inheritance of these traits in chilli.

According to Patil (2011) gene actions *i.e.* additive, dominance and interaction components were found to play role in their inheritance of fruit characters and yield. However, their degree varied with crosses which were attributed to the differences in magnitude of gene effects and genetic background of the parents.

According to Sood and Kumar (2011), inheritance of days to 50 per cent flowering, plant height, fruit length, fruit width, pericarp thickness and lobes per fruit was controlled by additive genes whereas non-additive actions were important in the control of days to first picking, harvest duration, fruit yield per plant, fruits per plant, marketable fruits per plant and average fruit weight.

Patil *et al.* (2012b) studied gene action and gene effects for fruit and seed attributes in chilli and observed duplicate type of epistasis for fruit length, fruit diameter and seed weight indicating that those were governed more by non- additive genes than additive genes whereas both duplicate and complementary type of epistasis were observed for number of seeds per fruit which indicated that seed noumber was governed by both additive and non-additive genes.

Prajapati and Agalodiya (2012) developed six generations from eleven inbred lines in chilli to study inheritance of earliness. They noticed the preponderance of dominance gene effects for inheritance of days to flowering and suggested heterosis breeding for improvement.

Prajapati *et al.,* (2012) studied nature and magnitude of gene action for fruit yield and yield attributing characters in six crosses of chilli and reported that the characters primary branches per plant, fruit length and no. of fruits per plant governed by fixable gene effects (additive and additive x additive epistasis). The dry fruit weight was controlled by non-additive gene effects whereas plant height, average fruit weight governed by additive as well as non-additive gene effects.

Savitha and Pugalendhi (2013) investigated a study to observe gene actions for plant height, no. of fruits per plant, fruit length, fruit girth, fruit weight and dry

fruit yield per plant and concluded that additive, dominance and epistasis components were governed their inheritance.

Silva *et al.* (2013) studied one cross (Pimenton Serrano x Aji Cayenne 958) through generation mean analysis and revealed that additive, dominance and the non-allelic interaction components were found to be significant for the phenotypic expression whereas additive X additive [i] effects found to be significant for fruit weight.

Tempeetikul *et al.* (2013) experimenting the inheritance of pungency in Thai hot pepper (*Capsicum annuum* L.) through generation mean analysis indicated that, a large magnitude of dominance and dominance X dominance gene effects were found for all capsaicinoids.

Anandhi and Khader (2014) studied generation mean analysis for fruit yield and its components in two interspecific crosses of chilli. The additive (d) component was found to be more important than dominance and epistasis gene interaction and also they reported duplicate epistasis with higher magnitude of dominance x dominance (l) interaction. The significance of all gene effects for most of the important traits indicating recurrent selection, multiple cross or diallel selective mating system were found to be effective in the exploitation of these characters.

Manu *et al.* (2014) detected the presence of additive and dominance gene effects for fruit length, additive gene effect for fruit weight but there were no gene effects found for fruit diameter. Further, fruit length also exhibited predominance of additive x additive gene effects.

All the three types of gene action *i.e*. additive, dominance and interaction components were found to play a major role in the inheritance of days to first picking, plant height (cm), number of branches per plant, fruit length (cm), fruit diameter (mm), number of seed per fruit, number of fruits per plant (green), number of fruits per plant (dry), dry fruit yield per plant (g) and capsaicin content (%) in chilli (Navhale *et al*., 2014a).

YiHu *et al.* (2014) evaluated six generations of one cross to study the gene action for fruit number per plant, fresh weight per fruit and dried fruit weight per plant and the results showed that the inheritance of fruit number per plant fitted the model of two additive-dominance-epitasis major genes (B-1), fresh weight per fruit fitted the model of two additive-dominance-epitasis major genes + additive-dominance-epitasis polygenes (E-0) and dried fruit weight per plant fitted the model of two additive-dominance-epitasis major genes + additive-dominance polygenes (E-1).

Patel and Patel (2015) developed six generations of six crosses from nine inbred lines and that generations were used to apply scaling tests for attributes of earliness *viz.*, days to flowering, days to fruit ripening and days for economic fruiting period. For days to economic fruiting period importance of both additive and dominance gene effect was found. The earliness being a complex character, preponderance of non-additive gene effect was evidenced.

2.4.2. Qualitative traits:

Shaw and Khan (1928) have used fruit position as a diagnostic character in classifying chillies. Deshpande (1933) has shown this character to be governed by a single factor while Singh and Roy (1945) observed dominance of pendent fruit position over erect fruit position.

Dale (1931) studied the inheritance of a dwarf plant habit arising from a cross between the cultivars 'Coral Gem' and 'Anaheim' and determined the trait to be a simply inherited recessive character.

Deshpande (1944) conducted an analysis of the inheritance of bunchy habit in chilli peppers. This mutant was described as bushy and compact with shortened internodes, flowers and fruits produced in clusters. The bunchy character was shown to be recessive and was later termed fasciculate (fa) by Lippert *et al.* (1965, 1966).

Kormos and Kormos (1956) crossed a fasciculate type of pepper with various non-fasciculate types and recovered F2 progeny exhibiting completely determinate growth (Producing a cluster of fruits without lateral shoots). This character was found to be recessive.

The inheritance of fruit bearing habit in *C.frutescens* L., was determined from a cross between two tabasco type cultivars, 'LP-I' and 'Almeda' and the results indicated that the cluster habit was controlled by a single recessive gene (Barrios and Mosokar, 1972).

In *capsicum chinense* Jack., *C. frutescens* L.and *C. baccatum* L., a single recessive gene for axillary shooting was demonstrated (Bergh and Lippert, 1975).

Shifriss and Hakim (1977) studied the inheritance of pre – bifurcation shooting in *C.annuum* L and they crossed 'Santaka' with 'Csokros Fellalo' and 'Yolo-Wonder Y'. The progenies of F_1 and F_2 from 'Santaka x Csokros Fellalo' cross showed partial dominance of many over few axillary shoots, while in the F_1 and F_2 from 'Santaka x Yolo-Wonder Y' the opposite occurred *i.e.* partial dominance of few over many shoots. They concluded that pre – bifurcation shooting though a quantitative character and is controlled by relatively few genes with different action and modified by environmental conditions.

Mc Cammon and Honma (1984) studied three inbred lines to determine the inheritance of the "umbrella" branching habit in peppers and they crossed MSU 79-221 with MSU78-191 and MSU74-230. Genetic analyses suggested that the umbrella phenotype was controlled by three major recessive genes, *ct* and *dt* determining plant habit, and *fa* determining fruit bearing habit and also reported that modifying genes were also involved in the control of umbrella branching habit, they also noticed linkage between the genes for indeterminate plant habit and non clustered bearing habit.

Thomas and peter (1986) evaluated two sets of segregating and non segregating populations of chilli to study inheritance of cluster bearing fruit habit

and reported that the cluster habit was recessive and governed by two gene pairs with specific dominant and recessive epistasis.

Gopalakrishnan *et al.* (1989) reported that clusterness was found to be monogenic recessive to solitary fruiting habit whereas the upright fruit orientation is controlled by two recessive genes in relation to pendent condition.

Dhamayanthi and Reddy (2001) conducted a study to transfer clustered and upright fruit characters from CA-33 and CA-219 into G4 and CO-2 through generation mean analysis. The results revealed that the genes responsible for the clustered fruit character are monogenic while, the upright fruit character is digenic, controlled by two genes with dominant and recessive epistasis.

Stommel and Griesbach (2008) found that fruit colour, shape, and fruits per cluster were simply inherited with modifying gene action. The fruit clustering was simply inherited and the number of fruit per cluster exhibited a quantitative mode of inheritance.

Joshi *et al.* (2011) reported the dominance of pendent over upright bearing habit and found to be governed by a single dominant gene. Similarly, the chilli type fruit shape was partially dominant over the bell shape.

2.2 HETEROSIS

Heterosis refers to the superiority/inferiority of the F_1 hybrid over the mean parental value (mid parent heterosis) or the better parent (heterobeltiosis) or the best commercial variety (standard heterosis). The term heterosis was coined by Shull (1908) to describe the stimulation resulting from increased heterozygosity. The term “heterobeltiosis” was proposed later (Bitzer *et al.*, 1968; Fonesco and Patterson, 1968) to denote the expression of heterosis over better parent. The potency of heterosis breeding is enormous in terms of increasing the productivity of crop plants. However, from the plant breeding point of view, increasing the productivity over

better parent and /or the popular commercial variety is more relevant. Heterosis breeding has already become popular in breeding of cross-pollinated crops and is increasingly being utilized for increasing the productivity of self-pollinated crops (Rai, 1979).

Heterosis is an important avenue for increasing yield and other economic traits in chilli (Joshi, 1986). Heterosis breeding is an important crop improvement method adopted in many crops all over the world and it is a quick and convenient way of combining desirable characters which has assumed greater significance in the production of F_1 hybrids (Ramesh *et al.*, 2013). East and Hays (1912) were the first to advocate heterosis breeding as an alternative crop improvement strategy. In chilli, heterosis was first reported by Despande (1933). Hybrids offer opportunities for improvement in productivity, earliness, uniformity, quality and wider adaptability and for rapid deployment of dominant genes for resistance to diseases and pests (Riggs, 1988). The negative heterosis is important for dwarfness and earliness whereas positive heterosis is essential for commercially important attributes (Kalloo, 1988).

The expression of heterosis may be due to such factors as heterozygosity, allelic and non-allelic interactions or epistasis, dominance or over dominance and plasmatic or maternal interaction. The degree of expression of heterosis depends upon the number of genes in heterozygous condition. Higher the number of heterozygous alleles, more is the heterosis expected (East and Hayes, 1912). There is a very possibility of exploiting heterosis in chilli, since the extent of natural cross pollination in chilli is found to be as high as 50-60 per cent (Murthy and Murthy, 1962) and upto 92 per cent (Gaddagimath, 1992).

Numerous studies were conducted to assess heterosis for individual characters of chilli *viz.*, plant height, plant spread, number of primary branches per plant, days to 50 per cent flowering, days to fruit maturity (red), number of fruits per plant, fruit length, fruit diameter, average dry fruit weight, fruit yield, number of seeds per fruit, seed weight, ascorbic acid, oleoresin, capsaicin, total colour value,

red carotenoids and yellow carotenoids over mid parent, better parent and commercial check. For the sake of brevity, the results of the above studies during the last 15 years *i.e.* from 2001 to 2015 are summarized in the form of table (Table 2.1).

Table 2.1: Review of literature on heterosis, heterobeltiosis and standard heterosis for various traits

S.No	Characters	No. of hybrids studied	Mid parent heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)	References
1	Plant height (cm)	12	-	25.18 to -4.18	-	Burli *et al*.(2001)
		24	-16.99 to 26.46	-26.17 to 25.09	-29.16 to 20.04	Patel *et al*. (2001)
		20	-28.40 to 75.67	-39.31 to 51.09	-13.18 to 40.15	Ajjappalavara (2003)
		27	-10.65 to 28.63	-18.45 to 22.90	-	Linganagouda *et al*. (2003)
		36	42.15 to 3.17	50.47 to 2.83	-	Nandadevi and Hosamani (2003)
		20	-28.40 to 75.67	39.31 to 51.09	-13.18 to 40.15	Prabhudeva (2003)
		21	1.30 to 73.80	- 6.00 to 47.20	-	Geleta and Labuschagne (2004)
		45	-	-23.37 to 23.22	-	Savitha (2004)
		30	-5.0 to 81.89	Highly Negative	Positive	Seneviratne and Kannangara (2004)
		18	-	Significant	-	Zate *et al*. (2005)
		21	Positive	-	-	Shankarnag *et al* (2006)
		21	-	37.22	57.10	Shankarnag and Madalgeri (2006)
		30	-	Significant	-	Sathish and Lad (2007)
		30	-1.50 to 49.06	-14.90 to 61.81	-	Chandan (2008)
		40	-12.92 to 39.07	-14.39 to 15.91	-28.99 to 4.63	Ganeshreddy *et al*. (2008)
		30	-	-	16.81 to 131.37	Prasath and Ponnuswami (2008)
		45	-	-21.36 to 24.57	-24.48 to -3.98	Kamble *et al*. (2009b)
		50	-	-25.52 to 70.36	-9.27 to 110.16	Patel *et al*. (2010)

		24	-	-	-35.51 to 17.81	Sood and Kumar (2010)
		3	-0.891 to 11.01	-10.83 to -1.27	-	Prajapati and Agalodia (2011)
		28	-	-22.68 to 7.75	-26.47 to 4.99	Patil *et al*. (2012a)
		9	-6.35 to 20.27	-19.92 to 8.74	-	Payakhapaab *et al*. (2012)
		10	-	-9.70 to 11.23	-	Rodrigues *et al.* (2012)
		51	-30.85 to 48.31	-37.41 to 44.48	-31.98 to 31.98	Tembhurne and Rao (2012)
		25	18.88 to 23.68	12.73 to 17.15	-	Chaudhary *et al.* (2013)
		72	-20.29 to 18.11	-24.70 to 15.94	-10.98 to 25.38	Kumar *et al.* (2013)
		15	-	-32.72 to 51.13	-9.24 to 18.74	Sharma *et al*. (2013)
		9	-	-	-34.22 to 21.24	Dhaliwal *et al.* (2014)
		66	-	-3.11 to 32.21	-	Singh *et al.* (2014)
		40	-30.87 to 38.49	-35.96 to 22.63	-16.52 to 59.82	Suryakumari *et al*. (2014)
		12	Positive, significant (4 hybrids)	Positive, significant (4 hybrids)	-	Herath *et al*. (2015)
		30	-16.06 to 16.05	-23.39 to 11.36	-28.05 to 19.68	Rekha (2015)
		30	-29.60 to 38.95	-49.19 to 34.39	-45.84 to 13.95	Savitha *et al*. (2015)
		30	-	-24.73 to 35.54	-	Spaldon *et al*. (2015)
2	Plant spread (cm)	30	High	High	High	Seneviratne and Kannangara (2004)
		40	-20.46 to 15.67	-26.18 to 14.80	-3.85 to 55.15	Ganeshreddy *et al*. (2008)
		50	-	-51.21 to 27.84	-39.29 to 49.97	Patel *et al*. (2010)
		9	-13.47 to 11.49	-15.74 to 8.67	-	Payakhapaab *et al*. (2012)

		10	-	-5.67 to 39.77	-	Rodrigues *et al.* (2012)
		66	-	-13.77 to 20.66	-	Singh *et al.* (2014)
		40	-1.30 to 64.56	-2.72 to 61.40	-4.40 to 191.8	Suryakumari *et al*. (2014)
		12	Positive, significant (8 hybrids)	Positive, significant (4 hybrids)	-	Herath *et al*. (2015)
		30	-12.10 to 30.93	-22.97 to 16.72	-18.69 to 41.92	Rekha (2015)
		30	-	-53.88 to 68.02	-	Spaldon *et al*. (2015)
3	Number of primary branches per plant	24	-20.22 to 28.14	-32.82 to 35.23	-28.43 to 31.70	Patel *et al*. (2001)
		27	-17.81 to 14.73	-18.92 to 80.32	-	Linganagouda *et al*. (2003)
		36	-50.70 to 127.66	-65.62 to 80.32	68.33	Nandadevi and Hosamani (2003)
		20	-17.56 to 114.45	-21.25 to 88.72	11.99 to 129.82	Prabhudeva (2003)
		45	-	-25.81 to 78.68	-	Savitha (2004)
		18	-	Significant	-	Zate *et al.* (2005)
		30	-8.20 to 71.43	-15.15 to 57.14	-	Chandan (2008)
		40	-14.29 to 55.13	-22.22 to 44.05	-42.47 to 17.26	Ganeshreddy *et al*. (2008)
		30	-	-	-42.22 to 82.68	Prasath and Ponnuswami (2008)
		50	-	39.06 to 53.11	-20.36 to 66.21	Patel *et al*. (2010)
		3	7.143 to 22.01	13.63 to 14.45	-	Prajapati and Agalodia (2011)
		28	-	-23.61 to 18.75	-26.70 to 6.92	Patil *et al*. (2012a)
		51	-20.87 to 83.88	-34.53 to 79.12	-5.01 to 97.70	Tembhurne and Rao (2012)
		72	-16.13 to 95.56	-21.87 to 91.30	-24.24 to 33.33	Kumar *et al*. (2013)

		15	-	-15.59 to 70.31	-44.72 to 33.52	Sharma *et al*. (2013)
		30	-25.81 to 27.45	-35.82 to 18.18	-29.63 to 38.30	Rekha (2015)
		30	-46.44 to 32.02	-50.94 to 12.00	-40.98 to 26.32	Savitha *et al*. (2015)
4	Days to 50% flowering	20	-	-19.67 to 0.82	-18.32 to 0.83	Ajjappalavara (2003)
		36	142.75 to 18.79	-35.11 to 43.55	-59.52 to -20.53	Nandadevi and Hosamani (2003)
		36		-3.54 to 22.85	-	Narasimha *et al*. (2003)
		20	-	-19.67 to 0.82	-18.32 to 0.83	Prabhudeva (2003)
		27	-18.7 to 1.3	-14.60 to3.10	-	Geleta and Labuschagne (2004)
		21	Positive	-	-	Shankarnag *et al*. (2006)
		30	-	Significant	-	Sathish and Lad (2007)
		30	-9.70 to5.84	-10.37 to 1.45	-	Chandan (2008)
		40	-6.62 to 4.51	-5.93 to 6.11	3.25 to 12.20	Ganesh reddy *et al*. (2008)
		24	-37.44 to 12.64	-38.65 to 12	-36.18 to 3.52	Patel *et al*. (2008)
		30	-	-	-3.99 to 14.62	Prasath and Ponnuswami (2008)
		45	-	-21 to24.57	-24 to -3.98	Kamble *et al*. (2009b)
		24	-	-	-9.84 to -1.64	Sood and Kumar (2010)
		3	0.893 to 1.963	2.86 to 4.00	-	Prajapati and Agalodia (2011)
		28	-	-15.03 to 25.58	-12.06 to 14.12	Patil *et al*. (2012a)
		51	-18.08 to 4.18	-23.45 to 0.74	-0.93 to 28.04	Tembhurne and Rao (2012)
		72	-12.99 to 5.45	-11.24 to 11.11	-13.48 to 4.49	Kumar *et al*. (2013)
		15	-	-12.86 to -9.67	-13.33 to -12.50	Sharma *et al*. (2013)

		40	-23.08 to 13.95	-28.57 to 12.09	-5.56 to 35.00	Suryakumari *et al*. (2014)
		30	-15.90 to 19.55	-21.25 to 15.38	-18.56 to 42.86	Rekha (2015)
		30	-26.10 to 15.88	-26.68 to -1.28	-9.46 to 26.81	Savitha *et al*. (2015)
5	Days to fruit maturity (Red)	3	-2.015 to 1.583	-2.015 to 2.66	-	Prajapati and Agalodia (2011)
		51	-13.69 to 0.74	-21.33 to 0.89	0.81 to 15.04	Tembhurne and Rao (2012)
		15	-	-16.14 to -11.87	-11.87 to -10.04	Sharma *et al*. (2013)
		40	-22.83 to 9.57	-27.05 to 3.28	-11.59 to 25.17	Suryakumari *et al*. (2014)
		30	-17.40 to 19.27	-26.35 to 13.73	-17.72 to 23.26	Rekha (2015)
		30	-	-10.97 to 1.72	-	Spaldon *et al*. (2015)
6	Number of fruits per plant	24	-21.26 to 46.73	-48.21 to -1.28	-48.21 to 26.42	Patel *et al*. (2001)
		36	Positive	High, positive	-44.82 to 344.02	Nandadevi and Hosamani (2003)
		36	-	-83.40 to 83.03	-85.82 to 56.36	Narasimha *et al*. (2003)
		45	-	-82.92 to 145.43	-	Savitha (2004)
		30	-19.18 to 234.86	-39.57 to 226.76	-50.18 to 208.64	Seneviratne and Kannangara (2004)
		15	-	Positive	-	Singh and Chaudhary (2005a)
		18	-	Significant	-	Zate *et al.* (2005)
		30	-4.54 to 277.73	-45.62 to 176.49	-	Chandan (2008)
		40	-28.13 to 98.73	-46.75 to 35.34	-10 to 250.67	Ganeshreddy *et al*. (2008)
		30	-	-	-22.94 to 137.61	Prasath and Ponnuswami (2008)
		45	-	-66.82 to -20.96	-26.87 to -17.37	Kamble *et al*. (2009b)

		15	-	-44 to 11	-	Perez *et al.* (2009)
		50	-	-43.47 to 170.62	12.97 to 277.69	Patel *et al*. (2010)
		10	7 to 69	-20 to 63	-	Sitaresmi *et al.* (2010)
		24		-	37.45 to 246.41	Sood and Kumar (2010)
		3	14.015 to 37.662	4.51 to 26.116	-	Prajapati and Agalodia (2011)
		28	-27.06 to 87.17	-57.75 to 39.69	-	Patil *et al*. (2012a)
		9	-41.99 to 51.09	-46.06 to 47.06	-	Payakhapaab *et al*. (2012)
		10	-	-0.19 to 98.09	-	Rodrigues *et al.* (2012)
		51	21.75 to 658.29	-1.8 to 651.37	43.02 to 397.94	Tembhurne and Rao (2012)
		28	3.93 to 41.6	-30.94 to 19.06	30.94 to 19.06	Berhate *et al*. (2013)
		25	110.57 to 163.71	96.43 to 161.55	-	Chaudhary *et al.* (2013)
		72	-29.81 to 55.77	-43.62 to 49.50	-18.12 to 83.29	Kumar *et al*. (2013)
		15	-	98.57 to 156.61	122.18 to 155.98	Sharma *et al*. (2013)
		15	-22.89 to 44.97	-46.22 to 10.15	-	Khalil and Hatem, (2014)
		15	-	-50 to 36	-	Artur *et al.* (2014)
		66	-	-79.30 to 205.95	-	Singh *et al.* (2014)
		40	-69.54 to 56.03	-74.90 to 27.48	-1.31 to 330.5	Suryakumari *et al*. (2014)
		12	Positive, significant (9 hybrids)	Positive, significant (7 hybrids)	-	Herath *et al*. (2015)
		30	-11.85 to 114.05	-26.06 to 100.36	-42.13 to 123.20	Rekha (2015)
		30	-64.22 to 250.31	-74.57 to 166.38	-75.83 to 39.19	Savitha *et al*. (2015)
		30	-	-45.30 to 86.76	-	Spaldon *et al*. (2015)

7	Fruit length (cm)	24	-8.42 to 24.98	-29.22 to 16.05	-35.87 to 15.84	Patel *et al*. (2001)
		36	-	-	-	Nandadevi and Hosamani (2003)
		36	-	-36.78 to 0.24	-	Narasimha *et al*. (2003)
		45	-	-43.90 to 4.93	-	Savitha (2004)
		30	High, positive	High, negative	High, positive	Seneviratne and Kannangara (2004)
		30	-14.96 to 46.19	-24.56 to 25.22	-	Chandan (2008)
		40	-34.08 to 47.48	-37.66 to 34.42	-34.21 to 40.79	Ganeshreddy *et al*. (2008)
		30	-	-	-20.59 to 39.85	Prasath and Ponnuswami (2008)
		50	-	-31.06 to 21.53	-40.86 to 5.67	Patel *et al*. (2010)
		3	5.128 to 25.844	-8.87 to 7.10	-	Prajapati and Agalodia (2011)
		28	-26.43 to 32.41	-33.61 to 5.52	-	Patil *et al*. (2012a)
		9	-12.43 to 40.36	-24.70 to 38.68	-	Payakhapaab *et al*. (2012)
		10	-	-2.51 to 25.96	-	Rodrigues *et al.* (2012)
		51	-25.88 to 86.13	-51.25 to 66.37	-67.39 to 17.72	Tembhurne and Rao (2012)
		25	59.42 to 74.91	37.99 to 52.38	-	Chaudhary *et al.* (2013)
		72	-25.15 to 56.60	-34.04 to 42.16	-25.29 to 34.54	Kumar *et al*. (2013)
		15	-	34.17 to 40.76	29.51 to 61.18	Sharma *et al*. (2013)
		9	-	-	-24.21 to 27.47	Dhaliwal *et al.* (2014)
		15	-34.59 to 32.50	-49.45 to 24.71	-	Khalil and Hatem (2014)
		15	-	-11 to 17	-	Artur *et al.* (2014)
		66	-	-5.13 to 39.64	-	Singh *et al.* (2014)

		40	-46.53 to 14.53	-49.79 to 14.04	-48.71 to 9.28	Suryakumari *et al*. (2014)
		12	Positive, significant (4 hybrids)	-	-	Herath *et al*. (2015)
		30	-10.48 to 15.19	-15.20 to 9.50	-12.68 to 39.05	Rekha (2015)
		30	-23.11 to 65.96	-48.22 to 46.88	-32.99 to 46.80	Savitha *et al*. (2015)
		30	-	-19.17 to 76.86	-	Spaldon *et al*. (2015)
8	Fruit diameter (cm)	24	-31.44 to 9.69	-50.22 to 3.28	-16.50 to 27.32	Patel *et al*. (2001)
		20	-40.94 to 27.34	-46.38 to 28.67	-54.62 to 8.40	Ajjappalavara (2003)
		36	High, positive	High, positive	-51.02 to 229.60	Nandadevi and Hosamani (2003)
		-	-	Negative, High	-34.78 to 124.35	Narasimha *et al*. (2003)
		20	-40.94 to 27.34	-46.38 to 28.67	-54.62 to 8.40	Prabhudeva (2003)
		30	High, positive	High, positive	Negative	Seneviratne and Kannangara (2004)
		40	40.79 to 63.98	-53.33 to 60.90	-44.83 to 47.59	Ganeshreddy *et al*. (2008)
		30	-	-	-41.82 to 29.90	Prasath and Ponnuswami (2008)
		50	-	-51.38 to 26.28	-29.34 to 38.42	Patel *et al*. (2010)
		3	5.194 to 11.929	-11.46 to 8.13	-	Prajapati and Agalodia (2011)
		28	-	-19.85 to 13.24	-26.04 to 7.29	Patil *et al*. (2012a)
		9	-29.64 to 7.92	-31.32 to 1.88	-	Payakhapaab *et al*. (2012)
		10	-	-19.44 to 12.80	-	Rodrigues *et al.* (2012)
		51	-50.69 to 19.59	-54.05 to -1.42	-49.51 to 28.74	Tembhurne and Rao (2012)
		25	9.04 to 34.62	7.57 to 20.69	-	Chaudhary *et al.* (2013)

		72	-17.57 to 67.47	-32.34 to 66.80	-31.22 to 8.29	Kumar *et al*. (2013)
		15	-	22.38 to 30.64	14.80 to 17.81	Sharma *et al*. (2013)
		9	-	-	-9.59 to 29.43	Dhaliwal *et al.* (2014)
		15	-45.83 to 25.67	-59.38 to 5.800	-	Khalil and Hatem (2014)
		15	-	-25 to 15	-	Artur *et al.* (2014)
		66	-	-20.60 to 10.41	-	Singh *et al.* (2014)
		40	-38.38 to 84.81	-41.84 to 67.82	1.76 to 186.27	Suryakumari *et al*. (2014)
		30	-20.32 to 20.93	-22.29 to 13.04	-37.25 to 57.28	Rekha (2015)
		30	-31.12 to 61.00	-34.14 to 59.93	-45.50 to 25.00	Savitha *et al*. (2015)
		12	Positive, significant (2 hybrids)	-	-	Herath *et al*. (2015)
		30	-	-35.90 to 46.43	-	Spaldon *et al*. (2015)
9	Average dry fruit weight (g)	12	-	-46.10 to 2.25	-	Burli *et al*. (2001)
		24	-28.45 to 47.24	-56.00 to 41.14	-36.47 to 57.29	Patel *et al*. (2001)
		24	-	-7.77 to 56.52	-	Thiruvelvan *et al*.(2002)
		20	-34.81 to 50.28	-63.00 to 47.13	-37.97 to 94.76	Ajjappalavara (2003)
		20	-34.81 to 50.28	-63.00 to 47.13	-37.97 to 94.76	Prabhudeva (2003)
		15	-	Positive, significant	-	Singh and Chaudhary (2005a)
		40	-56.76 to 59.37	-64.29 to 54.55	-41.67 to 112.50	Ganeshreddy *et al*. (2008)
		30	-	-	-44.60 to 90.60	Prasath and Ponnuswami (2008)
		45	-	-79.23 to -96.93	-82.63 to -4.37	Kamble *et al*. (2009b)

		24		24	-42.69 to 11.79	Sood and Kumar (2010)
		50	-	-51.19 to 3.60	36.04 to 33.93	Patel *et al*. (2010)
		3	7.847 to 56.882	5.73 to 52.59	-	Prajapati and Agalodia (2011)
		9	-48.02 to 51.33	-56.09 to 16.73	-	Payakhapaab *et al*. (2012)
		10	-	-21.92 to 20.82	-	Rodrigues *et al.* (2012)
		51	-1.09 to 84.38	-62.51 to 70.94	-84.81 to -44.15	Tembhurne and Rao (2012)
		25	49.35 to 123.33	22.34 to 123.33	-	Chaudhary *et al.* (2013)
		72	-33.46 to 193.9	-35.46 to 86.79	-44.72 to 21.70	Kumar *et al*. (2013)
		15	-	-20.96 to 102.73	-31.38 to 49.50	Sharma *et al*. (2013)
		9	-	-	-30.25 to 43.77	Dhaliwal *et al.* (2014)
		15	-23.58 to 70.11	-45.35 to 54.17	-	Khalil and Hatem (2014)
		15	-	-25 to 27	-	Artur *et al.* (2014)
		66	-	-28.65 to 57.52	-	Singh *et al.* (2014)
		30	-15.07 to 17.65	-28.57 to 9.09	-45.35 to 53.06	Rekha (2015)
		30	-31.60 to 125.96	-46.96 to 104.12	-21.59 to 96.53	Savitha *et al*. (2015)
		30	-	-37.11 to 96.69	-	Spaldon *et al*. (2015)
10	Fruit yield (g/plant)	12	-	-12.79 to 30.68	-	Burli *et al*. (2001)
		24	-1.67 to 92.04	-17.26 to 85.38	-24.10 to 15.30	Patel *et al*. (2001)
		12	-	-38.07 to 35.95	-	Kanthaswamy *et al*. (2003)
		36	-	-62.33 to 77.03	58.42 to 95.40	Narasimha *et al*. (2003)
		20	-71.96 to 120.98	-78.57 to 71.74	-70.78 to 64.61	Prabhudeva (2003)

		21	-0.30 to 327.70	-27.60 to 175.70	-	Geleta and Labuschagne (2004)
		45	-	-74.41 to 76.63	-	Savitha (2004)
		30	-81.09 to 44.45	-85.25 to 44.44	-	Chandan (2008)
		40	-52.80 to 152.67	-56.87 to 88.27	-62.18 to 60.51	Ganeshreddy *et al*.(2008)
		30	-	-	-51.84 to 99.04	Prasath and Ponnuswami (2008)
		15	-	-22 to 51	-	Perez *et al.* (2009)
		50	-	-36.33 to 197.55	21.47 to 448.55	Patel *et al*. (2010)
		10	4.47 to 29.76	-31.41 to 25.60	-	Sitaresmi *et al.* (2010)
		3	-5.33 to 34.22	-4.52 to 11.86	-	Prajapati and Agalodia (2011)
		9	-44.40 to 78.03	-48.33 to 73.03	-	Payakhapaab *et al*. (2012)
		28	-	-31.30 to 90.57	-63.23 to 41.91	Patil *et al*. (2012a)
		51	-0.92 to 493.44	-42.79 to 402.78	-62.88 to 48.47	Tembhurne and Rao (2012)
		28	-30.07 to 49.55	38.69 to 39.22	-39.19 to 38.72	Berhate *et al*. (2013)
		25	264.47 to 312.85	205.53 to 239.00	-	Chaudhary *et al.* (2013)
		72	-8.44 to 71.04	-24.67 to 70.24	-26.36 to 49.09	Kumar *et al*. (2013)
		15	-	-49.18 to 58.84	120.24 to 170.37	Sharma *et al*. (2013)
		9	-	-	-7.56 to 65.94	Dhaliwal *et al.* (2014)
		15	-24.24 to 86.38	-35.60 to 74.63	-	Khalil and Hatem (2014)
		15	-	-60 to 70	-	Artur *et al.* (2014)
		66	-	-71.82 to 331.11	-	Singh *et al.* (2014)
		40	-65.40 to 57.70	-68.16 to 82.10	14.68 to 51.61	Suryakumari *et al*. (2014)
		30	-11.20 to 86.83	-23.57 to 72.22	-26.24 to 53.03	Rekha (2015)

		30	-43.76 to 160.33	-57.60 to 79.70	-69.16 to 30.70	Savitha *et al*. (2015)
11	Number of seeds per fruit	45		-57.14 to 86.22	-	Savita (2004)
		40	-38.26 to 84.42	-33.15 to 114.29	30.83 to 77.50	Ganeshreddy *et al*. (2008)
		30	-	-	-8.24 to 87.65	Prasath and Ponnuswami (2008)
		15	-	-28 to 22	-	Perez *et al*. (2009)
		51	-54.41 to 52.92	-68.98 to 40.68	-91.11 to -20.78	Tembhurne and Rao (2012)
		72	-44.32 to 48.95	-38.40 to 80.43	-39.79 to 23.29	Kumar *et al*. (2013)
		9	-	-	-31.71 to 400.77	Dhaliwal *et al.* (2014)
		66	-	-80.70 to 89.94	-	Singh *et al.* (2014)
		40	-34.46 to 87.27	-39.49 to 83.85	-53.91 to 17.39	Suryakumari *et al*. (2014)
		30	-17.72 to 39.94	-33.64 to 34.62	-56.72 to 17.55	Rekha (2015)
		30	-42.12 to 99.47	-56.48 to 19.81	-52.30 to 38.00	Savitha *et al*. (2015)
		30	-	-53.18 to 117.50	-	Spaldon *et al*. (2015)
12	Seed weight (g/1000)	40	-84.14 to 68.12	-82.69 to 114.81	-60.00 to 180.00	Ganeshreddy *et al*. (2008)
		15	-	-19.00 to 38.00	-	Perez *et al*. (2009)
		51	-36.05 to 69.38	-45.65 to 60.88	-38.90 to 39.62	Tembhurne and Rao (2012)
		72	-51.89 to 135.1	-44.44 to 266.6	-51.11 to 71.10	Kumar *et al*. (2013)
		9	-	-	-51.30 to 406.32	Dhaliwal *et al.* (2014)
		40	-51.2 to 96.9	-57.32 to 59.45	-60.85 to 62.77	Suryakumari *et al*. (2014)
		30	-10.63 to 17.82	-14.55 to 13.65	-28.13 to 39.90	Rekha (2015)

		30	-69.91 to 50.32	-76.25 to 28.42	-69.04 to 34.67	Savitha *et al*. (2015)
13	Ascorbic acid (mg/100g)	45	-	High positive heterosis	-	Pandey *et al.* (2002)
			High	High	High	Geleta and Latuschagne (2004)
		30	-44.50 to 140.00	-58.57 to 120.41	-	Chandan (2008)
		50	-	-45.11 to 21.10	-22.82 to 59.07	Patel *et al*. (2010)
		18	-31.37 to 149.85	-48.60 to 137.68	-48.60 to 15.13	Asish and Pugalendhi (2012)
		15	-	20.36 to 30.89	6.63 to 37.61	Sharma *et al*. (2013)
		15	0.19 to 20.20	-4.12 to 6.45	-	Khalil and Hatem (2014)
		28	-	-55.00 to 34.43	-57.50 to 78.26	Jindal *et al.* (2015)
		30	-49.10 to 118.58	-54.45 to 112.50	-48.28 to 129.61	Rekha (2015)
14	Oleoresin (%)	30	-	-	-9.43 to 21.83	Prasath and Ponnuswami (2008)
		18	-12.90 to 4.09	-12.96 to 11.51	-21.62 to 6.31	Asish and Pugalendhi (2012)
		40	-51.46 to 42.86	-56.97 to 38.16	-46.85 to 62.77	Suryakumari *et al*. (2014)
		28	-	-45.14 to 49.52	-35.05 to 70.52	Jindal *et al.* (2015)
		30	-18.53 to 31.18	-27.77 to 28.41	-59.22 to 13.54	Rekha (2015)
15	Capsaicin (%)	Positive heterosis				Anandanayaki (1997), Tanki (1999), Hemavathy (2000), Doshi and Shukla (2000) and Sathiyamurthy (2002)

		10	-42.00 to 153.00	-	-	Zewdie *et al.* (2001)
		30	-	-	-53.57 to 202.38	Prasath and Ponnuswami (2008)
		50	-	-28.58 to 32.48	-31.66 to 10.94	Patel *et al*. (2010)
		3	-11.238 to 4.161	-17.80 to -0.49	-	Prajapati and Agalodia (2011)
		18	-27.47 to 26.87	-46.07 to 9.50	-70.00 to -4.34	Asish and Pugalendhi (2012)
		40	-49.06 to 222.73	-65.12 to 140.68	-57.38 to 32.79	Suryakumari *et al*. (2014)
		28	-	-41.75 to 71.75	-38.92 to 124.82	Jindal *et al.* (2015)
		30	-34.60 to 97.14	-36.21 to 94.37	-53.10 to 47.42	Rekha (2015)
16	Red carotenoids (%)	30	-47.62 to 50.66	-50.46 to 45.99	-50.12 to 49.54	Rekha (2015)
17	Yellow carotenoids (%)	30	-52.76 to 28.05	-61.37 to 10.60	-58.59 to 23.99	Rekha (2015)
18	Total colour value (ASTA units)	30	-	-	-53.09 to 33.03	Prasath and Ponnuswami (2008)
		18	-0.94 to 64.92	-10.32 to 8.04	-69.77 to 7.53	Asish and Pugalendhi (2012)
		40	-72.28 to 52.76	-77.82 to 249.31	-64.96 to 73.86	Suryakumari *et al*. (2014)
		28	-	-57.83 to 28.76	-58.75 to 36.19	Jindal *et al.* (2015)
		30	-50.78 to 57.22	-54.05 to 54.15	-52.08 to 47.73	Rekha (2015)

From the above review, it is observed that the degree and direction of heterosis for various characters varies in chilli. The negative heterosis for days to 50 per cent flowering indicated earliness in hybrids over their parents. For plant height, a majority of the reports suggest positive heterosis, however; negative heterosis for the trait suggesting dwarfness of the hybrids has also been reported. The fruit yield attributes *viz.,* fruit length, fruit diameter, number of fruits and fruit weight showed high range of heterosis, which was positive for dry fruit yield. In view of this the heterosis for component characters should also be considered in a breeding programme.

2.3 COMBINING ABILITY

The knowledge of the relative importance of additive and non-additive gene action is essential to a plant breeder for the development of an efficient hybridization programme (Dudley and Moll, 1969). In any hybridization programme, proper choice of parents based on their combining ability is a prerequisite to gain better heterotic effects. Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its crosses.

The concept of combining ability, originally developed in maize by Richey and Meyar (1925), is now extensively applied in all crop plants. However, Sprauge and Tatum (1942) defined the terms ‘general combining ability’ (GCA) and ‘specific combining ability’ (SCA) while working with maize. Combing ability analysis is a common tool used in breeding programme for testing the performance of parents in hybrid combinations and also for characterizing the nature and magnitude of gene action involved in the expression of quantitative traits because the ultimate objective in any crop improvement programme is to identify the best parent(s) and hybrid(s).

General Combining Ability is the average performance of a strain or genotype in a series of hybrid combinations and Specific Combining Ability is defined as “the performance of a parent in a specific cross or it refers to the deviation of a particular cross from the *gca”*. The general combing ability is

primarily due to additive effects of genes and specific combining ability due to non-additive effects of genes.

Griffing (1956), showed the relationship between various components of variance *viz.,* GCA and SCA variances. Thus, GCA variance is due to additive variance as well as inter-allelic interaction (additive x additive), whereas SCA variance is due to those of dominance and three epistatic variances (additive x dominance, dominance x additive, dominance x dominance interaction variances). Additive genetic variance (s) arises due to the allelic interaction of the segregating genes. The ratio of the GCA variance to SCA variance indicates the predominance of the additive or non-additive variance. Top crossing, line x tester, diallel and partial diallel crossing techniques are used to study the combining ability.

But a more precise estimate of GCA, SCA and other parameters can be estimated from Line x tester (L x T) mating design which is basically an extension of top cross analysis in which only one tester is used, while several testers are used in Line x Tester mating design (Kempthorne, 1957). Owing to more than one tester used, L x T design is the first simple design which provides both full-sib (FS) and half-sib (HS) relatives simultaneously and hence, L x T is referred to as FS / HS analysis.

The important advantage of this model is that, the estimates of specific combining ability (SCA) of each cross can be determined. L x T analysis involves hybridization between lines and broad based testers in one to one fashion. Generally, the lines (test genotypes) are used as females and testers are used as pollen or male parents.

A knowledge of GCA and SCA helps in choice of parents / hybrids and the nature of gene action as a basis for choosing an effective breeding methodology. The literature pertaining to combining ability and gene action governing different traits in chilli is summarized and presented in table 2.2.

Table 2.2: Review of literature on combining ability and gene action for various traits

Sl.No.	Characters	Materials used for the study	Combining ability		Gene action		References
			GCA	SCA	Additive	Non-Additive	
1	Plant height (cm)	4 x 5 Line x Tester	Significant	Highly significant	-	+	Ajjappalavara (2003)
		6 x 6 Diallel	Highly significant	Highly significant	+	+	Nandadevi *et al*. (2003)
		4 x 5 Line x Tester	Significant	Highly significant	-	+	Prabhudeva (2003)
		5 x 9 Line x Tester	-	-	+	+	Savitha (2004)
		3 x 15 Line x Tester	Significant	Significant	+	-	Jagadeesha and Wali (2005)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		15 x 3 Line x Tester	Significant	Significant	-	+	Kamble *et al.* (2009a)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		3 x 3 Line x Tester	Significant	Significant	+	+	Payakhapaab *et al.* (2012)
		5 x 5 Diallel	Significant	-	-	-	Rodrigues *et al*. (2012)
		5x5 Line x Tester	Significant	Significant	-	+	Chaudhary *et al.* (2013)
		6 x 6 Half diallel	Significant	-	-	+	Nsabiyera *et al.* (2013)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x 5 Line x Tester	-	-	-	+	Suryakumari *et al*. (2014)

		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
2	Plant spread (cm)	6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		3 x 3 Line x Tester	Highly significant	Highly significant	-	+	Payakhapaab *et al.* (2012)
		5 x 5 Diallel	Significant	Significant	+	+	Rodrigues *et al*. (2012)
		6 x 6 Half diallel	Significant	Significant	-	+	Nsabiyera *et al.* (2013)
		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	+	-	Rekha (2015)
3	Number of primary branches per plant	4 x 5 Line x Tester	Significant	Significant	-	+	Ajjappalavara (2003)
		6 x 6 Diallel	Highly significant	Highly significant	+	+	Nandadevi *et al*.(2003)
		4 x 5 Line X Tester	significant	Significant	-	+	Prabhudeva (2003)
		3 x 15 Line x Tester	Significant	Significant	-	+	Jagadeesha and Wali (2005)
		12 x 6 Line x Tester	-	-	-	+	Kumar (2005)
		5 x 9 Line x Tester	Significant	Significant	+	-	Saritha *et al.* (2005)
		4 x 12 Line x Tester	Significant	Significant	+	+	Singh and Chaudhary (2005b)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		6 x 6 Half diallel	Significant	Significant	-	+	Nsabiyera *et al.* (2013)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)

		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
4	Days to 50% flowering	4 x 5 Line x Tester	Significant	Significant	-	-	Ajjappalavara (2003)
		6 x 6 Diallel	Highly significant	Highly significant	-	+	Nandadevi *et al*. (2003)
		4 x 5 Line x Tester	Significant	Significant	-	+	Prabhudeva (2003)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		15 x 3 Line x Tester	Significant	Significant	-	+	Kamble *et al.* (2009a)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
5	Days to fruit maturity (Red)	6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		6 x 6 Half diallel	Significant	Significant	-	+	Nsabiyera *et al.* (2013)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		4 x 5 Line x Tester	Significant	High	+	+	Ajjappalavara (2003)

6	Number of fruits per plant	10 x 10 Diallel	-	-	+	-	Doshi (2003)
		6 x 6 Diallel	Highly significant	Highly significant	+	+	Nandadevi *et al*. (2003)
		4 x 5 Line x Tester	Significant	High	-	+	Prabhudeva (2003)
		3 x 15 Line x Tester	Significant	Significant	+	-	Jagadeesha and Wali (2005)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		15 x 3 Line x tester	Significant	Significant	-	+	Srivastava *et al*. (2005)
		7 x 7 Diallel	Significant	Significant	+	-	Geleta and Labuschagne (2006)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		15 x 3 Line x Tester	Significant	Significant	+	-	Kamble *et al.* (2009a)
		6 x 6 Diallel	-	Significant	+	-	Perez *et al.* (2009)
		5 x 5 Half diallel	Significant	-	+	-	Sitaresmi *et al.* (2010)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		12 x 12 Diallel	Significant	Significant	+	-	Pandey *et al.* (2012)
		3 x 3 Line x Tester	Significant	Significant	+	+	Payakhapaab *et al.* (2012)
		5 x 5 Diallel	Significant	Significant	+	+	Rodrigues *et al*. (2012)
		5x5 Line x Tester	Significant	Significant	-	+	Chaudhary *et al.* (2013)
		6 x 6 Half diallel	Significant	Significant	-	+	Nsabiyera *et al.* (2013)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Artur *et al.* (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Mendes *et al*. (2014)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)

		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
7	Fruit length (cm)	8 x 3 Line x Tester	-	Highly significant	+	+	Ahmed *et al.* (2003)
		4 x 5 Line x Tester	Significant	Significant	-	+	Ajjappalavara (2003)
		6 x 6 Diallel	Highly significant	Highly significant	+	-	Nandadevi *et al*. (2003)
		4 x 5 Line x Tester	Significant	High	-	+	Prabhudeva (2003)
		4 x 4 Line x Tester	-	-	-	+	Sabita and Baruah (2003)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		5 x 9 Line x Tester	Significant	Significant	-	+	Saritha *et al*. (2005)
		4 x 12 Line Tester	Significant	Significant	+	+	Singh and Chaudhary (2005b)
		15 x 3 Line x Tester	Significant	Significant	+	-	Srivastava *et al*. (2005)
		8 x 8 Diallel	Significant	Significant	+	+	Venkataramana *et al*.(2005)
		7 x 7 Diallel	Significant	Significant	+	-	Geleta and Labuschagne (2006)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		12 x 12 Diallel	Significant	Significant	+	-	Pandey *et al.* (2012)
		3 x 3 Line x Tester	Highly significant	Highly significant	-	-	Payakhapaab (2012)
		5 x 5 Diallel	Significant	Significant	+	+	Rodrigues *et al*. (2012)

		5 x 5 Line x Tester	Significant	Significant	-	+	Chaudhary *et al.* (2013)
		6 x 6 Half diallel	Significant	Significant	+	-	Nsabiyera *et al.* (2013)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Artur *et al.* (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Mendes *et al*. (2014)
		6 x 6 Diallel	Significant	Significant	+	-	Nascimento *et al.* (2014)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	+	-	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
8	Fruit diameter (cm)	4 x 5 Line x Tester	Significant	High	-	+	Ajjappalavara (2003)
		6 x 6 Diallel	Highly significant	Highly significant	+	-	Nandadevi *et al*. (2003)
		12 x 6 Line x Tester	Significant	-	-	+	Kumar (2005)
		4 x 12 Line Tester	Significant	Significant	+	+	Singh and Chaudhary (2005b)
		7 x 7 Diallel	Significant	Significant	+	-	Geleta and Labuschagne (2006)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		12 x 12 Diallel	Significant	Significant	-	+	Pandey *et al.* (2012)
		5 x 5 Diallel	Significant	Significant	+	+	Rodrigues *et al*. (2012)

		6 x 6 Half diallel	Significant	-	+	-	Nsabiyera *et al.* (2013)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Artur *et al.* (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Mendes *et al*. (2014)
		6 x 6 Diallel	Significant	Significant	+	-	Nascimento *et al.* (2014)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		12 x 12 Half diallel	Significant	Significant	+	-	Singh *et al.* (2014)
		8 x5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	+	-	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
9	Average dry fruit weight (g)	6 x2 Diallel	High	High	+	+	Jadhav and Dhumal (2001)
		4 x 5 Line x Tester	Significant	High	-	+	Prabhudeva (2003)
		3 x 15 Line x Tester	Significant	Significant	+	-	Jagadeesha and Wali (2005)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		7 x 7 Diallel	Significant	Significant	+	-	Geleta and Labuschagne (2006)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		15 x 3 Line x Tester	Significant	Significant	+	-	Kamble *et al.* (2009a)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		12 x 12 Diallel	Significant	Significant	+	-	Pandey *et al.* (2012)
		5 x 5 Diallel	Significant	-	+	-	Rodrigues *et al*. (2012)

		5x5 Line x Tester	Significant	Significant	+	_	Chaudhary *et al.* (2013)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Artur *et al.* (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Mendes *et al*. (2014)
		6 x 6 Diallel	Significant	-	+	-	Nascimento *et al.* (2014)
		12 x 12 Half diallel	Significant	Significant	+	-	Singh *et al.* (2014)
		6 x 5 Line x Tester	Significant	Significant	+	-	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
10	Fruit yield (g/plant)	5 x 9 Line x Tester	-	Significant	+	+	Savitha (2004)
		3 x 15 Line x Tester	Significant	Significant	+	-	Jagadeesha and Wali (2005)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		5 x 9 Line x Tester	Significant	Significant	+	+	Saritha *et al.* (2005)
		8 x 8 Diallel	Significant	Significant	+	+	Venkataramana *et al.* (2005)
		7 x 7 Diallel	Significant	Significant	+	-	Geleta and Labuschagne (2006)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		15 x 3 Line x Tester	Significant	Significant	+	-	Kamble *et al.* (2009a)
		6 x 6 Diallel	Significant	Significant	+	-	Perez *et al.* (2009)
		5 x 5 Half diallel	Significant	-	+	-	Sitaresmi *et al.* (2010)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		12 x 12 Diallel	Significant	Significant	+	-	Pandey *et al.* (2012)

		3 x 3 Line x Tester	Significant	Significant	+	+	Payakhapaab *et al.* (2012)
		5x5 Line x Tester	Significant	Significant	+	-	Chaudhary *et al.* (2013)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		5 x 5 Diallel	Significant	Significant	-	+	Artur *et al.* (2014)
		5 x 5 Diallel	Significant	Significant	+	-	Mendes *et al*. (2014)
		6 x 6 Diallel	Significant	Significant	+	-	Nascimento *et al.* (2014)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
11	Number of seeds per fruit	6 x6 Diallel	Significant	Significant	+	+	Nandadevi *et al.* (2003)
		12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		6 x6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		6 x 6 Diallel	-	Significant	+	-	Perez *et al.* (2009)
		6 x 6 Diallel	Significant	Significant	-	+	Hasanuzzaman *et al*. (2012)
		6 x 6 Half diallel	Significant	Significant	-	+	Nsabiyera *et al.* (2013)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		12 x 12 Half diallel	Significant	Significant	-	+	Singh *et al.* (2014)
		8 x 5 Line x Tester	-	Significant	-	+	Suryakumari *et al*. (2014)

		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
12	Seed weight (g)	12 x 6 Line x Tester	Significant	Significant	-	+	Kumar (2005)
		6 x 6 Diallel	-	Significant	+	-	Perez *et al.* (2009)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		6 x 5 Line x Tester	Significant	Significant	+	-	Rekha (2015)
		15 x 2 Line x Tester	Significant	Significant	-	+	Savitha *et al*. (2015)
13	Ascorbic acid (mg/100g)	12 x 12 Diallel	Significant	Significant	-	+	Pandey *et al.* (2012)
		6 x 6 Diallel	Significant	Significant	+	-	Khalil and Hatem (2014)
		6 x 6 Diallel	Significant	Significant	+	-	Nascimento *et al.* (2014)
		8 x 8 Half diallel	-	Significant	-	+	Jindal *et al.* (2015)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
14	Oleoresin (%)	3 x 14 Line x Tester	-	Significant	-	+	Rajinder *et al*. (2001)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		8 x 8 Half diallel	Significant	Significant	-	+	Jindal *et al.* (2015)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)

15	Capsaicin (%)	5 x 5 Diallel	Significant	Significant	+	-	Zewdie *et al*. (2001)
		6 x 6 Diallel	Significant	Significant	-	+	Prasath and Ponnuswami (2008)
		7 x 7 Diallel	Significant	Significant	-	+	Navhale *et al.* (2014b)
		8 x 5 Line x Tester	Significant	Significant	-	+	Suryakumari *et al*. (2014)
		8 x 8 Half diallel	-	Significant	-	+	Jindal *et al.* (2015)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
16	Red carotenoids (%)	6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
17	Yellow carotenoids (%)	6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)
18	Total colour value (ASTA units)	3 x 14 Line x Tester	-	Significant	-	+	Rajinder *et al*. (2001)
		6 x 6 Diallel	-	Significant	-	+	Nandadevi *et al.* (2003)
		6 x 6 Diallel	Significant	Significant	+	-	Prasath and Ponnuswami (2008)
		8 x 5 Line x Tester	-	-	+	-	Suryakumari *et al*. (2014)
		8 x 8 Half diallel	Significant	Significant	-	+	Jindal *et al.* (2015)
		6 x 5 Line x Tester	Significant	Significant	-	+	Rekha (2015)

'+' Predominance

From the above review, it is understood that both additive and non additive gene action plays an important role in inheritance of characters *viz.*, fruit length, fruit diameter, fruit weight, number of fruits per plant, seed yield and fruit yield per plant, but showed predominance of additive gene action. while, predominance of non-additive gene action was observed for plant height, plant spread, number of primary branches per plant, days to 50 per cent flowering, days to fruit maturity, number of seeds per fruit, vitamin C, oleoresin, capsaicin and total colour value in chilli. The yield is a complex character where a majority of workers have reported the predominance of SCA variance implying non-additive gene action.

CHAPTER III

MATERIAL AND METHODS

The present investigation on "Genetic analysis for yield, quality traits and plant ideotype in chilli (*Capsicum annuum* L.)" was carried out at Horticultural Research Station, Lam Farm, Guntur, Andhra Pradesh during *kharif*, 2013-14 and 2014-15 to estimate the heterosis, general combining ability (*gca*) of parents and specific combining ability (*sca*) of the crosses for yield and quality traits and to study the nature and magnitude of gene effects involved in the expression of yield, yield related traits, quality traits and plant ideotype in chilli. The details pertaining to the experimental location, materials used, materials generated and the methods followed are described below.

3.1 LOCATION, CLIMATE AND SOIL PROPERTIES OF THE EXPERIMENTAL SITE

Geographically, the site of the experiment is situated on 16^0.28' North latitude and 80^0.44' East longitude at an altitude of 31.5 m above mean sea level and falls under humid tropical climate. The soil of the experimental site is rich black cotton soil and has p^H of 8.4, EC of 0.16 m. mhos/cm and good moisture retentive capacity. The available nitrogen, phosphorus and potassium (NPK) contents were 200-250, 70-90 and 800-850 kg ha^{-1} respectively. The meteorological data during the period of investigation recorded at the Agricultural Meteorological Observatory Research Station, Lam is presented in Annexure I.

3.2 EXPERIMENTAL DETAILS

The investigation was carried out in two separate experiments *viz*.

3.2.1 Line x Tester analysis to estimate heterosis and combining ability studies for yield and quality traits in chilli

3.2.2 Generation mean analysis to study genetics of inheritance for yield, quality traits and plant ideotype in chilli.

3.2.1 LINE X TESTER ANALYSIS TO ESTIMATE HETEROSIS AND COMBINING ABILITY STUDIES FOR YIELD AND QUALITY TRAITS IN CHILLI

Nine female parents (lines) and six male parents (testers) selected from genetic material available at Horticultural Research Station, Lam, Guntur, A.P. were used to produce F_1 hybrids for further investigation. Details of parent materials used in the experiment are presented in Table 3.1 and Plate 1, 2 & 3.

3.2.1.1 Production of F_1 hybrids

Nine lines (LCA 504, LCA 615, LCA 446, LCA 466, LCA 442, LCA 654, LCA 607, LCA 655 and LCA 355) were crossed with six testers (G4, LCA 678, LCA 453, LCA 703-2, LCA 705-2 and LCA 315) during *kharif* 2013-14 and produced 54 F_1 hybrids. The fruits on female parents resulting from natural pollination were removed to avoid competition between hand crossed and natural crossed fruits for water and nutrients. Irrigation was given to induce healthy profuse flowering and pure white, mature flower buds which will open on next day morning were hand emasculated using forceps in the evening hours between 3.00 pm to 6.00 pm. Then they were covered to avoid natural pollen contamination by foreign pollen. The emasculated flowers were pollinated next day morning during anthesis time (8 am - 12 noon) by touching the stigma gently with pollen of dehisced anthers collected from the tester parents and the pollinated flowers were covered immediately. The pollinated flowers were then tagged indicating the details of parents and date of pollination. At maturity, red ripen fruits were harvested and dried for one week. Seeds extracted manually from the fruits, dried in shade, packed and stored for use in the ensuing season.

The parents (lines and testers) were maintained through selfing by covering mature flower buds destined to open next day for use in the ensuing season. The seeds were extracted from fruits resulted from selfing and stored.

The parental lines and generated F_1 hybrids served as the experimental material for evaluation in replicated yield trial to find out heterosis and combining ability status of the genotypes for yield and quality characters.

3.2.1.2 Evaluation of F_1s, parents along with standard checks for heterosis and combining ability

The 54 F_1 hybrids, their parents (15) were evaluated along with two commercial checks *i.e.* Indam-5 and Tejaswini during *kharif* 2014-15 in a Randomized Block Design with three replications. The plants of each genotype were planted in two rows (one row of 4 m length) at spacing of 75 cm x 30 cm. The crop was raised as per the recommended package of practices. Data on morphological, quantitative and biochemical characters were recorded from five randomly selected plants.

Design	:	Randomized Block Design with 3 replications
No. of treatments	:	71 (54 hybrids + 15 parents + 2 commercial checks Tejaswini and Indam-5)
Spacing	:	75 x 30 cm
Plot size	:	Two row plots (One row of 4 m length)
Season	:	*Late kharif*, 2014 -15
Location	:	HRS, Lam Farm, Guntur, A.P.

3.2.2 GENERATION MEAN ANALYSIS TO STUDY GENETICS OF INHERITANCE FOR YIELD, QUALITY TRAITS AND PLANT IDEOTYPE IN CHILLI.

3.2.2.1 Generation of F_1, BC_1, BC_2 and F_2 populations

Four better performing crosses (F_1s - LCA 710 x HC-28, LCA 712 x HC-28, LCA 712 x LCA 710 and LCA 764 x LCA 315) derived from parents which have contrasting characters for yield and plant ideotype were identified in chillies improvement scheme at HRS, Lam, Guntur, A.P. The selected F_1s and their maintained parents (P_1, P_2) were used to generate their F_2 (Selfing of F_1), BC_1 (F_1 x P_1), BC_2 (F_1 x P_2) seed material for respective 4 crosses. Details of parent materials used in this experiment are presented in Table 3.2 and Plate 4 & 5. The parents (P_1, P_2) of each cross were again crossed to generate F_1 seed and the parents (P_1, P_2) of each cross were also maintained through selfing for evaluating

in following season along with F_2, BC_1 and BC_2. Thus crossing, selfing and backcrossing programmes were done during *kharif*, 2013-14 to generate six generations for respective four crosses and were analyzed in generation mean analysis to study genetic inheritance of plant ideotype, yield and quality parameters in chilli.

3.2.2.2 Evaluation of P_1, P_2, F_1, F_2, BC_1 and BC_2 to study inheritance pattern of yield, yield components, quality parameters and plant ideotype in chilli

The four crosses along with their parents, F_2's, BC_1's and BC_2's were raised in a compact family block design with two replications during *kharif*, 2014-15. The parents and F_1s were planted in five rows (one row of 4 m length), F_2's in thirty rows and BC_1's / BC_2's in twenty rows were planted at a spacing of 75 cm x 30 cm. Thirteen plants were maintained in a single row and the crop was raised as per the recommended package of practices. Data on morphological, quantitative and biochemical characters were recorded.

Among the four crosses, the cross LCA 712 x HC-28 was selected to study the inheritance pattern of fruit bearing habit and fruit orientation in chilli as the parents involved in this cross have contrasting characters in respect to these traits. The parent LCA 712 is solitary bearing accession with pendent fruit position while HC-28 is the cluster bearing genotype with erect fruit position. The cross LCA 712 x LCA 710 was selected to study the inheritance pattern of branching habit in chilli as the parents involved in this cross have contrasting characters. The parent LCA 712 is intermediate branching type while LCA 710 is dense branching type. The populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of these crosses were raised in a uniformly fertile field and the data on these three characters were recorded by counting the plants for particular character. The plants were grouped into solitary *vs* clustering for fruit bearing habit, pendent *vs* erect for fruit position and intermediate *vs* dense for branching habit. The data were analysed for the best fit with standard expected ratios using chi-square test.

3.3 OBSERVATIONS RECORDED

Data on the following qualitative, quantitative and biochemical traits was recorded during the course of the experimentation. The observations were recorded on five randomly selected plants in parents and F_1s and on forty plants in F_2 progeny and on fifteen plants in B_1 and B_2 cross progeny for each replication.

3.3.1 Morphological characters

Qualitative characters were observed according to the descriptors given by National Bureau of Plant Genetic Resources (NBPGR), Pusa Campus, New Delhi, India.

3.3.1.1 Plant growth habit

Plant growth habit was recorded at fruit maturity stage and classified as prostrate (3), intermediate (5) and erect (7).

3.3.1.2 Branching habit

Branching habit was recorded when plants have ceased their growth and classified as sparse, intermediate and dense.

3.3.1.3 Fruit position

Fruit position was noted as pendant (3), semi pendent (5) and erect (7) fruit and it was recorded at mature fruit stage.

3.3.1.4 Fruit bearing habit

Fruit bearing habit was observed as solitary and cluster and it was recorded at mature fruit stage.

3.3.1.5 Fruit shape

In *Capsicum* genus the fruit shape was classified as elongate (1), almost round (2), triangular (3), companulate (4) and blocky (5).

3.3.1.6 Fruit colour at mature green stage

The fruit color of the each genotype at mature green stage was noted as green, parrot green and dark green.

Among the morphological traits, only three characters branching habit, fruit position and fruit bearing habit were studied for generation mean analysis.

3.3.2. Quantitative traits

3.3.2.1 Plant height (cm)

Height of the plant was measured from the ground level to tip of the plant in centimeters at the time of harvest.

3.3.2.2 Plant spread (cm)

The spread of the plant at final harvest in N-S and E-W directions was measured in centimeters and their mean was recorded as plant spread.

3.3.2.3 Number of primary branches per plant

The no. of primary branches arising from the main stem at final harvest was counted.

3.3.2.4 Days to 50 per cent flowering

Number of days taken from the date of transplanting to 50 per cent of plants in a plot start flowering was recorded.

3.3.2.5 Days to fruit maturity (ripe)

Number of days taken from the date of fruit set to red ripe fruit maturity stage was recorded.

3.3.2.6 Number of fruits per plant

The total no. of fruits per plant at harvest on five randomly selected plants was counted and the mean was calculated.

3.3.2.7 Fruit length (cm)

Average length of five fruits collected from five randomly selected plants was measured from base to the tip of the fruit and expressed in centimeters.

3.3.2.8 Fruit diameter (cm)

Average diameter of five fruits from five randomly selected plants was measured at the top shoulder and expressed in centimeters.

3.3.2.9 Average dry fruit weight (g)

Average fruit weight of five dry fruits from five randomly selected plants was recorded in grams.

3.3.2.10 Fruit yield (g/plant)

Mature fruits harvested from five randomly selected plants were dried and the mean weight in grams was recorded as dry fruit yield per plant.

3.3.2.11 Number of seeds per fruit

The number of seeds from five fruits collected on five randomly selected plants was counted and average was worked out.

3.3.2.12 Seed weight (g/1000 seed)

Weight of 1000 seeds extracted from randomly selected fruits was recorded in grams.

3.3.3 Biochemical traits

3.3.3.1 Ascorbic acid (mg /100g)

Ascorbic acid content of mature green fruits was estimated by volumetric method described by Sadasivam and Balasubramanian (1987).

Dye solution:

42 mg of sodium bicarbonate was weighed into a 200 ml volumetric flask in distilled water and 52 mg of 2-6 dichlorophenol indophenol was dissolved in it and then the volume was made up with distilled water.

Standard stock solution:

Stock solution was prepared by dissolving 100 mg ascorbic acid in 100 ml of 4% oxalic acid solution. 10 ml of stock solution was diluted to 100 ml with 4% oxalic acid to get the working standard of 100 mg per ml.

Procedure:

5 ml of the working standard solution was pipetted into a 100 ml of conical flask to which 10 ml of 4% oxalic acid was added. The contents were titrated against the dye (V_1ml) to get a pink end point which persisted for a few minutes. The chilli sample (5 g) was extracted in 4% oxalic acid and the volume was made up to 100 ml and the contents were centrifuged. 5 ml of this supernatant was pipetted out, to which 10 ml of 4 per cent oxalic acid was added and titrated against the dye (V_2 ml). The ascorbic acid content was calculated using the formula given below.

Amount of ascorbic acid (mg/100 g) sample

$$= \frac{0.5 \text{ mg}}{V_1} \times \frac{V_2}{5 \text{ ml}} \times \frac{100 \text{ ml}}{\text{Wt. of the sample}} \times 100$$

3.3.3.2 Oleoresin (%)

The oleoresin content was estimated as per the procedure given by Ranganna (1986).

Principle: Acetone being an organic solvent, dissolves whole oleoresin content of chillies when passed through chilli powder. Acetone can be evaporated after dissolving by mild heating at 15^{o}C for 15 min to separate oleoresin that can be quantified.

Procedure:

Finely mashed 25g chilli powder was transferred to a glass column, which was plugged by cotton plug on its narrow end. A thin layer of cotton was placed over chilli powder in the glass column and 25 ml of acetone was added. After all the acetone was decanted, 25 ml acetone was added each time till a total of 250 ml acetone was added to the contents. After decantatation, the resulting red coloured liquid in beaker contains all the principle constituents of chilli. The collected filtrate was transferred to a 250 ml volumetric flask and the volume was made up with acetone.

The chilli extract was transferred to a 250 ml beaker of known weight (W_I g) and was kept in water bath at 50-60^oC for 15-30 minutes so that acetone gets evaporated. Then, weight of the beaker along with contents was recorded as W_2 g. The weight of the oleoresin content in the 25 g chilli powder was calculated and expressed in percentage using the given formula

$$\text{Oleoresin content (\%)} = \frac{W_2 - W_1}{\text{Weight of sample}} \times 100$$

3.3.3.3 Capsaicin (%)

The capsaicin content of fruits was estimated by colorimetric method described by Balasubramanian *et al.* (1982).

Principle: The phenolic group in capsaicin reduces phosphomolybdic acid to lower acids of molybdenum. The resulting component is blue in colour and is read at 650nm. The color intensity is directly proportional to the concentration of capsaicin.

Chemicals:

- 0.4% sodium hydroxide
- 3% phosphomolybdic acid
- Dry acetone (25g anhydrous sodium sulphate added to 500ml of acetone at least one day before use)
- Stock standard capsaicin solution (50mg capsaicin was dissolved in 50ml of 0.4% NaOH solution (1000µg/ ml)). Working standard

(10ml of the stock standard was diluted to 50ml with 0.4% NaOH solution (200µg/ ml)).

Procedure:

0.5g dry chilli powder was weighed into glass-stoppard test tube; 10ml dry acetone was added to it and kept overnight for extraction. Next day, the samples were centrifuged at 10000 rpm for 10min to get clear supernatant. 1ml of the supernatant was taken into a test tube and evaporated to dryness in a hot water bath. Then, the residue was dissolved in 5ml of 0.4% of NaOH solution and 3ml of 3% phosphomolybdic acid was added. The contents were shaken and left undisturbed for 1hr. After 1hr, the solution was quickly filtered into centrifuge tubes to remove any floating debris, and then centrifuged at 5000 rpm for 15min. The clear blue coloured solution was directly transferred into the cuvette and absorbance was read at 650nm along with a reagent blank.

Preparation of standard graph: A standard graph was prepared using 0-200µg pure capsaicin. Simultaneously 0.2, 0.4, 0.6, 0.8 and 1ml of working standard solution were taken into new test tubes and proceeded as mentioned above.

Per cent capsaicin was calculated using the formula mentioned below

$$\text{Capsaicin content (\%)} = \frac{\text{µg capsaicin X 100 X 100}}{1000000 \text{ X } 1 \text{ X } 0.5}$$

3.3.3.4 Determination of red and yellow carotenoids in chilli powder

All the carotenoid pigments present in hot pepper have chromophore properties that allow their grouping in two isochromic families *i.e.* red (R) and yellow (Y). The R fraction contains pigments capsanthin, capsorubin and capsanthin-5, 6-epoxide, whereas Y fraction contains remaining pigments such as zeaxanthin, violaxanthin, antheraxanthin, β-cryptoxanthin, β-carotene and cucurbitaxanthin A, which act as precursors of the former (Minguez and Perez, 1998). Yellow and red fractions were determined using UV-visible spectrophotometric measurements at two characteristic wavelengths and

application of Lambert-Beer law for multi-component mixtures according to procedure developed by Hornero-Mendez and Minguez-Mosquera (2001).

Procedure:

Dried fruits were ground into a fine powder and 100mg of powder was extracted four times with 25ml acetone until the complete exhaustion of the colour. The extract was filtered and transferred to 50ml volumetric flask and the volume was made up with acetone. The samples absorbance was read at two wavelengths *i.e.,* 472 and 508nm using acetone as blank. The red and yellow fractions were calculated using the following formulae.

$$C^R\ (\mu g/ml) = \frac{A_{508} \times 2144.0 - A_{472} \times 403.3}{270.9}$$

$$C^Y\ (\mu g/ml) = \frac{A_{472} \times 1724.3 - A_{508} \times 2450.1}{270.9}$$

$$\text{Total colour} = C^R + C^Y$$

µg/ml values were converted into percentage on dry weight basis.

3.3.3.5 Total color value (ASTA units)

Total extractable color of fruits measured in ASTA (American Spice Trade Association) units was determined using the procedure outlined by ASTA (1986).

Procedure: 100mg of sieved fine chilli powder was weighed into a volumetric flask. Acetone was added and flask was closed tightly with stopper. The contents were kept for 16hr at room temperature in dark and shaken intermittently. Solution was filtered using Whatman filter paper and final volume was made up to 100ml. Absorbance of final extract was read at 460nm using acetone as blank.

ASTA color units were calculated as per the formula given below,

$$\text{ASTA} = \frac{\text{Absorbance at 460nm X 16.4}}{\text{Weight of sample in g}}$$

3.4 STATISTICAL PROCEDURES

The data recorded on different traits were subjected to the following statistical analyses.

3.4.1 Line x Tester analysis

This analysis was carried out to know the combining ability and magnitude of heterosis among the chilli lines. To derive the above information, line × tester analysis developed by Kempthorne (1957) was followed.

3.4.1.1 Analysis of variance (ANOVA)

Variance is the measure of variability and is defined as the average of the squared deviation from mean. There are two main objectives due to analysis of variance. Firstly, it helps in sorting out the variance due to different sources and secondly it helps to provide the basis for test of significance (Singh and Chaudhary, 1999).

i) ANOVA for RBD

Data were analyzed by the method outlined by Panse and Sukhatme (1985) using the mean values of random plants in each replication from all genotypes to find out the significance of genotypes effect.

$$Y_{ij} = m + g_i + v_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation of i^{th} genotype in j^{th} replication

m = General mean

g_i = Effect of i^{th} genotype

v_j = Effect of j^{th} replication

e_{ij} = Random error

Table 3.3: ANOVA for RBD analysis:

Sources of variation	Df	MSS	F ratio
Replications	r-1	rMSS	rMSS/eMSS
Treatments	t-1	tMSS	tMSS/eMSS
Error	(r-1) (t-1)	eMSS	
Total	(rt-1)		

Where,

r = Number of replications

t = Number of genotypes or treatments

e = Error

df = degrees of freedom

MSS = Mean sum of squares

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' test (Fisher and Yates, 1967).

ii) ANOVA for Line x Tester Analysis

The data recorded on the material generated as per Line x Tester model of Kempthorne (1957) were subjected to analysis of variance as per the Line x Tester model given by Singh and Chaudhary (1999).

Table 3.4: ANOVA for Line x Tester Analysis

S. No	Source of variation	df	MSS	F ratio
1.	Replications	(r-1)	rMSS	rMSS/eMSS
2.	Treatments	(t-1)	tMSS	tMSS/eMSS
a.	Parents	(f + m-1)	pMSS	pMSS/eMSS
i)	Females (lines)	(f-1)	fMSS	fMSS/eMSS
ii)	Males (testers)	(m-1)	mMSS	mMSS/eMSS
iii)	Females Vs Males	1	fmMSS	fmMSS/eMSS
b.	Hybrids	(fm-1)	hMSS	hMSS/eMSS
c.	Parent Vs Hybrids	1	phMSS	phMSS/eMSS
3.	Error	(t-1)(r-1)	eMSS	
4.	Total	(fmr-1)		

Where

r = number of replications

t = number of treatments

p = number of parents

f = number of females

m = number of males

h = number of hybrids

e = error

MSS = mean sum of squares

The significant differences among the genotypes and replications were verified by applying 'F' test (Fisher and Yates, 1967).

3.4.1.2 Estimation of heterosis

The mean values of hybrids were used for the calculation of heterosis. The per cent heterosis of the derived F_1 over mid parent value (Average heterosis, AH), better parent (Heterobeltiosis, HB) and standard check (Standard heterosis, SH) was calculated using the following formulae.

a) Average/Relative/Mid parent heterosis (%) = $\frac{\bar{\bar{F}}_1 - \overline{MP}}{\overline{MP}} x100$

Where,

$\bar{\bar{F}}_1$ = Mean of F_1

$\overline{MP}$ = Mean value of mid parent = $\frac{P1 + P2}{2}$

b) Heterobeltiosis (%) = $\frac{\bar{\bar{F}}_1 - \overline{BP}}{\overline{BP}} x100$

Where,

$\overline{BP}$ = Mean of better parent

Note: For the characters like days to 50% flowering, days to fruiting *etc.* earliness is desirable so the early parents are taken as better parents.

c) Standard heterosis (%) = $\frac{\overline{F1} - \overline{SC}}{\overline{SC}}$

Where,

$\overline{SC}$ = Mean value of standard check

Test of significance for heterosis:

The significance of the difference between any two estimates of heterosis was tested by comparing them with critical difference (CD) values obtained separately for MP, BP and SC employing the formula given below.

CD = SE x 't'

SE = Standard error

CD = Critical difference

t = 't' table value at respective error degrees of freedom at desired level of probability.

To compute the standard error (SE) of estimates for heterosis, the mean sum of squares due to error (eMSS) from RBD analysis was used.

SE for mid parent (MP) $= \frac{\sqrt{3 \times eMSS}}{2r}$

SE for Better parent (BP) and standard check (SC) $= \frac{\sqrt{2 \times eMSS}}{r}$

3.4.1.3 Combining ability analysis

The variation among the hybrids was partitioned into genetic components attributable to general combining ability (GCA) and specific combining ability (SCA) following the method suggested by Kempthorne (1957). The model for analysis of variance is given below.

Table 3.5: ANOVA for combining ability

Source	Degrees of freedom	Mean sum of squares	Expectations
Replication	(r-1)	-	-
Hybrids	(lt-1)	-	-
Lines	(l-1)	M_1	σ^2e+ r Cov(FS) - 2Cov(HS) + rt [Cov(HS)]
Testers	(t-1)	M_2	σ^2e + r Cov(FS) - 2Cov(HS) + rl [Cov(HS)]
Line ×tester	(l-1) (t-1)	M_3	σ^2e + r Cov(FS) - 2Cov(HS)]
Error	(r-1) (lt-1)	M_4	σ^2e

Where,

r = Number of replications

l	=	Number of lines (females)
t	=	Number of testers (males)
Cov (HS)	=	Covariance of half sibs
Cov (FS)	=	Covariance of full sibs
M_1	=	Mean sum of squares due to lines (females)
M_2	=	Mean sum of squares due to testers (males)
M_3	=	Mean sum of squares due to line x tester
M_4	=	Mean sum of squares due to error
$\sigma^2 e$	=	Error variance

Covariance of full sibs and covariance of half sibs were estimated by using the formula (Kempthorne, 1957) given below:

$$\text{Cov (HS)} = \frac{M_1 + M_2 - 2M_3}{r\,(l+t)}$$

$$\text{Cov (FS)} = \frac{1}{3r}\,[M_1 + M_2 + M_3 - 3M_4 + 6r\ \text{Cov (HS)} - r\,(l+t)\ \text{Cov (HS)}]$$

3.4.1.3.1 Estimation of variance

The GCA and SCA variances were expressed in terms of covariances of full sibs (FS) and half sibs (HS).

$\sigma^2 gca$	=	Cov (HS)
$\sigma^2 sca$	=	Cov (FS) – 2 Cov (HS)
GCA variance for lines	=	Cov (HS) for lines = $\frac{M_1 - M_3}{rt}$
GCA variance for testers	=	Cov (HS) for testers = $\frac{M_2 - M_3}{rl}$
SCA variance for hybrids	=	$\frac{M_3 - M_4}{r}$

3.4.1.3.2 Estimation of combining ability effects

The additive model used to analyze the GCA and SCA effects is given below.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + e_{ijk}$$

Y_{ijk} = Any character measured of the cross (i x j) in the k^{th} replication

μ = Population mean

g_i = *gca* effect of i^{th} (line) parent

g_j = *gca* effect of j^{th} (tester) parent

s_{ij} = *sca* effect of (i x j)th cross

e_{ijk} = Error associated with observation ijk

i = Number of lines (females)

j = Number of testers (males)

k = Number of replications

The population mean was calculated by the following formulae

$$\text{Population mean } (\mu) = \frac{X_{...}}{ltr}$$

Where,

X… = Total number of hybrid combinations over all replications

The individual effects were estimated as indicated below.

A) General combining ability effect (*gca*) for lines

$$\text{Lines: } g_i = \frac{X_{i...}}{tr} - \frac{X_{...}}{ltr}$$

B) General combining ability effect (*gca*) for testers

$$\text{Testers: } g_j = \frac{X_{j...}}{lr} - \frac{X_{...}}{ltr}$$

C) Specific combining ability effect (*sca*) for hybrids

$$S_{ij} = \frac{X_{ij...}}{r} - \frac{X_{i...}}{tr} - \frac{X_{j...}}{lr} - \frac{X_{...}}{ltr}$$

Where,

X… = Total number of hybrid combinations over all replications

$X_{i...}$ = Total of i^{th} female parent over all male parents and replications

$X_{j...}$ = Total of j^{th} male parent over all female parents and replications

$X_{ij...}$ = Total of ij_{th} combinations over all replications

g_i = *gca* of i^{th} line

g_j = *gca* of j^{th} tester

S_{ij} = *sca* effects of i x j crosses

r = Number of replications

l = Number of lines

t = Number of testers

3.4.1.3.3 Standard errors for combining ability effects

The standard error (SE) and critical difference (CD) pertaining to the *gca* effects of male and female parents and *sca* effects of different combinations were calculated as follows.

i) SE (*gca* for line) = $\frac{\sqrt{M_4}}{tr}$

ii) SE (*gca* for tester) = $\frac{\sqrt{M_4}}{lr}$

iii) SE (*sca* effect) = $\frac{\sqrt{M_4}}{r}$

Where,

M_4 = Mean sum of squares due to error (eMSS)

r = Replication

l = Lines

t = Testers

The critical differences were calculated by multiplying the standard errors with table *t* value at 5 and 1 per cent levels of probabilities for error degrees of freedom

Critical difference (CD) = SE x *t* value

3.4.1.3.4 Proportional contribution of lines, testers and their interactions

a) Contribution of lines (%) = $\frac{\text{SS (Lines)}}{\text{SS (Crosses)}} \times 100$

b) Contribution of testers (%) = $\frac{\text{SS (Testers)}}{\text{SS (Crosses)}} \times 100$

c) Contribution of Line x Tester = $\frac{\text{SS (Line} \times \text{Tester)}}{\text{SS (Crosses)}} \times 100$

Where,

SS = Sum of squares

3.4.2. GENERATION MEAN ANALYSIS

The concept of Generation Mean Analysis (GMA) was developed by Hayman (1958) and Jinks and Hayman (1958) for the estimation of genetic components of variation. Since this technique involves six different generations *viz.*, parents (P_1 and P_2), their F_1, F_2 and back crosses (B_1 and B_2).

The means were computed for each generation of P_1, P_2, F_1, F_2, B_1 and B_2 for each cross over three replications. The variance and corresponding standard errors of the means were computed from the deviations of the individual values from the pooled mean for each of the generation in each cross.

3.4.2.1 Computation of Generation Means

Means of various generations were calculated from individual plant data as:

$$X = \Sigma x_i / n$$

Where,

X = Generation mean,

Σx_i = Grand total,

X_i = i^{th} observation in a particular generation, and

n = Number of plants

3.4.2.2 Estimation of Variance of Generation Means (V_X)

The generation means were subjected to sampling variation which can be estimated by normal statistical procedure. The estimate of variance of generation means (V_X) was obtained by dividing the variance within generation (V_X):

$$V_X = V_X/n$$

Where,

V_X (variance of the generation mean) = $1/ (n – 1) [\Sigma x_i^2 – (\Sigma x_i)^2/n]$

x_i = i^{th} observation of a population and

n = number of observations within generation

The value thus obtained was used for further analysis.

3.4.2.3 Scaling Tests

3.4.2.3.1 Simple scaling tests

The test which provides information regarding presence / absence of gene interaction is termed as scaling test. The test of adequacy of scales is important because in most of the cases the estimation of additive and dominance components of variance is made assuming the absence of gene interactions. Mather (1949), and Hayman and Mather (1955) gave four scaling tests.

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1}$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2}$$

Where,

$\overline{P}_1, \overline{P}_2, \overline{F}_1, \overline{F}_2, \overline{B}_1$ and $\overline{B}_2$ are means of different generations over the replications. The deviation of these scaling tests from zero was tested using the respective standard errors. The deviations from zero of any of these quantities indicated the inadequacy of additive-dominance model.

The variances of the quantities A, B, C and D were calculated from respective variances of different generations as follows:

$$V_A = 4V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})$$

$$V_B = 4V(\overline{B_2}) + V(\overline{P_2}) + V(\overline{F_1})$$

$$V_C = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

$$V_D = 4V(\overline{F_2}) + V(\overline{B_1}) + V(\overline{B_2})$$

Where,

V_A, V_B, V_C and V_D are the variances of A, B, C and D; $V\overline{P_1}, V\overline{P_2}, V\overline{F_1}, V\overline{F_2}, V\overline{B_1}$ and $V\overline{B_2}$ are the variances of P_1, P_2, F_1, F_2, B_1 and B_2 generation means, respectively.

The standard error of A, B, C and D were worked out by taking the square root of respective variances.

$$\text{S.E. A} = \sqrt{VA}$$

$$\text{S.E. B} = \sqrt{VB}$$

$$\text{S.E. C} = \sqrt{VC}$$

$$\text{S.E. D} = \sqrt{VD}$$

The *t* values are calculated by dividing the scale effects of A, B, C and D by their respective standard error.

t cal for A-test = Scale A / S.E. A

t cal for B-test = Scale B / S.E. B

t cal for C-test = Scale C / S.E. C

t cal for D-test = Scale D/ S.E. D

The calculated *t* values of these four tests are compared against 1.96 and 2.58 which are the table values of *t* at 5 per cent and 1 per cent level of significance respectively. If the *t* calculated value of these scales is higher than 1.96, it is considered significant and *vice versa*. The significance of any scaling test indicates the presence of epistasis. The significant of A and B

tests indicates the presence of all three types of epistatic interactions *viz.*, additive × additive [*i*], additive × dominance [*j*] and dominance × dominance [*l*], the significance of C scaling test reveals the presence of dominance × dominance [*l*] type of interaction, the significance of D scaling test indicates the presence of additive × additive [*i*] type of gene interaction whereas significance of both C and D scales indicates presence of additive × additive [*i*] and dominance × dominance [*l*] types of non-allelic gene interactions.

3.4.2.3.2 Joint scaling test

The main drawback of simple scaling tests is that out of six generations only three or four are included in the test at a time. In order to overcome this problem another test, known as joint scale test has been developed. Estimation of various gene effects and test of fitness of appropriate genetic model was done according to joint scaling test of Cavalli (1952), as described in detail by Mather and Jinks (1982). This test permits any combination of the six populations at a time. This test also provides estimates of three genetic parameters or gene effects *viz.* mean (*m*), additive effects (*d*) and dominance effects (*h*).

3.4.2.4 Models of generation mean analysis

Based on the presence or absence of non-allelic interactions or epistasis there are two models *viz.* three parameter model and six parameter model are followed. Estimation of gene effects, variances and chi-square test of goodness of fit were carried out, using three-parameter and six-parameter models.

3.4.2.4.1Three parameter model (additive-dominance model)

This model was proposed by Jinks and Jones (1958) to estimate gene effects when absence of epistasis. The following gene effects were estimated.

m = Inbred population mean = $1/2P_1+1/2P_2+4F_2-2B_1-2B_2$

[d] = additive gene effects = $1/2\ P_1-1/2P_2$

[h] = dominance gene effects = $6B_1+6B_2-8F_2-F_1-3/2P_1-3/2P_2$

The variances for these estimates are calculated as follows.

V_m = $1/4VP_1+1/4VP_2+16VF_2+4VB_1+4VB_2$

V_d = $1/4VP_1+1/4VP_2$

V_h = $36VB_1+36VB_2+64VF_2+VF_1+9/4VP_1+9/4VP_2$

3.4.2.4.2 Six parameter model (digenic interaction or epistatic model)

The six parameter model was first suggested by Hayman (1958) for estimation of various genetic components from the generation means. This method is used when non-allelic interactions are present. The analysis of this model is based on six generations *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 and six parameters are obtained. These parameters are mean (*m*), additive gene effects (*d*), dominance gene effects (*h*) and three types of non-allelic gene interactions *viz.*, additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*).

m = mean effects $= \overline{F}_2$

d = additive effects $= \overline{B}_1 - \overline{B}_2$

h = dominance effects $= \overline{F}_1 - 4\overline{F}_2 - (1/2)\overline{P}_1 - (1/2)\overline{P}_2 + 2\overline{B}_1 + 2\overline{B}_2$

i = additive x additive gene interaction $= 2\overline{B}_1 + 2\overline{B}_2 - 4\overline{F}_2$

j = additive x dominance gene interaction $= \overline{B}_1 - (1/2)\overline{P}_1 - \overline{B}_2 + (1/2)\overline{P}_2$

l = dominance x dominance gene interaction $= \overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$

Where,

$\overline{P}_1, \overline{P}_2, \overline{F}_1, \overline{F}_2, \overline{B}_1$ and $\overline{B}_2$ are mean values of P_1, P_2, F_1, F_2, B_1 and B_2 generations, respectively.

The variances for these estimates are calculated as follows.

$$V_m = V(\bar{F}_2)$$

$$V_d = V(\bar{B}_1) + V(\bar{B}_2)$$

$$V_h = V(\bar{F}_1) + 16V(\bar{F}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2) + 4V(\bar{B}_1) + 4V(\bar{B}_2)$$

$$V_i = 4V(\bar{B}_1) + 4V(\bar{B}_2) + 16V(\bar{F}_2)$$

$$V_j = V(\bar{B}_1) + \frac{1}{4}V(\bar{P}_1) + V(\bar{B}_2) + \frac{1}{4}V(\bar{P}_2)$$

$$V_l = V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)$$

$V(P_1), V(P_2), V(F_1), V(F_2), V(B_1)$ and $V(B_2)$ are the variance of P_1, P_2, F_1, F_2, B_1 and B_2 generations, respectively.

The genetic expectation of different generation means used in the present study for the estimation of various gene effects in the presence of digenic interactions, were as follow:

For three parameter model

$P_1 = m + d$

$P_2 = m - d$

$F_1 = m + h$

$F_2 = m + ½\ h$

$B_1 = m + ½\ h + ½\ d$

$B_2 = m + ½\ h - ½\ d$

For six-parameter model

$P_1 = m + d + i$

$P_2 = m - d + i$

$F_1 = m + h + l$

$F_2 = m + ½\ h + 1/4l$

$B_1 = m + ½\ d + ½\ h + 1/4i + 1/4j + 1/4l$

$B_2 = m - ½\ d + ½\ h + 1/4i - 1/4j + 1/4l$

3.4.2.5 Test of significance of various gene effects

The test of significance of the gene effects is tested with the help of *t* value. First standard error (S.E.) is worked out for each component separately by taking the square root of the variance of respective component.

The standard error of each of the gene effects was estimated as follows

S.E (*m*) = $\sqrt{Vm}$

S.E (*d*) = $\sqrt{Vd}$

S.E (*h*) = $\sqrt{Vh}$

S.E (*i*) = $\sqrt{Vi}$

S.E (*j*) = $\sqrt{Vj}$

S.E (*l*) = $\sqrt{Vl}$

Then the *t* value is calculated for each component by dividing the gene effect of respective components by their S.E.

The *t* values were worked out using following formulae

t(*m*) = m / S.E (*m*)

t(*d*) = d / S.E (*d*)

t(*h*) = h / S.E (*h*)

t(*i*) = i / S.E (*i*)

t(*j*) = j / S.E (*j*)

t(*l*) = l / S.E (*l*)

The calculated value of *t* is compared with 1.96, which is the table value of *t* at 5 per cent level of significance. If the calculated value greater than 1.96, it is considered significant and vice versa.

The statistical analysis was carried out by using 'Windostat' software programme. The programme first tries to fit *m*, *d* and *h* parameter model and deletes any parameter whose *t* value is less than 2.0 and thereafter it tests the model significance by Chi-square test and if this test is significant then the programme fit six-parameter model (*m, d, h, i, j* and *l*) and does a step

down for non significant parameters. When all the parameters are significant then it computes Chi-square for joint scaling. The significance of Chi-square were tested at '6-p' degree of freedom where 'p' denotes the number of significant parameter. Thus best fit model was indentified with minimum non-significant value of Chi- square and with maximum number of significant parameter as suggested by Mather and Jinks (1982).

3.4.2.6 Chi-square test

χ^2 test was applied for testing the deviation of an observed segregation for theoretical observation. Chi-square was calculated using the formula.

$$\chi^2 = \frac{\Sigma(O-E)^2}{E}$$

Where,

O = Observed frequency

E = Expected frequency

$\sum$ = Summation of the data

If the calculated values of χ^2 is significant at 5 per cent level of significance, we can say that the fit is poor, one or more observed frequencies are not in accordance with the hypotheses assumed and *vice versa*. So, it is also known as goodness of fit. The degree of freedom (df) in χ^2 test is (n-1).

Where n = number of classes.

Table 3.1: Salient features of parents used in Line x Tester analysis of chilli

S.No	Parents	Features
Lines		
1	LCA-504	Drought resistant, highly pungent
2	LCA-615	High yielding line with parrot green fruits
3	LCA-446	Bold pod, high colour and oleoresin
4	LCA-466	Bold and long pod, high colour and oleoresin
5	LCA-442	Bold and long pod, high colour and mild pungent
6	LCA-654	Medium bold, shiny fruit surface, light green in colour
7	LCA-607	Light green pod, profuse branching
8	LCA-655	Dual purpose variety, bold light green pod
9	LCA-355	High colour with wrinkled surface
Testers		
1	G4	Dark green (olive green) fruits, virus resistant
2	LCA-678	More primary branches, semi erect plant habit
3	LCA-453	Bold pod, erect growth habit
4	LCA-703-2	Virus resistant, dark green fruits
5	LCA-705-2	More no. of fruits, shiny dry pod
6	LCA-315	Virus resistant, fruits are long and dark green

Checks

S. No.	Check name	Source
1	Indam-5	Indo-American Hybrid Seeds (India) Pvt.Ltd. (IAHS)
2	Tejaswini	Maharashta Hybrid Seeds Co.Ltd. (MAHYCO)

Table 3.2: Salient features of five parents involved in four crosses used in generation mean analysis of chilli

S. No	**Crosses**	
1	LCA-710 x HC-28	
2	LCA-712 x HC-28	
3	LCA-712 x LCA-710	
4	LCA-764 x LCA-315	
S. No.	**Parents**	**Features**
1	LCA-710	Erect but dwarf plant, cluster and pendent bearing habit
2	HC-28	Erect plant with two or three primary branches, cluster and erect bearing habit
3	LCA-712	High yielding line, more no. of fruits, solitary and pendent fruit bearing
4	LCA-764	Dense branching habit, solitary and pendent fruit bearing
5	LCA-315	Virus resistant, fruits are long and dark green

Chapter IV

RESULTS AND DISCUSSION

The information on nature and magnitude of generation means, heterosis and gene action for yield, its components and quality characters is a prerequisite for the development of high yielding and better quality cultivars. Besides the presence of additive [*d*] and dominance [*h*] gene effects, estimation of their relative magnitudes and types of epistasis is essential in adopting an appropriate breeding methodology to evolve disease resistant and horticulturally desirable pure line varieties/hybrids in chilli.

In view of limited studies to ascertain the nature and magnitude of gene effects using generation mean analysis, the present investigation entitled "Genetic analysis for yield, quality traits and plant ideotype in chilli (*Capsicum annuum* L.)" was undertaken to throw more light on gene action of important horticultural and biochemical traits, extent of heterosis and hybrid performance and also to generate the breeding material for further genetic improvement. The results obtained have been discussed here under:

LINE x TESTER ANALYSIS

4.1 Morphological characterization of genotypes

4.2 Analysis of variance

4.3 Mean performance of parents and crosses

4.4 Estimates of heterosis

4.5 Combining ability

4.5.1 Analysis of variance

4.5.2 Combining ability variances and gene action

4.5.3 Combining ability effects

GENERATION MEAN ANALYSIS

4.6 Generation means, scaling tests and gene effects

4.7 Inheritance of fruit bearing habit, fruit position and branching habit in chilli

LINE x TESTER ANALYSIS

4.1 MORPHOLOGICAL CHARACTERIZATION OF GENOTYPES

Characterization and evaluation of germplasm are prerequisite for the utilization of the available diversity in the chilli improvement programme. Desirable parental combinations provide the basis for selection through exploitation of heterosis.

All the 71 genotypes including 54 crosses, nine lines, six testers and two checks were described morphologically according to the descriptors given by National Bureau of Plant Genetic Resources (NBPGR), Pusa Campus, New Delhi, India. The genotypes were scored for six morphological characters on appropriate scales ranging from 0-9 (Table 4.1).

In respect of plant growth habit, 17, 49 and five genotypes showed prostrate (3), intermediate (5) and erect (7) plant growth habit respectively. Four genotypes recorded sparse branching habit (3), 52 genotypes exhibited intermediate branching habit (5) while 15 genotypes showed dense branching habit (7).

In respect of fruit position, pendent fruits (3) were observed by 54 genotypes while semi pendent fruits (5) were recorded by 17 genotypes. There was no variation among 71 genotypes with respect to fruit bearing habit, fruit shape and all genotypes produced solitary fruits (1) with elongated fruit shape (1).

The colour of mature fruits in 33 genotypes was green (1) while nine genotypes produced parrot green fruits (3), 20 genotypes recorded dark green fruits (5) and nine genotypes registered olive green colored fruits (7). The olive green color was expressed by the parents LCA-466, LCA-442, LCA-315 and the crosses LCA-466 x G-4, LCA-466 x LCA-678, LCA-466 x LCA-453, LCA-466 x LCA-

703-2, LCA-466 x LCA-705-2 and LCA-466 x LCA-315. The parrot green fruits were observed in genotypes LCA-654, LCA-607, LCA-654 X G-4, LCA-654 x LCA-678, LCA-607 x LCA-678, LCA-607 x LCA-453, LCA-607 x LCA-703-2, LCA-607 x LCA-705-2 and LCA-607 x LCA-315.

Genetic cataloguing based on standard descriptors helps to easily describe the morphological features of a genotype and thus helps exchange of information about new genotypes. This also helps in locating some accessions with specific morphological traits which can be used for crop improvement. In the present investigation, the chilli genotypes showed variation for plant growth habit, branching habit, fruit position and mature fruit colour whereas the variation was not observed for fruit bearing habit and fruit shape. Maximum genotypes had intermediate growth habit (49), intermediate branching habit (52) with green colored (33) and pendent fruits (54). The collection and characterization of chilli germplasm was earlier attempted by Sreelathakumary (2000), Manju and Sreelathakumary (2002), Pradheep and Veeraragavathatham (2006), Chattopadhyay *et al.* (2011), Chaudhary *et al.,* 2013, Datta and Das (2013) and Rekha (2015) who have reported this kind of variability among chilli germplasm lines.

4.2 ANALYSIS OF VARIANCE

The analysis of variance for 19 characters studied is furnished in Table 4.2. The analysis of variance showed significant differences among the genotypes studied (parents, crosses and checks) for all the traits indicating presence of significant variability among the genotypes which can be exploited through simple selection. These findings are in line with earlier reports of Ganeshreddy *et al.* (2008), Patel *et al.* (2010), Chaudhary *et al.* (2013) and Savitha *et al.* (2015).

4.3 MEAN PERFORMANCE OF PARENTS AND CROSSES

The mean values of parents, hybrids and standard checks on 19 characters studied are presented in Tables 4.3 - 4.5.

4.3.1 Plant height (cm)

The plant height among the parents and hybrids ranged between 74.57 cm and 109.77 cm with a general mean of 91.37 cm (Table 4.3). The plant height for the lines ranged from 75.57 cm (LCA 442) to 103.87 cm (LCA 504) and for the testers, it varied from 78.00 cm (LCA 315) to 109.70 cm (LCA 703-2). In case of hybrids, the hybrid LCA 446 x LCA 705-2 was found to be dwarf with a minimum plant height of 74.57 cm and the hybrid LCA 355 x LCA 703-2 was observed to be the tallest (109.77 cm) as compared to the height of checks *i.e.* Indam-5 (82.60 cm) and Tejaswini (106.40 cm).

4.3.2 Plant spread (cm)

The plant spread ranged from of 70.93 cm to 106.70 cm with a general mean of 88.41 cm. Among the lines, it ranged from 79.53 cm (LCA 607 and LCA 355) to 94.03 cm (LCA 655) and varied from 75.90 cm (LCA 678) and 95.63 cm (G4) among the testers. Among hybrids, the spread varied from 70.93 cm (LCA 355 x LCA 315) to 106.70 cm (LCA 504 x LCA 703-2) while the checks Indam-5 and Tejaswini recorded a mean spread of 82.60 cm and 105.57 cm respectively (Table 4.3).

4.3.3 Number of primary branches per plant

On an average, 4.18 primary branches per plant with were recorded a range of 3.03 to 5.23 branches (Table 4.3). For lines, the range varied from 3.63 (LCA 446) to 4.93 (LCA 655) and for the testers it varied from 3.43 (LCA 453) to 5.23 branches (LCA 703-2). In hybrids the no. of primary branches ranged from 3.03 (LCA 355 x LCA 705-2) to 5.03 (LCA 466 x LCA 678 and LCA 466 x LCA 315) as against 4.23 and 4.73 branches recorded in Indam-5 and Tejaswini respectively.

4.3.4 Days to 50% flowering

The data from Table 4.3 revealed that days to 50% flowering ranged from 22.67 days to 38.00 days with an overall mean of 30.10 days. The lines recorded 50% flowering in 25.00 days (LCA 615) to 37.67 days (LCA 355) after planting and the testers in 30.00 days (LCA 678) to 36.67 days (LCA 453) after planting. The hybrid LCA 446 x LCA 453 was the earliest (Fig: 4.1) to flower (22.67 days) whereas the hybrid LCA 466 x LCA 315 recorded maximum days to 50% flowering (38.00 days) compared to the standard checks Indam-5 (31.33 days) and Tejaswini (33.33 days).

4.3.5 Days to fruit maturity (red)

The number of days taken to fruit maturity ranged from 48.67 days to 69.33 days with an overall mean of 60.42 days (Table 4.3). The lines carried fruits to maturity in 53.67 days (LCA 355) to 64.67 days (LCA 504) whereas the testers took 53.67 days (LCA 678) to 67.67 days (LCA 703-2). Among the hybrids, the days to fruit maturity ranged between 48.67 days (LCA 442 x G4) and 69.33 days (LCA 615 x LCA 678) compared to the standard checks Indam-5 (63.33 days) and Tejaswini (55.67 days).

4.3.6 Number of fruits per plant

The number of fruits produced by the parents and hybrids ranged from 124.93 to 373.53 with a general mean of 230.41 fruits. Among the lines, LCA 504 produced the lowest no. of fruits (124.93) and LCA 607 recorded the highest no. of fruits per plant (228.87). The fruits produced by testers ranged from 133.67 (LCA 453) to 308.80 fruits (LCA 703-2) while those of hybrids showed a range of 135.87 (LCA 446 x LCA 453) to 373.53 fruits (LCA 655 x G4). Among the hybrids, 37 hybrids recorded more no. of fruits per plant than standard check Indam-5 (194.00 fruits) while the standard check Tejaswini recorded more no. of fruits than lines, testers and crosses with 447.03 fruits (Table 4.3 and Fig: 4.2).

4.3.7 Fruit length (cm)

The genotypes recorded a mean fruit length ranging from 7.54 cm to 15.18 cm with a general mean of 11.04 cm. Among the lines, it ranged from 8.19 cm (LCA 615) to 12.76 cm (LCA 607) whereas for testers it ranged from 7.54 cm (LCA 703-2) to 11.91 cm (LCA 705-2). Among hybrids, the fruit length varied from 8.67 cm (LCA 615 x LCA 703-2) to 15.18 cm (LCA 355 x LCA 315) as compared to standard checks Indam-5 (9.85 cm) and Tejaswini (8.29 cm) (Table 4.4).

4.3.8 Fruit Diameter (cm)

The data on fruit diameter indicated a range of 1.04 to 2.08 cm among the parents and hybrids with a general mean of 1.42 cm (Table 4.4). The fruit diameter among the lines varied from 1.04 cm (LCA 655) to 1.95 cm (LCA 466) and among the testers it ranged from 1.12 cm (G4) to 2.08 cm (LCA 453). The fruit diameter of hybrids varied from 1.05 cm (LCA 655x LCA 453) to 1.85 cm (LCA 466 x LCA 453 and LCA 654 x LCA 453) compared to standard checks Indam-5 (1.46 cm) and Tejaswini (0.98 cm).

4.3.9 Average dry fruit weight (g)

As indicated by the data from Table 4.4, the fruit weight among the genotypes varied from 0.79 g to 1.83 g with a general mean of 1.25 g. The range of fruit weight for lines varied from 1.05 g (LCA 355) to 1.64 g (LCA 607) and among the testers it was ranged from 0.79 g (G4) to 1.74 g (LCA 453). The hybrids were in the range of 0.89 g (LCA 615 x G4) to 1.83 g (LCA 607 x LCA 453) compared to standard checks Indam-5 (1.37 g) and Tejaswini (0.75 g) (Fig: 4.3).

4.3.10 Fruit yield (g/plant)

It is evident from the data (Table 4.4) that the mean fruit yield of parents and hybrids ranged from 151.93 g to 328.53 g with a general mean of 225.29 g. The fruit yield of lines varied from 151.93 g (LCA 504) to 292.55 g (LCA 607) and among the testers it varied from 172.99 g (LCA 678) to 283.96 g (LCA 705-2). The hybrids recorded a range of 156.97 g (LCA 355 x LCA 315) to 328.53 g (LCA 607 x LCA

703-2). Among the hybrids, 20 hybrids have recorded higher yield than standard check Indam-5 (242.18 g) while only five hybrids could record higher yield over Tejaswini (271.53 g) (Fig: 4.4).

4.3.11 Number of seeds per fruit

The number of seeds per fruit varied from 41.80 to 90.47 with a general mean of 68.32 (Table 4.4). The female parents exhibited a range of 53.63 (LCA 655) to 88.90 (LCA 615) and the no. of seeds in male parents was in the range of 47.93 (LCA 703-2) to 90.47 (LCA 453). The hybrids exhibited a range varying from 41.80 (LCA 446 x G4) to 89.60 (LCA 615 x G4) as compared to standard checks Indam-5 (84.93) and Tejaswini (76.00).

4.3.12 Seed weight (g/1000 seed)

The seed weight of genotypes ranged from 5.05 g to 7.74 g with a general mean of 6.38 g as seen from the data Table 4.4. The lines showed a range of 5.05 g (LCA 504) to 7.58 g (LCA 654) and among the testers it ranged from 5.28 g (LCA 703-2) to 7.35 g (LCA 453). The hybrids were in the range of 5.06 g (LCA 442 x G4) to 7.74 g (LCA 607 x LCA 705-2) compared to standard checks Indam-5 (6.91 g) and Tejaswini (5.06 g).

4.3.13 Ascorbic acid (mg/100g)

Among the parents and hybrids, the ascorbic acid content of fruits ranged from 16.08 to 128.83 mg/100g with a general mean of 80.55 mg/100g (Table 4.5). The ascorbic acid content of lines varied from 30.08 (LCA 446) to 126.82 mg/100g (LCA 466) and that of testers from 16.08 (LCA 678) to 89.48 mg/100g (LCA 453). The ascorbic acid content of hybrids was in the range of 33.64 (LCA 607 x LCA 453) to 128.83 mg/100g (LCA 355 x LCA 678) compared to standard checks Indam-5 (98.00 mg/100g) and Tejaswini (44.04 mg/100g).

4.3.14 Oleoresin (%)

The oleoresin content of the parents and hybrids ranged from 6.80 to 20.97 per cent with a general mean of 12.39 per cent (Table 4.5). It varied from 10.21 (LCA 504) to 19.77 per cent (LCA 446) for lines and from 8.21 (LCA 315) to 11.75 per cent (LCA 703-2) for testers. The hybrids had a range of 6.80 (LCA 442 x LCA 453) to 20.97 per cent (LCA 504 x G4) as compared to standard checks Indam-5 (10.89 %) and Tejaswini (15.21 %).

4.3.15 Capsaicin (%)

The capsaicin content of different genotypes varied from 0.08 to 0.69 per cent with a general mean of 0.36 per cent (Table 4.5). The capsaicin content among the lines varied from 0.08 (LCA 442) to 0.69 per cent (LCA 615) and among the testers it ranged from 0.24 (G4) to 0.59 per cent (LCA 703-2). The hybrids recorded capsaicin in the range of 0.22 (LCA 446 x LCA 315) to 0.68 per cent (LCA 654 x G4) as compared to standard checks Indam-5 (0.40 %) and Tejaswini (0.74 %) and all the genotypes were recorded lower capsaicin than Tejaswini (Fig: 4.5).

4.3.16 Red carotenoids (mg/100g)

The content of red carotenoids among all the genotypes ranged from 81.91 to 266.17 mg/100g with a general mean of 172.61 mg/100g. The lines showed a range of 81.91 (LCA 615) to 266.17 mg/100g (LCA 355) and the testers from 129.97 (LCA 315) to 166.44 mg/100g (LCA 705-2). The hybrids were ranged from 89.63 (LCA 607 x LCA 453) to 219.86 mg/100g (LCA 654 x LCA 705-2) compared to standard checks Indam-5 (189.59 mg/100g) and Tejaswini (115.07 mg/100g) (Table 4.5).

4.3.17 Yellow carotenoids (mg/100g)

The content of yellow carotenoids among the parents and hybrids varied from 28.12 to 180.62 mg/100g with a general mean of 97.53 mg/100g (Table 4.5). Among the nine lines, LCA 615 recorded the lowest yellow carotenoids (33.95

mg/100g) and LCA 355 recorded the highest yellow carotenoids (153.74 mg/100g). The range of yellow carotenoids among the testers varied from 70.65 (LCA 315) to 90.82 mg/100g (LCA 703-2). The hybrid LCA 654 x G4 recorded minimum (28.12 mg/100g) and LCA 355 x LCA 678 recorded maximum (180.62 mg/100g) for this trait against the checks Indam-5 (91.61 mg/100g) and Tejaswini (75.48 mg/100g).

4.3.18 Total carotenoids (mg/100g)

The total carotenoids of the parents and hybrids ranged from 115.86 to 419.90 mg/100g with a general mean of 270.14 mg/100g (Table 4.5). The total carotenoids of the lines varied from 115.86 (LCA 615) to 419.90 mg/100g (LCA 355) and among the testers, they ranged from 200.62 (LCA 315) to 250.66 mg/100g (LCA 678). The hybrids recorded a range of 186.49 (LCA 607 x G4) to 397.32 mg/100g (LCA 466 x LCA 453) as compared to standard checks Indam-5 (281.20 mg/100g) and Tejaswini (190.55 mg/100g).

4.3.19 Total colour value (ASTA units)

Data on total colour value indicated a range of 51.54 to 163.68 with a general mean of 105.71 ASTA units for this trait (Table 4.5). Among the nine lines, LCA 615 recorded the lowest value of 51.54 while LCA 355 recorded the highest value of 163.68. The range of total colour value among the testers varied from 79.77 (G4) to 104.91 (LCA 705-2). The hybrid LCA 607 x LCA 453 recorded the minimum colour value of 66.44 while LCA 355 x LCA 678 recorded the maximum of 151.97 ASTA units (Fig: 4.6). The checks Indam-5 and Tejaswini recorded a colour value of 89.71 and 59.43 ASTA units respectively.

Based on mean performance best two lines, two testers and two crosses for each character are summarized in Table 4.6. Plant height, plant spread and number of primary branches per plant are important growth parameters from production

point of view. The genotypes having medium height, maximum plant spread with higher number of primary branches are reported to produce higher yields. In the present study, parents and hybrids differed significantly among themselves for growth characters. The hybrid LCA 355 x LCA 703-2 recorded highest plant height while highest canopy spread was observed in LCA 504 x LCA 703-2. Maximum number of primary branches was observed in LCA 703-2 (tester), LCA 466 x LCA 678 and LCA 466 x LCA 315 (hybrids). Similar kind of conclusions are also found in earlier reports of Kumar *et al*. (2013), Sharma *et al*. (2013), Dhaliwal *et al.* (2014), Suryakumari *et al*. (2014) and Spaldon *et al*. (2015).

Earlier flowering and early fruit maturity were observed in LCA 446 x LCA 453 and LCA 442 x G4 respectively and these two hybrids were earlier than the checks (Indam-5 and Tejaswini). Earlier hybrids are also reported by Tembhurne and Rao (2012), Kumar *et al*. (2013), Sharma *et al*. (2013) and Suryakumari *et al*. (2014) in their earlier findings.

No. of fruits per plant, fruit length, fruit diameter, fruit weight, no. of seeds per fruit and seed weight are the important yield attributing characters. The genotype LCA 655 x G4 has recorded maximum number of fruits per plant followed by LCA 655 x LCA 703-2 and LCA 607 x LCA 703-2. Maximum fruit length was recorded in LCA 654 x LCA 315 while highest fruit diameter was noticed in LCA 453 (tester), LCA 466 x LCA 453 and LCA 654 x LCA 453 (hybrids). The genotype LCA 607 x LCA 453 exhibited highest average fruit weight. The no. of seeds per fruit was maximum in the genotypes LCA 453 (tester), LCA 615 x G4 (hybrid) whereas highest seed weight was recorded in the genotype LCA 607 x LCA 705-2. Similar differential response for yield and yield attributes in different genotypes of chilli was earlier reported by Tembhurne and Rao (2012), Chaudhary *et al.* (2013), Kumar *et al*. (2013), Sharma *et al*. (2013), Dhaliwal *et al.* (2014), Suryakumari *et al*. (2014) and Spaldon *et al*. (2015).

Among the hybrids, twenty have recorded higher yields over Indam-5 while five hybrids over Tejaswini. Five hybrids *viz.*, LCA 607 x LCA 703-2, LCA 655 x

LCA 703-2, LCA 655 x LCA 315, LCA 446 x 703-2 and LCA 466 x LCA 705-2 have recorded significantly higher yield per plant than the both commercial checks Indam5 and Tejaswini. The above results are in agreement with the findings of Payakhapaab *et al*. (2012), Tembhurne and Rao (2012), Chaudhary *et al.* (2013), Kumar *et al*. (2013), Sharma *et al*. (2013), Dhaliwal *et al.* (2014), Singh *et al.* (2014) and Suryakumari *et al.* (2014) who have also reported heterotic hybrids over checks in chilli.

Biochemical traits are very important in any crop because biochemical characters impart nutritional quality. In the present study, different genotypes showed significant variation in biochemical characters like ascorbic acid content, oleoresin content, capsaicin content, red carotenoids, yellow carotenoids, total carotenoids and total colour value. The genotype LCA 355 x LCA 678 recorded highest ascorbic acid content among all genotypes. Oleoresin content was highest in LCA 504 x G4. Capsaicin is responsible for pungency in chilli and the genotype LCA 654 x G4 (0.68 %) recorded the highest levels of capsaicin among the genotypes but they were lower than those recorded in highly pungent check Tejaswini (0.74 %). The genotype LCA 355 recorded highest red and total carotenoids and highest total colour value. Among the hybrids LCA 654 x LCA 705-2, LCA 355 x LCA 678, LCA 466 x LCA 453 and LCA 355 x LCA 678 recorded highest red, yellow, total carotenoids and total colour value respectively. Similar kinds of observations are also reported in earlier findings of mambers Zewdie *et al*., (2001), Prasath and Ponnuswami (2008), Patel *et al*. (2010), Sharma *et al.* (2013), Suryakumari *et al*. (2014) and Jindal *et al.* (2015) in chilli.

4.4 HETEROSIS

The study of *per se* performance of hybrids will be incomplete, unless it is supplemented with information on the heterotic behaviour of these hybrids. High heterosis for fruit yield in chilli is due to simultaneous heterosis for more than one component. Hence, in the present study an attempt has been made to measure the

magnitude of heterosis in chilli with due emphasis laid on contributions of different traits for yield and quality.

The commercial exploitation of heterosis in chilli has been a recent development. It is obviously important that the crosses are compared with released hybrids rather than merely comparing with their mid/better parent. So in the present study the performance of the experimental crosses were compared with that of the most popular released hybrids *viz.*, Indam-5 and Tejaswini in order to estimate the magnitude of standard heterosis so that the crosses with high heterotic potential could be isolated for further evaluation and commercial cultivation.

In the present investigation, heterosis was estimated for yield and its components studied in 54 hybrids and were expressed as per cent increase or decrease over mid parental value (heterosis, h_1), over better parent (heterobeltiosis, h_2) and over standard check (standard heterosis, h_3) and the results (Tables 4.7 – 4.16) are discussed here under.

4.4.1 Plant height

The increase in height over mid parental value (average heterosis) exhibited a range of -14.32 (LCA 446 x LCA 705-2) to 13.15 per cent (LCA 655 x LCA 678) (Table 4.7). The heterobeltiosis ranged from -20.51 (LCA 615 x LCA 703-2) to 11.21 per cent (LCA 355 x LCA 453). Standard heterosis ranged from -29.92 (LCA 446 x LCA 705-2) to 3.16 per cent (LCA 355 x LCA 703-2) and from -9.73 (LCA 446 x LCA 705-2) to 32.89 per cent (LCA 355 x LCA 703-2) over the checks Tejaswini and Indam-5 respectively.

Among the 54 hybrids, 13 hybrids recorded significant positive heterosis and five hybrids recorded negative heterosis respectively. 17 hybrids showed significant heterobeltiosis, out of which, 14 hybrids showed significant negative heterobeltiosis and three hybrids *viz.*, LCA 355 x LCA 453 (11.36), LCA 655 x LCA 678 (9.85) and LCA 466 x LCA 678 (8.79) showed significant positive heterobeltiosis. 41 hybrids had significant standard negative heterosis and only four hybrids recorded

positive but non-significant standard heterosis over Tejaswini. Nine hybrids registered significantly more plant height than check Indam-5.

Since presence of both negative and positive heterosis, heterobeltiosis and standard heterosis, plant height is an important yield contributing factor as earlier reported by Ajjappalavara (2003), Ganeshreddy *et al*. (2008), Tembhurne and Rao (2012), Kumar *et al.* (2013), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) in chilli.

4.4.2 Plant spread (cm)

The mid parent heterosis was observed to range from -12.91 (LCA 655 x LCA 705-2) to 23.31 per cent (LCA 504 x LCA 678). The range of heterobeltiosis varied from -18.57 (LCA 655 x LCA 315) to 16.12 per cent (LCA 504 x LCA 678). The standard heterosis ranged from -32.8 to 1.07 per cent and from -17.33 to 24.36 per cent over Tejaswini and Indam-5 respectively. Higher magnitude of standard heterosis was registered by hybrid LCA 504 x LCA 703-2 whereas its lesser magnitude was observed in the hybrid LCA 355 x LCA 315 for both the checks (Table 4.7).

Among 54 hybrids, 16 hybrids expressed significant positive heterosis and four hybrids registered significant negative heterosis. With respect to heterosis over better parent, significant positive and negative heterosis expressed by 10 crosses each. Forty three hybrids recorded negatively significant standard heterosis and only two hybrids showed positive heterosis over Tejaswini whereas 14 and three hybrids manifested significant positive and negative standard heterosis over Indam-5 respectively.

Plant spread is also an important growth parameter from productivity point of view. The presence of both negative and positive heterosis, heterobeltiosis and standard heterosis is in accordance with earlier findings of Ganeshreddy *et al*. (2008), Suryakumari *et al*. (2014) and Rekha (2015) in chilli.

4.4.3 Number of primary branches per plant

The relative heterosis in respect of no. of primary branches ranged from -26.61 (LCA 355 x LCA 705-2) to 21.29 per cent (LCA 466 x LCA 315) while heterobeltiosis from -28.03 (LCA 504 x LCA 703-2) to 12.69 per cent (LCA 466 x LCA 315). In respect of standard heterosis, the hybrid LCA 355 x LCA 705-2 recorded lower magnitude of heterosis *i.e.* -35.92 per cent and -28.35 per cent over Tejaswani and Indam-5 respectively while the hybrids LCA 466 x LCA 315 (over Tejaswani - 6.34) and LCA 466 x LCA 678 (over Indam 5 - 18.90) recorded higher magnitude of heterosis (Table 4.8).

Eleven, 16, 27 and nine crosses showed significant negative standard heterosis over mid parent, better parent, the checks Tejaswini and Indam-5 respectively. Among hybrids only one hybrid (LCA 466 x LCA 315) and three hybrids (LCA 466 x LCA 315, LCA 466 x LCA 678 and LCA 355 x LCA 703-2) showed significant positive heterosis over mid parent and check Indam-5 respectively.

Primary branches are one of the most important growth parameters contributing to productivity. The findings of earlier workers Ganeshreddy *et al*. (2008), Tembhurne and Rao (2012), Kumar *et al*. (2013) and Savitha *et al*. (2015) have indicated both positive and negative heterosis, heterobeltiosis and standard heterosis and these reports support the findings of present investigation.

4.4.4 Days to 50% flowering

Negative heterosis for days to 50 per cent flowering is considered as desirable, since early parent is treated as better parent for comparison. The observed heterosis, heterobeltiosis and standard heterosis among the hybrids was in the range of -38.46 to 14.00 per cent, -38.74 to 10.68, -32.00 to 14.00 and -27.66 to 21.28 per cent respectively (Table 4.8). The hybrids LCA 446 x LCA 453 and LCA 466 x LCA 315 recorded lesser and higher magnitude of heterosis respectively over mid parent, better parent, Tejaswini and Indam-5.

Twenty nine, 35, 34 and 27 hybrids recorded significant negative heterosis (Fig: 4.1) whereas eight, one, four and seven hybrids manifested significant positive heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively.

Earliness is considered an important character in any crop improvement programme and is required for realizing the potential economic yield in as less time as possible. Thus, earliness is an important trait from the vegetable grower's point of view. In the present study, days to 50 per cent flowering was recorded to find out earliness of genotypes. Among 54 hybrids, 34 and 27 hybrids exhibited significant negative heterosis over Tejaswini and Indam-5 respectively. This indicates that, most of the hybrids evaluated were early compared to the standard checks. Superiority of this trait in chilli hybrids was earlier reported by Ganeshreddy *et al*. (2008), Patel *et al*. (2008), Tembhurne and Rao (2012), Kumar *et al*. (2013), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) in chilli.

4.4.5 Days to fruit maturity (red):

The observed range of heterosis, heterobeltiosis and standard heterosis among the hybrids was -18.21 to 24.92 per cent, -22.66 to 20.93, -12.57 to 24.55 and -23.16 to 9.47 per cent respectively. The hybrid LCA 442 x G4 and LCA 615 x LCA 678 recorded lesser and higher magnitude of heterosis respectively over mid parent, better parent, Tejaswini and Indam-5 (Table 4.9).

Seven, 15, one and 13 hybrids recorded significant negative heterosis whereas nine, three, 26 and one hybrids manifested significant positive heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively.

In respect of days to maturity negative heterosis is desirable as early parent is considered better for comparison. The genotypes with high yield coupled with earliness are preferred for commercial cultivation and such F_1's are considered superior. The hybrid LCA 442 x G4 was significantly earlier than check Tejaswani with -12.57 per cent. The negative and positive heterosis observed for this trait is in

agreement with similar findings of Prajapati and Agalodia (2011), Patil *et al*. (2012a), Berhate *et al*. (2013), Sharma *et al*. (2013), Suryakumari *et al*. (2014) and Spaldon *et al*. (2015) in chilli.

As evident from the data on days to 50 per cent flowering and days to fruit maturity, though most of hybrids recorded early flowering over parents and checks, very limited of them could attain maturity earlier than parents and checks. This obviously indicated longer period of fruit development which includes attainment of size as well as colour.

4.4.6 Number of fruits per plant

The heterosis for no. of fruits per plant as indicated by the data from Table 4.9 ranged from -27.11 (LCA 355 x LCA 315) to 88.47 per cent (LCA 442 x LCA 453). The heterobeltiosis ranged from -40.34 (LCA 466 x G4) to 70.45 per cent (LCA 442 x LCA 453). The standard heterosis was observed to range from -69.61 (LCA 446 x LCA 453) to -16.44 per cent (LCA 655 x G4) over Tejaswini and from -29.97 (LCA 446 x LCA 453) to 92.54 per cent (LCA 655 x G4) over Indam-5.

Significant positive heterosis was observed in 20 over the mid parent and eight hybrids exhibited significantly superiority over better parent. Twenty four hybrids were significantly superior by exhibiting significant positive heterosis over Indam-5 whereas all hybrids were significantly inferior by exhibiting significant negative heterosis over Tejaswini (Fig: 4.2). Four, ten, 54 and two hybrids recorded significant negative heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively.

Number of fruits per plant is one of the most important characters as it directly contributes to yield per plant and positive heterosis in respect of this trait is desirable. In the present study, both positive and negative average heterosis, heterobeltiosis and standard heterosis was recorded. These results are in conformity

with the findings of Seneviratne and Kannangara (2004), Ganeshreddy *et al*. (2008), Kumar *et al*. (2013), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) in chilli.

4.4.7 Fruit length (cm)

Among the hybrids, the relative heterosis for fruit length (Table 4.10) ranged from -12.73 (LCA 607 x LCA 705-2) to 31.77 per cent (LCA 355 x LCA 315) while heterobeltiosis was in the range of -20.98 (LCA 466 x 705-2) to 31.09 per cent (LCA 355 x LCA 315). The standard heterosis ranged from -4.58 to 83.04 per cent over Tejaswini and from -11.98 to 54.06 per cent over Indam- 5. The hybrids LCA 615 x LCA 703-2 and LCA 355 x LCA 315 have registered minimum and maximum heterosis respectively over both checks.

Significant positive heterosis was observed in 35 hybrids over the mid parent and 13 hybrids exhibited significant superiority over better parent. Fifty one and 30 hybrids were significantly superior by exhibiting significant positive heterosis over Tejaswini and Indam-5. All hybrids were showed higher magnitude of heterosis than Tejaswini. One, three and eight hybrids were significantly inferior recording significant negative heterosis over Indam-5, mid parent and better parent respectively.

Fruit length contributes positively to yield. Superiority of this trait as observed in this study is also supported by earlier reports of Patil *et al*. (2012a), Payakhapaab *et al*. (2012), Tembhurne and Rao (2012), Kumar *et al*. (2013), Khalil and Hatem (2014), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) in chilli.

4.4.8 Fruit diameter (cm)

A perusal of the data on heterosis for fruit diameter indicated an increase over mid parent value in the range of -32.33 (LCA 655 x LCA 453) to 24.60 per cent (LCA 442 x LCA 705-2) (Table 4.10). Heterobeltiosis was ranged from -49.28 (LCA 655 x LCA 453) to 13.24 per cent (LCA 615 x LCA 678). The standard heterosis was in the range of -7.85 to 89.76 per cent over Tejaswini and from -

28.02 to 26.65 per cent over Indam- 5. The hybrids LCA 655 x LCA 453 and LCA 466 x LCA 453 were registered minimum and maximum heterosis respectively over both checks.

Seven hybrids and one hybrid showed significant positive relative heterosis and heterobeltiosis respectively whereas seven and 23 hybrids showed significant negative relative heterosis and heterobeltiosis respectively. Fifty two and seven hybrids were significantly superior by exhibiting significant positive heterosis over Tejaswini and Indam-5 respectively. All hybrids have recorded higher magnitude of heterosis than Tejaswini while seven, 23 and 15 hybrids were significantly inferior as they have recorded significant negative heterosis over mid parent, better parent and Indam-5 respectively.

Fruit diameter is also an important character as that of fruit length and contributes to yield. In the present study, both positive and negative average heterosis and heterobeltiosis were recorded. Similar findings were reported by Payakhapaab *et al*. (2012), Khalil and Hatem (2014) and Suryakumari *et al*. (2014) in chilli.

4.4.9 Average dry fruit weight (g)

The heterosis in respect of average dry fruit weight as observed from the data (Table 4.11) ranged from -19.82 (LCA 655 x LCA 453) to 35.17 per cent (LCA 442 x LCA 703-2). Heterobeltiosis ranged from -33.40 (LCA 607 x G4) to 22.01 per cent (LCA 442 x LCA 705-2). Standard heterosis over Tejaswini and Indam-5 ranged from 18.75 (LCA 615 x G4) to 144.64 per cent (LCA 607 x LCA 453) and from -35.12 (LCA 615 x G4) to 33.66 per cent (LCA 607 x LCA 453) respectively.

Fourteen hybrids exhibited significant positive relative heterosis and only one hybrid exhibited significant and positive heterosis over better parent. Fifty three and three hybrids registered significant and positive standard heterosis over Tejaswini and Indam-5 respectively (Fig: 4.3). All hybrids showed superiority over Tejaswini

as they exhibited positive heterosis. Two, 19 and 23 hybrids were significantly inferior exhibiting significant negative heterosis over mid parent, better parent and check Indam-5 respectively.

Fruit weight is one of the yield component characters which directly influences fruit yield. Heterosis for this trait can be added an advantage along with fruit length for yield. Superiority of this trait was earlier observed in chilli by Ganeshreddy *et al*. (2008), Kumar *et al*. (2013), Sharma *et al*. (2013), Dhaliwal *et al*. (2014), Khalil and Hatem (2014) and Savitha *et al*. (2015).

4.4.10 Fruit yield (g/plant)

The observed range of heterosis and heterobeltiosis among the hybrids was -22.38 (LCA 446 x LCA 705-2) to 53.61 per cent (LCA 655 x LCA 703-2) and from -34.83 (LCA 607 x LCA 678) to 47.71 per cent (LCA 655 x LCA 315) respectively. Standard heterosis over Tejaswini and Indam-5 ranged from -42.19 (LCA 355 x LCA 315) to 20.99 per cent (LCA 607 x LCA 703-2) and from -35.18 (LCA 355 x LCA 315) to 35.66 per cent (LCA 607 x LCA 703-2) respectively (Table 4.11).

Significant positive heterosis was observed in 27 hybrids over the mid parent and in 17 hybrids over better parent. Two and four hybrids were significantly superior by exhibiting significant positive heterosis over Tejaswini and Indam-5 respectively. Six, 11, 28 and 13 hybrids recorded significant negative heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively. Five and 20 hybrids have expressed in desirable direction *i.e.* positive heterosis but non-significant over checks Tejaswini and Indam-5 respectively (Fig: 4.4 and plate 6).

Fruit yield is the ultimate and most important trait. Heterosis for fruit yield is the product of simultaneous manifestation of heterosis for yield attributing traits. Significant positive heterosis was observed in 27 and 17 hybrids exhibited significantly superiority over mid parent and better parent respectively. Significant positive heterosis and heterobeltiosis for this trait was reported by Ganeshreddy *et al*. (2008), Prajapati and Agalodia (2011), Payakhapaab *et al*. (2012), Kumar *et al*.

(2013), Khalil and Hatem (2014) and Savitha *et al*. (2015) in chilli. Two hybrids (LCA 607 x LCA 703-2 and LCA 655 x LCA 703-2) and four hybrids (LCA 607 x LCA 703-2, LCA 655 x LCA 703-2, LCA 446 x LCA 703-2 and LCA 655 x LCA 315) recorded significant standard heterosis over the checks Tejaswini and Indam-5 respectively. Significant positive standard heterosis for yield per plant also exhibited by earlier findings of Berhate *et al*. (2013), Sharma *et al*. (2013), Dhaliwal *et al*. (2014) and Suryakumari *et al*. (2014). The hybrid which exhibited highest heterosis for yield per plant among the different crosses in the present study was LCA 607 x LCA 703-2 over best check Tejaswini. This cross also expressed significant positive heterosis for fruit length, fruit diameter, average fruit weight and seed weight indicating that these quantitative traits contributed to high magnitude of heterosis for fruit yield in chilli.

4.4.11 Number of seeds per fruit

The heterosis for no. of seeds per fruit was observed to be in the range of -43.31 (LCA 446 x G4) to 51.46 per cent (LCA 655 x LCA 315) whereas heterobeltiosis ranged from -52.73 (LCA 442 x LCA 453) to 41.38 per cent (LCA 655 x LCA 315) (Table 4.12). The standard heterosis over Tejaswini ranged from -45.00 (LCA 446 x G4) to 17.89 per cent (LCA 615 x G4) and over Indam-5 it ranged from -50.78 (LCA 446 x G4) to 5.49 per cent (LCA 615 x G4).

Seven hybrids and only one hybrid were significantly superior by exhibiting significant positive heterosis over mid and better parents respectively. Nine, 17, 17 and 31 hybrids were significantly inferior over mid parent, better parent, Tejaswini and Indam-5 respectively as indicated by significant negative heterosis registered. 15 and six hybrids were superior over Tejaswini and Indam-5 as they recorded positive heterosis but not-significant.

The seed number is also one of the yield component characters. The findings of earlier workers Tembhurne and Rao (2012), Kumar *et al*. (2013), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) have reported both positive and negative

heterosis, heterobeltiosis and standard heterosis and these reports support the findings of present investigation.

4.4.12 Seed weight (g/1000 seed)

The average heterosis in respect of seed weight ranged from -21.86 (LCA 442 x G4) to 20.17 per cent (LCA 466 x LCA 703-2) (Table 4.12). The heterosis over better parent ranged from -23.18 (LCA 607 x LCA 678) to 18.19 per cent (LCA 466 x LCA 703-2). Standard heterosis over Tejaswini and Indam-5 ranged from 0.13 (LCA 442 x G4) to 53.07 per cent (LCA 607 x LCA 705-2) and from -26.69 (LCA 442 x G4) to 12.07 per cent (LCA 607 x LCA 705-2) respectively.

Seven hybrids and only one hybrid exhibited significant positive heterosis whereas six and 14 hybrids recorded significant negative heterosis over mid and better parents respectively. All the 54 hybrids exhibited positive heterosis but among them 39 hybrids showed significant and positive heterosis over the check Tejaswini. 12 and 10 hybrids registered significant negative and positive standard heterosis over the check Indam-5 respectively.

The seed weight is also one of the yield component characters. In the present investigation both negative and positive heterosis, heterobeltiosis and standard heterosis were recorded. These findings are in accordance with earlier reports of Ganeshreddy *et al*. (2008), Tembhurne and Rao (2012), Kumar *et al*. (2013), Suryakumari *et al*. (2014) and Savitha *et al*. (2015) in chilli.

4.4.13 Ascorbic acid (mg/100g)

The observed range of heterosis, heterobeltiosis and standard heterosis (Tejaswini and Indam-5) among the hybrids was -65.33 to 390.84 per cent, -79.05 to 276.64, -54.24 to 192.54 and -79.44 to 31.46 per cent respectively (Table 4.13). The hybrid LCA 442 x LCA 315 exhibited lesser magnitude of heterosis over mid, better parents, Tejaswini and Indam-5 whereas the hybrid LCA 446 x LCA 678

recorded higher magnitude of heterosis over mid parent, better parent and LCA 355 x LCA 678 showed higher magnitude of heterosis over Tejaswini and Indam-5.

Thirty three, 17, 47 and 15 hybrids recorded significant positive heterosis whereas eight, 23, two and 32 hybrids manifested significant negative heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively. Most of the hybrids (47) showed significant positive standard heterosis over check Tejaswini.

The positive average heterosis is desirable for this trait. In the present investigation, both positive and negative average heterosis, heterobeltiosis and standard heterosis was recorded. The results are in conformity with earlier reports of Chandan (2008), Patel *et al*. (2010), Asish and Pugalendhi (2012) and Jindal *et al*. (2015) in chilli.

4.4.14 Oleoresin (%)

The increase in oleoresin over mid parental value exhibited a range of -54.83 (LCA 442 x LCA 453) to 116.44 per cent (LCA 504 x G4) (Table 4.14). Heterobeltiosis for this trait ranged from -64.52 (LCA 442 x LCA 453) to 105.49 per cent (LCA 504 x G4). Standard heterosis ranged from -55.28 (LCA 442 x LCA 453) to 37.92 per cent (LCA 504 x G4) and from –37.54 (LCA 442 x LCA 453) to 92.65 per cent (LCA 504 x G4) over checks Tejaswini and Indam-5 respectively.

Nine, five, four and 13 hybrids showed significant positive heterosis over mid parent, better parent, Tejaswini and Indam-5 respectively. Nineteen, 29, 41 and four hybrids registered significant negative heterosis over mid parent, better parent, Tejaswini and Indam-5 respectively.

With respect to this trait, the positive average heterosis is desirable. In the present investigation, both positive and negative heterosis recorded. Four and 13 hybrids showed significant positive heterosis over checks Tejaswini and Indam-5

respectively. These results are in line with earlier reports of Asish and Pugalendhi (2012), Suryakumari *et al*. (2014) and Jindal *et al.* (2015) in chilli.

4.4.15 Capsaicin (%)

The range of heterosis over mid parent varied from -64.10 (LCA 615 x LCA 703-2) to 264.95 per cent (LCA 654 x G4). The range of heterosis over better parent varied from -66.67 (615 x LCA 703-2) to 184.07 per cent (LCA 654 x G4). The range of standard heterosis was varied from -69.63 (LCA 446 x LCA 315) to -7.32 per cent (LCA 654 x G4) over Tejaswini and from -44.60 (LCA 446 x LCA 315) to 69.08 per cent (LCA 654 x G4) over Indam-5.

Twenty two, 11 and seven hybrids significantly recorded high heterosis than mid, better parents and Indam-5 respectively. All the hybrids were significantly inferior to Tejaswini (Fig: 4.5 and Plate 7) in respect of this trait. 18, 33 and 34 hybrids had significantly lesser capsaicin content than mid, better parents and Indam-5 respectively (Table 4.14).

In respect of capsaicin content, the positive average heterosis is desirable. The superiority of this trait was observed by Zewdie *et al.* (2001), Patel *et al*. (2010), Prasath and Ponnuswami (2008), Prajapati and Agalodia (2011), Asish and Pugalendhi (2012) Suryakumari *et al*. (2014) and Jindal *et al.* (2015) in chilli.

4.4.16 Red carotenoids (mg/100g)

A perusal of the data on heterosis for red carotenoids indicated an increase over mid parent value in the range of -33.19 (LCA 607 x LCA 453) to 75.19 per cent (LCA-615 x G4) (Table 4.15). Heterobeltiosis ranged from -43.81 (LCA 355 x LCA 703-2) to 43.23 per cent (LCA 442 x LCA 453). The standard heterosis ranged from -22.10 to 91.07 per cent over Tejaswini and from -52.72 to 15.97 per cent over Indam- 5. The hybrids LCA 607 x LCA 453 and LCA 654 x LCA 705-2 have registered minimum and maximum heterosis respectively over both checks.

Thirty six hybrids over mid parent and 26 hybrids over better parent, 49 hybrids over Tejaswini and eight hybrids over Indam-5 were found superior by exhibiting significant positive heterosis. Six, 15, one and 17 hybrids showed significant negative heterosis over mid parent, better parent, Tejaswini and Indam-5 respectively.

Red carotenoids are the most important quality parameter because it contributes to not only red colour in particular and also to the total colour value and positive heterosis for this trait is desirable. In respect of colour, Indam-5 is the best check. Eight hybrids over Indam-5 were found superior by exhibiting significant positive heterosis. These results are in agreement with earlier reports of Rekha (2015).

4.4.17 Yellow carotenoids (mg/100g)

The relative heterosis among the hybrids for yellow carotenoids (Table 4.15) ranged from -59.94 (LCA 442 x LCA 705-2) to 95.65 per cent (LCA 654 x LCA 705-2) and the heterobeltiosis ranged from -62.01 (LCA 442 x LCA 705-2) to 66.70 per cent (LCA 442 x LCA 453). The standard heterosis ranged from -62.75 (LCA 654 x G4) to 139.29 per cent (LCA 355 x LCA 678) over Tejaswini and from -69.31 (LCA 654 x G4) to 97.16 per cent (LCA 355 x LCA 678) over Indam-5.

Significant negative heterosis was recorded in nine, 11, three and nine hybrids over the mid parent, better parent, Tejaswini and Indam-5 respectively. Significant positive heterosis was observed in 34, 22, 33 and 21 hybrids over mid parent, better parent, Tejaswini and Indam-5 respectively.

Yellow carotenoids are one of the components which contribute to total colour value. For this trait, negative heterosis is desirable. In respect of colour Indam-5 is the best check. Nine hybrids over Indam-5 were found superior by exhibiting significant negative heterosis. These results are in agreement with earlier reports of Rekha (2015).

4.4.18 Total carotenoids (mg/100g)

The range of heterosis over mid parent varied from -30.69 (LCA 355 x LCA 703-2) to 78.88 per cent (LCA-615 x G4) (Table 4.16) and the heterobeltiosis ranged from -45.13 (LCA 355 x LCA 703-2) to 51.36 per cent (LCA 442 x LCA 453). The standard heterosis ranged from -2.13 to 108.51 per cent over Tejaswini and from -33.68 to 41.29 per cent over Indam- 5. The hybrids LCA 607 x G4 and LCA 466 x LCA 453 have registered lesser and higher magnitude of heterosis respectively over both checks.

Thirty seven, 24, 47 and 16 hybrids recorded significant positive heterosis whereas three, 13, zero and 19 hybrids manifested significant negative heterosis over mid parent, better parent, checks Tejaswini and Indam-5 respectively.

Total carotenoids are the most important quality parameter which is sum of red and yellow carotenoids and they are used in many food and beverage industries for colour. For this trait, positive heterosis is desirable. In respect of colour Indam-5 is the best check. 47 and 16 hybrids recorded significant positive heterosis over checks Tejaswini and Indam-5 respectively.

4.4.19 Total colour value (ASTA units)

A perusal of the data on heterosis for total colour value indicated an increase over mid parent value in the range of -33.72 (LCA 607 x LCA 453) to 70.57 per cent (LCA-615 x G4) (Table 4.16). Heterobeltiosis ranged from -43.53 (LCA 607 x LCA 453) to 51.24 per cent (LCA 442 x LCA 315). The standard heterosis ranged from 11.79 to 155.70 per cent over Tejaswini and from -25.94 to 69.40 per cent over Indam- 5. The hybrids LCA 607 x LCA 453 and LCA 355 x LCA 678 have registered lesser and higher magnitude of heterosis respectively over both checks.

Thirty one hybrids over mid parent and 20 hybrids over better parent, 53 hybrids over Tejaswini and 33 hybrids over Indam-5 were found superior by exhibiting significant positive heterosis (Fig: 4.6 and Plate 8). Eight, 19 and four hybrids showed significant negative heterosis over mid parent, better parent and Indam-5 respectively.

Total colour value is the most important quality parameter as it adds to the appearance of produce and improves marketability of fruits. The carotenoids of chilli are one of the major sources of natural dyes and the colour used in many food and beverage industries. Thus, for this trait positive heterosis is desirable. In respect of colour Indam-5 is the best check. 53 and 33 hybrids over Tejaswini and Indam-5 were found superior by exhibiting significant positive heterosis. These results are in agreement with earlier reports of Prasath and Ponnuswami (2008), Asish and Pugalendhi (2012), Suryakumari *et al*. (2014) and Jindal *et al.* (2015) in chilli.

Among 54 hybrids, the best five hybrids for total colour value are LCA 355 x LCA 678, LCA 466 x LCA 453, LCA 466 x LCA 678, LCA 466 x G4 and LCA 355 x LCA 705-2 which exhibited higher magnitude of positive heterosis over best check Indam-5 and these hybrids also recorded significant positive heterosis for red carotenoids. The red caroteanoids include capsanthin, capsorubin and capsanthin-5, 6-epoxide and contribute to red colour and these red carotenoids are in great demand in food and beverage industries for colouring of food products. The best five hybrids for red carotenoids are LCA 654 x LCA 705-2, LCA 466 x LCA 453, LCA 655 x LCA 705-2, LCA 607 x LCA 705-2 and LCA 442 x LCA 705-2 which recorded higher magnitude of positive heterosis over best check Indam-5 and also recorded significant positive heterosis for total colour value. The change in magnitude of heterosis in above hybrids is due to yellow carotenois because total colur value is the sum of red and yellow carotenoids.

Only five crosses exhibited heterosis in desired direction for fruit yield over best check (Tejaswini), among those five crosses only two were heterotic crosses which recorded significant positive heterosis. The correlation between *per se*

performance and heterosis of crosses for the characters indicated that heterosis of a cross can reasonably be predicted from *per se* performance (Table 4.17).

The top five heterotic crosses over best check Tejaswini were LCA 607 x LCA 703-2, LCA 655 X LCA 703-2, LCA 446 X LCA 703-2, LCA 655 X LCA 315 and LCA 466 X LCA 705-2 and among these five hybrids only two crosses have registered significant positive standard heterosis for fruit yield. The above five productive crosses had higher *per se* value over the check Tejaswini in respect of fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red, yellow, total carotenoids and total colour value.

4.5 COMBINING ABILITY

The concept of combining ability assumed greater importance in plant breeding as an effective means of selecting parents that have potential in developing superior hybrids. Sprague and Tatum (1942) proposed the concept of *gca* and *sca* as a measure of gene action. Kempthorne (1957) advanced a technique of line x tester analysis to explain *gca* and *sca* variances in terms of co-variance of half sibs and co-variance of full sibs in a population. This mating design facilitates screening of a large number of entries for their relative potential to produce outstanding hybrids.

The estimates of general combining ability of 15 parents and specific combining ability of 54 hybrids for yield and its components were studied at HRS, Lam, Guntur. The results with respect to analysis of variance, ratio of *gca* to *sca* variance and estimates of *gca* and *sca* effects are discussed here under character-wise.

4.5.1 Analysis of Variance

The mean data on 19 characters *viz*., plant height, plant spread, number of primary branches, days to 50% flowering, days to fruit maturity, no. of fruits per plant, fruit length, fruit diameter, average dry fruit weight, fruit yield, no. of seeds

per fruit, seed weight, ascorbic acid, oleoresin, capsaicin, red carotenoids, yellow carotenoids, total carotenoids and total colour value were collected and analyzed.

The analysis of variance (Table 4.18) revealed significant differences among the parents and crosses for all the nineteen characters studied indicating the variability among them. Significant differences were observed among the parents vs. hybrids for fourteen characters and the characters plant height, days to fruit maturity, fruit diameter, no. of seeds per fruit and seed weight recorded non significant differences. All genotypes were partitioned into lines, testers and lines x testers and the significant differences were observed among lines and testers for all the characters studied. The differences due to lines x testers were significant for all the traits studied except for plant height, plant spread, no. of primary branches per plant, days to fruit maturity, fruit yield and seed weight.

This indicates the existence of wide variability in the material studied and there is a good scope for identifying promising parents and hybrid combinations, and improving the yield through its components. These results are in accordance with the earlier findings of Patel *et al*. (2010), Payakhapaab *et al*. (2012), Tembhurne and Rao (2012), Kumar *et al*. (2013), Sharma *et al*. (2013), Savitha *et al*. (2015) and Spaldon *et al*. (2015).

Study of proportional contribution of each character (Table 4.19) is required to know the contribution of lines, testers and line x tester interactions in getting total variance of each character. The contribution of lines was more for days to fruit maturity, fruit length, fruit diameter, capsaicin, yellow and total carotenoids and total colour value whereas the contribution of testers was more for plant height and dry fruit weight. Line x Tester interactions contributed more for plant spread, no. of primary branches per plant, days to 50% flowering, no. of fruits per plant, no. of seeds per fruit, seed weight, fruit yield, ascorbic acid, oleoresin content and red carotenoids. The contribution to total variance can be concluded that the contribution due to Line x Tester interactions was highest (42.66%) followed by lines (35.42%) and testers (21.93%).

4.5.2 Combining ability variances and gene action

It is necessary to assess the genetic potentiality of the parents in hybrid combination through systematic studies in relation to general and specific combining abilities which are due to additive and non additive gene actions, respectively. In this direction, Line x Tester analysis was adopted to evaluate fifty four hybrids (nine lines and six testers) for combing ability studies.

Average performance of a parental line in a series of cross combinations is generally referred to as general combining ability and is mainly attributed to additive and additive x additive gene effects, which is mainly an intra allelic interaction and indicate the part of inter allelic interaction also. However, deviation in the performance of a cross expected on the basis of average performance of parental lines is mainly attributed to dominant / epistatic effects and is termed as specific combining ability *i.e.,* non- additive part. Additive component of genetic variation is fixable and it could be fixed through normal selection procedures, whereas non-additive component is not fixable and its presence for the controlling traits necessitates exploitation of hybrid vigour through heterosis breeding.

The estimates of *gca* and *sca* variances, their ratios and gene action are presented in Table 4.20. Variances due to general combining ability (*gca*) and specific combining ability (*sca*) were found to be significant for all the characters studied *viz.,* plant height, plant spread, number of primary branches, days to 50% flowering, days to fruit maturity, no. of fruits per plant, fruit length, fruit diameter, average dry fruit weight, fruit yield, no. of seeds per fruit, seed weight, ascorbic acid, oleoresin, capsaicin, red carotenoids, yellow carotenoids, total carotenoids and total colour value except for seed weight which is non-significant in case of variance due to *sca*.

General combining ability is genetically associated with additive gene action while specific combining ability is due to non-additive gene action *i.e.* dominance and epistasis. The ratio of σ^2_{gca} to σ^2_{sca}, is an index of additive / non-additive gene

action. If the ratio of *gca* to *sca* variance less than unity, it indicates predominance of non additive gene action whereas the ratio of more than unity indicates predominance of additive gene action. In present investigation, 13 characters exhibited higher *sca* variances than *gca* variances and recorded less than unity indicating predominance of non additive gene action whereas additive gene action was predominant for characters plant height, no. of primary branches, fruit length, fruit diameter, average dry fruit weight and seed weight due to higher *gca* variances than *sca* variances.

The results of this kind of gene action are in conformity with earlier findings of Hasanuzzaman *et al*. (2012), Nsabiyera *et al.* (2013), Nascimento *et al.* (2014), Navhale *et al.* (2014b), Suryakumari *et al*. (2014) and Jindal *et al.* (2015) in chilli.

4.5.3 Combining ability effects

The estimates of general combining ability effects of nine lines, six testers and specific combining ability effects of fifty four hybrids for nineteen characters are presented character wise below.

4.5.3.1 Plant height (cm)

***gca* effects**

The significant positive *gca* effects were exhibited by lines LCA 504 (7.14), LCA 607 (6.60), LCA 655 (3.52) and the testers LCA 703-2 (10.58), LCA 678 (2.07). These were regarded as good general combiners. The lines LCA 615, LCA 446, LCA 442 and LCA 654, LCA 710 and the testers LCA 453, LCA 705-2, LCA 315 exhibited significant negative *gca* effects and these were regarded as poor combiners (Table 4.21).

***sca* effects**

The *sca* effects for plant height ranged from -12.66 (LCA 615 x LCA 703-2) to 9.25 (LCA 615 x G4). The evaluation of the 54 hybrids for *sca* effects revealed that nine crosses recorded significant positive *sca* effects (Table 4.21) and seven

crosses showed significant negative *sca* effects. Among all hybrids, the good specific combiners with high positive significant *sca* effects are LCA 615 x G4 (9.25), LCA 446 x LCA 453 (8.19), LCA 615 x LCA 453 (7.82), LCA 355 x LCA 703-2 (7.68) and LCA 655 x G4 (7.59).

For this trait, the ratio of *gca* to *sca* variance was more than unity indicating the predominance of additive gene action (Table 4.20) and this trait can be improved through simple selection procedure in segregating generations. These observations are in accordance with the earlier findings of Jagadeesha and Wali (2005), Singh and Chaudhary (2005b), Prasath and Ponnuswami (2008) in chilli.

4.5.3.2 Plant spread (cm)

gca effects

For this trait, the good general combiners are lines LCA 504 (5.67), LCA 466 (3.17) and testers LCA 678 (5.33), LCA 703-2 (5.38) as they exhibited significant positive *gca* effects (Table 4.21). The lines LCA 442, LCA 654, LCA 355 and the testers LCA 453, LCA 705-2, LCA 315 showed significant negative *gca* effects.

***sca* effects**

Evaluation of the hybrids for *sca* effects revealed significant positive *sca* effects were registered in seven crosses whereas nine crosses exhibited significant negative *sca* effects. The range of *sca* effects was varied from -10.70 (LCA 607 x LCA 703-2) to 14.48 (LCA 355 x LCA 703-2) (Table 4.21). The best three specific combiners for this trait are LCA 355 x LCA 703-2 (14.48), LCA 655 x G4 (13.46) and LCA 466 x LCA 315 (13.18) as they exhibited significant and positive *sca* effects.

For plant spread, the ratio of *gca* to *sca* variance was less than unity indicating that non-additive gene action played a role in the inheritance of this trait (Table 4.20) and improvement can be made through heterosis breeding. Similar

results were reported by Hasanuzzaman *et al*. (2012), Nsabiyera *et al.* (2013), Singh *et al.* (2014) and Suryakumari *et al*. (2014).

4.5.3.3 Number of primary branches per plant

***gca* effects**

Among lines and testers, line LCA 466 (0.56) and tester LCA 703-2 (0.42) registered significant positive *gca* effects and these two are considered as good general combiners. The line LCA 504 and testers LCA 453 and LCA 705-2 recorded significant negative *gca* effects (Table 4.21).

***sca* effects**

For primary branches per plant, three crosses *viz.*, LCA 504 x LCA 705-2 (0.57), LCA 355 x LCA 703-2 (0.54) and LCA 355 x LCA 453 (0.48) recorded significant positive *sca* effects and these are regarded as good specific combiners. Two crosses exhibited significant negative *sca* effects (Table 4.21). For this trait the *sca* effects varied from -0.59 (LCA 355 x LCA 705-2) to 0.57 (LCA 504 x LCA 705-2).

For no. of primary branches per plant, the ratio of *gca* to *sca* variance was more than unity indicating predominance of additive gene action in governing this character (Table 4.20) and improvement can be made through simple selection procedure in segregating generations. These results are in accordance with earlier findings of Saritha *et al.* (2005), Singh and Chaudhary (2005b) and Prasath and Ponnuswami (2008).

4.5.3.4 Days to 50% flowering

***gca* effects**

This trait was studied for earliness and negative direction was desirable. For this character, the lines LCA 504 (-2.11), LCA 446 (-2.33), LCA 355 (-2.17) and the

testers G4 (-1.28), LCA 705-2 (-1.06) were found to be good general combiners as they recorded significant negative *gca* effects while the lines LCA 466, LCA 442 and LCA 607 (Table 4.21) and the tester LCA 678 recorded significant positive *gca* effects.

***sca* effects**

Out of 54 hybrids studied, significant negative specific combining ability effects which are desirable for this trait were exhibited by 10 crosses and the significant positive *sca* effects were exhibited by 12 crosses (Table 4.21). The range of *sca* effects varied from -5.50 (LCA 466 x G4) to 5.94 (LCA 442 x LCA 453). The best three specific combiners for this trait are LCA 466 x G4 (-5.50), LCA 655 x LCA 315 (-4.70) and LCA 615 x LCA 453 (-4.56) with significant negative *sca* effects.

The predominance of non-additive gene action was observed for this trait (Table 4.20) as indicated by the ratio of *gca* to *sca* variances (<1) and thus the improvement can be made through heterosis breeding for this trait. These results are in agreement with the earlier reports of Kamble *et al.* (2009a), Hasanuzzaman *et al*. (2012), Suryakumari *et al*. (2014) and Savitha *et al*. (2015).

4.5.3.5 Days to fruit maturity (red)

***gca* effects**

This trait was studied for earliness and negative direction was desirable. Among the nine lines, two lines *viz*., LCA 466 (-3.37) and LCA 355 (-4.20) recorded significant negative *gca* effects while, the lines LCA 504, LCA 615 and LCA 655 showed significant positive *gca* effects (Table 4.21). Among the six testers, G4 (-3.24) registered significant negative *gca* effects while LCA 703-2 recorded significant positive *gca* effects. The genotypes which showed significant negative *gca* effects were recored as good general combiners.

***sca* effects**

Out of 54 hybrids studied, the significant negative specific combining ability effects which are desirable for this trait were exhibited by three crosses *viz.,* LCA 466 x LCA 678 (-7.48), LCA 442 x G4 (-7.20) and LCA 355 x LCA 703-2 (-6.35) which are regarded as good specific combiners whereas significant positive *sca* effects were exhibited by four crosses (Table 4.21). The range of *sca* effects varied from -7.48 (LCA 466 x LCA 678) to 5.20 (LCA 442 x LCA 315).

The ratio of *gca* to *sca* variances less than unity have revealed the predominance of non-additive gene action over additive gene action in controlling days to fruit maturity (Table 4.20) and exploitation of this trait can be made through heterosis breeding. Similar results were reported by Hasanuzzaman *et al*. (2012), Nsabiyera *et al.* (2013), Navhale *et al.* (2014b) and Suryakumari *et al*. (2014).

4.5.3.6 Number of fruits per plant

gca effects

For this character, two lines *viz.,* LCA 442 (28.27), LCA 655 (64.01) and three testers G4 (22.62), LCA 678 (19.60), LCA 703-2 (49.39) recorded significant positive *gca* effects and were considered as good general combiners. Three lines (LCA 615, LCA 466 and LCA 654) and two testers (LCA 453 and LCA 315) showed significant negative *gca* effects (Table 4.21).

sca effects

The *sca* effects are in the range of -77.36 (LCA 442 x LCA 705-2) to 79.72 (LCA 466 x LCA 705-2). Hybrids evaluated for number of fruits per plant revealed that 11 crosses possessed significant positive *sca* effects while seven crosses had significant negative *sca* effects (Table 4.21). The best five hybrids with respect to this trait are LCA 466 x LCA 705-2 (79.72), LCA 442 x LCA 453 (73.06), LCA 504 x LCA 705-2 (71.08), LCA 355 x LCA 678 (70.11) and LCA 607 x LCA 703-2

(61.30) which recorded higher magnitude of significant positive *sca* effects and these are good specific combiners.

The ratio of *gca* to *sca* variances was less than unity for number of fruits per plant which indicated the importance of non-additive gene action for this character (Table 4.20) and improvement can be made through heterosis breeding. These results are in conformity with earlier reports of Hasanuzzaman *et al*. (2012), Chaudhary *et al*. (2013), Nsabiyera *et al.* (2013), Navhale *et al.* (2014b), Singh *et al.* (2014), Suryakumari *et al*. (2014) and Savitha *et al*. (2015).

4.5.3.7 Fruit length (cm)

***gca* effects**

The good general combiners are the lines LCA 442 (0.69), LCA 654 (0.92) and LCA 355 (1.42) and the tester LCA 315 (1.47) as they recorded significant positive *gca* effects. The lines LCA 615, LCA 466, LCA 655 and two testers LCA 678, LCA 703-2 showed significant negative *gca* effects (Table 4.22).

***sca* effects**

The *sca* effects for this trait ranged from -1.10 (LCA 466 x LCA 315) to 1.28 (LCA 466 x LCA 678). Evaluation of cross combinations revealed that six hybrids exhibited significant positive *sca* effects whereas two hybrids exhibited significant negative effects (Table 4.22). The higher magnitude of significant and positive *sca* effects were observed in LCA 466 x LCA 678 (1.28), LCA 615 x LCA 678 (1.04), LCA 504 x LCA 453 (1.00), LCA 355 x LCA 315 (0.96), LCA 655 x LCA 703-2 (0.82) and LCA 607 x G4 (0.81) and these regarded as good specific combiners.

The ratio of *gca* to *sca* variances (>1) indicated the predominance of additive gene action for this trait (Table 4.20) and improvement can be made through simple selection. Similar results were revealed by Prasath and Ponnuswami (2008), Pandey *et al*. (2012), Nsabiyera *et al.* (2013), Artur *et al.* (2014), Khalil and Hatem (2014), Mendes *et al*. (2014) and Nascimento *et al.* (2014).

4.5.3.8 Fruit diameter (cm)

***gca* effects**

The results on *gca* effects for fruit diameter revealed that five lines *viz.*, LCA 615 (0.07), LCA 446 (0.08), LCA 466 (0.16), LCA 442 (0.06), LCA 654 (0.05) and one tester LCA 453 (0.18) exhibited significant positive *gca* effects and these are regarded as good general combiners (Table 4.22). The lines LCA 655, LCA 355 and the tester G4 had significant negative *gca* effects.

***sca* effects**

For fruit diameter, four hybrids are regarded as good specific combiners *viz.*, LCA 442 x LCA 705-2 (0.20), LCA 654 x LCA 453 (0.20), LCA 446 x LCA 705-2 (0.19) and LCA 466 x G4 (0.14) as they exhibited significant positive *sca* effects while five hybrids registered significant negative *sca* effects (Table 4.22). The range of sca effects was in between of -0.33 (LCA 655 x LCA 453) to 0.20 (LCA 442 x LCA 705-2 and LCA 654 x LCA 453).

The ratio of *gca* to *sca* variances (>1) indicated the predominance of additive gene action for this trait (Table 4.20) and improvement can be made through simple selection. These results are in accordance with earlier reports of by Prasath and Ponnuswami (2008), Nsabiyera *et al.* (2013), Artur *et al.* (2014), Khalil and Hatem (2014), Mendes *et al*. (2014), Nascimento *et al.* (2014) and Singh *et al.* (2014).

4.5.3.9 Average dry fruit weight (g)

***gca* effects**

Among the lines and testers, good general combiners are three lines *viz.*, LCA 615 (0.06), LCA 654 (0.12), LCA 607 (0.11) and two testers *viz.*, LCA 453 (0.24), LCA 315 (0.07) as they registered significant positive *gca* effects while the lines LCA 655, LCA 355 and the testers G4, LCA 678 showed significant negative *gca* effects (Table 4.22).

***sca* effects**

The *sca* effects for this trait varied from -0.25 (LCA 655 x LCA 453) to 0.26 (LCA 655 x LCA 678). Evaluation of 54 hybrids for this trait revealed that nine hybrids recorded significant positive *sca* effects while seven hybrids showed significant negative *sca* effects (Table 4.22). The hybrids which showed comparatively higher magnitude of significant and positive *sca* effects are LCA 655 x LCA 678 (0.26), LCA 466 x G4 (0.23), LCA 442 x LCA 705-2 (0.21) and LCA 607 x LCA 453 (0.21) and these are regarded as good specific combiners for this trait.

The predominance of additive gene action was observed for this trait as indicated by the ratio of *gca* to *sca* variances (>1) (Table 4.20) and improvement can be made through simple selection procedure in segregating generations. These results are in line with findings of Prasath and Ponnuswami (2008), Pandey *et al*. (2012), Rodrigues *et al*. (2012), Chaudhary *et al.* (2013), Artur *et al.* (2014), Khalil and Hatem (2014), Mendes *et al*. (2014), Nascimento *et al.* (2014) and Singh *et al.* (2014) who made similar observations in chilli.

4.5.3.10 Fruit yield (g/plant)

***gca* effects**

For fruit yield , two lines *viz.*, LCA 442 (11.69), LCA 655 (36.99) and the tester LCA 703-2 (40.04) are good general combiners as they recorded significant positive *gca* effects whereas three lines *viz.,* LCA 615, LCA 466, LCA 355 and the tester G4 registered significant negative *gca* effects (Table 4.22).

***sca* effects**

For fruit yield , nine hybrids are good specific combiners *viz*., LCA 466 x LCA 705-2 (64.49), LCA 607 x LCA 703-2 (47.57), LCA 355 x LCA 678 (39.95), LCA 504 x LCA 705-2 (38.64), LCA 446 x LCA 703-2 (38.45), LCA 615 x LCA 453 (37.50), LCA 442 x LCA 453 (33.61), LCA 607 x G4 (32.30) and LCA 654 x

LCA 678 (31.11) as they have manifested significant positive *sca* effects and nine crosses registered significant negative *sca* effects (Table 4.22). The range of *sca* effects varied from -49.13 (LCA 607 x LCA 678) to 64.49 (LCA 466 x LCA 705-2).

Fruit yield is the most important trait which determines the worthiness of a hybrid. The ratio of *gca* to *sca* variances was less than unity for fruit yield suggesting that this trait is under the control of non-additive gene action (Table 4.20) and exploitation of this trait could be through heterosis breeding. These results are supported by the earlier findings of Hasanuzzaman *et al*. (2012), Artur *et al.* (2014), Navhale *et al.* (2014b), Singh *et al.* (2014), Suryakumari *et al*. (2014) and Savitha *et al*. (2015).

4.5.3.11 Number of seeds per fruit

***gca* effects**

Data from Table 4.22 indicated two lines *viz.,* LCA 615 (17.21), LCA 654 (5.52) and two testers LCA 453 (6.93), LCA 315 (4.99) recorded as good general combiners as they registered significant positive *gca* effects. Three lines (LCA 446, LCA 442 and LCA 355) and two testers (G4 and LCA 678) showed significant negative *gca* effects.

***sca* effects**

The *sca* effects ranged in between of -21.26 (LCA 504 x LCA 705-2) to 18.08 (LCA 655 x LCA 315). Hybrids evaluated for this trait revealed that, nine crosses possessed significant positive *sca* effects while seven crosses had significant negative *sca* effects (Table 4.22). The best two specific combiners for this trait are LCA 655 x LCA 315 (18.08) and LCA 466 x G4 (17.02) as they showed significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the preponderance of non additive gene action over additive gene action in controlling no. of seeds per fruit (Table 4.20). Similar results were also reported by Hasanuzzaman *et al*. (2012),

Nsabiyera *et al.* (2013), Navhale *et al.* (2014b), Singh *et al.* (2014), Suryakumari *et al*. (2014) and Savitha *et al*. (2015). This trait can be exploited through heterosis breeding.

4.5.3.12 Seed weight (g/1000 seed)

***gca* effects**

Among the lines and testers, two lines LCA 615 (0.64), LCA 607 (0.28) and three testers LCA 453 (0.37), LCA 703-2 (0.30), LCA 705-2 (0.26) recorded significant positive *gca* effects and these are regarded as good general combiners whereas the lines LCA 504, LCA 446, LCA 466, LCA 442 and the testers G4, LCA 678 showed significant negative *gca* effects (Table 4.22).

***sca* effects**

Evaluation of cross combinations revealed that three hybrids are good specific combiners *viz.,* LCA 446 x LCA 705-2 (0.84), LCA 607 x LCA 705-2 (0.82) and LCA 615 x LCA 678 (0.76) as they exhibited significant positive *sca* effects whereas one hybrid showed significant negative *sca* effects (Table 4.22). The range of *sca* effects varied from -1.01 (LCA 607 x LCA 678) to 0.84 (LCA 446 x LCA 705-2).

The ratio of *gca* to *sca* variances (>1) indicated the predominance of additive gene action over the non-additive action in controlling this trait (Table 4.20) and improvement can be made through simple selection procedure in segregating generations. This is in confirmity with findings of Singh and Chaudhary (2005b), Perej *et al.* (2009) and Rekha (2015) who also reported additive gene action plays an important role in inheritance of this trait.

4.5.3.13 Ascorbic acid (mg/100g)

***gca* effects**

Among the lines and testers significant positive *gca* effects were exhibited by two lines *viz.*, LCA 504 (17.14), LCA 446 (5.04) and three testers *viz.*, G4 (4.46), LCA 678 (7.83), LCA 703-2 (9.15) and these are regarded as good general combiners for this trait whereas the lines LCA 442, LCA 654 and the tester LCA 315 recorded significant negative *gca* effects (Table 4.23).

***sca* effects**

The range of *sca* effects was in between -49.94 (LCA 607 x LCA 453) to 38.79 (LCA 504 x LCA 315). Evaluation of the hybrids for *sca* effects revealed significant positive *sca* effects in 21 crosses whereas significant negative *sca* effects were recorded 23 crosses (Table 4.23). The best three specific combiners are LCA 504 x LCA 315 (38.79), LCA 615 x LCA 705-2 (36.09) and LCA 355 x LCA 678 (34.18) as they showed higher magnitude of significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling ascorbic acid (Table 4.20) and improvement can be made through heterosis breeding as reported by Pandey *et al.* (2012), Jindal *et al.* (2015) and Rekha (2015).

4.5.3.14 Oleoresin (%)

***gca* effects**

The lines LCA 615 (3.88), LCA 446 (1.24) and the tester G4 (2.08) registered significant positive *gca* effects (Table 4.23) and these are regarded as good general combiners whereas the lines LCA 466, LCA 442, LCA 655 and the testers LCA 453, LCA 703-2, LCA 315 recorded significant negative *gca* effects.

***sca* effects**

For oleoresin content, the range of *sca* effects varied from -4.70 (LCA 615 x LCA 315) to 7.04 (LCA 504 x G4). Nine crosses have manifested desirable significant positive *sca* effects while 13 crosses exhibited undesirable significant

negative *sca* effects (Table 4.23). For this trait, the best three specific combiners are LCA 504 x G4 (7.04), LCA 466 x LCA 453 (5.06) and LCA 615 x LCA 678 (4.42).

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling this trait (Table 4.20) and improvement can be made through heterosis breeding. These results are in accordance with earlier findings of Suryakumari *et al*. (2014), Jindal *et al.* (2015) and Rekha (2015).

4.5.3.15 Capsaicin (%)

***gca* effects**

Among lines and testers, the good general combiners are lines LCA 504 (0.02), LCA 654 (0.19) and the testers G4 (0.03), LCA 678 (0.02), LCA 453 (0.03) registered significant positive *gca* effects (Table 4.23) whereas the lines LCA 615, LCA 446, LCA 466, LCA 442, LCA 655 and the testers LCA 703-2, LCA 315 recorded significant negative *gca* effects.

***sca* effects**

The *sca* effects varied from -0.11 (LCA 654 x LCA 678) to 0.16 (LCA 615 x LCA 315). For capsaicin content, 12 crosses have manifested desirable significant positive *sca* effects while 12 crosses exhibited undesirable significant negative *sca* effects (Table 4.23). The hybrids LCA 615 x LCA 315 (0.16), LCA 504 x LCA 678 (0.11), LCA 504 x LCA 453 (0.11) and LCA 654 x G4 (0.11) are best specific combiners for this trait as they registered significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) for capsaicin content suggested that this trait is under the control of non-additive gene action (Table 4.20) and improvement can be made through heterosis breeding. The results are supported by earlier reports of Prasath and Ponnuswami (2008), Navhale *et al.* (2014b), Suryakumari *et al*. (2014) and Jindal *et al.* (2015).

4.5.3.16 Red carotenoids (mg/100g)

***gca* effects**

For this trait, the good general combiners are the lines LCA 466 (23.23), LCA 654 (20.38), LCA 355 (17.01) and the testers LCA 453 (5.23), LCA 705-2 (16.62) as they exhibited significant positive *gca* effects (Table 4.23). The lines LCA 615, LCA 607 and the testers LCA 703-2, LCA 315 showed significant negative *gca* effects.

***sca* effects**

The *sca* effects for red carotenoids were in between the -56.46 (LCA 607 x LCA 453) and 65.38 (LCA 607 x LCA 703-2). Thirteen crosses showed significant positive *sca* effects while 13 crosses exhibited significant negative *sca* effects (Table 4.23). The best three specific combiners are LCA 607 x LCA 703-2 (65.38), LCA 607 x LCA 705-2 (59.67) and LCA 615 x G4 (39.80) as they recorded higher magnitude of significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling red carotenoids (Table 4.20) and improvement can be made through heterosis breeding and the results are in conformity with earlier findings of Rekha (2015).

4.5.3.17 Yellow carotenoids (mg/100g)

***gca* effects**

For this trait, negative direction is desirable. Among lines and testers, the lines LCA 504 (-14.43), LCA 615 (-19.92), LCA 442 (-13.84), LCA 654 (-10.31), LCA 607 (-12.87) and the testers G4 (-10.89), LCA 703-2 (-15.70) registered significant negative *gca* effects and these are considered as good general combiners for this trait. The lines LCA 446, LCA 466, LCA 355 and the testers LCA 678, LCA 453 registered significant positive *gca* effects (Table 4.23).

***sca* effects**

The range of *sca* effects varied from -54.10 (LCA 442 x LCA 705-2) to 49.10 (LCA 355 x LCA 678). For yellow carotenoids, 13 crosses exhibited significant negative *sca* effects while 14 crosses showed significant positive *sca* effects (Table 4.23). The best three hybrids are LCA 442 x LCA 705-2 (-54.10), LCA 654 x G4 (-52.21) and LCA 607 x LCA 703-2 (-32.88) and were regarded as good specific combiners as they registered significant negative *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling yellow carotenoids (Table 4.20) and improvement can be made through heterosis breeding. These results are in accordance with earlier findings of Rekha (2015).

4.5.3.18 Total carotenoids (mg/100g)

***gca* effects**

The general combiners for this trait are the lines LCA 446 (11.85), LCA 466 (80.38), LCA 654 (10.07), LCA 355 (25.65) and the testers LCA 678 (17.34), LCA 453 (14.11), LCA 705-2 (14.17) as they registered significant positive *gca* effects (Table 4.23). The lines LCA 504, LCA 615, LCA 442, LCA 607 and the testers G4, LCA 703-2, LCA 315 recorded significant negative *gca* effects.

***sca* effects**

The range of *sca* effects varied from -60.48 (LCA 655 x LCA 703-2) to 84.61 (LCA 607 x LCA 705-2). For total carotenoids, 17 crosses each showed significant positive and significant negative *sca* effects (Table 4.23). The best three specific combiners were LCA 607 x LCA 705-2 (84.61), LCA 615 x G4 (69.06) and LCA 355 x LCA 678 (67.07) as they registered higher magnitude of desirable significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling total carotenoids (Table

4.20) and improvement can be made through heterosis breeding. These results are in accordance with earlier findings of Rekha (2015).

4.5.3.19 Total colour value (ASTA units)

***gca* effects**

The significant positive *gca* effects were exhibited by the lines LCA 446 (8.71), LCA 466 (18.92), LCA 442 (6.20), LCA 654 (4.30), LCA 355 (19.66) and the testers LCA 678 (5.97), LCA 453 (2.95), LCA 705-2 (5.82) and these genotypes are regarded as good general combiners for this trait. The lines LCA 615, LCA 607, LCA 655 and the testers LCA 703-2, LCA 315 recorded significant negative *gca* effects (Table 4.23).

***sca* effects**

The range of *sca* effects varied in between -35.91 (LCA 466 x LCA 315) to 27.88 (LCA 442 x LCA 315). Evaluation of the hybrids for *sca* effects for total colour value revealed that 16 crosses each showed significant positive and significant negative *sca* effects (Table 4.23). The best three specific combiners for this trait are LCA 442 x LCA 315 (27.88), LCA 615 x G4 (25.27) and LCA 655 x LCA 315 (22.51) as they showed higher magnitude of desirable significant positive *sca* effects.

The ratio of *gca* to *sca* variances (<1) revealed the predominance of non additive gene action over additive gene action in controlling total colour value (Table 4.20) and improvement can be made through heterosis breeding. These results are in line with earlier findings of Nandadevi *et al.* (2003), Jindal *et al.* (2015) and Rekha (2015).

Based on *gca* and *sca* effects, good general combiners and top three specific combiners for each character were summarized in Table 4.24. Based on *gca* effects, the genotypes LCA-442, LCA-654, LCA-655, LCA-703-2 and LCA-453 found to be promising general combiners for yield, yield components and quality traits. All

these parents might be contributing positive alleles for yield and yield attributes (Table 4.25). Among the lines, LCA-442 was found to be good general combiner for no. of fruits per plant, fruit length, fruit diameter and fruit yield, yellow carotenoids and total colour value, LCA-654 was found to be good general combiner for fruit length, fruit diameter, dry fruit weight, no. of seeds per fruit, capsaicin, red, yellow and total carotenoids and total colour value (fruit yield in desired direction) while LCA-655 was found to be good general combiner for plant height, no. of fruits per plant and fruit yield, yellow carotenoids. Among the testers, LCA-703-2 was found to be good general combiner for plant height, plant spread, no. of primary branches per plant, no. of fruits per plant, seed weight, fruit yield, ascorbic acid and yellow carotenoids while LCA-453 for fruit diameter, dry fruit weight, no. of seeds per fruit, seed weight, oleoresin, red, yellow and total carotenoids, total colour value.

The parents with good general combining ability for a trait also exhibited high *per se* performance for that trait. Therefore, these parents were noted as good source of favourable genes for increasing fruit yield through various yield contributing characters and use of these parental lines would be more rewarding for boosting fruit yield in chilli. It was further noted that using of these parents had resulted in crosses expressing useful heterosis for various traits.

Based on the *sca* effects nine crosses *viz*., LCA 466 x LCA 705-2 (for no. of fruits per plant, fruit yield , Ascorbic acid), LCA 607 x LCA 703-2 (for no. of fruits per plant, fruit yield, oleoresin, capsaicin, red, yellow and total carotenoids), LCA 355 x LCA 678 (for no. of fruits per plant, fruit yield, Ascorbic acid, capsaicin, red and yellow carotenoids, total colour value), LCA 504 x LCA 705-2 (for no. of primary branches, no. of fruits per plant, fruit yield), LCA 446 x LCA 703-2 (for plant height, fruit yield, capsaicin), LCA 615 x LCA 453 (for plant height, days to 50% flowering, no. of fruits per plant, dry fruit weight, fruit yield, yellow carotenoids), LCA 442 x LCA 453 (for plant spread, no. of fruits per plant, fruit yield, Ascorbic acid, total carotenoids), LCA 607 x G4 (for plant spread, days to 50% flowering, no. of fruits per plant, fruit length, fruit yield, Ascorbic acid) and

LCA 654 x LCA 678 (for no. of seeds per fruit, fruit yield) were identified as promising specific combiners for fruit yield, yield components and quality traits (Table 4.25).

The parents were estimated for general combining ability and accordingly were classified as good, average and poor combiners based on the estimates of *gca* effects (Table 4.26). The crosses which had both parents as good general combiners involving high x high general combiners may be advanced through pedigree method of selection. In crosses which had only one parent as good general combiner involving high x low or low x high general combiners, it would be improved through recurrent selection. The crosses which had both parents as poor general combiners involving low x low general combiners, it would be difficult to improve the trait by selection. Hence, improvement of this character is possible through heterosis breeding only.

The crosses exhibiting high *per se* performance may result from either good x good, good x average, average x average and poor x poor general combining parents. The good general combining parents when crossed do not always produce high *sca* effects, while poor general combining parents not always produce low *sca* effects. So, any parental combination either good x good, average x good, average x average or poor x poor may result into high *sca* effects.

For exploitation of heterosis, the information on *gca* should be supplemented with *sca* and hybrid performance. The estimates of *sca* effects revealed that none of the crosses was constantly superior for all the traits. This indicated that the specific combining ability of the crosses was not always dependent on the *gca* of the parents involved. These results are supported by the findings of Prasath and Ponnuswami (2008), Pandey *et al*. (2012), Chaudhary *et al.* (2013), Khalil and Hatem (2014), Suryakumari *et al*. (2014) and Jindal *et al*. (2015).

From the studies of line x tester analysis, it is concluded that three hybrids *viz*., LCA 607 x LCA 703-2, LCA 446 x LCA 703-2 and LCA 466 x LCA 705-2

were most promising hybrids with desirable *sca* effects, heterosis and *per se* performance for fruit yield, fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red, total carotenoids and total colour value. These hybrids may be further tested over locations and seasons and recommended for commercial release and the material generated in the present investigation could be utilized for future chilli breeding programmes.

GENERATION MEAN ANALYSIS

With a view to study the inheritance pattern of yield and its components, four crosses were selected *viz.*, LCA-710 x HC-28 (cross 1), LCA-712 x HC-28 (cross 2), LCA-712 x LCA-710 (cross 3) and LCA-764 x LCA-315 (cross 4). The above mentioned four crosses are here after referred to as cross 1, cross 2, cross 3 and cross 4 respectively.

Mean data on various quantitative traits recoded on different generations *viz.*, parents (P_1 and P_2), F_1, F_2, BC_1 and BC_2 of four cross combinations of chilli, were subjected to scaling test. First, the data were subjected to three parameter model to test adequacy of the additive-dominance model. If scaling tests were found to be significant in three parameter model indicating the inadequacy of the additive-dominance model, in such cases data was subjected to Hayman (1958) six parameter model. The results are elaborated character wise here under.

4.6 Generation means, scaling tests and gene effects

4.6.1 Plant height (cm)

4.6.1.1 Generation means

The parent 2 (P_2) recorded more plant height than parent 1 (P_1) in all crosses except in cross 3 where parent 1 (P_1) recorded more plant height (Table 4.27). The F_1 mean of the cross 3 surpassed both of its parental means indicating over dominance for plant height. In crosses 1, 2 and 4, the F_1 means were intermediate between their respective parental means indicating partial dominance. The F_2 means

were less than their corresponding F_1 means in cross 1 and 3 indicating some degree of inbreeding depression. The behaviour of back cross generations *viz.*, BC_1 and BC_2 were on expected lines except in cross 4, in which the mean of BC_2 (85.35) was almost equal to mean of BC_1 (85.55) but the recurrent parent involved in BC_2 has higher plant height than the recurrent parent involved in BC_1 indicating a slight deviation in performance of back cross generations from the expectations. The variation in expression of different generations was also observed in earlier findings of Hasanuzzaman and Golam (2011) and Prajapati *et al.* (2012).

4.6.1.2 Scaling tests and gene effects

The scaling tests and gene effects for plant height are presented in Table 4.28 and 4.29 respectively. The scaling test B was significant in only cross 4, indicating the presence of all the three types of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) type of gene interactions. Additive – dominance model was adequate in crosses 1, 2 and 3 due to absence of significant scaling tests.

In cross 1 and 2, the plant height was governed by significant additive (*d*) gene effects and improvement can be made through simple pedigree selection in segregating generations. The cross 4 showed significant dominance (*h*) and dominance x dominance (*l*) type of non-allelic gene interactions with opposite sign indicating duplicate type of epistasis for plant height (Table 4.29) and in such cases it would be better to exploit this trait by heterosis breeding, reciprocal recurrent selection or full sib selection. These results are in agreement with the findings of Hasanuzzaman and Golam (2011), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013) and Navhale *et al*. (2014a).

4.6.2 Plant spread (cm)

4.6.2.1 Generation means

The parent 2 (P_2) recorded more plant spread than parent 1 (P_1) in crosses 1 and 4 whereas parent 1 (P_1) recorded more plant spread in crosses 2 and 3 (Table 4.30). The F_1 mean of the cross 4 surpassed both of its parental means indicating over dominance for plant spread and the F_2 mean of cross 4 also higher than their corresponding parental means, which could be due to the presence of large number of transgressive segregates. In crosses 1, 2 and 3, the F_1 means were intermediate between their respective parental means indicating partial dominance. The F_2 means were less than their corresponding F_1 means in cross 1, 3 and 4 indicating some degree of inbreeding depression. The behaviour of back cross generations *viz.*, BC_1 and BC_2 were on expected lines except in cross 4, in which the mean of BC_2 (79.72) was near to mean of BC_1 (81.03) but the recurrent parent involved in BC_2 has higher plant height than the recurrent parent involved in BC_1 indicating a slight deviation in the performance of back cross generations from expectations. This kind of variation in different generations was also observed in earlier reports of Hasanuzzaman and Golam (2011).

4.6.2.2 Scaling tests and gene effects

One or two scaling tests were found to be significant in all the crosses, indicating the presence of non-allelic interactions in all the crosses. The scaling tests C and D in cross 1, while D in cross 2, A in cross 3, B and D in cross 4 were found significant (Table 4.31).

The additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were significant in cross 1 whereas dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were significant in cross 2 and 4 (Table 4.32). In crosses 1, 2 and 4 dominance (*h*) and dominance x dominance (*l*) type of gene interactions were significant with opposite signs revealed duplicate epistasis. All the 4 crosses showed duplicate epistasis as dominance (*h*) and dominance x dominance (*l*) type of epistasis were in opposite directions. In such cases selection in the early generation would be ineffective. Hence, under such a situation, growing of larger populations in

segregating generations, intermating and delayed selection would be helpful to get transgressive segregants. The heterosis breeding and reciprocal recurrent selection would be helpful in improvement of this trait due to presence of duplicate epistasis coupled with higher magnitude of dominance (*h*) and dominance x dominance (*l*) epistasis. The findings of earlier workers *viz.*, Kamboj *et al*. (2007), Jabeen *et al.* (2009) and Hasanuzzaman and Golam (2011) also supported the findings of present investigation.

4.6.3 Number of primary branches per plant

4.6.3.1 Generation means

The parent 1 (P_1) recorded more number of primary branches per plant in crosses 1(4.00) and 4 (4.20) (Table 4.33) whereas in cross 2 both the parents having equal number of primary branches and parent 2 (P_2) recorded more number of primary branches (4.00) in cross 3 than parent 1. The F_1 means of the crosses 2 and 4 having lower number of primary branches than both the parents whereas the F_1 means of the crosses 1 and 3 were slightly equal and above the parents. The F_2 means were less than their corresponding F_1 means in all crosses except in cross 2 indicating some degree of inbreeding depression. In cross 3, the behaviour of back cross generations was on expected lines whereas in remaining three crosses the mean of back cross generations were slightly deviated from expectations. These kinds of variations in generation means are also reported by Prajapati *et al.* (2012) in their earlier findings.

4.6.3.2 Scaling tests and gene effects

The scaling tests A, B in cross 1; A, B, C scaling tests in cross 2 and A, C scaling tests in cross 4 were significant (Table 4.34) indicating the presence of non-allelic interactions in crosses1, 2 and 4 whereas non-allelic interactions were absent in cross 3.

Dominance x dominance (*l*) type of gene interactions was significant in cross 1 whereas additive (*d*) gene effects were significant in cross 3 (Table 4.35). The improvement in cross 1 can be made through heterosis breeding and reciprocal recurrent selection due to presence of duplicate epistasis coupled with higher magnitude of dominance x dominance (*l*) epistasis whereas the improvement of crosses 2, 3 and 4 can be made through pedigree method of selection due to predominance of additive gene effects (*d*) (cross 3) and presence of complementary epistasis (cross 2 and 4). These results are in accordance with earlier findings of Somashekhar *et al.* (2008), Jabeen *et al.* (2009), Anandhi and Khader (2011), Prajapati *et al.* (2012) and Navhale *et al.* (2014a).

4.6.4 Days to 50% flowering

4.6.4.1 Generation means:

The parent 1 (P_1) have taken less number of days to 50% flowering in crosses 1 (23.00) and 2 (28.80) (Table 4.36) whereas in crosses 3 and 4, the P_2 was earlier. The F_1 means of the crosses 1 and 2 are intermediary between the parents which showed partial dominance whereas the F_1's of the crosses 3 and 4 taken more days to 50% flowering comparative to both the parents which indicating that presence of over dominance. The F_2 means were less than their corresponding F_1 means in crosses 1 and 4 indicating some degree of inbreeding depression. The behaviour of back cross generations BC_1 and BC_2 were on expected lines except in crosses 3 and 4, in which BC_1 and BC_2 are equal but the recurrent parents involved showed variation. This kind of variations in generation means are also reported by Hasanuzzaman and Golam (2011) and Prajapati and Agalodiya (2012) in their earlier findings.

4.6.4.2 Scaling tests and gene effects

One or more scaling tests were found to be significant in all the crosses, indicating the presence of non-allelic interactions in all the crosses. The scaling tests B and C were significant in cross 1; while A and C in cross 2; B, C and D in cross 3 and A, B and D in cross 4 (Table 4.37) indicating presence of non-allelic interactions.

Additive (*d*) and dominance x dominance (*l*) type of gene interactions in cross 1, additive (*d*) gene effects in cross 2 and dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions in cross 3 and 4 were found to be significant (Table 4.38). All the 4 crosses showed duplicate epistasis as dominance (*h*) and dominance x dominance (*l*) type of epistasis were in opposite signs. The improvement of earliness in chilli can be made by simple selection, pedigree selection, heterosis breeding and delayed selection as this trait governed by both additive, non - additive as well as non-allelic gene interactions. The results of this investigation are in line with earlier findings of Hasanuzzaman and Golam (2011), Prajapati and Agalodiya (2012) and Patel and Patel (2015).

4.6.5 Days to fruit maturity

4.6.5.1 Generation means:

The parent P_1 have taken less number of days to fruit maturity in crosses 1 (43.20) and 2 (54.80) whereas in crosses 3 and 4 P_2 was earlier (Table 4.39). The F_1 means of the crosses 1 and 2 are intermediary between the parents which showed partial dominance whereas the F_1's of the crosses 3 and 4 recorded over dominance as they have taken more days to fruit maturity comparative to both the parents. The F_2 means were less than their corresponding F_1 means in crosses 1 and 4 which indicating presence of inbreeding depression. The behaviour of back crosses BC_1 and BC_2 were on expected lines except in cross 4, in which BC_1 and BC_2 were slightly deviated from expectations. Similar kind of variations and expressions are also observed by Hasanuzzaman and Golam (2011) in their earlier reports.

4.6.5.2 Scaling tests and gene effects

The scaling tests B and D in cross 1; A, B, C and D in cross 2 and 3; A, B and D in cross 4 recorded significant values indicating presence of all types of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) type of gene interactions (Table 4.40).

Dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were significant in all crosses whereas cross 1 and 2 also recorded significant additive (*d*) gene effects (Table 4.41). In all four crosses the dominance (*h*) and dominance x dominance (*l*) type of gene interactions recorded opposite signs indicating duplicate epistasis. The improvement of early maturity in chilli can be made by simple selection, pedigree selection, heterosis breeding and delayed selection as this trait governed by both additive, non -additive as well as non-allelic gene interactions. These results are in agreement with earlier findings of Kamboj *et al.* (2007), Jabeen *et al*. (2009), Hasanuzzaman and Golam (2011) and Prajapati and Agalodiya (2012).

4.6.6 Number of fruits per plant

4.6.6.1 Generation means:

Regarding this trait, the parent 2 (P_2) recorded more fruits than parent 1 (P_1) in crosses 1 (417.00) and 2 (421.00) whereas parent 1 (P_1) recorded more number of fruits per plant in crosses 3 (306.00) and 4 (248.40). The F_1 mean of the crosses 1 and 2 are intermediary between the parents which indicating the presence of partial dominance. The crosses 3 and 4 are surpassed both of its parental means indicating over dominance for number of fruits per plant. The F_2 means were more than their corresponding F_1 means in cross 1 and 2 (Table 4.42) whereas in crosses 3 and 4 the F_2 means were lower than the F_1 means indicating some degree of inbreeding depression. The performance of back cross generations *viz.*, BC_1 and BC_2 were on expected lines except in crosses 2 and 3. In cross 2 the mean of BC_1 (351.55) was more than BC_2 (304.25) but the recurrent parent involved in BC_2 has more number of fruits per plant (421.00) than the recurrent parent involved in BC_1 (306.00) and in

cross 3, mean of BC_2 (332.35) was more than BC_1 (325.85) but the recurrent parent involved in BC_1 has more number of fruits per plant (306.00) than the recurrent parent involved in BC_2 (228.20) which indicating that mean of back cross generations were a little deviated from expectations. For this trait, the similar kinds of expressions are also observed by Marame *et al*. (2009), Hasanuzzaman and Golam (2011), Patil (2011) and Prajapati *et al.* (2012) in their findings.

4.6.6.2 Scaling tests and gene effects

The scaling tests for this trait are presented in Table 4.43 and showed significant B, C and D scaling tests for cross 2 indicating the presence of all non-allelic gene interactions whereas significant D scaling test for cross 1 indicating the presence of additive x additive (*i*) type of gene interaction. Additive – dominance model was adequate in crosses 3 and 4 due to absence of significant scaling tests.

Regarding gene effects, additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were significant in cross 1 and 2 (Table 4.44) while interaction effects were absent for crosses 3 and 4. The magnitude of dominance gene effects were more than that of additive gene effects which confirms that dominance gene effects found to contribute substantially in the inheritance of number of fruits per plant and also observed duplicate epistasis in crosses 1 and 2. In such cases selection in the early generation would be ineffective. Hence, under such a situation, growing of larger populations in segregating generations, intermating and delayed selection would be helpful to get transgressive segregants and the heterosis breeding also would be helpful in improvement of this trait due to presence of duplicate epistasis coupled with higher magnitude of dominance (*h*) and dominance x dominance (*l*) epistasis. These results are in conformity with the findings of Marame *et al*. (2009), Anandhi and Khader (2011), Patil (2011), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013) and Navhale *et al*. (2014a).

4.6.7 Fruit length (cm)

4.6.7.1 Generation means

The parent 1 (P_1) recorded maximum fruit length than parent 2 (P_2) in all crosses except in cross 4, in which parent 2 (P_2) recorded highest fruit length (11.30) (Table 4.45). The F_1 means of the crosses 3 and 4 surpassed both of its parental means indicating over dominance for fruit length. In crosses 1 and 2, the F_1 means were intermediate between their respective parental means indicating partial dominance and the F_2 means of all crosses lower than their corresponding F_1 means indicating some degree of inbreeding depression. The performance of all back cross generations were on expected lines. The similar kinds of expressions are also observed by Hasanuzzaman and Golam (2011), Patil (2011), Prajapati *et al.* (2012) and Manu *et al.* (2014) in their findings.

4.6.7.2 Scaling tests and gene effects

For fruit length the scaling tests C and D were found significant in cross 1 and 2 indicating the presence of both additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions and the scaling tests A, B and C were significant for cross 3 revealed presence of all three types of non-allelic gene interactions (Table 4.46). Additive – dominance model was adequate for cross 4 due to non significance of scaling tests.

Additive (*d*) gene effects in cross 1, 2 and 3; dominance (*h*) gene effects in all crosses; additive x additive (*i*) type of gene interactions in cross 1 and 2 and dominance x dominance (*l*) gene interactions in cross 1 recorded significant effects (Table 4.47). The magnitude of dominance gene effects were more than that of additive gene effects in all crosses revealed that the dominance gene effects plays an important role in the inheritance of fruit length. The improvement of this trait can be made by simple selection, pedigree selection, heterosis breeding and recurrent selection as this trait governed by both additive, non -additive as well as non-allelic gene interactions and also presence of duplicate (cross 1 and 2) and complementary

(cross 3) epistasis. These results in this study was also supported by earlier reports of Anandhi and Khader (2011), Patil *et al.* (2012b), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013), Manu *et al.* (2014) and Navhale *et al*. (2014a).

4.6.8 Fruit diameter (cm)

4.6.8.1 Generation means

The parent 1 (P_1) recorded maximum fruit diameter than parent 2 (P_2) in crosses 2 (1.10) and 3 (1.10) whereas in crosses 1 (0.97) and 4 (1.30), the parent 2 (P_2) recorded maximum fruit diameter. The F_1 means were intermediate between their respective parental means indicating partial dominance. The F_2 means were lower than their corresponding F_1 means in all crosses (Table 4.48) except in cross1 indicating some degree of inbreeding depression. The behaviour of back cross generations *viz.,* BC_1 and BC_2 were on expected lines except in crosses 1 and 4. In cross 1 the mean of BC_1 (1.01) was higher than BC_2 (0.88) but the recurrent parent involved in BC_2 has higher fruit diameter (0.97) than the recurrent parent involved in BC_1 (0.82) and in cross 4 , BC_1 (1.21) was higher than BC_2 (1.19) but the recurrent parent involved in BC_2 has higher fruit diameter (1.30) than the recurrent parent involved in BC_1 (1.07) indicating a slight deviation in performance of back cross generations from expectations. The variation in expression of generations is also observed by Hasanuzzaman and Golam (2011), Patil (2011), Prajapati *et al.* (2012) and Manu *et al.* (2014) in their earlier findings.

4.6.8.2 Scaling tests and gene effects

The significance of one or two scaling tests in all the crosses clearly indicated the presence of all the three types of non-allelic interactions *viz*., additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions (Table 4.49).

The dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) gene interactions were significant in cross 2 and 3 with higher magnitude of

dominance x dominance (*l*) gene interactions (Table 4.50) revealed that dominance gene effects play an important role in inheritance of fruit diameter. In all crosses, duplicate epistasis was observed. Hence, it would be better to exploit this trait by heterosis breeding and recurrent selection. These results in this study was also supported by earlier reports of Anandhi and Khader (2011), Patil *et al.* (2012b), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013), Manu *et al.* (2014) and Navhale *et al*. (2014a).

4.6.9 Average dry fruit weight (g)

4.6.9.1 Generation means

The parent 2 (P_2) recorded maximum fruit weight than parent 1 (P_1) in crosses 1 (0.58) and 4 (1.35) whereas parent 1 (P_1) recorded maximum fruit weight in crosses 2 (0.81) and 3 (0.80) (Table 4.51). The F_1 mean of the all crosses are intermediary between both the parents indicating partial dominance. The F_2 means were lower than their corresponding F_1 means in all crosses indicating some degree of inbreeding depression. The behaviour of back cross generations were on expected lines except in cross 1, in which the mean of BC_1 (0.59) was more than BC_2 (0.54) but the recurrent parent involved in BC_2 has higher fruit weight (0.58) than the recurrent parent involved in BC_1 (0.53) indicating a slight deviation in performance of back cross generations from expectations. For this trait, the similar kinds of expressions are also observed by Marame *et al*. (2009), Hasanuzzaman and Golam (2011), Prajapati *et al.* (2012) and Manu *et al.* (2014).

4.6.9.2 Scaling tests and gene effects

The scaling test B was found significant in cross 4 (Table 4.52) indicating the presence of all three types of non-allelic gene interactions and additive – dominance model was adequate in crosses 1, 2 and 3 due to absence of significant scaling tests.

Additive (*d*) gene effects were significant in crosses 2, 3 and 4 and dominance x dominance (*l*) gene interactions were significant in cross 4 (Table

4.53). The exploition of cross 4 can be done by following the heterosis breeding and pedigree method as predominance of both additive (*d*) and dominance x dominance (*l*) epistasis and the remaining crosses could be improved by simple pedigree method due to predominance of additive gene action. Similar findings were reported by Somashekar *et al.* (2008), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013) and Manu *et al.* (2014) in chilli.

4.6.10 Fruit yield (g/plant)

4.6.10.1 Generation means

For this trait, the parent 1 (P_1) recorded highest yield than parent 2 (P_2) in crosses 2 (242.00) and 3 (242.00) whereas parent 2 (P_2) recorded maximum yield in crosses 1 (170.00) and 4 (179.40) (Table 4.54). The F_1 mean of all the crosses surpassed both of its parental means except cross 1 which revealed presence of over dominance, while in cross 1 the F_1 mean was in between the parents indicating partial dominance. The F_2 means were lower than their corresponding F1 means for all the crosses indicating some degree of inbreeding depression. The performance of back cross generations *viz.,* BC_1 and BC_2 were on predictable lines except in cross 4, in which the mean of BC_1 (236.50) was more than BC_2 (190.00) but the recurrent parent involved in BC_2 had maximum yield (179.40) than the recurrent parent involved in BC_1 (130.00) indicating a slight deviation in performance of back cross generations from expectations. Similar kinds of variations are also observed by Marame *et al*. (2009), Hasanuzzaman and Golam (2011), Patil (2011) and Prajapati *et al.* (2012) in their earlier findings.

4.6.10.2 Scaling tests and gene effects

The significance of one or all of the scaling tests A, B, C and D in all the crosses clearly indicated the presence of all the three types of non-allelic gene interactions *viz.,* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions for this trait. The scaling tests C and D in cross 1; A,

B, and D in cross 2; A and C in cross 3 and A in cross 4 showed significant values (Table 4.55)

The gene effects *viz.*, additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) gene interactions in cross 1; additive (*d*), additive x additive (*i*) and dominance x dominance (*l*) gene interactions in cross 2 and additive (*d*), dominance (*h*) and dominance x dominance (*l*) gene interactions in cross 4 were found significant and the crosses 1,2 and 4 recorded duplicate epistasis as dominance (*h*) and dominance x dominance (*l*) gene interactions were significant with opposite signs (Table 4.56). The magnitude of dominance gene effects was higher than that of additive and epistasis indicating that fruit yield per plant governed by dominance gene effects. Exploiting of this character can be made by following the heterosis breeding, recurrent selection and pedigree method of selection as predominance of both additive and non-additive gene effects. These results in accordance with earlier reports of Anandhi and Khader (2011), Patil (2011), Prajapati *et al.* (2012), Savitha and Pugalendhi (2013) and Navhale *et al*. (2014a).

4.6.11 Number of seeds per fruit

4.6.11.1 Generation means

The parent 2 (P_2) recorded more number of seeds per fruit than parent 1 (P_1) in crosses1 (59.60) and 2 (59.60) (Table 4.57) whereas parent 1 (P_1) recorded more number of seeds per fruit in crosses 3 (41.32) and 4 (69.88). The F_1 mean of the crosses 1, 2 and 3 are intermediary between the parents which indicating the presence of partial dominance whereas the cross 4 surpassed both of its parental means indicating over dominance. The F_2 means were lower than their corresponding F_1 means in cross 1, 2 and 4 except cross 3 indicating presence of some degree of inbreeding depression. The means of back cross generations *viz.*, BC_1 and BC_2 were on expected lines for crosses 1 and 2 whereas in crosses 3 and 4 the means of back cross generations were slightly deviated from expectations. For

this trait, the similar kinds of variations are also observed in earlier reports of Marame *et al*. (2009) Hasanuzzaman and Golam (2011).

4.6.11.2 Scaling tests and gene effects

The scaling tests A and D in cross 1; B and C in cross 3; B and D in cross 4 (Table 4.58) recorded significant values indicating presence of all types of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) type of gene interactions whereas non-allelic gene interactions were absent in cross 2 as all the scaling tests were non-significant.

Dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were found significant in crosses 1 and 4 while in crosses 2 and 4 significant additive (*d*) gene effects were found (Table 4.59). The duplicate epistasis was recorded in crosses 1, 3 and 4. Therefore, it would be better to exploit the this character by heterosis breeding and recurrent selection due to higher magnitude of dominance (*h*) and dominance x dominance (*l*) type of gene interactions and presence of duplicate epistasis. Similar findings reported in earlier works of Somashekhar *et al*. (2008), Marame *et al*. (2009), Hasanuzzaman and Golam (2011), Patil *et al*. (2012b) and Navhale *et al.* (2014a).

4.6.12 Seed weight (g/1000 seed)

4.6.12.1 Generation means

The parent 1 (P_1) recorded maximum seed weight than parent 2 (P_2) for all crosses. The F_1 mean of the cross 2 (5.50) was intermediate between the both parents (Table 4.60) indicating partial dominance and the F_1 means were higher than their corresponding parents in crosses 3 and 4 indicating presence of over dominance whereas the F_1 mean was lower than their corresponding parents in cross 1. The F_2 means were lower than their corresponding F_1 means in cross 2, 3 and 4 except in cross 1 indicating presence of some degree of inbreeding depression. The behaviour

of back cross generations were on expected lines in crosses 2 and 4 whereas the crosses 1 and 3 slightly deviated from the expectations.

4.6.12.2 Scaling tests and gene effects

One or two scaling tests were found to be significant for all the crosses except for cross 2 indicating the presence of non-allelic interactions in all the crosses. The scaling tests C was in cross 1, while A in cross 3; A, B and C in cross 4 were found significant (Table 4.61) whereas non-significant scaling tests were found in cross 2 which indicated that absence of non-allelic gene interactions.

The additive (*d*) gene effects were significant in cross 3 whereas dominance x dominance (*l*) type of gene interactions were significant in cross 4 (Table 4.62). The complementary type of epistasis was observed in all crosses for this trait and thus can be exploited effectively through pedigree method of selection. These reports are in line with earlier reports of Patil *et al.* (2012b) in chilli.

4.6.13 Ascorbic acid (mg/100g)

4.6.13.1 Generation means

The parent 2 (P_2) recorded highest ascorbic acid in crosses 1 (29.24), 2 (29.64) and 4 (31.29) whereas parent 1 (P_1) exhibited highest (29.30) for cross 3 (Table 4.63). The F_1 means of the crosses 2 and 4 were highest over both of their parents which revealed presence of over dominance whereas the crosses 1 and 3 recorded lowest F_1 means than their corresponding parents. The F_2 means were less than their corresponding F_1 means for only cross 2 indicating presence of some inbreeding depression. The behaviour of back cross generations BC_1 and BC_2 were on expected lines for all crosses except in cross 2 indicating that the means of back cross generations were slightly deviated from expectations.

4.6.13.2 Scaling tests and gene effects

The significance of one or all of the scaling tests A, B, C and D in all the crosses clearly indicated the presence of all the three types of non-allelic gene

interactions *viz.*, additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions for this trait. The scaling tests A, B, C and D in cross 1, 4; A, B and D in cross 2; A, B and C in cross 3 were found significant (Table 4.64).

The gene effects *viz.*, additive (*d*), dominance (*h*) and additive x additive (*i*) gene interactions in cross 1 and 2; dominance x dominance (*l*) gene interactions in cross 2 and 3; additive (*d*) gene effects in cross 3 and additive x additive (*i*) gene interactions in cross 4 were found significant (Table 4.65). The magnitude of dominance and dominance x dominance (*l*) gene interactions were found more than that of additive gene effects in crosses 1, 2 and 3 revealed that the dominance gene effects plays an important role in the inheritance of ascorbic acid. The improvement of this trait can be made by simple selection, pedigree selection, heterosis breeding and recurrent selection as this trait governed by both additive, non - additive as well as non-allelic gene interactions and also presence of duplicate (cross 1 and 2) and complementary (cross 3 and 4) epistasis. These results are in agreement with findings of earlier works of Kamboj *et al*. (2006).

4.6.14 Oleoresin (%)

4.6.14.1 Generation means

The highest oleoresin content was recorded by parent 2 (P_2) in crosses 1 (11.55), 2 (11.55) and 3 (10.88) whereas parent 1 (P_1) exhibited highest (11.85) for cross 4 (Table 4.66). The F_1 means of the crosses 2 and 3 were highest over both of their parents which revealed presence of over dominance whereas the crosses 1 and 4 recorded intermediate F_1 means between their corresponding parents indicating the presence of partial dominance. The F_2 means were less than their corresponding F_1 means for crosses 2, 3 and 4 indicating presence of some inbreeding depression whereas cross 1 recorded highest F_2 means than their corresponding F_1 means. The behaviour of back cross generations BC_1 and BC_2 were on expected lines for crosses

2 and 3 whereas the back cross generations of crosses 1 and 4 were deviated from expectations.

4.6.14.2 Scaling tests and gene effects

The scaling tests A, B and D in cross 1 and 2; A, B, C and D in cross 4 and A in cross 3 were found significant (Table 4.67). The significance of one or all of the scaling tests A, B, C and D in all the crosses clearly indicated the presence of all the three types of non-allelic gene interactions *viz.*, additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions for this trait.

The gene effects *viz.*, additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) gene interactions in crosses 1, 2 and 4 and additive x additive (*i*) gene interactions in cross 3 were found significant (Table 4.68). The improvement of this trait can be made by simple selection, pedigree method of selection, heterosis breeding and recurrent selection as this trait governed by both additive, non -additive and non-allelic gene interactions and also due to presence of duplicate (cross 3) and complementary (cross 1,2 and 4) epistasis with higher magnitude of dominance x dominance (*l*) gene interactions.

4.6.15 Capsaicin (%)

4.6.15.1 Generation means

Among the two parents, the parent 1 (P_1) recorded maximum capsaicin content than parent 2 (P_2) in all crosses except in cross 4 where the parent 2 (P_2) recorded maximum capsaicin content (0.38) (Table 4.69). The F_1 means of the cross 1 surpassed both of its parental means indicating over dominance for capsaicin content and in crosses 2 and 4, the F_1 means were intermediate between their respective parental means indicating partial dominance, but in cross 4, F_1 means lower than their corresponding mid parental means suggesting partial dominance towards the lowest capsaicin content (P_1). The F_2's in all crosses exhibited highest capsaicin than their corresponding parents and F_1's, which could be due to the

presence of large number of transgressive segregates. The performance of BC_1 and BC_2 were on predictable lines except in cross 1, in which the mean of BC_2 (0.66) was near to mean of BC_1 (0.61) but the recurrent parent involved in BC_2 recorded highest capsaicin (0.38) than the recurrent parent involved in BC_1 (0.27) indicating a little deviation in performance of back cross generations from expectations. The similar type of generation means also observed in earlier findings of Dhall and Hundal (2005a).

4.6.15.2 Scaling tests and gene effects

The scaling tests were significant for all the crosses indicating the presence of all three types of non- allelic gene interactions. The scaling tests B, C and D in cross 1; A, B and C in crosses 2 and 4; C and D in cross 3 were found significant for capsaicin (Table 4.70).

In cross 1, dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene effects were significant while in cross 2, additive type (*d*) of gene effects were significant. Additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) types of gene interactions were significant in cross 3 whereas only dominance x dominance (*l*) types of gene effects were significant in cross 4 (Table 4.71). The dominance (*h*) and dominance x dominance (*l*) types of gene effects were significant and have opposite signs indicated that presence of duplicate epistasis. According those gene effects, this trait was governed by both additive and non-additive gene effects. Therefore it would be better to exploit these crosses by pedigree selection and heterosis breeding. Similar findings are reported by Zewdie and Bosland (2000), Dhall and Hundal (2005a), Tempeetikul *et al*. (2013) and Navhale *et al*. (2014a).

4.6.16 Red carotenoids (mg/100g)

4.6.16.1 Generation means

In crosses 1 (166.10) and 2 (134.49), the maximum red carotenoids were recorded by the parent 1 (P_1) than parent 2 (P_2) whereas the parent 2 (P_2) recorded maximum red carotenoids in crosses 3 (166.10) and 4 (162.39). The F_1mean of the cross 1 (179.52) and cross 3 (189.03) surpassed both of its parental means (Table 4.72) revealed presence of over dominance for this trait and in cross 2, the F_1 mean was intermediate between their respective parental means but higher than mid parent mean indicating partial dominance towards the parent 1 (134.49) which recorded maximum carotenoids. The F_2 means were less than their corresponding F_1means in all crosses except in cross 2 indicating some degree of inbreeding depression. The means performance of back cross generations were on expected lines for all crosses.

4.6.16.2 Scaling tests and gene effects

The scaling tests A, B, C and D in cross 3; A, B, C in crosses 2 and 4; C and D in cross 1 were found significant (Table 4.73). The significance of one or all of the scaling tests A, B, C and D in all the crosses clearly indicated the presence of all the three types of non-allelic gene interactions *viz.*, additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions for this trait.

The gene effects *viz.,* additive (*d*), dominance (*h*) and additive x additive (*i*) gene interactions in cross 1, additive (*d*) and dominance x dominance (*l*) gene interactions in cross 2 and 4; dominance (*h*) and additive x additive (*i*) gene interactions in cross 3 were found significant (Table 4.74). Duplicate epistasis was observed in crosses 1, 2 and 4 whereas complimentary epistasis was observed in cross 3 with higher magnitude of dominance (*h*) gene effects (cross 1 and 3) and dominance x dominance (*l*) gene interactions (cross 2 and 4) indicating that dominance gene effects plays an important role in the inheritance of this trait. Hence heterosis breeding and delay selection would be effectively used to exploit these crosses.

4.6.17 Yellow carotenoids (mg/100g)

4.6.17.1 Generation means

The maximum yellow carotenoids in crosses 2, 3 and 4 were observed by parent 2 (P_2) whereas in cross 1, the maximum yellow carotenoids were exhibited by parent 1 (146.06) (Table 4.75). In crosses 2 and 3, the F_1means were intermediate in between their respective parental means indicating partial dominance. The F_2 means were less than their corresponding F_1 means in crosses 1, 2 and 4 indicating some degree of inbreeding depression. The behaviour of back cross generations were on predictable lines for crosses 2 and 3 but in crosses 1 and 4, the mean of back cross generations were somewhat deviated from expectations.

4.6.17.2 Scaling tests and gene effects

The scaling tests were significant for all the crosses except for cross 1 indicating the presence of all three types of non- allelic gene interactions. The scaling tests B, C in cross 2; A in cross 3; A, B and C in cross 4 were found significant for yellow cerotenoids (Table 4.76) and scaling tests for cross 1 were non-significant which indicated that absence of non-allelic interactions.

Additive (*d*) gene effects were significant in crosses 2, 3 and 4 whereas dominance (*h*) gene effects were significant in cross 3 and dominance x dominance (*l*) type of gene effects were significant in cross 4 (Table 4.77). This trait was governed by both additive and non-additive gene effects and thus it would be better to exploit this trait by pedigree selection and heterosis breeding.

4.6.18 Total carotenoids (mg/100g)

4.6.18.1 Generation means

The parent 2 (P_2) recorded maximum total carotenoids than parent 1 (P_1) in all crosses except in cross 1 where parent 1 (P_1) recorded maximum total carotenoids (312.15) (Table 4.78). In crosses 1, 2 and 3, the F_1 means were intermediate in between their respective parental means indicating partial dominance, but in cross 4, F_1 mean (223.57) was lower than its corresponding parental means. The F_2 means were less than their corresponding F_1means in cross

1, 3 and 4 indicating presence of some degree of inbreeding depression. The performance of back cross generations *viz.,* BC_1 and BC_2 were on expected lines for all crosses except in cross 2, in which the means of back cross generations were a little deviated from expectations.

4.6.18.2 Scaling tests and gene effects

The scaling tests A, B and C in cross 4; C in cross 1; A in cross 2; B and C in cross 3 were found significant (Table 4.79). The significance of one or all of the scaling tests A, B, C and D in all the crosses clearly indicated the presence of all the three types of non-allelic gene interactions *viz.,* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) gene interactions for this trait.

The additive (*d)* effects in cross 2 and dominance x dominance (*l*) gene interactions in cross 4 were found significant (Table 4.80). Higher magnitude of dominance x dominance (*l*) gene interactions was observed in cross 4. This trait can be exploited effectively by heterosis breeding and selection as presence of duplicate (cross 1 and 2) as well as complimentary (3 and 4) epistasis.

4.6.19 Total colour value (ASTA Units)

4.6.19.1 Generation means

The maximum colour value was recorded by parent 2 (P_2) in crosses 2 (96.20), 3 (122.03) and 3 (103.51) whereas parent 1 (P_1) exhibited highest (122.43) for cross 1(Table 4.81). The F_1 mean of the cross 2 was highest over both of their parents which revealed presence of over dominance whereas the crosses 1 and 3 recorded intermediate F_1 means between their corresponding parents indicating the presence of partial dominance. The F_2 means were less than their corresponding F_1 means for crosses 1, 3 and 4 indicating presence of some inbreeding depression whereas cross 2 recorded highest F_2 means than their corresponding F_1 means. The

behaviour of BC_1 and BC_2 were on expected lines for crosses 1, 3 and 4 whereas the backcross generations of crosses 2 were deviated from expectations. Similar types of observations are recorded by Dhall and Hundal (2005b) in their earlier findings.

4.6.19.2 Scaling tests and gene effects

The scaling tests were significant for all the crosses indicating the presence of all three types of non- allelic gene interactions. The scaling tests C, D in cross 1; A in cross 2; B in cross 3; A, B and C in cross 4 were found significant for total colour value (Table 4.82).

Additive (*d*) gene effects in cross 2; additive (*d*) and dominance x dominance (*l*) gene interactions in cross 4; dominance (*h*) and additive x additive (*i*) type of gene interactions in cross 1 were found significant (Table 4.83). The dominance (*h*) and dominance x dominance (*l*) types of gene effects were observed with opposite signs which indicated that presence of duplicate epistasis in cross 1, 2 and 4 and this trait governed by both additive and non-additive gene action. Therefore it would be better to exploit this trait by heterosis breeding and selection. These results are in line with earlier findings of Dhall and Hundal (2005b).

In general, the F_1 means were intermediate between their respective parental means indicating that F_1's showed partial dominance. But the F_1's showed over dominance for number of primary branches per plant, capsaicin and red carotenoids in cross 1 (LCA-710 x HC-28); for fruit yield, ascorbic acid, oleoresin and total colour value in cross 2 (LCA-712 x HC-28); for plant height, days to 50% flowering, days to fruit maturity, number of fruits per plant, fruit length, fruit yield, seed weight, oleoresin and red carotenoids in cross 3 (LCA-712 x LCA-710); for plant spread, days to 50% flowering, days to fruit maturity, number of fruits per plant, fruit length, average dry fruit weight, fruit yield, number of seeds per fruit, seed weight and ascorbic acid in cross 4 (LCA-764 x LCA-315). Hence, it can be concluded that the F_1's in crosses 3 and 4 showed over dominance for more number of characters. The means of segregating generations (F_2, BC_1 and BC_2) were on

expected lines in some crosses for some traits whereas in some crosses for other traits they have been deviated from expectations.

The superiority of F_1 could be due to an accumulation of favorable dominant alleles while the superiority in performance of segregating generations (F_2, BC_1 and BC_2) might suggest a higher frequency of their transgressive segregants. Transgressions in segregating generations could occur due to a wider genetic distance between genotypes of their parents. The particular cases in which the backcross generations (BC_1 and BC_2) were superior to their matching generations (P_1 and P_2) might also indicate an accumulation of some favorable alleles in them. The reverse case, in which the F_2 generation was inferior to its matching progeny generations (F_1, BC_1 and BC_2), could be due to the maximum segregation of their desirable alleles which may result in higher frequency of inferior segregants in some crosses (Marame *et al*., 2009). The differences in performances among the generations could be caused by both the additive and dominance genes as well as their interaction effects, most of which might be manipulated through recombination and selection (Perera *et al*. 2001). Thus, the pattern of generation means in the current study indicates a simple selection method within parental lines does not seem feasible for the improvement of fruit traits in hot pepper. The variation in generation means by itself neither clearly specified the magnitude and nature of gene effects involved in inheritance of any of the traits nor confidently enabled to propose correct breeding procedures (Marame *et al.,* 2009).

Non significance of all the scaling tests (A, B, C and D) indicates the absence of non-allelic gene interactions. In the present investigation, the significance of one or more scales in one or more crosses was observed for all the characters indicating the presence of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) type of gene interactions in the inheritance of all characters. The non-significance of all scaling tests found for plant height and average dry fruit weight in crosses 1, 2 and 3; for yellow carotenoids in cross 1; for number of seeds per fruit, seed weight in cross 2; for number of primary

branches per plant in cross 3; for number of fruits per plant in crosses 3 and 4 and for fruit length in cross 4 indicated the adequacy of simple additive dominance model due to absence of non-allelic gene interactions.

From the view of gene effects, additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions were found significant for majority of characters in four crosses. The additive (*d*) type of gene effects were found significant for 10, 14, seven, eight characters in cross 1, 2, 3 and 4 respectively whereas the dominance (*h*) type of gene effects were found significant for 12, seven, seven, eight characters in cross 1, 2, 3 and 4 respectively. The additive x additive (*i*) type of epistasis were found significant for 11, eight, five, six characters in cross 1, 2, 3 and 4 respectively whereas the dominance x dominance (*l*) type of epistasis were found significant for 10, eight, five, 14 characters in cross 1, 2, 3 and 4 respectively. Hence it can be concluded that in all the four crosses, the characters were governed by all or either additive, non-additive or epistatic interactions which indicates that these four crosses can be improved by either pedigree selection, heterosis breeding or reciprocal recurrent selection (Comstock *et al*., 1949). But in cross 2, additive gene effects were predominant in governing the majority of the characters compare to other gene effects and thus revealed that pedigree method of selection will be effective compared to others. In cross 4, dominance x dominance (*l*) type of epistasis were predominant in governing the majority of the characters compared to other gene effects revealing that either heterosis breeding, reciprocal recurrent selection or full sib selection were effective compare to other breeding methods.

In general, duplicate epistasis for many traits in four crosses was found as dominance (*h*) and dominance x dominance (*l*) type of epistasis have opposite signs. This will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistatic effects (Dhall and Hundal, 2006). However, Jindal *et al.* (1993) and Amawate and Behl, (1995) suggested that duplicate epistasis might restrict the expression and selection of a trait in early segregating generations. The

selection in early generations would not be effective for fixable components of variation. Such gene effects can however be exploited by intermating the selected segregants and delaying the selection to the advanced generations (Jindal *et al*., 1993). Delayed selection (Sharma and Sharma, 1995) or selection after biparental intermating (Misra *et al.,* 1994) would be more effective to get a good response in such cases. The complementary epistasis (same signs) was found for seed weight in cross 1; for number of primary branches and capsaicin in cross 2; for fruit length, fruit yield, seed weight, ascorbic acid, oleoresin, red carotenoids, total carotenoids and total colour value in cross 3 and for number of primary branches, seed weight, ascorbic acid and total carotenoids in cross 4. The additive, additive × additive or any other digenic complementary gene interaction is fixable and thus can be exploited effectively for the improvement of the traits through pedigree method of selection (Ram, 1994). Considering all these observations together, the pedigree or recurrent selection is recommended for varietal improvement of chilli.

4.7 Inheritance of fruit bearing habit, fruit position and branching habit:

Cross: LCA 712 x HC-28 for fruit bearing habit and fruit position

In cross LCA 712 x HC-28, all the F_1 plants produced solitary fruits (Table 4.84 and plate 9) indicating the dominance of solitary bearing over the clustered bearing habit. The F_2 plants segregated into 245 plants with solitary fruits and 88 plants with clustered fruit habit fitted the expected genetic ratio of 3:1. In BC_1 generation, out of 195 plants, 190 plants were with solitary fruits and only five plants were with clustered fruits, which fitted the generation ratio of 1:0. The BC_2 generation was segregated into 140 plants with solitary fruits and 121 plants with clustered fruits which fitted the segregation ratio of 1:1. Non significance of chi square value also confirmed that the observed ratio was fitted to expected ratio. The present results confirmed the monogenic dominant nature of solitary fruit bearing and monogenic recessive nature of cluster fruit bearing habit. These results are in agreement with earlier findings of Gopalakrishnan *et al.* (1989), Ahmed *et al*. (1994) and Dhamayanthi and Reddy (2001) in chilli.

The pendent fruit position was observed in all the F_1 plants of LCA 712 x HC-28 (Table 4.85 and plate 9) indicating the dominance of pendent fruit position over the erect fruit character. The F_2 plants were segregated into 155 plants with pendent fruits and 44 plants with erect fruits, which fitted the expected genetic ratio of 3:1. In BC_1 generation, out of 179 plants, 170 plants produced pendulous fruits and only nine plants were with erect fruits, which fitted the generation ratio of 1:0. The BC_2 generation was segregated into 115 pendulous and 99 erect fruited plants fitting the segregation ratio of 1:1. Non significance of chi square value also confirmed that the observed ratio was fitted to expected ratio. The present results confirmed the monogenic dominant nature of pendent fruit position and monogenic recessive nature of erect fruit position. These results are in agreement with earlier findings of Gopalakrishnan *et al.* (1989), Ahmed *et al*. (1994) and Dhamayanthi and Reddy (2001) who also reported that the nature of pendent fruit position was monogenic and dominant.

Cross: LCA 712 x LCA 710 for branching habit

In cross LCA 712 x LCA 710, all the F_1's were intermediate plants like the female parent LCA 712 (Table 4.86). In F_2 generation, 309 plants showed intermediate branching habit while 92 plants showed dense branching habit and fitted the genetic ratio of 13:3 indicating the epistatic gene interaction. Out of 250 BC_1 plants, 244 plants were intermediate plants and six were dense plants which clearly fitted to genetic ratio of 1:0. The BC_2 fitted to genetic ratio of 1:1 from 115 intermediate and 125 dense plants. The results revealed that the nature of this character is digenic and governed by two gene pairs with dominant suppression epistasis *i.e.* inhibitory gene action.

From the studies of line x tester analysis, it was concluded that three hybrids *viz*., LCA 607 x LCA 703-2, LCA 446 x LCA 703-2 and LCA 466 x LCA 705-2 were most promising hybrids with desirable *sca* effects, heterosis and *per se* performance for fruit yield and other desirable traits. From the generation mean analysis studies, it can be concluded that all the characters in one or more crosses are

controlled by either additive, dominant or epistatic interactions or all gene effects. The crosses, in which the characters governed by additive, additive x additive and complementary epistasis can be improved effectively by pedigree method of selection whereas the crosses, in which the characters controlled by dominant, dominant x dominant and duplicate epistasis can be exploited effectively by either heterosis breeding, reciprocal recurrent selection or full sib selection or delayed selection. From the chi-square analysis, it was concluded that the nature of solitary fruit bearing habit and pendent fruit position were monogenic and dominant whereas the nature of the branching habit was digenic and governed by two gene pairs with dominant suppression epistasis.

Table 4.1: Morphological characterization of chilli hybrids, parents and checks

Hybrid/Parent/Check	Plant growth habit	Branching habit	Fruit position	Fruit bearing habit	Fruit shape	Mature fruit colour
LCA-504 X G-4	5	7	3	1	1	5
LCA-504 X LCA-678	5	7	3	1	1	1
LCA-504 X LCA-453	5	5	3	1	1	1
LCA-504 X LCA-703-2	7	5	3	1	1	1
LCA-504 X LCA-705-2	5	5	3	1	1	5
LCA-504 X LCA-315	5	5	3	1	1	5
LCA-615 X G-4	5	5	3	1	1	1
LCA-615 X LCA-678	5	7	5	1	1	1
LCA-615 X LCA-453	5	3	3	1	1	1
LCA-615 X LCA-703-2	5	5	3	1	1	1
LCA-615 X LCA-705-2	5	5	3	1	1	1
LCA-615 X LCA-315	5	5	3	1	1	5
LCA-446 X G-4	5	5	3	1	1	5
LCA-446 X LCA-678	5	7	3	1	1	1
LCA-446 X LCA-453	5	5	3	1	1	1
LCA-446 X LCA-703-2	5	5	3	1	1	1
LCA-446 X LCA-705-2	3	7	5	1	1	5
LCA-446 X LCA-315	3	7	3	1	1	5
LCA-466 X G-4	5	5	3	1	1	7
LCA-466 X LCA-678	5	5	3	1	1	7
LCA-466 X LCA-453	5	5	3	1	1	7
LCA-466 X LCA-703-2	5	5	3	1	1	7
LCA-466 X LCA-705-2	5	7	5	1	1	7
LCA-466 X LCA-315	5	3	5	1	1	7
LCA-442 X G-4	3	5	3	1	1	5
LCA-442 X LCA-678	5	5	3	1	1	1
LCA-442 X LCA-453	5	5	5	1	1	5

Table 4.1: Contd…

Hybrid/Parent/Check	Plant growth habit	Branching habit	Fruit position	Fruit bearing habit	Fruit shape	Mature fruit colour
LCA-442 X LCA-703-2	5	7	3	1	1	1
LCA-442 X LCA-705-2	5	5	5	1	1	5
LCA-442 X LCA-315	3	5	3	1	1	5
LCA-654 X G-4	3	5	3	1	1	3
LCA-654 X LCA-678	3	7	3	1	1	3
LCA-654 X LCA-453	5	5	5	1	1	1
LCA-654 X LCA-703-2	5	7	3	1	1	1
LCA-654 X LCA-705-2	5	5	5	1	1	1
LCA-654 X LCA-315	3	5	5	1	1	1
LCA-607 X G-4	5	7	3	1	1	1
LCA-607 X LCA-678	5	5	3	1	1	3
LCA-607 X LCA-453	5	5	5	1	1	3
LCA-607 X LCA-703-2	5	5	3	1	1	3
LCA-607 X LCA-705-2	5	5	3	1	1	3
LCA-607 X LCA-315	3	5	5	1	1	3
LCA-655 X G-4	5	5	3	1	1	5
LCA-655 X LCA-678	5	5	3	1	1	1
LCA-655 X LCA-453	5	5	3	1	1	1
LCA-655 X LCA-703-2	5	7	3	1	1	1
LCA-655 X LCA-705-2	3	5	3	1	1	5
LCA-655 X LCA-315	3	5	3	1	1	1
LCA-355 X G-4	5	5	3	1	1	1
LCA-355 X LCA-678	3	5	3	1	1	1
LCA-355 X LCA-453	5	5	5	1	1	1
LCA-355 X LCA-703-2	5	7	3	1	1	1
LCA-355 X LCA-705-2	3	5	3	1	1	1
LCA-355 X LCA-315	3	5	3	1	1	5
LCA-504	7	5	3	1	1	5
LCA-615	3	5	3	1	1	1
LCA-446	7	5	3	1	1	5

Table 4.1: Contid…

Hybrid/Parent/Check	Plant growth habit	Branching habit	Fruit position	Fruit bearing habit	Fruit shape	Mature fruit colour
LCA-466	5	3	3	1	1	7
LCA-442	5	3	3	1	1	7
LCA-654	5	5	5	1	1	3
LCA-607	3	5	3	1	1	3
LCA-655	3	5	5	1	1	1
LCA-355	5	7	5	1	1	5
G4	5	7	3	1	1	1
LCA-678	3	5	3	1	1	5
LCA-453	7	5	3	1	1	1
LCA-703-2	5	5	3	1	1	1
LCA-705-2	5	5	5	1	1	1
LCA-315	7	5	3	1	1	7
Tejaswani	5	5	3	1	1	5
Indam-5	5	5	5	1	1	5

Description of scores:

Plant growth habit	3 Prostrate	5 Intermediate	7 Erect		
Branching habit	3 Sparse	5 Intermediate	7 Dense		
Fruit position	3 Pendent	5 Semi pendent	7 Erect		
Fruit bearing habit	1 Solitary	3 cluster			
Fruit shape	1 Elongate	2 Almost Round	3 Triangular	4 Companulate	5 Blocky
Mature fruit colour	1 Green	3 Parrot green	5 Dark green	7 Olive Green	

Table 4.2. General ANOVA for various characters in chilli (*Capsicum annuum* L.)

S. No.	Characters	Mean Sum of Squares		
		Replications	Treatments	Error
1	Plant height (cm)	38.02	253.36**	23.13
2	Plant spread (cm)	54.44	191.81**	27.89
3	No. of primary branches per plant	0.15	0.71**	0.18
4	Days to 50 % flowering	2.80	39.65**	2.16
5	Days to fruit maturity (red)	14.89	60.69**	12.88
6	No. of fruits per plant	1207.15	11584.90**	1053.79
7	Fruit length (cm)	0.49	6.46**	0.45
8	Fruit diameter (cm)	0.00	0.14**	0.01
9	Dry fruit weight (g)	0.03	0.14**	0.01
10	Fruit yield (g/plant)	53.05	4456.41**	601.5
11	No. of seeds per fruit	260.34	539.22**	88.22
12	Seed weight (g/1000 seed)	0.67	1.35**	0.36
13	Ascorbic Acid (mg/100g)	11.41	2418.73**	37.5
14	Oleoresin (%)	0.05	33.18**	1.76
15	Capsaicin (%)	0.00	0.05**	0.00
16	Red carotenoids (mg/100g)	2.86	4039.6**	140.97
17	Yellow carotinoids (mg/100g)	31.99	3072.99**	67.22
18	Total carotenoids (mg/100g)	5.04	10572.02**	273.67
19	Total colour value (ASTA units)	21.81	1717.09**	49.05

Table 4.3: Mean performance of parents and hybrids for plant height (cm), plant spread (cm), number of primary branches per plant, days to 50% flowering, days to fruit maturity (red) and number of fruits per plant in chilli

	Plant height (cm)	Plant spread (cm)	Number of primary branches per plant	Days to 50% flowering	Days to fruit maturity (red)	Number of fruits per plant
Lines						
LCA-504	103.87	85.92	4.33	28.33	64.67	124.93
LCA-615	91.67	87.97	4.43	25.00	57.33	207.10
LCA-446	87.60	85.70	3.63	37.00	62.33	201.53
LCA-466	90.97	89.43	4.47	34.33	61.67	170.50
LCA-442	75.57	85.97	4.27	29.00	62.67	165.27
LCA-654	79.57	84.57	4.23	34.00	60.33	175.57
LCA-607	93.47	79.53	4.63	32.00	64.33	228.87
LCA-655	95.40	94.03	4.93	29.33	63.67	211.13
LCA-355	84.47	79.53	4.13	37.67	53.67	225.90
Mean	**89.18**	**85.85**	**4.34**	**31.85**	**61.19**	**190.09**
Testers						
G4	99.87	95.63	4.53	32.67	56.33	284.37
LCA-678	89.83	75.90	4.93	30.00	53.67	230.80
LCA-453	83.80	84.70	3.43	36.67	57.33	133.67
LCA-703-2	109.70	91.97	5.23	34.00	67.67	308.80
LCA-705-2	86.47	88.70	4.13	33.00	64.67	211.93
LCA-315	78.00	76.03	3.83	32.33	57.67	198.50
Mean	**91.28**	**85.49**	**4.35**	**33.11**	**59.56**	**228.01**
Parental Mean	**90.02**	**85.71**	**4.34**	**32.36**	**60.53**	**205.26**
Crosses						
LCA-504 x G4	100.80	93.67	3.30	25.00	65.67	244.70
LCA-504 x LCA-678	100.03	99.77	3.57	32.00	63.67	227.30
LCA-504 x LCA-453	92.80	86.87	3.33	27.33	61.33	154.42
LCA-504 x LCA-703-2	106.77	106.70	3.77	26.67	66.33	240.53
LCA-504 x LCA-705-2	98.30	92.50	3.87	25.67	63.00	288.53
LCA-504 x LCA-315	93.97	87.90	4.03	27.00	64.67	209.03

Table 4.3 Contd…..

LCA-615 x G4	98.27	81.73	4.37	30.00	65.33	198.70
LCA-615 x LCA-678	89.75	97.93	4.07	30.67	69.33	183.43
LCA-615 x LCA-453	95.03	88.57	3.83	25.00	62.67	189.70
LCA-615 x LCA-703-2	87.20	93.43	4.73	31.33	67.67	231.23
LCA-615 x LCA-705-2	83.80	86.90	3.57	31.00	64.33	211.93
LCA-615 x LCA-315	81.63	86.90	3.87	29.00	65.33	214.27
LCA-446 x G4	82.80	94.70	4.13	27.00	55.33	245.90
LCA-446 x LCA-678	90.43	89.43	3.93	28.67	62.33	267.17
LCA-446 x LCA-453	93.60	81.70	3.27	22.67	60.67	135.87
LCA-446 x LCA-703-2	103.97	94.63	4.87	26.00	63.00	302.00
LCA-446 x LCA-705-2	74.57	83.73	3.53	28.67	57.67	183.80
LCA-446 x LCA-315	79.47	81.83	4.17	29.33	62.00	193.43
LCA-466 x G4	86.63	83.63	4.53	27.00	52.33	169.67
LCA-466 x LCA-678	98.97	100.93	5.03	36.00	50.33	278.27
LCA-466 x LCA-453	92.70	82.87	4.13	34.67	60.33	142.10
LCA-466 x LCA-703-2	108.50	96.80	4.73	34.00	63.67	261.57
LCA-466 x LCA-705-2	92.97	89.67	4.67	33.00	60.33	286.27
LCA-466 x LCA-315	80.83	98.53	5.03	38.00	55.33	161.20
LCA-442 x G4	80.97	84.53	3.93	31.00	48.67	292.67
LCA-442 xLCA-678	83.93	93.95	4.63	31.67	61.67	294.03
LCA-442 x LCA-453	77.40	88.50	4.27	37.00	59.33	281.70
LCA-442 x LCA-703-2	102.67	82.93	4.83	30.00	60.67	299.87
LCA-442 x LCA-705-2	88.67	80.63	3.83	29.00	58.67	175.00
LCA-442 x LCA-315	75.90	76.40	4.17	27.33	65.67	230.70
LCA-654 x G4	81.87	84.53	4.27	28.67	53.33	226.60
LCA-654 x LCA-678	92.93	88.07	4.53	31.33	65.67	262.53
LCA-654 x LCA-453	82.70	85.00	3.97	26.67	59.67	147.33
LCA-654 x LCA-703-2	89.63	83.70	3.93	26.33	62.33	237.93
LCA-654 x LCA-705-2	89.97	84.47	3.87	27.33	59.67	170.47
LCA-654 x LCA-315	78.47	81.67	3.73	32.67	58.67	224.47
LCA-607 x G4	98.70	102.80	4.63	28.00	56.33	293.67
LCA-607 x LCA-678	95.60	89.87	3.93	33.33	55.67	185.80
LCA-607 x LCA-453	91.20	89.70	3.43	36.00	54.33	147.80

Table 4.3 Contd…..

LCA-607 x LCA-703-2	103.93	85.83	4.63	31.67	62.67	336.33
LCA-607 x LCA-705-2	90.60	99.93	3.83	26.67	61.67	191.77
LCA-607 x LCA-315	90.90	78.83	4.43	31.00	63.67	198.47
LCA-655 x G4	105.57	105.97	4.73	31.00	62.33	373.53
LCA-655 x LCA-678	104.80	97.42	4.53	31.00	64.67	255.90
LCA-655 x LCA-453	86.77	87.98	3.93	25.67	61.67	254.50
LCA-655 x LCA-703-2	107.47	99.43	4.53	34.00	67.33	345.00
LCA-655 x LCA-705-2	88.97	79.57	3.83	26.67	58.33	290.77
LCA-655 x LCA-315	95.87	76.57	4.33	24.00	60.33	268.70
LCA-355 x G4	86.73	80.67	4.23	25.33	55.33	264.67
LCA-355 x LCA-678	86.90	90.67	3.73	27.67	57.33	328.50
LCA-355 x LCA-453	93.93	78.93	4.13	30.00	53.67	169.97
LCA-355 x LCA-703-2	109.77	105.00	4.93	27.33	52.33	296.60
LCA-355 x LCA-705-2	89.77	84.67	3.03	27.00	58.33	218.33
LCA-355 x LCA-315	81.97	70.93	3.73	26.00	60.33	154.67
Crosses Mean	**91.64**	**88.90**	**4.13**	**29.39**	**60.43**	**234.06**
Checks						
Tejaswini	106.40	105.57	4.73	33.33	55.67	447.03
Indam-5	82.60	85.80	4.23	31.33	63.33	194.00
Grand Mean	**91.37**	**88.41**	**4.18**	**30.10**	**60.42**	**230.41**
C.D. 5%	7.76	8.52	0.68	2.37	5.79	52.40
S.E.	2.78	3.05	0.24	0.85	2.07	18.74

Table 4.4: Mean performance of parents and hybrids for fruit length (cm), fruit diameter (cm), dry fruit weight (g), fruit yield (g/plant), number of seeds per fruit and seed weight (g/1000 seed) in chilli

	Fruit length (cm)	Fruit diameter (cm)	Dry fruit weight (g)	Fruit yield (g/plant)	Number of seeds per fruit	Seed weight (g/1000 seed)
Lines						
LCA-504	11.33	1.38	1.18	151.93	81.90	5.05
LCA-615	8.19	1.36	1.25	201.41	88.90	6.76
LCA-446	10.05	1.78	1.45	206.99	80.60	6.03
LCA-466	9.01	1.95	1.36	184.94	78.93	5.46
LCA-442	11.23	1.55	1.23	174.81	57.60	6.55
LCA-654	12.56	1.59	1.34	200.62	82.47	7.58
LCA-607	12.76	1.38	1.64	292.55	63.97	6.87
LCA-655	10.31	1.04	1.17	194.28	53.63	7.15
LCA-355	11.58	1.19	1.05	191.81	69.43	7.53
Mean	**10.78**	**1.47**	**1.29**	**199.93**	**73.05**	**6.55**
Testers						
G4	8.43	1.12	0.79	184.88	66.87	6.41
LCA-678	8.98	1.30	0.99	172.99	63.80	5.63
LCA-453	8.37	2.08	1.74	212.86	90.47	7.35
LCA-703-2	7.54	1.24	0.83	212.62	47.93	5.28
LCA-705-2	11.91	1.18	1.03	283.96	50.53	6.28
LCA-315	11.46	1.31	1.36	190.98	61.87	6.69
Mean	**9.45**	**1.37**	**1.12**	**209.72**	**63.58**	**6.27**
Parental Mean	**10.25**	**1.43**	**1.23**	**203.84**	**69.26**	**6.44**
Crosses						
LCA-504 x G4	10.95	1.21	1.06	215.82	65.53	5.62
LCA-504 x LCA-678	10.77	1.35	1.16	213.86	58.50	5.87
LCA-504 x LCA-453	12.52	1.55	1.44	224.59	86.97	6.81
LCA-504 x LCA-703-2	10.83	1.44	1.23	235.98	78.97	6.06
LCA-504 x LCA-705-2	10.31	1.41	1.10	265.62	47.30	5.87
LCA-504 x LCA-315	13.07	1.33	1.31	232.90	71.27	5.78
LCA-615 x G4	9.35	1.41	0.89	176.93	89.60	6.75

Table 4.4 Contd…..

LCA-615 x LCA-678	10.79	1.54	1.21	176.94	76.60	7.40
LCA-615 x LCA-453	10.08	1.72	1.72	243.95	88.80	7.39
LCA-615 x LCA-703-2	8.67	1.43	1.28	227.45	79.47	6.72
LCA-615 x LCA-705-2	10.00	1.39	1.32	229.60	88.87	6.95
LCA-615 x LCA-315	11.79	1.49	1.50	228.51	85.57	6.90
LCA-446 x G4	11.78	1.19	1.17	205.85	41.80	5.90
LCA-446 x LCA-678	10.45	1.51	1.13	235.67	54.67	5.41
LCA-446 x LCA-453	11.04	1.63	1.46	186.93	63.77	6.04
LCA-446 x LCA-703-2	10.46	1.49	1.18	297.99	59.50	5.97
LCA-446 x LCA-705-2	11.57	1.71	1.17	190.54	77.80	7.18
LCA-446 x LCA-315	13.70	1.53	1.27	200.05	77.43	5.99
LCA-466 x G4	9.91	1.57	1.27	171.58	80.67	5.76
LCA-466 x LCA-678	10.90	1.51	1.06	234.88	52.73	5.18
LCA-466 x LCA-453	10.12	1.85	1.40	166.94	74.23	6.54
LCA-466 x LCA-703-2	9.24	1.44	1.12	249.98	67.20	6.45
LCA-466 x LCA-705-2	9.41	1.57	1.24	271.92	75.77	6.35
LCA-466 x LCA-315	10.35	1.59	1.30	176.10	71.97	6.08
LCA-442 x G4	11.74	1.22	0.95	226.88	44.47	5.06
LCA-442 xLCA-678	11.59	1.41	1.19	249.65	56.53	6.10
LCA-442 x LCA-453	12.78	1.69	1.31	267.93	42.77	6.20
LCA-442 x LCA-703-2	11.60	1.49	1.39	265.65	67.60	6.76
LCA-442 x LCA-705-2	11.65	1.70	1.50	189.96	60.97	6.56
LCA-442 x LCA-315	12.79	1.40	1.37	250.52	47.40	5.86
LCA-654 x G4	12.33	1.35	1.18	206.54	66.37	6.09
LCA-654 x LCA-678	11.15	1.49	1.16	267.51	81.87	6.54
LCA-654 x LCA-453	12.19	1.85	1.78	238.52	84.43	6.43
LCA-654 x LCA-703-2	11.87	1.41	1.46	268.97	63.60	7.49
LCA-654 x LCA-705-2	12.27	1.29	1.36	213.74	63.50	6.40
LCA-654 x LCA-315	13.73	1.47	1.38	229.99	78.97	6.44
LCA-607 x G4	12.00	1.24	1.09	253.83	58.40	5.90
LCA-607 x LCA-678	10.78	1.37	1.22	190.66	67.67	5.28
LCA-607 x LCA-453	11.83	1.50	1.83	200.71	86.60	7.55
LCA-607 x LCA-703-2	10.49	1.39	1.20	328.53	68.77	6.92

Table 4.4 Contd…..

LCA-607 x LCA-705-2	10.77	1.40	1.49	231.43	66.67	7.74
LCA-607 x LCA-315	12.61	1.43	1.43	240.37	78.87	6.59
LCA-655 x G4	9.58	1.10	1.12	256.81	54.57	6.64
LCA-655 x LCA-678	10.29	1.25	1.34	245.84	54.83	6.18
LCA-655 x LCA-453	9.99	1.05	1.17	270.70	74.87	6.45
LCA-655 x LCA-703-2	10.61	1.29	1.18	312.51	46.77	7.43
LCA-655 x LCA-705-2	10.87	1.24	1.04	229.59	67.87	6.53
LCA-655 x LCA-315	11.98	1.28	1.19	286.97	87.47	6.50
LCA-355 x G4	12.42	1.16	0.93	181.93	46.00	5.93
LCA-355 x LCA-678	11.98	1.28	1.08	245.41	58.50	6.05
LCA-355 x LCA-453	12.47	1.60	1.45	203.39	68.40	7.39
LCA-355 x LCA-703-2	11.31	1.35	1.09	243.93	72.53	6.28
LCA-355 x LCA-705-2	13.15	1.20	1.15	207.97	63.93	6.19
LCA-355 x LCA-315	15.18	1.28	1.22	156.97	54.43	6.11
Crosses Mean	**11.33**	**1.43**	**1.26**	**230.07**	**67.60**	**6.38**
Checks						
Tejaswini	8.29	0.98	0.75	271.53	76.00	5.06
Indam-5	9.85	1.46	1.37	242.18	84.93	6.91
Grand Mean	**11.04**	**1.42**	**1.25**	**225.29**	**68.32**	**6.38**
C.D. 5%	1.0794	0.1635	0.1723	39.5906	15.1623	0.9634
S.E.	0.3860	0.0585	0.0616	14.1598	5.4229	0.3446

Table 4.5: Mean performance of parents and hybrids for ascorbic acid (mg/100g), capsaicin (%), oleoresin (%), red carotenoids (mg/100g), yellow carotenoids (mg/100g), total carotenoids (mg/100g) and total colour value (ASTA units) in chilli

	Ascorbic acid (mg/100g)	Oleoresin (%)	Capsaicin (%)	Red carotenoids (mg/100g)	Yellow carotenoids (mg/100g)	Total carotenoids (mg/100g)	Total colour value (ASTA units)
Lines							
LCA-504	77.98	10.21	0.66	149.30	74.24	223.54	86.98
LCA-615	71.78	13.80	0.69	81.91	33.95	115.86	51.54
LCA-446	30.08	19.77	0.14	198.59	110.43	309.02	119.74
LCA-466	126.82	19.50	0.14	162.41	130.00	292.41	120.97
LCA-442	96.19	19.17	0.08	102.32	73.50	175.83	90.81
LCA-654	68.51	11.96	0.13	165.55	44.88	210.44	103.35
LCA-607	70.89	14.65	0.51	129.12	78.22	207.34	117.66
LCA-655	121.00	12.55	0.17	153.33	97.91	251.24	62.33
LCA-355	57.67	19.67	0.15	266.17	153.74	419.90	163.68
Mean	**80.10**	**15.70**	**0.30**	**156.52**	**88.54**	**245.06**	**101.90**
Testers							
G4	62.57	9.17	0.24	132.88	73.40	206.28	79.77
LCA-678	16.08	10.99	0.49	162.87	87.79	250.66	99.70
LCA-453	89.48	10.94	0.26	139.18	73.76	212.95	82.83
LCA-703-2	84.78	11.75	0.59	154.16	90.82	244.98	84.83
LCA-705-2	20.05	9.49	0.36	166.44	81.97	248.41	104.91
LCA-315	20.09	8.21	0.44	129.97	70.65	200.62	83.52
Mean	**48.84**	**10.09**	**0.39**	**147.58**	**79.73**	**227.32**	**89.26**
Parental Mean	**67.60**	**13.46**	**0.34**	**152.95**	**85.02**	**237.96**	**96.84**
Crosses							
LCA-504 x G4	78.64	20.97	0.40	205.94	70.11	276.05	127.37
LCA-504 x LCA-678	117.79	10.48	0.51	199.82	128.78	328.61	127.67
LCA-504 x LCA-453	112.21	9.21	0.52	206.40	90.22	296.62	126.40
LCA-504 x LCA-703-2	114.00	10.87	0.33	169.12	78.57	247.68	111.19

Table 4.5 Contd…..

LCA-504 x LCA-705-2	69.78	9.99	0.29	143.59	75.53	219.11	89.93
LCA-504 x LCA-315	117.42	9.59	0.23	143.30	79.40	222.71	90.81
LCA-615 x G4	75.19	19.59	0.31	188.15	99.98	288.12	111.99
LCA-615 x LCA-678	82.37	20.83	0.29	132.96	80.56	213.52	82.88
LCA-615 x LCA-453	87.96	16.83	0.28	151.46	78.35	229.81	79.54
LCA-615 x LCA-703-2	78.97	11.98	0.23	156.46	84.19	240.66	93.80
LCA-615 x LCA-705-2	121.75	16.67	0.30	135.10	76.16	211.27	81.48
LCA-615 x LCA-315	61.95	9.81	0.41	134.52	70.41	204.93	79.81
LCA-446 x G4	116.82	16.70	0.23	160.79	88.47	249.25	97.63
LCA-446 x LCA-678	113.29	17.96	0.30	161.17	120.85	282.02	129.61
LCA-446 x LCA-453	98.12	8.53	0.35	200.81	131.99	332.80	140.45
LCA-446 x LCA-703-2	70.42	9.81	0.34	181.58	88.89	270.48	105.82
LCA-446 x LCA-705-2	80.22	10.86	0.31	201.58	107.35	308.93	120.09
LCA-446 x LCA-315	58.36	16.03	0.22	199.04	110.70	309.74	114.61
LCA-466 x G4	112.72	10.43	0.34	212.67	176.83	389.50	140.68
LCA-466 x LCA-678	68.11	8.60	0.35	207.93	169.74	377.67	146.50
LCA-466 x LCA-453	73.30	15.64	0.35	219.66	177.65	397.32	151.21
LCA-466 x LCA-703-2	100.19	11.03	0.33	178.78	117.14	295.92	113.99
LCA-466 x LCA-705-2	110.59	11.73	0.25	200.40	150.62	351.02	130.82
LCA-466 x LCA-315	51.04	9.77	0.33	192.85	160.13	352.98	86.27
LCA-442 x G4	51.78	9.59	0.39	144.92	86.12	231.04	89.60
LCA-442 xLCA-678	85.59	9.96	0.34	190.94	104.43	295.37	112.26
LCA-442 x LCA-453	102.50	6.80	0.25	199.35	122.96	322.32	121.70
LCA-442 x LCA-703-2	74.74	11.09	0.31	179.00	94.57	273.56	105.96
LCA-442 x LCA-705-2	81.85	10.72	0.36	214.99	31.14	246.13	126.27
LCA-442 x LCA-315	20.15	8.43	0.27	175.47	86.91	262.38	137.35
LCA-654 x G4	112.04	11.52	0.68	190.81	28.12	218.93	100.64
LCA-654 x LCA-678	57.02	10.96	0.46	194.89	110.25	305.14	118.08
LCA-654 x LCA-453	93.27	12.08	0.56	197.23	89.78	287.01	111.61
LCA-654 x LCA-703-2	77.05	13.88	0.56	200.81	110.47	311.29	120.94
LCA-654 x LCA-705-2	53.09	11.95	0.62	219.86	124.10	343.96	127.24
LCA-654 x LCA-315	60.40	10.13	0.41	191.61	84.59	276.19	103.24
LCA-607 x G4	119.36	13.01	0.40	108.39	78.10	186.49	81.23

Table 4.5 Contd…..

LCA-607 x LCA-678	111.40	11.53	0.37	98.32	97.00	195.32	76.59
LCA-607 x LCA-453	33.64	12.86	0.37	89.63	103.75	193.39	66.44
LCA-607 x LCA-703-2	82.27	13.54	0.41	196.85	40.08	236.93	72.75
LCA-607 x LCA-705-2	90.30	12.00	0.36	217.16	111.15	328.30	99.57
LCA-607 x LCA-315	60.85	11.62	0.28	134.85	101.87	236.72	90.47
LCA-655 x G4	87.88	11.99	0.34	175.16	92.15	267.31	91.73
LCA-655 x LCA-678	66.60	10.75	0.32	177.51	113.67	291.18	92.16
LCA-655 x LCA-453	89.09	9.19	0.39	184.30	111.36	295.66	93.27
LCA-655 x LCA-703-2	117.73	10.67	0.26	112.69	77.71	190.40	72.84
LCA-655 x LCA-705-2	69.74	11.91	0.35	217.80	98.53	316.33	122.93
LCA-655 x LCA-315	72.46	9.84	0.27	184.80	110.13	294.93	114.33
LCA-355 x G4	46.19	13.60	0.34	209.71	95.86	305.57	129.33
LCA-355 x LCA-678	128.83	11.73	0.45	209.79	180.62	390.41	151.97
LCA-355 x LCA-453	75.85	11.95	0.37	207.58	87.65	295.23	119.85
LCA-355 x LCA-703-2	127.49	10.82	0.30	149.56	80.86	230.42	122.28
LCA-355 x LCA-705-2	91.78	13.54	0.34	208.53	117.12	325.66	138.00
LCA-355 x LCA-315	50.75	10.47	0.32	189.81	98.91	288.72	112.52
Crosses Mean	**84.50**	**12.07**	**0.36**	**178.82**	**101.53**	**280.35**	**109.33**
Checks							
Tejaswini	44.04	15.21	0.74	115.07	75.48	190.55	59.43
Indam-5	98.00	10.89	0.40	189.59	91.61	281.20	89.71
Grand Mean	**80.55**	**12.39**	**0.36**	**172.61**	**97.53**	**270.14**	**105.71**
C.D. 5%	9.88	2.14	0.05	19.17	13.24	26.70	11.31
S.E.	3.54	0.77	0.02	6.85	4.73	9.55	4.04

Table 4.6: Best parents and crosses for various characters in chilli (Based on mean performance)

S.No.	Character	Best parent		Best cross
		Line	Tester	
1	Plant height (cm)	LCA 504 LCA 655	LCA 703-2 G4	LCA 355 x LCA 703-2 LCA 466 x LCA 703-2
2	Plant spread (cm)	LCA 655 LCA 466	G4 LCA 703-2	LCA 504 x LCA 703-2 LCA 655 x G4
3	No. of primary branches per plant	LCA 655 LCA 607	LCA 703-2 LCA 678	LCA 466 x LCA 678 LCA 466 x LCA 315
4	Days to 50 % flowering	LCA 615 LCA 504	LCA 678 LCA 315	LCA 466 x LCA 453 LCA 655 x LCA 315
5	Days to fruit maturity (red)	LCA 355 LCA 615	LCA 678 G4	LCA 442 x G4 LCA 466 x LCA 678
6	No. of fruits per plant	LCA 607 LCA 355	LCA 703-2 G4	LCA 655 x G4 LCA 655 x LCA 703-2
7	Fruit length (cm)	LCA 607 LCA 654	LCA 705-2 LCA 315	LCA 355 x LCA 315 LCA 654 x LCA 315
8	Fruit diameter (cm)	LCA 466 LCA 446	LCA 453 LCA 315	LCA 466 x LCA 453 LCA 654 x LCA 453
9	Dry fruit weight (g)	LCA 607 LCA 446	LCA 453 LCA 315	LCA 607 x LCA 453 LCA 654 x LCA 453
10	Fruit yield (g/plant)	LCA 607 LCA 446 LCA 615 LCA 654 LCA 655	LCA 705-2 LCA 453 LCA 703-2 LCA 315 G4	LCA 607 x LCA 703-2 LCA 655 x LCA 703-2 LCA 446 x LCA 703-2 LCA 655 x LCA 315 LCA 466 x LCA 705-2
11	No. of seeds per fruit	LCA 615 LCA 654	LCA 453 G4	LCA 615 x G4 LCA 615 x 453
12	Seed weight (g/1000 seed)	LCA 654 LCA 355	LCA 453 LCA 315	LCA 607 x LCA 705-2 LCA 607 x LCA 453
13	Ascorbic Acid (mg/100g)	LCA 466 LCA 655	LCA 453 LCA 703-2	LCA 355 x LCA 678 LCA 355 x LCA 703-2
14	Oleoresin (%)	LCA 446 LCA 355	LCA 703-2 LCA 678	LCA 504 x G4 LCA 615 x LCA 678
15	Capsaicin (%)	LCA 615 LCA 504	LCA 703-2 LCA 678	LCA 654 x G4 LCA 654 x LCA 705-2

Table 4.6 Contd…..

16	Red carotenoids (mg/100g)	LCA 355 LCA 446	LCA 705-2 LCA 678	LCA 654 x LCA 705-2 LCA 466 x LCA 453
17	Yellow carotinoids (mg/100g)	LCA 615 LCA 654	LCA 315 G4	LCA 654 x G4 LCA 442 x LCA 705-2
18	Total carotenoids (mg/100g)	LCA 355 LCA 446	LCA 678 LCA 705-2	LCA 466 x LCA 453 LCA 355 x LCA 678
19	Total colour value (ASTA units)	LCA 355 LCA 466	LCA 705-2 LCA 678	LCA 355 x LCA 678 LCA 466 x LCA 453

Table 4.7: Estimates of heterosis, heterobeltiosis and standard heterosis for plant height (cm) and plant spread (cm) in chilli

Cross	Plant height (cm)				Plant spread (cm)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	-1.05	-2.95	-5.26	22.03**	3.19	-2.06	-11.27**	9.17
LCA-504 x LCA-678	3.29	-3.69	-5.98	21.11**	23.31**	16.12**	-5.49	16.28**
LCA-504 x LCA-453	-1.10	-10.65**	-12.78**	12.35*	1.83	1.11	-17.71**	1.24
LCA-504 x LCA-703-2	-0.02	-2.67	0.34	29.26**	19.97**	16.02**	1.07	24.36**
LCA-504 x LCA-705-2	3.29	-5.36	-7.61*	19.01**	5.95	4.28	-12.38**	7.81
LCA-504 x LCA-315	3.34	-9.53*	-11.69**	13.76**	8.55	2.31	-16.74**	2.45
LCA-615 x G4	2.61	-1.60	-7.64*	18.97**	-10.97**	-14.53**	-22.58**	-4.74
LCA-615 x LCA-678	-1.10	-2.09	-15.65**	8.66	19.53**	11.33*	-7.23	14.14**
LCA-615 x LCA-453	8.32*	3.67	-10.68**	15.05**	2.59	0.68	-16.10**	3.22
LCA-615 x LCA-703-2	-13.39**	-20.51**	-18.05**	5.57	3.85	1.59	-11.49**	8.90
LCA-615 x LCA-705-2	-5.91	-8.58	-21.24**	1.45	-1.62	-2.03	-17.68**	1.28
LCA-615 x LCA-315	-3.77	-10.95*	-23.28**	-1.17	5.98	-1.21	-17.68**	1.28
LCA-446 x G4	-11.66**	-17.09**	-22.18**	0.24	4.45	-0.98	-10.29*	10.37*
LCA-446 x LCA-678	1.93	0.67	-15.01**	9.48	10.68*	4.36	-15.28**	4.23
LCA-446 x LCA-453	9.22*	6.85	-12.03**	13.32**	-4.11	-4.67	-22.61**	-4.78
LCA-446 x LCA-703-2	5.39	-5.23	-2.29	25.87**	6.53	2.90	-10.36*	10.30*
LCA-446 x LCA-705-2	-14.32**	-14.88**	-29.92**	-9.73*	-3.98	-5.60	-20.68**	-2.41
LCA-446 x LCA-315	-4.03	-9.28*	-25.31**	-3.79	1.20	-4.51	-22.48**	-4.62
LCA-466 x G4	-9.21*	-13.25**	-18.58**	4.88	-9.62*	-12.55**	-20.78**	-2.53
LCA-466 x LCA-678	9.48*	8.79*	-6.99	19.81**	22.10**	12.86**	-4.39	17.64**
LCA-466 x LCA-453	6.08	1.91	-12.88**	12.23*	-4.82	-7.34	-21.50**	-3.42
LCA-466 x LCA-703-2	8.14*	-1.09	1.97	31.36**	6.73	5.26	-8.30*	12.82*
LCA-466 x LCA-705-2	4.79	2.20	-12.63**	12.55*	0.67	0.26	-15.06**	4.51
LCA-466 x LCA-315	-4.32	-11.14*	-24.03**	-2.14	19.10**	10.18*	-6.66	14.84**
LCA-442 x G4	-7.70	-18.93**	-23.90**	-1.98	-6.90	-11.61*	-19.92**	-1.48
LCA-442 xLCA-678	1.49	-6.57	-21.12**	1.61	16.08**	9.29	-11.00**	9.50

*; Significant at 5% level; **; Significant at 1% level

Table 4.7 contd…….

LCA-442 x LCA-453	-2.87	-7.64	-27.26**	-6.30	3.71	2.95	-16.17**	3.15
LCA-442 x LCA-703-2	10.83**	-6.41	-3.51	24.29**	-6.78	-9.82*	-21.44**	-3.34
LCA-442 x LCA-705-2	9.44*	2.54	-16.67**	7.34	-7.67	-9.09	-23.62**	-6.02
LCA-442 x LCA-315	-1.15	-2.69	-28.67**	-8.11	-5.68	-11.13*	-27.63**	-10.96*
LCA-654 x G4	-8.75*	-18.02**	-23.06**	-0.89	-6.18	-11.61*	-19.92**	-1.48
LCA-654 x LCA-678	9.72*	3.45	-12.66**	12.51*	9.76*	4.14	-16.58**	2.64
LCA-654 x LCA-453	1.24	-1.31	-22.27**	0.12	0.43	0.35	-19.48**	-0.93
LCA-654 x LCA-703-2	-5.28	-18.29**	-15.76**	8.51	-5.17	-8.99	-20.71**	-2.45
LCA-654 x LCA-705-2	8.37*	4.05	-15.44**	8.92	-2.50	-4.77	-19.99**	-1.55
LCA-654 x LCA-315	-0.40	-1.38	-26.25**	-5.00	1.70	-3.43	-22.64**	-4.82
LCA-607 x G4	2.10	-1.17	-7.24	19.49**	17.37**	7.49	-2.62	19.81**
LCA-607 x LCA-678	4.31	2.28	-10.15**	15.74**	15.63**	12.99*	-14.87**	4.74
LCA-607 x LCA-453	2.90	-2.43	-14.29**	10.41*	9.23*	5.90	-15.03**	4.55
LCA-607 x LCA-703-2	2.31	-5.26	-2.32	25.83**	0.10	-6.67	-18.69**	0.04
LCA-607 x LCA-705-2	0.70	-3.07	-14.85**	9.69*	18.80**	12.66**	-5.34	16.47**
LCA-607 x LCA-315	6.03	-2.75	-14.57**	10.05*	1.35	-0.88	-25.32**	-8.12
LCA-655 x G4	8.13*	5.71	-0.78	27.80**	11.74**	10.81*	0.38	23.50**
LCA-655 x LCA-678	13.15**	9.85*	-1.50	26.88**	14.65**	3.60	-7.72	13.54**
LCA-655 x LCA-453	-3.16	-9.05*	-18.45**	5.04	-1.55	-6.43	-16.66**	2.54
LCA-655 x LCA-703-2	4.79	-2.04	1.00	30.10**	6.92	5.74	-5.81	15.89**
LCA-655 x LCA-705-2	-2.16	-6.74	-16.38**	7.71	-12.91**	-15.38**	-24.63**	-7.26
LCA-655 x LCA-315	10.57**	0.49	-9.90**	16.06**	-9.96*	-18.57**	-27.47**	-10.76*
LCA-355 x G4	-5.90	-13.15**	-18.48**	5.00	-7.90	-15.65**	-23.59**	-5.98
LCA-355 x LCA-678	-0.29	-3.27	-18.33**	5.21	16.66**	14.00*	-14.11**	5.67
LCA-355 x LCA-453	11.65**	11.21*	-11.72**	13.72**	-3.88	-6.81	-25.23**	-8.00
LCA-355 x LCA-703-2	13.06**	0.06	3.16	32.89**	22.45**	14.17**	-0.54	22.38**
LCA-355 x LCA-705-2	5.03	3.82	-15.63**	8.68	0.65	-4.55	-19.80**	-1.32
LCA-355 x LCA-315	0.90	-2.96	-22.96**	-0.77	-8.81	-10.81*	-32.81**	-17.33**

*; Significant at 5% level; **; Significant at 1% level

Table 4.8: Estimates of heterosis, heterobeltiosis and standard heterosis for number of primary branches per plant and days to 50% flowering in chilli

Cross	Number of primary branches per plant				Days to 50% flowering			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	-25.56**	-27.21**	-30.28**	-22.05**	-18.03**	-23.47**	-25.00**	-20.21**
LCA-504 x LCA-678	-23.02**	-27.70**	-24.65**	-15.75*	9.71**	6.67	-4.00	2.13
LCA-504 x LCA-453	-14.16	-23.08**	-29.58**	-21.26**	-15.90**	-25.45**	-18.00**	-12.77**
LCA-504 x LCA-703-2	-21.25**	-28.03**	-20.42**	-11.02	-14.44**	-21.57**	-20.00**	-14.89**
LCA-504 x LCA-705-2	-8.66	-10.77	-18.31*	-8.66	-16.30**	-22.22**	-23.00**	-18.09**
LCA-504 x LCA-315	-1.22	-6.92	-14.79*	-4.72	-10.99**	-16.49**	-19.00**	-13.83**
LCA-615 x G4	-2.60	-3.68	-7.75	3.15	4.05	-8.16*	-10.00**	-4.26
LCA-615 x LCA-678	-13.17*	-17.57*	-14.08*	-3.94	11.52**	2.22	-8.00*	-2.13
LCA-615 x LCA-453	-2.54	-13.53	-19.01**	-9.45	-18.92**	-31.82**	-25.00**	-20.21**
LCA-615 x LCA-703-2	-2.07	-9.55	0.00	11.81	6.21	-7.84*	-6.00	0.00
LCA-615 x LCA-705-2	-16.73*	-19.55*	-24.65**	-15.75*	6.90	-6.06	-7.00	-1.06
LCA-615 x LCA-315	-6.45	-12.78	-18.31*	-8.66	1.16	-10.31**	-13.00**	-7.45
LCA-446 x G4	1.22	-8.82	-12.68	-2.36	-22.49**	-27.03**	-19.00**	-13.83**
LCA-446 x LCA-678	-8.17	-20.27**	-16.90*	-7.09	-14.43**	-22.52**	-14.00**	-8.51*
LCA-446 x LCA-453	-7.55	-10.09	-30.99**	-22.83**	-38.46**	-38.74**	-32.00**	-27.66**
LCA-446 x LCA-703-2	9.77	-7.01	2.82	14.96	-26.76**	-29.73**	-22.00**	-17.0**
LCA-446 x LCA-705-2	-9.01	-14.52	-25.35**	-16.54*	-18.10**	-22.52**	-14.00**	-8.51*
LCA-446 x LCA-315	11.61	8.70	-11.97	-1.57	-15.38**	-20.72**	-12.00**	-6.38
LCA-466 x G4	0.74	0.00	-4.23	7.09	-19.40**	-21.36**	-19.00**	-13.83**
LCA-466 x LCA-678	7.09	2.03	6.34	18.90*	11.92**	4.85	8.00*	14.89**
LCA-466 x LCA-453	4.64	-7.46	-12.68	-2.36	-2.35	-5.45	4.00	10.64**
LCA-466 x LCA-703-2	-2.41	-9.55	0.00	11.81	-0.49	-0.97	2.00	8.51*
LCA-466 x LCA-705-2	8.53	4.48	-1.41	10.24	-1.98	-3.88	-1.00	5.32
LCA-466 x LCA-315	21.29**	12.69	6.34	18.90*	14.00**	10.68**	14.00**	21.28**
LCA-442 x G4	-10.61	-13.24	-16.90*	-7.09	0.54	-5.10	-7.00	-1.06
LCA-442 xLCA-678	0.72	-6.08	-2.11	9.45	7.34*	5.56	-5.00	1.06
LCA-442 x LCA-453	10.82	0.00	-9.86	0.79	12.69**	0.91	11.00**	18.09**

*; Significant at 5% level; **; Significant at 1% level

Table 4.8 contd…….

LCA-442 x LCA-703-2	1.75	-7.64	2.11	14.17	-4.76	-11.76**	-10.00**	-4.26
LCA-442 x LCA-705-2	-8.73	-10.16	-19.01**	-9.45	-6.45	-12.12**	-13.00**	-7.45
LCA-442 x LCA-315	2.88	-2.34	-11.97	-1.57	-10.87**	-15.46**	-18.00**	-12.77**
LCA-654 x G4	-2.66	-5.88	-9.86	0.79	-14.00**	-15.69**	-14.00**	-8.51*
LCA-654 x LCA-678	-1.09	-8.11	-4.23	7.09	-2.08	-7.84*	-6.00	0.00
LCA-654 x LCA-453	3.48	-6.30	-16.20*	-6.30	-24.53**	-27.27**	-20.00**	-14.89**
LCA-654 x LCA-703-2	-16.90**	-24.84**	-16.90*	-7.09	-22.55**	-22.55**	-21.00**	-15.96**
LCA-654 x LCA-705-2	-7.57	-8.66	-18.31*	-8.66	-18.41**	-19.61**	-18.00**	-12.77**
LCA-654 x LCA-315	-7.44	-11.81	-21.13**	-11.81	-1.51	-3.92	-2.00	4.26
LCA-607 x G4	1.09	0.00	-2.11	9.45	-13.40**	-14.29**	-16.00**	-10.64**
LCA-607 x LCA-678	-17.77**	-20.27**	-16.90*	-7.09	7.53*	4.17	0.00	6.38
LCA-607 x LCA-453	-14.88*	-25.90**	-27.46**	-18.90*	4.85	-1.82	8.00*	14.89**
LCA-607 x LCA-703-2	-6.08	-11.46	-2.11	9.45	-4.04	-6.86	-5.00	1.06
LCA-607 x LCA-705-2	-12.55	-17.27*	-19.01**	-9.45	-17.95**	-19.19**	-20.00**	-14.89**
LCA-607 x LCA-315	4.72	-4.32	-6.34	4.72	-3.63	-4.12	-7.00	-1.06
LCA-655 x G4	0.00	-4.05	0.00	11.81	0.00	-5.10	-7.00	-1.06
LCA-655 x LCA-678	-8.11	-8.11	-4.23	7.09	4.49	3.33	-7.00	-1.06
LCA-655 x LCA-453	-5.98	-20.27**	-16.90*	-7.09	-22.22**	-30.00**	-23.00**	-18.09**
LCA-655 x LCA-703-2	-10.82	-13.38*	-4.23	7.09	7.37*	0.00	2.00	8.51*
LCA-655 x LCA-705-2	-15.44*	-22.30**	-19.01**	-9.45	-14.44**	-19.19**	-20.00**	-14.89**
LCA-655 x LCA-315	-1.14	-12.16	-8.45	2.36	-22.16**	-25.77**	-28.00**	-23.40**
LCA-355 x G4	-2.31	-6.62	-10.56	0.00	-27.96**	-32.74**	-24.00**	-19.15**
LCA-355 x LCA-678	-17.65**	-24.32**	-21.13**	-11.81	-18.23**	-26.55**	-17.00**	-11.70**
LCA-355 x LCA-453	9.25	0.00	-12.68	-2.36	-19.28**	-20.35**	-10.00**	-4.26
LCA-355 x LCA-703-2	5.34	-5.73	4.23	16.54*	-23.72**	-27.43**	-18.00**	-12.77**
LCA-355 x LCA-705-2	-26.61**	-26.61**	-35.92**	-28.35**	-23.58**	-28.32**	-19.00**	-13.83**
LCA-355 x LCA-315	-6.28	-9.68	-21.13**	-11.81	-25.71**	-30.97**	-22.00**	-17.02**

*; Significant at 5% level; **; Significant at 1% level

Table 4.9: Estimates of heterosis, heterobeltiosis and standard heterosis for days to fruit maturity (red) and number of fruits per plant in chilli

Cross	Days to fruit maturity (red)				Number of fruits per plant			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	8.54*	1.55	17.96**	3.68	19.57	-13.95	-45.26**	26.13*
LCA-504 x LCA-678	7.61	-1.55	14.37**	0.53	27.79*	-1.52	-49.15**	17.16
LCA-504 x LCA-453	0.55	-5.15	10.18	-3.16	19.43	15.53	-65.46**	-20.40
LCA-504 x LCA-703-2	0.25	-1.97	19.16**	4.74	10.91	-22.11**	-46.19**	23.99
LCA-504 x LCA-705-2	-2.58	-2.58	13.17*	-0.53	71.30**	36.14**	-35.46**	48.73**
LCA-504 x LCA-315	5.72	0.00	16.17**	2.11	29.26*	5.31	-53.24**	7.75
LCA-615 x G4	14.96**	13.95**	17.37**	3.16	-19.14*	-30.13**	-55.55**	2.42
LCA-615 x LCA-678	24.92**	20.93**	24.55**	9.47*	-16.22	-20.52	-58.97**	-5.45
LCA-615 x LCA-453	9.30*	9.30	12.57*	-1.05	11.34	-8.40	-57.56**	-2.22
LCA-615 x LCA-703-2	8.27*	0.00	21.56**	6.84	-10.36	-25.12**	-48.27**	19.19
LCA-615 x LCA-705-2	5.46	-0.52	15.57**	1.58	1.15	0.00	-52.59**	9.24
LCA-615 x LCA-315	13.62**	13.29*	17.37**	3.16	5.65	3.46	-52.07**	10.45
LCA-446 x G4	-6.74	-11.23*	-0.60	-12.63**	1.21	-13.53	-44.99**	26.75*
LCA-446 x LCA-678	7.47	0.00	11.98*	-1.58	23.59*	15.76	-40.24**	37.71**
LCA-446 x LCA-453	1.39	-2.67	8.98	-4.21	-18.93	-32.58**	-69.61**	-29.97*
LCA-446 x LCA-703-2	-3.08	-6.90	13.17*	-0.53	18.35*	-2.20	-32.44**	55.67**
LCA-446 x LCA-705-2	-9.19*	-10.82*	3.59	-8.95	-11.09	-13.27	-58.88**	-5.26
LCA-446 x LCA-315	3.33	-0.53	11.38*	-2.11	-3.29	-4.02	-56.73**	-0.29
LCA-466 x G4	-11.30*	-15.14**	-5.99	-17.37**	-25.40**	-40.34**	-62.05**	-12.54
LCA-466 x LCA-678	-12.72**	-18.38**	-9.58	-20.53**	38.68**	20.57	-37.75**	43.44**
LCA-466 x LCA-453	1.40	-2.16	8.38	-4.74	-6.56	-16.66	-68.21**	-26.75*
LCA-466 x LCA-703-2	-1.55	-5.91	14.37**	0.53	9.15	-15.30	-41.49**	34.83**
LCA-466 x LCA-705-2	-4.49	-6.70	8.38	-4.74	49.71**	35.07**	-35.96**	47.56**
LCA-466 x LCA-315	-7.26	-10.27*	-0.60	-12.63**	-12.63	-18.79	-63.94**	-16.91
LCA-442 x G4	-18.21**	-22.34**	-12.57*	-23.16**	30.18**	2.92	-34.53**	50.86**
LCA-442 xLCA-678	6.02	-1.60	10.78*	-2.63	48.48**	27.40**	-34.23**	51.56**

*; Significant at 5% level; **; Significant at 1% level

Table 4.9 contd…….

LCA-442 x LCA-453	-1.11	-5.32	6.59	-6.32	88.47**	70.45**	-36.98**	45.21**
LCA-442 x LCA-703-2	-6.91	-10.34*	8.98	-4.21	26.51**	-2.89	-32.92**	54.57**
LCA-442 x LCA-705-2	-7.85	-9.28*	5.39	-7.37	-7.21	-17.43	-60.85**	-9.79
LCA-442 x LCA-315	9.14*	4.79	17.96**	3.68	26.84*	16.22	-48.39**	18.92
LCA-654 x G4	-8.57	-11.60*	-4.19	-15.79**	-1.46	-20.31*	-49.31**	16.80
LCA-654 x LCA-678	15.20**	8.84	17.96**	3.68	29.21**	13.75	-41.27**	35.33**
LCA-654 x LCA-453	1.42	-1.10	7.19	-5.79	-4.71	-16.08	-67.04**	-24.05
LCA-654 x LCA-703-2	-2.60	-7.88	11.98*	-1.58	-1.75	-22.95**	-46.78**	22.65
LCA-654 x LCA-705-2	-4.53	-7.73	7.19	-5.79	-12.02	-19.57	-61.87**	-12.13
LCA-654 x LCA-315	-0.56	-2.76	5.39	-7.37	20.01	13.08	-49.79**	15.70
LCA-607 x G4	-6.63	-12.44**	1.20	-11.05*	14.44	3.27	-34.31**	51.37**
LCA-607 x LCA-678	-5.65	-13.47**	0.00	-12.11*	-19.16*	-19.50	-58.44**	-4.23
LCA-607 x LCA-453	-10.68*	-15.54**	-2.40	-14.21**	-18.46	-35.42**	-66.94**	-23.81
LCA-607 x LCA-703-2	-5.05	-7.39	12.57*	-1.05	25.11**	8.92	-24.76**	73.37**
LCA-607 x LCA-705-2	-4.39	-4.64	10.78*	-2.63	-12.99	-16.21	-57.10**	-1.15
LCA-607 x LCA-315	4.37	-1.04	14.37**	0.53	-7.12	-13.28	-55.60**	2.30
LCA-655 x G4	3.89	-2.09	11.98*	-1.58	50.77**	31.36**	-16.44**	92.54**
LCA-655 x LCA-678	10.23*	1.57	16.17**	2.11	15.81	10.88	-42.76**	31.91*
LCA-655 x LCA-453	1.93	-3.14	10.78*	-2.63	47.62**	20.54	-43.07**	31.19*
LCA-655 x LCA-703-2	2.54	-0.49	20.96**	6.32	32.71**	11.72	-22.82**	77.84**
LCA-655 x LCA-705-2	-9.09*	-9.79*	4.79	-7.89	37.46**	37.20**	-34.96**	49.88**
LCA-655 x LCA-315	-0.55	-5.24	8.38	-4.74	31.19**	27.27*	-39.89**	38.51**
LCA-355 x G4	0.61	-1.78	-0.60	-12.63**	3.74	-6.93	-40.79**	36.43**
LCA-355 x LCA-678	6.83	6.83	2.99	-9.47*	43.86**	42.33**	-26.52**	69.33**
LCA-355 x LCA-453	-3.30	-6.40	-3.59	-15.26**	-5.46	-24.76*	-61.98**	-12.39
LCA-355 x LCA-703-2	-13.74**	-22.66**	-5.99	-17.37**	10.94	-3.95	-33.65**	52.89**
LCA-355 x LCA-705-2	-1.41	-9.79*	4.79	-7.89	-0.27	-3.35	-51.16**	12.54
LCA-355 x LCA-315	8.38	4.62	8.38	-4.74	-27.11**	-31.53**	-65.40**	-20.27

*; Significant at 5% level; **; Significant at 1% level

Table 4.10: Estimates of heterosis, heterobeltiosis and standard heterosis for fruit length (cm) and fruit diameter (cm) in chilli

Cross	Fruit length (cm)				Fruit diameter (cm)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	10.86*	-3.35	32.07**	11.16*	-3.34	-12.56*	23.55**	-17.54**
LCA-504 x LCA-678	6.07	-4.94	29.90**	9.34	1.12	-1.93	38.57**	-7.52
LCA-504 x LCA-453	27.11**	10.47*	50.96**	27.06**	-10.51*	-25.52**	58.36**	5.69
LCA-504 x LCA-703-2	14.80**	-4.41	30.63**	9.95	9.81	4.11	47.10**	-1.82
LCA-504 x LCA-705-2	-11.33**	-13.49**	24.28**	4.60	10.30	2.17	44.37**	-3.64
LCA-504 x LCA-315	14.71**	14.08**	57.64**	32.68**	-1.12	-3.62	36.18**	-9.11
LCA-615 x G4	12.56*	11.00	12.78	-5.07	13.59*	3.43	44.03**	-3.87
LCA-615 x LCA-678	25.70**	20.19**	30.14**	9.54	15.93**	13.24*	57.68**	5.24
LCA-615 x LCA-453	21.70**	20.44**	21.50**	2.27	0.29	-17.01**	76.45**	17.77**
LCA-615 x LCA-703-2	10.25	5.86	4.58	-11.98*	10.40	5.39	46.76**	-2.05
LCA-615 x LCA-705-2	-0.53	-16.06**	20.58**	1.49	9.86	2.45	42.66**	-4.78
LCA-615 x LCA-315	20.01**	2.91	42.20**	19.69**	11.61*	9.56	52.56**	1.82
LCA-446 x G4	27.54**	17.25**	42.04**	19.55**	-17.97**	-33.21**	21.50*	-18.91**
LCA-446 x LCA-678	9.88	4.05	26.05**	6.09	-1.52	-14.82**	54.95**	3.42
LCA-446 x LCA-453	19.91**	9.89	33.12**	12.04*	-15.22**	-21.35**	67.24**	11.62*
LCA-446 x LCA-703-2	18.95**	4.11	26.13**	6.16	-0.88	-15.95**	52.90**	2.05
LCA-446 x LCA-705-2	5.40	-2.85	39.55**	17.46**	16.03**	-3.56	75.43**	17.08**
LCA-446 x LCA-315	27.40**	19.55**	65.19**	39.04**	-0.86	-13.88**	56.66**	4.56
LCA-466 x G4	13.65*	9.99	19.45**	0.54	2.06	-19.80**	60.41**	7.06
LCA-466 x LCA-678	21.20**	21.02**	31.43**	10.62	-7.28	-22.87**	54.27**	2.96
LCA-466 x LCA-453	16.50**	12.36*	22.03**	2.71	-8.02*	-10.75**	89.76**	26.65**
LCA-466 x LCA-703-2	11.68*	2.59	11.41	-6.22	-9.93*	-26.45**	47.10**	-1.82
LCA-466 x LCA-705-2	-10.01*	-20.98**	13.50*	-4.47	0.53	-19.45**	61.09**	7.52
LCA-466 x LCA-315	1.17	-9.66*	24.84**	5.07	-2.55	-18.60**	62.80**	8.66
LCA-442 x G4	19.47**	4.57	41.56**	19.15**	-8.39	-21.12**	24.91**	-16.63**
LCA-442 xLCA-678	14.75**	3.27	39.79**	17.66**	-1.06	-9.05	44.03**	-3.87

*; Significant at 5% level; **; Significant at 1% level

Table 4.10 contd…….

LCA-442 x LCA-453	30.45**	13.84**	54.10**	29.70**	-6.53	-18.46**	73.38**	15.72**
LCA-442 x LCA-703-2	23.62**	3.33	39.87**	17.73**	7.07	-3.66	52.56**	1.82
LCA-442 x LCA-705-2	0.66	-2.24	40.43**	18.20**	24.60**	9.70	73.72**	15.95**
LCA-442 x LCA-315	12.72**	11.58*	54.18**	29.77**	-1.75	-9.27	43.69**	-4.10
LCA-654 x G4	17.53**	-1.80	48.71**	25.17**	-0.49	-15.30**	37.88**	-7.97
LCA-654 x LCA-678	3.50	-11.25*	34.41**	13.13*	3.00	-6.50	52.22**	1.59
LCA-654 x LCA-453	16.47**	-2.97	46.95**	23.68**	0.91	-10.91**	89.42**	26.42**
LCA-654 x LCA-703-2	18.14**	-5.47	43.17**	20.50**	-0.24	-11.32*	44.37**	-3.64
LCA-654 x LCA-705-2	0.25	-2.34	47.91**	24.49**	-6.75	-18.87**	32.08**	-11.85*
LCA-654 x LCA-315	14.35**	9.34*	65.59**	39.38**	1.15	-7.76	50.17**	0.23
LCA-607 x G4	13.28**	-5.96	44.69**	21.79**	-0.80	-10.17	26.62**	-15.49**
LCA-607 x LCA-678	-0.83	-15.52**	29.98**	9.40	2.74	-0.24	40.61**	-6.15
LCA-607 x LCA-453	11.96**	-7.31	42.60**	20.03**	-13.13**	-27.77**	53.58**	2.51
LCA-607 x LCA-703-2	3.32	-17.82**	26.45**	6.43	6.63	1.21	42.66**	-4.78
LCA-607 x LCA-705-2	-12.73**	-15.62**	29.82**	9.27	9.66	1.69	43.34**	-4.33
LCA-607 x LCA-315	4.10	-1.20	52.01**	27.94**	6.20	3.63	46.08**	-2.51
LCA-655 x G4	2.24	-7.11	15.51*	-2.77	2.48	-1.19	12.97	-24.60**
LCA-655 x LCA-678	6.70	-0.19	24.12**	4.47	7.14	-3.60	27.99**	-14.58*
LCA-655 x LCA-453	7.00	-3.10	20.50**	1.42	-32.33**	-49.28**	7.85	-28.02**
LCA-655 x LCA-703-2	18.82**	2.84	27.89**	7.65	13.78*	4.58	32.42**	-11.62*
LCA-655 x LCA-705-2	-2.22	-8.79	31.03**	10.28	12.05	5.38	26.96**	-15.26**
LCA-655 x LCA-315	10.04*	4.54	44.45**	21.58**	9.09	-2.29	31.06**	-12.53*
LCA-355 x G4	24.16**	7.25	49.76**	26.05**	0.72	-2.25	18.77*	-20.73**
LCA-355 x LCA-678	16.54**	3.45	44.45**	21.58**	3.09	-1.29	31.06**	-12.53*
LCA-355 x LCA-453	25.07**	7.71	50.40**	26.59**	-2.15	-23.11**	63.48**	9.11
LCA-355 x LCA-703-2	18.34**	-2.30	36.41**	14.82**	11.69*	9.43	38.57**	-7.52
LCA-355 x LCA-705-2	11.92**	10.35*	58.52**	33.42**	1.55	1.12	22.87**	-18.00**
LCA-355 x LCA-315	31.77**	31.09**	83.04**	54.06**	2.27	-2.54	30.72**	-12.76*

*; Significant at 5% level; **; Significant at 1% level

Table 4.11: Estimates of heterosis, heterobeltiosis and standard heterosis for dry fruit weight (g) and fruit yield (g/plant) in chilli

Cross	Dry fruit weight (g)				Fruit yield (g/plant)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	7.43	-10.17	41.96**	-22.44**	28.16**	16.74	-20.52**	-10.88
LCA-504 x LCA-678	6.61	-1.98	54.91**	-15.37*	31.64**	23.63*	-21.24**	-11.69
LCA-504 x LCA-453	-1.48	-17.40**	92.86**	5.37	23.14*	5.51	-17.29*	-7.26
LCA-504 x LCA-703-2	22.72**	4.52	65.18**	-9.76	29.46**	10.99	-13.09	-2.56
LCA-504 x LCA-705-2	-0.90	-7.06	46.88**	-19.76**	21.88**	-6.46	-2.18	9.68
LCA-504 x LCA-315	3.41	-3.43	75.89**	-3.90	35.84**	21.95*	-14.23	-3.83
LCA-615 x G4	-13.07	-28.88**	18.75	-35.12**	-8.40	-12.15	-34.84**	-26.94**
LCA-615 x LCA-678	8.20	-2.94	62.05**	-11.46	-5.48	-12.15	-34.84**	-26.94**
LCA-615 x LCA-453	14.83**	-1.53	129.91**	25.61**	17.77*	14.60	-10.16	0.73
LCA-615 x LCA-703-2	23.60**	2.94	71.88**	-6.10	9.87	6.97	-16.23*	-6.08
LCA-615 x LCA-705-2	16.08*	6.15	77.23**	-3.17	-5.39	-19.14**	-15.44*	-5.19
LCA-615 x LCA-315	15.09*	10.29	100.89**	9.76	16.47	13.46	-15.84*	-5.64
LCA-446 x G4	4.46	-19.12**	56.70**	-14.39*	5.06	-0.55	-24.19**	-15.00
LCA-446 x LCA-678	-6.98	-21.66**	51.79**	-17.07**	24.04**	13.86	-13.21	-2.69
LCA-446 x LCA-453	-8.25	-16.06**	95.98**	7.07	-10.95	-12.18	-31.16**	-22.81**
LCA-446 x LCA-703-2	3.95	-18.20**	58.48**	-13.41*	42.03**	40.15**	9.74	23.05**
LCA-446 x LCA-705-2	-5.91	-19.35**	56.25**	-14.63*	-22.38**	-32.90**	-29.83**	-21.32*
LCA-446 x LCA-315	-9.26	-11.98	70.54**	-6.83	0.54	-3.35	-26.32**	-17.39*
LCA-466 x G4	18.45*	-6.14	70.54**	-6.83	-7.21	-7.22	-36.81**	-29.15**
LCA-466 x LCA-678	-9.66	-21.87**	41.96**	-22.44**	31.24**	27.01*	-13.50	-3.01
LCA-466 x LCA-453	-9.68	-19.69**	87.50**	2.44	-16.07	-21.57*	-38.52**	-31.07**
LCA-466 x LCA-703-2	2.13	-17.69**	49.55**	-18.29**	25.76**	17.57	-7.94	3.22
LCA-466 x LCA-705-2	4.04	-8.35	66.52**	-9.02	15.98*	-4.24	0.14	12.28
LCA-466 x LCA-315	-4.05	-4.17	74.55**	-4.63	-6.31	-7.79	-35.14**	-27.28**
LCA-442 x G4	-5.61	-22.28**	27.68*	-30.24**	26.15**	22.72*	-16.44*	-6.32
LCA-442 xLCA-678	7.07	-3.26	58.93**	-13.17*	43.56**	42.81**	-8.06	3.09

*; Significant at 5% level; **; Significant at 1% level

Table 4.11 contd…….

LCA-442 x LCA-453	-11.78*	-24.86**	75.45**	-4.15	38.22**	25.87**	-1.33	10.63
LCA-442 x LCA-703-2	35.17**	13.32	86.16**	1.71	37.13**	24.94**	-2.17	9.69
LCA-442 x LCA-705-2	32.45**	22.01**	100.45**	9.51	-17.19*	-33.11**	-30.04**	-21.56*
LCA-442 x LCA-315	5.67	0.49	83.04**	0.00	36.97**	31.17**	-7.74	3.44
LCA-654 x G4	10.49	-11.97	57.59**	-13.90*	7.16	2.95	-23.93**	-14.71
LCA-654 x LCA-678	-0.29	-13.22*	55.36**	-15.12*	43.20**	33.34**	-1.48	10.46
LCA-654 x LCA-453	15.58**	2.10	138.39**	30.24**	15.37	12.05	-12.16	-1.51
LCA-654 x LCA-703-2	34.77**	9.23	95.54**	6.83	30.17**	26.50**	-0.94	11.06
LCA-654 x LCA-705-2	14.49*	1.50	81.70**	-0.73	-11.79	-24.73**	-21.28**	-11.74
LCA-654 x LCA-315	2.35	1.47	84.82**	0.98	17.46	14.64	-15.30*	-5.03
LCA-607 x G4	-10.29	-33.40**	45.98**	-20.24**	6.33	-13.23	-6.52	4.81
LCA-607 x LCA-678	-7.36	-25.66**	62.95**	-10.98	-18.09*	-34.83**	-29.78**	-21.27*
LCA-607 x LCA-453	8.09	4.78	144.64**	33.66**	-20.57**	-31.39**	-26.08**	-17.12*
LCA-607 x LCA-703-2	-2.70	-26.68**	60.71**	-12.20	30.07**	12.30	20.99**	35.66**
LCA-607 x LCA-705-2	11.86*	-8.76	100.00**	9.27	-19.71**	-20.89**	-14.77*	-4.44
LCA-607 x LCA-315	-4.78	-12.83*	91.07**	4.39	-0.57	-17.83*	-11.47	-0.74
LCA-655 x G4	14.29	-4.00	50.00**	-18.05**	35.46**	32.19**	-5.42	6.04
LCA-655 x LCA-678	24.27**	14.86	79.46**	-1.95	33.87**	26.54*	-9.46	1.51
LCA-655 x LCA-453	-19.82**	-33.08**	56.25**	-14.63*	32.97**	27.17**	-0.31	11.78
LCA-655 x LCA-703-2	18.20*	1.14	58.04**	-13.66*	53.61**	46.98**	15.09*	29.04**
LCA-655 x LCA-705-2	-5.45	-10.86	39.29**	-23.90**	-3.99	-19.15**	-15.45*	-5.20
LCA-655 x LCA-315	-5.54	-12.25	59.82**	-12.68	48.97**	47.71**	5.69	18.50*
LCA-355 x G4	0.54	-11.75	24.11*	-32.20**	-3.41	-5.15	-33.00**	-24.88**
LCA-355 x LCA-678	5.56	2.54	44.20**	-21.22**	34.55**	27.94**	-9.62	1.34
LCA-355 x LCA-453	3.82	-16.83**	94.20**	6.10	0.52	-4.45	-25.09**	-16.02
LCA-355 x LCA-703-2	15.96	3.81	45.98**	-20.24**	20.63*	14.73	-10.16	0.73
LCA-355 x LCA-705-2	10.72	9.84	54.46**	-15.61*	-12.58	-26.76**	-23.41**	-14.13
LCA-355 x LCA-315	1.52	-10.05	63.84**	-10.49	-17.99*	-18.16	-42.19**	-35.18**

*; Significant at 5% level; **; Significant at 1% level

Table 4.12: Estimates of heterosis, heterobeltiosis and standard heterosis for number of seeds per fruit and seed weight (g/1000 seed) in chilli

Cross	Number of seeds per fruit				Seed weight (g/1000 seed)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	-11.90	-19.98*	-13.77	-22.84*	-1.92	-12.32	11.14	-18.63*
LCA-504 x LCA-678	-19.70*	-28.57**	-23.03*	-31.12**	9.96	4.32	16.08	-15.01*
LCA-504 x LCA-453	0.91	-3.87	14.43	2.39	9.76	-7.43	34.61**	-1.45
LCA-504 x LCA-703-2	21.64*	-3.58	3.90	-7.03	17.39*	14.84	19.91*	-12.21
LCA-504 x LCA-705-2	-28.57**	-42.25**	-37.76**	-44.31**	3.62	-6.53	16.08	-15.01*
LCA-504 x LCA-315	-0.86	-12.98	-6.23	-16.09	-1.48	-13.55	14.37	-16.26*
LCA-615 x G4	15.04	0.79	17.89	5.49	2.56	-0.10	33.55**	-2.22
LCA-615 x LCA-678	0.33	-13.84	0.79	-9.81	19.54**	9.52	46.41**	7.19
LCA-615 x LCA-453	-0.98	-1.84	16.84	4.55	4.77	0.54	46.21**	7.05
LCA-615 x LCA-703-2	16.15	-10.61	4.56	-6.44	11.57	-0.64	32.83**	-2.75
LCA-615 x LCA-705-2	27.47**	-0.04	16.93	4.63	6.60	2.81	37.44**	0.63
LCA-615 x LCA-315	13.51	-3.75	12.59	0.75	2.65	2.12	36.52**	-0.05
LCA-446 x G4	-43.31**	-48.14**	-45.00**	-50.78**	-5.17	-7.96	16.68	-14.58*
LCA-446 x LCA-678	-24.28**	-32.18**	-28.07**	-35.64**	-7.15	-10.28	7.05	-21.62**
LCA-446 x LCA-453	-25.45**	-29.51**	-16.10	-24.92**	-9.81	-17.91**	19.38*	-12.60
LCA-446 x LCA-703-2	-7.42	-26.18**	-21.71*	-29.95**	5.48	-1.10	18.00	-13.61
LCA-446 x LCA-705-2	18.66	-3.47	2.37	-8.40	16.62*	14.33	41.99**	3.96
LCA-446 x LCA-315	8.70	-3.93	1.89	-8.83	-5.84	-10.46	18.46	-13.27
LCA-466 x G4	10.65	2.20	6.14	-5.02	-2.95	-10.14	13.91	-16.60*
LCA-466 x LCA-678	-26.11**	-33.19**	-30.61**	-37.91**	-6.49	-7.88	2.50	-24.95**
LCA-466 x LCA-453	-12.36	-17.94*	-2.32	-12.60	2.13	-11.02	29.40**	-5.26
LCA-466 x LCA-703-2	5.94	-14.86	-11.58	-20.88*	20.17*	18.19*	27.62**	-6.56
LCA-466 x LCA-705-2	17.04	-4.01	-0.31	-10.79	8.23	1.17	25.64**	-8.01
LCA-466 x LCA-315	2.23	-8.83	-5.31	-15.27	0.03	-9.17	20.17*	-12.02
LCA-442 x G4	-28.55**	-33.50**	-41.49**	-47.65**	-21.86**	-22.70**	0.13	-26.69**
LCA-442 xLCA-678	-6.86	-11.39	-25.61*	-33.44**	0.25	-6.82	20.70*	-11.63

*; Significant at 5% level; **; Significant at 1% level

Table 4.12 contd…….

LCA-442 x LCA-453	-42.23**	-52.73**	-43.73**	-49.65**	-10.86	-15.73*	22.54*	-10.28
LCA-442 x LCA-703-2	28.11*	17.36	-11.05	-20.41*	14.34	3.26	33.75**	-2.08
LCA-442 x LCA-705-2	12.76	5.84	-19.78	-28.22**	2.31	0.20	29.80**	-4.97
LCA-442 x LCA-315	-20.65	-23.38	-37.63**	-44.19**	-11.43	-12.36	15.95	-15.11*
LCA-654 x G4	-11.12	-19.52*	-12.68	-21.86*	-12.96*	-19.67**	20.37*	-11.87
LCA-654 x LCA-678	11.94	-0.73	7.72	-3.61	-0.93	-13.68*	29.33**	-5.31
LCA-654 x LCA-453	-2.35	-6.67	11.10	-0.59	-13.82*	-15.09*	27.22**	-6.85
LCA-654 x LCA-703-2	-2.45	-22.88*	-16.32	-25.12**	16.52*	-1.14	48.12**	8.45
LCA-654 x LCA-705-2	-4.51	-23.00*	-16.45	-25.24**	-7.67	-15.57*	26.50**	-7.38
LCA-654 x LCA-315	9.42	-4.24	3.90	-7.03	-9.72	-15.00*	27.36**	-6.76
LCA-607 x G4	-10.73	-12.66	-23.16*	-31.24**	-11.22	-14.21	16.61	-14.62*
LCA-607 x LCA-678	5.92	5.78	-10.96	-20.33*	-15.52*	-23.18**	4.42	-23.55**
LCA-607 x LCA-453	12.15	-4.27	13.95	1.96	6.19	2.72	49.37**	9.36
LCA-607 x LCA-703-2	22.91	7.50	-9.52	-19.03*	13.93	0.73	36.91**	0.24
LCA-607 x LCA-705-2	16.45	4.22	-12.28	-21.51*	17.69**	12.61	53.07**	12.07
LCA-607 x LCA-315	25.35*	23.29	3.77	-7.14	-2.78	-4.07	30.39**	-4.54
LCA-655 x G4	-9.43	-18.39	-28.20**	-35.75**	-2.04	-7.13	31.38**	-3.81
LCA-655 x LCA-678	-6.61	-14.05	-27.85**	-35.44**	-3.34	-13.65	22.15*	-10.57
LCA-655 x LCA-453	3.91	-17.24*	-1.49	-11.85	-11.12	-12.33	27.49**	-6.66
LCA-655 x LCA-703-2	-7.91	-12.80	-38.46**	-44.94**	19.57**	3.91	47.00**	7.63
LCA-655 x LCA-705-2	30.30*	26.54	-10.70	-20.09*	-2.73	-8.67	29.20**	-5.41
LCA-655 x LCA-315	51.46**	41.38**	15.09	2.98	-6.09	-9.13	28.54**	-5.89
LCA-355 x G4	-32.50**	-33.75**	-39.47**	-45.84**	-14.89*	-21.24**	17.34	-14.09
LCA-355 x LCA-678	-12.18	-15.75	-23.03*	-31.12**	-8.05	-19.69**	19.64*	-12.40
LCA-355 x LCA-453	-14.45	-24.39**	-10.00	-19.47*	-0.76	-1.95	46.08**	6.95
LCA-355 x LCA-703-2	23.60*	4.46	-4.56	-14.60	-1.93	-16.59*	24.26*	-9.03
LCA-355 x LCA-705-2	6.59	-7.92	-15.88	-24.73**	-10.42	-17.88**	22.35*	-10.42
LCA-355 x LCA-315	-17.09	-21.60	-28.38**	-35.91**	-14.04*	-18.85**	20.90*	-11.49

*; Significant at 5% level; **; Significant at 1% level

Table 4.13: Estimates of heterosis, heterobeltiosis and standard heterosis for ascorbic acid (mg/100g) in chilli

Cross	Ascorbic acid (mg/100g)			
	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	11.90	0.84	78.56**	-19.76**
LCA-504 x LCA-678	150.45**	51.05**	167.47**	20.19**
LCA-504 x LCA-453	34.01**	25.40**	154.78**	14.49**
LCA-504 x LCA-703-2	40.08**	34.47**	158.85**	16.32**
LCA-504 x LCA-705-2	42.36**	-10.52	58.45**	-28.79**
LCA-504 x LCA-315	139.45**	50.57**	166.61**	19.81**
LCA-615 x G4	11.94	4.76	70.74**	-23.27**
LCA-615 x LCA-678	87.50**	14.75*	87.03**	-15.96**
LCA-615 x LCA-453	9.10	-1.69	99.74**	-10.24*
LCA-615 x LCA-703-2	0.89	-6.85	79.32**	-19.42**
LCA-615 x LCA-705-2	165.17**	69.63**	176.46**	24.23**
LCA-615 x LCA-315	34.87**	-13.69	40.67**	-36.79**
LCA-446 x G4	152.18**	86.71**	165.26**	19.20**
LCA-446 x LCA-678	390.84**	276.64**	157.25**	15.60**
LCA-446 x LCA-453	64.13**	9.66	122.79**	0.12
LCA-446 x LCA-703-2	22.62**	-16.93**	59.90**	-28.15**
LCA-446 x LCA-705-2	220.04**	166.70**	82.16**	-18.14**
LCA-446 x LCA-315	132.65**	94.00**	32.51**	-40.45**
LCA-466 x G4	19.04**	-11.12**	155.95**	15.02**
LCA-466 x LCA-678	-4.68	-46.30**	54.65**	-30.51**
LCA-466 x LCA-453	-32.22**	-42.20**	66.44**	-25.21**
LCA-466 x LCA-703-2	-5.30	-20.99**	127.51**	2.23
LCA-466 x LCA-705-2	50.60**	-12.79**	151.12**	12.85*
LCA-466 x LCA-315	-30.52**	-59.76**	15.89	-47.92**
LCA-442 x G4	-34.76**	-46.16**	17.58	-47.16**
LCA-442 xLCA-678	52.47**	-11.02*	94.35**	-12.67*
LCA-442 x LCA-453	10.42*	6.57	132.75**	4.59

*; Significant at 5% level; **; Significant at 1% level

Table 4.13 contd…….

LCA-442 x LCA-703-2	-17.39**	-22.29**	69.72**	-23.73**
LCA-442 x LCA-705-2	40.84**	-14.90**	85.86**	-16.48**
LCA-442 x LCA-315	-65.33**	-79.05**	-54.24**	-79.44**
LCA-654 x G4	70.94**	63.53**	154.40**	14.32**
LCA-654 x LCA-678	34.80**	-16.78*	29.47*	-41.82**
LCA-654 x LCA-453	18.07**	4.24	111.79**	-4.83
LCA-654 x LCA-703-2	0.53	-9.11	74.95**	-21.38**
LCA-654 x LCA-705-2	19.89*	-22.51**	20.55	-45.83**
LCA-654 x LCA-315	36.34**	-11.84	37.15**	-38.37**
LCA-607 x G4	78.87**	68.37**	171.03**	21.79**
LCA-607 x LCA-678	156.17**	57.14**	152.95**	13.67**
LCA-607 x LCA-453	-58.05**	-62.40**	-23.61*	-65.67**
LCA-607 x LCA-703-2	5.70	-2.96	86.80**	-16.06**
LCA-607 x LCA-705-2	98.59**	27.38**	105.04**	-7.86
LCA-607 x LCA-315	33.76**	-14.17*	38.16**	-37.91**
LCA-655 x G4	-4.25	-27.37**	99.55**	-10.33*
LCA-655 x LCA-678	-2.84	-44.96**	51.22**	-32.05**
LCA-655 x LCA-453	-15.34**	-26.37**	102.30**	-9.09
LCA-655 x LCA-703-2	14.43**	-2.70	167.33**	20.13**
LCA-655 x LCA-705-2	-1.11	-42.36**	58.36**	-28.84**
LCA-655 x LCA-315	2.71	-40.12**	64.52**	-26.07**
LCA-355 x G4	-23.17**	-26.18**	4.87	-52.87**
LCA-355 x LCA-678	249.38**	123.41**	192.54**	31.46**
LCA-355 x LCA-453	3.09	-15.23**	72.22**	-22.61**
LCA-355 x LCA-703-2	79.00**	50.38**	189.48**	30.08**
LCA-355 x LCA-705-2	136.19**	59.16**	108.41**	-6.35
LCA-355 x LCA-315	30.54**	-11.99	15.24	-48.22**

*; Significant at 5% level; **; Significant at 1% level

Table 4.14: Estimates of heterosis, heterobeltiosis and standard heterosis for oleoresin (%) and capsaicin (%) in chilli

Cross	Oleoresin (%)				Capsaicin (%)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	116.44**	105.49**	37.92**	92.65**	-10.74*	-39.15**	-45.37**	-0.33
LCA-504 x LCA-678	-1.13	-4.67	-31.08**	-3.74	-10.30*	-22.24**	-30.19**	27.37**
LCA-504 x LCA-453	-12.93	-15.84	-39.46**	-15.43	13.63**	-20.94**	-29.01**	29.51**
LCA-504 x LCA-703-2	-0.97	-7.49	-28.50**	-0.12	-47.12**	-50.13**	-55.22**	-18.30**
LCA-504 x LCA-705-2	1.42	-2.16	-34.33**	-8.27	-43.90**	-56.87**	-61.27**	-29.35**
LCA-504 x LCA-315	4.09	-6.07	-36.96**	-11.94	-57.62**	-64.87**	-68.46**	-42.46**
LCA-615 x G4	70.54**	41.97**	28.80**	79.91**	-34.03**	-55.43**	-58.61**	-24.48**
LCA-615 x LCA-678	68.08**	51.00**	37.00**	91.37**	-50.19**	-57.42**	-60.46**	-27.86**
LCA-615 x LCA-453	36.10**	22.01**	10.70	54.62**	-40.56**	-59.03**	-61.95**	-30.59**
LCA-615 x LCA-703-2	-6.22	-13.17	-21.22**	10.04	-64.10**	-66.67**	-69.05**	-43.53**
LCA-615 x LCA-705-2	43.16**	20.80*	9.60	53.09**	-42.43**	-56.25**	-59.38**	-25.89**
LCA-615 x LCA-315	-10.83	-28.87**	-35.47**	-9.86	-26.59**	-39.95**	-44.24**	1.73
LCA-446 x G4	15.41*	-15.51**	9.82	53.40**	21.08	-4.16	-68.73**	-42.95**
LCA-446 x LCA-678	16.78**	-9.14	18.11*	64.97**	-4.63	-38.55**	-59.51**	-26.13**
LCA-446 x LCA-453	-44.46**	-56.86**	-43.93**	-21.68*	73.81**	33.93**	-52.91**	-14.10*
LCA-446 x LCA-703-2	-37.73**	-50.35**	-35.47**	-9.86	-5.32	-41.34**	-53.32**	-14.84*
LCA-446 x LCA-705-2	-25.75**	-45.06**	-28.58**	-0.24	24.11**	-13.48	-58.25**	-23.83**
LCA-446 x LCA-315	14.58*	-18.90**	5.41	47.24**	-22.22**	-48.58**	-69.63**	-44.60**
LCA-466 x G4	-27.28**	-46.54**	-31.43**	-4.23	81.16**	42.52**	-53.50**	-15.17*
LCA-466 x LCA-678	-43.60**	-55.90**	-43.45**	-21.00*	12.39	-27.85**	-52.46**	-13.27*
LCA-466 x LCA-453	2.75	-19.81**	2.85	43.66**	76.01**	34.83**	-52.60**	-13.52*
LCA-466 x LCA-703-2	-29.44**	-43.46**	-27.49**	1.29	-8.97	-43.78**	-55.26**	-18.38**
LCA-466 x LCA-705-2	-19.05**	-39.84**	-22.84**	7.78	0.54	-30.24**	-66.34**	-38.58**
LCA-466 x LCA-315	-29.48**	-49.89**	-35.73**	-10.23	15.40	-24.02**	-55.13**	-18.14**
LCA-442 x G4	-32.30**	-49.95**	-36.91**	-11.88	143.10**	60.94**	-47.49**	-4.20
LCA-442 xLCA-678	-33.95**	-48.03**	-34.50**	-8.51	20.21*	-30.25**	-54.04**	-16.16*
LCA-442 x LCA-453	-54.83**	-64.52**	-55.28**	-37.54**	50.99**	-1.80	-65.48**	-37.02**
LCA-442 x LCA-703-2	-28.24**	-42.12**	-27.05**	1.90	-6.67	-47.13**	-57.93**	-23.25**

*; Significant at 5% level; **; Significant at 1% level

Table 4.14 contd…….

LCA-442 x LCA-705-2	-25.17**	-44.07**	-29.50**	-1.53	67.43**	2.06	-50.75**	-10.14
LCA-442 x LCA-315	-38.40**	-56.00**	-44.54**	-22.54*	5.52	-37.80**	-63.26**	-32.98**
LCA-654 x G4	9.02	-3.68	-24.24**	5.82	264.95**	184.07**	-7.32*	69.08**
LCA-654 x LCA-678	-4.50	-8.36	-27.93**	0.67	47.96**	-5.62	-37.82**	13.44*
LCA-654 x LCA-453	5.50	1.00	-20.56**	10.96	185.76**	116.71**	-23.81**	38.99**
LCA-654 x LCA-703-2	17.09*	16.08	-8.70	27.53**	56.45**	-3.92	-23.54**	39.49**
LCA-654 x LCA-705-2	11.41	-0.11	-21.44**	9.74	154.97**	75.47**	-15.32**	54.49**
LCA-654 x LCA-315	0.46	-15.27	-33.36**	-6.92	44.29**	-5.66	-44.28**	1.65
LCA-607 x G4	9.18	-11.24	-14.47*	19.47	7.49	-20.98**	-45.19**	0.00
LCA-607 x LCA-678	-10.06	-21.29**	-24.16**	5.94	-26.50**	-28.34**	-50.29**	-9.32
LCA-607 x LCA-453	0.49	-12.24	-15.43*	18.13	-2.81	-26.78**	-49.21**	-7.34
LCA-607 x LCA-703-2	2.55	-7.60	-10.96	24.37*	-25.67**	-30.44**	-44.65**	0.99
LCA-607 x LCA-705-2	-0.58	-18.11*	-21.09**	10.23	-16.63**	-29.32**	-50.97**	-10.55
LCA-607 x LCA-315	1.60	-20.72**	-23.61**	6.71	-41.03**	-45.41**	-62.13**	-30.92**
LCA-655 x G4	10.37	-4.46	-21.17**	10.10	64.04**	41.55**	-53.82**	-15.75*
LCA-655 x LCA-678	-8.64	-14.29	-29.29**	-1.22	-4.44	-35.05**	-57.21**	-21.93**
LCA-655 x LCA-453	-21.71**	-26.73**	-39.54**	-15.55	80.34**	50.90**	-46.95**	-3.22
LCA-655 x LCA-703-2	-12.21	-14.98	-29.86**	-2.02	-31.38**	-55.48**	-64.57**	-35.37**
LCA-655 x LCA-705-2	8.08	-5.10	-21.70**	9.37	30.40**	-2.81	-53.10**	-14.43*
LCA-655 x LCA-315	-5.20	-21.57*	-35.29**	-9.61	-12.51	-38.71**	-63.80**	-33.97**
LCA-355 x G4	-5.69	-30.85**	-10.57	24.92*	74.55**	41.55**	-53.82**	-15.75*
LCA-355 x LCA-678	-23.46**	-40.34**	-22.84**	7.78	40.33**	-8.23	-39.54**	10.31
LCA-355 x LCA-453	-21.93**	-39.25**	-21.44**	9.74	81.74**	43.32**	-49.62**	-8.08
LCA-355 x LCA-703-2	-31.13**	-44.98**	-28.85**	-0.61	-17.83**	-48.44**	-58.97**	-25.14**
LCA-355 x LCA-705-2	-7.11	-31.15**	-10.96	24.37*	32.50**	-5.90	-54.59**	-17.15**
LCA-355 x LCA-315	-24.92**	-46.78**	-31.17**	-3.86	8.43	-27.16**	-56.98**	-21.52**

*; Significant at 5% level; **; Significant at 1% level

Table 4.15: Estimates of heterosis, heterobeltiosis and standard heterosis for red carotenoids (mg/100g) and yellow carotenoids (mg/100g) in chilli

Cross	Red carotenoids (mg/100g)				Yellow carotenoids (mg/100g)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	45.97**	37.94**	78.97**	8.63	-5.02	-5.56	-7.11	-23.47**
LCA-504 x LCA-678	28.02**	22.69**	73.66**	5.40	58.96**	46.69**	70.61**	40.57**
LCA-504 x LCA-453	43.10**	38.25**	79.38**	8.87	21.91**	21.52*	19.52*	-1.52
LCA-504 x LCA-703-2	11.46*	9.70	46.98**	-10.80*	-4.80	-13.49	4.08	-14.24
LCA-504 x LCA-705-2	-9.05	-13.73*	24.79**	-24.26**	-3.30	-7.86	0.06	-17.56*
LCA-504 x LCA-315	2.63	-4.02	24.54**	-24.41**	9.60	6.95	5.19	-13.33
LCA-615 x G4	75.19**	41.59**	63.51**	-0.76	86.26**	36.20**	32.45**	9.13
LCA-615 x LCA-678	8.63	-18.36**	15.55	-29.87**	32.34**	-8.24	6.73	-12.07
LCA-615 x LCA-453	37.01**	8.82	31.63**	-20.11**	45.48**	6.22	3.80	-14.47
LCA-615 x LCA-703-2	32.55**	1.49	35.98**	-17.47**	34.96**	-7.29	11.54	-8.10
LCA-615 x LCA-705-2	8.80	-18.83**	17.41*	-28.74**	31.40**	-7.09	0.90	-16.86*
LCA-615 x LCA-315	26.98**	3.50	16.91*	-29.05**	34.63**	-0.34	-6.72	-23.14**
LCA-446 x G4	-2.98	-19.03**	39.73**	-15.19**	-3.75	-19.89**	17.20	-3.43
LCA-446 x LCA-678	-10.82*	-18.84**	40.07**	-14.99**	21.93**	9.44	60.10**	31.91**
LCA-446 x LCA-453	18.90**	1.12	74.51**	5.92	43.32**	19.52**	74.86**	44.07**
LCA-446 x LCA-703-2	2.95	-8.56	57.81**	-4.22	-11.66*	-19.50**	17.77	-2.97
LCA-446 x LCA-705-2	10.44*	1.51	75.18**	6.32	11.59	-2.79	42.22**	17.18*
LCA-446 x LCA-315	21.16**	0.23	72.98**	4.99	22.26**	0.24	46.65**	20.83**
LCA-466 x G4	44.04**	30.95**	84.83**	12.18*	73.87**	36.03**	134.26**	93.02**
LCA-466 x LCA-678	27.85**	27.67**	80.71**	9.68	55.87**	30.57**	124.87**	85.28**
LCA-466 x LCA-453	45.67**	35.25**	90.90**	15.86**	74.37**	36.66**	135.35**	93.91**
LCA-466 x LCA-703-2	12.95*	10.08	55.37**	-5.70	6.10	-9.89	55.19**	27.86**
LCA-466 x LCA-705-2	21.88**	20.41**	74.16**	5.71	42.11**	15.86**	99.54**	64.40**
LCA-466 x LCA-315	31.92**	18.74**	67.60**	1.72	59.62**	23.18**	112.14**	74.79**
LCA-442 x G4	23.23**	9.06	25.94**	-23.56**	17.25*	17.17	14.10	-5.99
LCA-442 xLCA-678	44.00**	17.24**	65.94**	0.72	29.48**	18.95*	38.34**	13.99
LCA-442 x LCA-453	65.09**	43.23**	73.25**	5.15	66.99**	66.70**	62.90**	34.22**

*; Significant at 5% level; **; Significant at 1% level

Table 4.15 contd…….

LCA-442 x LCA-703-2	39.58**	16.11*	55.56**	-5.59	15.108*	4.13	25.29**	3.23
LCA-442 x LCA-705-2	59.98**	29.17**	86.84**	13.40*	-59.94**	-62.01**	-58.74**	-66.01**
LCA-442 x LCA-315	51.08**	35.01**	52.49**	-7.45	20.58*	18.24	15.14	-5.13
LCA-654 x G4	27.88**	15.26*	65.83**	0.65	-52.45**	-61.69**	-62.75**	-69.31**
LCA-654 x LCA-678	18.68**	17.72**	69.37**	2.80	66.20**	25.58**	46.06**	20.35**
LCA-654 x LCA-453	29.45**	19.14**	71.41**	4.03	51.34**	21.71*	18.94*	-2.00
LCA-654 x LCA-703-2	25.62**	21.30**	74.52**	5.92	62.82**	21.64**	46.35**	20.59**
LCA-654 x LCA-705-2	32.45**	32.09**	91.07**	15.97**	95.65**	51.39**	64.41**	35.46**
LCA-654 x LCA-315	29.68**	15.74**	66.52**	1.07	46.43**	19.73*	12.06	-7.67
LCA-607 x G4	-17.26**	-18.43*	-5.80	-42.83**	3.02	-0.16	3.47	-14.75*
LCA-607 x LCA-678	-32.66**	-39.63**	-14.55	-48.14**	16.85*	10.48	28.50**	5.88
LCA-607 x LCA-453	-33.19**	-35.60**	-22.10*	-52.72**	36.53**	32.64**	37.45**	13.25
LCA-607 x LCA-703-2	38.98**	27.69**	71.08**	3.83	-52.58**	-55.87**	-46.90**	-56.25**
LCA-607 x LCA-705-2	46.95**	30.47**	88.73**	14.54**	38.76**	35.59**	47.25**	21.32**
LCA-607 x LCA-315	4.10	3.76	17.19*	-28.87**	36.85**	30.23**	34.95**	11.19
LCA-655 x G4	22.40**	14.24*	52.23**	-7.61	7.58	-5.88	22.08*	0.59
LCA-655 x LCA-678	12.28*	8.99	54.27**	-6.37	22.42**	16.10*	50.59**	24.07**
LCA-655 x LCA-453	26.01**	20.20**	60.17**	-2.79	29.73**	13.74*	47.52**	21.55**
LCA-655 x LCA-703-2	-26.70**	-26.90**	-2.06	-40.56**	-17.65**	-20.63**	2.95	-15.18*
LCA-655 x LCA-705-2	36.22**	30.86**	89.28**	14.88**	9.55	0.64	30.54**	7.55
LCA-655 x LCA-315	30.46**	20.52**	60.60**	-2.53	30.68**	12.49	45.90**	20.22**
LCA-355 x G4	5.11	-21.21**	82.25**	10.61*	-15.60**	-37.65**	26.99**	4.63
LCA-355 x LCA-678	-2.20	-21.18**	82.32**	10.66*	49.57**	17.49**	139.29**	97.16**
LCA-355 x LCA-453	2.42	-22.01**	80.40**	9.49	-22.95**	-42.99**	16.12	-4.33
LCA-355 x LCA-703-2	-28.84**	-43.81**	29.98**	-21.11**	-33.87**	-47.40**	7.12	-11.74
LCA-355 x LCA-705-2	-3.59	-21.65**	81.23**	9.99	-0.62	-23.82**	55.16**	27.85**
LCA-355 x LCA-315	-4.17	-28.69**	64.95**	0.12	-11.84*	-35.66**	31.04**	7.97

*; Significant at 5% level; **; Significant at 1% level

Table 4.16: Estimates of heterosis, heterobeltiosis and standard heterosis for total carotenoids (mg/100g) and total colour value (ASTA units) in chilli

Crosses	Total carotenoids (mg/100g)				Total colour value (ASTA units)			
	Mid	Better	Tejaswani	Indam-5	Mid	Better	Tejaswani	Indam-5
LCA-504 x G4	28.45**	23.49**	44.87**	-1.83	52.76**	46.44**	114.30**	41.98**
LCA-504 x LCA-678	38.59**	31.10**	72.45**	16.86**	36.78**	28.06**	114.81**	42.31**
LCA-504 x LCA-453	35.91**	32.69**	55.67**	5.48	48.88**	45.33**	112.68**	40.90**
LCA-504 x LCA-703-2	5.73	1.10	29.98**	-11.92*	29.43**	27.84**	87.08**	23.94**
LCA-504 x LCA-705-2	-7.15	-11.79*	14.99*	-22.08**	-6.27	-14.28*	51.31**	0.24
LCA-504 x LCA-315	5.01	-0.37	16.88*	-20.80**	6.52	4.40	52.79**	1.22
LCA-615 x G4	78.88**	39.68**	51.21**	2.46	70.57**	40.38**	88.42**	24.83**
LCA-615 x LCA-678	16.51*	-14.82**	12.05	-24.07**	9.61	-16.87**	39.45**	-7.61
LCA-615 x LCA-453	39.78**	7.92	20.60**	-18.28**	18.39*	-3.97	33.83**	-11.34
LCA-615 x LCA-703-2	33.39**	-1.76	26.30**	-14.42**	37.57**	10.57	57.82**	4.56
LCA-615 x LCA-705-2	15.99*	-14.95**	10.87	-24.87**	4.16	-22.33**	37.09**	-9.17
LCA-615 x LCA-315	29.51**	2.15	7.55	-27.12**	18.19*	-4.44	34.29**	-11.03
LCA-446 x G4	-3.26	-19.34**	30.81**	-11.36*	-2.13	-18.47**	64.27**	8.83
LCA-446 x LCA-678	0.78	-8.74	48.00**	0.29	18.13**	8.24	118.08**	44.48**
LCA-446 x LCA-453	27.52**	7.70	74.65**	18.35**	38.67**	17.29**	136.32**	56.56**
LCA-446 x LCA-703-2	-2.35	-12.47**	41.95**	-3.81	3.45	-11.63*	78.04**	17.95**
LCA-446 x LCA-705-2	10.84*	-0.03	62.13**	9.86*	6.91	0.29	102.06**	33.87**
LCA-446 x LCA-315	21.55**	0.23	62.55**	10.15*	12.77*	-4.29	92.84**	27.76**
LCA-466 x G4	56.21**	33.20**	104.41**	38.51**	40.16**	16.30**	136.71**	56.82**
LCA-466 x LCA-678	39.09**	29.16**	98.20**	34.31**	32.78**	21.11**	146.49**	63.30**
LCA-466 x LCA-453	57.24**	35.88**	108.51**	41.29**	48.40**	25.00**	154.43**	68.56**
LCA-466 x LCA-703-2	10.13*	1.20	55.30**	5.24	10.78*	-5.77	91.79**	27.06**
LCA-466 x LCA-705-2	29.81**	20.04**	84.22**	24.83**	15.83**	8.14	120.11**	45.82**
LCA-466 x LCA-315	43.19**	20.71**	85.24**	25.53**	-15.62**	-28.68**	45.15**	-3.83
LCA-442 x G4	20.93**	12.01	21.25**	-17.84**	5.05	-1.34	50.76**	-0.12
LCA-442 xLCA-678	38.51**	17.84**	55.01**	5.04	17.85**	12.60*	88.88**	25.14**
LCA-442 x LCA-453	65.81**	51.36**	69.15**	14.62**	40.18**	34.01**	104.77**	35.66**

*; Significant at 5% level; **; Significant at 1% level

Table 4.16 contd…….

LCA-442 x LCA-703-2	30.02**	11.67*	43.57**	-2.72	20.65**	16.68*	78.28**	18.11**
LCA-442 x LCA-705-2	16.03**	-0.92	29.17**	-12.47*	29.03**	20.36**	112.46**	40.75**
LCA-442 x LCA-315	39.40**	30.79**	37.70**	-6.69	57.56**	51.24**	131.09**	53.10**
LCA-654 x G4	5.08	4.04	14.90*	-22.14**	9.91	-2.63	69.33**	12.18
LCA-654 x LCA-678	32.35**	21.73**	60.14**	8.51	16.31**	14.25*	98.68**	31.62**
LCA-654 x LCA-453	35.58**	34.78**	50.62**	2.07	19.90**	8.00	87.80**	24.42**
LCA-654 x LCA-703-2	36.71**	27.07**	63.36**	10.70*	28.53**	17.02**	103.48**	34.81**
LCA-654 x LCA-705-2	49.92**	38.46**	80.51**	22.32**	22.19**	21.28**	114.09**	41.83**
LCA-654 x LCA-315	34.38**	31.25**	44.95**	-1.78	10.49	-0.11	73.70**	15.08*
LCA-607 x G4	-9.83	-10.06	-2.13	-33.68**	-17.72**	-30.96**	36.67**	-9.46
LCA-607 x LCA-678	-14.71**	-22.08**	2.50	-30.54**	-29.52**	-34.90**	28.87**	-14.62*
LCA-607 x LCA-453	-7.97	-9.19	1.49	-31.23**	-33.72**	-43.53**	11.79	-25.94**
LCA-607 x LCA-703-2	4.76	-3.28	24.34**	-15.74**	-28.14**	-38.17**	22.41*	-18.91**
LCA-607 x LCA-705-2	44.07**	32.16**	72.29**	16.75**	-10.53*	-15.38**	67.53**	10.99
LCA-607 x LCA-315	16.05**	14.17*	24.23**	-15.82**	-10.06*	-23.11**	52.22**	0.84
LCA-655 x G4	16.85**	6.40	40.29**	-4.94	29.10**	14.99*	54.35**	2.26
LCA-655 x LCA-678	16.03**	15.90**	52.81**	3.55	13.76*	-7.56	55.06**	2.73
LCA-655 x LCA-453	27.39**	17.68**	55.16**	5.14	28.51**	12.61	56.93**	3.97
LCA-655 x LCA-703-2	-23.26**	-24.22**	-0.08	-32.29**	-1.00	-14.13*	22.56*	-18.80**
LCA-655 x LCA-705-2	26.62**	25.91**	66.01**	12.49*	47.01**	17.18**	106.84**	37.03**
LCA-655 x LCA-315	30.54**	17.39**	54.78**	4.88	56.77**	36.88**	92.36**	27.44**
LCA-355 x G4	-2.40	-27.23**	60.36**	8.67	6.24	-20.99**	117.61**	44.16**
LCA-355 x LCA-678	16.44**	-7.02*	104.89**	38.84**	15.40**	-7.16*	155.70**	69.40**
LCA-355 x LCA-453	-6.70	-29.69**	54.93**	4.99	-2.76	-26.78**	101.65**	33.60**
LCA-355 x LCA-703-2	-30.69**	-45.13**	20.92**	-18.06**	-1.59	-25.30**	105.74**	36.30**
LCA-355 x LCA-705-2	-2.54	-22.44**	70.91**	15.81**	2.76	-15.69**	132.19**	53.83**
LCA-355 x LCA-315	-6.94	-31.24**	51.52**	2.67	-8.97*	-31.26**	89.32**	25.43**

*; Significant at 5% level; **; Significant at 1% level

4.17: Promising hybrids for fruit yield, yield components and quality traits in chilli

Heterotic crosses	Mean Fruit yield per plant (g) (Tejaswini, 271.53g)	Heterosis (%) for yield over best check Tejaswini	The characters showing significant standard heterosis over best check Tejaswini in desired direction
LCA 607 x LCA 703-2	328.53	20.99**	Fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red, yellow and total carotenoids, total colour value
LCA 655 X LCA 703-2	312.51	15.09*	Fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red and total carotenoids
LCA 446 X LCA 703-2	297.99	9.74	Fruit length, fruit diameter, dry fruit weight, ascorbic acid, red and total carotenoids, total colour value
LCA 655 X LCA 315	286.97	5.69	Fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red and total carotenoids, total colour value
LCA 466 X LCA 705-2	271.92	0.14	Fruit length, fruit diameter, dry fruit weight, seed weight, ascorbic acid, red and total carotenoids and total colour value

Table 4.18: Analysis of variance for combining ability (L x T) for yield and yield components in chilli

	Df	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	Days to 50 % flowering	Days to fruit maturity (red)	No. of fruits per plant	Fruit length (cm)	Fruit diameter (cm)	Dry fruit weight (g)	Fruit yield (g/plant)
Replications	2	35.36	35.31	0.11	3.27	16.71	233.40	0.47	0.00	0.03	50.82
Treatments	68	247.43**	184.04**	0.72**	40.28**	61.11**	9776.15**	6.25**	0.13**	0.13**	4478.00**
Parents	14	272.38**	107.87**	0.71**	37.40**	55.51**	7290.72**	8.87**	0.28**	0.22**	4302.95**
Lines	8	219.22**	62.17*	0.38*	54.34**	39.01**	3414.52**	7.06**	0.24**	0.09**	4457.92**
Testers	5	402.36**	202.30**	1.39**	14.36**	87.29**	11844.51**	9.72**	0.38**	0.40**	4708.59**
Line x Tester	1	47.80	1.41	0.00	17.13**	28.68	15531.43**	19.17**	0.10**	0.31**	1034.96
Parents vs Crosses	1	92.42	358.89**	1.65**	309.95**	0.41	29217.10**	41.66**	0.00	0.05*	24233.62**
Crosses	53	243.76**	200.86**	0.71**	35.95**	63.73**	10065.87**	4.89**	0.09**	0.11**	4151.50**
Error	136	23.79	27.19	0.17	2.14	13.18	860.72	0.46	0.01	0.01	602.37

	Df	No. of seeds per fruit	Seed weight (g/1000 seed)	Ascorbic acid (mg/100g)	Oleoresin (%)	Capsaicin (%)	Red carotenoids (mg/100g)	Yellow carotinoids (mg/100g)	Total carotenoids (mg/100g)	Total colour (ASTA units)
Replications	2	285.78*	0.68	14.92	0.00	0.06	7.95	22.72	5.92	23.40
Treatments	68	539.91**	1.30**	2417.40**	0.05**	33.70**	3998.56**	3139.88**	10595.07**	1659.34**
Parents	14	577.65**	1.99**	3597.82**	0.13**	51.35**	5302.04**	2697.75**	13994.68**	2209.20**
Lines	8	457.92**	2.34**	2779.55**	0.18**	44.09**	8709.48**	4484.69**	23066.37**	3448.91**
Testers	5	691.03**	1.66**	3515.78**	0.05**	5.42*	737.85*	210.62*	1598.45**	322.66**
Line x Tester	1	968.63**	0.85	10554.25**	0.10**	339.05**	863.46*	837.83**	3402.25**	1724.30**
Parents vs Crosses	1	96.68	0.13	10059.97**	0.02**	67.09**	23579.70**	9601.24**	63274.96**	5490.19**
Crosses	53	538.30**	1.14**	1961.39**	0.03**	28.41**	3284.78**	3134.75**	8703.10**	1441.81**
Error	136	89.20	0.37	38.45	0.00	1.80	141.50	68.83	278.48	50.22

*; Significant at 5% level; **; Significant at 1% level

Table 4.19: Proportional contribution of lines, testers and their interactions to total variance in chilli

S.No.	Character	Lines	Testers	Lines x Testers
1	Plant height (cm)	29.37	38.22	32.42
2	Plant spread (cm)	17.97	30.29	51.75
3	No. of primary branches per plant	31.85	30.39	37.76
4	Days to 50 % flowering	37.97	9.6	52.43
5	Days to fruit maturity (red)	42.26	16.22	41.53
6	No. of fruits per plant	23.15	35.92	40.93
7	Fruit length (cm)	50.64	31.13	18.23
8	Fruit diameter (cm)	40.45	31.14	28.41
9	Dry fruit weight (g)	16.82	49.5	33.68
10	Fruit yield (g/plant)	24.01	25.93	50.06
11	No. of seeds per fruit	40.22	13.83	45.95
12	Seed weight (g/1000 seed)	29.77	28.13	42.1
13	Ascorbic acid (mg/100g)	11.04	18.08	70.88
14	Oleoresin (%)	31.58	13.12	55.3
15	Capsaicin (%)	57.87	8.25	33.88
16	Red carotenoids (mg/100g)	37.19	7.12	55.68
17	Yellow carotinoids (mg/100g)	48.25	14.74	37.01
18	Total carotenoids (mg/100g)	49.43	9.07	41.5
19	Total colour (ASTA units)	53.09	5.95	40.96
	Total	672.93 (35.42%)	416.63 (21.93%)	810.46 (42.66%)

Table 4.20: Estimates of general and specific combining ability variances and proportionate gene action for 12 quantitative and biochemical characters in chilli

Source of variation	Plant height (cm)	Plant spread (cm)	Number of primary branches per plant	Days to 50% flowering	Days to fruit maturity (red)	Number of fruits per plant
σ^2gca	31.43**	18.43*	0.076**	2.73**	5.81**	1156.53*
σ^2sca	26.97**	36.84**	0.063*	7.61**	7.29**	1532.72**
σ^2gca/σ^2sca	1.17	0.50	1.22	0.36	0.80	0.75

*; Significant at 5% level; **; Significant at 1% level

Source of variation	Fruit length (cm)	Fruit diameter (cm)	Dry fruit weight (g)	Fruit yield (g/plant) (g)	Number of seeds per fruit	Seed weight (g/1000 seed)
σ^2gca	0.70**	0.012**	0.015*	373.57**	45.45**	0.11*
σ^2sca	0.24**	0.008**	0.013**	717.03**	79.51**	0.09
σ^2gca/σ^2sca	2.92	1.43	1.20	0.52	0.57	1.22

*; Significant at 5% level; **; Significant at 1% level

Source of variation	Ascorbic Acid (mg/100g)	Oleoresin (%)	Capsaicin (%)	Red carotenoids (mg/100g)	Yellow carotenoids (mg/100g)	Total carotenoids (mg/100g)	Total colour value (ASTA units)
σ^2gca	113.69*	2.12**	0.003**	228.68**	328.46**	806.88**	130.67**
σ^2sca	601.22**	6.34**	0.004**	760.69**	489.49**	1502.44**	244.09**
σ^2gca/σ^2sca	0.19	0.33	0.75	0.30	0.67	0.54	0.54

*; Significant at 5% level; **; Significant at 1% level

Table 4.21: Estimates of general and specific combining ability effects for plant height (cm), plant spread (cm), number of primary branches per plant, days to 50% flowering, days to fruit maturity (red) and number of fruits per plant in chilli

	Plant height (cm)	Plant spread (cm)	Number of primary branches per plant	Days to 50% flowering	Days to fruit maturity (red)	Number of fruits per plant
Lines						
LCA-504	7.14**	5.67**	-0.48**	-2.11**	3.69**	-6.64
LCA-615	-2.35*	0.35	-0.06	0.11	5.35**	-29.18**
LCA-446	-4.16**	-1.23	-0.14	-2.33**	-0.26	-12.70
LCA-466	1.80	3.17*	0.56**	4.39**	-3.37**	-17.55*
LCA-442	-6.71**	-4.41**	0.15	1.61**	-1.31	28.27**
LCA-654	-5.71**	-4.33**	-0.08	-0.56	-0.54	-22.51**
LCA-607	3.52**	2.26	0.02	1.72**	-1.37	-8.42
LCA-655	6.60**	2.26	0.19	-0.67	2.02*	64.01**
LCA-355	-0.12	-3.75**	-0.16	-2.17**	-4.20**	4.73
SE (gi)	**1.15**	**1.23**	**0.10**	**0.35**	**0.86**	**6.92**
Testers						
G4	-0.27	1.35	0.11	-1.28**	-3.24**	22.62**
LCA-678	2.07*	5.33**	0.09	1.98**	0.76	19.60**
LCA-453	-2.07*	-3.33**	-0.32**	0.06	-1.13	-53.68**
LCA-703-2	10.58**	5.38**	0.42**	0.31	2.46**	49.39**
LCA-705-2	-3.01**	-2.00*	-0.35**	-1.06**	-0.20	-9.96
LCA-315	-7.30**	-6.72**	0.04	-0.02	1.35	-27.96**
SE (gj)	**0.94**	**1.00**	**0.08**	**0.28**	**0.70**	**5.65**
Crosses						
LCA-504 x G4	2.29	-2.25	-0.45	-1.00	4.80*	-5.34
LCA-504 x LCA-678	-0.81	-0.13	-0.17	2.74**	-1.20	-19.72
LCA-504 x LCA-453	-3.91	-4.37	0.01	0.00	-1.65	-19.31

*; Significant at 5% level; **; Significant at 1% level

Table 4.21 contd…….

LCA-504 x LCA-703-2	-2.59	6.76*	-0.30	-0.93	-0.24	-36.28*
LCA-504 x LCA-705-2	2.54	-0.07	0.57*	-0.56	-0.91	71.08**
LCA-504 x LCA-315	2.49	0.06	0.35	-0.26	-0.80	9.57
LCA-615 x G4	9.25**	-8.86**	0.19	1.78*	2.80	-28.79
LCA-615 x LCA-678	-1.60	3.36	-0.10	-0.81	2.80	-41.04*
LCA-615 x LCA-453	7.82**	2.65	0.08	-4.56**	-1.98	38.51*
LCA-615 x LCA-703-2	-12.66**	-1.19	0.24	1.52	-0.57	-23.04
LCA-615 x LCA-705-2	-2.47	-0.34	-0.16	2.56**	-1.24	17.02
LCA-615 x LCA-315	-0.35	4.38	-0.24	-0.48	-1.80	37.35*
LCA-446 x G4	-4.41	5.68	0.04	1.22	-1.59	1.92
LCA-446 x LCA-678	0.89	-3.57	-0.14	-0.37	1.41	26.21
LCA-446 x LCA-453	8.19**	-2.64	-0.40	-4.44**	1.63	-31.81
LCA-446 x LCA-703-2	5.92*	1.58	0.46	-1.37	0.37	31.25
LCA-446 x LCA-705-2	-9.89**	-1.94	-0.10	2.67**	-2.30	-27.60
LCA-446 x LCA-315	-0.70	0.88	0.14	2.30**	0.48	0.03
LCA-466 x G4	-6.53*	-9.79**	-0.26	-5.50**	-1.48	-69.46**
LCA-466 x LCA-678	3.46	3.53	0.25	0.24	-7.48**	42.16*
LCA-466 x LCA-453	1.33	-5.88	-0.24	0.83	4.41*	-20.73
LCA-466 x LCA-703-2	4.49	-0.65	-0.38	-0.09	4.15	-4.34
LCA-466 x LCA-705-2	2.55	-0.40	0.32	0.28	3.48	79.72**
LCA-466 x LCA-315	-5.30	13.18**	0.31	4.24**	-3.07	-27.35
LCA-442 x G4	-3.69	-1.31	-0.45	1.28	-7.20**	7.72
LCA-442 xLCA-678	-3.06	4.13	0.26	-1.31	1.80	12.11
LCA-442 x LCA-453	-5.46	7.34*	0.31	5.94**	1.35	73.06**
LCA-442 x LCA-703-2	7.17*	-6.93*	0.13	-1.31	-0.91	-11.85
LCA-442 x LCA-705-2	6.76*	-1.86	-0.10	-0.94	-0.24	-77.36**
LCA-442 x LCA-315	-1.72	-1.37	-0.15	-3.65**	5.20*	-3.67
LCA-654 x G4	-3.80	-1.39	0.11	1.11	-3.31	-7.57

*; Significant at 5% level; **; Significant at 1% level

Table 4.21 contd…….

LCA-654 x LCA-678	4.94	-1.83	0.39	0.52	5.02*	31.38
LCA-654 x LCA-453	-1.16	3.76	0.23	-2.22**	0.91	-10.54
LCA-654 x LCA-703-2	-6.87*	-6.25*	-0.54*	-2.81**	-0.02	-23.01
LCA-654 x LCA-705-2	7.05*	1.90	0.16	-0.44	-0.02	-31.12
LCA-654 x LCA-315	-0.16	3.82	-0.36	3.85**	-2.57	40.87*
LCA-607 x G4	3.81	10.29**	0.37	-1.83*	0.52	45.41**
LCA-607 x LCA-678	-1.63	-6.62*	-0.31	0.24	-4.15	-59.44**
LCA-607 x LCA-453	-1.89	1.87	-0.40	4.83**	-3.59	-24.15
LCA-607 x LCA-703-2	-1.80	-10.70**	0.06	0.24	1.15	61.30**
LCA-607 x LCA-705-2	-1.54	10.77**	0.03	-3.39**	2.81	-23.91
LCA-607 x LCA-315	3.05	-5.60	0.24	-0.09	3.26	0.78
LCA-655 x G4	7.59**	13.46**	0.31	3.56**	3.13	52.85**
LCA-655 x LCA-678	4.49	0.93	0.13	0.30	1.46	-61.77**
LCA-655 x LCA-453	-9.41**	0.16	-0.07	-3.11**	0.35	10.12
LCA-655 x LCA-703-2	-1.35	2.90	-0.21	4.96**	2.43	-2.46
LCA-655 x LCA-705-2	-6.26*	-9.59**	-0.14	-1.00	-3.91	2.66
LCA-655 x LCA-315	4.93	-7.87*	-0.02	-4.70**	-3.46	-1.41
LCA-355 x G4	-4.51	-5.83	0.16	-0.61	2.35	3.26
LCA-355 x LCA-678	-6.68*	0.19	-0.32	-1.54	0.35	70.11**
LCA-355 x LCA-453	4.49	-2.88	0.48*	2.72**	-1.43	-15.14
LCA-355 x LCA-703-2	7.68**	14.48**	0.54*	-0.20	-6.35**	8.42
LCA-355 x LCA-705-2	1.27	1.52	-0.59*	0.83	2.31	-10.49
LCA-355 x LCA-315	-2.24	-7.49*	-0.27	-1.20	2.76	-56.17**
SE (gij)	**2.82**	**3.01**	**0.24**	**0.85**	**2.10**	**16.94**

*; Significant at 5% level; **; Significant at 1% level

Table 4.22: Estimates of general and specific combining ability effects for fruit length (cm), fruit diameter (cm), dry fruit weight (g), fruit yield (g/plant), number of seeds per fruit and seed weight (g/1000 seed) in chilli

	Fruit length (cm)	Fruit diameter (cm)	Dry fruit weight (g)	Fruit yield (g/plant)	Number of seeds per fruit	Seed weight (g/1000 seed)
Lines						
LCA-504	0.08	-0.05	-0.05	1.39	0.49	-0.38**
LCA-615	-1.22**	0.07**	0.06*	-16.18**	17.21**	0.64**
LCA-446	0.17	0.08**	-0.03	-10.57	-5.11*	-0.30*
LCA-466	-1.35**	0.16**	-0.03	-18.17**	2.82	-0.32*
LCA-442	0.69**	0.06*	0.02	11.69*	-14.31**	-0.29*
LCA-654	0.92**	0.05*	0.12**	7.47	5.52*	0.18
LCA-607	0.08	-0.04	0.11**	10.85	3.56	0.28*
LCA-655	-0.78**	-0.22**	-0.09**	36.99**	-3.21	0.24
LCA-355	1.42**	-0.12**	-0.11**	-23.47**	-6.97**	-0.06
SE (gi)	**0.16**	**0.02**	**0.03**	**5.78**	**2.23**	**0.14**
Testers						
G4	-0.22	-0.16**	-0.19**	-19.39**	-6.78**	-0.42**
LCA-678	-0.37**	-0.01	-0.09**	-1.14	-5.17**	-0.38**
LCA-453	0.11	0.18**	0.24**	-7.45	6.93**	0.37**
LCA-703-2	-0.77**	-0.01	-0.03	40.04**	-0.45	0.30*
LCA-705-2	-0.23	0.01	0.00	-4.48	0.47	0.26*
LCA-315	1.47**	-0.01	0.07**	-7.59	4.99**	-0.13
SE (gj)	**0.13**	**0.02**	**0.02**	**4.72**	**1.82**	**0.12**
Crosses						
LCA-504 x G4	-0.24	-0.02	0.03	3.74	4.23	0.04
LCA-504 x LCA-678	-0.27	-0.01	0.03	-16.46	-4.42	0.25

Table 4.22 contd……. *; Significant at 5% level; **; Significant at 1% level

LCA-504 x LCA-453	1.00*	-0.01	-0.02	0.58	11.94*	0.43
LCA-504 x LCA-703-2	0.19	0.07	0.04	-35.52*	11.33*	-0.23
LCA-504 x LCA-705-2	-0.88*	0.02	-0.12	38.64**	-21.26**	-0.39
LCA-504 x LCA-315	0.20	-0.05	0.03	9.02	-1.82	-0.09
LCA-615 x G4	-0.55	0.07	-0.24**	-17.58	11.56*	0.15
LCA-615 x LCA-678	1.04**	0.06	-0.02	-35.82*	-3.05	0.76*
LCA-615 x LCA-453	-0.15	0.05	0.15*	37.50**	-2.95	0.00
LCA-615 x LCA-703-2	-0.67	-0.05	-0.01	-26.48	-4.90	-0.60
LCA-615 x LCA-705-2	0.11	-0.11	0.00	20.19	3.58	-0.33
LCA-615 x LCA-315	0.21	0.00	0.11	22.20	-4.24	0.01
LCA-446 x G4	0.50	-0.17**	0.13*	5.73	-13.91*	0.24
LCA-446 x LCA-678	-0.68	0.02	-0.01	17.30	-2.66	-0.29
LCA-446 x LCA-453	-0.57	-0.06	-0.01	-25.13	-5.66	-0.42
LCA-446 x LCA-703-2	-0.27	-0.01	-0.02	38.45**	-2.55	-0.41
LCA-446 x LCA-705-2	0.30	0.19**	-0.06	-24.48	14.83**	0.84*
LCA-446 x LCA-315	0.73	0.02	-0.03	-11.86	9.95	0.04
LCA-466 x G4	0.13	0.14*	0.23**	-20.93	17.02**	0.12
LCA-466 x LCA-678	1.28**	-0.07	-0.08	24.12	-12.52*	-0.50
LCA-466 x LCA-453	0.02	0.09	-0.08	-37.52**	-3.13	0.11
LCA-466 x LCA-703-2	0.02	-0.14*	-0.09	-1.96	-2.78	0.10
LCA-466 x LCA-705-2	-0.35	-0.02	0.01	64.49**	4.87	0.03
LCA-466 x LCA-315	-1.10**	0.01	0.00	-28.21*	-3.45	0.15
LCA-442 x G4	-0.07	-0.11	-0.14*	4.50	-2.04	-0.61
LCA-442 xLCA-678	-0.06	-0.06	0.00	9.03	8.41	0.39
LCA-442 x LCA-453	0.64	0.03	-0.22**	33.61*	-17.46**	-0.27
LCA-442 x LCA-703-2	0.35	0.02	0.13*	-16.15	14.76**	0.38
LCA-442 x LCA-705-2	-0.15	0.20**	0.21**	-47.33**	7.21	0.21
LCA-442 x LCA-315	-0.70	-0.08	0.02	16.34	-10.88*	-0.10

Table 4.22 contd…….

*; Significant at 5% level; **; Significant at 1% level

LCA-654 x G4	0.29	0.03	-0.02	-11.61	0.03	-0.06
LCA-654 x LCA-678	-0.74	0.03	-0.13*	31.11*	13.91*	0.35
LCA-654 x LCA-453	-0.18	0.20**	0.15*	8.42	4.38	-0.50
LCA-654 x LCA-703-2	0.39	-0.05	0.10	-8.61	-9.07	0.63
LCA-654 x LCA-705-2	0.24	-0.19**	-0.03	-19.33	-10.09	-0.43
LCA-654 x LCA-315	0.01	0.00	-0.07	0.03	0.85	0.01
LCA-607 x G4	0.81*	0.00	-0.09	32.30*	-5.98	-0.35
LCA-607 x LCA-678	-0.26	0.00	-0.07	-49.13**	1.68	-1.01**
LCA-607 x LCA-453	0.30	-0.07	0.21**	-32.76*	8.50	0.52
LCA-607 x LCA-703-2	-0.15	0.02	-0.15*	47.57**	-1.95	-0.04
LCA-607 x LCA-705-2	-0.42	0.00	0.12	-5.01	-4.97	0.82*
LCA-607 x LCA-315	-0.27	0.04	-0.02	7.04	2.71	0.06
LCA-655 x G4	-0.76	0.06	0.14*	9.13	-3.05	0.44
LCA-655 x LCA-678	0.11	0.06	0.26**	-20.09	-4.39	-0.07
LCA-655 x LCA-453	-0.67	-0.33**	-0.25**	11.07	3.54	-0.55
LCA-655 x LCA-703-2	0.82*	0.10	0.03	5.41	-17.18**	0.52
LCA-655 x LCA-705-2	0.54	0.03	-0.13*	-33.00*	3.00	-0.35
LCA-655 x LCA-315	-0.04	0.08	-0.05	27.49	18.08**	0.01
LCA-355 x G4	-0.12	0.01	-0.04	-5.28	-7.85	0.03
LCA-355 x LCA-678	-0.41	-0.02	0.02	39.95**	3.04	0.10
LCA-355 x LCA-453	-0.39	0.11	0.05	4.23	0.83	0.69
LCA-355 x LCA-703-2	-0.67	0.05	-0.04	-2.70	12.35*	-0.34
LCA-355 x LCA-705-2	0.62	-0.12*	0.00	5.84	2.83	-0.40
LCA-355 x LCA-315	0.96*	-0.03	0.00	-42.04**	-11.19*	-0.08
SE (gij)	**0.39**	**0.06**	**0.06**	**14.17**	**5.45**	**0.35**

*; Significant at 5% level; **; Significant at 1% level

Table 4.23: Estimates of general and specific combining ability effects for ascorbic acid (mg/100g), capsaicin (%), oleoresin (%), red carotenoids (mg/100g), yellow carotenoids (mg/100g), total carotenoids (mg/100g) and total colour value (ASTA units) in chilli

	Ascorbic acid (mg/100g)	Oleoresin (%)	Capsaicin (%)	Red carotenoids (mg/100g)	Yellow carotenoids (mg/100g)	Total carotenoids (mg/100g)	Total colour value (ASTA units)
Lines							
LCA-504	17.14**	-0.22	0.02**	-0.79	-14.43**	-15.22**	2.90
LCA-615	0.20	3.88**	-0.05**	-29.05**	-19.92**	-48.97**	-21.08**
LCA-446	5.04**	1.24**	-0.06**	5.34	6.51**	11.85**	8.71**
LCA-466	1.49	-0.87**	-0.03**	23.23**	57.15**	80.38**	18.92**
LCA-442	-15.06**	-2.64**	-0.04**	5.29	-13.84**	-8.55*	6.20**
LCA-654	-9.02**	-0.32	0.19**	20.38**	-10.31**	10.07*	4.30*
LCA-607	-1.53	0.35	0.01	-37.95**	-12.87**	-50.83**	-28.15**
LCA-655	-0.58	-1.35**	-0.04**	-3.45	-0.94	-4.38	-11.45**
LCA-355	2.32	-0.06	0.00	17.01**	8.64**	25.65**	19.66**
SE (gi)	**1.46**	**0.32**	**0.01**	**2.80**	**1.96**	**3.93**	**1.67**
Testers							
G4	4.46**	2.08**	0.03**	-1.43	-10.89**	-12.32**	-1.53
LCA-678	7.83**	0.46	0.02**	-4.01	21.35**	17.34**	5.97**
LCA-453	0.61	-0.62*	0.03**	5.23*	8.88**	14.11**	2.95*
LCA-703-2	9.15**	-0.55*	-0.01*	-9.39**	-15.70**	-25.09**	-7.15**
LCA-705-2	0.96	0.08	0.00	16.62**	-2.45	14.17**	5.82**
LCA-315	-23.01**	-1.44**	-0.05**	-7.02**	-1.19	-8.21*	-6.06**
SE (gj)	**1.19**	**0.26**	**0.01**	**2.29**	**1.60**	**3.21**	**1.36**
Crosses							
LCA-504 x G4	-27.46**	7.04**	0.00	29.34**	-6.10	23.24*	16.67**

Table 4.23 contd…….

*; Significant at 5% level; **; Significant at 1% level

LCA-504 x LCA-678	8.32*	-1.83*	0.11**	25.80**	20.33**	46.14**	9.47*
LCA-504 x LCA-453	9.96**	-2.02*	0.11**	23.15**	-5.77	17.38	11.23**
LCA-504 x LCA-703-2	3.20	-0.42	-0.04*	0.48	7.16	7.64	6.11
LCA-504 x LCA-705-2	-32.82**	-1.94*	-0.09**	-51.06**	-9.12	-60.19**	-28.12**
LCA-504 x LCA-315	38.79**	-0.82	-0.10**	-27.71**	-6.51	-34.22**	-15.36**
LCA-615 x G4	-13.97**	1.55*	-0.02	39.80**	29.26**	69.06**	25.27**
LCA-615 x LCA-678	-10.17**	4.42**	-0.03	-12.81	-22.40**	-35.21**	-11.34**
LCA-615 x LCA-453	2.66	1.50	-0.05**	-3.54	-12.14*	-15.68	-11.66**
LCA-615 x LCA-703-2	-14.88**	-3.42**	-0.06**	16.08*	18.28**	34.36**	12.70**
LCA-615 x LCA-705-2	36.09**	0.64	0.00	-31.29**	-3.00	-34.29**	-12.59**
LCA-615 x LCA-315	0.26	-4.70**	0.16**	-8.24	-10.01*	-18.24	-2.37
LCA-446 x G4	22.82**	1.31	-0.09**	-21.95**	-8.68	-30.63**	-18.88**
LCA-446 x LCA-678	15.92**	4.19**	-0.01	-18.98**	-8.54	-27.52**	5.60
LCA-446 x LCA-453	7.97*	-4.17**	0.03	11.42	15.07**	26.49**	19.47**
LCA-446 x LCA-703-2	-28.27**	-2.95**	0.07**	6.82	-3.45	3.37	-5.06
LCA-446 x LCA-705-2	-10.27**	-2.53**	0.02	0.79	1.76	2.56	-3.76
LCA-446 x LCA-315	-8.17*	4.16**	-0.02	21.90**	3.85	25.74**	2.64
LCA-466 x G4	22.27**	-2.85**	-0.01	12.05	29.04**	41.09**	13.97**
LCA-466 x LCA-678	-25.72**	-3.06**	0.01	9.89	-10.30*	-0.41	12.28**
LCA-466 x LCA-453	-13.30**	5.06**	0.00	12.39	10.08*	22.47*	20.02**
LCA-466 x LCA-703-2	5.05	0.38	0.02	-13.87*	-25.85**	-39.72**	-7.10
LCA-466 x LCA-705-2	23.64**	0.46	-0.07**	-18.27**	-5.62	-23.88*	-3.25
LCA-466 x LCA-315	-11.94**	0.02	0.06**	-2.19	2.64	0.45	-35.91**
LCA-442 x G4	-22.11**	-1.92*	0.04*	-37.76**	9.33	-28.44**	-24.40**
LCA-442 xLCA-678	8.32*	0.07	0.00	10.84	-4.61	6.23	-9.24*
LCA-442 x LCA-453	32.46**	-2.01*	-0.09**	10.02	26.39**	36.41**	3.23
LCA-442 x LCA-703-2	-3.85	2.21**	0.00	4.28	22.58**	26.85**	-2.41
LCA-442 x LCA-705-2	11.46**	1.21	0.05*	14.25*	-54.10**	-39.84**	4.93

Table 4.23 contd…….

*; Significant at 5% level; **; Significant at 1% level

LCA-442 x LCA-315	-26.27**	0.44	0.00	-1.63	0.41	-1.21	27.88**
LCA-654 x G4	32.10**	-2.31**	0.11**	-6.96	-52.21**	-59.17**	-11.46**
LCA-654 x LCA-678	-26.30**	-1.25	-0.11**	-0.31	-2.31	-2.62	-1.52
LCA-654 x LCA-453	17.19**	0.95	-0.02	-7.19	-10.32*	-17.52	-4.96
LCA-654 x LCA-703-2	-7.58*	2.68**	0.03	11.00	34.95**	45.96**	14.47**
LCA-654 x LCA-705-2	-23.35**	0.12	0.08**	4.03	35.33**	39.36**	7.80
LCA-654 x LCA-315	7.94*	-0.18	-0.09**	-0.58	-5.44	-6.02	-4.33
LCA-607 x G4	31.93**	-1.50	0.01	-31.05**	0.33	-30.71**	1.58
LCA-607 x LCA-678	20.60**	-1.35	-0.02	-38.54**	-13.01**	-51.55**	-10.56*
LCA-607 x LCA-453	-49.94**	1.05	-0.02	-56.46**	6.21	-50.25**	-17.68**
LCA-607 x LCA-703-2	-9.86**	1.67*	0.06**	65.38**	-32.88**	32.50**	-1.27
LCA-607 x LCA-705-2	6.37	-0.50	0.00	59.67**	24.94**	84.61**	12.57**
LCA-607 x LCA-315	0.89	0.63	-0.03	1.00	14.40**	15.40	15.35**
LCA-655 x G4	-0.50	-0.82	0.00	1.22	2.45	3.67	-4.62
LCA-655 x LCA-678	-25.16**	-0.43	-0.02	6.14	-8.27	-2.13	-11.69**
LCA-655 x LCA-453	4.57	-0.91	0.04*	3.70	1.88	5.58	-7.56
LCA-655 x LCA-703-2	24.66**	0.50	-0.04*	-53.29**	-7.19	-60.48**	-17.88**
LCA-655 x LCA-705-2	-15.13**	1.11	0.03	25.80**	0.39	26.19**	19.23**
LCA-655 x LCA-315	11.55**	0.56	0.00	16.44*	10.73*	27.17**	22.51**
LCA-355 x G4	-45.09**	-0.50	-0.04*	15.31*	-3.42	11.89	1.87
LCA-355 x LCA-678	34.18**	-0.74	0.07**	17.97*	49.10**	67.07**	17.00**
LCA-355 x LCA-453	-11.57**	0.55	-0.01	6.52	-31.40**	-24.88*	-12.09**
LCA-355 x LCA-703-2	31.52**	-0.64	-0.03	-36.88**	-13.61**	-50.49**	0.44
LCA-355 x LCA-705-2	4.01	1.45	-0.01	-3.92	9.40	5.49	3.19
LCA-355 x LCA-315	-13.05**	-0.11	0.02	1.00	-10.07*	-9.07	-10.41*
SE (gij)	**3.58**	**0.77**	**0.02**	**6.87**	**4.79**	**9.63**	**4.09**

*; Significant at 5% level; **; Significant at 1% level

Table 4.25: Promising general and specific combiners for yield, yield components and quality traits in chilli

Parents (general combiners)	Characters
LCA-442 (line)	No. of fruits per plant, fruit length, fruit diameter and fruit yield, yellow carotenoids and total colour value (no. of primary branches and fruit weight in desired direction)
LCA-654 (line)	Fruit length, fruit diameter, dry fruit weight, no. of seeds per fruit, capsaicin, red, yellow and total carotenoids and total colour value (days to 50% flowering and fruit yield in desired direction)
LCA-655 (line)	Plant height, no. of fruits per plant and fruit yield, yellow carotenoids (plant spread, no. of primary branches per plant, days to 50% flowering in desired direction)
LCA-703-2 (tester)	Plant height, plant spread, no. of primary branches per plant, no. of fruits per plant, seed weight, fruit yield, Ascorbic acid, yellow carotenoids
LCA-453 (tester)	Fruit diameter, dry fruit weight, no. of seeds per fruit, seed weight, oleoresin, red, yellow and total carotenoids, total colour value (days to fruit maturity, fruit length Ascorbic acid in desired direction)
Crosses (specific combiners)	
LCA-466 x LCA-705-2	No. of fruits per plant, dry fruit yield, Ascorbic acid
LCA-607 x LCA-703-2	No. of fruits per plant, fruit yield, oleoresin, capsaicin, red, yellow and total carotenoids
LCA-355 x LCA-678	No. of fruits per plant, fruit yield, Ascorbic acid, capsaicin, red and yellow carotenoids, total colour value
LCA-504 x LCA-705-2	No. of primary branches, no. of fruits per plant, fruit yield
LCA-446 x LCA-703-2	Plant height, fruit yield, capsaicin
LCA-615 x LCA-453	Plant height, days to 50% flowering, no. of fruits per plant, dry fruit weight, fruit yield, yellow carotenoids
LCA-442 x LCA-453	Plant spread, no. of fruits per plant, fruit yield, Ascorbic acid, total carotenoids
LCA-607 x G4	Plant spread, days to 50% flowering, no. of fruits per plant, fruit length, fruit yield, Ascorbic acid
LCA-654 x LCA-678	No. of seeds per fruit, fruit yield
LCA-355 x LCA-703-2	Plant height, plant spread, no. of primary branches per plant, days to fruit maturity, no. of seeds per fruit, Ascorbic acid, yellow carotenoids (fruit yield in desired direction)

Table 4.24: Good general combiners and promising three specific combiners for different characters in chilli

S. No.	characters	General combiners		Specific combiners
		Lines	Testers	Crosses
	Growth parameters			
1	Plant height (cm)	LCA 504, LCA 607, LCA 655	LCA 703-2, LCA 678	LCA 615 x G4, LCA 446 x LCA 453, LCA 615 x LCA 453
2	Plant spread (cm)	LCA 504, LCA 466	LCA 678, LCA 703-2	LCA 355 x LCA 703-2, LCA 655 x G4, LCA 466 x LCA 315
3	No. of primary branches per plant	LCA 466	LCA 703-2	LCA 504 x LCA 705-2, LCA 355 x LCA 703-2, LCA 355 x LCA 453
	Promising combiners for growth parameters	LCA-504, LCA-466, LCA-678 and LCA-703-2		LCA-655 x G4, LCA-355 x LCA-703-2, LCA-654 x LCA-705-2, LCA-446 x LCA-703-2, LCA-615 x LCA-453
Earliness parameters				
4	Days to 50 % flowering	LCA 504, LCA 446, LCA 355	G4, LCA 705-2	LCA 466 x G4, LCA 655 x LCA 315, LCA 615 x LCA 453
5	Days to fruit maturity (red)	LCA 466, LCA 355	G4	LCA 466 x LCA 678, LCA 442 x G4, LCA 355 x LCA 703-2
	Promising combiners for earliness	LCA-355, G4		LCA-615 x LCA-453, LCA-466 x G4, LCA-654 x LCA-703-2, LCA-654 x LCA-703-2 LCA-355 x LCA-703-2
Fruit and seed parameters				
6	No. of fruits per plant	LCA 442, LCA 655	G4, LCA 678, LCA 703-2	LCA 466 x LCA 705-2, LCA 442 x LCA 453, LCA 504 x LCA 705-2
7	Fruit length (cm)	LCA 442, LCA 654, LCA 355	LCA 315	LCA 466 x LCA 678, LCA 615 x LCA 678, LCA 504 x LCA 453
8	Fruit diameter (cm)	LCA 615, LCA 446, LCA 466, LCA 442, LCA 654	LCA 453	LCA 442 x LCA 705-2, LCA 654 x LCA 453, LCA 446 x LCA 705-2
9	Dry fruit weight (g)	LCA 615, LCA 654, LCA 607	LCA 453, LCA 315	LCA 655 x LCA 678, LCA 466 x G4, LCA 442 x LCA 705-2, LCA 607 x LCA 453
10	No. of seeds per fruit	LCA 615, LCA 654	LCA 453, LCA 315	LCA 655 x LCA 315, LCA 466 x G4, LCA 446 x LCA 705-2

Table 4.24 contd….

11	Seed weight (g/1000 seed)	LCA 615, LCA 607	LCA 453, LCA 703-2, LCA 705-2	LCA 446 x LCA 705-2, LCA 607 x LCA 705-2, LCA 615 x LCA 678
	Promising combiners for fruit and seed parameters	LCA-615, LCA-442, LCA-654, LCA-453 and LCA-315		LCA-446 x LCA-705-2, LCA-466 x G4, LCA-442 x LCA-703-2, LCA-442 x LCA-705-2 LCA-504 x LCA-453
12	Fruit yield	LCA 442, LCA 655	LCA 703-2	LCA 466 x LCA 705-2, LCA 607 x LCA 703-2, LCA 355 x LCA 678
Quality parameters				
13	Ascorbic acid (mg/100g)	LCA 504, LCA 446	G4, LCA 678, LCA 703-2	LCA 504 x LCA 315, LCA 615 x LCA 705-2 LCA 355 x LCA 678
14	Oleoresin (%)	LCA 615, LCA 446	G4	LCA 504 x G4, LCA 466 x LCA 453, LCA 615 x LCA 678
15	Capsaicin (%)	LCA 504, LCA 654	G4, LCA 678, LCA 453	LCA 615 x LCA 315, LCA 504 x LCA 678, LCA 504 x LCA 453
16	Red carotenoids (mg/100g)	LCA 466, LCA 654, LCA 355	LCA 453, LCA 705-2	LCA 607 x LCA 703-2, LCA 607 x LCA 705-2, LCA 615 x G4
17	Yellow carotinoids (mg/100g)	LCA 504, LCA 615, LCA 442, LCA 654, LCA 607	G4, LCA 703-2	LCA 442 x LCA 705-2, LCA 654 x G4, LCA 607 x LCA 703-2
18	Total carotenoids (mg/100g)	LCA 446, LCA 466, LCA 654, LCA 355	LCA 678, LCA 453, LCA 705-2	LCA 607 x LCA 705-2, LCA 615 x G4, LCA 355 x LCA 678
19	Total colour (ASTA units)	LCA 446, LCA 466, LCA 442, LCA 654, LCA 355	LCA 678, LCA 453, LCA 705-2	LCA 442 x LCA 315, LCA 615 x G4, LCA 655 x LCA 315
	Promising combiners for quality parameters	LCA-446, LCA-654, LCA-355, G4, LCA-678 LCA-453		LCA-504 x G4, LCA-504 x LCA-678, LCA-504 x LCA-453, LCA-615 x G4, LCA-442 x LCA-705-2, LCA-607 x LCA-703-2, LCA-655 x LCA-315 LCA-355 x LCA-678

Table 4.26: Summary of *gca* effects of the parents for yield, yield components and quality traits in chilli

		PH	PS	NPBP	DFF	DFM	NFP	FL	FD	DFW	NSF	SW	DFYP	AA	OC	CC	RC	YC	TC	TCV
	Lines																			
1	LCA-504	G	G	P	G	P	P	A	P	P	A	P	A	G	P	G	P	G	P	A
2	LCA-615	P	A	P	P	P	P	P	G	G	G	G	P	A	G	P	P	G	P	P
3	LCA-446	P	P	P	G	A	P	A	G	P	P	P	P	G	G	P	A	P	G	G
4	LCA-466	A	G	G	P	G	P	P	G	P	A	P	P	A	P	P	G	P	G	G
5	LCA-442	P	P	A	P	A	G	G	G	A	P	P	G	P	P	P	A	G	P	G
6	LCA-654	P	P	P	A	A	P	G	G	G	G	A	A	P	P	G	G	G	G	G
7	LCA-607	G	A	A	P	A	P	A	P	G	A	G	A	P	A	A	P	G	P	P
8	LCA-655	G	A	A	A	P	G	P	P	P	P	A	G	P	P	P	P	G	P	P
9	LCA-355	P	P	P	G	G	A	G	P	P	P	P	P	A	P	A	G	P	G	G
	Testers																			
1	G4	P	A	A	G	G	G	P	P	P	P	P	P	G	G	G	P	G	P	P
2	LCA-678	G	G	A	P	P	G	P	P	P	P	P	P	G	A	G	P	P	G	G
3	LCA-453	P	P	P	P	A	P	A	G	G	G	G	P	A	P	G	G	P	G	G
4	LCA-703-2	G	G	G	P	P	G	P	P	P	P	G	G	G	P	P	P	G	P	P
5	LCA-705-2	P	P	P	G	A	P	P	A	A	A	G	P	A	A	A	G	A	G	G
6	LCA-315	P	P	A	A	P	P	G	P	G	G	P	P	P	P	P	P	A	P	P

Where,

G: Good combiner (Significant in desired direction)

A: Average combiner (Non-significant but in desired direction)

P: Poor combiner (Undesired direction)

PH – Plant Height (cm), PS – Plant Spread (cm), NPBP – Number of Primary Branches per Plant, DFF – Days to 50 per cent Flowering , DFM – Days to Fruit Maturity, NFP – Number of Fruits per Plant, FL – Fruit Length (cm), FD – Fruit Diameter (cm), DFW – Dry Fruit Weight (g), NSF – Number of Seeds per Fruit, SW – Seed Weight (g/1000 seed), DFYP –Fruit yield (g), AA - Ascorbic Acid (mg /100g), OC - Oleoresin Content (%), CC - Capsaicin Content (%), RC - Red Carotenoids (mg/100g), YC - Yellow Carotenoids (mg/100g), TC - Total carotenoids((mg/100g) and TCV - Total Colour Value (ASTA Units)

Table 4.27: Generation means of six generations for plant height in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	66.00	117.40	99.40	97.39	78.20	106.85
C2	96.80	117.40	103.00	104.00	98.15	110.35
C3	94.60	72.00	105.00	93.63	94.05	87.55
C4	85.80	117.00	87.60	90.18	85.55	85.35

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.28: Estimates of scaling test for plant height in four crosses of chilli

Cross	A	B	C	D
C1	-9.01±6.34	-3.11±7.47	7.35±12.66	9.73±7.41
C2	-3.50±6.29	0.30±6.40	-4.21±10.46	-0.50±4.87
C3	-11.50±6.49	-1.90±6.75	-2.10±10.68	5.65±5.35
C4	-2.30±8.00	-33.91±7.24**	-17.30±12.56	9.46±6.03

Table 4.29: Estimates of gene effects for plant height in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	97.39±2.97**	-28.66±4.42**	-11.75±14.97	-19.46±14.81	-2.96±4.87	31.56±21.74	-
C2	104.00±1.79**	-12.20±3.32**	-3.11±10.47	1.00±9.74	-1.91±3.82	2.21±16.89	-
C3	93.63±2.00**	6.50±3.55	10.41±11.26	-11.30±10.69	-4.81±4.33	24.70±17.75	-
C4	90.18±2.28**	0.21±3.94	-32.71±12.80*	-18.91±12.05	15.81±4.91	55.11±20.15**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.30: Generation means of six generations for plant spread in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	55.00	94.40	69.90	62.34	66.76	83.10
C2	109.60	94.40	94.50	102.44	95.93	92.03
C3	107.20	55.60	104.50	91.91	95.20	91.38
C4	75.00	88.90	93.40	89.91	81.03	79.72

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.31: Estimates of scaling test for plant spread in four crosses of chilli

Cross	A	B	C	D
C1	8.63±11.51	1.90±5.46	-39.85±11.82**	-25.19±8.35**
C2	-12.25±7.98	-4.85±5.80	16.75±14.44	16.93±7.78*
C3	-21.31±6.10**	22.66±18.62	-4.16±13.05	-2.75±11.10
C4	-6.35±6.63	-22.86±6.38**	8.95±9.85	19.08±6.30**

Table 4.32: Estimates of gene effects for plant spread in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	62.34±2.81**	-16.34±6.18*	45.58±16.80**	50.38±16.69**	3.37±6.29	-60.91±27.39*	Duplicate
C2	102.44±3.26**	3.91±4.26	-41.35±15.86*	-33.85±15.55*	-3.70±4.55	50.95±22.33*	Duplicate
C3	91.92±2.89**	3.83±9.48	28.61±22.40	5.50±22.19	-21.98±9.63	-6.86±40.10	Duplicate
C4	89.92±2.29**	1.31±4.34	-26.71±12.73*	-38.15±12.59**	8.26±4.49	67.36±19.94**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.33: Generation means of six generations for number of primary branches per plant in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	4.00	3.60	4.40	3.80	3.35	3.35
C2	3.60	3.60	3.20	4.28	4.05	4.20
C3	3.60	4.00	4.00	3.83	3.85	4.60
C4	4.20	3.80	3.60	2.90	3.00	3.20

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.34: Estimates of scaling test for number of primary branches per plant in four crosses of chilli

Cross	A	B	C	D
C1	-1.71±0.56**	-1.31±0.49*	-1.21±1.04	0.91±0.49
C2	1.31±0.62*	1.60±0.64*	3.51±1.16**	0.31±0.51
C3	0.10±0.58	1.20±0.64	-0.30±0.99	-0.80±0.45
C4	-1.80±0.59**	-1.00±0.60	-3.60±0.97**	-0.40±0.43

Table 4.35: Estimates of gene effects for number of primary branches per plant in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	3.80±0.21**	0.00±0.00	-1.20±1.03	-1.81±0.98	-0.21±0.33	4.81±1.47**	Duplicate
C2	4.28±0.21**	-0.15±0.31	-1.00±1.10	-0.61±1.02	-0.15±0.36	-2.30±1.70	Complementary
C3	3.83±0.16**	-0.75±0.31*	1.80±0.96	1.60±0.89	-0.55±0.37	-2.90±1.57	-
C4	2.91±0.16**	-0.21±0.28	0.40±0.92	0.80±0.85	-0.40±0.39	2.00±1.47	Complementary

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.
* Significant at 5% level; ** Significant at 1% level

Table 4.36: Generation means of six generations for days to 50% flowering in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	23.00	37.40	30.80	28.48	26.50	29.35
C2	28.80	37.00	33.60	34.42	33.70	35.25
C3	28.80	23.00	29.20	33.10	29.45	29.60
C4	33.80	31.60	36.20	34.45	36.25	36.05

Where, P_1, P_2 = Parents, $F_1=P_1xP_2$, F_2 = Selfing of F_1, $BC_1= F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 4.37: Estimates of scaling test for days to 50% flowering in four crosses of chilli

Cross	A	B	C	D
C1	-0.80±0.93	-9.50±0.89**	-8.10±1.69**	1.11±0.86
C2	5.01±0.91**	-0.10±1.19	4.71±1.19*	-0.11±0.92
C3	0.91±0.73	7.00±0.77**	22.20±1.80**	7.15±0.84**
C4	2.50±0.92*	4.30±0.90**	0.01±1.56	-3.40±0.72**

Table 4.38: Estimates of gene effects for days to 50% flowering in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	28.48±0.35**	-2.86±0.51**	-1.61±1.78	-2.21±1.72	4.36±0.59	12.50±2.63**	Duplicate
C2	34.43±0.38**	-1.55±0.52**	0.90±1.95	0.20±1.83	2.56±0.66	-5.11±2.88	Duplicate
C3	33.10±0.39**	-0.15±0.35	-11.00±1.75**	-14.30±1.68**	-3.05±0.46	6.40±2.28**	Duplicate
C4	34.46±0.29**	0.21±0.44	10.31±1.53**	6.81±1.43**	-0.90±0.59	-13.60±2.35**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.39: Generation means of six generations for days to fruit maturity (red) in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	43.20	70.40	62.40	59.08	52.75	56.35
C2	54.80	70.00	62.80	67.13	67.95	69.60
C3	54.60	43.20	59.40	64.82	58.85	58.60
C4	63.80	63.00	69.00	66.45	68.00	69.10

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.40: Estimates of scaling test for days to fruit maturity (red) in four crosses of chilli

Cross	A	B	C	D
C1	-0.11±1.02	-20.11±1.12**	-2.10±2.24	9.06±1.07**
C2	18.30±1.23**	6.40±1.17**	18.10±2.21**	-3.30±1.12**
C3	3.70±0.93**	14.60±0.92**	42.70±1.97**	12.20±0.84**
C4	3.20±1.11**	6.20±1.21**	1.00±1.96	-4.21±0.87**

Table 4.41: Estimates of gene effects for days to fruit maturity (red) in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	59.08±0.46**	-3.60±0.54**	-12.50±2.23**	-18.11±2.13**	10.00±0.67	38.31±3.11**	Duplicate
C2	67.13±0.46**	-1.66±0.65*	7.00±2.33**	6.60±2.24**	5.95±0.81	-31.30±3.39**	Duplicate
C3	64.83±0.38**	0.25±0.39	-13.90±1.80**	-24.40±1.68**	-5.45±0.55	6.11±2.50*	Duplicate
C4	66.45±0.34**	-1.10±0.56	14.01±1.88**	8.41±1.74**	-1.50±0.73	-17.81±2.97**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.42: Generation means of six generations for number of fruits per plant in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	228.40	417.00	308.60	313.38	301.00	438.05
C2	306.00	421.00	307.40	397.42	351.55	304.25
C3	306.00	228.20	388.20	359.95	325.85	332.35
C4	248.40	186.12	262.60	235.07	262.60	241.75

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.43: Estimates of scaling test for number of fruits per plant in four crosses of chilli

Cross	A	B	C	D
C1	65.00±49.38	150.50±70.47	-9.11±112.38	-112.30±44.29*
C2	89.70±49.13	-119.90±50.85*	247.90±114.29*	139.05±55.65*
C3	-42.50±65.09	48.30±64.66	129.21±109.08	61.71±51.26
C4	14.21±38.27	34.78±25.12	-19.43±58.48	-34.21±36.04

Table 4.44: Estimates of gene effects for number of fruits per plant in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	313.38±17.99**	-137.05±25.84**	210.50±98.53*	224.60±88.57*	-42.75±34.22	-440.10±152.67**	Duplicate
C2	397.43±24.78**	47.30±25.33	-334.20±114.87**	-278.10±111.29*	104.80±32.37	308.31±152.72*	Duplicate
C3	359.96±18.87**	-6.50±34.70	-2.31±109.83	-123.41±102.52	-45.40±38.12	117.61±176.53	-
C4	235.08±14.23**	20.86±22.11	113.75±72.38	68.41±72.07	-10.29±22.67	-117.39±106.01	-

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.45: Generation means of six generations for fruit length in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	9.18	5.08	7.30	6.71	8.39	6.38
C2	11.12	5.02	9.20	7.85	9.93	6.80
C3	10.44	9.28	10.52	8.94	9.60	8.99
C4	8.62	11.30	11.46	10.33	9.76	11.34

Where, P_1, P_2 = Parents, $F_1=P_1xP_2$, F_2 = Selfing of F_1, $BC_1= F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 4.46: Estimates of scaling test for fruit length in four crosses of chilli

Cross	A	B	C	D
C1	0.31±0.75	0.39±0.51	-2.02±0.93*	-1.35±0.40**
C2	-0.48±0.33	-0.62±0.39	-3.15±0.65**	-1.04±0.38**
C3	-1.77±0.63**	-1.82±0.58**	-5.01±0.97**	-0.72±0.48
C4	-0.56±0.62	-0.09±0.58	-1.52±0.94	-0.45±0.45

Table 4.47: Estimates of gene effects for fruit length in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	6.72±0.11**	2.01±0.34**	2.87±0.90**	2.70±0.80**	-0.05±0.37	-3.39±1.62*	Duplicate
C2	7.85±0.15**	3.13±0.23**	3.20±0.76**	2.07±0.75**	0.08±0.25	-0.98±1.10	Duplicate
C3	8.94±0.19**	0.61±0.32	2.10±1.02*	1.44±0.96	0.03±0.41	2.16±1.58	Complementary
C4	10.34±0.17**	-1.58±0.31**	2.39±0.96*	0.89±0.90	-0.24±0.39	-0.26±1.54	-

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.48: Generation means of six generations for fruit diameter in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	0.82	0.97	0.81	0.87	1.01	0.88
C2	1.10	0.97	1.02	0.97	1.07	1.04
C3	1.10	0.80	0.93	0.93	0.89	0.83
C4	1.07	1.30	1.25	1.22	1.21	1.19

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.49: Estimates of scaling test for fruit diameter in four crosses of chilli

Cross	A	B	C	D
C1	0.39±0.15*	-0.03±0.08	0.10±0.13	-0.14±0.09
C2	0.02±0.06	0.10±0.05	-0.24±0.10*	-0.17±0.05**
C3	-0.25±0.07**	-0.08±0.07	-0.02±0.11	0.16±0.06**
C4	0.11±0.06	-0.17±0.06**	0.02±0.09	0.04±0.06

Table 4.50: Estimates of gene effects for fruit diameter in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	0.88±0.03**	0.14±0.08	0.19±0.18	0.27±0.17	0.21±0.08	-0.63±0.32	Duplicate
C2	0.98±0.02**	0.03±0.03	0.33±0.10**	0.34±0.10**	-0.04±0.04	-0.45±0.15**	Duplicate
C3	0.94±0.02**	0.07±0.04	-0.34±0.11**	-0.31±0.11**	-0.09±0.04	0.64±0.17**	Duplicate
C4	1.23±0.02**	0.02±0.04	-0.01±0.11	-0.08±0.11	0.14±0.04	0.13±0.17	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.51: Generation means of six generations for average dry fruit weight in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	0.53	0.58	0.57	0.53	0.59	0.54
C2	0.81	0.58	0.76	0.69	0.77	0.63
C3	0.80	0.53	0.72	0.66	0.74	0.66
C4	0.89	1.35	1.19	1.15	1.01	1.14

Where, P_1, P_2 = Parents, $F_1=P_1xP_2$, F_2 = Selfing of F_1, $BC_1= F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 4.52: Estimates of scaling test for average dry fruit weight in four crosses of chilli

Cross	A	B	C	D
C1	0.08±0.08	-0.07±0.08	-0.12±0.14	-0.07±0.07
C2	-0.03±0.07	-0.10±0.07	-0.15±0.14	-0.02±0.07
C3	-0.05±0.07	0.06±0.06	-0.15±0.11	-0.09±0.06
C4	-0.06±0.08	-0.26±0.09**	-0.01±0.15	0.16±0.08

Table 4.53: Estimates of gene effects for average dry fruit weight in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	0.54±0.03**	0.05±0.04	0.14±0.13	0.13±0.13	0.07±0.05	-0.15±0.20	-
C2	0.70±0.03**	0.15±0.04**	0.10±0.14	0.03±0.13	0.04±0.04	0.09±0.20	-
C3	0.66±0.03**	0.09±0.04*	0.23±0.12	0.17±0.11	-0.05±0.05	-0.18±0.18	-
C4	1.16±0.04**	-0.13±0.05*	-0.24±0.16	-0.31±0.16	0.11±0.06	0.62±0.24*	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.54: Generation means of six generations for fruit yield per plant in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	94.00	170.00	156.00	113.13	128.00	168.50
C2	242.00	162.00	266.00	211.25	210.00	148.50
C3	242.00	97.60	246.00	184.75	202.00	177.50
C4	130.00	179.40	240.00	192.25	236.50	190.00

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.55: Estimates of scaling test for fruit yield per plant in four crosses of chilli

Cross	A	B	C	D
C1	6.00±17.10	11.00±18.99	-123.50±40.26**	-70.25±17.50**
C2	-88.00±29.08**	-131.00±27.23**	-91.00±62.04	64.00±31.64*
C3	-84.00±24.27**	11.40±27.30	-92.60±44.22*	-10.00±27.01
C4	103.00±25.81**	-39.40±22.35	-20.40±41.92	-42.00±23.40

Table 4.56: Estimates of gene effects for fruit yield per plant in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	113.13±7.79**	-40.50±7.98**	164.50±37.25**	140.50±35.00**	-2.50±10.01	-157.50±51.37**	Duplicate
C2	211.25±13.62**	61.50±16.10**	-64.00±64.99	-128.00±63.27*	21.50±17.71	347.00±89.41**	Duplicate
C3	184.75±10.44**	24.50±17.13	96.21±54.50	20.00±54.02	-47.70±17.90	52.60±81.55	Complementary
C4	192.25±9.16**	46.50±14.57**	169.30±47.90**	84.00±46.80	71.21±16.32	-147.60±71.79*	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.57: Generation means of six generations for number of seeds per fruit in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	28.48	59.60	59.00	47.53	53.49	56.82
C2	41.32	59.60	57.36	53.61	52.64	61.26
C3	41.32	30.48	40.12	44.11	42.94	43.89
C4	69.88	66.48	77.36	68.93	72.72	83.16

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.58: Estimates of scaling test for number of seeds per fruit in four crosses of chilli

Cross	A	B	C	D
C1	19.51±7.67*	-4.97±7.44	-15.96±13.03	-15.26±5.70**
C2	6.61±6.81	5.57±7.84	-1.22±12.97	-6.69±5.46
C3	4.45±5.42	17.19±5.06**	24.39±9.75*	1.38±4.84
C4	-1.80±8.39	22.49±6.53**	-15.35±12.77	-18.02±6.39**

Table 4.59: Estimates of gene effects for number of seeds per fruit in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	47.54±2.21**	-3.33±3.61	45.47±12.36**	30.51±11.39**	12.24±4.58	-45.06±19.44*	Duplicate
C2	53.61±2.13**	-8.62±3.42*	20.28±11.96	13.38±10.91	0.53±4.28	-25.55±18.84	-
C3	44.11±1.98**	-0.96±2.79	1.47±10.09	-2.76±9.67	-6.38±3.39	-18.87±14.82	Duplicate
C4	68.94±2.47**	-10.44±4.07*	45.21±13.41**	36.03±12.78**	-12.14±4.85	-56.71±20.68**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.60: Generation means of six generations for seed weight in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	4.66	4.41	4.27	4.98	4.79	4.84
C2	5.62	4.41	5.50	5.43	5.45	5.12
C3	5.54	4.66	6.11	5.57	5.01	5.89
C4	6.91	6.90	7.87	6.91	6.83	6.53

Where, P_1, P_2 = Parents, $F_1=P_1xP_2$, F_2 = Selfing of F_1, $BC_1= F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 4.61: Estimates of scaling test for seed weight in four crosses of chilli

Cross	A	B	C	D
C1	0.66±0.65	1.00±0.65	2.30±1.11*	0.33±0.53
C2	-0.22±0.43	0.33±0.45	0.67±0.74	0.28±0.42
C3	-1.63±0.66*	1.01±0.64	-0.16±1.04	0.24±0.50
C4	-1.13±0.54*	-1.71±0.31**	-1.90±0.77*	0.47±0.47

Table 4.62: Estimates of gene effects for seed weight in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	4.98±0.20**	-0.05±0.35	-0.92±1.13	-0.65±1.06	-0.18±0.40	-1.01±1.77	Complementary
C2	5.43±0.17**	0.34±0.27	-0.07±0.86	-0.56±0.84	-0.27±0.30	0.45±1.29	-
C3	5.57±0.19**	-0.88±0.34*	0.55±1.06	-0.47±1.00	-1.32±0.42	1.08±1.70	Complementary
C4	6.92±0.19**	0.30±0.29	0.05±0.94	-0.93±0.93	0.29±0.31	3.75±1.38**	Complementary

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.63: Generation means of six generations for ascorbic acid in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	28.10	29.24	22.33	48.19	30.03	37.92
C2	29.10	29.64	51.20	41.95	58.93	46.64
C3	29.30	27.90	23.54	51.50	56.57	44.30
C4	27.49	31.29	36.58	53.50	42.35	49.85

Where, P_1, P_2 = Parents, $F_1=P_1xP_2$, F_2 = Selfing of F_1, $BC_1= F_1 \times P_1$, $BC_2 = F_1 \times P_2$

Table 4.64: Estimates of scaling test for ascorbic acid in four crosses of chilli

Cross	A	B	C	D
C1	9.63±3.63*	24.28±3.69**	90.75±9.01**	28.43±4.70**
C2	37.57±5.43**	12.45±5.32**	6.66±8.44	-21.68±5.53**
C3	60.31±8.37**	37.15±6.22**	101.73±16.29**	2.14±9.49
C4	20.64±5.52**	31.83±6.17**	82.06±11.80**	14.80±6.97**

Table 4.65: Estimates of gene effects for ascorbic acid in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	48.19±2.08**	-7.90±2.18**	-63.19±9.55**	-56.85±9.40**	-7.33±2.38	22.94±12.54	Duplicate
C2	41.95±2.06**	12.30±3.71**	65.19±11.10**	43.36±11.06**	12.57±3.77	-93.37±17.04**	Duplicate
C3	51.51±4.01**	12.28±5.07*	-9.33±19.03	-4.27±18.97	11.58±5.15	-93.19±2601**	Complementary
C4	53.50±2.87**	-7.50±3.97	-22.41±14.01	-29.60±13.93*	-5.60±4.07	-22.87±19.76	Complementary

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.
* Significant at 5% level; ** Significant at 1% level

Table 4.66: Generation means of six generations for oleoresin in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	10.48	11.55	10.93	11.19	15.39	13.57
C2	9.46	11.55	12.27	11.33	7.72	9.70
C3	9.80	10.88	12.36	10.53	9.85	10.92
C4	11.85	8.46	11.62	9.48	10.69	12.09

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.67: Estimates of scaling test for oleoresin in four crosses of chilli

Cross	A	B	C	D
C1	9.38±1.47**	4.68±1.53**	0.87±2.87	-6.60±1.41**
C2	-6.29±0.85**	-4.41±0.88**	-0.24±1.38	5.24±0.69**
C3	-2.47±0.92*	-1.40±0.93	-3.31±1.71	0.29±0.76
C4	-2.08±0.77*	4.11±0.67**	-5.63±1.23**	-3.83±0.56**

Table 4.68: Estimates of gene effects for oleoresin in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	11.19±0.57**	1.82±0.83*	13.10±2.94**	13.19±2.81**	2.36±0.90	-27.23±4.37**	Duplicate
C2	11.34±0.26**	-1.99±0.46**	-8.70±1.45**	-10.47±1.37**	-0.94±0.57	21.16±2.30**	Duplicate
C3	10.53±0.31**	-1.08±0.44*	1.46±1.62	-0.57±1.51	-0.54±0.56	4.43±2.44	Complementary
C4	9.49±0.22**	-1.40±0.36**	9.11±1.21**	7.65±1.12**	-3.10±0.45	-9.67±1.88**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.69: Generation means of six generations for capsaicin in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	0.40	0.23	0.48	0.69	0.47	0.49
C2	0.44	0.23	0.39	0.59	0.60	0.46
C3	0.46	0.40	0.29	0.59	0.41	0.30
C4	0.27	0.38	0.27	0.58	0.61	0.66

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.70: Estimates of scaling test for capsaicin in four crosses of chilli

Cross	A	B	C	D
C1	0.07±0.10	0.27±0.07**	1.16±0.16**	0.41±0.08**
C2	0.38±0.12**	0.30±0.10**	0.90±0.17**	0.12±0.09
C3	0.06±0.10	-0.10±0.07	0.89±0.15**	0.47±0.08**
C4	0.69±0.09**	0.67±0.09**	1.14±0.14**	-0.12±0.07

Table 4.71: Estimates of gene effects for capsaicin in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	0.69±0.03**	-0.02±0.05	-0.66±0.16**	-0.82±0.15**	-0.10±0.06	0.49±0.25*	Duplicate
C2	0.59±0.04**	0.15±0.06*	-0.17±0.18	-0.23±0.18	0.05±0.07	-0.44±0.29	Complementary
C3	0.59±0.04**	0.11±0.05*	-1.07±0.17**	-0.93±0.16**	0.08±0.06	0.97±0.25**	Duplicate
C4	0.59±0.03**	-0.05±0.05	0.17±0.15	0.23±0.14	0.02±0.06	-1.58±0.23**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.72: Generation means of six generations for red carotenoids in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	166.10	112.19	179.52	120.99	171.90	133.72
C2	134.49	112.19	130.86	145.25	174.36	138.31
C3	140.49	166.10	189.03	143.26	153.05	154.95
C4	134.45	162.39	124.93	105.21	88.69	112.23

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.73: Estimates of scaling test for red carotenoids in four crosses of chilli

Cross	A	B	C	D
C1	-1.83±30.74	-24.27±20.56	-153.38±47.14**	-63.65±27.38**
C2	83.37±18.66**	33.57±15.19*	72.61±34.70*	-22.17±17.05
C3	-23.43±10.41*	-45.23±9.97**	-111.60±20.52**	-21.48±9.98*
C4	-82.02±14.34**	-62.86±15.00**	-125.86±22.89**	9.51±10.54

Table 4.74: Estimates of gene effects for red carotenoids in four crosses of chilli using six parameter model

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	120.99±10.81**	38.18±16.81*	167.68±55.55**	127.30±54.75*	11.23±17.69	-101.21±82.10	Duplicate
C2	145.26±7.23**	36.06±9.06**	51.85±35.43	44.33±34.10	24.91±10.74	-161.26±50.15**	Duplicate
C3	143.27±4.24**	-1.91±5.28	78.68±20.78**	42.95±19.95*	10.90±6.51	25.71±29.44	Complementary
C4	105.22±3.88**	-23.55±7.15**	-42.50±22.70	-19.01±21.07	-9.58±9.65	163.88±36.61**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.75: Generation means of six generations for yellow carotenoids in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	146.06	133.88	129.51	128.79	125.43	129.68
C2	100.51	145.88	120.59	107.89	100.05	115.19
C3	100.51	153.46	104.11	122.55	110.54	121.40
C4	98.53	109.29	94.64	65.73	74.05	60.59

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.76: Estimates of scaling test for yellow carotenoids in four crosses of chilli

Cross	A	B	C	D
C1	-24.72±22.45	-4.02±19.08	-23.82±41.03	2.46±19.94
C2	-21.01±11.16	-36.09±9.18**	-56.00±17.91**	0.55±10.40
C3	16.46±7.59*	-14.76±9.75	28.00±22.38	13.16±11.74
C4	-45.08±9.75**	-82.75±10.93**	-134.19±16.62**	-3.19±7.03

Table 4.77: Estimates of gene effects for yellow carotenoids in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	128.79±8.43**	-4.26±10.67	-15.38±41.56	-4.92±39.88	-10.35±13.53	33.65±59.19	-
C2	107.90±4.08**	-15.15±6.44*	-3.70±21.12	-1.10±20.79	7.54±7.03	58.19±31.37	Duplicate
C3	122.55±5.26**	-10.87±5.21*	-49.18±23.78*	-26.31±23.47	15.61±5.90	24.62±30.56	Duplicate
C4	65.73±2.59**	13.46±4.77**	-2.90±15.49	6.38±14.06	18.84±6.49	121.45±25.30**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.78: Generation means of six generations for total carotenoids in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	312.15	246.06	309.03	250.41	285.44	260.65
C2	235.01	266.06	251.46	253.15	280.70	248.50
C3	235.01	312.15	296.14	260.48	267.63	274.91
C4	234.98	253.68	223.57	167.39	171.92	183.57

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.79: Estimates of scaling test for total carotenoids in four crosses of chilli

Cross	A	B	C	D
C1	-50.31±31.22	-33.81±27.57	-174.64±51.48**	-45.27±25.01
C2	74.95±25.61**	-20.52±18.65	8.62±40.67	-22.91±20.80
C3	4.12±18.56	-58.48±16.50**	-97.54±35.92**	-21.59±18.01
C4	-114.72±20.64**	-110.12±19.98**	-266.25±31.60**	-20.71±16.08

Table 4.80: Estimates of gene effects for total carotenoids in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	250.42±9.72**	24.80±15.73	120.46±52.78	90.54±50.01	-8.26±18.31	-6.43±81.29	Duplicate
C2	253.15±8.42**	32.21±12.23*	46.74±43.13	45.82±41.59	47.74±14.90	-100.24±63.60	Duplicate
C3	260.48±7.79**	-7.28±9.04	65.74±37.10	43.18±36.01	31.30±12.11	11.18±50.95	Complementary
C4	167.39±5.93**	-11.65±10.87	20.67±33.81	41.42±32.15	-2.30±13.61	183.42±53.74**	Complementary

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.

* Significant at 5% level; ** Significant at 1% level

Table 4.81: Generation means of six generations for total colour value in four crosses of chilli

Cross	P_1	P_2	F_1	F_2	BC_1	BC_2
C1	122.43	96.20	121.48	97.49	114.18	102.44
C2	90.77	96.20	97.09	98.22	106.84	96.15
C3	90.77	122.03	111.95	101.95	103.55	107.24
C4	90.76	103.51	81.12	65.44	60.98	73.56

Where, P_1, P_2 = Parents, F_1=P_1xP_2, F_2 = Selfing of F_1, BC_1= F_1 x P_1, BC_2 = F_1 x P_2

Table 4.82: Estimates of scaling test for total colour value in four crosses of chilli

Cross	A	B	C	D
C1	-15.56±12.81	-12.80±10.73	-71.65±20.39*	-21.66±10.17*
C2	25.84±10.27*	-1.00±8.06	11.75±16.51	-6.55±8.07
C3	4.39±8.02	-19.49±7.57*	-28.91±16.29	-6.90±7.20
C4	-49.92±8.48**	-37.52±8.17**	-94.77±13.43**	-3.67±5.89

Table 4.83: Estimates of gene effects for total colour value in four crosses of chilli

Cross	*m*	*d*	*h*	*i*	*j*	*l*	Type of epistasis
C1	97.49±3.92**	11.74±6.48	55.47±21.36*	43.31±20.33*	-1.38±7.42	-14.96±32.98	Duplicate
C2	98.23±3.27**	10.70±4.73*	16.70±16.91	13.10±16.14	13.42±6.13	-37.94±25.09	Duplicate
C3	101.95±3.17**	-3.70±3.44	19.35±15.29	13.80±14.40	11.94±4.76	1.31±21.31	Complementary
C4	65.44±2.18**	-12.58±3.96**	-8.69±12.83	7.34±11.77	-6.21±5.25	80.10±20.76**	Duplicate

Where C1=LCA-710 x HC-28, C2=LCA-712 x HC-28, C3=LCA-712 x LCA-710 and C4=LCA-764 x LCA-315; m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.
* Significant at 5% level; ** Significant at 1% level

Table 4.84 Inheritance of fruit bearing habit in F_2, BC_1 and BC_2 generations for cross LCA 712 x HC-28

	Observed frequencies			Expected Ratio	χ2-calculated	Probability
Generations	Solitary	Clustering	Total plants			
P_1	50	0	50	-	-	-
P_2	0	50	50	-	-	-
F_1	55	0	55	-	-	-
F_2	245	88	333	3:1	0.37	0.7-0.50
B_1	190	5	195	1:0	-	-
B_2	140	121	261	1:1	1.39	0.30-0.20

Table 4.85 Inheritance of fruit position in F_2, BC_1 and BC_2 generations for cross LCA 712 x HC-28

	Observed frequencies			Expected Ratio	χ2-calculated	Probability
Generations	Pendent	Erect	Total plants			
P_1	55	0	55	-	-	-
P_2	0	66	66	-	-	-
F_1	70	0	70	-	-	-
F_2	155	44	199	3:1	0.75	0.30-0.5
B_1	170	9	179	1:0	-	-
B_2	115	99	214	1:1	1.12	0.20-0.3

Table 4.86 Inheritance of branching habit in F_2, BC_1 and BC_2 generations for cross LCA 712 x LCA 710

	Observed frequencies			Expected Ratio	χ^2-calculated	Probability
Generations	Intermediate	Dense	Total plants			
P_1	45	0	45	-	-	-
P_2	0	41	41	-	-	-
F_1	55	0	55	-	-	-
F_2	309	92	392	13:3	5.584	0.02-0.01
B_1	244	6	250	1:0	-	-
B_2	115	125	240	1:1	0.417	0.7-0.5

G 4

LCA 678

LCA 453

LCA 703-2

LCA 705-2

LCA 315

Plate 2 : The Testers used in Line x Tester analysis

LCA 442

LCA 654

LCA 607

LCA 655

LCA 355

Plate 1 : The lines used in Line x Tester analysis

LCA 504

LCA 615

LCA 446

LCA 466

Plate 1 : The lines used in Line x Tester analysis

LCA 607 x LCA 706 - 2

LCA 655 x LCA 703 - 2

LCA 446 x LCA 703 - 2

LCA 655 x LCA 315

LCA 446 x LCA 705 - 2

Plate 6 : The promising hybrids for fruit yield per plant

LCA 355 x LCA 678

LCA 466 x LCA 453

LCA 466 x LCA 678

LCA 466 x G4

LCA 466 x LCA 453

Plate 8 : The promising hybrids for total colour value

LCA 654 x G4

LCA 654 x LCA 705-2

LCA 654 x LCA 703 - 2

LCA 654 x LCA 453

LCA 504 x LCA 453

Plate 7 : The promising hybrids for capsaicin

LCA 710 X HC- 28

LCA 712 X HC- 28

LCA 712 X LCA 710

LCA 764 X LCA 315

Plate 5 : The F_1 crosses obtained in Generation mean analysis

LCA 710

HC - 28

LCA 712

LCA 764

LCA 315

Plate 4 : The Parents used in Generation mean analysis

Plate 9 : F_2 segregants of the cross LCA 712 x HC 28 for fruit bearing and fruit position

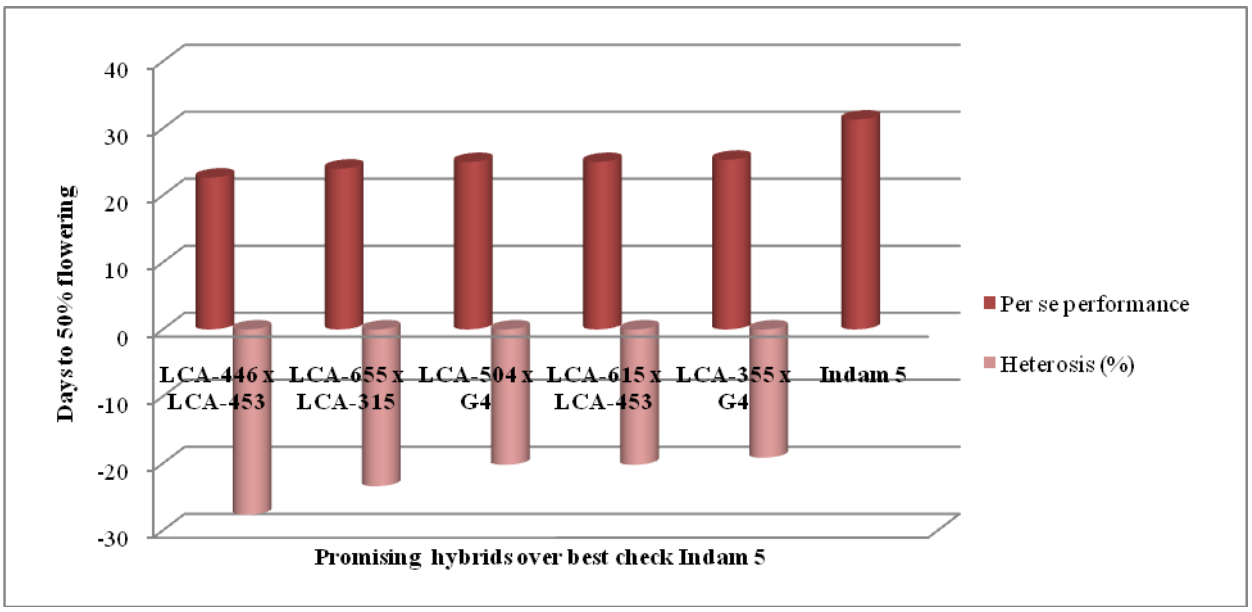

Fig 4.1: Standard heterosis of five promising hybrids over best check Inadam-5 for days to 50% flowering in chilli

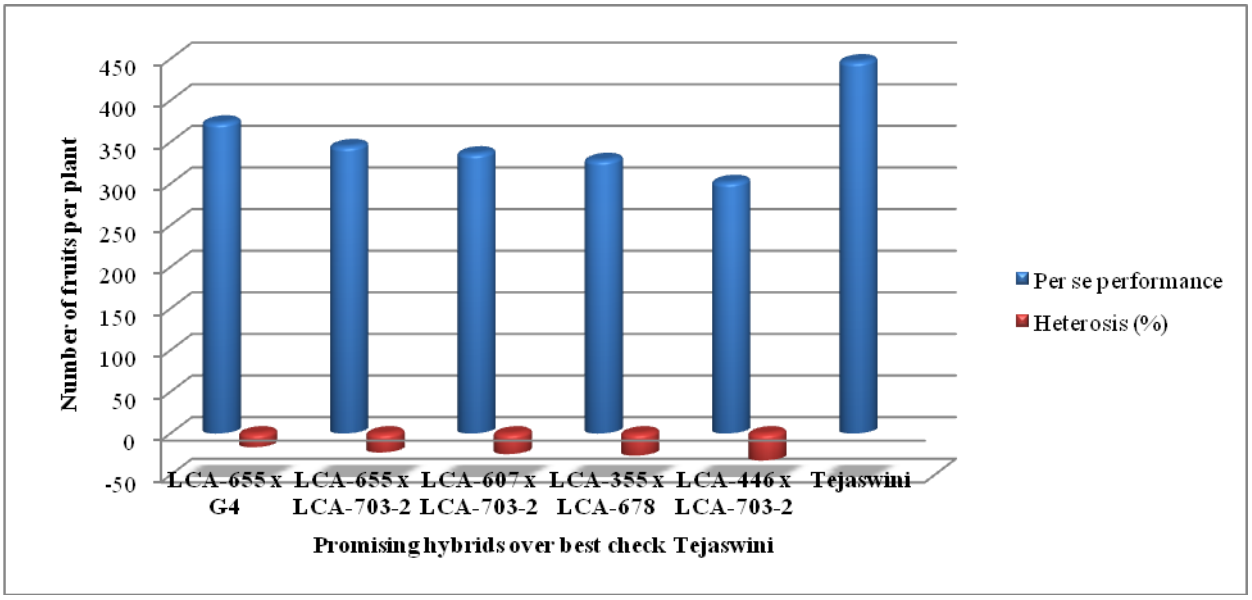

Fig 4.2: Standard heterosis of five promising hybrids for number of fruits per plant in chilli

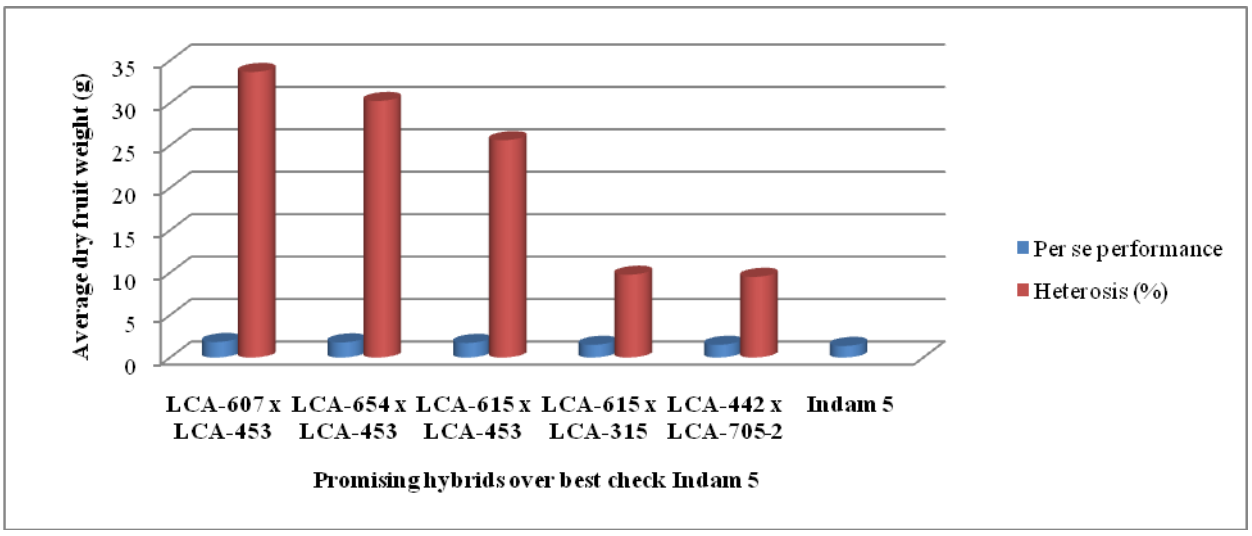

Fig 4.3: Standard heterosis of five promising hybrids over best check Indam-5 for average dry fruit weight (g) in chilli

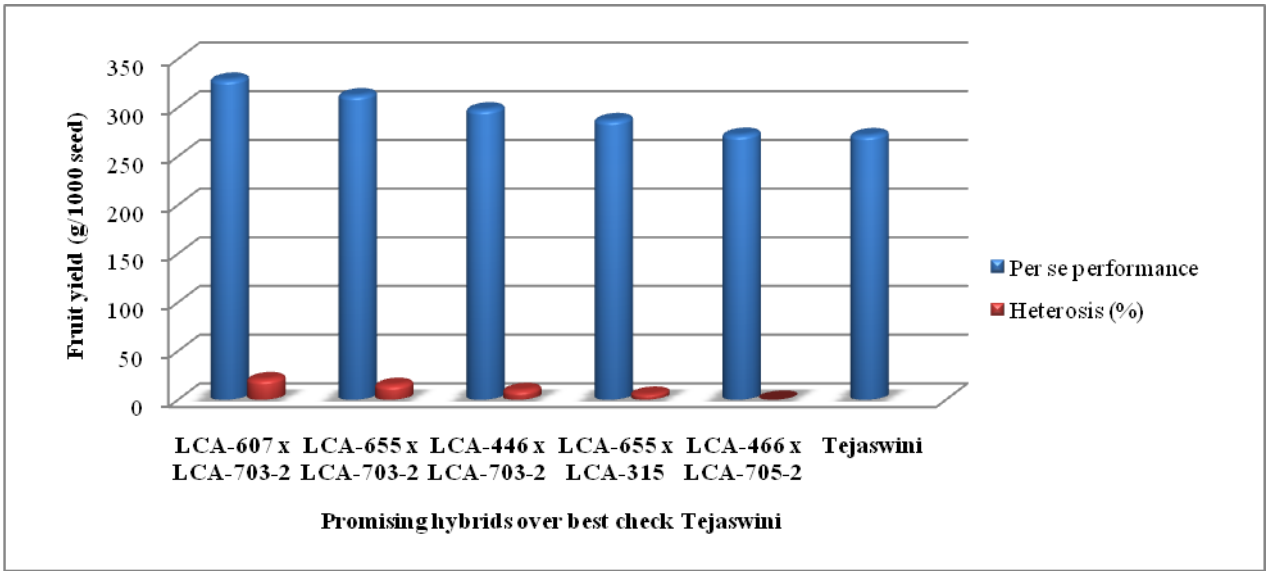

Fig 4.4: Standard heterosis of five promising hybrids over best check Tejaswini for fruit yield (g/plant) in chilli

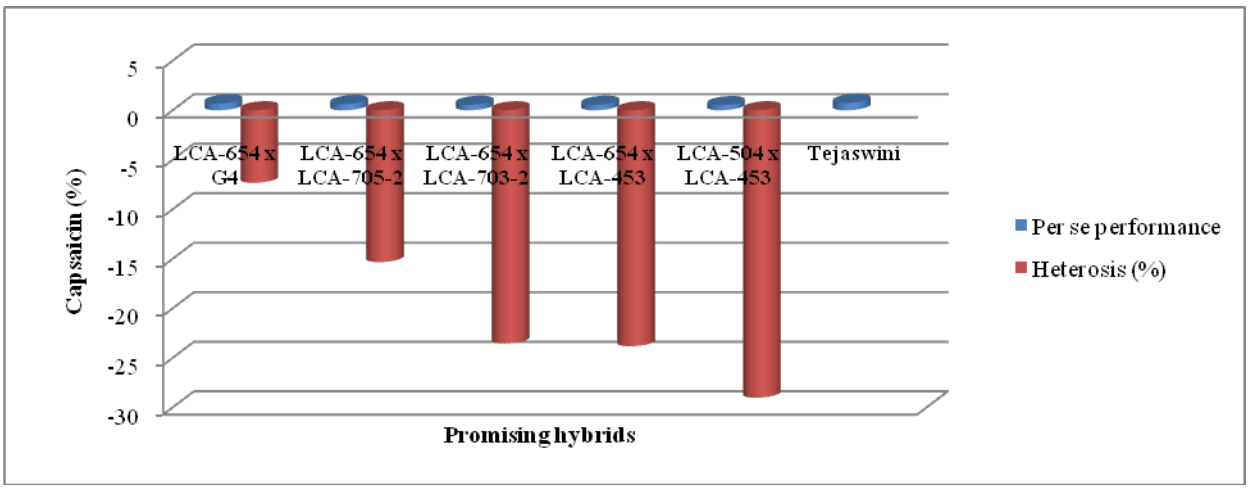

Fig 4.5: Standard heterosis of five promising hybrids for capsaicin (%) in chilli

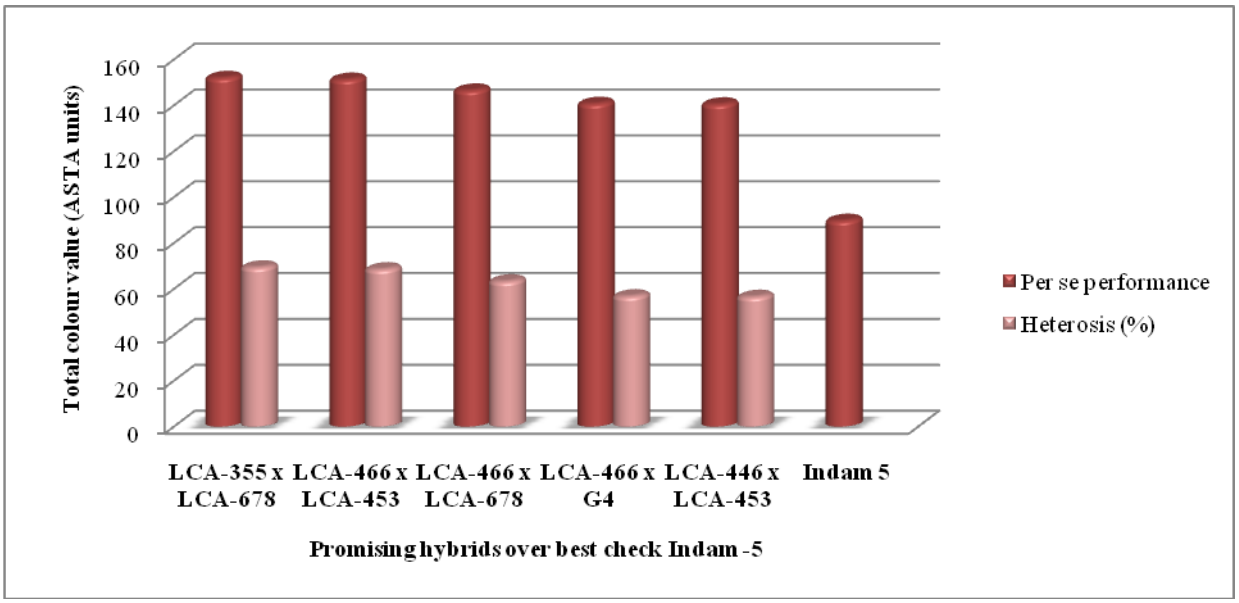

Fig 4.6: Standard heterosis of five promising hybrids over best check Indam-5 for total colour value (ASTA units) in chilli

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis for yield, quality traits and plant ideotype in chilli (*Capsicum annuum* L.)” was carried out at Horticultural Research Station, Lam farm, Guntur, Andhra Pradesh during *kharif*, 2013-14 and 2014-15 to estimate the heterosis, combining ability and gene action employing line x tester mating design and to study the nature and magnitude of gene effects involved in the expression of yield, yield components, quality traits and plant ideotype using generation mean analysis. For line x tester analysis, the planting material consisted of nine lines (LCA 504, LCA 615, LCA 446, LCA 466, LCA 442, LCA 654, LCA 607, LCA 655 and LCA 355), six testers (G4, LCA 678, LCA 453, LCA 703-2, LCA 705-2 and LCA 315), the resultant 54 F_1 hybrids and two commercial checks *i.e.* Indam-5 and Tejaswini which were grown in randomized block design with three replications and the plants of each genotype were planted in two rows at a spacing of 75 cm x 30 cm. For generation mean analysis, the planting material consisted of four crosses (F_1s – LCA 710 x HC-28, LCA 712 x HC-28, LCA 712 x LCA-710 and LCA 764 x LCA-315), their P_1’s, P_2’s, F_2’s, BC_1’s and BC_2’s. The parents and F_1s were planted in five rows, F_2s in thirty rows and BC_1’s and BC_2’s in twenty rows were planted at a spacing of 75 cm x 30 cm. Among these four crosses, the cross LCA 712 x HC-28 was selected to study the inheritance pattern of fruit bearing habit and fruit position whereas the cross LCA 712 x LCA 710 was selected to study the inheritance pattern of branching habit.

The observations on six morphological (plant growth habit, branching habit, fruit position, fruit bearing habit, fruit shape and mature fruit colour), 12 quantitative characters (plant height, plant spread, number of primary branches per plant, days to 50% flowering, days to fruit maturity, number of fruits per plant, fruit length, fruit diameter, average dry fruit weight, fruit yield per plant, number of seeds per fruit and 1000 seed weight) and seven biochemical traits

(vitamin C, oleoresin, capsaicin, red carotenoids, yellow carotenoids, total carotenoids and total colour value) were recorded.

In respect of line x tester analysis, the chilli genotypes showed variation for plant growth habit, branching habit, fruit position and mature fruit colour whereas the variation was not observed for fruit bearing habit and fruit shape.

A perusal of *per se* performance revealed that five genotypes *viz.*, LCA 607 x LCA 703-2, LCA 655 x LCA 703-2, LCA 655 x LCA 315, LCA 446 x 703-2 and LCA 466 x LCA 705-2 were the most promising hybrids over the both commercial checks Indam5 and Tejaswini for fruit yield per plant and other desirable traits.

The data on heterosis calculated over better parent and standard checks Indam5 and Tejaswini revealed the superiority of some of the outstanding cross combinations. The top five heterotic crosses over best check Tejaswini were LCA 607 x LCA 703-2, LCA 655 x LCA 703-2, LCA 446 x LCA 703-2, LCA 655 x LCA 315 and LCA 466 x LCA 705-2 as they showed desirable standard heterosis for fruit yield and yield components. The correlation between *per se* performance and heterosis of crosses for the characters indicated that heterosis of a cross can reasonably be predicted from *per se* performance.

The analysis of variance for combining ability revealed that the significant differences due to parents and crosses were observed for all the characters whereas the significant differences due to parents *vs* hybrids were observed for only fourteen characters indicating the existence of wide variability in the material studied and greater scope for identifying promising parents and hybrid combinations. With respect to contribution of genotypes to total variance, the contribution due to Line x Tester interactions was highest (42.66%) followed by lines (35.42%) and testers (21.93%).

Thirteen characters exhibited higher *sca* variances than *gca* variances and the ratio of *gca* to *sca* variance was less than unity indicating the predominance of non additive gene action and improvement of those traits can be made through heterosis breeding. The additive gene action was predominant for characters *viz.*

plant height, no. of primary branches, fruit length, fruit diameter, average dry fruit weight and seed weight due to higher *gca* variances than *sca* variances and in these traits the improvement can be made through simple selection.

Based on *gca* effects, the lines LCA 442, LCA 654 and LCA 655 and the testers LCA 703-2 and LCA 453 were found to be promising general combiners for yield, yield components and quality traits as they recorded significant positive *gca* effects.

Based on the *sca* effects, nine crosses *viz*., LCA 466 x LCA 705-2, LCA 607 x LCA 703-2, LCA 355 x LCA 678, LCA 504 x LCA 705-2, LCA 446 x LCA 703-2, LCA 615 x LCA 453, LCA 442 x LCA 453, LCA 607 x G4 and LCA 654 x LCA 678 were identified as promising specific combiners for fruit yield, yield components and quality traits.

If the crosses had both parents as good general combiners involving high x high general combiners they may be advanced through pedigree method of breeding. In case of crosses involving only one parent as good general combiner (high x low or low x high), it would be difficult to improve the trait by simple selection. Hence, improvement of such character is possible only through heterosis breeding.

Based on the studies of line x tester analysis, it was concluded that three hybrids *viz*., LCA 607 x LCA 703-2, LCA 446 x LCA 703-2 and LCA 466 x LCA 705-2 were most promising hybrids with desirable *sca* effects, heterosis and *per se* performance for fruit yield and other desirable traits. These hybrids may be further tested over locations and seasons and recommended for commercial release and the material generated in the present investigation could be utilized for future chilli breeding programmes.

With respect to generation mean analysis, non significance of all the scaling tests (A, B, C and D) indicates the absence of non-allelic gene interactions. In the present investigation, the significance of one or more scales in one or more crosses was observed for all the characters indicating the presence of non-allelic interactions *i.e.* additive x additive (*i*), additive x dominance (*j*) and

dominance x dominance (*l*) type of gene interactions in the inheritance of all characters.

From the view of gene effects, either additive (*d*), dominance (*h*), additive x additive (*i*) and dominance x dominance (*l*) type of gene interactions or all found to be significant in one or more crosses indicating their role in inheritance of majority of characters. In combination of four crosses, additive (*d*) type of gene effects have controlled most of characters followed by dominance x dominance (*l*), dominance (*h*), and additive x additive (*i*) type of gene interactions. Hence it can be concluded that in all the four crosses, the characters were governed by all or either additive, non-additive and epistatic interactions suggesting that these four crosses can be improved by either pedigree method of selection, heterosis breeding or reciprocal recurrent selection. Among the crosses, in cross 2, additive gene effects and in cross 4, dominance x dominance (*l*) type of epistasis were predominant in governing the majority of the characters compared to other gene effects which revealed that pedigree method of selection for cross 2 and heterosis breeding or reciprocal recurrent selection or full sib selection for cross 4 are effective compared to other breeding methods.

In general, duplicate epistasis for many traits in four crosses was found and this will reduce the net gain occurring from heterozygosity due to the cancellation of dominance and epistatic effects and those crosses can be improved by delayed selection or selection after biparental intermating. The complementary epistasis was also found for one character in cross 1, for two characters in cross 2, for eight characters in cross 3 and for four characters in cross 4 and this will increase the heterosis and these crosses can be exploited effectively through pedigree method of selection. Considering all the results of the present investigation, the pedigree or recurrent selection is recommended for varietal improvement of chilli.

From the studies of generation mean analysis, it can be concluded that all the characters in one or more crosses controlled by either additive, dominant and epistatic interactions or all gene effects. The crosses, in which the characters governed by additive, additive x additive and complementary epistasis can be

improved effectively by pedigree method of selection whereas the crosses, in which the characters controlled by dominant, dominant x dominant and duplicate epistasis can be exploited effectively by heterosis breeding or reciprocal recurrent selection or full sib selection or delayed selection.

From the chi-square analysis, it was concluded that the nature of solitary fruit bearing habit and pendent fruit position were monogenic and dominant whereas the nature of the branching habit was digenic and governed by two gene pairs with dominant supression epistasis.

Future line of work

1. The identified superior general combiners (LCA 442, LCA 654, LCA 655, LCA 703-2 and LCA 453) can be used in multiple crosses and their segregating population can be screened for segregants which possess all the favourable alleles distributed among the population.
2. Evaluation of promising crosses (LCA 607 x LCA 703-2, LCA 446 x LCA 703-2 and LCA 466 x LCA 705-2) over locations or seasons in larger plots would be essential to draw valid conclusion for their commercial exploitation on their hybrid vigour.
3. Pedigree method of selection can be followed to select superior recombinants from the segregating generations which on attaining homozygosity can be released as varieties for cultivation.
4. Information generated on fruit position, fruit bearing habit and branching habit can be utilized to develop varieties with desired ideotype in chilli.

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Pattern of 'literature cited' presented above is in accordance with the 'Guidelines for thesis presentation of 'Dr. Y. S. R. Horticultural University'.

APPENDIX

Meteorological data: RARS, Lam during 2013-2014

Month & year	Lam			
	Rainfall (mm)	Mean temperature (^{0}C)		Relative humidity (%)
		Max.	Min.	
June, 13	88.50	36.10	26.20	62.75
July, 13	138.30	32.70	25.40	72.05
August, 13	238.50	29.95	23.27	71.75
Sepptember,13	222.20	32.20	24.70	80.50
October,13	287.00	29.10	23.00	79.00
November,13	40.40	29.10	20.30	75.00
December,13	0.00	27.60	15.50	66.50
January, 14	0.00	28.94	17.40	75.50
February, 14	1.00	30.90	18.50	75.00
March, 14	0.00	34.60	21.70	67.50
April,14	0.00	38.90	25.40	62.95
Total/Mean	**1015.90**	**31.83**	**21.94**	**71.68**

Meteorological data: RARS, Lam during 2014-2015

Month & year	Lam			
	Rainfall (mm)	Mean temperature (^{0}C)		Relative humidity (%)
		Max.	Min.	
June, 14	8.30	39.80	25.40	62.50
July, 14	149.00	34.40	20.10	74.80
August, 14	130.60	34.19	19.72	82.71
Sepptember,14	228.40	32.70	18.70	89.30
October,14	133.00	31.80	17.00	93.30
November,14	45.20	30.60	21.50	95.80
December,14	0.00	29.80	18.40	89.50
January, 15	0.00	29.90	17.60	92.60
February, 15	0.00	32.10	19.50	94.50
March, 15	0.00	35.60	24.10	92.30
April,15	33.40	36.70	27.10	93.00
Total/Mean	**727.90**	**33.42**	**20.83**	**87.30**