

Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]

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UTTAR BANGA KRISHI VISWAVIDYALAYA
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IN
GENETICS AND PLANT BREEDING

BY
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FACULTY OF AGRICULTURE
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**APPROVAL OF EXAMINERS FOR THE AWARD OF THE
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We, the undersigned, having been satisfied with the performance of Sanghamitra Rout, in the viva-voice examination on Final evaluation of the thesis, conducted today, the 6th September 2021, recommended that the thesis be accepted for the award of the degree of Doctor of Philosophy (Agriculture) in Genetics and Plant Breeding.

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This is to certify that the work recorded in the thesis entitled “**Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]**” submitted by **Ms. Sanghamitra Rout** in partial fulfilment of the requirement for the degree of Doctor of Philosophy (Agriculture) in Genetics and Plant Breeding of the *Uttar Banga Krishi Viswavidyalaya*, is the faithful and bonafide research work carried out under my personal supervision and guidance. The results of the investigation reported in the thesis have not so far been submitted for any other Degree or Diploma. The assistance and help received from various sources during the course of investigation have been duly acknowledged.

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Abstract

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Thesis title: Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]

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The present investigation entitled “**Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]**” was conducted to elicit information on identification of genetically divergent mustard genotypes based on yield and its attributing characters, combining ability analysis and heterotic hybrids for morphological, physiological and aphid related characters and evaluation of parents and their F₁ progenies having elevated level of resistance against mustard aphid. 71 genotypes of Indian mustard were evaluated and observations were taken for various yield and its attributing characters. Analysis of variance revealed significant differences for all the characters studied. The character association studied revealed that secondary branches plant⁻¹ and siliquae plant⁻¹ had positive significant association with seed yield plant⁻¹. PHR- 2, RNWR-09-3, Giriraj, Kranti, SKJM-05, DRMR-15-16, RW-85-59 (Sarna) and NPJ-194 considered as diverse genotype for crossing programme. Combining ability and heterosis studies were carried out by involving 8 parents and 28 F₁s developed from half diallel mating design. Significant differences were observed for both GCA and SCA effects for almost all the characters studied. RW-85-59, DRMR-15-16, Kranti and NPJ-194 seemed to be a good general combiner for most of the yield attributing characters; PHR-2, NPJ-194, RNWR-09-3 and Kranti for physiological characters and SKJM-05, DRMR-15-16, Kranti, NPJ-194, PHR-2 and Giriraj for aphid- related characters. SKJM-05 × Kranti, RW-85-59 × SKJM-05 and NPJ-194 × SKJM-05 showed positively significant sca for seed yield per plant; NPJ-194 × PHR-2, NPJ-194 × Giriraj, DRMR-15-16 × RNWR-09-3, Giriraj × PHR-2 and RW-85-59 × PHR-2 showed positively significant sca effect for total chlorophyll; RW-85-59 × Giriraj, RW-85-59 × SKJM-05, DRMR-15-16 × Kranti, NPJ-194 × RW-85-59, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, NPJ-194 × DRMR-15-16, SKJM-05 × PHR-2, NPJ-194 × SKJM-05, DRMR-15-16 × RNWR-09-3 showed positively significant sca effect for aphid count. Positively significant heterosis for seed yield over mid parent namely NPJ-194 × SKJM-05, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, Kranti × PHR-2 whereas, only two crosses showed significant positive heterosis over better parent namely NPJ-194 × SKJM-05 and Kranti × PHR-2. Crosses namely NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Kranti, RW-85-59 × PHR-2 and Giriraj × PHR-2 revealed positive significant heterosis while, the crosses namely NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × Kranti, Giriraj × PHR-2 exhibited positive significant heterosis over better parent for total chlorophyll. Crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2 and Giriraj × RNWR-09-3 revealed negative significant heterosis over mid parent while the crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Kranti, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Kranti, DRMR-15-16 × RNWR-09-3, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Giriraj × RNWR-09-3 exhibited negative significant heterosis over better parent for aphid count. Genotype RW-85-59, Giriraj and RNWR-09-3 were resistant for A1, A5 and A10 aphid number respectively while the genotype Kranti and SKJM-05 were considered susceptible for A1, A10 and A5 respectively. In crosses, genotype RW-85-59 × Giriraj was resistant and the susceptible cross was NPJ-194 × SKJM-05.

Key words : Genetic diversity, Combining ability, Heterosis and Aphid resistance

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INTRODUCTION

CHAPTER- 1

INTRODUCTION

Brassica juncea, very well known as Indian mustard, leaf mustard, brown mustard or Chinese mustard is an annual herb that is indigenous to Southern and Eastern Asia. It is included in the family of *Brassicaceae* (*Cruciferae*). Over the last decades, mustard crop has to turn into one of the prominent sources of vegetable oil in the world. Indian mustard is a major cash crop as well as a source of edible oil in the worldwide diet especially in Eastern and North-Western India. *B. juncea* is grown as a pure crop or as a mixed crop with wheat, lentil, chickpea, pea, sugarcane, linseed etc. Earlier its cultivation was narrowed to the Northern belt has now extended to unconventional areas in Eastern, Western and Southern regions of the country. The crop flourishes well under both irrigated and rainfed conditions. Continued development in rapeseed-mustard has yielded nutritionally quality edible oil and meal as an essential source of protein in animal feed. A high level of erucic acid (~40-50%) and glucosinolates (180-200 micro moles) are found in traditional varieties of Indian mustard. Worldwide erucic acid is considered an unsafe constituent in food material in the OECD-WHO Food Safety Standards and FAO's Manual on Food Safety Assessment (2008). Interspecific cross between *Brassica nigra* (2n=18) and *B. campestris* (2n=20) yields an amphidiploid species *Brassica juncea* (2n=36).

East and Southern Iran is the region where their wild forms of *Brassica juncea* have been found. There are contradictory views about the origin of *B. juncea* (Bhowmik, 1980). In the middle of the 19th century, it was considered that *B. juncea* has its origin in China and entered India through the North Eastern route independent of any Aryan incursion. According to (Vavilov, 1949), the primary center of its origin was Afghanistan and its adjoining regions (Central Asia) while central and western China, Eastern India and Asia minor with Iran

comprised the secondary centers of origin. The height of Indian mustard plant is 160 cm tall when its flowers; erect, often unbranched annual to biennial plant. It has an ovate, simple, and petiole leaf having a bisexual flower with raceme inflorescences. The flower of Indian mustard consists of four free sepals and four yellow petals, as well as two long and two shorter stamens. The seed and oil of mustard are used in the preparation of pickles and for flavoring curries and vegetables. Grounded seeds are used in powdered form, prepared pastes and sauces. Sulphur containing glucosinolates is the major cause of pungency in mustard. The paste of mustard is used for salad dressings and for preparing sandwiches. Oil of mustard is used in cooking in most Asian countries. The oil cakes are rich in protein and are mostly used as cattle feed. However, it is also used as concentrated organic manure. The tender leaves of these plants are consumed as green vegetables. The use of leaves (also referred to as mustard green) is particularly popular in the cuisine of Punjab where a famous dish called 'sarson ka saag' is prepared. Mustard seeds and oil are traditionally used to relieve muscle pain, rheumatism and arthritic pain. Oil of mustard is considered to promote hair growth when applied to the scalp especially in India. To stimulant gastric mucosa and increase intestinal secretion ground mustard seeds are used as it act as a laxative. At present biofuels are prepared from edible oils and are studied to be the best alternative for traditional fossil diesel fuel as it minimizes greenhouse gas emissions (Cardone *et al.* 2003).

B. juncea is a predominantly self-pollinated crop and self-compatible crop (Labana *et al.* 1992). However, in some environments out crossing varies from 7.6% to 22% (Dhillon and Labana, 1988; Bhajan *et al.* 1991; Abhram, 1994). Pollen can last for 4 or 5 days when the temperature is low and humidity is high. With warmer temperatures and lower humidity, survival time can fall to 1 or 2 days (Mayers, 2006). *Brassica* pollen is viable even after 4 hours

of stress at 60° C (Rao *et al.*, 1992). However, under experimental conditions, it has been observed that pollen can remain active in dry storage for years or more at -20° C (Brown and Dyer, 1990). The stigma receptivity is for 3 days before blooming to 3 days after blooming of the flowers (Singh and Rai, 2004). Throughout the flowering time, numerous insects visit this crop however honeybee is the primary pollinator in brown mustard because of its yellow flowers for nectar and pollen. The growth and productivity of this crop reduce drastically because of mustard aphid (*Lipaphis erysimi*). It is one of the major constraints among the biotic stresses and the key pest of Rapeseed-mustard crops in India. It generally invades the plant during November- February month when the temperature is low. Aphid with the help of narrow piercing-sucking mouthparts called stylets cause severe damage to the mustard plant during flowering by penetrating the stylet into the plant tissue and suck the phloem sap. Its capacity to produce progeny is extremely quick. The mustard aphid (*Lipaphis erysimi*), family (Homoptera: Aphididae) are also known called as Mahoo, Tela, Chenpa or Moyala. The moment aphid's stylets pierce the epidermal layer, parenchyma cells and mesophyll cells of host plant, the mechanical damage may persuade the plant responses to get infected (Tjallingii *et al.* 1993). Due to the attack by *L. erysimi* yield losses of oilseed *Brassica* has been stated repeatedly and the average loss in yield has been assessed to deviate from 35.4 to 91.3% (Singh and Sachan, 1994) within several agro-climatic conditions and is nearly 54.2% on all India based (Bakhetia and Sekhon, 1989). The extent of yield loss in the host crop is relying on the growth stage of the crop while aphid infestation, the period of time and severity of the infestation, soil and environmental influence etc. Several newer pests like *Myzus persicae*, *Agrotis segetum*, *Crocidolomia binotalis*, *Plutella xylostella*, *Odontotermus obesus* and *Monomorium* sp. are minor probable threats to Rapeseed-mustard.

The defensive photochemical liberated by the infected plant in response to aphid infestation become inactivated by no enzymatic reducing compounds in the presence of oxidizes that is secreted by aphid saliva (Miles, 1999). The losses caused by *L. erysimi* may be reduced by following the natural cultural practices or by using resistant varieties as such practices are reviewed economic and environmental friendly approach for pest management. However, the intrusion of the resistance gene(s) accompanied by linkage drag may influence the agronomic traits of *B. juncea* which may be unsuitable. In this respect, genetic engineering-mediated resistant gene transfer can serve to be a more suitable technique.

Genetic diversity showed a prominent role in plant breeding because greater heterosis has been shown by the hybrids between lines of diverse origin than the closely related parents. The degree of diversification is the measure of the distance between the two clusters. The larger the distance between the two clusters, the more is the divergence and vice versa. The genotypes pooled in the same cluster show close association than those belonging to different clusters *i.e.* genotype clump together in one cluster are less diverse than those which are arranged in a different cluster.

The study of heterosis in mustard has been realized as a practical expedient in providing breeders a means of improving yield and other yield attributing traits. The major objective of Indian mustard breeding is to attain high production and productivity. This can be attained by effective exploitation of hybrid vigour, which would rely on the identification of hybrids that are more productive than either of the parents and standard check cultivars (Kumar *et al.*, 2017). Both positive and negative heterosis is suitable for crop improvement. In overall, positive heterosis is anticipated for yield and negative heterosis is desired for early maturity and plant height (Synrem *et al.*, 2014).

Mustard is the chief oil yielding crop in West Bengal. In any case, the general creation of mustard is much underneath the prerequisite for the state because of different reasons. One of such reasons has been the lack of genetic improvement of the crop keeping pace with the growing demand. Combining ability analysis helps in the genetic improvement of crop plants. It gives valuable information for the selection of good combiners, which are anticipated to give an elite performance in their crosses, and progenies. It is also useful to get information on the nature of gene actions involved in the inheritance of character under study. General combining ability is chiefly a function of additive gene action however, non-additive type of gene action is revealed by specific combining ability variance, initiating primarily from dominance and epistasis deviations (Malik *et al.*, 2004). Nature, and the extent of combining ability effects help in detecting superior parents, and their exploitation in the further breeding programme. Environmental factors play a significant role in the performance of various quantitative characters (Sinhamahapatra and Ghosh Dastidar, 1990). Among various mating plans, the diallel examination is a precise methodology that has been broadly utilized in crop plants for testing the exhibition of genotypes in hybrid combinations and furthermore for characterizing the magnitude and nature of gene action associated with controlling quantitative characters (Griffing, 1956).

The present study is performed to recognize the best general combiners and their F₁ hybrids based on their general and specific combining ability. Moreover, it is also necessary to know about the nature and magnitude of gene action along with combining ability of the parent and their cross combination and to determine the level of heterosis for yield and its component characters of mustard through diallel crossing system. With these broad perspectives in view, the present investigation was undertaken with the following objectives:

Objectives:

- Identification of genetically divergent mustard genotypes based on yield and its attributing characters.
- Combining ability analysis of mustard for yield and its attributing characters
- Study on heterotic hybrids for seed yield and aphid resistance.
- Evaluation of mustard parental lines and their F₁ progenies having elevated level of resistance against aphid.



REVIEW OF LITERATURE

CHAPTER-2

REVIEW OF LITERATURE

A relevant review of literature in Indian mustard available on the following aspects which have direct relation to the present study is reviewed briefly under the following heads:

2.1 Selection parameters

2.1.1 Genetic variability

2.1.2 Heritability and Genetic advance

2.1.3 Correlation coefficients

2.1.4 Path analysis

2.1.5 Genetic diversity

2.2 Combining ability and gene action

2.3 Nature and magnitude of heterosis for yield and its components

2.4 Screening for mustard aphid resistance

2.1.1 Genotypic and phenotypic coefficient of variation and other genetic parameters

Singh *et al.* (1990) estimated high amount of genotypic and phenotypic coefficient of variance for 1000-seed weight, plant height, seed yield, primary branches per plant and low for oil content.

Singh and Singh (1994) observed high genotypic and phenotypic coefficient of variation for dry matter, days to flowering, days to maturity, siliquae on main raceme, siliquae per plant, length of raceme and grain yield.

Uddin *et al.* (1995) revealed high genotypic and phenotypic coefficients of variation for seed weight, seeds per siliquae, biological yield, oil content, secondary branches per plant and seed yield per plant.

Meena *et al.* (2000) reported highest GCV and PCV for plant height, branches per plant, test weight, seeds per siliquae, plant and seed yield per plant while found moderate for days to maturity.

Pant and Singh (2001) estimated high genotypic and phenotypic coefficient of variation for days to flower, harvest index, length of raceme, seed yield per plant and number of siliquae per plant.

Choudhary *et al.* (2003) observed genotypic and phenotypic coefficient of variation for branches per plant, biological yield, siliquae on main raceme, seed yield per plant and number of siliquae per plant.

Mehla *et al.* (2003) noted high genotypic and phenotypic coefficient of variation for seed yield per plant, test weight, days to maturity, siliquae per plant, length of raceme and harvest index.

Variability for different quantitative characters in Mustard

Sl. No.	Character	PCV	Reference (S)
1	Plant Height	High	Labana <i>et al.</i> , (1980), Ali <i>et al.</i> , (1985), Pant <i>et al.</i> , (2001), Ali <i>et al.</i> , (2002), Kardam and Singh (2005), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> ,(2011), Helal <i>et al.</i> , (2014)
		Medium	Pandey <i>et al.</i> , (2002), Bind <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Rameeh <i>et al.</i> , (2016), Meena <i>et al.</i> , (2017) and Singh <i>et al.</i> , (2018)
		Low	Ali <i>et al.</i> , (2002), Mahmood <i>et al.</i> , (2003) Sial, P. (2003), Singh <i>et al.</i> , (2011), Gangapur <i>et al.</i> (2011), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Tripathi <i>et</i>

			<i>al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), Kumar <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
2	Height up to first fruiting branch	High	Roy <i>et al.</i> , (2017) and Roy <i>et al.</i> , (2018)
3	Days to 50% flowering	High	Singh and Singh <i>et al.</i> , (1994), Kardam and Singh (2005) and Yadava <i>et al.</i> , (2011)
		Medium	Rameeh (2016) and Meena <i>et al.</i> , (2017)
		Low	Pant <i>et al.</i> , (2001), Sial, P. (2003), Singh <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Yadava <i>et al.</i> , (2011), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Roy <i>et al.</i> , (2018), Singh <i>et al.</i> , (2018), Kumar <i>et al.</i> , (2019)
4	Primary branches per plant	High	Singh <i>et al.</i> , (1990), Pandey <i>et al.</i> , (2002), Kardam and Singh (2005), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Pal <i>et al.</i> , (2019) and Kumar <i>et al.</i> , (2019)

		Medium	Ali <i>et al.</i> , (2002), Mahmood <i>et al.</i> , (2003), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Islam <i>et al.</i> , (2015), Rameeh (2016), Meena <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018) and Singh <i>et al.</i> , (2018)
5	Secondary branches per plant	High	Uddin <i>et al.</i> , (1995), Pandey <i>et al.</i> , (2002), Singh (2004), Rai <i>et al.</i> , (2005), Kardam and Singh (2005), Kumar and Mishra (2007), Singh <i>et al.</i> , (2008), Yadava <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Ram and Verma (2011), Yadava <i>et al.</i> , (2011), Singh <i>et al.</i> (2013), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Roy <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018), Singh <i>et al.</i> , (2018) and Pal <i>et al.</i> , (2019)
		Medium	Afrin <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Meena <i>et al.</i> , (2017) and Kumar <i>et al.</i> , (2019)
6	Siliqua per	High	Ali <i>et al.</i> , (1985), Pant and Singh <i>et al.</i> ,

	plant		(2001), Ali <i>et al.</i> , (2002), Mehla <i>et al.</i> , (2003), Naazar <i>et al.</i> , (2003), Mahmood <i>et al.</i> , (2003), Helal <i>et al.</i> , (2014), Roy <i>et al.</i> , (2015), Kumar <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
		Medium	Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011) and Islam <i>et al.</i> , (2015)
		Low	Rameeh <i>et al.</i> , (2016)
7	Seeds per silliqua	High	Nigam <i>et al.</i> , (2009) and Pal <i>et al.</i> , (2019)
		Medium	Ali <i>et al.</i> , (2003), Afrin <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Yadava <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Bind <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Meena <i>et al.</i> , (2017) and Kumar <i>et al.</i> , (2018)
		Low	Synrem <i>et al.</i> , (2014), Rameeh <i>et al.</i> , (2016), Kumar <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
8	1000 seed wt.(g)	High	Singh <i>et al.</i> , (1990), Singh (2004), Kardam and Singh (2005), Meena <i>et al.</i> , (2006), Patel <i>et al.</i> , (2006), Yadava <i>et al.</i> , (2011), Lodhi <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Meena <i>et al.</i> , (2017), Singh <i>et al.</i> , (2018)
		Medium	Pandey <i>et al.</i> , (2002), Ali <i>et al.</i> , (2003), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011),

			Afrin <i>et al.</i> , (2011), Helal <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019) and Kumar <i>et al.</i> , (2019)
		Low	Gangapur <i>et al.</i> , (2011)
9	Seed yield/plant	High	Ali <i>et al.</i> , (2002), Mahmood <i>et al.</i> , (2003), Naazar <i>et al.</i> , (2003), Singh (2004), Kardam and Singh (2005), Rai <i>et al.</i> , (2005), Kumar and Mishra (2007), Singh <i>et al.</i> , (2008), Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Ram and Verma (2011), Yadava <i>et al.</i> , (2011), Singh <i>et al.</i> , (2013), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Roy <i>et al.</i> , (2015), Vermai <i>et al.</i> , (2016), Meena <i>et al.</i> , (2017), Sikarwar <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018), Singh <i>et al.</i> , (2018) and Pal <i>et al.</i> , (2019)
		Medium	Ali <i>et al.</i> , (2002), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Synrem <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015) and Kumar <i>et al.</i> , (2019)
		Low	Rameeh (2016) and Helal <i>et al.</i> , (2014)

10	Oil content	Low	Singh <i>et al.</i> , (2011), Meena <i>et al.</i> , (2014), Meena <i>et al.</i> , (2017) and Singh <i>et al.</i> , (2018)
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Magnitude of GCV

Sl no	Character	GCV	Reference (s)
1	Plant Height	High	Labana <i>et al.</i> , (1980), Ali <i>et al.</i> , (1985), Ali <i>et al.</i> , (2002), Kardam and Singh (2005), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011) and Helal <i>et al.</i> , (2014)
		Medium	Pandey <i>et al.</i> , (2002), Bind <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Rameeh (2016), Meena <i>et al.</i> , (2017) and Singh <i>et al.</i> , (2018)
		Low	Ali <i>et al.</i> , (2002), Sial P., (2003), Pant <i>et al.</i> , (2001), Singh <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Kumar <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
2	Height upto first fruiting branch	High	Roy <i>et al.</i> , (2015), Roy <i>et al.</i> , (2018) and Roy <i>et al.</i> , (2017)
3	Days to 50% flowering	High	Kardam and Singh (2005) and Yadava <i>et al.</i> , (2011)
		Medium	Rameeh (2016), Meena <i>et al.</i> , (2017)

		Low	Pant <i>et al.</i> , (2001), Singh <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Synrem <i>et al.</i> , (2014) Bind <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Singh <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
4	Primary branches per plant	High	Pandey <i>et al.</i> , (2002), Kardam and Singh (2005), Yadava <i>et al.</i> , (2011) and Roy <i>et al.</i> , (2015)
		Medium	Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Meena <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018), Singh <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019) and Kumar <i>et al.</i> , (2019)
		Low	Singh <i>et al.</i> (2011), Yadava <i>et al.</i> (2011)
5	Secondary branches per plant	High	Pandey <i>et al.</i> , (2002), Singh (2004), Kardam and Singh (2005), Rai <i>et al.</i> , (2005), Kumar and Mishra (2007), Singh <i>et al.</i> , (2008), Yadava <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Ram and Verma (2011), Singh <i>et al.</i> , (2013), Tripathi <i>et al.</i> , (2013), Meena <i>et al.</i> , (2014), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Synrem <i>et al.</i> ,

			(2014), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Singh <i>et al.</i> , (2018), Yadava <i>et al.</i> , (2011) and Pal <i>et al.</i> (2019)
		Medium	Singh <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Bind <i>et al.</i> , (2015), Meena <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
6	Siliqua per plant	High	Ali <i>et al.</i> , (1985), Mahmood <i>et al.</i> , (2003), Naazar <i>et al.</i> , (2003), Helal <i>et al.</i> , (2014) and Roy <i>et al.</i> , (2015)
		Medium	Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Lodhi <i>et al.</i> , (2014), Islam <i>et al.</i> , (2015), and Kumar <i>et al.</i> , (2019)
		Low	Ali <i>et al.</i> , (2002) and Rameeh <i>et al.</i> , (2016)
7	Seeds per siliqua	High	Pal <i>et al.</i> (2019)
		Medium	Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Tripathi <i>et al.</i> , (2013), Islam <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017) and Kumar <i>et al.</i> , (2018)
		Low	Ali <i>et al.</i> , (2002), Yadava <i>et al.</i> , (2011), Synrem <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Bind <i>et al.</i> , (2015), Rameeh <i>et al.</i> , (2016), Meena <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018),

			Singh <i>et al.</i> , (2018) and Kumar <i>et al.</i> , (2019)
8	1000 seed wt.(g)	High	Singh <i>et al.</i> , (1990), Singh (2004), Kardam and Singh (2005), Meena <i>et al.</i> , (2006), Patel <i>et al.</i> , (2006), Yadava <i>et al.</i> , (2011), Lodhi <i>et al.</i> , (2014), Meena <i>et al.</i> , (2014), Meena <i>et al.</i> , (2017), Yadava <i>et al.</i> , (2011) and Singh <i>et al.</i> , (2018)
		Medium	Pandey <i>et al.</i> , (2002), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Bind <i>et al.</i> , (2014), Helal <i>et al.</i> , (2015), Islam <i>et al.</i> , (2015), Bind <i>et al.</i> , (2015), Kumar <i>et al.</i> , (2018) and Pal <i>et al.</i> , (2019)
		Low	Ali <i>et al.</i> , (2002), Gangapur <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Meena <i>et al.</i> , (2017), Sikarwar <i>et al.</i> , (2017) and Kumar <i>et al.</i> , (2019)
9	Seed yield/plant	High	Ali <i>et al.</i> , (2002), Naazar <i>et al.</i> , (2003), Singh (2004), Kardam and Singh (2005), Rai <i>et al.</i> , (2005), Kumar and Mishra (2007), Singh <i>et al.</i> , (2008), Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Ram and Verma (2011), Yadava <i>et al.</i> (2011), Singh <i>et al.</i> , (2013), Tripathi

			<i>et al.</i> , (2013), <i>Amit et al.</i> , (2013), <i>Lodhi et al.</i> (2014), <i>Bind et al.</i> , (2014), <i>Meena et al.</i> , (2014), <i>Lodhi et al.</i> , (2014), <i>Bind et al.</i> , (2015), <i>Roy et al.</i> , (2015), <i>Roy et al.</i> , (2015), <i>Meena et al.</i> , (2017), <i>Sikarwar et al.</i> , (2017) and <i>Pal et al.</i> , (2019)
		Medium	<i>Ali et al.</i> , (2002), <i>Singh et al.</i> , (2011), <i>Yadava et al.</i> , (2011), <i>Islam et al.</i> , (2015), <i>Kumar et al.</i> , (2018), <i>Singh et al.</i> , (2018) and <i>Kumar et al.</i> , (2019)
		Low	<i>Mahmood et al.</i> , (2003), <i>Helal et al.</i> , (2014), <i>Synrem et al.</i> , (2014) and <i>Rameeh</i> (2016)
10	Oil Content	Low	<i>Singh et al.</i> , (2011), <i>Meena et al.</i> , (2014) and <i>Singh et al.</i> , (2018)

2.1.2 Heritability and genetic advance

It is useful measure of considering the ratio of genetic variance to the total phenotypic variance. This concept has been one of the major significances in the development of quantitative genetics. Heritability is of concern to the plant breeder primarily a measure of the values of selection for a particular character, various types of progenies and as an index of transmissibility.

Lush (1949) partitioned heritability in broad sense and narrow sense. Broad sense heritability is the ratio of total genetic variance to total phenotypic variance, expressed in

percentage. Narrow sense heritability is the ratio of additive genetic variance to the total phenotypic variance, expressed in percentage.

Robinson *et al.* (1949) considered that additive genetic variance indicates the degree to which progeny is likely to be resemble the parents. Hence, narrow sense heritability can be defined as the ratio of additive genetic variance to the total phenotypic variance.

Diwakar and Singh (1993) reported high heritability coupled with high genetic advance for days to flowering, plant height, biological yield, harvest index and seed yield.

Sangwan *et al.* (1994) recorded high heritability and high genetic advance for length of main raceme, seed yield, test weight, seeds per siliquae, siliquae on main raceme and branches per plant.

Uddin *et al.* (1995) reported high heritability coupled with high genetic advance for 100-seed weight, seed yield per plant and siliquae per plant.

Singh *et al.* (1996) reported high heritability and high genetic advance for oil content, number of siliquae per plant, plant height, harvest index and biological yield.

Zhang *et al.* (1996) reported high heritability coupled with high genetic advance for seed yield, plant height, days to flowering, days to maturity, branches per plant and number of siliquae per plant.

Mondal *et al.* (2000) studied on genotypic coefficients of variation, heritability and genotypic and phenotypic correlation coefficients in thirty-five genotype of (*Brassica juncea*)

genotypes. Days to maturity and 1000-grain weight showed high heritability and genetic advance.

Mahmood *et al.* (2003) estimated broad- sense heritability and genetic advance values for primary branches, plant height, siliqua per plant and seed yield per plant in four single crosses. Number of siliqua per plant was highly heritable coupled with high genetic advance.

Heritability for different quantitative characters in Indian mustard

Character	Heritability	Reference (s)
Plant height (cm)	High	Diwakar and Singh <i>et al.</i> , (1993), Afrin <i>et al.</i> , (2011), Yadava <i>et al.</i> , (2011), Islam <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017) and Roy <i>et al.</i> , (2015)
	Medium	Bind <i>et al.</i> , (2014) and Tiwari <i>et al.</i> , (2017)
	Low	Ali <i>et al.</i> , (2002)
Primary branches per plant	High	Lodhi <i>et al.</i> , (2014), Sikarwar <i>et al.</i> , (2017), Tiwari <i>et al.</i> , (2017), Meena <i>et al.</i> , (2017) and Gupta <i>et al.</i> , (2019)
	Medium	Bind <i>et al.</i> , (2014), Sandhu <i>et al.</i> , (2017) and Islam <i>et al.</i> , (2015)
	Low	Mahmood <i>et al.</i> , (2003) and Afrin <i>et al.</i> , (2011)
Seeds per siliqua	High	Islam <i>et al.</i> , (2015), Sikarwar <i>et al.</i> , (2017), Tiwari <i>et al.</i> , (2017), Meena <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2019) and Gupta <i>et al.</i> , (2019)
	Medium	Afrin <i>et al.</i> , (2011) and Sandhu <i>et al.</i> , (2017)
	Low	Bind <i>et al.</i> , (2014)

Height upto first fruiting branch (cm)	High	Roy <i>et al.</i> , (2018) and Roy <i>et al.</i> , (2018)
	Low	Roy <i>et al.</i> , (2015)
1000 Seed Weight (g)	High	Mondal <i>et al.</i> , (2000), Kumar <i>et al.</i> , (2007), Lodhi <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014) and Gupta <i>et al.</i> , (2019)
	Medium	Sikarwar <i>et al.</i> , (2017)
Seed Yield (g/plant)	High	Upadhyay <i>et al.</i> , (2009), Yadava <i>et al.</i> , (2011), Singh <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Roy <i>et al.</i> , (2015), Tiwari <i>et al.</i> , (2017), Sikarwar <i>et al.</i> , (2017), Roy <i>et al.</i> , (2018) and Gupta <i>et al.</i> , (2019)
	Medium	Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011) and Islam <i>et al.</i> , (2015)
	Low	Ali <i>et al.</i> , (2002) and Bind <i>et al.</i> , (2014)

Genetic advance for different quantitative characters in Indian mustard

Character	Genetic advance	Reference (s)
Plant height (cm)	High	Sandhu <i>et al.</i> , (2017), Singh <i>et al.</i> , (2013), Afrin <i>et al.</i> , (2011), Meena <i>et al.</i> , (2017), Bind <i>et al.</i> , (2014), Diwakar <i>et al.</i> , (1993), Zhang <i>et al.</i> , (1996) and Uzair <i>et al.</i> , (2016)
	Medium	Islam <i>et al.</i> , (2015) and Roy <i>et al.</i> , (2015)
	Low	Sikarwar <i>et al.</i> , (2017), Tiwari <i>et al.</i> , (2017) and Ali <i>et al.</i> , (2002)

Primary branches per plant	High	Lodhi <i>et al.</i> , (2014), Sikarwar <i>et al.</i> , (2017), Tiwari <i>et al.</i> , (2017), Afrin <i>et al.</i> , (2011) and Meena <i>et al.</i> , (2017)
	Medium	Islam <i>et al.</i> , (2015)
	Low	Bind <i>et al.</i> , (2014) and Gupta <i>et al.</i> , (2019)
Seeds per siliqua	High	Sikarwar <i>et al.</i> , (2017), Tiwari <i>et al.</i> , (2017), Afrin <i>et al.</i> , (2011), Gangapur <i>et al.</i> , (2011) and Sangwan <i>et al.</i> , (1994)
	Medium	Islam <i>et al.</i> , (2015) and Gupta <i>et al.</i> , (2019)
	Low	Bind <i>et al.</i> , (2014) and Ali <i>et al.</i> , (2002)
Height upto first fruiting branch (cm)	High	Roy <i>et al.</i> , (2018)
1000 Seed Weight (g)	High	Lodhi <i>et al.</i> , (2014) and Mondal <i>et al.</i> , (2000),
	Medium	Ali <i>et al.</i> , (2002)
	Low	Bind <i>et al.</i> , (2014) and Gupta <i>et al.</i> , (2019)
Seed Yield (g/plant)	High	Ali <i>et al.</i> , (2002), Mahmood <i>et al.</i> , (2003), Upadhayay <i>et al.</i> , (2009), Yadava <i>et al.</i> , (2011), Afrin <i>et al.</i> , (2011), Lodhi <i>et al.</i> , (2014), Bibi <i>et al.</i> , (2016), Uzair <i>et al.</i> , (2016), Tiwari <i>et al.</i> , (2017), Singh <i>et al.</i> , (2017) and Roy <i>et al.</i> , (2018)
	Medium	Gangapur <i>et al.</i> , (2011)
	Low	Bind <i>et al.</i> , (2014) and Gupta <i>et al.</i> , (2019)

2.1.3 Correlation among yield and other yield attributing characters: Correlation of seed yield with different yield contributing characters has been studied. Some significant results have been summarized here:

Sl.	Character	Association with yield	References
1	Plant height	Positively significant	Sadhu and Gupta (1996), Ali <i>et al.</i> , (2002), Pant <i>et al.</i> , (2002), Akbar <i>et al.</i> , (2003), Singhet <i>et al.</i> , (2003), Kardam and Singh(2005), Mitra <i>et al.</i> , (2006), Afrin <i>et al.</i> , (2011), Zehra <i>et al.</i> , (2008), Singh and Singh (2010) Shazia <i>et al.</i> , (2011),Tahira <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Singh <i>et al.</i> , (2013), Patel <i>et al.</i> , (2014), Mekonnen <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Helal <i>et al.</i> ,(2014), Bhuiyan <i>et al.</i> , (2015), Akabari <i>et al.</i> , (2015), Vermai <i>et al.</i> , (2016), Tiwari <i>et al.</i> , (2017), Tantuway <i>et al.</i> , (2018), Ompal <i>et al.</i> , (2018) and Swetha <i>et al.</i> , (2019)
		Negatively Significant	Kumar <i>et al.</i> , (2019)
3	Days to 50%	Positively significant	Sadhu and Gupta (1996), Pant <i>et al.</i> ,

	flowering		(2002), Afrin <i>et al.</i> , (2011), Shazia <i>et al.</i> (2011), Singh <i>et al.</i> , (2011), Roy <i>et al.</i> ,(2015), Singh <i>et al.</i> , (2017), Swetha <i>et al.</i> , (2019) and Lakra <i>et al.</i> , (2020)
		Negatively Significant	Shekhawat <i>et al.</i> , (2014), Mekonnen <i>et al.</i> , (2014), Ompal <i>et al.</i> , (2018) and Roy <i>et al.</i> , (2018)
4	Primary branches plant- _1	Positively significant	Thakur and Zager (1989), Sadhu and Gupta (1996), Shalini <i>et al.</i> , (1998), Verma <i>et al.</i> , (2001), Srivastava and Singh (2002), Pant <i>et al.</i> , (2002), Singh (2004), Sudan <i>et al.</i> , (2004), Kardam and Singh (2005), Acharya <i>et al.</i> , (2006), Gangapur <i>et al.</i> , (2011), Doddabhimappa <i>et al.</i> , (2009), Singh and Singh (2010), Afrin <i>et al.</i> , (2011), Shazia <i>et al.</i> , (2011), Uddin <i>et al.</i> , (2013), Patel <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Lodhi <i>et al.</i> , (2014), Bhuiyan <i>et al.</i> , (2015), Vermai <i>et al.</i> , (2016), Tiwari <i>et al.</i> , (2017), Solanki <i>et al.</i> , (2017), Tantuway <i>et al.</i> , (2018), Ompal <i>et al.</i> , (2018), Chaurasiya <i>et al.</i> ,

			(2019) and Lakra <i>et al.</i> , (2020)
		Negatively Significant	Mekonnen <i>et al.</i> , (2014)
5	Secondary branches plant ⁻¹	Positively significant	Thakur and Zager (1989), Shalini <i>et al.</i> , (1998), Verma <i>et al.</i> , (2001), Srivastava and Singh (2002), Pant <i>et al.</i> , (2002), Sudan <i>et al.</i> , (2004), Sharad and Singh (2005), Acharya <i>et al.</i> , (2006), Doddabhimappa <i>et al.</i> , (2009), Singh and Singh (2010), Shazia <i>et al.</i> , (2011), Uddin <i>et al.</i> , (2013), Meena <i>et al.</i> , (2014), Mekonnen <i>et al.</i> , (2014), Bind <i>et al.</i> , (2014), Tiwari <i>et al.</i> , (2017), Gupta <i>et al.</i> , (2018), Tantuway <i>et al.</i> , (2018), Ompal <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019), Chaurasiya <i>et al.</i> , (2019) and Kumar <i>et al.</i> , (2019)
		Negatively Significant	Tripathi <i>et al.</i> , (2019)
6	Siliquae plant ⁻¹	Positively significant	Thakur and Zager (1989), Shalini <i>et al.</i> , (1998), Henry and Gupta (1993), Sadhu and Gupta (1996), Thakral <i>et al.</i> , (1997), Khulbe and Pant (1999), Verma <i>et al.</i> , (2001), Badsra and

			Choudhary (2001), Ali <i>et al.</i> , (2002), Akbar <i>et al.</i> , (2003), Kardam and Singh (2005), Mitra <i>et al.</i> , (2006), Acharya <i>et al.</i> , (2006), Afrin <i>et al.</i> , (2011), Uddin <i>et al.</i> , (2013), Doddabhimappa <i>et al.</i> , (2009), Shazia <i>et al.</i> , (2011), Shekhawat <i>et al.</i> , (2014), Helal <i>et al.</i> , (2014), Patel <i>et al.</i> , (2014), Bhuiyan <i>et al.</i> , (2015), Akabari <i>et al.</i> , (2015), Rameeh <i>et al.</i> , (2016), Vermai <i>et al.</i> , (2016), Singh <i>et al.</i> , (2017), Tantuwai <i>et al.</i> , (2018), Ompal <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019), Chaurasiya <i>et al.</i> , (2019), Kumar <i>et al.</i> , (2019) and Lakra <i>et al.</i> , (2020)
		Negatively Significant	Mekonnen <i>et al.</i> , (2014)
7	Seeds siliqua ⁻¹	Positively significant	Shalini <i>et al.</i> , (1998) Khulbe and Pant (1999), Verma <i>et al.</i> , (2001), Ali <i>et al.</i> , (2002), Singh <i>et al.</i> , (2003), Singh (2004), Kardam and Singh (2005), Acharya <i>et al.</i> , (2006), Zehra <i>et al.</i> , (2008), Doddabhimappa <i>et al.</i> , (2009),

			<p>Singh and Singh (2010), Shazia <i>et al.</i>, (2011), Singh <i>et al.</i>, (2013), Shekhawat <i>et al.</i>, (2014), Patel <i>et al.</i>, (2014), Bind <i>et al.</i>, (2014), Bhuiyan <i>et al.</i>, (2015), Roy <i>et al.</i>, (2015), Tiwari <i>et al.</i>, (2017), Roy <i>et al.</i>, (2018), Ompal <i>et al.</i>, (2018), Chaurasiya <i>et al.</i>, (2019), Kumar <i>et al.</i>, (2019), Pandey <i>et al.</i>, (2020) and Lakra <i>et al.</i>, (2020)</p>
		Negatively Significant	Mekonnen <i>et al.</i> , (2014)
8	1000 seed wt.(g)	Positively significant	<p>Henry and Gupta (1993), Sadhu and Gupta (1996), Khulbe and Pant (1999), Srivastava and Singh (2002), Singh (2004), Sudan <i>et al.</i>. (2004), Kardam and Singh (2005), Sharad and Singh (2005), Mitra <i>et al.</i>, (2006), Doddabhimappa <i>et al.</i>, (2009), Singh and Singh (2010), Singh <i>et al.</i>, (2011), Shekhawat <i>et al.</i>, (2014), Hela <i>et al.</i>, (2014) Mekonnen <i>et al.</i>, (2014),</p>

			Tiwari <i>et al.</i> , (2017), Kumar <i>et al.</i> , (2018), Ompal <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019), Swetha <i>et al.</i> , (2019), Chaurasiya <i>et al.</i> , (2019) Kumar <i>et al.</i> , (2019) and Pandey <i>et al.</i> , (2020)
		Negatively Significant	Pant <i>et al.</i> , (2002)
9	Oil content	Positively significant	Thakral <i>et al.</i> , (1997), Shalini <i>et al.</i> , (1998), Badsra and Choudhary (2001) Pant <i>et al.</i> , (2002), Srivastava and Singh (2002), Sharad and Singh (2005), Tahira <i>et al.</i> , (2011), Singh <i>et al.</i> , (2011), Mekonnen <i>et al.</i> , (2014), Singh <i>et al.</i> , (2017), Roy <i>et al.</i> , (2018), Chandra <i>et al.</i> , (2018) and Chaurasiya <i>et al.</i> , (2019)
		Negatively Significant	Sharad and Singh (2005), Shazia <i>et al.</i> , (2011), Ompal <i>et al.</i> , (2018), Pal <i>et al.</i> , (2019)

2.1.4 Path Analysis

Sl no	Character	Effect on yield (dependent character)	References

1	Plant height	Direct	Afrin <i>et al.</i> ,(2011), Helal <i>et al.</i> ,(2014), Roy <i>et al.</i> ,(2018), Roy <i>et al.</i> ,(2017), Roy <i>et al.</i> ,(2015), Tyagi <i>et al.</i> , (1996), Singh <i>et al.</i> , (1997), Ghosh and Mukhopadhyay (1994)
		Indirect	Bind <i>et al.</i> , (2014)
2	Height up to first fruiting branch	Direct	Roy <i>et al.</i> , (2018), Roy <i>et al.</i> , (2017)
3	50% flowering	Direct	Uddin <i>et al.</i> , (2013), Singh <i>et al.</i> , (2013), Rameeh <i>et al.</i> , (2016), Roy <i>et al.</i> , (2018)
		Indirect	Bind <i>et al.</i> , (2014)
4	Primary branches/plant	Direct	Lodhi <i>et al.</i> , (2014)
5	Secondary branches/plant	Direct	Uddin <i>et al.</i> , (2013), Roy <i>et al.</i> , (2018), Roy <i>et al.</i> , (2015), Roy <i>et al.</i> , (2011)
		Indirect	
6	Silliqua/plant	Direct	Afrin <i>et al.</i> , (2011), Uddin <i>et al.</i> , (2013), Rameeh <i>et al.</i> , (2016), Ali <i>et al.</i> , (2002), Roy <i>et al.</i> , (2011), Roy <i>et al.</i> , (2015), Ghosh and Mukhopadhyay (1994)
		Indirect	Mondal <i>et al.</i> , (2000)
7	Seeds/silliqua	Direct	Uddin <i>et al.</i> , (2013), Lodhi <i>et al.</i> , (2014), Singh <i>et al.</i> , (2013), Ali <i>et al.</i> , (2002), Roy <i>et al.</i> ,

			(2015), Roy <i>et al.</i> , (2015), Mustafa <i>et al.</i> , (2014) and Behl <i>et al.</i> , (1992)
		Indirect	Mondal <i>et al.</i> , (2000)
8	1000 seed wt.(g)	Direct	Afrin <i>et al.</i> , (2011), Uddin <i>et al.</i> , (2013), Singh <i>et al.</i> , (2013), Singh <i>et al.</i> , (2011), Ali <i>et al.</i> , (2002), Mondal <i>et al.</i> , (2000), Sheikh <i>et al.</i> , (1999) and Mustafa <i>et al.</i> , (2014)
		Indirect	Bind <i>et al.</i> , (2014)

2.1.5 Genetic diversity

P.C. Mahalanobis in 1928 originally developed the concept of D^2 statistics to measure a group of distance based on multiple characters. This technique was used by him for the study of Anthropometry and Psychometry. The application of this technique was used for assessment of genetic diversity in plant breeding which was suggested by Rao (1952). This is one of the effective techniques for determining genetic divergence in numerous plant breeding materials. The assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding program. In plant breeding, genetic diversity plays an important role because, hybrids between the genotype of diverse origin, generally display a greater heterosis and throw more recombinants than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barrier to cross ability or due to different patterns of evolution. Replicated data is required for analysis of D^2 statistics and the consistent outcomes are attained from multilocational or multiseasonal data. Distinct cluster is formed by ordering the D^2 values of all the genotypes and after arranging, a method suggested by Tocher (Rao, 1952) is used for cluster formation. Studies in

different crops on genetic divergence pattern based on D^2 statistics in different environments demonstrated that the clusters based on genetic divergence and their constituents differ from environment to environment (Upadhaya and Murti, 1970; Jatsara and Paroda, 1970). However, such instability was restricted only to those characters, which are separated by low inter-cluster distances. The widely divergent clusters, however, remained divergent over different environments.

Narain (1981) studied the geographical distribution of species, concept and nomenclature of oliferous species of *Brassica* in India, with a view to find out genetic conservation and the history of their early cultivation. Anand and Rawat (1984) grouped geographically diverse, *B. juncea* lines into nine clusters using the Mahalanobis D^2 statistic by considering seed yield per plant and five related characters. They further suggested that geographical diversity of a line does not necessarily reflect on index of its genetic diversity and genetic estimates may be useful in the cross-breeding programme. Seed yield per plant along with ten related characters in seven varieties of *B. juncea* and their 21 F_1 hybrids was studied by Yadav *et al.* (1985). The parents and hybrids were assigned to 5 clusters. Forty-eight apparently diverse genotypes were classified into 5 distinct groups on the basis of D^2 analysis for seed yield and component traits. The clustering pattern suggested that geographical diversity was not necessarily an index of genetic diversity. The selection of parents based on diversity estimates, coupled with combining ability analysis would be effective Gupta *et al.* (1991). Swamy Gowda (1993) found 16 clusters from ten principal components where cluster III had the maximum number of genotypes. The maximum inter cluster distances occurred between cluster xiv and remaining clusters. Similarly, between cluster VI and VII, XVI between X and XVI and between V and X. The cluster XIV followed by XV included outstanding genotypes in respect to high siliqua per plant, number of racemes per plant, number

of primary branches per plant and higher plant height which results in higher seed yield per plant. The pooled data of nine characters over environments was studied on genotypes of mustard. Genotypes were grouped into 3 clusters based on D^2 analysis. Genotypes x Environment interactions were significant for characters like number of seeds per siliquae, siliquae on main raceme, days to flowering, days to maturity, harvest index and number of branches per plant Mahto (1996). The greatest contribution to genetic divergence was exhibited by number of siliquae per plant, plant height, and days to 50% flowering which, can be the basis for the selection of genetically diverse parents for hybridization Shalini *et al.* (2000). Sandhu and Gupta (2001) assessed the genetic divergence in *Brassica* species and reported wide physio-morphological divergence for the traits days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, length of main shoot, number of siliquae on main shoot, seed yield per plant, seeds per siliquae and seed weight both within and between species. Based on cluster analysis 36 genotypes were divided into five groups. Ghosh and Gulati (2002) showed D^2 values which were used to estimate genetic diversity and then the genotypes were classified into four divergence classes based on mean and standard deviation of all D^2 values. The percent contribution of the characters to genetic divergence was high for number of siliquae per plant, seed yield per plant, biological yield per plant, harvest index, plant height, 1000 seed weight, length of main raceme. Maximum intra cluster distance was observed in the cluster III which was highest with 11 genotypes followed by cluster I with 9 genotypes, cluster V and VI consisted of 4 and 3 genotypes respectively. The cluster II and VII both had two genotypes each and similarly, cluster IV and VIII included one genotype each. The crosses among the genotypes are expected to provide enough genetic variability to select for high seed yield was observed by Aunwinithul *et al.* (2004). Genotypes which were grouped into 5 clusters and cluster I having the highest number of genotypes (11). The intra-cluster distance was highest in cluster II,

whereas the lowest intra-cluster distance was recorded in cluster I. Inter cluster divergence was highest between clusters IV and V. Genotypes in cluster IV recorded the siliquae on main raceme, siliquae per plant, length of main raceme, oil content, test weight and biological yield contributed to more than 60% of the total divergence in the genotypes examined by Sinha and Singh (2004). Monalisam *et al.* (2005) estimated highly significant differences for all the characters, indicating a wide range of genetic diversity in the material. Siliqua per plant had the highest contribution toward total genetic divergence, followed by days to maturity, harvest index, days to flowering, seed yield and plant height. Singh *et al.* (2005) analyzed genetic divergence among 50 genotypes of Indian mustard (*Brassica juncea*). Four genotypes (RAURD-9602, NDR-190, NDYR-23 and NDM-87-1) could be grouped together and formed separate clusters. The most diverse groups were clusters VII and VIII. The genotypes present in different clusters may be selected for hybridization for exploiting heterosis.

Goswami and Behl (2006) considered genetic divergence and the characters contributing to genetic diversity among 43 genotypes of 13 homozygous diverse lines and their 30 F₁ hybrids derived from a line x tester mating design in Indian mustard using D² statistics. Based on divergence analysis, the genotypes were grouped into 6 and 15 clusters, respectively. The intra-cluster distances were almost equal and relatively lower than the inter-cluster distances. Days to 50% flowering, days to maturity, plant height, primary branches, secondary branches, main shoot length, siliquae on main shoot, siliquae length, seeds per siliquae, 1000 seed weight, seed-yield per plant and oil content contributed to total divergence in varietal improvement programme. 33 genotypes of mustard were evaluated by Singh *et al.* (2010) where seed yield, 1000 seed weight, number of secondary branches, number of seed per siliqua, siliqua length, number of primary branches, plant height, number of silique on main raceme were the maximum contributors for genetic diversity among the genotypes. Cluster I and IX included maximum genotypes and cluster IV was having only one genotype. Maximum

divergence was observed between clusters IV and VIII followed by cluster IV and VI, cluster IV and V and cluster V and VIII. Doddabhimappa *et al.* (2010) studied genetic diversity by using Mahalanobis D^2 statistics in 46 genotypes of Indian mustard. The 46 genotypes were grouped into seven clusters based on D^2 analysis in both conditions. Cluster III was the largest with genotypes followed by cluster IV and cluster I in protected condition. In unprotected condition, cluster II comprised of largest genotypes followed by cluster III, cluster I and cluster IV.

Again Doddabhimappa *et al.* (2012) considered genetic diversity employing Mahalanobis D^2 statistics for 46 germplasm lines of Indian mustard. The 46 genotypes were grouped into seven clusters. The intra cluster distance varied from cluster VII to cluster III in protected condition, and cluster VII to cluster II under unprotected condition. Similarly, intercluster distance varied from cluster VI to cluster II in protected condition, and under unprotected condition from cluster VI to cluster V. Number of secondary branches per plant showed maximum per cent contribution towards divergence followed by biological yield per plant, days to maturity and seed yield. Identification of similar cluster combinations inculcated both quantitative and qualitative traits in a positive direction for more effective selection. Khan *et al.* (2013) grouped the genotypes into 6 clusters on the basis of D^2 analysis. Cluster III had the maximum number of 11 genotypes, while the cluster IV and cluster V had only 2 genotypes each. The highest inter cluster distance was observed between cluster I and V (21.871), while the lowest in the cluster II and III (4.237). The intra cluster distance was the maximum in cluster V (0.469) and minimum in cluster III (0.116). The characters, yield per plant, number of siliquae per plant, and days to maturity were found prominent towards the genetic divergence. The genotypes G-15 and G-19 from cluster IV and G-1, G-3, G-4, G-10, G-18, and G-24 from cluster I were suitable for creating more variability for higher yield per plant through hybridization. Field experiment was conducted by Jahan *et al.* (2013) to study

on genetic diversity in 10 F₄ lines obtained through intervarietal crosses along with 8 released varieties of *Brassica rapa*. All the genotypes were grouped into four clusters. Cluster IV was the largest comprised of 7 genotypes and cluster II was the smallest with 2 genotypes. Cluster II had the highest intra-cluster distance and Cluster I had the lowest intra cluster distance. Inter cluster distance was maximum between clusters II and III. The results revealed that genotypes chosen for hybridization from clusters with highest distances would give high heterotic F₁ and broad spectrum of variability in segregating generations. The characters like number of primary branches/plant, number of secondary branches/plant and days to 50% flowering contributed maximum towards divergence among *Brassica* genotypes.

Singh *et al.* (2013) studied genetic divergence among 50 genotypes of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] using D^2 statistics which indicated the presence of substantial genetic diversity among the material. The analysis enabled grouping of all the genotypes into six clusters. Based on the inter cluster distances, C V and C VI were found to be the most divergent followed by C IV and C VI, C II and C VI and C I and C VI. Genetic divergence in ninety genotypes of Indian mustard [*Brassica juncea* (L.) Czern and Coss.] was assessed using D^2 statistics for fifteen characters enabled grouping of all the genotypes into nine clusters. Number of primary branches/ plants, number of secondary branches/plants, siliqua angle, siliquae on main shoot, primary branch angle, 1000 seed weight, and main shoot length were the major contributors for genetic diversity among the genotypes. Out of 9 clusters, cluster I was the largest comprising 20 genotypes followed by cluster II consisting of 18 genotypes, cluster III with 15 genotypes, whereas, clusters IV, V, VI, VII, VIII and IX contained 10, 8, 7, 7, 3 and 2 genotypes, respectively. The cluster V exhibited maximum intra-cluster distance, while maximum inter cluster distance was observed between cluster VIII and IX Lodhi *et al.*, (2013). 60 genotypes were considered by Shekhawat *et al.* (2014). They grouped the genotypes into 13 clusters based on D^2 analysis. The maximum inter-cluster

distance was found between cluster VI and VII, followed by VI and XI. The minimum inter-cluster distance was observed between cluster II and XII.

Chaurasia *et al.* (2015) estimated 13 quantitative characters including seed yield and oil content in Indian mustard [*Brassica juncea* (L.) Czern and Coss] to study genetic diversity using Mahalanobis D^2 statistics. The maximum number of genotypes were grouped in Cluster-III (17) followed by Cluster-I (14), Cluster-II (13), Cluster-V (6), Clusters-VI and VII (5 in each), and Cluster-IV (4). No regular geographical demarcation was discernible from clustering pattern of the genotypes. Clusters pair III and IV followed by VII and VI found to be most divergent. Days to flowering followed by days to maturity and plant height contributed maximum towards genetic diversity. Thirty genotypes were assessed by Bind *et al.* (2015) for genetic diversity using Mahalanobis D^2 statistics. Based on thirteen characters the genotypes were grouped into 7 clusters. Cluster I had largest number of genotypes followed by cluster III, IV, VII, VI, V and II. Maximum intra cluster divergence was found in cluster III, cluster IV and maximum inter cluster distance was found between cluster V and cluster VI which indicated that efficient breeding programme can be formulated to improve yield potential. Gupta *et al.* (2015) observed thirty-nine genotypes of Indian mustard. The maximum numbers of genotypes (14) were observed in cluster II, cluster I had six genotypes whereas cluster III, IV and V had one genotype in each. Cluster III exhibited maximum intra cluster distance, which indicated that these genotypes may be used to produce superior hybrid and transgressive segregants. The minimum intra cluster distance was observed for cluster I. Genetic diversity studies on 302 indigenous accessions of Indian mustard [*Brassica juncea* (L.) Czern and Coss] was carried out by Singh *et al.* (2016). The Indian mustard germplasm was evaluated for eight important morpho-agronomic traits. Geographic information system (GIS), principal component and cluster analysis were carried out to analyse major clusters. The cluster analysis grouped mainly in two major clusters I and II and further sub-divided into a and

b sub-groups. In cluster I sub-group b which indicated a close relationship between traits, days to mean flowering and days to mean maturity while the plant height was grouped individually. In cluster II, number of primary branches and number of seeds/siliquae showed close relationship with oil content as compared to other traits.

Vermai *et al.* (2016) deliberate the genetic divergence in Indian mustard and grouped them into different clusters based on yield and yield contributing traits for the hybridization programme. Genetic divergence analysis was performed on the basis of discriminant analysis using Mahalanobis D^2 statistics. Based on the relative magnitude of D^2 values, 60 genotypes of Indian mustard were grouped into five clusters and plant height, number of siliquae on main shoot and days to maturity were found the best discriminatory characters for the selection of diverse genotypes. 41 lines of Indian mustard which were grouped in 7 clusters following Tocher's method. Cluster I constituted of 10 genotypes and was the largest one followed by Cluster II consisting 7, cluster IV and cluster VI consisting of 6 genotypes. Cluster V was consisted of 5 genotypes, whereas cluster III and VII consisted of 4 and 3 genotypes, respectively. For yield improvement cluster VII exhibited highest cluster mean value for siliqua length, number of seeds/ siliquae, total seed weight/plant and test weight whereas cluster II number of primary branches/ plants, number of secondary branches/ plant, number of siliquae/plant and lowest mean value for number of total number of seeds/plant and total seed yield/plant Kumar *et al.* (2017). 25 genotypes of Indian mustard were assessed by Mohan *et al.* (2017) for genetic divergent study. Genotypes were grouped into 6 clusters. Maximum genotypes were present in cluster-I. The maximum inter cluster distance was observed between cluster-III and cluster-IV. The maximum intra cluster distance was observed for cluster-III followed by cluster-II and cluster-I. The maximum character contribution towards divergence was observed for days to 50% flowering.

Kumari *et al.* (2018) investigated the genetic diversity pattern in thirty-one *Brassica juncea* genotypes, using morphological traits. The cluster analysis based on Tocher's method classified the genotypes into four major groups of different sizes. Cluster I was the largest with 28 genotypes or constituting closer to 90 % of the total population, while cluster II, III and IV had one genotype each. The intra- cluster distance was comparable for cluster I, while for clusters II, III and IV, intracluster distance was zero as the clusters were constituted by single genotype each. The maximum intercluster distance was found between clusters II and III. The second most divergent clusters were III and IV. Among the traits, 1000- seed weight contributed maximum to genetic divergence followed by days to flower initiation and siliqua length. Genetic divergence in 36 Mustard genotypes and observations on 13 traits of were recorded by Nagda *et al.* (2018). Genetic divergence assessed using D^2 statistics for characters enabled grouping of all the genotypes in seven clusters. Among seven clusters, cluster I was the biggest with 13 genotypes followed by cluster II with 11 genotypes, cluster IV with 5 genotypes and cluster III with 4 genotypes. Cluster V, VI and VII were solitary. Maximum differences among the genotypes within the same cluster (intra-cluster) were shown by cluster IV (267.22) followed by cluster III (217.06), cluster II (133.07) and cluster I (92.53). Solitary clusters V, VI and VII showed zero intra-cluster distances. Diversity among the clusters varied from 171.51 to 1645.64 inter-cluster distances. Cluster VI and VII showed maximum inter cluster distance (1645.64). Tabassum *et al.* (2020) observed diversity among thirty *Brassica rapa* germplasm accessions were analyzed through Mahalanobis's D^2 statistic. Cluster I was largest containing 20 accessions followed by cluster II and III each with three germplasm accessions and cluster IV having two accessions. All remaining cluster contained one accession each. Cluster II had the highest mean values for shoot length while cluster IV had highest mean for number of siliqua and siliqua density. Similarly, cluster V possessed highest cluster mean value for siliqua length and beak length. Cluster VI had highest mean

value for number of seeds per siliqua and cluster VIII exhibited highest mean value for plant height and seed yield per plant. Highest intra cluster distance was observed for cluster IV followed by cluster III, cluster II and cluster I. Maximum inter cluster distance was observed between cluster VI and IV, followed by between cluster VII and V, cluster VIII and IX, cluster IV and V, Cluster II and Cluster IV and between cluster IV and IX.

2.2 Combining ability

Combining ability of seed yield with different yield contributing characters have been studied by different works.

Chauhan *et al.* (1990) stated that when crosses and their 15 parents were verified, there were significant differences for seed yield between genotypes. NOR 8602, Krishna, Pusa Bold and TM 9 had good general combining ability. The type of gene action involved in the inheritance of oil content in Indian mustard was studied by Pal and Kumar (1991). They reported the presence of both additive and non-additive gene actions. Recurrent selection might be used to exploit both the types of gene actions for improving oil content. The predominance of additive gene effects for 1000-seed weight and oil content, non-additive gene action for primary and secondary branches and both additive and non-additive types of gene effects for plant height and seed yield reported by Verma *et al.* (1991). Yadav *et al.* (1992) evaluated 45 F_{1s} of Indian mustard along with their 10 parents. They reported that all the traits (seed yield, its components and oil content) were governed by both additive and non-additive genetic variances. Parents Varuna, Kranti, RLC 1359 and RLC 1357 were identified as good general combiners for earliness, siliqua length, seeds per siliqua, 1000- seed weight, primary and secondary branches and oil content.

Diwakar and Singh (1993) derived the information on combining ability of 7 yield components and oil content in parents and their hybrids. K2 and K4 were superior for gca. Crosses K7 x K8, K2 x K4 and K x K5 had the highest sca for seed yield per plant. Significant variation was observed in gca and sca for all the traits studied. Both additive and

non - additive gene actions were involved in controlling the traits. Among all the traits, number of branches per plant played the most important role in the improvement of seed yield suggested by Malkhandale (1993). Rishipal *et al.* (1993) concluded that gene effects were considerably influenced by environment and cross the expression of number of primary branches, seeds per siliqua. 1000-seed weight and seed yield were governed by additive and non-additive effects.

Sharma and Singh (1994) observed that additive gene action was predominated for seed volume, whereas for remaining traits, non-additive gene action was important. Predominance of non-additive gene action through line x tester analysis was reported by Bharteria *et al.* (1995). The cross RLM 198 x Varuna has high sca effects for several characters and was also high yielder. Patel *et al.* (1996) found that variances due to gca and sca were significant for most of the traits except number of seeds per siliqua for gca variance and 1000-seed weight for sca variance. Non-additive gene action appeared to be predominant for all the characters except days to maturity, which was governed by additive gene action.

Singh *et al.* (1996) reported high magnitude of variance of sca for days to flower, number of secondary branches, seeds per siliqua, seed yield and oil content. However, estimates of gca variance were high for plant height. Both additive and non-additive gene actions were important in most of characters studied was found by Chaudhary *et al.* (1997). Hybridization system such as multiple or reciprocal recombinant crossing, which exploit both additive and non-additive gene effects simultaneously were recommended for the improvement of such characters. Khulbe *et al.* (1998) reported that significant differences existed for gca and sca for all the traits and were important for all the characters. Indicating the presence of both additive and non-additive gene effects in controlling the expression of various traits. Yield was found to be controlled predominantly by non- additive gene action. The crosses with high sca effects did not have parents with good gca effects. The

predominance of non-additive gene action for most of the traits including the seed yield and oil content observed by Sheikh and Singh (1998). Verma and Kushwaha (1999) found the significant differences for the combining ability variances for all the characters. Variance due to sca was greater than gca indicating the predominance of non-additive gene effects in the expression of seed quantity traits.

Chauhan *et al.* (2000) reported significant differences for days to maturity and oil content in males and for 311 the characters in females except for secondary branches and seed yield per plant. Basudev *et al.* (2001) observed the presence of gca and sca variances for seed yield per plant, days to 50 per cent flowering, days to maturity, early vigour, plant height, number of primary branches, number of siliquae on main axis, length of siliqua, seeds per siliqua, oil content and 1000-seed weight. Reciprocal cross effects were also significant for all the traits except early vigour and length of siliqua. Ghosh *et al.* (2002) reported that both additive and non-additive gene actions were of prime importance through studies carried out on line x tester analysis involving 29 female and 7 male parents.

Katiyar *et al.* (2004) studied combining ability and heterosis in 90 inter- varietals crosses of *B. Campestris*. Existence of significant variation among parents and crosses indicated the presence of adequate genetic variance between parents which reflected in differential performance of individual cross combinations. The presence of both additive and non-additive genetic variance and adequate heterosis provided the possibility of improvement of this crop not only by hybridization and selection but also by developing hybrids.

Goswami *et al.* (2006) thirteen genotypes and their 30 F₁ and F₂ progenies obtained from lines x tester mating were evaluated in the field less than two year for seed yield and its major components. The cross were had moderate genetic divergence between them and had good general combining ability (GCA) effects and had high SCA and high mean/value in F₁ had the highest frequency of transgressive segregates in F₁ and the magnitude of transgression were high the crossed RH 9710 x RH 30, RH 9624 x RH-30, RH 9617 x RWH-1 and RH-9615 x

RWA-1 involved parents with average to good GCA effects, high and SCA effect and moderate divergence resulted into the highest frequency of transgressive segregates.

A 6x6 diallel experiment was conducted on brown mustard (*Brassica juncea*) to perform a combining ability analysis for yield and its components by Nashim *et al.*, (2007). The good general combines for all the characters formed superior specific and reciprocal combination with RL-18 and Early raya and is therefore recommended for inclusion in the breeding programme for the evaluation high yielding mustard cultivars.

Combining ability analysis of 10 × 10 diallel set of crosses in Indian mustard for ten quantitative traits revealed preponderance of non-additive gene effects for plant height, number of primary branches per plant and seed yield per plant, whereas additive gene effect was found to be predominant for the inheritance of rest of the characters. The parent Durgamani, RLM-198 and Varuna were the good general combiners for seed yield and oil content. Varuna and Durgamani also exhibited desirable general combining ability effect for earliness and dwarfness. Among the cross combinations, cross Kanti × Pusa Agrani exhibited superior specific combining ability effects for seed yield, oil content and other yield attributing traits.

Most of the crosses involving high \times low general combining parents, exhibited high sca effects for various traits reported by Singh *et al.*, (2010). A diallel experiment was conducted to determine better general and specific combiners in 8x8 *Brassica juncea* L., genotypes for seed yield and its associated traits. Analysis of variance revealed highly significant differences among all the genotypes for pod length, 1000 seed weight and seed yield plant⁻¹, while significant differences were noted for pods plant⁻¹ and seeds pods⁻¹. According to combining ability analysis, the general combining ability (GCA) mean squares was highly significant for seed yield plant⁻¹ and significant for 1000 seed weight, while found non-significant for pods plant⁻¹, pod length and seeds pod⁻¹. The specific combining ability (SCA) and reciprocal combining ability (RCA) mean squares were highly significant for all the traits except seeds pod⁻¹. GCA effects were of greater magnitude than SCA and RCA for pods plant⁻¹, pod length and seed yield plant⁻¹ indicating that these traits were controlled by additive type of gene action. The parental genotypes MYT009, MYT113, MYT123, MYT120 and MYT117 were found the best general combiners, while hybrids MYT117 \times MYT123, MYT113 \times MYT009, MYT123 \times MYT113, MYT124 \times MYT117, MYT105 \times MYT103 and MYT113 \times MYT120 were found the best specific combiners for majority of the traits and could be exploited through further selection in segregating population was reported by Turi *et al.*, (2011)..

Significant differences were observed for both general combining ability (gca) and specific combining ability (sca) for almost all the traits studied by Patel *et al.*, (2012). The high magnitude of gca and sca effects indicated the presence of both additive and non-additive gene interactions for the inheritance of different traits. Parents RK 9501, GM 1, GM 2, GM 3 and SKM 139 were detected to be good general combiners for seed yield and they also presented good general combining ability for most of the other characters, in addition to, on the basis of sca effects out of 45 crosses six crosses were found better for seed yield per plant *viz*; GM 3 \times SKM 139, GM 1 \times GM 3, GM 1 \times RK 9501, SKM 139 \times PM 67, SKM 149

x PM 67 and RK 9501 x GM 2. Out of these 6 crosses only three crosses namely GM 1 x GM 3, GM 3 x SKM 139 and GM 1 x RK 9501 had shown high heterotic response for seed yield. Saheed *et al.*, (2013) reported that the analysis of variance indicated significant differences among parents and their hybrids in the F1 generation for all the traits studied. The cross combinations namely CR-5 x RAS 3189, DP 7-91 x INDIA III, RAS 3189 x DP 7-91, RAS 3189 x 0714-A and RAS 3189 x INDIA III exhibited significant heterosis for most of the studied traits thus may be exploited using heterosis breeding. The parent INDIA III and DP 18-9 was best general combiners for majority of traits. The cross-combination DP 7-91 x INDIA III proved best specific combiner for plant height, number of siliquae per plant, number of seeds per siliquae and seed yield per plant. The GCA and SCA mean squares significance determined the presence of both additive and nonadditive gene action that execute role for the expression of these traits. Nasim *et al.*, (2014) observed that the primary branches plant⁻¹, pods main raceme⁻¹, pod length, 100-seed weight and seed yield plant⁻¹ were significantly different. Heritability and genetic advance estimates were moderate for primary branches plant⁻¹, pods main raceme⁻¹, 100 seed weight whereas were high for seed yield plant⁻¹. Parental line G-909 for primary branches plant⁻¹, pods main raceme⁻¹ and seed yield plant⁻¹, genotype G-902 for pod length and genotype G-403 for 100-seed weight were the best general combiners.

Combining ability estimates were worked out by Gopikannan and Ganesh (2013) through Line x Tester analysis of 25 hybrids developed by crossing five lines with five testers to know the genetic architecture of 13 physio-morphological traits under sodic environment. The analysis of variance of combining ability showed variances of specific combining ability (SCA) and were higher in magnitude than the corresponding general combining ability (GCA) variances for all the traits under study which indicated preponderance of non-additive gene action governing these traits. Results of *per se* and *gca* effects of parents revealed that

multiple crosses involving IR 20, CO (R) 50, FL 478, TRY (R) 2 and CSR 23 would be considered as invaluable sources of genetic materials. An outset on perusal of data for hybrids based on *per se*, sca effects and standard heterosis, three hybrids viz., IR 20 / FL 478, IR 20 / CSR 23 and ADT 49 / TRY (R) 2 were found to be suitable for heterosis breeding under sodicity. As there was dominance gene action involved, inter se matings followed by recombination breeding might be advocated for improvement of yield under sodicity.

Line × tester analysis involving nine breeding lines and four testers revealed the operation of both additive and non-additive gene actions with predominance of nonadditive gene action in controlling yield and contributing traits. Four lines, namely, DRMR 2243, DRMR 2341, DRMR 2486, DRMR 2613, and one tester, NRCHB 101, were adjudged the best general combiner possessing highly significant positive GCA effects for seed yield and yield contributing traits. Significant SCA effects for seed yield, 1000-seed weight, oil content, and other attributing traits in desirable direction were recorded in a series of hybrids and a close association between SCA effects reported by Meena *et al.*, (2015). Chaurasiya *et al.*, (2019) stated that the ANOVA study of GCA variances significant for all the characters and SCA variances significant for nine characters except in case of days to maturity, plant height and biological yield per plant. The ratio of GCA and SCA variances were below unity in 6 characters. Out of twelve characters, Urvashi, Pusa Bold are the best parent for almost all traits as their GCA and *per se* performance are highest. Maya x NRCDR-2, Maya x Urvashi, Maya x Pusa Bold, NRCDR-2 x Urvashi, NRCHB-101 x Pusa M-21 and Urvashi x Pusa Bold showed high *per se* performance as well as SCA effects. The above best parent and best crosses can be used in hybridization and heterosis breeding respectively.

Proline concentration has been often suggested as an indicator of osmotic stress. A better understanding of the genetics of this trait is however needed. The study was carried out by Khalil *et al.*, (2016) proline concentration has been assessed, together with root and stem

growth, potassium, calcium and total soluble sugars concentration and stress injury symptoms, in seedlings of sunflower hybrids and their parents grown under control and osmotic conditions. Proline strongly accumulated with osmotic stress. Its concentration exhibited a large variation among genotypes and was higher in hybrids than in parental lines. In the control treatment, dominance effects explained most of the genetic variation for proline concentration while under osmotic stress both dominance and additive variance were high. The importance of dominance and additive effects suggested that several genomic regions are controlling this trait. Good general combiners, presumably carrying positive additive alleles affecting proline concentration, were identified.

Singh *et al.*, (2017) studied the effects of high temperature stress during terminal stage were investigated on canopy temp. ($^{\circ}\text{C}$) at 40 DAS, 50 DAS, 60 DAS, 70 DAS, chlorophyll fluorescence at 40 DAS, 50 DAS, 60 DAS, 70 DAS and seedling mortality (%) of 36 Indian mustard [*B. juncea* (L.) Czern & Coss.] genotypes along with their F_1 s. The genotypes were grown in randomized complete block design with three replications in two environments, *viz.*, E1 and E2. The analysis of variance based on Griffing's method revealed significant mean squares of general combining ability (gca) and specific combining ability (sca) for all most the traits. Mean squares due to parent v/s crosses were also significant for all the traits which depicted presence of heterosis for all the traits, except for canopy temperature at 50 DAS, chlorophyll fluorescence (Fv/Fm) at 40 DAS, chlorophyll fluorescence (Fv/Fm) at 50DAS and 60 DAS in timely sown condition and canopy temperature at 50 DAS and 70DAS in late sown condition. In the present study, an overall appraisal of gca effects revealed that parent RH0735 and BPR349-9 in timely sown condition and RH0116 and RH0555A late sown condition were good combiners for the majority of characters. High gca effects are related to additive gene effects or additive x additive interaction effects which represent the fixable genetic component of variation. Hence these

parents could be efficiently used for exploiting seed yield. For seed yield the crosses RH 8814 x RH0555A, RH0644 x BPR543-3 and BPR 349-9 x RH0644 in normal environment and crosses RH0555A x RH0644, RH 0735 x RH 0116 and BPR 349-9 x RH0644 were identified as promising on the basis of their high significant SCA effects. These crosses could be extensively used in breeding programme to develop superior segregants could be derived in further breeding programmes.

Dahiya *et al.*, (2018) carried out experiment considering ten parents comprising six selected local germplasm lines (PWR 15-8, PRHC 17-1, FS-14-24, PWR 158-1, PRHC 12-14, PRHC 13-14) and four released varieties (RGN-73, Maya, Kranti, PM 25) were crossed in diallel fashion (excluding reciprocals). Ten parents and their 45 F₁'s were evaluated. Results indicated that predominance of additive gene action for expression for all traits barring oil and glucosinolate content. Combining ability studies revealed that PRHC 17-1, RGN73, Maya, Kranti, PRHC 13-14 were good combiners for seed yield per plant but none had good GCA for oil content. Out of 45 crosses, 13 crosses *viz.*, PWR 15-8×PRHC 12-14, PWR 15-8×Kranti, PRHC 17-1×FS-14-24, PRHC 17-1×PWR 15-8-1, PRHC 17-1×RGN73, PRHC 17-1×PRHC 13-14, FS-14-24×Maya, PWR 15-8-1×RGN73, PWR 15-8-1×PM 25, RGN73×Maya, RGN73×Kranti, Maya × PRHC 12-14, PRHC 12-14 × PRHC 13-14 were good specific combinations for high yield/plant.

Ram *et al.*, (2018) identify parents for suitable use in a breeding programme for development of high yielding varieties of Indian mustard with heat stress tolerant traits, the combining ability and gene action for certain physiological traits were investigated in half-diallel crossings among eight parental lines. Analysis of variance for general combining ability (GCA) and specific combining ability (SCA) displayed significant general and specific combining effects for the seven seed yield and physiological traits *i.e.* population survival (%) 10 DAS, population survival (%) 25 DAS, membrane stability index (%), excised- leaf

water loss (%), relative water content (%), water retention capacity of leaves (%) 24hrs and seed yield per plant (g). For all the traits the GCA effects were relatively more important than the SCA effects, indicating that additive genetic effects were predominant. Crosses displaying high SCA effects for relative water content (%), membrane stability index (%) and seed yield per plant (g) were observed to be derived from parents having various types of GCA effects (high x high, high x low, low x low and medium x low). Among the parents, genotypes BPR-549-9, BPR-543-2 and Urvashi were found to be superior general combiners for seed yield and heat stress tolerance traits. Likewise, crosses involving diverse parents showed significant SCA effects for seed yield and other heat stress tolerance traits.

Six sensitive and ten salinity tolerant lines along with their resultant crosses obtained after crossing in Line \times Tester mating design were evaluated by Kanwal *et al.*, (2019) at maturity stage in a pot experiment. Data were recorded on various yield attributing trait and salinity tolerance related traits (proline content, Na⁺/K⁺ ratio, osmotic potential). Results showed that breeding material being studied had genetic variability that can be used in development of high yielding salinity tolerant types of *Brassica napus* L. Combining ability analysis revealed that lines R-3 and 23627 and tester Faisal were best general combiners under control conditions and on exposure to higher levels of salinity also. Crosses R-3 \times Laclone, RBJ-8007 \times Laclone and ZMR-1 \times ZMR-3 were observed to have positive significant specific combining ability effects for most of the traits under control and salinity stress conditions that can be further evaluated for growing under saline conditions. Proline content, Na⁺/K⁺ ratio and osmotic potential might be used as salinity tolerance indicators.

Twelve Indian mustard genotype and physiological parameters *i.e.*, Chlorophyll Content was recorded at anthesis and siliquae initiation stage; Chlorophyll Stability Index (CSI %), Net Photosynthesis Rate, Relative Water Content (RWC %) and Canopy Temperature Depression (CTD ⁰C) were estimated at pre-flowering and post-flowering stage

by Tripathi *et al.*, (2020). Study revealed that DRMRIJ16-3, RGN-403 and RH-1556 recorded higher CSI, net photosynthesis rate, Relative Water Content and canopy temperature depression at post-flowering stage, while higher chlorophyll content was recorded at siliquae initiation stage. The study indicated that mustard genotypes DRMRIJ16-3, RGN-403 and RH-1556 had tolerance to high temperature stress with delayed sowing, as they maintained higher values of these physiological parameters.

2.3 Nature and magnitude of heterosis for yield and its components

Primarily hybrid vigour was described by Koelreuter (1763). By artificial plant crosses Knight (1799) and Darwin (1877) described hybrid vigour in various crosses. Genetic basis of heterosis has been reported by East (1908).

Jinks (1955) suggested that non-allelic interactions might be the cause of heterosis rather than relation between the genes at the same locus. Mather (1955) detected heterosis to be an expression of genetic balance, which depends upon adjustment and integration of polygenes. Allard (1960) painstaking heterosis as hybrid vigour such that an F₁ hybrid falls outside the range of the parents with respect to some traits, heterosis in common use represents percent increase/decrease in the mean value of the F₁ hybrid over its mid parental value.

Jinks and Jones (1958) also stated that heterosis is a complex genetical phenomenon which depends upon the additive, dominance and interaction of homozygous/homogeneous and homozygous/ heterogeneous components as well as on the contribution of the genes in the parental lines. Highest heterosis over better parent for seed yield and significant heterosis for seed yield contributing traits reported by Hirve and Tiwari (1991). Patel *et al.*, (1993) crossed six lines of Indian mustard with four testers and found that only three crosses *viz.*, RC 1277 x Kranti (41.4%), RH 7811 x Kranti (279%) and RSK2 x Kranti (259%) had significant

heterosis for seed yield over better parent. Heterosis over better parents to the tune of 77.6 per cent for seed yield and 131 percent for oil content observed by Singh *et al.*, (1996). 18 hybrids out yielded the best control variety RLM 18 was noted by Agarwal and Badwal (1998). Three of them *viz.*, MS x Pant Raj 1002, MS x RH 818 and MS x RLC 1017 were superior over the best control in seed yield by 81.18 50.56 and 64.65 percent, respectively. Over all heterosis for seed yield was very high (59.69%). Khulbe *et al.*, (1998) reported that heterosis was high for length of main shoot, number of primary branches, seeds per siliqua, seed yield per plant and 1000-seed weight. The range of heterosis was quite low for days to maturity and oil content A large number of crosses exhibited significant negative heterosis for days to maturity and oil content.

Verma *et al.* (1998) reported significant positive heterosis for seed yield and oil content. Crosses RK 8801 x Krnati and JGM 88-A x Kranti exhibited the best hybrid vigour. The highest heterotic response for seed yield, followed by number of primary and secondary branches over better parent, when compared with standard check highest being 78 per cent for seed yield was found by Chauhan *et al.*, (2000). Katiyar *et al.*, (2000) reported that seven combinations exhibited >30 per cent heterosis and 11 crosses showed 31.3 to 71.3% heterosis. It is concluded that there should be adequate genetic divergence among lines to support a successful hybrid breeding programme. Tyagi *et al.*, (2000) revealed that desirable significant and negative heterosis for plant height was observed in seven crosses, with Varuna x SKNM 90-14 exhibiting the negative value (14%), Maximum positive heterosis was recorded for seed yield per plant with crosses pe R-7 x 5 KNM-13, RH 30 x TM 18-18 and per7 x JM90-12, giving values of 93.13,81.3 and 77.31 per cent, respectively. In general, positive heterosis for seed yield was accompanied with positive heterosis for siliqua length, seeds per siliqua, 1000-seed weight. biological yield and harvest index.

Sood *et al.*, (2001) noted that none of the hybrids was consistently good with regard to high heterosis and sca effects. The highest heterosis for seed yield was observed in the cross NOR 860 x RLM619 (141%). Sheikh and Singh (2001) reported the manifestation of higher degree of heterosis for seed yield and other component characters in mustard. Tyagi *et al.* (2001) reported that the selective heterosis was desirable for plant height, number of primary branches and secondary branches per plant, seeds per siliqua, number of siliqua on main shoots biological and seed yields and oil content. Heterobeltiosis was desirable for primary and secondary branches per plant. siliqua on main shoots and biological and seed yields. Standard heterosis was desirable for the number of primary and secondary per plant. siliqua length, seeds per siliqua number of siliqua on main shoots, biological yield, seed yields and oil content The mean level of heterosis was highest for biological yield. The highest standard heterosis (206.14%) and Heterobeltiosis (240.56%) for seed yield per plant was recorded in the cross. 810 772 x Rohini.

Five hybrids with the highest heterosis for seed yield were RN-505 x RN-440 RN-505 x PER-43. RNN – 393 x RN-481, RN- 393 x RN-453 and RN-505 x RN-481, and these crosses offer the best possibilities of further exploitation for the development of high yielding varieties stated by Kumar *et al.*, (2002). Singh *et al.*, (2003) found that heterobeltiosis in Indian mustard for seed yield per plant was observed in eight crosses namely KR-5610x PR-15, YRT-3 x PR-15, RK-1467x T-6342. Varun x YRT-3, KRV-Tall x T- 6342, RLM-198 x RT-3, Varuna x RLM- 198 and KR-5610 x KRV. The cross RH 9404 x RH30 had the maximum heterosis for seed yield per plant during E1 and E2, respectively. This cross also presented high heterosis for 1000 – seed weight was observed by Goswami *et al.*, (2005). Kumar and

Rathore Neetu (2004) studied heterosis on yield and its components in Indian mustard. The crosses NDR-9501 x RH-30 and Kranti x NDR-9501 and NDR-9501 x RK-30 showed the highest heterosis effect on seed yield. There was no cross showing significant positive heterosis for seed yield.

Shweta *et al.*, (2006) diverse lines of Indian mustard (*Brassica juncea*) were crossed to study the heterosis for Geeta, its component and oil content. Forty-eight crosses obtained by crossing twelve lines and four testers in a line x tester fashion along with their parent were used in the experiment. The higher significant heterosis over the controls Varuna and Kanti, was recorded to hybrid Pusa Basant x Rohini, Jagannath x Vardan and Vaibhav. The level of heterosis observed in these crosses justifies the development of commercial hybrid in Indian mustard. Monapara *et al.*, (2007) the maximum estimate of significant heterosis over best parent for seed yield 23% and over the significant heterosis for number of primary &

Singh *et al.*, (2009) reported high significant and positive heterosis was observed for 1000 seed weight and seed yield/ plant in crosses RC-781 x Basanti, Varuna x Maya, Vardan x Basanti and Pusa Jaikisan x Kanti. Three crosses, Vardan x Basanti, RC-781 x Kanti and RLM-198 x Maya showed significant heterosis for number of primary branches/plants, number of secondary branches/ plant and number of siliquae/ plants. For high oil content, Varuna x Basanti, Varuna x Kanti and RLM-198 x Basanti showed significant and positive heterosis. However, RK-2001 x Kanti, RK-01-02 x Kanti and Urvashi x Kanti showed negative heterosis for days to flowering and days to maturity. The above crosses can be utilized for development of early maturing, high yielding, bold seed size and having high oil content.

Heterosis estimates were worked out by Gopikannan and Ganesh (2013) through Line \times Tester analysis of 25 hybrids developed by crossing five lines with five testers to know the genetic architecture of 13 physio-morphological traits under sodic environment. An outset on perusal of data for hybrids based on *per se*, sca effects and standard heterosis,

three hybrids viz., IR 20 / FL 478, IR 20 / CSR 23 and ADT 49 / TRY (R) 2 were found to be suitable for heterosis breeding under sodicity. As there was dominance gene action involved, inter se matings followed by recombination breeding might be advocated for improvement of yield under sodicity.

20 F₁ hybrids and their parents were sown in a randomized complete block design with 3 replicates by Sincik *et al.*, (2014). During both years, the mean squares of the general combining ability (GCA), specific combining ability (SCA) and reciprocal combining ability (RCA) were statistically significant for all traits evaluated. The parent Malvira was a good general combiner because this parent had the highest significant positive GCA effects for all the characteristics evaluated. In addition, Lenox proved to be a good general combiner for plant height. The significant positive mid-parent and high-parent heterosis values were obtained with several crosses in important yield components. The parents used in this study exhibited positive GCA effects for seed yield.

Liton *et al.*, (2017) studied six parents of *Brassica rapa* (L.) viz., SAU Sarisha-1, SAU Sarisha-2, SAU Sarisha-3, BARI Sarisha6, BARI Sarisha-15, and Tori-7 were crossed in a half diallel fashion. Results indicated that, all the parameters except 1000-seed weight and seed yield/plant were significantly differed among the parents indicated existing variation in the parents. The best performance was observed from the parents BARI Sarisha-15 and Tori-7. The growth as well as yield and yield attributes of all hybrids were also significantly differed. The highest seed yield was obtained from the hybrid CC6 followed by CC15 with a moderate day to flowering. The most heterotic hybrids for seed yield per plant were CC14, which produced significantly positive heterosis over mid-parent and better-parent in our study. However, the parent BARI Sarisha-6, BARI Sarisha-15, and Tori-7 can be used in any breeding program and the hybrids CC14 can be selected for further study towards a variety development.

Analysis of variance revealed that the genotypes were genetically-differ to each for all the characters. Out of 21 Crosses the cross combinations namely; Varuna x RK-9101, Varuna x Pusa Jagannath, Varuna x RH-819, Varuna x Rohini and RK-9101 x Pusa Jagannath showed positive and significant heterosis over economic parents for seed yield per plant was studied by Mohan *et al.*, (2017).

Line x Tester analysis involving two females (CMS lines) and twenty males of safflower yielding forty hybrids was conducted by Rathod *et al.*, (2020) to estimate the magnitude of heterosis, heterobeltiosis and standard heterosis over three checks *viz.*, PKV PINK, PBNS 12 and CO 1 for the biochemical traits associated with aphid tolerance and seed yield (under aphid infestation). Considerable range of variability for heterosis over mid parent, better parent and standard check was observed for aphid infestation index, phenol content and seed yield as compared to chlorophyll content. Additionally, the female parent AKS CMS 2A performed well in combination with male parents for all the traits as compared to AKS CMS 3A. The highest, significant heterosis over mid parent, better parent and best check in desirable direction for the trait and chlorophyll content index was observed in cross AKS CMS 2A x AKS/S-33. The highest magnitude of average heterosis, heterobeltiosis and useful heterosis for phenol content was observed in cross AKS CMS 2A x S-518. Further, the highest positive and significant heterosis, heterobeltiosis and standard heterosis in desirable direction were recorded for seed yield per plant (under aphid infestation) by the cross AKS CMS 2A x GMU 3876. Hence, these three crosses *viz.*, AKS CMS 2A X AKS/S-33, AKS CMS 2A X S-518 and AKS CMS 2A X GMU 3876 found to have immense value as far as the traits associated with aphid tolerance is concerned.

2.4 Screening for aphid resistance

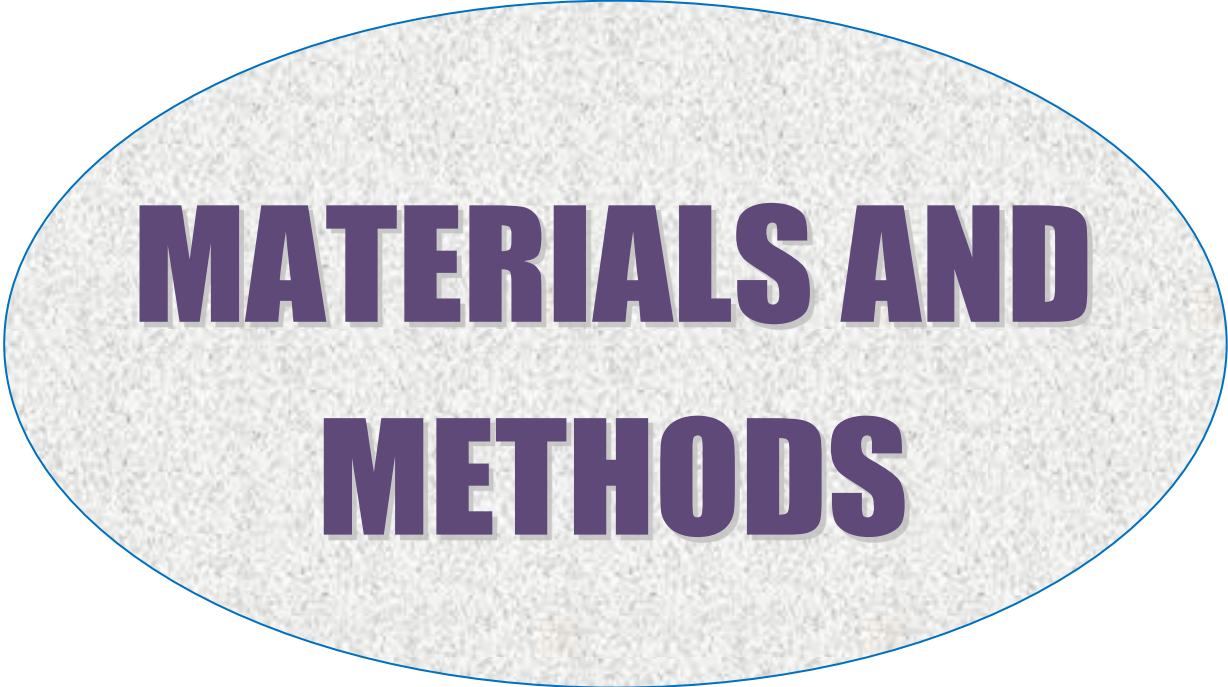
Sharma *et al.*, (2017) studied few parameters *i.e.* comparison of water content in aphid itself, comparison of water content between aphid probed twig and aphid unprobed twig

and comparison of water content in aphid probed twig and aphid itself that can probe the elevated levels of resistance in open field condition at early period of aphid infestation. The water content of aphid grown in different genotypes could able to differentiate the elevated level of resistance among the genotypes except between B2 and B3 which belong to the same class of resistance group (susceptible). Water content of aphid probed twig was significantly lower as compared to aphid unprobed twig due to aphid infestation in B2 and B3 genotypes whereas water content of aphid probed twig and aphid itself was comparable and in genotypes B4 and B12 water content of aphid probed twig was comparable to aphid unprobed twig whereas water content of aphid probed twig was significantly higher as compared to water content of aphid itself.

Experiment was carried out by Maurya *et al.*, (2018) to study the screening of rapeseed-mustard varieties *Brassica* spp. and evaluation of novel insecticides against aphid, *Lipaphis erysimi* (Kalt.). The screening was done based on the parameters of aphid infestation index and aphid population count. The result revealed that differential reaction among varieties ranged from highly susceptible to highly tolerant. Among the twenty varieties tested, Pusa Jagarnath and RLM-619 possessed highly tolerant and susceptible to mustard aphid.

Varietal screening was done with 51 genotypes of Indian mustard against mustard aphid *Lipaphis erysimi* to evaluate the resistant or tolerant genotypes on the basis of aphid population density by Sreedhar *et al.*, (2019). Categorization of resistant or tolerant genotypes was done on the basis of aphid infestation index (AII) scale, one germplasm was recorded as highly resistant, 20 were recorded as resistant and 30 were recorded as susceptible. None of the genotype recorded as immune and highly susceptible to aphid infestation.

Dhillon *et al.*, (2018) developed and evaluated various screening techniques to differentiate diverse mustard genotypes for resistance to *L. erysimi* under field conditions. Artificial infestation at bud formation stage with 20 mixed stage aphids pinned with bell pins on the top third branch near inflorescence was found most appropriate and effective for establishment of aphids at inoculation site. Evaluation of mustard genotypes under multi-choice natural infestation revealed maximum variability in *L. erysimi* resistance indices, but plot cage artificial screening technique was found appropriate over natural infestation for multi-choice assays. Genotypes Heera and PDZM 31 showed susceptible to highly susceptible reaction against *L. erysimi* under all the artificial infestation screening techniques. However, PM 30, PM 21, Pusa Bold and Pusa Vijay displayed variable resistance reactions under different screening techniques. PM 21, Pusa Bold and Pusa Vijay displayed variable resistance reactions under different screening techniques.



**MATERIALS AND
METHODS**

The details of the experimental material used, and methods applied during the present study are described in this chapter under the various heads.

3.1 Experimental material

The experimental material consisted of seventy-one diverse genotypes of Indian mustard (*Brassica juncea*) that were obtained from three different sources *i.e.* Pulses and Oilseed Research Station, Kanpur; Banaras Hindu University, Varanasi, Uttar Pradesh and Directorate of Rapeseed and Mustard Research (ICAR-DRMR), Bharatpur, Rajasthan for selection of eight divergent parents. The experimental trial was planted in a Randomized Block Design with three replications during the *rabi* season of 2017-2018. The list of the seventy-one diverse genotypes is given in Table 3.1. Based on the D² analysis, eight divergent parents were selected, and the crossing was done among the parents in half diallel fashion during *rabi* season of 2018-2019. To carry out the hybridization programme, the experimental material consisted of eight morphologically diverse parental genotypes namely, NPJ-194, RW-85-59 (Sarma), DRMR-15-16, SKJM-05, Kranti, Giriraj, RNWR-09-3 and PHR-2 that were crossed in a diallel fashion to obtain 28 direct crosses. All the 36 treatments *i.e.* 8 parents and 28 F₁s were grown in Randomized Block Design with three replications during *rabi* season of 2019-2020.

The experimental material for screening for aphid resistance consisted of eight diverse genotypes of Indian mustard (*Brassica juncea*) and their 28 F₁ population. The experiment was conducted at Central Instrumental Center laboratory, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, West Bengal. The experimental material was

sown in a Complete Randomize Block Design, with three replications during *khariif* season, 2019-20.

Table 3.1 List of Indian mustard genotypes evaluated during 2017-18.

S.No.	Genotype	S.No.	Genotype
1.	B-85(Seeta)	36.	DRMR-15-16
2.	RW-351(Bhagirathi)	37.	NPJ-198
3.	RW-85-59(Sarna)	38.	JMM-927-RC
4.	RW-4C-6-3(Sanjukta Asech)	39.	DRMR-15-47
5.	NPJ-194	40.	RGN-389
6.	TM-276	41.	RAURD-214
7.	Rohini (SC)	42.	DRMR-15-14
8.	KMR-15-4	43.	DRMR-4001
9.	PR-2012-9	44.	RGN-384
10.	Divya-88	45.	NPJ-197
11.	RL-JEB-52	46.	RB-81
12.	Kranti-NC	47.	NPJ-200
13.	DRMRIJ-15-85	48.	DRMR-15-9
14.	RH-1202	49.	KMR-L-15-6
15.	NPJ-196	50.	PRD-2013-9
16.	RMM-09-10	51.	DRMRIJ-15-66
17.	JMM-927-RC	52.	RH-1368
18.	RRN-871	53.	RH-1325
19.	KM-126	54.	RGN-386
20.	SKM-1313	55.	RNWR-09-3
21.	RB-77	56.	PRD-2013-2
22.	DRMR-15-5	57.	RH-749
23.	KMR-53-3	58.	Giriraj
24.	RL-JEB-84	59.	RH-406
25.	Ganga	60.	BPR-540-6
26.	RGN-73-JC	61.	RGIN-73
27.	RH-1209	62.	DRMR-IJ-31
28.	PR-2012-12	63.	NRCHB-101
29.	RGN-385	64.	DRMR-150-35
30.	NPJ-195	65.	Pusa mustard-25(NPJ 112)
31.	Maya-C	66.	Pusa mustard26(NPJ 113)
32.	SKJM-05	67.	Pusa mustard27(EJ 17)
33.	SVJ-64	68.	CS 54
34.	Sitara-Sreenagar	69.	PHR 2
35.	RH-0923	70.	RL 1359
		71.	Kranti

3.2 Experimental location and agro-climatic conditions of the experimental site

The field trial was laid out at Instructional Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, during *rabi* seasons. The farm is situated at 26° 40' N latitude and 89° 39' E longitude and an altitude of 47 meters above mean sea level. The soil at the experimental site is sandy loam in texture, and the agro-climatic zone is lower Gangetic plain region (III); New Alluvial Zone (WB-4)-NARP. The crop was sown on 10th November, 2017-18 in the first year, on 27th October, 2018-2019 in the second year and on 3rd October, 2019-2020 in the third year for experimental trials. During the period when the experiment was in the field, the weather condition remained suitable for the normal healthy growth of the crop. The meteorological data is given below

Table 3.2 Meteorological parameter of the location during the experiment 2017-2020

Month	Year	Temperature (°C)		Relative humidity (%)		Rainfall (mm)
		Maximum	Minimum	Maximum	Minimum	
November	2017	29.50	15.69	95	55	0
December		26.94	12.78	97.25	55.41	0
January	2018	21.84	9.25	95	60	0.00
February		26.23	12.69	84	53	0.14
March		30.03	16.54	71	49	3.26
October		30.9	20.5	76	63.9	3.9
November		29	15.1	75.2	51.7	0
December		25.9	10.8	76.3	48.5	5.8
January	2019	26	9	79	43	0.50
February		26.1	12.0	81.3	54.3	13.6
March		29.5	15.5	70	45	81.1
October		30.7	21.5	84.5	69	54.9
November		30.1	17.7	79.8	57.6	4.2
December		23.9	10.6	83.9	57.7	0
January	2020	22.8	9.9	91.1	59.7	0.8
February		26	10.8	8.4	49.7	11
March		29	16.1	74.7	51.8	43.4

Source: Integrated Agro-met Advisory Service Unit: Pundibari (Uttar Banga Krishi Viswavidyalaya, Pundibari).

3.3 Experimental details

The present research work was conducted with 71 genotypes of Indian mustard in Randomized Complete Block Design in three replications. Genotypes were represented by 3-row plots of 3-meter length. The second experimental trial was carried out including eight diverse parents selected in the first year of the trial based on a wide range of genetic diversity and adaptability for various yield attributing and aphid related traits. The crossing program was carried out in the second year. The third field trial involves both eight divergent parents and 28 F₁s for evaluation of the combining ability analysis and identification of heterotic hybrids using the diallel method based on yield, physiological and aphid-related traits. Genotypes were grown with proper spacing of 60cm between row to row 15 cm distance was maintained for the plant to plant by proper thinning. Standard cultural practices essential for the good crop of mustard were followed for obtaining a healthy and competitive crop stand.

3.4 Experimental methods

All possible non direct crosses were made during *rabi* 2018-19 in a half diallel fashion (8×8). Crossing was accomplished by removing the stamens from the female parent (emasculation) and by transferring pollen from the desired parent to its stigma (pollination). Emasculation was performed during the evening hours by hand picking the tubular petal cone in one go and removing the stamens with the help of needle without causing injury to other floral parts. After emasculation, flower buds were covered with thin film of cotton. Cotton was removed for a short while for pollination in the next day morning hours when male flowers had just opened and relative humidity in the atmosphere was at its maximum. At that time stigma was receptive and the pollen grains were viable. For effective pollination dusting

of freshly collected desired pollen grains was done on the stigmas of pistils. After pollination floral buds were again bagged and tagged. After maturity siliquae were harvested separately and kept in envelopes with proper labeling. Seeds of each siliquae were threshed and finally separated for raising F₁ generation in the subsequent year. A total of 36 treatments (28 crosses + 8 parents) were evaluated during *rabi* 2019-2020.

3.5 Recording of observations

In each replication five plants are randomly selected from each genotype and the observations were recorded for seed yield and its attributing, physiological and aphid-related characters. The details of the observations recorded are given below:

3.5.1 Seed yield and its attributing characters

3.5.1.1 Plant height (cm)

Plant height is the length from the base of the plant to the tip of the plant at maturity expressed in cm.

3.5.1.2 Height up to first branching (cm)

Length from the ground level up to the first capsule bearing a branch of the main stem. It was recorded in cm.

3.5.1.3 Days to 50% flowering

It is the number of days from the date of sowing to the date when 50 per cent of plants flowered in the plot. It was recorded on plot basis.

3.5.1.4 Primary branches per plant

At maturity the first order of branches emerging from main shoot were counted in each selected plant and the average of this was considered as number of primary branches

per plant.

3.5.1.5 Secondary branches per plant

The number of second order of fruiting branches emerging from the primary branches was counted at maturity as secondary branches and the average of five plants was recorded as the number of secondary branches per plant.

3.5.1.6 Siliquae per plant

Siliquae in each selected five plants were counted at maturity and the average of five plant siliquae was recorded as the number of siliquae per plant.

3.5.1.7 Seeds per siliqua

Ten siliquae from each selected plant were selected and seeds were counted and the average was recorded as the number of seeds per siliqua.

3.5.1.8 1000 seed weight (g)

The weight of 1000-seeds were counted randomly from the total yield of five randomly selected plant of a genotype and weighed in gram (g) with the help of an electronic balance up to two decimal places.

3.5.1.9 Seed yield per plant (g)

At maturity all the siliquae from the selected five plants per genotype were threshed, cleaned and dried. The average weight of the seeds was recorded as seed yield per plant in gram.

3.5.1.10 Oil content

Oil content was determined by Soxhlet method. Seed from each sample were first air dried. Two -gram of seed from each treatment was weighed on an analytical balance. Weighed seed was crushed with the help of mortar-pestle. The crushed sample was transferred to the thimble. A pre weighed empty round-bottomed flask was

taken. The thimble was put in soxhlet apparatus along with n-Hexane (100ml) and boiled at 90⁰C for 45 mins and then at 180⁰C for 10 mins. The oil was extracted in a soxhlet apparatus till the seed powder was completely free from the last traces of oil. The solvent from the extracted oil was first removed by condensation and the last traces of solvent were removed by evaporation. After evaporating the solvent, the weight of the flask containing the oil was taken till a constant weight was obtain. Oil content has been reported as the weight of the oil obtained from a hundred grams of the seed.

3.5.2 Physiological traits

3.5.2.1 Percentage of leaf membrane stability index (MSI)

Leaf membrane stability index was determined following the method of Premachandra *et al.*, (1990) as modified by Sairam (1994). Leaf sample was collected from selected plants of a genotype. The leaf was cut into small strips of 0.2g, which are placed in two separate test tubes in 10 ml distilled water. One set of the test tube with the sample was placed in a water bath at 40 degree Celsius for 30 minutes and then EC of the water was measured using a conductivity bridge (C1). Another set of test tube with leaf strip was incubated at 100 degree Celsius for 15 minutes and measure the EC of the sample water (C2). Leaf membrane stability index (MSI) was calculated using the formula:

$$\text{MSI (\%)} = [1 - C1/C2] \times 100$$

3.5.2.2 Percentage of excised- leaf water loss (ELWL)

It was suggested by Clarke (1987). The leaf sample was collected from selected plants of a genotype and fresh weight of the leaf was taken followed by weight after 6 hrs. of drying in an incubator at 28 degree Celsius and 50 % relative humidity. After that dry weight of the sample was recorded by placing the sample in a hot air oven for 24 hrs. at 70 degrees Celsius. ELWL was calculated using the following formula:

$$\text{ELWL (\%)} = \frac{[\text{Fresh weight} - \text{Weight after 6 hrs.}]}{[\text{Fresh weight} - \text{Dry weight}]} \times 100$$

3.5.2.3 Percentage of relative water content (RWC)

RWC was suggested by Barrs and Weatherley (1962). Leaf sample collected from the selected plant, cut into 2cm leaf section and immediately weighed for fresh weight. After fresh weight, the 2cm leaf section was placed in distilled water for 4 hrs., blot dried the leaf to remove excess water and weighed the turgid weight of the sample. The same 2 cm leaf sections were oven-dried at 60-degree Celsius for 24 hrs. and weight to obtain the dry weight. RWC was calculated using the following formula:

$$\text{RWC (\%)} = \frac{[\text{Fresh weight} - \text{Dry weight}]}{[\text{Turgid weight} - \text{Dry weight}]} \times 100$$

3.5.2.4 Proline estimation

(a) Reagent required:

- 3% sulphosalicylic acid
- Ninhydrin solution: In a 100 ml beaker, 1.25g ninhydrin was taken. To it, 3 ml of glacial acetic acid and 20 ml of 6 (M) orthophosphoric acid was added, warmed the solution with agitation until the crystal was dissolved. The solution was stored at 4⁰C and used within 24 hours.
- Glacial acetic acid
- Toluene
- Proline

(b) Extraction of proline:

0.2gm of the newly harvested leaf was collected. Homogenized the leaf sample with 2ml of 3% sulphosalicylic acid. Homogenate was centrifuged at 10,000rpm for 15 minutes. The supernatant was collected and discard the ruminants. This step was repeated thrice in

the same solvent. The supernatants were combined and volume was made to 10 ml with distilled water. This aliquot was used for the estimation of proline.

(c) Estimation of proline:

The method for proline estimation was suggested by Bates *et al.*, (1973). 2.0 ml aliquot from different extracts was taken separately in test tubes to which 2.0 ml of glacial acid and 2.0ml of ninhydrin solution was added. The mixture was heated in a boiling water bath for 1 hour with glass marbles placed at the top of it. After 1 hour, the reaction was terminated by placing the tubes in the ice bath. 4ml toluene was added to each tube and shaken well for 20-30 seconds. The tube was allowed to stand at room temperature for 10 minutes. The Toluene layer was then separated and the intensity of the red color was measured in a spectrophotometer at 520nm. A blank was run similarly in a separate test tube in which 2.0ml of distilled water was taken instead of the extract. The amount of proline in the test sample was calculated from the standard curve, prepared from known concentrations of proline and expressed as (mg/gm).

3.5.2.5 Chlorophyll content

The chlorophyll content was estimated according to the method of Arnon (1949). About 0.2g of leaf sample was cut into small pieces and placed in test tubes having (10 ml) 80% (V/V) acetone. The clear solution of acetone turn green as the chlorophyll from the leaf comes out in the solution. The spectrophotometer reading was measured at 645 and 663 nm against an 80% acetone as blank. The levels of chlorophyll 'a', chlorophyll 'b' and total chlorophyll were determined using the equation given below:

$$\text{Chlorophyll 'a' (mg/g fr.wt.)} = (12.7 \times \text{O.D. at } 663\text{nm} - 2.69 \times \text{O.D. at } 645 \text{ nm}) \times V/A \times 1000 \times W$$

Chlorophyll 'b' (mg/g fr.wt.) = $(22.9 \times \text{O.D. at } 645\text{nm} - 4.68 \times \text{O.D. at } 663\text{ nm}) \times V/A \times 1000 \times W$

Total chlorophyll (mg/g fr.wt.) = $(22.9 \times \text{O.D. at } 645\text{ nm}) + (8.02 \times \text{O.D. at } 663\text{ nm}) \times V/A \times 1000 \times W$

The chlorophyll content was expressed as mg chlorophyll per gram fresh weight of the leaf.

3.5.3 Aphid related traits

3.5.3.2 Water content of aphid uninfected twig (%)

The water content of aphid uninfested twig was suggested by Sharma *et al.*, (2017). Uninfected twigs of 10 cm from the tip of the selected plants per genotype were selected and placed in a sealed polythene bag to reduce the evaporation rates. The fresh weight of the uninfected twig was recorded and then the twig was placed in a dry oven for 24 hrs. at 50^odegree. After drying the twigs, dry weight was recorded with the help of power balance and the available moisture was calculated.

3.5.3.3 Water content of aphid probed twig (%)

The water content of aphid probed twig was suggested by Sharma *et al.*, (2017). Aphid probed twigs were collected from the selected plants and placed in polyethylene seal packets. Aphids were separated from the twigs with the help of a brush and the fresh weight of the twigs was considered. After fresh weighing, the twigs were placed in a dry air oven for 24 hrs. and dry weight was recorded.

3.5.3.4 Water content of aphid itself (%)

The water content of aphid itself was suggested by Sharma *et al.*, (2017). Aphid from the infested twig was separated and the fresh weight of the aphid was measured with the help of a high precision weighing balance (mg). After that, aphids were placed in a hot

air oven in a small paper envelope at 50 °Celsius for 24 hrs. for a day. The dry weight of the aphid was recorded, and the calculation was done accordingly.

3.5.3.5 Aphid count

A 10 cm twig was collected from the tip of the selected five plants. The aphid-infested twig was cut gently, placed in a sealed polythene packet and brought to the lab. The aphids were well removed from the twigs on top of the white sheet with the help of a brush. The large aphids were separated with the help of magnifying glass and a fine brush. Large and small aphids were counted separately and the counts of both types of aphids were recorded on average as aphid count.

3.5.3.6 Penetration force

The texture analyzer instrument was used to measure positive and negative pressures by following protocol suggested by Mondal *et al.*, (2017)

Stable microsystem; 2 mm needle stainless (Plant code-P/2N)

Sequence manure; (Texture analyzer)

Caption	Value	units
Test mode	Compression	
Pre-test mode	1.00	/mm/sec
Test speed	1.00	/mm/sec
Post-test Speed	10.00	/mm/sec
Target mode	Distance	
Distance	1.00	/mm
Trigger type	Auto (force)	
Trigger force	5.0	g.
Advance option	off	

The positive pressure was measured and represented in the forms of graphs in the system attached to the Texture analyzer. Positive pressure is the pressure that is needed to puncture the plant twig tissue. Positive pressure was considered by the analyzer as the pressure exerted by the aphid upon entering the twig while the negative pressure is the pressure exerted to retract back the tip of the probe from the punctured tissue of the twig. This negative pressure was assumed to be the same force exerted by the aphid to remove the stylet from the twigs.

3.6 Screening for aphid resistance for parents and F₁

a) Sterilization of potting mixture

Artificial soil formation was packed in an autoclaved bag until it was filled up by about an inch from the top with a scooper and a piece of autoclave tape was placed on the autoclaved bag. The autoclave was done at 121°C, 15 atmospheric pressures for 15 mins. After the autoclave, the pressure was released, and the bag was removed from the autoclave. The mouth of the bag was opened and set aside to cool. After the soil cooled, the autoclaved soil was moved to an airtight basket to prevent the contamination of seeds and fungi. Autoclaved soil was used for further seedbed preparation and can be used for up to 2 weeks.

b) Seedbed preparation

Eight medium-sized pots for each parent's genotype and 28 F₁s were filled with artificial soil, lightly packed and sprinkled with the help of a sprinkler. Thirty seeds of mustard were sown in each pot and the pot was kept in a transparent box with less water for maintenance of moisture condition. The box was then placed in the refrigerator for 2 days at 4° Celsius for attaining even sprouting. The box was removed from the refrigerator and placed in a controlled environment chamber (8000 LUX of light intensity, 14:10 hrs. light: dark condition per day and 70% of relative humidity) for suitable growth of plants.

c) Sub culturing of plant

In the lab condition, germination of mustard seed takes 3-4 days and a regular visit is required to focus on germination status. A few days of germination when the plant attains a height of 4-5 cm having the cotyledonary leaf, is the best time to sub-culture the seedlings usually 7 days after germination. For sub-culturing tray was washed properly and filled with little water and pots were placed over it. Each parent and F₁ requires 21 pots for subculture. Plants are transferred from the seedbed pot to the small pots over the tray and retained in the growth chamber to grow until the true leaves arrived.

d) Aphid rearing

Lipaphis erysimi was reared on Indian mustard. Artificial growth conditions were provided for the development of aphids at Plant Growth Chamber (PGC). Large and medium-sized aphids were used for the experiment.

e) Screening experiment

Three transparent boxes were taken and filled with 1/3rd of water. Place the pots in the boxes. For each genotype, three transparent boxes were required, and each box contains six small pots having the plants. Transparent boxes are labeled properly mentioning the genotype name and aphid number per plant as 1, 5 and 10 aphids per plant. Aphids were collected from the Plant Growth Chamber (PGC) on a small tray and relocate the collected aphid on the shoot of the plant with the help of a thin paintbrush. Aphid was released at 6 PM and observations of aphid proliferation were recorded as aphid count at 0,12,36,60 and 80 hrs. time.

3.7 Transformation of the replicated mean data

3.7.2 Percentage data transformation

Physiological and aphid-related characters are subjected to arcsine and square root transformation in the case of percentage data. If the mean value is less than 30 or more than 70 square root transformation is done. If the mean value is between 30-70 no transformation is required and when the mean value is across 30 or 70 arcsine transformation is required to be carried out. In the current study, percentage of membrane stability index, the water content of aphid probed twig, the water content of aphid unprobed twig, the water content of aphid and percentage of water differential between aphid probed twig and aphid itself undergo the arcsine transformation while only one character *i.e.* the percentage of relative water content square root transformation was done.

3.7.3 Test for Normality of the traits

All the mean values of the nine morphological, physiological and aphid related characters in Indian mustard were subjected to a normality test. If the computed P-value is found to be greater than the significance level of the different normality tests, then the trait follows normality distribution or else it deviates and log transformation [$\log(x)$] of the data is to be done. Also, if the individual value of the data for a character is all lower than 10 then instead of $\log(x)$, the transformation is $\log(x+1)$. In the present study, it was found that among the morphological characters siliquae per plant, height up to first fruiting branch, plant height seed yield per plant and 1000 seed weight; in case of physiological characters except for proline content of leaf and among aphid related characters water content of aphid, percentage of water differential between aphid probed twig and aphid itself and aphid count didn't show the normal distribution. Hence, both $\log(x)$ and $\log(x+1)$ transformations were carried out for the characters depending upon whether their values were greater or less than 10. Subsequently, all other statistical analysis was done using the log-transformed values of the characters.

3.8 Statistical analysis

3.8.2 Randomized Block Design Analysis

The subsequent statistical parameters were used to find the final result from the raw data for the respective traits.

3.8.2.2 Arithmetic mean

The average of a set of numerical values, as calculated by adding them together and dividing by the number of terms in the set.

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n X_i$$

Where, \bar{X} = Mean

X_i = i^{th} observation

N = number of observations

Least significant difference (LSD)

The least significant difference (LSD) test is used in the context of the analysis of variance, when the F -ratio suggests the rejection of the null hypothesis H_0 , that is, when the difference between the population means is significant. This test helps to identify the populations whose means are statistically different. Critical difference (CD), as it is also called, are a form of t -test which tests the significance of observed differences simultaneously among various means. CD is used at (0.05) and (0.01) percent level to signify the differences among the two treatment means.

$$CD = SE_D \times t$$

Where,

SE_D = standard error of the difference of the treatment means to be compared, and is equal to

$$SE_D = \sqrt{\frac{2EMS}{r}}$$

and 't' is the tabulated value at 5% and 1% level of significance.

3.8.3 Analysis of variance

The mean values of genotypes in each replication were used for statistical analysis. The data were analyzed for a randomized block design to test the significance of variance among the genotypes (treatment) for various characters. The steps involved in the analysis of the randomized block design were as described by Panse and Sukhatme (1969).

The analysis of variance was based on the following linear model of Fischer (1918).

The following mathematical model was used in the analysis

$$y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

- I = 1, 2,----- r (replication)
- j = 1, 2,----- t (treatment)
- Y_{ij} = Phenotypic observation of the ith genotype in the jth replication
- M = general mean
- g_i = effect of ith genotype
- r_j = effect of jth replication
- e_{ij} = random error associated with the ith genotype
in the jth replication

Table 3.3 Analysis of variance for all the treatments including check- ANOVA for the experiment.

Source variation	of	d.f.	Sum of square (S.S.)	Mean sum of square (M.S.)	F value
Replication		(r-1)	R.S.S.	$RSS/(r-1) = MSR$	MSR/MSE
Treatment		(t-1)	T.S.S.	$TSS/(t-1) = MST$	MST/MSE
Error		(r-1) (t-1)	E.S.S.	$ESS/(r-1) (t-1) = MSE$	
Total		(rt-1)			

Where,

r = number of replications

t = number of treatments

d.f. = degree of freedom

MSR = mean square of replication

MST = mean square of treatment

MSE = mean square of error

The significance of variance in the treatment for all the characters was tested by the 'F' test. The calculated value of 'F' is compared with the table value 'F' for treatment of degree of freedom. If the observed value of 'F' is less than the value of the table, it is considered to be non-significant and vice-versa. If the observed value of 'F' is higher than the table value is considered to significant. Wherever the 'F' value was found to be significant, the critical difference (CD) was calculated to test the significance of the difference between two treatment means as follows: $C.D. (0.5) = \sqrt{t}2MSe/r \times t$ at error degree of freedom at 5 % level of probability.

Where, r = number of replications.

t = number of strains/genotypes.

$ESS = \text{Total sum of square} - TSS - RSS.$

The test for difference among treatments was made by the following F test.

$$F(t), m = \frac{MST}{MSE}$$

Where,

(t-1) and m are the degrees of freedom associated with the numerator and denominator of the F ratio, respectively and MST and MSE are the treatment and error mean squares, respectively.

If the calculated F value is greater than the Table F value, the F ratio would be significant and the null hypothesis would be rejected with the assumption that there were genotypic differences.

Based on above model, the data obtained on treatments, parents and F₁s were subjected to randomized complete block analysis. The skeleton of the analysis of variance is given as under.

Table 3.4 Skeleton of analysis of variance (ANOVA) for parents and F₁s,

Source of variation	d.f.	Mean sum of squares	F --test
Replication	(r-1)	MSR	MSR/MSE
Treatments	(t-1)	MST	MST/MSE
Parents	(p-1)	MSP	MSP/MSE
F ₁ s	(f-1)	MSF	MSF/MSE
Parents vs. F ₁ s	1	MSPF	MSPF/MSE
Error	(r-1)(t-1)	MSE	

Where,

r = number of replications

t = number of treatments

p = number of parents

f = number of F₁s

d.f. = degree of freedom

- MSR = mean sum of square of replication
- MST = mean sum of square of treatment
- MSP = mean sum of square of parents
- MSF = mean sum of square of F1s
- MSPF = mean sum of square of parents vs. F1s
- MSE = mean sum of square of error

3.8.4 Genetic Variability

The following parameters were estimated following Burton (1952) and Johnson *et al.*, (1955).

$$GCV = \frac{\text{Genotypic standard deviation } \sqrt{\sigma_g^2}}{\text{Mean}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation } \sqrt{\sigma_p^2}}{\text{Mean}} \times 100$$

The estimates of genotypic and phenotypic standard deviations were obtained from the respective analysis of variance table for different characters.

For convenience following classifications were used for describing various parameters of variability in the text:

PCV and GCV	>25%	High
	10-25%	Moderate
	<10%	Low
Heritability (h^2)	>80%	high

	60-80% Medium
	<60% Low
Genetic advance	>20% High
	10-20% Moderate
	<10%

3.8.5 Heritability and Genetic advance

3.8.5.2 Heritability

A quantitative measure that provides information about correspondence between genotypic variance and phenotypic variance is heritability. The heritability in a broad sense was computed by the method of Burton (1951) and the formula is:

$$h^2 (bs) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,

$h^2 (bs)$ = Heritability in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

3.8.5.3 Genetic advance

Genetic advance, i.e., improvement in the genotypic value of new population as compared with the base population, depends among other things upon the magnitude of difference among the genotypic values of individuals in the base population Allard (1960).

Thus, Genetic advance $G_s = \frac{\sigma_g^2}{\sigma_p} \times K$

Where,

K is the selection differential which is the difference between the mean phenotypic

value of n selected lines, i.e. \bar{a}_s and the mean phenotypic value of n original tested lines, a .

$$\text{Thus, } G_s = Kh^2\sigma_p$$

Where,

G_s = Genetic advance,

K = Selection differential at 5% selection intensity = 2.06

h^2 = heritability of the character

σ_p and σ_g are the phenotypic and genotypic standard deviations, respectively. The genetic advance was computed by the method used by Lush (1940).

3.8.6 Estimation of the Correlation coefficient

Correlation was estimated as the association between various character-pairs (between two variables). The correlations at genotypic, phenotypic and environmental levels were estimated from the analysis of variance and covariance as suggested by Searle (1961).

Phenotypic correlation between character x and y

$$r_{xy}(p) = \frac{\text{Cov}_{xy}(p)}{\sqrt{\text{Var}_x(p) \times \text{Var}_y(p)}}$$

Where,

$\text{Cov}_{xy}(p)$ = Phenotypic covariance between two characters x and y.

$\text{Var}_x(p)$ = Phenotypic variance for characters x.

$\text{Var}_y(p)$ = Phenotypic variance for characters y.

Genotypic correlation between character x and y

$$r_{xy}(g) = \frac{\text{Cov}_{xy}(g)}{\sqrt{\text{Var}_x(g) \times \text{Var}_y(g)}}$$

Where,

$Cov_{xy}(g)$ = Genotypic covariance between two character x and y

$Var_x(g)$ = Genotypic variance for characters x

$Var_y(g)$ = Genotypic variance for characters y

The significance of correlation coefficient (r) was tested by comparing the observed value of correlation coefficient with the tabulated value for (n-2) degree of freedom. If the observed value is more than the table value, the correlation coefficient is said to be significant.

$$tc = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

Where,

r = correlation coefficient

n = number of genotypes

tc = t calculated

3.8.7 Path coefficient analysis

The analysis of path-coefficient was conducted following the procedure suggested by Wright (1921) and as elaborated by Dewey and Lu (1959).

Eleven yield contributing characters were considered in path coefficient analysis to estimate their direct and indirect effect on seed yield.

Path coefficients were obtained by solving the simultaneous equation which expresses the basic relationship between correlation and path coefficient. The equation is as follows:

$$ry_1 = Py_1 + Py_1r_{12} + Py_3r_{13} + \dots\dots\dots Pynr_{1n}$$

$$ry_2 = Py_2 + Py_1r_{21} + Py_3r_{23} + \dots\dots\dots Pynr_{2n}$$

$$ryn = Pyn + Py_1rn_1 + Pynrn_2 + \dots\dots\dots Pynrn(n-1)$$

Where,

$r_{y1}, r_{y2}, \dots, r_{yn}$ are the correlation coefficient of dependent variable (y) with various independent variables (1, 2,..... n).

$P_{y1}, P_{y2}, \dots, P_{yn}$ are the direct path effects of independent variables (1, 2,.....n) on dependable variable (y).

$r_{12}, r_{13}, \dots, r_{1n}, \dots, r_{n(n-1)}$ are the correlation coefficient between various independent variables (1, 2,.....n).

Path coefficients were obtained by replacing the corresponding elements in A and B matrix by correlation coefficients. B matrix was inverted and the inverted B matrix was multiplied by matrix to obtain path coefficients.

Residual factor which measures the contribution of rest on the characters of causal scheme was obtained as given below:

$$P_{xy} = \sqrt{1-R^2}$$

Where, $R^2 = \sum_{i=1}^n P_{iy} r_{iy}$

Where R_{iy} denotes correlation between all possible combinations of independent character Y. The correlation is r_{12} to r_{11} $12 P =$ direct effect of i th character on Y. $r_{iy} =$ coefficient correlation between i th and y factor.

3.8.8 Genetic divergence analysis

The genetic divergence in seventy-one genotypes was estimated using Mahalanobis D^2 statistics (1936) following Rao (1952). The clustering pattern was followed as suggested by Ward (1963).

$$D^2 = \lambda^{ij} \delta_i \delta_j$$

Where,

λ^{ij} = reciprocal matrix to the common dispersion matrix.

δ_i = Difference between the mean values of the two populations for i^{th} character.

δ_j = Difference between the mean values of the two populations for j^{th} character.

The parameter D^2 can be estimated as D^2 statistics Rao (1952)

$$D^2 = \sum \sum \delta_{ij}, d_i d_j = \text{Sample estimate of } X_{ij}$$

Where,

δ_{ij} = Sample estimates of X^{ij}

d_i = Sample estimates of δ_i

d_j = Sample estimates of δ_j

Unstandardized and correlated variables (mean value of character) are transformed into standardized uncorrelated variables. After transformation X_1, X_2, \dots, X_p variable (unstandardized and correlated) becomes Y_1, Y_2, \dots, Y_p variable (standardized and uncorrelated variables). This transformation was done according to the square root of Dwyer, described by Rao (1952). The variable transformations is done because this formula requires the inversion of n order of determinants and then evaluation of $(n+1) / 2$ term whose sum is D^2 .

Inter and intra-cluster distances were calculated by Ward's method (1963) to form the clusters. This criterion was based on the principle that any two populations belonging to the

same cluster should at least on average show smaller D^2 than those belonging to different clusters.

3.8.9 Combining ability analysis

3.8.8.1 Analysis of variance for combining ability (diallel)

Combining ability was analyzed for mean value of 36 entries (parents and hybrids) according to the procedure given by Griffing (1956a) as per Method II (in which parents and the set of F_1 s without reciprocals are included) and Model I [which assumes that the genotypes and block effects are constant (fixed) but the environment effects are variable].

The combining ability analysis was carried out as per the method suggested by Griffing (1956 a, b) Method-II, Model-1 which assume that variety and block effects are constant (fixed).

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + [1/r] \sum e_{ijk}$$

Where,

Y_{ijk} =Performance of hybrid of ij th cross in k th replication,

$i, j=1,2,3, \dots, P$ (Number of parents)

$k=1,2,3, \dots, b$ (Number of replications)

μ = General mean,

g_i = General combining ability effect of i^{th} parent,

g_j = General combining ability effect of j^{th} parent,

s_{ij} =Specific combining ability effect of the cross between i^{th} and j^{th} parent,

e_{ijk} = Environment effect pertaining to ijk^{th} observation

Based on this model, the analysis of variance for combining ability is done as shown in

below table

Table 3.5 ANOVA for combining ability analysis as per Model I, Method 2 (Griffings,1956)

Source	Df	S.S.	M.S.S	E.M.S.
GCA	(p-1)	S_g	M_g	$\sigma_e^2 + p + 2 \left(\frac{1}{p-1} \right) \sum g_i^2$
SCA	p(p-1)/2	S_s	M_s	$\sigma_e^2 + \left(\frac{2}{p(p-1)} \right) \sum \sum s_{ij}^2$
Error	(g-1)(r-1)	S_e	M_e	σ_e^2

The sum of squares due to various sources was calculated as follows:

$$S_g = \frac{1}{p+2} \left[\sum (Y_i + Y_{ii})^2 - \frac{4}{p} Y^2 \dots \right]$$

Sum of square due to sca (S_s) was estimated as:

$$S_s = \sum \sum Y_{ij}^2 - \frac{1}{p+2} \left[\sum (Y_i + Y_{ii})^2 \right] + \frac{2}{(p+1)(p+2)} Y^2$$

Where,

p = Number of parents

g =Number of progenies

S_g =Sum of squares due to general combining ability

S_s = Sum of squares due to specific combining ability

Y_i = Array totals of ith parent

Y_{ii} = Mean value of ith parent

Y = Grant total, parents and half diallel matrix

Y_{ij} = Mean value of ij^{th} cross

M_e' = Error mean square in the analysis of the experimental design (R.B.D) M_e/r

M_s = Mean sum of square of sca

M_g = Mean sum of square of gca

r = Number of replications,

M_e was used for calculation of variance ratio (F) as a test of gca and sca mean squares

3.8.8.2 Genetic component of variance

Variance due to gca (g_i^2) = $1/p + 2 (M_g - M_s)$

Variance due to sca (S_{ij}^2) = $M_s - M_e'$

Where,

g_i^2 = Variance due to gca

S_{ij}^2 = Variance due to sca

M_g = Mean sum of square of gca

M_e' = Error mean square in the analysis of the experimental design (R.B.D) M_e/r

p = Number of parents

3.8.8.3 Estimates of general and specific combining ability effects

The gca and sca effects were calculated by applying the following formulae

gca effect $g_i = 1/(p+2) [(Y_{i.} + Y_{.i}) - 2/p Y_{..}]$

sca effect $S_{ij} = Y_{ij} - 1/(p+2) [Y_{i.} + Y_{.i} + Y_{.j} + Y_{jj}] + 2 / (p+1) (p+2) Y_{..}$

Where,

$Y_{i.} + Y_{ii} = \text{Total of } i^{\text{th}} \text{ array} + \text{mean value of } i^{\text{th}} \text{ parent}$

$Y_{.j} + Y_{jj} = \text{Total of } j^{\text{th}} \text{ array} + \text{mean value of } j^{\text{th}} \text{ parent}$

The estimation of standard errors of general combining ability and specific combining ability effects were obtained as under:

$$\text{S.E. for gca effect of parents } (g_i) = \sqrt{\frac{(p-1)}{p(p+2)} \sigma_e^2}$$

(to test individual gca effect)

$$\text{S.E. for sca effect of hybrids } (s_{ij}) = \sqrt{\frac{p(p-1)}{(p+1)(p+2)} \sigma_e^2}$$

(to test individual sca effect)

$$\text{S.E. } (g_i - g_j) = \sqrt{\frac{2\sigma_e^2}{p+2}}$$

(to test the difference between two gca effects)

$$\text{S.E. } (S_{ij} - S_{ik}) = \sqrt{\frac{2\sigma_e^2}{p+2}}$$

(to test the difference between sca of the same array or column)

$$\text{S.E. } (S_{ij} - S_{ik}) = \sqrt{\frac{2\sigma_e^2}{p+2}}$$

(to test the sca of any two crosses)

Where,

p= Number of parents

σ_e^2 = Error mean square (Me)

Each gca and sca effects were subjected to “t” test for testing of significance

Since error degree of freedom are greater than 30, the value of calculated “t” is regarded as significant if it exceeds 1.96 and 2.58 at 5 percent and 1 percent levels of significance, respectively.

Alternatively, gca and sca effects were compared with critical difference calculated by following formula:

$$C.D. (g_i) = S.E. (g_i) \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

$$C.D (s_{ij}) = S.E. (s_{ij}) \times \text{table } t_{0.05} \text{ and } t_{0.01}$$

Predictability ratio = $\sigma^2 A / (\sigma^2 A + \sigma^2 D)$, where, $\sigma^2 A$ is the additive variance and $\sigma^2 B$ is the dominance variance. If the value of predictability ratio is greater than 0.5 for any trait, it is considered to be high and it indicates predominance of additive gene action for the said trait. If the predictability ratio is equal to or near to 0.5, it is considered to be moderate and it indicates predominance of both additive and dominance gene action whereas, a predictability ratio less than 0.5 indicates predominance of non-additive gene action Baker (1978).

3.8.8.3 Graphical analysis

F₁ values were set out in the diallel tables and crosses were arranged in arrays. The statistics like variance (Vr) of the family means with an array and covariance (Wr) of these means with no non-recurrent parents were calculated from each diallel table.

Genetic parameters	Symbols	Formulae
Environment variance	E	{(ESS+RSS)/Edf + Rdf}/nR

Additive variance	D	VOLO1-E
Variation due to dominant effect of genes	H1	VOLO1-4WOLO1+4V1L1- E (3n-2/n)
Variation due to dominant effect of gene correlated with gene distribution	H2	4V1L1-4VOL1-2E
Over all dominant effect of heterozygous loci	h2	4 (ML1-MLO) ² - 4(n-1) E / n ²
Relative frequency of dominant to recessive alleles	F	(H1 / D) ½
Mean degree of dominance		H2 / 4H1
Proportion of genes with positive and negative effect in the parents	KD/KR	(4DH1) ½ + F/(4DH1)- ½ F
Proportion of dominant and recessive genes in the parents		
The number of groups of gene which control the character and exhibit dominance		h2/H2
Narrow sense heritability	h2 _{ns}	½ D+ ½ H1-½ H2-½F/½D+ ½ H1- ¼

		H ³ -½F+E1
--	--	-----------------------

This can be presented as:

Variance of family means with an array

$$\text{Var (Vr)} = [\sum x^2 - (\sum x)^2/n] / (n-1)$$

Covariance of these means with non-recurrent parent

$$\text{Var (Wr)} = [\sum xy - (\sum x \cdot \sum y)/n] / n-1$$

Parabola

By plotting covariance (Wr) of each array against its variance (Vr), information on gene action, diversity among parents, presence or absence of epistasis, degree of dominance and distribution of dominant and recessive genes among the parents was obtained. The limiting parabola was constructed on the basis of the formula $Wr^2 = Vr \cdot Vp$ i.e by plotting $Vr \cdot (Wr \times Vr)$ points. The corresponding values for Wri were calculated for all observed Vri values using the formula.

$$Wri = (Vri \times VOLO)^{1/2}$$

The different arrays were fitted within the limits of the parabola using the individual variance and covariance as their limiting points. Array nearest to the point of origin possessed most dominant genes, while the array that lay the farthest, possessed most recessive genes and the intermediate position showed the presence of both dominant and recessive genes in the array.

The slope of the regression lines

The regression line was calculated from the mean of variance (V_r) and the mean of covariance (W_r). The expected W_{ri} values were calculated by the formula.

$$W_{rei} = \bar{W}_r + b\bar{V}_r + b\bar{V}_{ri} = \bar{W}_r - \bar{V}_r(b = 1)$$

The point of interception of the regression line with W_r ordinate was determined as

$$A = W_r - bV_r$$

The slope and the position of the regression line were fitted to the array points. If the line of a unit slope ($b=1$) passed through the origin then complete dominance was indicated. In case, it cut the axis below the origin, there was over dominance and if it touched the axis above the origin, it indicated partial dominance. The position of the points on the regression line indicated the distribution of the dominant and recessive genes among the parents.

3.8.10 Estimation of Heterosis

Heterosis was suggested by Mather and Jinks (1971). Heterosis expressed as percentage increase or decrease of F_1 's over better parent and mid parent was calculated using following formula:

$$\text{Heterosis (\% over better parent)} = \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100$$

$$\text{Heterosis (\% over mid parent)} = \frac{\bar{F}_1 - \bar{MP}}{\bar{MP}} \times 100$$

Where,

\bar{F}_1 = mean value of F_1

BP = mean value of better parent

MP = mean value of mid parent

Test of significance of heterosis

Test of significance for heterosis was done following Bitzer et al., (1967).

$$SE_1 = \frac{\sqrt{3MSe}}{2r}$$

$$SE_2 = \frac{\sqrt{2MSe}}{r}$$

Where,

SE₁ = Standard error of heterosis over mid parent

SE₂ = Standard error of heterosis over better parent


MSe = Error mean square of ANOVA

r = Number of replications

t value for Relative Heterosis = [(F1-MP)/SE₁]

t value for Heterobeltiosis = [(F1-BP)/ SE₂]

t value for Standard Heterosis = [(F1-SV)/SE₂]



**RESULT AND
DISCUSSION**

The present investigation entitled “Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]” was carried out with 8 parent and 28 F₁s developed from half diallel mating (excluding reciprocals). Observations were recorded for nine yield characters (days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliqua plant⁻¹, seed siliqua⁻¹, height upto first fruiting branch, plant height, seed yield plant⁻¹ and 1000 seed weight), nine physiological characters (oil content, percentage of membrane stability index, percentage of excised leaf water loss, percentage of relative water content, canopy temperature depression, proline content, chlorophyll a, chlorophyll b and total chlorophyll b) and six aphid related characters (water content of aphid probed twig, water content of aphid uninfested twig, water content of aphid, percentage of water differential between aphid probed twig and aphid itself, aphid count and penetration force) both parents and F₁ for combining ability and heterosis studies. Screening for aphid resistance was done for both parents and F₁s based on lab-based counting of aphid and the correlation as well path analysis of aphid count and its influencing characters in Indian mustard was studied. The data recorded for these characters were subjected to the statistical and biometrical analysis and the results obtained are described under the following heads:

4.1 Analysis of variance

Before subjecting the data for analysis of various genetic parameters, the analysis of variance (ANOVA) was estimated to test the significance of variance among the 71 diversified genotypes of mustard for all the 11 seed yield and its attributing characters namely plant height, height upto first fruiting branch, days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliquae⁻¹, 1000 seed weight, aphid count, penetration

force and seed yield plant⁻¹. The analysis of variance, as given in Table 4.1, revealed that the mean sum of squares was highly significant for all the characters studied.

Analysis of variance of 71 genotypes of mustard revealed significant differences among the genotypes for all the eleven characters studied *viz*; Plant height (cm), height upto first fruiting branch (cm), days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹ (cm), seeds siliqua⁻¹, 1000 seed weight (g), penetration force (kpasascal), aphid count (% incidence) and seed yield plant⁻¹ (g).

4.2 Estimation of genetic parameters

4.2.1 Phenotypic coefficient of variation and genotypic coefficient of variation

The mean, range and estimates of genetic parameters for the 11 characters are presented in Table 4.2. The values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated as per the method suggested by Sivasubramanian and Madhavamenon (1973). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low (<10%) for plant height (9.13 and 9.18) and seeds per siliqua (4.34 and 7.78).

Moderate GCV and PCV (10-25%) were observed for days to 50% flowering (10.32 and 10.51), primary branches plant⁻¹ (21.06 and 23.83), secondary branches plant⁻¹ (21.05 and 22.99), siliquae per plant (21.75 and 23.59) and 1000 seed weight (20.39 and 20.54).

High GCV and PCV (>25%) for height up to first fruiting branch (31.07 and 31.71), aphid count (28.69 and 49.19) and penetration force (25.50 and 34.05). It was interesting to note that seed yield plant⁻¹ had moderate GCV (20.55) but high PCV (32.89).

4.2.2 Heritability

The estimates of heritability in broad sense for the eleven characters under study are shown in Table 4.2. The estimates of heritability were categorized into 3 major groups, *i.e.*

Table 4.1 Analysis of variance (ANOVA) for eleven characters in Indian mustard (*Brassica juncea*)

Sources of variation	df	Plant height (cm)	Height upto first fruiting branch (cm)	Days to 50 % flowering	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seeds per siliqua	1000 seed weight (g)	Aphid count (% incidence)	Penetration force (Kpascal)	Seed yield per plant (g)
Replication	2	2.71	14.36	0.33	0.62	4.77	1091.91	0.31	1.45	7.82	321.78	75.10
Treatment	70	727.92**	999.71**	67.10**	2.37**	12.44**	4181.39**	1.66**	2.90**	42.40**	2069.92**	16.71**
Error	140	2.82	13.64	0.85	0.20	0.75	213.49	0.70	0.015	16.65	428.39	5.72

** significant at 1% level of probability

Table 4.2 Genetic parameters for eleven characters in Indian mustard (*Brassica juncea*)

Sl. No.	Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (broad sense) (%)	Genetic advance as percent of mean
			Lowest	Highest				
1	Plant height (cm)	170.25	125.67	212.93	9.13	9.18	98.86	18.70
2	Height upto first fruiting branch (cm)	58.35	21.33	153.00	31.07	31.71	96.02	62.72
3	Days to 50 % flowering	45.55	35.00	57.00	10.32	10.51	96.30	20.86
4	Primary branches per plant	4.04	2.33	7.13	21.07	23.83	78.13	38.36
5	Secondary branches per plant	9.38	3.47	15.20	21.05	22.99	83.84	39.71
6	Siliquae per plant	166.81	72.27	252.40	21.75	23.59	85.05	41.33
7	Seeds per siliqua	12.99	10.60	14.93	4.34	7.78	31.12	4.99
8	1000- seed weight(g)	4.81	2.20	9.07	20.38	20.55	98.46	41.67
9	Aphid count (% incidence)	10.21	4.35	25.47	28.69	49.19	34.01	34.46
10	Penetration force (kpascal)	91.74	46.93	192.70	25.50	34.05	56.09	39.34
11	Seed yield per plant (g)	9.31	3.19	15.50	20.55	32.89	39.03	26.44

high heritability (> 60 %), moderate heritability (30 to 60%), and low heritability (<30%). The characters exhibiting high heritability for plant height (98.86), height upto first fruiting branch (96.02), days to 50% flowering (96.30), primary branches plants⁻¹ (78.13), secondary branches plant⁻¹ (83.84), siliquae plant⁻¹ (85.05) and 1000 seed weight (98.46).

Moderate heritability for seeds siliqua⁻¹ (31.12), aphid count (34.01), penetration force (56.09) and seed yield plant⁻¹ (39.03).

4.2.3 Genetic advance as percentage of mean

The data of genetic advance as percentage of mean are presented in Table 4.2. The estimates of genetic advance were categorized into three major groups, *i.e.* high genetic advance (above 20 per cent), moderate genetic advance (10-20%), low genetic advance (less than 10 per cent). Genetic advance as percentage of mean was exhibited low (<10%) by seeds per siliquae (4.99). Moderate (10-20%) for plant height (18.70); high (> 20%) for height up to first fruiting branch (62.72), days to 50% flowering (20.86), primary branches plant⁻¹ (38.36), secondary branches plant⁻¹ (39.71), siliquae per plant (41.33), 1000 seed weight (41.67), aphid count (34.46), penetration force (39.33) and seed yield plant⁻¹ (26.44).

The characters height up to first fruiting branch (96.02 and 62.72), primary branches plant⁻¹ (78.13 and 38.36), secondary branches plant⁻¹ (83.84 and 39.71), siliquae plant⁻¹ (85.05 and 41.33) and 1000 seed weight (98.46 and 41.67) expressed high heritability along with high genetic advance as percentage of mean.

4.3 Character association analysis

To analyze the extent of the mutual relationship among different characters, the study of correlation coefficient would be quite beneficial in formulating a suitable selection criterion. This information may be used in predicting the correlated response to direct selection as well as in practicing indirect selection. In the present investigation, the estimates

Table 4.3 Association (correlation) between the yield and its attributing characters at genotypic level in Indian mustard (*Brassica juncea*)

Characters	Height upto first fruiting branch (cm)	Days to 50 % flowering	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seeds per siliqua	1000- seed weight (g)	Aphid count (% incidence)	Penetration force (Kpascal)	Seed yield per plant (g)
Plant height (cm)	0.715*	0.625*	0.244*	0.014	0.181	-0.138	-0.162	-0.219*	-0.397*	0.002
Height upto first fruiting branch (cm)		0.571*	0.301*	-0.088	0.008	-0.149	-0.236*	-0.200*	-0.280*	-0.461*
Days to 50 % flowering			0.070	-0.048	0.127	-0.108	0.069	-0.298*	-0.528*	0.085
Primary branches per plant				0.303*	-0.072	-0.337	-0.058	0.153	-0.197*	-0.215*
Secondary branches per plant					0.501*	-0.191	-0.135	-0.217*	-0.244*	0.354*
Siliquae per plant						0.066	0.093	-0.060	-0.112	0.560*
Seeds per siliqua							0.140	-0.006	0.137	0.077
1000- seed weight (g)								0.178	-0.133	0.152
Aphid count (% incidence)									0.412*	-0.199*
Penetration force (kpascal)										0.116

* significant at 5% level of probability

of correlation coefficients were worked out at the genotypic level for all the eleven characters as presented in Table 4.3.

In genotypic correlation analysis, it was found that the significant positive correlation of seed yield was observed with secondary branches plant⁻¹ and siliquae plant⁻¹ while plant height had a positive association with height up to first fruiting branch, days to 50% flowering (0.625) and primary branches plant⁻¹ (0.244). Height up to first fruiting branch had a positive association with days to 50% flowering (0.571) and primary branches plant⁻¹ (0.301). Primary branches plant⁻¹ was positively associated with only one character *i.e.* secondary branches plant⁻¹ (0.303) whereas secondary branches plant⁻¹ was positively associated with siliquae plant⁻¹ (0.501) and seed yield plant⁻¹ (0.354). The siliquae plant⁻¹ had a positive association with seed yield plant⁻¹ (0.560). Aphid count had a positive association with penetration force (0.412) which is quite contradictory to the natural situation where the aphid count should decrease with an increase in penetration force as increased penetration force reduces the suction of sap from the twigs. In the overall assessment of the character association analysis, it was found that secondary branches plant⁻¹ and siliquae plant⁻¹ had a positive association with seed yield plant⁻¹.

It was also observed that plant height (-0.219; -0.397), height upto first fruiting branch (-0.200; -0.280) and days to 50% flowering (-0.298; -0.528) had a negative association with aphid count and penetration force. Secondary branches plant⁻¹ showed a significant negative association with penetration force. Height up to first fruiting branch had a negative association with 1000 seed weight (-0.236), aphid count (-0.200), penetration force (-0.280) and seed yield plant⁻¹ (-0.461). Primary branches plant⁻¹ was negatively associated with seeds siliqua⁻¹ (-0.337), penetration force (-0.197) and seed yield plant⁻¹ (-0.215). Aphid count was negatively associated with seed yield plant⁻¹ (-0.199) while seed yield plant⁻¹ itself was negatively correlated with height upto first fruiting branch (-0.461), primary branches plant⁻¹ (-0.215) and

aphid count (-0.199). It was observed that seed yield was negatively correlated with height up to first fruiting branch, primary branches plant⁻¹ and aphid count. From the correlation study involving the present set of 71 mustard genotypes, a positive correlation (significant) with seed yield was observed only in the case of secondary branches plant⁻¹ and siliquae plant⁻¹.

4.4 Path coefficient analysis

Even though the correlation coefficient is quite helpful in determining the components of complex characters like yield, however, an exact picture of the relative importance of the direct and indirect influence of each component character is not provided by such studies. Path coefficient analysis (Sewall Wright, 1921; Dewey and Lu, 1959) under such circumstances plays an important role in the partitioning of the correlation coefficient into direct and indirect effects of a set of independent variables on the dependent variable and determines the component characters on which selection can be based for improvement in yield.

In the present investigation, the path coefficient analysis was estimated among the eleven characters Table 4.4. Correlation of height up to first fruiting branch with seed yield plant⁻¹ was negative and its direct effect (-0.983) was also negative. But the coefficient of correlation was more than the direct effect. This indicates the high positive indirect effect of height upto the first fruiting branch on seed yield via plant height and days to 50% flowering, is nullified by the high negative direct effect of height upto the first fruiting branch on seed yield. So, this character can never help to improve seed yield in the given set of 71 mustard genotypes.

Primary branches plant⁻¹ had a negative correlation with seed yield plant⁻¹ although its direct effect (0.086) was positive and low. But the direct effect was more than the coefficient of correlation. This indicates that the indirect negative effects through other attributes *i.e.* height up to first fruiting branch, siliquae plant⁻¹, 1000 seed weight, aphid count and penetration

force have enhanced the negative relationship of primary branches per plant with seed yield per plant.

Association of siliquae plant⁻¹ with seed yield plant⁻¹ was positive and its direct effect (0.407) was also high and positive. But the coefficient of correlation was more than the direct effect. This indicates that the indirect positive effects of siliquae plant⁻¹ are supplemented through plant height, days to 50% flowering, secondary branches plant⁻¹, 1000 seed weight and aphid count, of which the *via* effect through plant height was highest. The highest positive direct effect on yield was of penetration force followed by days to 50% flowering. However, penetration force had no association with seed yield and it was evident from the low coefficient of correlation with seed yield (0.116) which was mainly due to the negative effects of penetration force as seed yield via plant height, days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seeds siliqua⁻¹, 1000 seed weight and aphid count. This negative effect could be the reason behind the positive correlation of penetration force with aphid count and subsequently not having any association with seed yield. An interesting finding here is that the very high direct effect of penetration force is nullified by the negative effects via the other characters. Hence for the present set of genotypes, the emphasis for selection cannot be laid on penetration force.

Secondary branches plant⁻¹ had a positive correlation with seed yield plant⁻¹ and its direct (0.111) effect was also positive, although low and was less than the coefficient of correlation. This indicated that the indirect positive effects are more than indirect negative effects and the former have supplemented the positive association of secondary branches plant⁻¹ with seed yield plant⁻¹. The indirect positive effect of secondary branches plant⁻¹ on seed yield was observed *via* plant height, height upto first fruiting branch, primary branches plant⁻¹, siliquae plant⁻¹, seeds siliqua⁻¹ and aphid count.

The highest direct negative effect was of the height upto first fruiting branch followed by aphid count. Aphid count had a negative correlation with seed yield per plant and its direct effect (-0.345) was also negative. But the coefficient of correlation was more than the direct effect. This indicated that the indirect negative effect of aphid count via other attributes i.e., plant height, days to 50% flowering, secondary branches plant⁻¹ and siliquae plant⁻¹ have enhanced the negative relationship of aphid count with seed yield plant⁻¹.

4.5 Ranking of mustard genotypes concerning yield parameters and aphid infestation

An overall ranking of 71 genotypes of mustard was done for eleven characters (Table 4.5), out of which nine were yield attributing characters and the remaining two were aphid count and penetration force, as per the rescaling index method suggested by Iyenger and Sudarshan (1982). From the rescaling index value, the ranking was done for 71 genotypes according to their rescaled index value (Roy *et al.* 2017). The genotypes which gave the same index value were given the same rank. It showed that based on all the eleven characters including aphid count, the genotype PRD-2013-9 was the best and had the highest rescaled index value of 6.62 and ranked first followed by the genotypes RH-0923 having rescaled index value of 6.41 (rank-2) which was closely followed by another genotype RGN-389 which had rescaled index value of 6.27 (rank 3). In this way, all the 71 genotypes were ranked according to their rescaled index values and the best among them could be selected.

4.6 Clustering of genotypes

The chi-square test indicated that the population of the mustard was divergent and therefore the D² analysis was carried out. The clustering pattern of the genotypes has been presented in Table 4.6. The seventy-one genotypes of mustard when subjected to D² analysis, using eleven yield attributing characters revealed that seven clusters were formed. From the pattern of clustering, it could be inferred that sufficient divergence was present to enable the formation of individual clusters. The clustering pattern could be utilized in the selection of

Table 4.4 Direct (diagonal) and indirect (off-diagonal) effects of different attributing characters on seed yield in Indian mustard (*Brassica juncea*)

Characters	Plant height (cm)	Height upto first fruiting branch (cm)	Days to 50 % flowering	Primary branches per plant	Secondary branches per plant	Siliquae per plant	Seeds per siliqua	1000- seed weight (g)	Aphid count (% incidence)	Penetration force (Kpascal)	Correlation with seed yield per plant (g)
Plant height (cm)	0.450	-0.703	0.297	0.021	0.002	0.074	0.002	-0.012	0.076	-0.204	0.002
Height upto first fruiting branch (cm)	0.322	-0.983	0.271	0.026	-0.010	0.003	0.002	-0.018	0.069	-0.144	-0.461*
Days to 50 % flowering	0.281	-0.561	0.475	0.006	-0.005	0.052	0.002	0.005	0.103	-0.272	0.085
Primary branches per plant	0.109	-0.296	0.033	0.086	0.034	-0.029	0.005	-0.004	-0.052	-0.101	-0.215*
Secondary branches per plant	0.006	0.086	-0.022	0.026	0.111	0.204	0.003	-0.010	0.075	-0.125	0.354*
Siliquae per plant	0.081	-0.008	0.060	-0.006	0.056	0.407	-0.001	0.007	0.021	-0.058	0.560*
Seeds per siliqua	-0.062	0.147	-0.051	-0.029	-0.021	0.027	-0.016	0.010	0.002	0.071	0.077
1000- seed weight (g)	-0.073	0.232	0.032	-0.005	-0.015	0.038	-0.002	0.074	-0.061	-0.068	0.152
Aphid count (% incidence)	-0.098	0.196	-0.141	0.013	-0.024	-0.024	0.0001	0.013	-0.345	0.021	-0.199*
Penetration force (kpascal)	-0.178	0.276	-0.251	-0.017	-0.027	-0.045	-0.002	-0.010	-0.142	0.514	0.116

* Significant at 5% level of probability; Residual values = 0.344

Table 4.5 Mean performance of the Indian mustard (*Brassica juncea*) genotypes and their ranking based on rescaled index value as suggested by Iyengar and Sudarshan (1982)

Sl. No.	Genotypes	Plant height (cm)		Height upto first fruiting branch (cm)		Days to 50 % Flowering		Primary branches per plant		Secondary branches per plant		Siliquae per plant		Seeds per siliqua	
		x	Rescaled Index value (A) = (x-Min)/(Max-Min)	x	Rescaled Index value (B) = (x-Min)/(Max-Min)	x	Rescaled Index value (C) = (x-Min)/(Max-Min)	x	Rescaled Index value (D) = (x-Min)/(Max-Min)	x	Rescaled Index value (E) = (x-Min)/(Max-Min)	x	Rescaled Index value (F) = (x-Min)/(Max-Min)	x	Rescaled Index value (G) = (x-Min)/(Max-Min)
1	B-85(Seeta)	140.87	0.17	24.40	0.02	36.00	0.05	4.47	0.45	11.13	0.65	210.40	0.77	13.00	0.55
2	RW-351(Bhagarathi)	143.60	0.21	32.00	0.08	37.00	0.09	4.13	0.38	9.80	0.54	191.93	0.66	14.40	0.88
3	RW-85-59(Sarna)	136.13	0.12	28.60	0.06	35.00	0.00	4.27	0.40	13.07	0.82	149.60	0.43	13.27	0.62
4	RW-4C-6-3	170.67	0.52	39.73	0.14	38.00	0.14	4.27	0.40	11.67	0.70	186.20	0.63	12.53	0.45
5	NPJ-194	125.67	0.00	35.07	0.10	36.00	0.05	3.60	0.26	11.60	0.69	114.13	0.23	13.27	0.62
6	TM-276	185.27	0.68	56.00	0.26	45.00	0.45	3.93	0.33	9.13	0.48	157.93	0.48	12.73	0.49
7	Rohini(SC)	163.73	0.44	69.47	0.37	46.00	0.50	4.13	0.38	9.93	0.55	151.33	0.44	10.60	0.00
8	KMR-15-4	166.53	0.47	54.33	0.25	46.00	0.50	4.53	0.46	11.27	0.66	252.40	1.00	13.07	0.57
9	PR-2012-9	185.07	0.68	73.87	0.40	51.00	0.73	4.93	0.54	9.80	0.54	122.07	0.28	14.13	0.82
10	Divya-88	181.20	0.64	55.00	0.26	46.00	0.50	4.60	0.47	14.07	0.90	232.33	0.89	12.93	0.54
11	RL-JEB-52	178.53	0.61	80.20	0.45	45.00	0.45	4.27	0.40	9.40	0.51	211.73	0.77	13.53	0.68
12	Kranti-NC	179.60	0.62	71.60	0.38	46.00	0.50	4.67	0.49	10.27	0.58	175.47	0.57	13.27	0.62
13	DRMRIJ-15-85	172.13	0.53	75.60	0.41	47.00	0.55	4.07	0.36	10.80	0.62	168.33	0.53	12.27	0.38
14	RH-1202	179.93	0.62	80.47	0.45	48.00	0.59	4.20	0.39	10.80	0.62	196.87	0.69	12.80	0.51
15	NPJ-196	176.07	0.58	75.47	0.41	47.00	0.55	4.33	0.42	9.60	0.52	225.67	0.85	11.87	0.29
16	RMM-09-10	179.40	0.62	60.67	0.30	47.00	0.55	3.60	0.26	8.20	0.40	175.20	0.57	13.20	0.60
17	JMM-927-RC	162.80	0.43	50.73	0.22	45.00	0.45	3.73	0.29	9.00	0.47	219.33	0.82	14.40	0.88
18	RRN-871	176.27	0.58	57.40	0.27	46.00	0.50	2.73	0.08	9.60	0.52	227.73	0.86	12.93	0.54
19	KM-126	177.87	0.60	59.80	0.29	47.00	0.55	2.40	0.01	9.87	0.55	154.13	0.45	13.13	0.59
20	SKM-1313	177.27	0.59	73.20	0.39	46.00	0.50	2.47	0.03	11.73	0.70	209.47	0.76	13.00	0.55
21	RB-77	161.80	0.41	70.20	0.37	49.00	0.64	2.33	0.00	4.80	0.11	72.27	0.00	12.80	0.51
22	DRMR-15-5	164.00	0.44	55.60	0.26	47.00	0.55	2.87	0.11	10.47	0.60	189.93	0.65	12.47	0.43
23	KMR-53-3	161.40	0.41	49.73	0.22	47.00	0.55	2.93	0.13	11.60	0.69	207.20	0.75	12.60	0.46
24	RL-JEB-84	162.13	0.42	44.13	0.17	43.00	0.36	2.60	0.06	9.13	0.48	206.33	0.74	12.53	0.45
25	Ganga	173.00	0.54	56.80	0.27	50.00	0.68	3.33	0.21	13.00	0.81	192.07	0.67	12.80	0.51
26	RGN-73-JC	165.93	0.46	61.60	0.31	49.00	0.64	3.47	0.24	9.53	0.52	189.13	0.65	12.80	0.51
27	RH-1209	179.00	0.61	64.73	0.33	47.00	0.55	3.53	0.25	9.53	0.52	198.07	0.70	13.40	0.65
28	PR-2012-12	177.40	0.59	65.40	0.33	50.00	0.68	3.53	0.25	7.73	0.36	159.33	0.48	12.67	0.48
29	RGN-385	172.33	0.53	62.80	0.31	46.00	0.50	3.27	0.20	8.80	0.45	165.07	0.52	12.67	0.48
30	NPJ-195	167.13	0.48	52.73	0.24	43.00	0.36	3.73	0.29	8.40	0.42	201.27	0.72	12.73	0.49
31	Maya-C	147.53	0.25	56.07	0.26	42.00	0.32	4.47	0.45	9.13	0.48	136.40	0.36	13.20	0.60
32	SKJM-05	141.80	0.18	47.93	0.20	43.00	0.36	4.53	0.46	9.53	0.52	174.67	0.57	13.00	0.55
33	SVJ-64	174.87	0.56	60.80	0.30	47.00	0.55	3.67	0.28	8.00	0.39	142.53	0.39	13.73	0.72
34	Sitara-Sreenagar	179.40	0.62	67.20	0.35	50.00	0.68	5.00	0.56	9.73	0.53	221.67	0.83	12.40	0.42
35	RH-0923	171.93	0.53	65.47	0.34	47.00	0.55	5.00	0.56	11.80	0.71	201.67	0.72	14.93	1.00

Table 4.5 Continued (Genotypes 1 to 35)

Sl. No.	Genotypes	1000 seed weight (g)		Aphid count		Penetration force (kpasca)		Seed yield per plant (g)		Total of the rescaled values (L)	Ranking based on
		x	Rescaled Index value (H) = (x-Min)/(Max-Min)	x	Rescaled Index value (I) = (Max-x)/(Max-Min)	x	Rescaled Index value (J) = (x-Min)/(Max-Min)	x	Rescaled Index value (K) = (x-Min)/(Max-Min)	L=(A+B+C+D+E+F+G+H+I+J)+K)	
1	B-85(Seeta)	3.27	0.16	10.91	0.69	152.57	0.72	13.51	0.84	5.07	37
2	RW-351(Bhagarathi)	3.70	0.22	15.93	0.45	115.25	0.47	11.30	0.66	4.63	53
3	RW-85-59(Sarna)	3.87	0.24	11.98	0.64	110.83	0.44	6.79	0.29	4.05	66
4	RW-4C-6-3	3.47	0.18	9.51	0.76	82.80	0.25	11.57	0.68	4.84	48
5	NPJ-194	4.77	0.37	12.01	0.64	141.45	0.65	10.20	0.57	4.18	65
6	TM-276	4.27	0.30	15.96	0.45	192.70	1.00	11.35	0.66	5.60	19
7	Rohini(SC)	4.97	0.40	15.39	0.48	93.15	0.32	8.45	0.43	4.29	62
8	KMR-15-4	4.67	0.36	8.44	0.81	103.20	0.39	10.71	0.61	6.07	6
9	PR-2012-9	4.07	0.27	9.36	0.76	88.95	0.29	9.94	0.55	5.85	11
10	Divya-88	4.27	0.30	9.71	0.75	82.80	0.25	8.58	0.44	5.93	9
11	RL-JEB-52	5.00	0.41	11.60	0.66	84.67	0.26	7.82	0.38	5.57	21
12	Kranti-NC	5.03	0.41	8.57	0.80	84.30	0.26	10.33	0.58	5.80	13
13	DRMRIJ-15-85	5.03	0.41	9.17	0.77	107.43	0.42	9.39	0.50	5.50	25
14	RH-1202	4.57	0.34	9.25	0.77	93.47	0.32	9.85	0.54	5.85	12
15	NPJ-196	4.57	0.34	10.51	0.71	78.62	0.22	9.41	0.51	5.39	27
16	RMM-09-10	5.47	0.48	8.91	0.78	87.17	0.28	9.80	0.54	5.37	30
17	JMM-927-RC	5.47	0.48	10.47	0.71	90.38	0.30	9.50	0.51	5.56	23
18	RRN-871	4.70	0.36	8.64	0.80	77.95	0.21	14.14	0.89	5.63	16
19	KM-126	4.67	0.36	5.50	0.95	77.68	0.21	9.58	0.52	5.07	38
20	SKM-1313	4.40	0.32	7.66	0.84	90.53	0.30	10.97	0.63	5.63	15
21	RB-77	4.07	0.27	7.13	0.87	69.52	0.15	5.81	0.21	3.55	71
22	DRMR-15-5	5.07	0.42	8.65	0.80	77.57	0.21	6.47	0.27	4.73	51
23	KMR-53-3	4.97	0.40	8.48	0.80	93.28	0.32	11.26	0.66	5.38	29
24	RL-JEB-84	4.67	0.36	7.47	0.85	116.50	0.48	10.41	0.59	4.96	42
25	Ganga	4.67	0.36	7.68	0.84	80.90	0.23	8.98	0.47	5.59	20
26	RGN-73-JC	4.63	0.35	6.37	0.90	82.82	0.25	9.36	0.50	5.32	31
27	RH-1209	4.97	0.40	25.47	0.00	95.15	0.33	8.76	0.45	4.78	49
28	PR-2012-12	4.17	0.29	7.13	0.87	90.43	0.30	6.66	0.28	4.92	45
29	RGN-385	4.67	0.36	5.47	0.95	101.20	0.37	7.77	0.37	5.04	39
30	NPJ-195	4.37	0.32	11.51	0.66	80.28	0.23	7.28	0.33	4.54	54
31	Maya-C	4.67	0.36	10.50	0.71	97.87	0.35	7.40	0.34	4.48	56
32	SKJM-05	9.07	1.00	5.26	0.96	78.10	0.21	9.31	0.50	5.52	24
33	SVJ-64	4.00	0.26	9.99	0.73	89.90	0.29	6.59	0.28	4.75	50
34	Sitara-Sreenagar	4.57	0.34	8.85	0.79	72.28	0.17	11.10	0.64	5.93	8
35	RH-0923	5.13	0.43	8.92	0.78	69.75	0.16	11.13	0.65	6.41	2

Table 4.5 Continued (Genotypes 36 to 71)

Sl. No.	Genotypes	Plant height (cm)		Height upto first fruiting branch (cm)		Days to 50 % flowering		Primary branches per plant		Secondary branches per plant		Siliquae per plant		Seeds per siliqua	
		x	Rescaled Index value (A) = (x-Min)/(Max-Min)	x	Rescaled Index value (B) = (x-Min)/(Max-Min)	x	Rescaled Index value (C) = (x-Min)/(Max-Min)	x	Rescaled Index value (D) = (x-Min)/(Max-Min)	x	Rescaled Index value (E) = (x-Min)/(Max-Min)	x	Rescaled Index value (F) = (x-Min)/(Max-Min)	X	Rescaled Index value (G) = (x-Min)/(Max-Min)
36	DRMR-15-16	147.67	0.25	42.13	0.16	42.00	0.32	3.53	0.25	10.80	0.62	191.73	0.66	13.20	0.60
37	NPJ-198	175.40	0.57	52.73	0.24	46.00	0.50	3.40	0.22	8.80	0.45	164.73	0.51	14.13	0.82
38	JMM-927-RC	183.60	0.66	58.80	0.28	48.00	0.59	4.00	0.35	8.20	0.40	162.20	0.50	13.40	0.65
39	DRMR-15-47	176.13	0.58	55.20	0.26	47.00	0.55	3.53	0.25	8.47	0.43	185.33	0.63	14.07	0.80
40	RGN-389	193.73	0.78	59.13	0.29	51.00	0.73	3.93	0.33	10.73	0.62	176.87	0.58	13.73	0.72
41	RAURD-214	187.47	0.71	61.67	0.31	52.00	0.77	3.53	0.25	8.27	0.41	187.33	0.64	13.53	0.68
42	DRMR-15-14	202.20	0.88	88.67	0.51	48.00	0.59	3.53	0.25	7.40	0.34	174.73	0.57	13.07	0.57
43	DRMR-4001	167.73	0.48	73.47	0.40	41.00	0.27	4.93	0.54	10.53	0.60	140.47	0.38	12.53	0.45
44	RGN-384	179.40	0.62	61.07	0.30	47.00	0.55	4.87	0.53	10.07	0.56	159.87	0.49	12.13	0.35
45	NPJ-197	179.00	0.61	67.13	0.35	47.00	0.55	4.67	0.49	10.00	0.56	142.47	0.39	12.20	0.37
46	RB-81	166.80	0.47	55.20	0.26	46.00	0.50	4.47	0.45	8.73	0.45	113.47	0.23	12.13	0.35
47	NPJ-200	141.47	0.18	21.33	0.00	39.00	0.18	4.67	0.49	10.93	0.64	88.27	0.09	11.80	0.28
48	DRMR-15-9	164.20	0.44	42.67	0.16	40.00	0.23	4.53	0.46	11.40	0.68	128.13	0.31	13.33	0.63
49	KMR-L-15-6	168.73	0.49	45.00	0.18	42.00	0.32	4.27	0.40	10.87	0.63	196.60	0.69	12.13	0.35
50	PRD-2013-9	184.13	0.67	66.47	0.34	53.00	0.82	5.60	0.68	15.20	1.00	201.80	0.72	13.00	0.55
51	DRMRIJ-15-66	183.93	0.67	57.73	0.28	52.00	0.77	4.13	0.38	7.67	0.36	168.33	0.53	12.47	0.43
52	RH-1368	178.53	0.61	49.00	0.21	43.00	0.36	4.20	0.39	9.80	0.54	118.73	0.26	12.73	0.49
53	RH-1325	181.37	0.64	56.93	0.27	50.00	0.68	4.60	0.47	8.87	0.46	128.40	0.31	12.60	0.46
54	RGN-386	191.80	0.76	58.73	0.28	53.00	0.82	4.07	0.36	10.73	0.62	179.40	0.59	12.73	0.49
55	RNWR-09-3	178.07	0.60	48.20	0.20	51.00	0.73	3.80	0.31	10.67	0.61	223.73	0.84	12.87	0.52
56	PRD-2013-2	161.73	0.41	37.67	0.12	48.00	0.59	4.13	0.38	7.60	0.35	166.87	0.53	12.67	0.48
57	RH-749	139.27	0.16	46.27	0.19	44.00	0.41	3.07	0.15	6.53	0.26	163.07	0.50	13.47	0.66
58	GIRIRAJ	166.40	0.47	50.40	0.22	43.00	0.36	2.67	0.07	5.27	0.15	126.93	0.30	13.87	0.75
59	RH-406	169.80	0.51	47.33	0.20	42.00	0.32	3.07	0.15	7.40	0.34	164.67	0.51	13.40	0.65
60	NRCHB-101	175.47	0.57	54.33	0.25	42.00	0.32	7.13	1.00	9.27	0.49	153.27	0.45	12.80	0.51
61	RGIN-73	176.07	0.58	51.60	0.23	42.00	0.32	5.53	0.67	7.47	0.34	152.07	0.44	11.20	0.14
62	DRMR-IJ-31	179.53	0.62	57.33	0.27	41.00	0.27	4.53	0.46	7.53	0.35	125.53	0.30	12.13	0.35
63	NRCHB-101	160.80	0.40	51.87	0.23	47.00	0.55	3.53	0.25	5.87	0.20	134.07	0.34	13.47	0.66
64	DRMR-150-35	152.27	0.30	44.40	0.18	54.00	0.86	3.67	0.28	6.53	0.26	99.87	0.15	13.27	0.62
65	Pusa mustard-25(NPJ 112)	162.47	0.42	47.33	0.20	38.00	0.14	3.87	0.32	7.33	0.33	123.93	0.29	13.53	0.68
66	Pusa mustard26(NPJ 113)	164.60	0.45	56.20	0.26	37.00	0.09	3.80	0.31	6.93	0.30	127.73	0.31	12.80	0.51
67	Pusa mustard27(EJ 17)	186.20	0.69	87.27	0.50	38.00	0.14	4.40	0.43	9.20	0.49	153.60	0.45	14.20	0.83
68	CS 54	154.47	0.33	49.00	0.21	47.00	0.55	4.13	0.38	7.73	0.36	146.07	0.41	13.53	0.68
69	PHR 2	212.93	1.00	153.00	1.00	57.00	1.00	6.20	0.81	8.13	0.40	132.47	0.33	11.87	0.29
70	RL 1359	182.60	0.65	100.20	0.60	54.00	0.86	6.13	0.79	9.40	0.51	136.93	0.36	13.20	0.60
71	Kranti	153.73	0.32	52.67	0.24	42.00	0.32	2.93	0.13	3.47	0.00	113.80	0.23	14.20	0.83

Table 4.5 Continued (Genotypes 36 to 71)

Sl. No.	Genotypes	1000 seed weight (g)		Aphid count (% incidence)		Penetration force (kpasal)		Seed yield per plant (g)		Total of the rescaled values (L) L=(A+B+C+D+E+F+G+H+I+J+K)	Ranking based on the total rescaled value*
		x	Rescaled Index value (H) = (x-Min)/(Max-Min)	x	Rescaled Index value (I) = (Max-x)/(Max-Min)	x	Rescaled Index value (J) = (x-Min)/(Max-Min)	x	Rescaled Index value (K) = (x-Min)/(Max-Min)		
36	DRMR-15-16	4.47	0.33	8.09	0.82	117.52	0.48	13.18	0.81	5.32	31
37	NPJ-198	5.57	0.49	8.80	0.79	85.45	0.26	11.97	0.71	5.57	22
38	JMM-927-RC	4.97	0.40	7.39	0.86	61.97	0.10	10.42	0.59	5.39	27
39	DRMR-15-47	5.07	0.42	6.93	0.88	121.43	0.51	12.27	0.74	6.03	7
40	RGN-389	5.17	0.43	7.78	0.84	61.22	0.10	13.70	0.85	6.27	3
41	RAURD-214	4.93	0.40	7.05	0.87	80.85	0.23	15.50	1.00	6.27	4
42	DRMR-15-14	4.50	0.33	4.35	1.00	97.78	0.35	8.01	0.39	5.78	14
43	DRMR-4001	4.27	0.30	4.43	1.00	93.25	0.32	7.00	0.31	5.04	40
44	RGN-384	4.93	0.40	7.90	0.83	87.43	0.28	10.17	0.57	5.47	26
45	NPJ-197	3.77	0.23	6.78	0.89	71.02	0.17	9.95	0.55	5.14	36
46	RB-81	4.67	0.36	6.41	0.90	46.93	0.00	8.75	0.45	4.42	59
47	NPJ-200	4.27	0.30	7.87	0.83	82.30	0.24	9.05	0.48	3.71	70
48	DRMR-15-9	4.53	0.34	9.58	0.75	72.38	0.17	6.21	0.25	4.42	60
49	KMR-L-15-6	5.37	0.46	12.00	0.64	55.28	0.06	11.49	0.67	4.90	46
50	PRD-2013-9	4.47	0.33	6.59	0.89	52.60	0.04	10.29	0.58	6.62	1
51	DRMRIJ-15-66	4.07	0.27	9.14	0.77	82.93	0.25	8.87	0.46	5.17	34
52	RH-1368	3.97	0.26	10.38	0.71	51.67	0.03	10.13	0.56	4.43	58
53	RH-1325	5.07	0.42	10.72	0.70	54.77	0.05	8.53	0.43	4.90	46
54	RGN-386	4.77	0.37	10.10	0.73	51.67	0.03	9.89	0.54	5.61	17
55	RNWR-09-3	8.83	0.97	16.62	0.42	51.67	0.03	10.94	0.63	5.86	10
56	PRD-2013-2	4.07	0.27	9.79	0.74	105.13	0.40	11.47	0.67	4.94	43
57	RH-749	5.30	0.45	19.34	0.29	96.62	0.34	7.00	0.31	3.73	68
58	GIRIRAJ	5.50	0.48	10.43	0.71	96.22	0.34	8.01	0.39	4.26	64
59	RH-406	5.10	0.42	9.29	0.77	139.52	0.64	11.30	0.66	5.15	35
60	NRCHB-101	6.20	0.58	15.74	0.46	95.68	0.33	7.29	0.33	5.30	33
61	RGIN-73	5.80	0.52	18.14	0.35	101.38	0.37	9.92	0.55	4.51	55
62	DRMR-IJ-31	5.10	0.42	15.90	0.45	136.98	0.62	10.85	0.62	4.73	51
63	NRCHB-101	5.30	0.45	13.77	0.55	98.03	0.35	9.17	0.49	4.48	56
64	DRMR-150-35	5.70	0.51	12.49	0.61	121.27	0.51	11.14	0.65	4.93	44
65	Pusa mustard-25(NPJ 112)	6.20	0.58	12.05	0.64	116.57	0.48	5.86	0.22	4.28	63
66	Pusa mustard26(NPJ 113)	3.90	0.25	17.30	0.39	147.98	0.69	5.23	0.17	3.71	69
67	Pusa mustard27(EJ 17)	3.50	0.19	9.31	0.76	100.35	0.37	5.01	0.15	5.00	41
68	CS 54	5.32	0.45	14.31	0.53	72.33	0.17	6.38	0.26	4.33	61
69	PHR 2	2.20	0.00	11.13	0.68	60.85	0.10	3.19	0.00	5.61	18
70	RL 1359	5.30	0.45	8.77	0.79	98.23	0.35	5.69	0.20	6.17	5
71	Kranti	5.60	0.49	10.03	0.73	115.05	0.47	5.94	0.22	3.98	67

×=Mean performance of the character; *Ranking has been done in descending order taking the highest rescaled value as 1 (first rank) followed by other lower rescaled values from rank 2 onwards. The formulas for the index value (rescaled value) are the same for all the characters except in the case of "Aphid Count" where this character was negatively associated with yield.

Table 4.6 Distribution of seventy-one genotypes of Indian mustard (*Brassica juncea*) in seven clusters

Cluster number	No. of genotypes	Genotypes
I	31	B-85(Seeta), RW-351(Bhagarathi),RW-85-59 (Sarna),RW-4C-6-3 (Sanjukta Asech), NPJ-194, TM-276, Rohini(SC), KMR-15-4, PR-2012-9, Divya-88, RL-JEB-52, Kranti- NC, DRMRIJ-15-85, RH1202, NPJ-196, RMM-09-10, JMM-927-RC, RRN-871, KM-126, SKM-1313, RB-77, DRMR-15-5, KMR-53-3, RL-JEB-84, Ganga, RGN-73-JC, RH-1209, PR-2012-12, RGN- 385, NPJ-195, Maya-C
II	2	JMM-927-RC, RH-1325
III	2	RGN-389, RGN-386
IV	21	SKJM-05,SVJ-64, Sitara-Sreenagar, RH-0923, DRMR-15-16, NPJ-198, JMM-927-RC, DRMR-15-47, RAURD-214, DRMR-15-14, DRMR-4001, RGN-384, NPJ-197, RB-81, NPJ-200, DRMR-15-9, KMR-L-15-6, PRD-2013-9, DRMRIJ-15-66, RH-1368, RH-406, CS 54
V	12	RNWR-09-3, PRD-2013-2, GIRIRAJ, NRCHB-101, RGIN-73, DRMR-IJ-31, NRCHB-101, DRMR-150-35, RH-749, Pusa mustard 25 (NPJ112), Pusa mustard 26 (NPJ113), Pusa mustard 27 (EJ17)
VI	2	RL1358, Kranti
VII	1	PHR2

parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various characters. Mahalanobis D^2 analysis of quantitative characters is a powerful tool for measuring genetic divergence among the material selected even from the same geographic region, reported by Mahalanobis (1936) followed by Rao (1952).

Based on D^2 values seventy-one genotypes of mustard were grouped into seven clusters. A total of thirty one genotypes were grouped into cluster I namely B-85 (Seeta), RW-351 (Bhagarathi), RW-85-59 (Sarna), RW-4C-6-3 (Sanjukta Asech), NPJ-194, TM276, Rohini (SC), KMR-15-4, PR-2012-9, Divya-88, RL-JEB-52, Kranti- NC, DRMRIJ-15-85, RH1202, NPJ-196, RMM-09-10, JMM-927-RC, RRN-871, KM126, SKM-1313, RB-77, DRMR-15-5, KMR-53-3, RLJEB-84, Ganga, RGN-73-JC, RH-1209, PR-2012-12, RGN- 385, NPJ-195 and Maya-C; twenty-one genotypes in cluster IV namely SKJM-05, SVJ-64, Sitara Sreenagar, RH-0923, DRMR-15-16, NPJ-198, JMM927-RC, DRMR-15-47, RAURD-214, DRMR-15-14, DRMR-4001, RGN-384, NPJ-197, RB-81, NPJ-200, DRMR-15-9, KMR-L-15-6, PRD-2013-9, DRMRIJ-15- 66, RH-1368, RH-406 and CS 54; twelve genotypes in cluster V namely RNWR-09-3, PRD-2013-2, GIRIRAJ, NRCHB-101, RGIN-73, DRMR-IJ-31, NRCHB-101, DRMR-150-35, RH-749, Pusa mustard 25 (NPJ112), Pusa mustard 26 (NPJ113) and Pusa mustard 27 (EJ17); two genotypes in cluster II namely JMM-927-RC, RH1325), as well as in cluster III namely RGN-389 and RGN-386; two genotypes in cluster VI namely RL1358 and Kranti and one genotype in cluster VII namely PHR-2.

4.7 Inter and intra-cluster distance

The average intra and inter cluster D^2 values are given in Table 4.7. In the present investigation, the inter cluster and intra cluster distance were estimated among eleven characters. The maximum intra cluster distance was recorded in cluster VI (943.87) followed by cluster V (524.72), cluster IV (472.12), cluster I (350.00), cluster III (22.21), cluster II

Table 4.7 Average intra (diagonal) and inter-cluster (off-diagonal) D^2 values in Indian mustard (*Brassica juncea*)

Cluster	I	II	III	IV	V	VI	VII
I	350.00	325.19	542.99	414.56	491.54	523.97	2507.42
II		19.692	83.99	303.98	410.53	372.20	1954.86
III			22.21	496.72	682.97	587.32	1591.24
IV				472.12	515.42	538.13	2560.63
V					524.72	557.07	3147.81
VI						943.87	2564.55
VII							0.00

(19.69) and cluster VII (0.00). The maximum intra cluster distance in cluster VI was because of wide genetic diversity among its genotypes.

The maximum inter cluster distance was between cluster VII and V (3147.81) followed by cluster VII and VI (2564.55), cluster VII and IV (2560.63) and cluster VII and I (2507.42).

4.8. Genetically divergent clusters and distance (D^2 value) between the genotypes selected for hybridization

Genetically divergent clusters and distance (D^2 value) between the genotypes selected for hybridization is presented in Table 4.8. On minute observation of distance between the genotypes into different divergent clusters, it was revealed that PHR-2 in cluster VII and RNWR09-3 in cluster V had a very high genotypic distance ($D^2 = 4662.847$). Similar findings with high genetic distance between the genotypes in other clusters like PHR-2 in cluster VII and Giriraj in cluster V had high genotypic distance ($D^2 = 4342.083$). Information from other clusters like PHR-2 in cluster VII and Kranti in cluster VI had high genotypic distance ($D^2 = 3811.183$). Similarly, PHR-2 in cluster VII and SKJM-05 in cluster IV had very high genotypic distance ($D^2 = 6745.971$) followed by PHR-2 in cluster VII and DRMR-15-16 in cluster IV ($D^2 = 3636.379$). PHR-2 in cluster VII and RW-85-59 (Sarma) in cluster I very high genotypic distance ($D^2 = 4950.465$) followed by PHR-2 in cluster VII and NPJ-194 in cluster I ($D^2 = 5853.214$). Hence, based on the higher inter-cluster distance value, the crosses could be made among the genotypes of cluster VII and cluster V (PHR 2 and RNWR-09-3; PHR 2 and Giriraj), cluster VII and cluster VI (PHR 2 and Kranti), cluster VII and cluster IV (PHR 2 and SKJM-05 ; PHR 2 and DRMR-15-16), cluster VII and cluster I (PHR 2 and RW-85-59 (Sarma); PHR 2 and NPJ-194) as per their D^2 values for expecting better segregants. This indicates that the genotypes included in these clusters are having a broad spectrum of genetic diversity and

Table 4.8 Description of the genetically divergent clusters and distance (D² value) between the genotypes selected

Cluster combination	Inter-cluster distance	Genotype selected from the cluster	Distance between the genotypes selected (D ² value)
Cluster VII and cluster V	3147.808	PHR -2 in cluster VII and RNWR-09-3 in cluster V	4662.847
Cluster VII and cluster V	3147.808	PHR -2 in cluster VII and Giriraj in cluster V	4342.083
Cluster VII and cluster VI	2564.546	PHR -2 in cluster VII and Kranti in cluster VI	3811.183
Cluster VII and cluster IV	2560.633	PHR -2 in cluster VII and SKJM-05 in cluster IV	6745.971
Cluster VII and cluster IV	2560.633	PHR -2 in cluster VII and DRMR-15-16 in cluster IV	3636.379
Cluster VII and cluster I	2507.415	PHR -2 in cluster VII and RW-85-59(Sarna) in cluster I	4950.465
Cluster VII and cluster I	2507.415	PHR -2 in cluster VII and NPJ-194 in cluster I	5853.214

Table 4.9 Cluster mean for the eleven characters in Indian mustard (*Brassica juncea*)

Clusters	Plant height (cm)	Height upto first fruiting branch (cm)	Days to 50 % flowering	Primary branches per plant (cm)	Secondary branches per plant (cm)	Siliquae per plant	Seeds per siliqua	1000-seed weight (g)	Aphid count (% incidence)	Penetration force (Kpascal)	Seed yield per plant (g)
I	167.43	57.85	44.94	3.72	10.09	182.24	12.94	4.55	10.17	97.47	9.46
II	182.48	57.87	49.00	4.30	8.53	145.30	13.00	5.02	9.05	58.37	9.48
III	192.77	58.93	52.00	4.00	10.73	178.13	13.23	4.97	8.94	56.44	11.80
IV	170.77	56.27	46.00	4.27	9.60	161.08	13.03	4.87	8.45	79.96	9.83
V	167.66	52.36	43.33	4.13	7.64	148.44	13.02	5.43	13.87	109.11	8.67
VI	168.17	76.43	48.00	4.53	6.43	125.37	13.70	5.45	9.40	106.64	5.81
VII	212.93	153.00	57.00	6.20	8.13	132.47	11.87	2.20	11.13	60.85	3.19
Contribution (%) of the characters	18.71	3.86	8.09	0.60	2.86	5.47	0.32	18.35	12.76	18.35	10.62

could very well be used in hybridization programmes for improving seed yield. Therefore, it would be logical to attempt crosses between the genotypes from the above-mentioned clusters.

4.9. Cluster mean and contribution percentage of various characters

The cluster mean calculated for 11 characters under study has been presented in Table 4.9. The highest cluster mean value for plant height was recorded in the case of cluster VII (212.93), for height upto first fruiting branch recorded in case of cluster VII (153.00), days to 50 % flowering in case of cluster VII (57.00), primary branches plant⁻¹ highest cluster mean value was recorded in case of cluster VII (6.20), secondary branches plant⁻¹ in case of cluster III (10.73), siliquae plant⁻¹ in case of cluster I (182.24), seeds per siliqua in case of cluster VI (13.70), 1000-seed weight in case of culture VI (5.45), aphid count in case of cluster V (13.86), penetration force in case of cluster V (109.11), seed yield plant⁻¹ in case of cluster III (11.80).

The percentage contribution (Table 4.9) of plant height (18.71%) has been maximum to divergence followed by 1000 seed weight (18.35%) as well as penetration force (18.35%), aphid count (12.76%), seed yield per plant (10.62%) and days to 50 % flowering (8.09%), contributed most towards genetic divergence, whereas remaining characters contributed very little towards genetic divergence *i.e.*, siliquae plant⁻¹ (5.47), height upto first fruiting branch (3.86), secondary branches plant⁻¹ (2.86), primary branches plant⁻¹ (0.60) and seeds per siliqua (0.32).

4.10 Analysis of variance for parents and crosses

4.10.1 Analysis of variance for seed yield and its attributing characters

Analysis of variance for the experiment with eight parents and twenty-eight crosses for nine seed yield and its attributing characters (days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliqua⁻¹, height up to first fruiting branch, plant height, seed yield plant⁻¹ 1000 seed weight and oil content); physiological

Table 4.10 Analysis of variance of seed yield and its attributing characters for parents and crosses in Indian mustard (*Brassica juncea*)

Sources of variation	df	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliqua e plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
Replication	2	2.3982	5.5033**	19.8031**	0.0003	0.7487	0.0012	0.0001	0.0000	7.4444**	74.3430**
Treatments	35	40.2632**	0.9641**	7.8982**	0.0214**	4.9412**	0.0122**	0.0042**	0.0040**	135.664**	132.3710**
Parents	7	31.9048**	1.1483*	8.8283*	0.0334**	2.7323	0.0109**	0.0065**	0.0059**	125.4050**	156.1850**
Crosses	27	42.5340**	0.9309*	7.9494**	0.0190**	5.4574**	0.0130**	0.0034**	0.0037**	139.2710**	129.1660**
Parents Vs Crosses	1	37.4630**	0.5717	0.0037	0.0007	6.4638	0.0001	0.0159**	0.0015	110.0950**	52.2223**
Error	70	3.2553	0.4904	3.1831	0.0002	2.5194	0.0009	0.0001	0.0009	1.4250	0.9810
Total	107	15.3447	0.7390	5.0361	0.0071	3.2785	0.0046	0.0014	0.0019	45.4480	45.3300

*, ** Significant at 5% and 1% levels of probability, respectively

Table 4.11: Analysis of variance of physiological characters for parents and crosses in Indian mustard (*Brassica juncea*)

Sources of variation	df	Percentage of membrane stability index (%)	Percentage of excised leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
Replication	2	0.0018**	0.0042	0.0003*	0.0030	0.1368	0.0006	0.0000	0.0158
Treatments	35	0.0020**	0.0588**	0.0002**	0.0019**	0.9706**	0.0053**	0.0017**	0.1433**
Parents	7	0.0013**	0.0284**	0.0004**	0.0010**	1.1748**	0.0089**	0.0013*	0.0958
Crosses	27	0.0022**	0.0674**	0.0002**	0.0022**	0.9529**	0.0042**	0.0018**	0.1446**
Parents Vs Crosses	1	0.0001	0.0402**	0.0000	0.0005	0.0178	0.0075*	0.0027*	0.4409**
Error	70	0.0002	0.0043	0.0001	0.0016	0.0694	0.0017	0.0006	0.0447
Total	107	0.0008	0.0221	0.0001	0.0017	0.3655	0.0028	0.0009	0.0764

*, ** Significant at 5% and 1% levels of probability, respectively

characters (percentage of percentage relative water content, canopy temperature depression, proline content of leaf, chlorophyll a, chlorophyll b and total chlorophyll); aphid related characters (water content of aphid probed twig (%), watercontent of aphid uninfested twig (%), water content of aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force) was carried out for testing the significance of variance among the treatments, parents and parent vs crosses for each character through 'F' test.

The analysis of variance of seed yield and its attributing characters for eight parents and twenty-eight crosses in Indian mustard was presented in Table 4.10. The results of the present study showed significant differences among the treatments for all the seed yield and its attributing characters. The mean sum of square revealed that parental lines and crosses showed significant differences at 5% and 1% probability level for all characters except seed siliqua⁻¹ in the case of parents while days to 50% flowering, plant height, 1000 seed weight and oil content exhibited significant variance for parents Vs crosses while other characters namely primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliqua⁻¹, height up to first fruiting branch and seed yield plant⁻¹ showed the non-significant difference.

4.10.2 Analysis of variance for physiological characters

The analysis of variance of nine physiological characters for eight parents and twenty-eight crosses in Indian mustard was presented in Table 4.11. The analysis of variance of treatment revealed significant differences at 5% and 1% probability levels for all eight physiological characters. Analysis of variance further indicated significant differences among the parents and crosses for all the characters except total chlorophyll. Parents Vs crosses showed significance for percentage of excised leaf water loss, chlorophyll a, chlorophyll b, total chlorophyll while other physiological characters were non-significant *viz.*, percentage of membrane stability index, percentage of relative water content, canopy temperature and proline content.

4.10.3 Analysis of variance for aphid related characters

The analysis of variance of aphid-related characters for eight parents and twenty-eight crosses in Indian mustard was presented in Table 4.12. The mean square for six aphid-related characters indicated that significant differences were recorded among the treatments for all the characters. Analysis of variance revealed significant differences existed at 5% and 1% probability level among the parents and crosses for water content of aphid probed twig (%), water content of aphid uninfested twig (%), water content of aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force. Significant differences were recorded among the parent Vs crosses for all the characters studied.

4.11 Mean performance of parents and crosses

4.11.1 Mean performance of parents and crosses for seed yield and its attributing characters

The mean performance of parents and crosses are presented in Table 4.13. The character-wise findings are described below:

4.11.1.1 Days to 50% flowering

Days to 50 % flowering for parental lines ranged from 68.000 (PHR-2) to 55.000 days (NPJ-194 and RW-85-59) with a mean value of 60.000 days, while in the case of crosses it ranged from 62.670 (RNWR-09-3 × PHR-2) to 51.000 days (NPJ-194 × RW-85-59) with a mean value of 56.917 days. The grand mean of parents and crosses was 57.602 day.

When both parents and crosses were considered together it was observed that in case of days to 50 % flowering, the crosses NPJ-194 × SKJM-05 (51.00) and NPJ-194 × RW-85-59 (51.00) exhibited the lowest mean value and considered as best performing. However, it did not differ significantly from other crosses namely NPJ-194 × DRMR-15-16 (51.33) and

Table 4.12 Analysis of variance of aphid related characters for parents and crosses in Indian mustard (*Brassica juncea*)

Sources of variation	df	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
Replication	2	15.0739**	5.2278	0.0004	0.0001	0.0176**	19.2504
Treatments	35	7.4779**	18.1967**	0.0192**	0.0209**	0.0836**	218.5200**
Parents	7	10.6000**	23.4567**	0.0357**	0.0225**	0.0884**	111.8798**
Crosses	27	6.7957**	15.9128**	0.0143**	0.0201**	0.0853**	253.9250**
Parents Vs Crosses	1	4.0434	43.0363*	0.0026**	0.0304	0.0048	9.0675
Error	70	2.3765	7.3806	0.0026	0.0036	0.0019	12.8896
Total	107	4.2825	10.8783	0.0080	0.0092	0.0019	80.2708

*, ** Significant at 5% and 1% levels of probability, respectively

RW-85-59 × RNWR-09-3 (52.33). The genotype PHR -2 (68.00) was the high-performing one which differs significantly from other genotypes.

4.11.1.2 Primary branches plant⁻¹

Primary branches plant⁻¹ for parents varied from 5.867 (PHR-2) to 3.933 (NPJ-194) with a parental mean value of 4.800. In the crosses, the range of primary branches plant⁻¹ was found from 5.933 (NPJ-194 × DRMR-15-16) to 3.667 (Kranti × Giriraj) with a mean value of 4.793. The general mean for whole genotypes was recorded as 4.794.

Both parents and crosses mean values were evaluated together and it was realized that cross RW-85-59 × Kranti (4.33) followed by SKJM-05 × PHR-2 (5.87) showed high mean value for primary branches plant⁻¹ which did not differ significantly from genotypes namely PHR -2 (5.87), DRMR-15-16 (5.07), SKJM-05 (5.00) RNWR-09-3 (5.33) and Kranti (4.87) and crosses NPJ-194 × RW-85-59 (5.53), NPJ-194 × Kranti (5.33), NPJ-194 × SKJM-05 (5.33), DRMR-15-16 × Kranti (5.27), Giriraj × PHR-2 (5.27), RW-85-59 × Kranti (4.33), Kranti × PHR-2 (5.20), Kranti × RNWR-09-3 (4.93), Giriraj × RNWR-09-3 (4.93), RW-85-59 × PHR-2 (4.80), DRMR-15-16 × SKJM-05 (4.80), SKJM-05 × Giriraj (4.80) and NPJ-194 × RNWR-09-3 (4.80) but not from each other while the cross Kranti × Giriraj (3.67) showed poor performance.

4.11.1.3 Secondary branches plant⁻¹

Among the parents, secondary branches plant⁻¹ ranged from 10.400 (PHR-2) to 7.400 (Giriraj), with a mean value of 8.883, while crosses reflected the range from 15.507 (NPJ-194 × Kranti) to 6.333 (Kranti × Giriraj) with an average value of 9.459. The grand mean for parents and crosses was 9.331.

In the case of secondary branches plant⁻¹ cross NPJ-194 × Kranti (15.51) was the best-performing one which differs significantly from other genotypes whereas lowest value was observed for cross NPJ-194 × Giriraj (9.47) which did not differ significantly from other genotypes *i.e.*, Kranti (8.93), DRMR-15-16 (8.93), Giriraj (7.40), NPJ-194 (8.00), RW-85-59

(8.60) and SKJM-05 (9.00), RW-85-59 × Giriraj (6.47), SKJM-05 × Giriraj (7.60), RW-85-59 × RNWR-09-3 (7.67), DRMR-15-16 × PHR-2 (7.93), RNWR-09-3 × PHR-2 (8.07), SKJM-05 × RNWR-09-3 (8.40), RW-85-59 × Kranti (8.73), DRMR-15-16 × RNWR-09-3 (8.73), DRMR-15-16 × Giriraj (8.80), Giriraj × PHR-2 (8.87).

4.11.1.4 Siliquae plant⁻¹

Parent (PHR-2) recorded the highest mean value for siliquae plant⁻¹ *i.e.* 329.80 whereas, the lowest mean value was recorded in (NPJ-194) *i.e.* 162.13, with a parental mean value of 2.328. While the crosses (NPJ-194 × Kranti) 2.430 and (Kranti × Giriraj) 2.110 showed maximum and minimum siliquae plant⁻¹ respectively, with an average value of 2.279. The grand mean value for this character was recorded as 219.37.

In the case of siliquae plant⁻¹ genotype PHR-2 (329.80) was the best performing one which differs significantly from other genotypes and crosses. Poor performance was shown by the crosses Kranti × Giriraj (128.80).

4.11.1.5 Seed siliqua⁻¹

Seed siliqua⁻¹ for parental entries ranged from 9.133 (PHR-2) to 13.000 (Giriraj) with an average value of 11.925. In the crosses, it ranged from 11.267 (Giriraj × PHR-2) to 15.427 (NPJ-194 × Kranti) with the crosses mean value of 13.408. The grand mean value for this character was 13.079.

In case of seed siliqua⁻¹ cross NPJ-194 × Kranti (15.43) was the best performing one which did not differ significantly from other genotypes namely RW-85-59 × Giriraj (14.93), RW-85-59 × RNWR-09-3 (14.80), RW-85-59 × PHR-2 (14.80), SKJM-05 × Giriraj (14.60), RNWR-09-3 × PHR-2 (14.40), RW-85-59 × SKJM-05 (14.33), NPJ-194 × Giriraj (14.20), DRMR-15-16 × Kranti (14.07), DRMR-15-16 × Giriraj (14.07), DRMR-15-16 × PHR-2 (14.07), RW-85-59 × Kranti (13.80), NPJ-194 × DRMR-15-16 (13.80), NPJ-194 × RNWR-09-3 (13.73), SKJM-05 × Kranti (13.33), NPJ-194 × PHR -2 (13.23), SKJM-05 × PHR-2 (13.13),

DRMR-15-16 × SKJM-05 (13.00), NPJ-194 × SKJM-05 (13.00) and Giriraj (13.00) whereas low performing genotype was PHR-2 (9.13).

4.11.1.6 Height up to first fruiting branch (cm)

Lowest height up to first fruiting branch was recorded in Giriraj (74.00) and maximum in DRMR-15-16 (95.13), with a parental mean value of 82.29. The corresponding values among the crosses ranged from 133.75 in (NPJ-194 × Kranti) to 63.87 (SKJM-05 × PHR-2), with an average value of 82.66. The grand mean value for this character was recorded as 82.58.

In the case of height up to first fruiting branch cross NPJ-194 × Kranti 133.5 was the best-performing one which differs significantly from other genotypes and crosses. Poor performance was shown by the cross SKJM-05 × PHR-2 (63.87) which did not differ significantly from other crosses namely Kranti × PHR-2 (64.93), Kranti × Giriraj (65.73), DRMR-15-16 × RNWR-09-3 (70.00), RW-85-59 × SKJM-05 (70.40) and NPJ-194 × PHR -2 (71.20).

4.11.1.7 Plant height (cm)

For plant height, the parent (NPJ-194) was short-statured 153.00 and (PHR-2) was tall statured 235.13 with mean of 193.87 whereas, among crosses (NPJ-194 × RW-85-59) exhibited the shortest stature 175.93 and (DRMR-15-16 × Kranti) 237.27 was tallest with mean of 199.62 cm. The grand mean was observed as 198.34cm.

In the case of plant height cross DRMR-15-16 × Kranti (175.93) was tall statured one which did not differ significantly from other genotypes namely PHR -2 (235.13) and Kranti × PHR-2 (234.73) whereas short and desirable genotype was NPJ-194 (153.00).

4.11.1.8 Seed yield plant⁻¹ (g)

Seed yield per plant, among the parents, ranged from 4.23 (DRMR-15-16) to 6.13 (SKJM-05) with a mean value of 5.03 per plant, while in case of crosses it ranged from 4.26

(DRMR-15-16 × Giriraj) to 6.33 (Kranti × Giriraj) with an average value of 4.86 per plant. was the 4.90 grand mean value for this character.

In case of seed yield per plant cross, Kranti × Giriraj (6.33) was the best performing one which did not differ significantly from other genotypes namely SKJM-05 (6.13), Giriraj (5.61) and cross NPJ-194 × SKJM-05 (5.73). Low yield was observed by genotype DRMR- 15-16 (4.23).

4.11.1.9 1000 seed weight (g)

In parents, 1000 seed weight varied from 1.97 (NPJ-194) to 3.56 (RNWR-09-3) with an average value of 2.84. Among crosses, it ranged from 1.820 (RW-85-59X Giriraj) to 4.25 (NPJ-194X DRMR-15-16) with a mean value of 3.12. Grand mean was 3.059 g.

Cross DRMR-15-16 × Giriraj (2.76) showed the best performance in case of 1000 seed weight and did not differ significantly from other genotypes namely DRMR-15-16 (2.00), RNWR-09-3 (3.56), SKJM-05 (2.57), Kranti (3.45) and crosses viz., Giriraj × PHR-2 (3.57), Giriraj × RNWR-09-3 (3.60), NPJ-194 × RW-85-59 (2.95), Kranti × PHR-2 (3.70), SKJM-05 × RNWR-09-3 (3.68), DRMR-15-16 × SKJM-05 (3.463), SKJM-05 × Giriraj (2.89), SKJM-05 × PHR-2 (2.98), NPJ-194 × RNWR-09-3 (2.85), SKJM-05 × Kranti (2.96), RW-85-59 × DRMR-15-16 (2.22), RW-85-59 × RNWR-09-3 (2.72), NPJ-194 × Giriraj (3.34), DRMR-15-16 × RNWR-09-3 (3.53) and DRMR-15-16 × Kranti (3.720).

4.11.1.10 Oil content

Among the parental lines, DRMR-15-16 (41.56) recorded the highest mean value and PHR-2 (16.85) had the minimum mean value for this character with an average value of 31.59 percentage for this character. The cross Giriraj × PHR-2 (42.02) recorded the highest value for this character and the lowest value was shown by SKJM-05X PHR-2 (16.87) with mean of 26.34 percentage.

Cross Giriraj × RNWR-09-3 (40.49) showed the best performance in case of oil content and did not differ significantly from other genotypes namely NPJ-194 (40.03), DRMR-15-16

(41.56), NPJ-194 × PHR -2 (40.77) and SKJM-05 × Giriraj (22.62) whereas genotype PHR -2 (16.85) followed by cross SKJM-05 × PHR-2 (16.87) showed poor performance

4.11.2 Mean performance of parents and crosses for physiological characters

The mean performance of parents and crosses are presented in Table 4.14. The character-wise findings are described below:

4.11.2.1 Percentage of membrane stability index (%)

Parent PHR-2(53.03) showed the minimum percentage of membrane stability index while RW-85-59 (73.96) showed the maximum percentage of membrane stability index. Among the crosses, DRMR-15-16 × Giriraj (75.29) showed maximum while NPJ-194 × DRMR-15-16(60.15) showed the minimum percentage of membrane stability index.

In case of percentage of membrane stability index cross DRMR-15-16 × Giriraj (75.29) was the best performing one which did not differ significantly from other genotypes namely NPJ-194 (74.13), RW-85-59 (73.96), NPJ-194 × RNWR-09-3 (74.50), RW-85-59 × Kranti (74.65), RW-85-59 × Giriraj (74.56), SKJM-05 × PHR-2 (74.39), Kranti × RNWR-09-3 (74.36), RNWR-09-3 × PHR-2 (73.87), RW-85-59 × DRMR-15-16 (72.54), DRMR-15-16 × Kranti (71.58), RW-85-59 × PHR-2 (70.52) and Giriraj × PHR-2 (69.84) whereas low performing genotype was PHR -2 (53.03).

4.11.2.2 Percentage of excised leaf water loss (%)

Among the parental genotypes, Kranti (34.63) recorded the highest mean value and SKJM-05 (14.46) had the minimum mean value for this character. The Cross RW-85-59 × RNWR-09-3 (49.96) recorded the highest value while DRMR-15-16 × RNWR-09-3(14.10) the least.

Table 4.13 Mean performance of parents and crosses for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
1	NPJ-194	55.00	3.93	8.00	162.13 (2.21)	11.73	82.47 (1.92)	153.00 (2.18)	4.59 (0.75)	1.973 (0.473)	40.027 (1.593)
2	RW-85-59 (Sarma)	55.00	4.20	8.60	192.00 (2.28)	12.27	85.73 (1.93)	167.80 (2.23)	4.97 (0.77)	3.173 (0.620)	31.383 (1.533)
3	DRMR-15-16	62.33	5.07	8.93	225.33 (2.35)	12.53	95.13 (1.98)	192.73 (2.28)	4.23 (0.72)	2.000 (0.477)	41.560 (1.600)
4	SKJM-05	62.67	5.00	9.00	215.60 (2.33)	12.07	82.73 (1.92)	196.07 (2.29)	6.13 (0.85)	2.570 (0.553)	27.840 (1.503)
5	Kranti	58.00	4.87	8.93	184.27 (2.26)	12.27	84.27 (1.93)	196.93 (2.29)	4.95 (0.77)	3.450 (0.647)	40.980 (1.600)
6	Giriraj	60.00	4.13	7.40	167.33 (2.22)	13.00	74.00 (1.87)	194.13 (2.29)	5.61 (0.82)	2.580 (0.553)	21.090 (1.437)
7	RNWR-09-3	59.00	5.33	9.80	278.53 (2.44)	12.40	77.53 (1.89)	215.20 (2.33)	4.52 (0.74)	3.557 (0.657)	32.963 (1.543)
8	PHR 2	68.00	5.87	10.40	329.80 (2.52)	9.13	76.47 (1.88)	235.13 (2.37)	5.27 (0.80)	3.453 (0.647)	16.853 (1.383)
	Mean (Parents)	60.00	4.80	8.88	219.37 (2.33)	11.93	82.29 (1.91)	193.87 (2.28)	5.03 (0.78)	2.845 (0.578)	31.587 (1.524)
	Crosses										
1	NPJ-194 × RW-85-59	51.00	5.53	11.60	257.20 (2.41)	12.43	104.66 (2.02)	175.93 (2.25)	4.83 (0.76)	2.953 (0.597)	18.333 (1.403)
2	NPJ-194 × DRMR-15-16	52.33	5.93	10.67	158.20 (2.20)	13.80	111.66 (2.05)	184.93 (2.27)	5.28 (0.80)	4.247 (0.720)	23.493 (1.463)
3	NPJ-194 × SKJM-05	51.00	5.33	9.40	172.07 (2.23)	13.00	86.93 (1.94)	185.20 (2.27)	5.73 (0.83)	3.750 (0.677)	26.923 (1.493)
4	NPJ-194 × Kranti	54.67	5.33	15.51	268.39 (2.43)	15.43	133.75 (2.13)	186.17 (2.27)	4.39 (0.73)	3.430 (0.643)	29.493 (1.517)
5	NPJ-194 × Giriraj	56.00	4.60	9.47	185.20 (2.27)	14.20	85.87 (1.93)	196.20 (2.29)	4.59 (0.75)	3.343 (0.637)	31.297 (1.533)
6	NPJ-194 × RNWR-09-3	56.00	4.80	9.87	185.60 (2.27)	13.73	81.80 (1.91)	186.13 (2.27)	4.59 (0.74)	2.850 (0.587)	24.307 (1.470)
7	NPJ-194 × PHR -2	57.00	4.47	9.27	173.73 (2.24)	13.23	71.20 (1.85)	198.47 (2.30)	5.09 (0.78)	2.967 (0.597)	40.773 (1.597)
8	RW-85-59 × DRMR-15-16	56.00	5.20	9.87	186.00 (2.27)	12.53	88.67 (1.95)	187.93 (2.27)	5.51 (0.81)	2.220 (0.510)	24.963 (1.473)
9	RW-85-59 × SKJM-05	55.00	4.13	9.27	186.00 (2.27)	14.33	70.40 (1.85)	188.80 (2.28)	5.31 (0.80)	3.893 (0.690)	25.443 (1.483)

Table 4.13 (Continued)

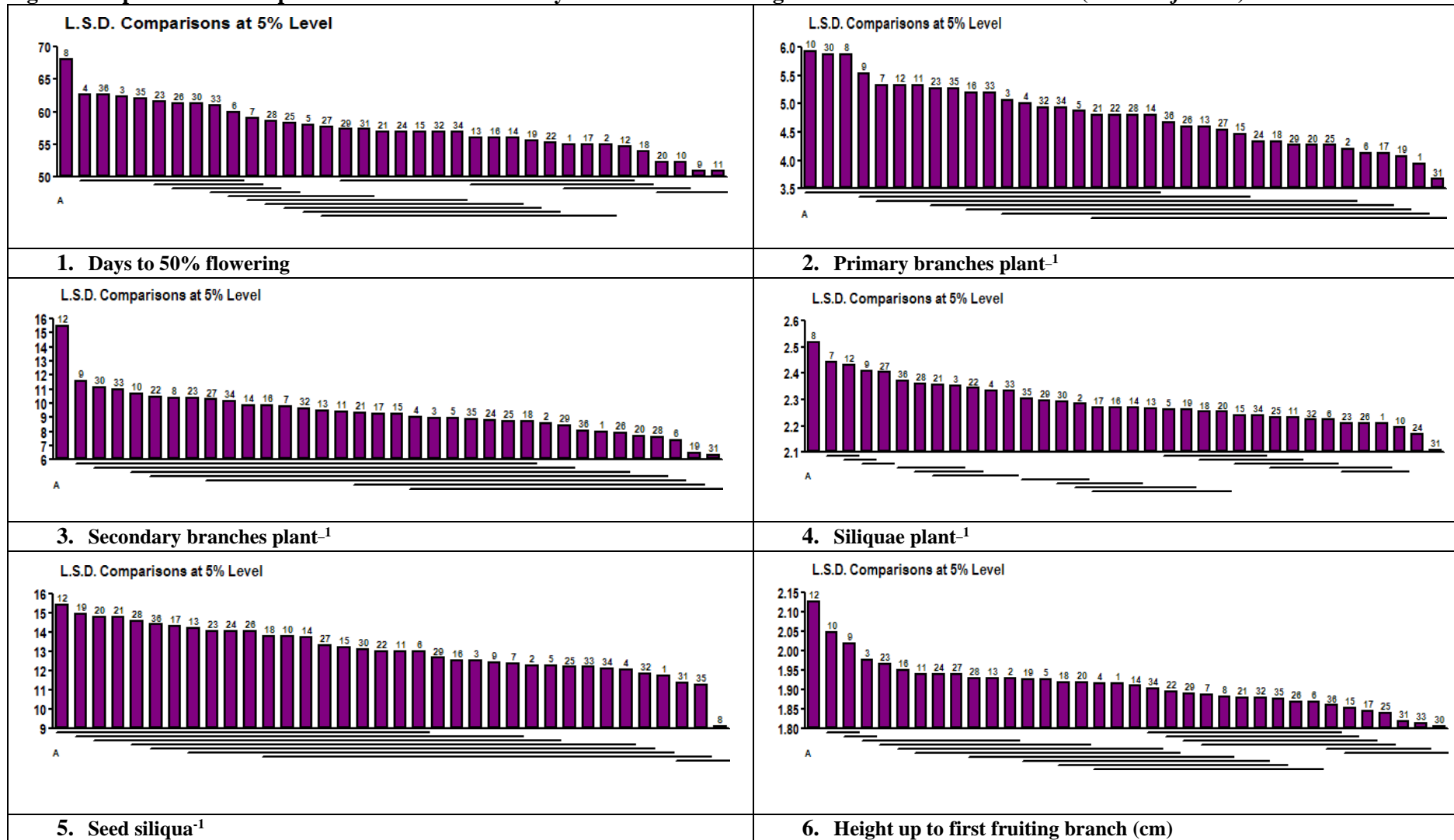
S.N o.	Parents	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
Crosses											
10	RW-85-59 × Kranti	54.00	4.33	8.73	178.33 (2.25)	13.80	83.47 (1.92)	196.67 (2.29)	4.41 (0.74)	2.520 (0.543)	24.780 (1.473)
11	RW-85-59 × Giriraj	55.67	4.07	6.47	183.27 (2.26)	14.93	85.07 (1.93)	215.13 (2.33)	4.65 (0.75)	1.820 (0.450)	26.123 (1.487)
12	RW-85-59 × RNWR-09-3	52.33	4.27	7.67	178.87 (2.25)	14.80	83.20 (1.92)	195.40 (2.29)	4.61 (0.75)	2.717 (0.570)	20.333 (1.430)
13	RW-85-59 × PHR-2	57.00	4.80	9.33	227.67 (2.36)	14.80	75.73 (1.88)	195.07 (2.29)	4.90 (0.77)	2.927 (0.593)	21.677 (1.443)
14	DRMR-15-16 × SKJM-05	55.33	4.80	10.47	220.80 (2.34)	13.00	79.20 (1.90)	206.67 (2.32)	5.17 (0.79)	3.463 (0.650)	21.843 (1.443)
15	DRMR-15-16 × Kranti	61.67	5.27	10.40	161.47 (2.21)	14.07	93.07 (1.97)	237.27 (2.37)	5.32 (0.80)	3.720 (0.673)	22.630 (1.453)
16	DRMR-15-16 × Giriraj	57.00	4.33	8.80	148.27 (2.17)	14.07	86.80 (1.94)	194.20 (2.29)	4.26 (0.72)	2.760 (0.577)	18.490 (1.407)
17	DRMR-15-16 × RNWR-09-3	58.33	4.27	8.73	172.00 (2.23)	12.20	70.00 (1.84)	199.87 (2.30)	4.44 (0.73)	3.530 (0.653)	20.283 (1.430)
18	DRMR-15-16 × PHR-2	61.33	4.60	7.93	162.47 (2.21)	14.07	73.93 (1.87)	213.93 (2.33)	4.43 (0.74)	3.183 (0.620)	35.287 (1.560)
19	SKJM-05 × Kranti	57.67	4.53	10.27	252.93 (2.40)	13.33	86.73 (1.94)	206.27 (2.31)	4.33 (0.73)	2.957 (0.597)	31.813 (1.533)
20	SKJM-05 × Giriraj	58.67	4.80	7.60	229.53 (2.36)	14.60	84.87 (1.93)	205.73 (2.31)	4.45 (0.74)	2.890 (0.590)	22.620 (1.453)
21	SKJM-05 × RNWR-09-3	57.33	4.27	8.40	196.33 (2.30)	12.67	77.87 (1.89)	193.07 (2.29)	4.77 (0.76)	3.667 (0.667)	28.747 (1.513)
22	SKJM-05 × PHR-2	61.33	5.87	11.13	195.87 (2.29)	13.13	63.87 (1.81)	207.13 (2.32)	5.53 (0.81)	2.983 (0.667)	16.873 (1.383)
23	Kranti × Giriraj	57.33	3.67	6.33	128.80 (2.11)	11.40	65.73 (1.82)	185.07 (2.27)	6.33 (0.86)	2.750 (0.667)	22.533 (1.453)
24	Kranti × RNWR-09-3	57.00	4.93	9.60	167.93 (2.22)	11.87	76.07 (1.88)	207.33 (2.32)	4.66 (0.75)	1.900 (0.577)	21.543 (1.440)
25	Kranti × PHR-2	61.00	5.20	11.00	214.60 (2.33)	12.20	64.93 (1.81)	234.73 (2.37)	4.53 (0.74)	3.700 (0.463)	19.573 (1.420)
26	Giriraj × RNWR-09-3	57.00	4.93	10.13	173.53 (2.24)	12.13	80.53 (1.90)	195.87 (2.29)	4.78 (0.76)	3.603 (0.673)	40.493 (1.600)
27	Giriraj × PHR-2	62.00	5.27	8.87	201.00 (2.30)	11.27	75.87 (1.88)	214.67 (2.33)	4.60 (0.75)	3.573 (0.663)	42.023 (1.610)
28	RNWR-09-3 × PHR-2	62.67	4.67	8.07	234.80 (2.37)	14.40	72.73 (1.86)	195.47 (2.29)	4.53 (0.74)	3.060 (0.660)	31.990 (1.537)

Table 4.13 (Continued)

S.No.	Parents	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
	Mean (Crosses)	56.92	4.79	9.46	192.89 (2.28)	13.41	82.66 (1.91)	199.62 (2.30)	4.86 (0.77)	3.121	26.239
	Grand Mean	57.60	4.79	9.33	198.77 (2.30)	13.08	82.58 (1.91)	198.34 (2.29)	4.90 (0.77)	3.059 (0.603)	27.427 (1.492)
	SEm (±)	0.90^t	0.35^t	0.89^t	0.01^t	0.79^t	0.01^t	0.00^t	0.02^t	0.007^t	0.005^t
	CD (P=0.05)	2.94^t	1.14^t	2.91^t	0.02^t	2.59^t	0.05^t	0.01^t	0.05^t	0.019^t	0.0161^t

The values in parenthesis indicate the transformed values of the original data. Here “t” in the superscript of SEm (±) and CD (P=0.05) indicate that they have been estimated from the transformed data. In the case of the characters for which the data has been transformed, the analysis was further carried out using the transformed values only.

Fig 1 Mean performance of parents and crosses for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)



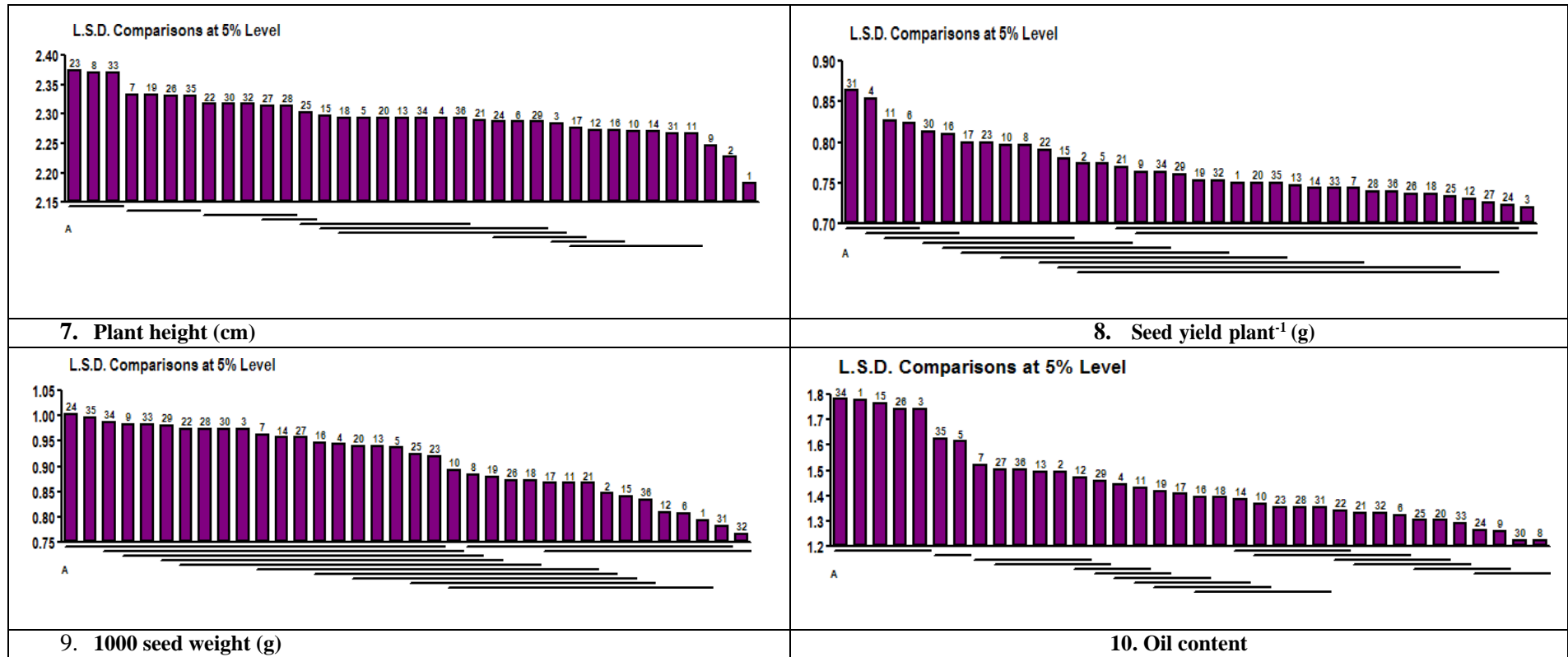


Fig 1 (Continued)

The lowest value observed for cross DRMR-15-16 × RNWR-09-3 (14.10) showed the best performance and didn't differ significantly from another cross like SKJM-05 (14.46), RW-85-59 × Kranti (15.40), PHR-2 (33.38), SKJM-05 × Giriraj (34.75), Giriraj × PHR-2 (16.78) and SKJM-05 × PHR-2 (16.99) while the cross RW-85-59 × RNWR-09-3 (49.96) was the poor performing one in case of the percentage of excised leaf water loss which did not differ significantly from other crosses namely RNWR-09-3 × PHR-2 (42.46).

4.11.2.3 Percentage relative water content (%)

The percentage relative water content among the parents ranged from 29.03 (NPJ-194) to 34.69 (Kranti). For crosses, the highest percentage relative water content was recorded by the cross SKJM-05 × Kranti (26.89) while it was lowest in RNWR-09-3 × PHR-2 (78.68).

In case of percentage relative water content cross SKJM-05 × Kranti (26.89) was the best performing one which did not differ significantly from other genotypes namely NPJ-194 (29.03) and crosses NPJ-194 × Kranti (31.12), NPJ-194 × PHR -2 (26.26), DRMR-15-16 × RNWR-09-3 (14.10), SKJM-05 × RNWR-09-3 (30.16), Kranti × PHR-2 (23.93), Giriraj × PHR-2 (16.78), RW-85-59 × Kranti (15.40), RW-85-59 × Giriraj (34.94), DRMR-15-16 × Kranti (35.03), DRMR-15-16 × Giriraj (28.44), DRMR-15-16 × PHR-2 (16.57), SKJM-05 × PHR-2 (16.99), Kranti × Giriraj (25.79), Giriraj × RNWR-09-3 (26.49), RW-85-59 × PHR-2 (21.57) and Kranti × RNWR-09-3 (17.69).

4.11.2.4 Canopy temperature depression (°C)

Parental genotype DRMR-15-16 (1.97) recorded highest mean value while it was least in SKJM-05 (1.54). Among the crosses, NPJ-194 × Giriraj (2.08) showed the highest value and the lowest value was shown by DRMR-15-16 × Giriraj (1.45).

In case of canopy temperature depression (°C) cross DRMR-15-16 × Giriraj (1.45) was the best performing one which did not differ significantly from other genotypes namely SKJM-05 (1.54), PHR-2 (1.62) and NPJ-194 (1.75) and crosses NPJ-194 × DRMR-15-16

(1.49), RW-85-59 × DRMR-15-16 (1.61), Giriraj × PHR-2 (1.62), DRMR-15-16 × Kranti (1.65), DRMR-15-16 × RNWR-09-3 (1.65), RNWR-09-3 × PHR-2 (1.79), RW-85-59 × PHR-2 (1.74) and SKJM-05 × PHR-2 (1.79).

4.11.2.5 Proline content of leaf (mg/gm)

Among the eight parents, the mean value of proline content of leaf varied from RNWR-09-3(4.60) to DRMR-15-16 (6.180) with mean of 5.436 whereas, among crosses, it ranged from DRMR-15-16 × SKJM-05 (4.157) to DRMR-15-16 × PHR-2 (6.540) with mean of 5.436. The grand mean for this character was 5.352.

In the case of proline content of leaf, cross DRMR-15-16 × PHR-2 (6.54) was the best-performing one which did not differ significantly from other genotypes namely DRMR-15-16 (6.18), PHR -2 (6.17) and NPJ-194 × RW-85-59 (6.11) cross SKJM-05 × Giriraj (6.32). Poor performance was shown by the cross DRMR-15-16 × SKJM-05 (4.16) followed by RW-85-59 × Kranti (4.35).

4.11.2.6 Chlorophyll a (mg/gm)

For chlorophyll a, the parental mean varied from 0.74 (Kranti) to 1.20 (PHR-2) with a mean value of 1.00 whereas, among crosses, NPJ-194 × RW-85-59 exhibited lowest of 0.43 while Kranti × PHR-2 showed highest mean value of 1.18 mg/gm. The overall mean of parents and crosses was observed to be 0.92 mg/gm.

In case of chlorophyll a genotype PHR -2 (1.20) was the best performing one which did not differ significantly from other genotypes namely Giriraj (1.13), RNWR-09-3 (1.14) and NPJ-194 (1.10) while crosses namely Kranti × PHR-2 (1.18), DRMR-15-16 × PHR-2 (1.12), DRMR-15-16 × SKJM-05 (1.05), DRMR-15-16 × RNWR-09-3 (1.03), Giriraj × RNWR-09-3 (1.04), RW-85-59 × Kranti (1.02), RW-85-59 (1.04), NPJ-194 × Giriraj (1.00), SKJM-05 × Giriraj (0.99), DRMR-15-16 × Kranti (0.97), SKJM-05 × RNWR-09-3 (0.98), SKJM-05 × PHR-2 (0.97), NPJ-194 × DRMR-15-16 (0.97), DRMR-15-16 × Giriraj (0.97), Kranti ×

RNWR-09-3 (0.97), RW-85-59 × PHR-2 (0.93), DRMR-15-16 (0.94), RW-85-59 × Kranti (1.02), Giriraj × PHR-2 (0.90) and RNWR-09-3 × PHR-2 (0.89) whereas low performing genotype was NPJ-194 × RW-85-59 (0.43).

4.11.2.7 Chlorophyll b (mg/gm)

Among the parental genotypes, PHR-2 (0.47) recorded the highest mean value and SKJM-05 (0.21) had the minimum mean value with the mean value of 0.35 for this character. The cross, DRMR-15-16 × RNWR-09-3 (0.47) recorded the highest value and lowest value was shown by NPJ-194 × RW-85-59 (0.18) with an average of 0.35 for this character.

Genotype PHR -2 (0.47) showed best performance in case of chlorophyll b and did not differ significantly from other genotypes namely Giriraj (0.44), RNWR-09-3 (0.39) crosses viz., DRMR-15-16 × RNWR-09-3 (0.47), RW-85-59 × RNWR-09-3 (0.44), NPJ-194 × PHR -2 (0.37) and DRMR-15-16 × PHR-2 (0.36).

4.11.2.8 Total Chlorophyll (mg/gm)

The estimates among parents, the mean value varied from 1.033 (SKJM-05) to 1.767 (PHR -2) whereas, among crosses, it ranged from 0.793 (NPJ-194 × RW-85-59) to 1.513 (Kranti × PHR-2). The average of parents and crosses are 1.376 and 1.153 respectively whereas, the grand mean for both parents and crosses is 1.203.

In the case of total chlorophyll genotype PHR-2 (1.77) was the best-performing one which did not differ significantly from other genotypes namely Giriraj (1.58), RNWR-09-3 (1.51) and crosses Kranti × PHR-2 (1.51), NPJ-194 × PHR -2 (1.46) and RW-85-59 × RNWR-09-3 (1.43) whereas lowest value was observed for genotype NPJ-194 × RW-85-59 (0.79).

4.11.3 Mean performance of parents and crosses for aphid related characters

The mean performance of parents and crosses are presented in Table 4.15. The character-wise findings are described below:

Table 4.14 Mean performance of parents and crosses for physiological characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Percentage of membrane stability index(%)	Percentage of excised leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
1	NPJ-194	74.13 (1.77)	29.03 (1.46)	86.35 (1.01)	1.75 (0.44)	5.45	1.10 (0.32)	0.33 (0.12)	1.09
2	RW-85-59 (Sarma)	73.96 (1.78)	26.16 (1.41)	85.56 (1.01)	1.91 (0.47)	5.12	1.04 (0.30)	0.30 (0.11)	1.34
3	DRMR-15-16	63.89 (1.73)	18.81 (1.27)	84.77 (1.01)	1.97 (0.47)	6.18	0.94 (0.29)	0.33 (0.12)	1.32
4	SKJM-05	58.77 (1.70)	14.46 (1.16)	84.41 (1.01)	1.54 (0.40)	5.96	0.72 (0.23)	0.21 (0.08)	1.03
5	Kranti	63.82 (1.72)	34.69 (1.54)	79.06 (0.99)	1.89 (0.46)	4.65	0.74 (0.23)	0.31 (0.12)	1.36
6	Giriraj	68.96 (1.75)	16.10 (1.20)	84.63 (1.01)	1.94 (0.47)	5.35	1.13 (0.33)	0.44 (0.15)	1.58
7	RNWR-09-3	69.24 (1.75)	18.71 (1.27)	85.29 (1.01)	1.79 (0.45)	4.60	1.14 (0.33)	0.39 (0.14)	1.51
8	PHR -2	53.03 (1.67)	33.38 (1.52)	80.82 (1.00)	1.62 (0.42)	6.17	1.20 (0.34)	0.47 (0.17)	1.77
	Mean (Parents)	65.72 (1.73)	23.92 (1.35)	83.86 (1.01)	1.80 (0.45)	5.44	1.00 (0.30)	0.35 (0.13)	1.38
	Crosses								
1	NPJ-194 × RW-85-59	63.10 (1.72)	25.08 (1.39)	84.13 (1.01)	1.73 (0.44)	6.11	0.43 (0.16)	0.18 (0.07)	0.79
2	NPJ-194 × DRMR-15-16	60.51 (1.71)	21.59 (1.33)	81.45 (1.00)	1.49 (0.39)	5.61	0.97 (0.29)	0.22 (0.09)	1.02
3	NPJ-194 × SKJM-05	65.12 (1.73)	36.66 (1.57)	82.46 (1.00)	1.82 (0.45)	5.67	0.82 (0.26)	0.23 (0.09)	1.05
4	NPJ-194 × Kranti	66.67 (1.74)	31.12 (1.49)	90.04 (1.02)	1.80 (0.45)	5.51	0.87 (0.27)	0.29 (0.11)	1.38
5	NPJ-194 × Giriraj	67.63 (1.74)	21.95 (1.34)	85.81 (1.01)	2.08 (0.49)	4.96	1.00 (0.30)	0.26 (0.10)	1.13
6	NPJ-194 × RNWR-09-3	74.50 (1.78)	21.69 (1.29)	84.42 (1.01)	1.99 (0.47)	4.82	0.84 (0.26)	0.23 (0.09)	1.18
7	NPJ-194 × PHR -2	68.09 (1.74)	26.26 (1.41)	89.79 (1.02)	1.81 (0.45)	4.95	0.87 (0.27)	0.37 (0.13)	1.46
8	RW-85-59 × DRMR-15-16	72.54 (1.76)	21.57 (1.33)	79.01 (0.99)	1.61 (0.42)	5.40	0.79 (0.25)	0.18 (0.07)	0.97

Table 4.14 (Continued)

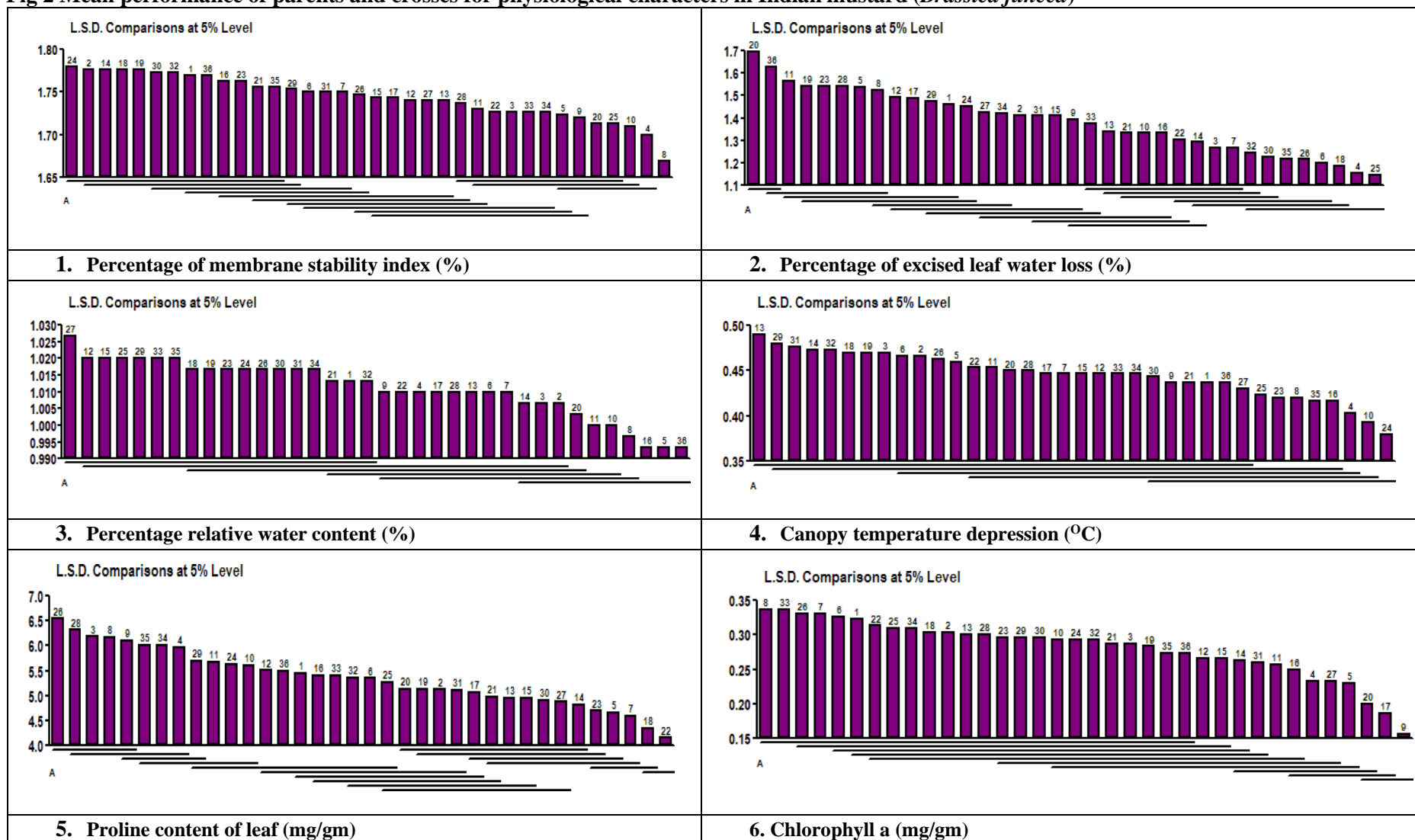
S.No	Parents	Percentage of membrane stability index (%)	Percentage of excised leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b(mg/gm)	Total Chlorophyll (mg/gm)
Crosses									
9	RW-85-59 × SKJM-05	67.78 (1.74)	32.53 (1.49)	85.21 (1.01)	1.79 (0.45)	5.06	0.54 (0.19)	0.22 (0.08)	0.88
10	RW-85-59 × Kranti	74.65 (1.78)	15.40 (1.19)	88.07 (1.02)	1.95 (0.47)	4.35	1.02 (0.30)	0.24 (0.09)	1.02
11	RW-85-59 × Giriraj	74.56 (1.78)	34.94 (1.54)	87.79 (1.02)	1.96 (0.47)	5.13	0.91 (0.28)	0.24 (0.09)	1.05
12	RW-85-59 × RNWR-09-3	61.63 (1.71)	49.96 (1.70)	82.95 (1.00)	1.82 (0.45)	5.14	0.58 (0.20)	0.44 (0.16)	1.43
13	RW-85-59 × PHR-2	70.72 (1.76)	21.57 (1.33)	87.22 (1.01)	1.74 (0.44)	4.97	0.93 (0.29)	0.31 (0.12)	1.22
14	DRMR-15-16 × SKJM-05	63.94 (1.73)	20.23 (1.30)	85.99 (1.01)	1.84 (0.45)	4.16	1.05 (0.31)	0.31 (0.12)	1.33
15	DRMR-15-16 × Kranti	71.58 (1.76)	35.03 (1.54)	88.18 (1.02)	1.65 (0.42)	4.70	0.97 (0.30)	0.26 (0.10)	1.05
16	DRMR-15-16 × Giriraj	75.29 (1.78)	28.44 (1.45)	88.86 (1.02)	1.45 (0.38)	5.64	0.97 (0.29)	0.28 (0.11)	1.03
17	DRMR-15-16 × RNWR-09-3	61.42 (1.71)	14.10 (1.15)	88.21 (1.02)	1.65 (0.42)	5.27	1.03 (0.31)	0.47 (0.16)	1.25
18	DRMR-15-16 × PHR-2	68.50 (1.75)	16.57 (1.22)	87.99 (1.02)	1.90 (0.46)	6.54	1.12 (0.33)	0.36 (0.13)	1.39
19	SKJM-05 × Kranti	67.37 (1.74)	26.89 (1.43)	92.41 (1.03)	1.72 (0.43)	4.88	0.71 (0.23)	0.24 (0.09)	0.98
20	SKJM-05 × Giriraj	66.02 (1.74)	34.75 (1.54)	84.28 (1.01)	1.80 (0.45)	6.32	0.99 (0.30)	0.24 (0.09)	0.94
21	SKJM-05 × RNWR-09-3	69.92 (1.75)	30.16 (1.48)	89.75 (1.02)	2.02 (0.48)	5.70	0.98 (0.30)	0.28 (0.11)	1.20
22	SKJM-05 × PHR-2	74.39 (1.77)	16.99 (1.23)	87.67 (1.02)	1.79 (0.44)	4.90	0.97 (0.30)	0.28 (0.11)	1.15
23	Kranti × Giriraj	68.43 (1.75)	25.79 (1.41)	88.97 (1.02)	2.00 (0.48)	5.12	0.82 (0.26)	0.28 (0.11)	1.07
24	Kranti × RNWR-09-3	74.36 (1.77)	17.69 (1.25)	86.95 (1.01)	1.99 (0.47)	5.36	0.97 (0.29)	0.27 (0.10)	1.02
25	Kranti × PHR-2	64.10 (1.73)	23.93 (1.38)	90.89 (1.02)	1.80 (0.45)	5.40	1.18 (0.34)	0.27 (0.10)	1.51
26	Giriraj × RNWR-09-3	64.53 (1.73)	26.49 (1.42)	88.24 (1.02)	1.81 (0.45)	6.01	1.04 (0.31)	0.31 (0.12)	1.32
27	Giriraj × PHR-2	69.84 (1.76)	16.78 (1.22)	88.92 (1.02)	1.62 (0.42)	6.02	0.90 (0.27)	0.32 (0.12)	1.37

Table 4.14 (Continued)

S.No.	Parents	Percentage of membrane stability index (%)	Percentage of excised leaf water loss (%)	Percentage relative water content (%)	Canopy temprature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
28	RNWR-09-3 × PHR-2	73.87 (1.77)	42.46 (1.63)	78.68 (0.99)	1.79 (0.44)	5.50	0.89 (0.27)	0.30 (0.11)	1.11
	Mean (Crosses)	68.61 (1.75)	26.31 (1.39)	86.58 (1.01)	1.80 (0.45)	5.33	0.90 (0.28)	0.28 (0.11)	1.15
	Grand Mean	67.97 (1.74)	25.78 (1.37)	85.98 (1.01)	1.80 (0.45)	5.35	0.92 (0.29)	0.30 (0.12)	1.20
	SEm (±)	0.01^t	0.03^t	0.00^t	0.02^t	0.13^t	0.02^t	0.01^t	0.12^t
	CD (P=0.05)	0.02^t	0.11^t	0.02^t	0.06^t	0.43^t	0.07^t	0.04^t	0.34^t

The values in parenthesis indicate the transformed values of the original data. Here “^t” in the superscript of SEm (±) and CD (P=0.05) indicate that they have been estimated from the transformed data. In the case of the characters for which the data has been transformed, the analysis was further carried out using the transformed values only.

Fig 2 Mean performance of parents and crosses for physiological characters in Indian mustard (*Brassica juncea*)



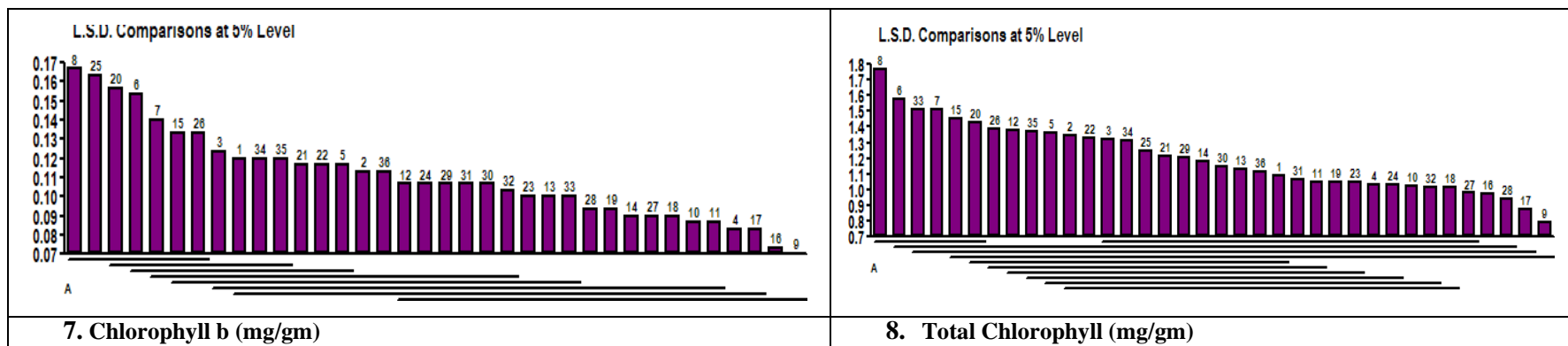


Fig 2 (Continued)

4.11.3.1 Water content of aphid probed twig (%)

Water content of aphid probed twig for parents ranged from RW-85-59 (71.99) to PHR-2 (80.65) percent with a mean value of 77.86 percent while in the case of crosses, it varied from 71.40 (RW-85-59 × SKJM-05) to 80.13 (Giriraj × RNWR-09-3) with a mean value of 76.15 percent. The grand mean value of this character for parents and crosses was 76.53 percent.

In the case of water content of aphid probed twig genotype PHR-2 (80.65) was the best-performing one which did not differ significantly from other genotypes namely Kranti (80.45), NPJ-194 (80.11), DRMR-15-16 (78.87), SKJM-05 (78.27), RNWR-09-3 (76.85) and crosses NPJ-194 × RW-85-59 (76.99), SKJM-05 × Kranti (76.85), Giriraj × RNWR-09-3 (80.13), NPJ-194 × Giriraj (80.09), DRMR-15-16 × SKJM-05 (79.72), DRMR-15-16 × Kranti (78.13), Giriraj × PHR-2 (77.88), SKJM-05 × Giriraj (77.61), NPJ-194 × RNWR-09-3 (77.44), DRMR-15-16 × RNWR-09-3 (77.32) and DRMR-15-16 × PHR-2 (77.20). Poor performance was showed by cross NPJ-194 × RW-85-59 (76.99).

4.11.3.2 Water content of aphid uninfested twig (%)

Water content of aphid uninfested twig, among the parents, ranged from 67.53 (RW-85-59) to 78.38 (Kranti) with a mean value of 73.69 percent, while in case of crosses it ranged from 68.15 (SKJM-05 × PHR-2) to 82.68 (SKJM-05 × Giriraj) with an average value of 75.32 percent. 74.96 percent was the grand mean value of this character for both parents and crosses.

Cross SKJM-05 × Giriraj (82.68) showed the best performance in case of the water content of aphid uninfested twig and did not differ significantly from other genotypes namely SKJM-05 × Kranti (81.67), RNWR-09-3 × PHR-2 (81.04), DRMR-15-16 × SKJM-05 (79.01), DRMR-15-16 × Kranti (79.01), RW-85-59 × Giriraj (78.77), Giriraj × RNWR-09-3 (78.76), Kranti (78.38), DRMR-15-16 × RNWR-09-3 (78.35), DRMR-15-16 × Giriraj (77.47) and RW-

85-59 × DRMR-15-16 (77.15) while the genotype RW-85-59 (67.53) showed poor performance.

4.11.3.3 Water content of aphid (%)

Parent (Giriraj) 37.01 percentage recorded lowest and (NPJ-194) 59.13 showed maximum water content of aphid. For crosses, the highest water content of aphid was recorded by the cross (NPJ-194 × Giriraj) 62.80 and lowest by (RNWR-09-3 × PHR-2) 17.42.

In the case of water content of aphid genotype cross, RNWR-09-3 × PHR-2 (17.42) was the best-performing one which did not differ significantly from other crosses namely RW-85-59 × DRMR-15-16 (19.53) while cross NPJ-194 × Giriraj (62.80) followed by RW-85-59 × Kranti (61.50) were low performing.

4.11.3.4 Percentage of water differential between aphid probed twig and aphid itself (%)

The percentage of water differential between aphid probed twig and aphid itself among the parents ranged from 20.98 (NPJ-194) to 38.69 (Giriraj), with a parental mean value of 28.96 percentage. Among the crosses, RW-85-59 × Kranti (14.51) showed minimum while it was the highest in RNWR-09-3 × PHR-2 (57.36), with an average value of 36.63 percentage. The grand mean value for this character was recorded as 37.48 percentage.

In case of the percentage of water differential between aphid probed twig and aphid itself cross RNWR-09-3 × PHR-2 (57.36) was the best-performing one which did not differ significantly from other crosses namely RW-85-59 × DRMR-15-16 (53.77), DRMR-15-16 × RNWR-09-3 (51.96), DRMR-15-16 × PHR-2 (51.27), DRMR-15-16 × Kranti (50.74), DRMR-15-16 × Giriraj (48.97), Kranti × Giriraj (47.28), NPJ-194 × PHR -2 (46.40), RW-85-59 × Giriraj (46.27), RW-85-59 × RNWR-09-3 (45.67), SKJM-05 × Kranti (45.34), DRMR-15-16 × SKJM-05 (44.12), RW-85-59 × PHR-2 (57.36) and NPJ-194 × SKJM-05 (42.13) whereas low performing genotype was RW-85-59 × Kranti (14.51).

4.11.4.5 Aphid count

Among the parents, the aphid count varied from 45.11 (RW-85-59) to 111.33 (RNWR-09-3) with a parental mean value of 82.14 while the corresponding range among the crosses varies from 28.67 (NPJ-194 × SKJM-05) to 150.44 (NPJ-194 × DRMR-15-16), with an average value of 82.14. The grand mean value for this character was recorded as 66.63.

In the case of aphid count cross, NPJ-194 × SKJM-05 (28.67) was the best-performing one which did differ significantly from cross NPJ-194 × RW-85-59 (32.00). The poor performance was showed by NPJ-194 × DRMR-15-16 (150.44) followed by RNWR-09-3 (111.33).

4.11.4.6 Penetration force

Among the parents, penetration force ranged from 66.417 (PHR-2) to 96.293 (RNWR-09-3) with a mean value of 81.906, while in case of crosses reflected range from 63.160 (NPJ-194 × Giriraj) to 94.710 (RW-85-59 × RNWR-09-3) with an average value of 77.235. The grand mean for parents and crosses was 78.273.

In the case of penetration force, genotype RNWR-09-3 (96.29) was the best-performing one which did not differ significantly from other genotypes namely RW-85-59 × RNWR-09-3 (94.71) and NPJ-194 × DRMR-15-16 (92.75) whereas low performing genotype was NPJ-194 × Giriraj (63.16).

4.12 Analysis of variance for combining ability

4.12.1 Analysis of variance for seed yield and its attributing characters

The analysis of variance for combining ability was carried out separately for all the characters involving eight parents and twenty-eight crosses, which are presented in Table 4.16. The mean sum of squares due to GCA was significant for all the ten seed yield and its attributing characters at 5% and 1% probability levels. The mean sum of squares due to SCA

Table 4.15 Mean performance of parents and crosses for aphid related characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
1	NPJ-194	80.11 (63.55)	73.54 (59.06)	59.13 (1.70)	20.98 (1.43)	108.44 (2.04)	76.37
2	RW-85-59 (Sarma)	71.99 (58.05)	67.53 (55.27)	48.31 (1.64)	23.68 (1.46)	45.11 (1.65)	85.43
3	DRMR-15-16	78.87 (62.64)	75.70 (60.50)	48.13 (1.64)	30.75 (1.52)	59.00 (1.77)	86.12
4	SKJM-05	78.27 (62.22)	73.12 (58.79)	51.18 (1.66)	27.09 (1.50)	61.67 (1.79)	87.65
5	Kranti	80.45 (63.79)	78.38 (62.35)	53.43 (1.67)	27.02 (1.49)	75.22 (1.88)	75.38
6	Giriraj	75.70 (60.47)	69.11 (56.24)	37.01 (1.57)	38.69 (1.59)	108.67 (2.04)	81.57
7	RNWR-09-3	76.85 (61.25)	76.11 (60.76)	39.13 (1.58)	37.72 (1.57)	111.33 (2.05)	96.29
8	PHR -2	80.65 (63.92)	75.99 (60.70)	46.89 (1.64)	33.76 (1.55)	87.67 (1.94)	66.42
	Mean (Parents)	77.86 (61.99)	73.69 (59.21)	47.90 (1.64)	29.96 (1.51)	82.14 (1.89)	81.91
	Crosses						
1	NPJ-194 × RW-85-59	76.99 (61.36)	71.43 (57.69)	48.09 (1.64)	28.90 (1.51)	32.00 (1.50)	84.67
2	NPJ-194 × DRMR-15-16	74.50 (59.72)	74.71 (59.85)	41.72 (1.60)	32.77 (1.54)	150.44 (2.18)	92.75
3	NPJ-194 × SKJM-05	74.74 (59.84)	75.66 (60.45)	32.61 (1.54)	42.13 (1.61)	28.67 (1.45)	77.97
4	NPJ-194 × Kranti	76.24 (60.84)	73.02 (58.82)	46.96 (1.63)	29.28 (1.51)	54.45 (1.73)	66.97
5	NPJ-194 × Giriraj	80.09 (63.53)	68.82 (56.06)	62.80 (1.72)	17.28 (1.39)	37.45 (1.57)	63.16
6	NPJ-194 × RNWR-09-3	77.44 (61.66)	73.14 (58.79)	42.15 (1.60)	35.29 (1.55)	89.22 (1.95)	79.76
7	NPJ-194 × PHR -2	74.56 (59.73)	75.74 (60.60)	28.16 (1.51)	46.40 (1.63)	66.55 (1.83)	65.10
8	RW-85-59 × DRMR-15-16	73.30 (58.91)	77.15 (61.48)	19.53 (1.41)	53.77 (1.67)	42.56 (1.63)	82.31

Table 4.15 (Continued)

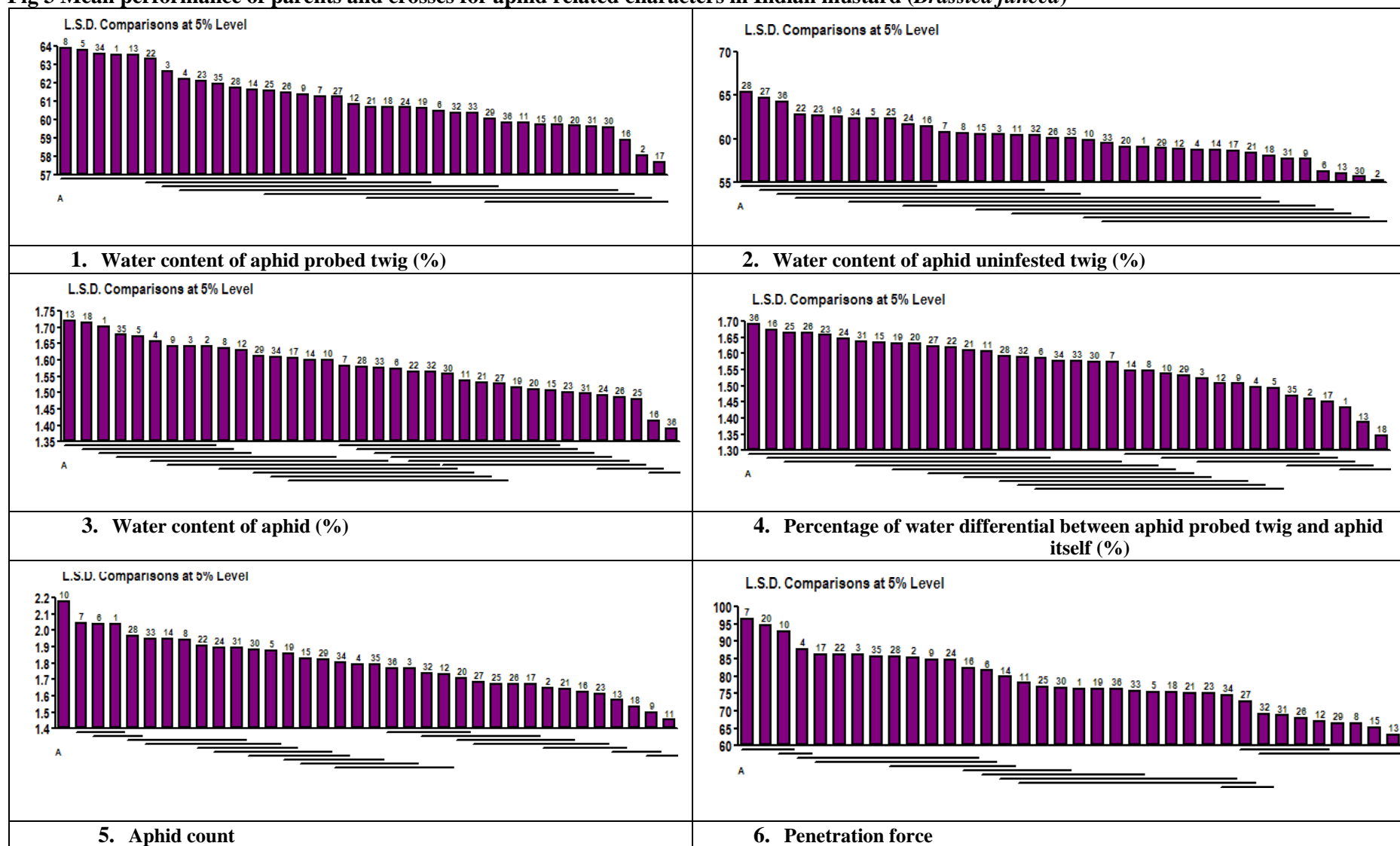
S.No.	Parents	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
9	RW-85-59 × SKJM-05	71.40 (57.68)	72.96 (58.68)	44.62 (1.61)	26.77 (1.45)	47.33 (1.67)	86.26
10	RW-85-59 × Kranti	76.00 (60.67)	71.96 (58.04)	61.50 (1.71)	14.51 (1.35)	34.44 (1.53)	75.31
11	RW-85-59 × Giriraj	75.96 (60.66)	78.77 (62.57)	29.69 (1.52)	46.27 (1.63)	73.56 (1.86)	76.37
12	RW-85-59 × RNWR-09-3	74.48 (59.67)	73.01 (59.11)	28.81 (1.51)	45.67 (1.63)	51.11 (1.71)	94.71
13	RW-85-59 × PHR-2	75.95 (60.68)	72.43 (58.41)	31.90 (1.53)	44.04 (1.61)	43.78 (1.64)	75.15
14	DRMR-15-16 × SKJM-05	79.72 (63.30)	79.01 (62.76)	35.60 (1.56)	44.12 (1.62)	80.56 (1.91)	86.20
15	DRMR-15-16 × Kranti	78.13 (62.13)	79.01 (62.74)	27.39 (1.50)	50.74 (1.66)	41.33 (1.61)	75.02
16	DRMR-15-16 × Giriraj	75.99 (60.67)	77.47 (61.70)	27.03 (1.49)	48.97 (1.65)	79.22 (1.90)	84.61
17	DRMR-15-16 × RNWR-09-3	77.32 (61.59)	78.35 (62.32)	25.35 (1.48)	51.96 (1.66)	47.00 (1.67)	76.82
18	DRMR-15-16 × PHR-2	77.20 (61.49)	75.14 (60.14)	25.93 (1.49)	51.27 (1.66)	47.44 (1.67)	67.92
19	SKJM-05 × Kranti	76.85 (61.25)	81.67 (64.76)	31.51 (1.53)	45.34 (1.62)	49.11 (1.69)	72.83
20	SKJM-05 × Giriraj	77.61 (61.76)	82.68 (65.43)	37.99 (1.58)	39.62 (1.59)	93.56 (1.97)	85.58
21	SKJM-05 × RNWR-09-3	75.05 (60.06)	73.00 (58.93)	43.36 (1.61)	31.69 (1.53)	66.78 (1.82)	66.50
22	SKJM-05 × PHR-2	74.39 (59.61)	68.15 (55.66)	35.50 (1.56)	38.88 (1.57)	76.56 (1.88)	76.72
23	Kranti × Giriraj	74.41 (59.63)	71.45 (57.74)	27.13 (1.50)	47.28 (1.64)	77.78 (1.89)	68.67
24	Kranti × RNWR-09-3	75.54 (60.38)	75.51 (60.41)	35.77 (1.56)	39.77 (1.59)	55.44 (1.74)	69.01
25	Kranti × PHR-2	75.56 (60.38)	74.20 (59.48)	37.78 (1.58)	37.78 (1.58)	90.00 (1.95)	75.68
26	Giriraj × RNWR-09-3	80.13 (63.59)	78.46 (62.37)	42.41 (1.61)	37.72 (1.58)	64.22 (1.81)	74.57
27	Giriraj × PHR-2	77.88 (61.96)	75.11 (60.12)	53.92 (1.68)	23.95 (1.47)	61.67 (1.79)	85.75

Table 4.15 (Continued)

S.No.	Parents	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
28	RNWR-09-3 × PHR-2	74.77 (59.86)	81.04 (64.26)	17.42 (1.39)	57.36 (1.69)	59.33 (1.77)	76.23
	Mean (Crosses)	76.15 (60.81)	75.32 (60.33)	36.52 (1.56)	39.63 (1.58)	62.20 (1.76)	77.24
	Grand Mean	76.53 (61.40)	74.96 (59.77)	39.05 (1.60)	37.48 (1.55)	66.63 (1.83)	78.27
	SEm (±)	0.83^t	1.35^t	0.02^t	0.03^t	0.02^t	1.81^t
	CD (P=0.05)	2.51^t	4.42^t	0.08^t	0.10^t	0.07^t	5.88^t

The values in parenthesis indicate the transformed values of the original data. Here “t” in the superscript of SEm (±) and CD (P=0.05) indicate that they have been estimated from the transformed data. In the case of the characters for which the data has been transformed, the analysis was further carried out using the transformed values only.

Fig 3 Mean performance of parents and crosses for aphid related characters in Indian mustard (*Brassica juncea*)



was also significant for all the characters except seed siliqua⁻¹.

4.12.2 Analysis of variance for physiological characters

Analysis of variance due to combining ability concerning physiological characters to check the significance of difference among the eight parents and their twenty-eight crosses are presented in Table 4.17. The results for combining ability analysis revealed that the mean square for GCA and SCA was significant for all the characters *viz.*, percentage membrane stability index (%), percentage excised- leaf water loss (%), percentage relative water content (%), proline content of leaf, chlorophyll a, chlorophyll b and total chlorophyll.

4.12.3 Analysis of variance for aphid related characters

The analysis of variance for combining ability was carried out separately for all the six aphid-related characters are presented in Table 4.18. It was observed that the mean square of both GCA and SCA were significant for all six aphid related characters *viz.*, water content of aphid probed twig (%), water content of aphid uninfested twig (%), water content of aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force.

4.13 Estimates of genetic components of variances

4.13.1 Estimates of genetic components of variances for seed yield and its attributing characters

The estimates of genetic components of variances and degree of dominance for ten seed yield and its attributing characters are presented in Table 4.19. The contribution of SCA component of variance (σ^2_{sca}) was higher than the GCA component of variance (σ^2_{gca}) for all the characters studied *viz.*, days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliqua⁻¹, height up to first fruiting branch, plant height, seed yield per plant, 1000 seed weight and oil content.

Table 4.16 Analysis of variance for combining ability for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)

Sources of variation	df	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height(cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
GCA	7	42.659**	0.390*	5.032**	100.810**	3.0036**	114.860**	29.574**	10.221**	83.056**	49.828**
SCA	28	6.111**	0.304*	2.033*	63.813**	1.308	22.137**	10.065***	14.240**	36.763**	42.698**
Error	70	1.085	0.163	1.061	0.708	0.840	2.960	0.181	3.051	0.475	0.327

*, ** Significant at 5% and 1% levels of probability, respectively

Table 4.17 Analysis of variance for combining ability for physiological characters in Indian mustard (*Brassica juncea*)

Sources of variation	df	Percentage of membrane stability index (%)	Percentage excised- leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyllb (mg/gm)	Total Chlorophyll (mg/gm)
GCA	7	0.0003**	0.0056**	0.0001**	0.0005	0.1723**	0.0025**	0.0012**	0.0883**
SCA	28	0.0007**	0.0231**	0.0001**	0.0007	0.3613**	0.0016**	0.0004**	0.0376**
Error	70	0.0001	0.0014	0.0000	0.0005	0.0231	0.0006	0.0002	0.0149

*, ** Significant at 5% and 1% levels of probability, respectively

Table 4.18 Analysis of variance for combining ability for aphid related characters in Indian mustard (*Brassica juncea*)

Sources of variation	Df	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force(Kpascal)
GCA	7	3.5472**	7.8858**	0.0128**	0.0108**	0.0412**	108.8149**
SCA	28	2.2290**	5.6104**	0.0048**	0.0060**	0.0245**	63.8463**
Error	70	0.7922	2.4602	0.0009	0.0012	0.0006	4.2965

*, ** Significant at 5% and 1% levels of probability, respectively

The GCA and SCA variance ratio ($\sigma_{gca}^2/\sigma_{sca}^2$) was less than 1 for all the characters. The mean degree of dominance ($\sigma_{sca}^2/\sigma_{gca}^2$)^{0.5} was found to be greater than 1 for all the characters which indicated the involvement of over dominance. The estimates of variance due to dominance (σ_D^2) were higher than corresponding additive genetic variance (σ_A^2) for all the characters *i.e.*, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliqua⁻¹, height up to first fruiting branch, plant height, seed yield plant⁻¹ and 1000 seed weight except days to 50% flowering. The ratio of additive variance to dominance variance (σ_A^2/σ_D^2) was lower than unity for all the characters except days to 50% flowering. The estimates of predictability ratio ($\sigma_A^2/\sigma_A^2+\sigma_D^2$) were higher than 0.05 for all the characters under study.

4.13.2 Estimates of components of variance for physiological characters

The variances of genetic components and degree of dominance for physiological characters are presented in Table 4.20. The magnitude of SCA variance (σ_{sca}^2) was higher than GCA variance (σ_{gca}^2) for all the physiological characters *i.e.*, oil content, percentage of membrane stability index, percentage of excised leaf water loss, percentage of relative water content, canopy temperature depression, proline content of leaf, chlorophyll a, chlorophyll b and total chlorophyll. The GCA and SCA variance ratio ($\sigma_{gca}^2/\sigma_{sca}^2$) was less than 1 for all the characters. The average degree of dominance ($\sigma_{sca}^2/\sigma_{gca}^2$)^{0.5} for majority of characters showed over dominance *i.e.*, percentage of relative water content, chlorophyll a, chlorophyll b and total chlorophyll. The dominance genetic variation (σ_D^2) was higher than the additive genetic variance (σ_A^2) for all the physiological characters studied. The ratio of additive variance to dominance variance (σ_A^2/σ_D^2) was lower than unity for all the characters. The predictability ratio ($\sigma_A^2/\sigma_A^2+\sigma_D^2$) was higher than 0.50 for all the characters.

Table 4.19 Estimates of genetic components of variance and degree of dominance for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)

Sources of variation	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
σ^2_{gca}	3.65481	0.00860	0.29986	0.00037	0.16956	0.00093	0.00020	-0.00004	4.72936	0.71300
σ^2_{sca}	5.02637	0.14070	0.97198	0.00631	0.46812	0.00192	0.00099	0.00112	35.28757	42.37082
$\sigma^2_{gca}/\sigma^2_{sca}$	0.72713	0.06115	0.30851	0.05863	0.36222	0.48350	0.19735	-0.03591	0.13402	0.01683
$(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$	1.17272	1.17272	1.80040	4.12965	1.66156	1.43684	2.22485	5.29150	2.73155	7.70883
σ^2_A	7.30961	0.01721	0.59973	0.00074	0.33913	0.00185	0.00039	0.00008	9.45873	1.42600
σ^2_D	5.02637	0.14070	0.97198	0.00631	0.46812	0.00192	0.00099	0.00112	35.28757	42.37082
σ^2_A/σ^2_D	1.45425	0.12232	0.61702	0.11727	0.72445	0.96354	0.39394	0.07143	0.26805	0.03366
$\sigma^2_A/\sigma^2_A+\sigma^2_D$	6.02637	1.14070	1.97198	1.00631	1.46812	1.00192	1.00099	1.00112	36.28757	43.37082

gca = general combining ability, sca = specific combining ability, σ^2_{gca} = gca variance, σ^2_{sca} = sca variance, $(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$ = degree of dominance, σ^2_A = additive variance, σ^2_D = dominance variance, $\sigma^2_A/(\sigma^2_A+\sigma^2_D)$ = predictability ratio

Table 4.20 Estimates of genetic components of variance and degree of dominance for physiological characters in Indian mustard (*Brassica juncea*)

Sources of variation	Percentage of membrane stability index (%)	Percentage excised-leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
σ^2_{gca}	-0.00004	-0.00176	0.00001	-0.00001	-0.01891	0.00010	0.00008	0.00507
σ^2_{sca}	0.00068	0.02169	0.00003	0.00014	0.33819	0.00100	0.00023	0.02270
$\sigma^2_{gca}/\sigma^2_{sca}$	-0.06491	-0.08105	0.16331	-0.09529	-0.05590	0.09857	0.35816	0.22337
$(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$	-4.12310	-3.51053	1.73205	-3.74165	-4.22897	3.16227	1.69558	2.11590
σ^2_A	-0.00009	-0.00352	0.00001	-0.00003	-0.03781	0.00020	0.00016	0.01014
σ^2_D	0.00068	0.02169	0.00003	0.00014	0.33819	0.00100	0.00023	0.02270
σ^2_A/σ^2_D	-0.13235	-0.16229	0.33333	-0.21429	-0.11180	0.20000	0.69565	0.44670
$\sigma^2_A/\sigma^2_A+\sigma^2_D$	1.00068	1.02169	1.00003	1.00014	1.33819	1.00100	1.00023	1.02270

gca = general combining ability, sca = specific combining ability, σ^2_{gca} = gca variance, σ^2_{sca} = sca variance, $(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$ = degree of dominance, σ^2_A = additive variance, σ^2_D = dominance variance, $\sigma^2_A/(\sigma^2_A+\sigma^2_D)$ = predictability ratio

4.13.3 Estimates of components of variance for aphid related characters

The variances of genetic components and degree of dominance for aphid-related characters are presented in Table 4.21. The SCA component of variance (σ^2_{sca}) was higher than GCA variance (σ^2_{gca}) for all aphid related characters *i.e.*, water content of aphid probed twig (%), water content of aphid uninfested twig (%), water content of aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force. The GCA and SCA variance ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was lesser than one. The mean degree of dominance ($(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$) was found more than unity for all the aphid related characters indicated the over-dominance. Estimates of dominance variance (σ^2_D) was larger in magnitude than additive variance for all the aphid characters under study. The additive and non-additive ratio (σ^2_A/σ^2_D) was lower than unity for all the characters. The estimates of predictability ratios ($\sigma^2_A/(\sigma^2_A+\sigma^2_D)$) higher than 0.50 in all the aphid related characters and much higher in case of penetration force.

4.14 Estimation of general combining ability (gca) effects

4.14.1 Estimation of general combining ability (gca) effects for seed yield and its attributing characters

The estimates of the general combining ability effects of eight parents for all the nine seed yield and its attributing characters are given in Table 4.22. The character-wise findings are described below:

4.14.1.1 Days to 50% flowering

General combiners with a negative value for this character was considered as desirable. Among the parental genotypes, RW-85-59 (-3.442) and DRMR-15-16 (-1.775) exhibited significant negative general combining ability effects and were found to be good general combiners for early flowering. The genotypes namely NPJ-194 (1.658) and PHR-2 (3.458) showed significant positive *gca* effects which indicated that they were good general combiners

Table 4.21 Estimates of genetic components of variance and degree of dominance for aphid related characters in Indian mustard (*Brassica juncea*)

Sources of variation	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
σ^2_{gca}	0.13182	0.22753	0.00081	0.00048	0.00167	4.49686
σ^2_{sca}	1.43685	3.15023	0.00391	0.00479	0.02391	59.54974
$\sigma^2_{gca}/\sigma^2_{sca}$	0.09174	0.07223	0.20641	0.10117	0.06969	0.07551
$(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$	3.30152	3.72093	2.19707	3.15898	3.78383	3.63902
σ^2_A	0.26364	0.45507	0.00161	0.00097	0.00333	8.99373
σ^2_D	1.43685	3.15023	0.00391	0.00479	0.02391	59.54974
σ^2_A/σ^2_D	0.18348	0.14446	0.41176	0.20251	0.13927	0.15103
$\sigma^2_A/\sigma^2_A+\sigma^2_D$	2.43685	4.15023	1.00391	1.00479	1.02391	60.54974

gca = general combining ability, sca = specific combining ability, σ^2_{gca} = gca variance, σ^2_{sca} = sca variance, $(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$ = degree of dominance, σ^2_A = additive variance, σ^2_D = dominance variance, $\sigma^2_A/(\sigma^2_A+\sigma^2_D)$ = predictability ratio

for a long time to flowering while the other parental genotypes showed non-significant *gca* effect is Kranti (0.258), Giriraj (0.158), RNWR-09-3 (-0.242) and SKJM-05 (-0.075).

4.14.1.2 Primary branches per plant

Out of eight parents, genotype RW-85-59 (0.258) showed significant positive general combining ability effects and were found to be a good general combiner while genotype Giriraj (-0.375) exhibited significant negative general combining ability effects and were poor general combiner for primary branches per plant. Kranti (0.065), PHR-2 (0.225), NPJ-194 (-0.082), DRMR-15-16 (-0.015), SKJM-05 (-0.062) and RNWR-09-3 (-0.015) showed non-significant *gca* effect for primary branches per plant.

4.14.1.3 Secondary branches plant⁻¹

The genotypes RW-85-59 (1.200) and Kranti (0.726) emerged as good general combiners for secondary branches plant⁻¹ which revealed significant positive general combining ability effects, while the genotype Giriraj (-1.098) showed significant negative general combining ability effects and were considered as poor general combiners for this character. The genotypes NPJ-194 (-0.491), DRMR-15-16 (-0.318), SKJM-05 (0.049), RNWR-09-3 (-0.078) and PHR-2 (0.009) presented non-significant *gca* effect for secondary branches plant-1.

4.14.1.4 Siliquae per plant

Parents NPJ-194 (0.023), RW-85-59 (0.013), Kranti (0.030) and PHR 2 (0.038) were found good general combiners for siliquae per plant by exhibiting significant positive general combining ability effects and the genotypes DRMR-15-16 (-0.012), SKJM-05 (-0.026), Giriraj (-0.055) and RNWR-09-3 (-0.011) recorded significant negative general combining ability effects and poor general combiners for this character.

4.14.1.5 Seeds per siliquae

Out of all parental lines, only one genotype DRMR-15-16 (0.636) revealed a significant positive general combining ability effect and was found to be the best general combiner for seeds per siliqua. The genotypes NPJ-194 (-1.057) showed significant negative general combining ability effects appeared to be poor general combiners whereas RW-85-59 (0.282), SKJM-05 (0.209), Kranti (0.492), Giriraj (-0.004), RNWR-09-3 (-0.451) and PHR-2 (-0.107) genotypes exhibited non-significant *gca* effect for this character

4.14.1.6 Height upto first fruiting branch

The significant and desirable general combining ability effects were marked for height upto first fruiting branch in the genotypes RW-85-59 (0.057), DRMR-15-16 (0.021) and Kranti (0.024) are the best general combiners while the genotypes Giriraj (-0.027), RNWR-09-3 (-0.019), PHR-2 (-0.050) exhibited significant negative general combining ability effects reflecting as poor general combiners for height upto first fruiting branch. The parental genotypes namely NPJ-194 (0.002) and SKJM-05 (-0.009) revealed a non-significant *gca* effect for this character.

4.14.1.7 Plant height

In the case of plant height genotypes NPJ-194 (-0.021), RW-85-59 (-0.027) and DRMR-15-16 (-0.008) were good general combiners for dwarfness and exhibited significant negative general combining ability effects, while genotypes SKJM-05 (0.010), Kranti (0.011), Giriraj (0.007), RNWR-09-3 (0.006) and PHR-2 (0.023) revealed significant positive general combining ability effects and were best general combiners for tall plants.

4.14.1.8 Seed yield per plant

Out of all parental lines, one genotype SKJM-05 (0.013) showed significant and positive general combining ability effects and were found to be a good general combiner for seed yield per plant, while the parents Kranti (-0.011) and RNWR-09-3 (-0.016) revealed significant negative general combining ability effects appeared to be poor general combiners for this character while the parental genotypes NPJ-194 (0.006), RW-85-59 (0.000), DRMR-15-16 (0.003), Giriraj (0.009) and PHR-2 (-0.005) revealed non-significant *gca* effect for seed yield per plant.

4.14.1.9 1000 seed weight

The genotypes RW-85-59 (2.458), SKJM-05 (3.158), Kranti (1.292), RNWR-09-3 (1.558) and PHR-2 (1.758) showed significant positive general combining ability effects and emerged as the best general combiner while the significant negative general combining ability effects were recorded for the genotypes NPJ-194 (-3.275) and DRMR-15-16 (-3.642) as poor general combiners for 1000 seed weight.

4.14.1.10 Oil content

The general combiner effects for oil content ranged from -3.408 (Giriraj) to 3.625 (NPJ-194). The parents namely NPJ-194 (3.625), Kranti (0.358), RNWR-09-3 (2.125) and PHR-2 (0.458) showed positive and significant *gca* effects which may be considered as good general combiners whereas RW-85-59 (-0.108), DRMR-15-16 (-0.975), SKJM-05 (-2.075) and Giriraj (-3.408) showed negative significant *gca* and considered as poor general combiners for this character.

4.14.2 Estimation of general combining ability (*gca*) effects for physiological characters

The estimates of the general combining ability effects of eight parents for all the eight physiological characters are given in Table 4.23. The character-wise findings are described below:

4.14.2.1 Percentage of membrane stability index

The general combiner effects for percentage of membrane stability index ranged from SKJM-05 (-0.007) to Giriraj (0.008). Good general combiners for percentage of membrane stability index with significant positive *gca* effects were observed in Kranti (0.005) and Giriraj (0.008). The highest negative and significant *gca* effect were exhibited in SKJM-05 (-0.007) and NPJ-194 (-0.006) resulting these were poor general combiners for this character whereas, RW-85-59(-0.004), RNWR-09-3 (-0.001), DRMR-15-16 (0.003) and PHR-2 (0.002) parental genotypes showed non-significant *gca* effects for the percentage of membrane stability index.

4.14.2.2 Percentage of excised - leaf water loss

General combiners with a negative value for this character was considered as desirable. Only two parents namely SKJM-05 (-0.029) and RNWR-09-3 (-0.028) was found as a good general combiner for the percentage of excised -leaf water loss by exhibiting significant negative *gca* effects, while the genotype Kranti (0.039) was considered as poor general combiner because of positive significant *gca* effects for this character. Parental genotypes NPJ-194 (-0.018), RW-85-59 (0.017), DRMR-15-16 (0.005), Giriraj (0.005) and PHR-2 (0.009) were found as poor general combiner for percentage of excised -leaf water loss as these genotypes showed non-significant *gca* effects.

4.14.2.3 Percentage of relative water content

Good general combiners for the percentage of relative water content with significant positive *gca* effects were observed one genotype *i.e.*, Kranti (0.005). Negative and significant *gca* effect was exhibited in NPJ-194 (-0.004) and DRMR-15-16 (-0.005) resulting these were poor general combiners for this character. However, RW-85-59 (-0.002), PHR-2 (-0.001), SKJM-05 (0.001), Giriraj (0.003) and RNWR-09-3 (0.003) had non-significant *gca* effects.

Table 4.22 General combining ability (gca) effects for parents for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
1	NPJ-194	1.658**	-0.082	-0.491	0.023**	-1.057**	0.002	-0.021**	0.006	-3.275*	3.625*
2	RW-85-59 (Sarma)	-3.442**	0.258*	1.200**	0.013**	0.282	0.057**	-0.027**	0.000	2.458*	-0.108*
3	DRMR-15-16	-1.775**	-0.015	-0.318	-0.012**	0.636*	0.021**	-0.008**	0.003	-3.642*	-0.975*
4	SKJM-05	-0.075	-0.062	0.049	-0.026**	0.209	-0.009	0.010**	0.013*	3.158*	-2.075*
5	Kranti	0.258	0.065	0.726*	0.030**	0.492	0.024**	0.011**	-0.011*	1.292*	0.358*
6	Giriraj	0.158	-0.375**	-1.098**	-0.055**	-0.004	-0.027**	0.007**	0.009	-3.308*	-3.408*
7	RNWR-09-3	-0.242	-0.015	-0.078	-0.011**	-0.451	-0.019**	0.006**	-0.016**	1.558*	2.125*
8	PHR 2	3.458**	0.225	0.009	0.038**	-0.107	-0.050**	0.023**	-0.005	1.758*	0.458*
	SE (gi)	0.308	0.120	0.305	0.002	0.271	0.005	0.001	0.005	0.203	0.1691
	SE(gi-gj)	0.466	0.181	0.461	0.004	0.410	0.008	0.002	0.008	0.3082	0.2556

*, ** Significant at 5% and 1% levels of probability, respectively

Table 4.23 General combining ability (gca) effects for parents for physiological characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Percentage of membrane stability index (%)	Percentage excised- leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
1	NPJ-194	-0.006*	-0.018	-0.004*	0.000	0.077	0.017*	0.014**	0.127**
2	RW-85-59 (Sarma)	-0.004	0.017	-0.002	0.003	0.070	-0.026**	-0.014**	-0.067
3	DRMR-15-16	0.003	0.005	-0.005**	-0.004	-0.092*	-0.019*	-0.010*	0.095*
4	SKJM-05	-0.007**	-0.029*	0.001	-0.011	-0.102*	0.001	-0.001	-0.049
5	Kranti	0.005*	0.039**	0.005**	0.002	-0.229**	-0.007	-0.010*	-0.077*
6	Giriraj	0.008**	0.005	0.003	0.012	0.023	0.013	-0.003	-0.043
7	RNWR-09-3	-0.001	-0.028*	0.003	0.005	0.076	0.006	0.012**	0.077*
8	PHR 2	0.002	0.009	-0.001	-0.006	0.179**	0.015*	0.011*	0.126**
	SE (gi)	0.002	0.011	0.002	0.007	0.045	0.007	0.004	0.036
	SE(gi-gj)	0.004	0.017	0.002	0.010	0.068	0.011	0.006	0.055

*, ** Significant at 5% and 1% levels of probability, respectively

4.14.2.4 Canopy temperature depression

In this character, none of the parents showed significant positive or significant negative *gca* effect indicating no parents showed be a good combiner of the canopy temperature depression.

4.14.2.5 Proline content of leaf

The proline content of leaf with significant positive *gca* effects was observed only in PHR-2 (0.179) and this genotype was considered a good general combiner while the genotypes DRMR-15-16 (-0.092), SKJM-05 (-0.102) and Kranti (-0.229) was considered as poor general combiner because of negative significant *gca* effects for this character. Parental genotypes NPJ-194 (0.077), RW-85-59 (0.070), Giriraj (0.023) and RNWR-09-3 (0.076) were found as poor general combiner for this character as these genotypes showed non-significant *gca* effects.

4.14.2.6 Chlorophyll a

The general combiner effects for chlorophyll a ranged from -0.026 (RW-85-59) to 0.015 (PHR-2). The parents namely NPJ-194 (0.017) and PHR-2 (0.015) showed positive and significant *gca* effects which may be considered as good general combiners for this character whereas, RW-85-59 (-0.026) and DRMR-15-16 (-0.019) showed negative significant *gca* effects and were recorded as poor general combiners for chlorophyll a. Parental genotypes Kranti (-0.007), SKJM-05 (0.001), Giriraj (0.013), RNWR-09-3 (0.006) were found as a poor general combiner for this character as these genotypes showed non-significant *gca* effects.

4.14.2.7 Chlorophyll b

Significant positive *gca* effects for chlorophyll b, was exhibited by NPJ-194 (0.014), RNWR-09-3 (0.012) and PHR-2 (0.011). Genotypes RW-85-59 (-0.014), DRMR-15-16 (-0.010), Kranti (-0.010) expressed significant negative *gca* effects and were recorded as poor

general combiners for chlorophyll a. All other genotypes namely SKJM-05 (-0.001) and Giriraj (-0.003) showed non-significant *gca* effects for chlorophyll b.

4.14.2.8 Total Chlorophyll

Positive and significant *gca* effect was observed in the parental genotypes *viz.*, NPJ-194 (0.127), DRMR-15-16 (0.095), RNWR-09-3 (0.077) and PHR-2 (0.126), resulting these genotypes were good general combiners for this character, whereas negative significant *gca* were observed in only one genotype *i.e.*, Kranti (-0.077). Other parental genotypes specifically RW-85-59 (-0.067), SKJM-05 (-0.049) and Giriraj (-0.043) showed non-significant *gca* effect for total chlorophyll.

4.14.3 Estimation of general combining ability (*gca*) effects for aphid related characters

The estimates of general combining ability effects of eight parents for all the nine seed yield and its attributing characters are given in Table 4.24. The character-wise findings are described below:

4.14.3.2 Water content of aphid probed twig (%)

Positive and significant *gca* effects were recorded for only one parent *i.e.*, NPJ-194 (0.098) and recorded as excellent general combiners. DRMR-15-16 (-1.007) exhibited a significant negative *gca* effect for this character and considered as poor general combiner whereas, other parental genotypes namely RW-85-59 (-0.354), Giriraj (-0.252), PHR-2 (-0.216), SKJM-05 (0.258), Kranti (0.174) and RNWR-09-3 (0.413) presented non-significant *gca* effect for water content of aphid probed twig.

4.14.3.3 Water content of aphid uninfested twig (%)

Significant positive GCA effects for water content of aphid uninfested twig were possessed by two parental genotypes *i.e.*, SKJM-05 (0.957) and Kranti (1.072). These genotypes were considered as good general combiner for this character while RW-85-59 (-1.554) having negative significant *gca* effect for water content of aphid uninfested twig

represented poor general combiner. Some genotypes *viz.*, NPJ-194 (-0.803), DRMR-15-16 (-0.063), Giriraj (-0.339), RNWR-09-3 (0.442) and PHR-2 (0.287) showed non-significant effect for this character results in no *gca* effect.

4.14.3.4 Water content of aphid (%)

For the water content of aphid, general combiners with negative values are desirable. The parents, DRMR-15-16 (-0.024), SKJM-05 (-0.030) and PHR-2 (-0.044) showed negative and significant *gca* effects and are considered as best general combiner for this character. A significant and positive *gca* effect was exhibited by NPJ-194 (0.063) and RW-85-59 (0.034) was considered as poor general combiner. However, Giriraj (-0.017), Kranti (0.013) and RNWR-09-3 (0.006) parental genotypes showed non-significant *gca* effects for percentage for water content of aphid.

4.14.3.5 Percentage of water differential between aphid probed twig and aphid itself (%)

Among parents, significant and positive *gca* effects were recorded by SKJM-05 (0.035), Giriraj (0.021) and PHR-2 (0.038) was found as good general combiner for percentage of water differential between aphid probed twig and aphid itself. NPJ-194 (-0.053) and RW-85-59 (-0.038) displayed a significant *gca* effect in the negative direction and measured as a poor general combiner. Parental genotypes Kranti (-0.012), DRMR-15-16 (0.000) and RNWR-09-3 (0.009) showed non-significant *gca* effects.

4.14.3.6 Aphid count

General combiners with a negative value for this character was considered as desirable. Only two parents *viz.*, RW-85-59 (-0.076), DRMR-15-16 (-0.050), SKJM-05 (-0.053) and Kranti (-0.031) was found as good general combiner for aphid count by exhibiting significant negative *gca* effects, while the genotype NPJ-194 (0.106), Giriraj (0.069) and RNWR-09-3 (0.023) was considered as poor general combiner because of positive significant

gca effects for this character. Parental genotypes PHR-2 (0.013) were found as a poor general combiner for this character as this genotype showed non-significant *gca* effects.

4.14.3.7 Penetration force

Significant and positive *gca* effects were showed by NPJ-194 (2.716), DRMR-15-16 (4.682), SKJM-05 (2.418), Giriraj (3.114) and RNWR-09-3 (1.352) and considered as good general combiner. Only two parents namely Kranti (-3.729) and PHR-2 (-3.929) was found as poor general combiner for penetration force by exhibiting significant negative *gca* effects, while the genotype RW-85-59 (-0.396) was considered as non-significant *i.e.* showed no *gca* effect for this character.

4.15 Estimation of specific combining ability (*sca*) effects

14.15.1 Estimation of specific combining ability (*sca*) effects for seed yield and its attributing characters

The estimates of specific combining ability (*sca*) effects of 28 crosses for nine seed yield and its attributing characters are presented in Table 4.25. The character-wise findings of *sca* effects are described as follows:

14.15.1.1 Days to 50% flowering

The crosses which have negative significant value of *sca* effects were considered as desirable because of early flowering. The total number of crosses with negative value was 15, out of which 5 crosses exhibited negative significant *sca* effects namely NPJ-194 × Kranti (-1.519), RW-85-59 × SKJM-05 (-3.085), DRMR-15-16 × Kranti (-2.085), DRMR-15-16 × RNWR-09-3 (-3.252) and DRMR-15-16 × PHR-2 (-2.285) were considered desirable as they were early flower types. Positive and significant *sca* effects were recorded for NPJ-194 × DRMR-15-16 (4.848), NPJ-194 × SKJM-05 (3.481), NPJ-194 × PHR-2 (5.281), RW-85-59 × Giriraj (1.681), RW-85-59 × RNWR-09-3 (2.081) and SKJM-05 × Kranti (3.881) was good for late flowering.

Table 4.24 General combining ability (gca) effects for parents for aphid related characters in Indian mustard (*Brassica juncea*)

S.No.	Parents	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
1	NPJ-194	0.098**	-0.803	0.063**	-0.053**	0.106**	2.716**
2	RW-85-59 (Sarma)	-0.354	-1.554**	0.034**	-0.038**	-0.076**	-0.396
3	DRMR-15-16	-1.007**	-0.063	-0.024**	0.000	-0.050**	4.682**
4	SKJM-05	0.258	0.957*	-0.030**	0.035**	-0.053**	2.418**
5	Kranti	0.174	1.072*	0.013	-0.012	-0.031**	-3.729**
6	Giriraj	-0.252	-0.339	-0.017	0.021*	0.069**	3.114**
7	RNWR-09-3	0.413	0.442	0.006	0.009	0.023**	1.352*
8	PHR 2	-0.216	0.287	-0.044**	0.038**	0.013	-3.929**
	SE (gi)	0.263	0.464	0.009	0.010	0.007	0.613
	SE(gi-gj)	0.398	0.701	0.013	0.015	0.011	0.927

*, ** Significant at 5% and 1% levels of probability, respectively

14.15.1.2 Primary branches per plant

The crosses which have a positively significant value of *sca* effects for primary branches plant⁻¹ were considered desirable. Total numbers of crosses with positive value were 14, out of which 6 crosses expressed positively significant *sca* effects viz., NPJ-194 × RNWR-09-3 (0.636), NPJ-194 × PHR-2 (0.929), RW-85-59 × DRMR-15-16 (0.896), Kranti × PHR-2 (0.782), Giriraj × RNWR-09-3 (0.529) and Giriraj × PHR-2 (0.556) and were considered as desirable specific combiners for this character whereas significant negative *sca* effects were showed by NPJ-194 × RW-85-59 (-0.771), RW-85-59 × PHR-2 (-0.811), DRMR -15-16 × SKJM-05 (-0.584) and Kranti × RNWR-09-3 (-0.578) and were found as poor *sca* for primary branches per plant.

14.15.1.3 Secondary branches plant⁻¹

For this character, four cross combinations showed significant positive *sca* effects i.e. NPJ-194 × PHR-2 (1.551), RW-85-59 × Kranti (4.250), Giriraj × RNWR-09-3 (1.445) and Giriraj × PHR-2 (2.758) was found as a good specific combiner for secondary branches plant⁻¹ while the crosses NPJ-194 × RW-85-59 (-1.439), DRMR-15-16 × Giriraj (-1.449), SKJM-05 × PHR-2 (-1.455), Kranti × Giriraj (-1.359) and Kranti × RNWR-09-3 (-1.579) exhibited negative *sca* effect and considered as poor specific combiner.

14.15.1.4 Siliquae per plant

Ten crosses exhibited positive and significant *sca* effects for this character namely NPJ-194 × DRMR-15-16 (0.053), NPJ-194 × SKJM-05 (0.047), NPJ-194 × RNWR-09-3 (0.141), NPJ-194 × PHR-2 (0.166), RW-85-59 × Kranti (0.097), RW-85-59 × Giriraj (0.019), DRMR-15-16 × SKJM-05 (0.019), DRMR-15-16 × Giriraj (0.041), DRMR-15-16 × PHR-2 (0.041), Kranti × Giriraj (0.095) and Giriraj × PHR-2 (0.060) was found as good specific combiner. NPJ-194 × RW-85-59 (-0.042), NPJ-194 × Kranti (-0.080), NPJ-194 × Giriraj (-

0.034), RW-85-59 × DRMR-15-16 (-0.094), RW-85-59 × SKJM-05 (-0.043), RW-85-59 × RNWR-09-3 (-0.022), RW-85-59 × PHR-2 (-0.101), DRMR-15-16 × Kranti (-0.055), DRMR-15-16 × RNWR-09-3 (-0.014), SKJM-05 × Kranti (-0.084), SKJM-05 × Giriraj (-0.039), SKJM-05 × RNWR-09-3 (-0.020), SKJM-05 × RNWR-09-3 (-0.092), Kranti × RNWR-09-3 (-0.013), Kranti × PHR-2 (-0.065) and RNWR-09-3 × PHR-2 (-0.014) was considered as poor specific combiner for this character as they showed negative significant *sca* effect.

14.15.1.5 Seed per siliqua

Based on *sca* effects of the crosses showed positive significant *sca* effect namely RW-85-59 × Kranti (1.574), DRMR-15-16 × Giriraj (1.223) and DRMR-15-16 × RNWR-09-3 (1.536) were good cross combinations for seeds per siliquae while the crosses NPJ-194 × PHR-2 (-2.781) and RNWR-09-3 × PHR-2 (-1.254) showed negative significant *sca* effect.

14.15.1.6 Height upto first fruiting branch

Out of 28 crosses, only 6 combinations showed significant and positive *sca* effects viz., NPJ-194 × DRMR-15-16 (0.042), RW-85-59 × DRMR-15-16 (0.056), RW-85-59 × Kranti (0.133), SKJM-05 × Kranti (0.040), SKJM-05 × Giriraj (0.065) and RNWR-09-3 × PHR-2 (0.034) and recorded as excellent specific combiners. NPJ-194 × RW-85-59 (-0.041), RW-85-59 × RNWR-09-3 (-0.040), RW-85-59 × PHR-2 (-0.066), DRMR-15-16 × SKJM-05 (-0.077), DRMR-15-16 × Kranti (-0.037), SKJM-05 × RNWR-09-3 (-0.043), Kranti × RNWR-09-3 (-0.27) , Kranti × PHR-2 (-0.079) exhibited significant negative *sca* effect for this character and considered as poor specific combiner.

14.15.1.7 Plant height (cm)

The specific combining ability effects for plant height varied from -0.026 (Kranti × RNWR-09-3) and SKJM-05 × Giriraj to 0.072 (NPJ-194 × PHR-2). Out of 28 F₁s, 13 crosses identified with negative *sca* values out of which only 10 crosses were negative and significant while with positive value were 15, out of which only 11 crosses combinations were positively

significant. Negative significant and best specific combining ability effects were showed in crosses NPJ-194 × RW-85-59 (-0.021), RW-85-59 × SKJM-05 (-0.012), RW-85-59 × Kranti (-0.007), DRMR- 15-16 × SKJM-05 (-0.022), DRMR- 15-16 × Kranti (-0.006), DRMR- 15-16 × PHR-2 (-0.021), SKJM-05 × Giriraj (-0.026), SKJM-05 × RNWR-09-3 (-0.008), Kranti × RNWR-09-3 (-0.026) and Kranti × PHR-2 (-0.013) while, positive and significant specific combining ability effects were observed in cross combinations, NPJ-194 × DRMR- 15-16 (0.016), NPJ-194 × SKJM-05 (0.008), NPJ-194 × Kranti (0.007), NPJ-194 × RNWR-09-3 (0.053), NPJ-194 × PHR-2 (0.072), RW-85-59 × DRMR- 15-16 (0.009), RW-85-59 × Giriraj (0.018), DRMR- 15-16 × Giriraj (0.038), SKJM-05 × Kranti (0.056), Giriraj × RNWR-09-3 (0.008) and Giriraj × PHR-2 (0.044).

14.15.1.8 Seed yield per plant (g)

The value of *sca* effects for seed yield per plant ranged from -0.068 (SKJM-05 × Giriraj) to 0.065 (NPJ-194 × SKJM-05). The total number of crosses with positive value was 13, out of which 7 were positive significant whereas with negative value were 15, out of which only 10 cross combination was expressing negatively significant value. The positive and significant value of specific combining ability effect of this character were obtained by the crosses namely, NPJ-194 × SKJM-05 (0.065), NPJ-194 × Giriraj (0.039), NPJ-194 × PHR-2 (0.026), RW-85-59 × DRMR-15-16 (0.025), RW-85-59 × SKJM-05 (0.044), SKJM-05 × Kranti (0.029) and Kranti × PHR-2 (0.061). However, the cross, with negative and significant *sca* effect, was NPJ-194 × DRMR-15-16 (-0.058), RW-85-59 × Kranti (-0.028), RW-85-59 × Giriraj (-0.032), DRMR-15-16 × Kranti (-0.024), DRMR-15-16 × Giriraj (-0.027), SKJM-05 × Giriraj (-0.068), SKJM-05 × RNWR-09-3 (-0.033), SKJM-05 × PHR-2 (-0.041), Kranti × Giriraj (-0.027) and Giriraj × PHR-2 (-0.030).

14.15.1.9 1000 seed weight

The specific combining ability effects for this character ranged from -12.222 (Giriraj × RNWR-09-3) to 12.878 (RW-85-59 × DRMR-15). Out of 28 F₁s, the total number of crosses with positive value was 17, out of which 14 were positively significant, whereas with negative value were 11, out of which all the 11 crosses combination were negatively significant. The crosses namely NPJ-194 × RW-85-59 (2.511), NPJ-194 × Kranti (6.344), NPJ-194 × Giriraj (1.611), NPJ-194 × RNWR-09-3 (7.078), NPJ-194 × PHR-2 (5.878), RW-85-59 × DRMR-15-16 (12.878), RW-85-59 × SKJM-05 (1.744), RW-85-59 × Giriraj (4.211), DRMR-15-16 × SKJM-05 (9.178), DRMR-15-16 × PHR-2 (0.911), SKJM-05 × Kranti (2.578), Kranti × RNWR-09-3 (3.511), Giriraj × PHR-2 (8.578) and RNWR-09-3 × PHR-2 (2.378) were having positive and significant value of specific combining ability effects while negative and significant *sca* effect was found in cross NPJ-194 × DRMR-15-16 (-5.722), NPJ-194 × SKJM-05 (-4.856), RW-85-59 × RNWR-09-3 (-5.656), RW-85-59 × PHR-2 (-4.856), DRMR-15-16 × Kranti (-3.622), DRMR-15-16 × Giriraj (-8.356), DRMR-15-16 × RNWR-09-3 (-1.222), SKJM-05 × Giriraj (-2.489), SKJM-05 × PHR-2 (-3.222), Kranti × PHR-2 (-3.356), Giriraj × RNWR-09-3 (-12.222).

14.15.1.10 Oil content (%)

The *sca* effects for this character varied from -14.907 (NPJ-194 × PHR-2) to 10.159 (RW-85-59 × PHR-2). The crosses NPJ-194 × DRMR-15-16 (8.193), NPJ-194 × Kranti (6.859), RW-85-59 × SKJM-05 (2.359), RW-85-59 × Kranti (2.259), RW-85-59 × Giriraj (7.693), RW-85-59 × PHR-2 (10.159), DRMR-15-16 × SKJM-05 (2.226), DRMR-15-16 × Giriraj (3.893), SKJM-05 × PHR-2 (8.459) and RNWR-09-3 × PHR-2 (9.259) showed significant positive *sca* effects and thus, were good for oil content.

Results

Table 4.25 Specific combining ability (sca) effects of crosses for seed yield and its attributing characters in Indian mustard (*Brassica juncea*)

S.No.	Crosses	Days to 50% flowering	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliquae plant ⁻¹	Seed siliqua ⁻¹	Height up to first fruiting branch (cm)	Plant height (cm)	Seed yield plant ⁻¹ (g)	1000 seed weight (g)	Oil content (%)
1	NPJ-194 × RW-85-59	-0.819	-0.771**	-1.439**	-0.042**	-0.037	-0.041**	-0.021**	-0.002	2.511**	0.659
2	NPJ-194 × DRMR-15-16	4.848**	0.369	0.411	0.053**	-0.124	0.042**	0.016**	-0.058**	-5.722**	8.193**
3	NPJ-194 × SKJM-05	3.481**	0.349	0.111	0.047**	-0.164	0.012	0.008**	0.065**	-4.856**	-0.374
4	NPJ-194 × Kranti	-1.519**	0.089	-0.633	-0.080**	-0.247	-0.011	0.007**	0.009	6.344**	6.859**
5	NPJ-194 × Giriraj	0.581	-0.204	-0.342	-0.034**	0.983	-0.016	0.005	0.039**	1.611**	-5.707**
6	NPJ-194 × RNWR-09-3	-0.019	0.636**	1.038	0.141**	0.829	-0.008	0.053**	-0.016	7.078**	-0.574
7	NPJ-194 × PHR -2	5.281**	0.929**	1.551**	0.166**	-2.781**	0.020	0.072**	0.026**	5.878**	-14.907**
8	RW-85-59 × DRMR-15-16	-0.052	0.896**	0.454	-0.094**	-0.197	0.056**	0.009**	0.025**	12.878**	-1.741**
9	RW-85-59 × SKJM-05	-3.085**	0.342	-1.179	-0.043**	-0.570	-0.020	-0.012**	0.044**	1.744**	2.359**
10	RW-85-59 × Kranti	0.248	0.216	4.250**	0.097**	1.574**	0.133**	-0.007**	-0.028**	0.278	2.259**
11	RW-85-59 × Giriraj	1.681**	-0.078	0.034	0.019**	0.843	-0.012	0.018**	-0.032**	4.211**	7.693**
12	RW-85-59 × RNWR-09-3	2.081**	-0.238	-0.586	-0.022**	0.823	-0.040**	-0.004	-0.010	-5.656**	-4.174**
13	RW-85-59 × PHR-2	-0.619	-0.811**	-1.273	-0.101**	-0.020	-0.066**	0.005	0.016	-4.856**	10.159**
14	DRMR-15-16 × SKJM-05	-0.752	-0.584**	0.205	0.019**	0.409	-0.077**	-0.022**	0.015	9.178**	2.226**
15	DRMR-15-16 × Kranti	-2.085**	-0.511	-1.006	-0.055**	-0.407	-0.037**	-0.006**	-0.024**	-3.622**	-1.207**
16	DRMR-15-16 × Giriraj	-0.319	-0.338	-1.449**	0.041**	1.223**	0.021	0.038**	-0.027**	-8.356**	3.893**
17	DRMR-15-16 × RNWR-09-3	-3.252**	-0.498	-1.269	-0.014**	1.536**	0.006	-0.001	-0.006	-1.222**	-7.307**
18	DRMR-15-16 × PHR-2	-2.285**	-0.204	0.311	0.041**	1.193	-0.003	-0.021**	0.003	0.911**	-4.307**
19	SKJM-05 × Kranti	3.881**	0.469	0.294	-0.084**	0.287	0.040**	0.056**	0.029**	2.578**	-2.107**
20	SKJM-05 × Giriraj	-0.685	-0.024	0.518	-0.039**	0.783	0.065**	-0.026**	-0.068**	-2.489**	-3.007**
21	SKJM-05 × RNWR-09-3	1.048	-0.451	-0.569	-0.020**	-0.637	-0.043**	-0.008**	-0.033**	0.311	-6.207**
22	SKJM-05 × PHR-2	0.348	-0.358	-1.455**	-0.092**	0.886	0.017	0.001	-0.041**	-3.222**	8.459**
23	Kranti × Giriraj	0.648	0.316	-1.359**	0.095**	1.033	0.021	-0.001	-0.027**	0.711	-0.774**
24	Kranti × RNWR-09-3	-0.285	-0.578**	-1.579**	-0.013**	-0.453	-0.027**	-0.026**	0.018	3.511**	-0.307
25	Kranti × PHR-2	0.015	0.782**	1.067	-0.065**	-0.330	-0.079**	-0.013**	0.061**	-3.356**	-11.641**
26	Giriraj × RNWR-09-3	-0.519	0.529**	1.445**	-0.001	-0.757	0.015	0.008**	-0.009	-12.222**	-3.874**
27	Giriraj × PHR-2	-0.219	0.556**	2.758**	0.060**	-0.767	-0.021	0.044**	-0.030**	8.578**	-4.207**
28	RNWR-09-3 × PHR-2	1.181	0.262	-0.395	-0.014**	-1.254**	0.034**	0.006	0.002	2.378**	9.259**
	SE(sij))	0.822	0.367	0.934	0.008	0.831	0.016	0.004	0.016	0.625	0.518

*, ** Significant at 5% and 1% levels of probability, respectively

14.15.2 Estimation of specific combining ability (*sca*) effects for physiological characters

The estimates of specific combining ability (*sca*) effects of 28 crosses for nine physiological characters are presented in Table 4.26. The character-wise findings of *sca* effects are described as follows:

14.15.2.1 Percentage membrane stability index (%)

Value for *sca* effects of this character varied from -0.070 (NPJ-194 × PHR-2) to 0.043 (NPJ-194 × RW-85-59). The total number of crosses with positive value was 16, out of which 9 crosses exhibited positively significant *sca* effects whereas, 12 crosses were having negative *sca* value out of which 9 were negatively significant. Positive and significant *sca* effects were recorded, in order of merit in NPJ-194 × RW-85-59 (0.043), NPJ-194 × RNWR-09-3 (0.013), RW-85-59 × RNWR-09-3 (0.037), DRMR-15-16 × Kranti (0.024), DRMR-15-16 × Giriraj (0.021), SKJM-05 × Kranti (0.021), SKJM-05 × Giriraj (0.034), Kranti × PHR-2 (0.023) and Giriraj × RNWR-09-3 (0.021) which were considered as good specific combiners for percentage membrane stability index whereas negative significant *sca* effect was shown by NPJ-194 × DRMR-15-16 (-0.015), NPJ-194 × SKJM-05 (-0.031), NPJ-194 × Kranti (-0.020), NPJ-194 × PHR-2 (-0.070), RW-85-59 × DRMR-15-16 (-0.033), DRMR-15-16 × RNWR-09-3 (-0.033), SKJM-05 × RNWR-09-3 (-0.023), Kranti × Giriraj (-0.021) and Giriraj × PHR-2 (-0.28) and considered as poor *sca* for this character.

14.15.2.2 Percentage of excised leaf water loss

The specific combining ability effect for percentage of excised leaf water loss ranged from -0.207 (Kranti × PHR-2) to 0.113 (Kranti × Giriraj). Out of 28 crosses, total number of crosses with negative value were 16, out of which 14 were significant in negative direction. The most promising crosses which exhibited negative and significant *sca* effects for percentage of excised leaf water loss were, NPJ-194 × DRMR-15-16 (-0.103), NPJ-194 × SKJM-05 (-

0.182), NPJ-194 × Giriraj (-0.173), NPJ-194 × RNWR-09-3 (-0.070), RW-85-59 × DRMR-15-16 (-0.074), RW-85-59 × Giriraj (-0.068), RW-85-59 × RNWR-09-3 (-0.081), DRMR-15-16 × Kranti (-0.243), DRMR-15-16 × PHR-2 (-0.066), SKJM-05 × RNWR-09-3 (-0.182), SKJM-05 × PHR-2 (-0.149), Kranti × PHR-2 (-0.207), Giriraj × RNWR-09-3 (-0.116) and RNWR-09-3 (-0.116) and RNWR-09-3 × PHR-2 (-0.147). The crosses showing poor positive significant *sca* effect are NPJ-194 × Kranti (0.130), NPJ-194 × PHR-2 (0.147), RW-85-59 × SKJM-05 (0.193), RW-85-59 × Kranti (0.052), DRMR-15-16 × SKJM-05 (0.128), DRMR-15-16 × Giriraj (0.147), DRMR-15-16 × RNWR-09-3 (0.334), SKJM-05 × Kranti (0.148), SKJM-05 × Giriraj (0.091), Kranti × Giriraj (0.113) and Kranti × RNWR-09-3 (0.080).

14.15.2.3 Percentage of relative water content (%)

The *sca* effects for this character ranged from -0.018 (NPJ-194 × Kranti) to 0.007 (Giriraj × PHR-2) and (DRMR-15-16 × Giriraj). The total number of crosses with positive value was 18, out of which 2 were positive significant while with negative value were 10, out of which 5 were negatively significant. Among the 24 F_{1s} , 2 crosses expressing high significant *sca* effects in positive direction were RW-85-59 × PHR-2 (0.012) and DRMR-15-16 × PHR-2 (0.008) while the negative significant *sca* effect was showed by NPJ-194 × Kranti (-0.018), NPJ-194 × PHR-2 (-0.009), RW-85-59 × SKJM-05 (-0.010), Kranti × Giriraj (-0.009) and RNWR-09-3 × PHR-2 (-0.016).

14.15.2.4 Canopy temperature depression (°C)

The specific combining ability effects for this character varied from -0.066 (SKJM-05 × Giriraj) to 0.029 (NPJ-194 × DRMR-15-16) and (RW-85-59 × Giriraj). Out of 24 crosses, total number of crosses with negative value was 11, out of which only three were negative significant while with positive value were 17, out of which only one crosses were found negatively significant. The high significant and negative specific combining ability effects were observed in the cross, *i.e.* NPJ-194 × SKJM-05 (-0.031), RW-85-59 × DRMR-15-16 (-0.052)

and SKJM-05 × Giriraj (-0.066) while the positively significant *sca* effects exhibiting for SKJM-05 × PHR-2 (0.035).

14.15.2.5 Proline content of leaf (mg/gm)

The *sca* effect for this character ranged from -0.904 (NPJ-194 × RNWR-09-3) to 1.171 (Kranti × Giriraj). Out of 28 F₁s, total number of crosses with positive significant *sca* effect were observed in 11 crosses, whereas with negative value were 17, out of which 10 crosses showed negatively significant *sca* effects. The cross combination like NPJ-194 × DRMR-15-16 (0.844), NPJ-194 × SKJM-05 (0.637), NPJ-194 × PHR-2 (0.562), RW-85-59 × DRMR-15-16 (0.278), RW-85-59 × SKJM-05 (0.351), RW-85-59 × Kranti (0.315), SKJM-05 × Giriraj (0.364), SKJM-05 × PHR-2 (1.111), Kranti × Giriraj (1.171), Kranti × RNWR-09-3 (0.499) and RNWR-09-3 × PHR-2 (0.414) were identified as good specific combiners these were exhibiting high positive significant *sca* effects for this character. The crosses NPJ-194 × RW-85-59 (-0.375), NPJ-194 × Kranti (-0.546), NPJ-194 × RNWR-09-3 (-0.904), RW-85-59 × Giriraj (-0.484), RW-85-59 × RNWR-09-3 (-0.674), RW-85-59 × PHR-2 (-0.647), DRMR-15-16 × Kranti (-0.680), DRMR-15-16 × PHR-2 (-0.468), SKJM-05 × Kranti (-0.324) and Kranti × PHR-2 (-0.401) showed negative significant *sca* effect for this character.

14.15.2.6 Chlorophyll a (mg/gm)

Out of 28 crosses studied, for this character, 6 cross combinations in F₁ showed significant positive *sca* effects. The crosses based on their desirable *sca* values were NPJ-194 × RW-85-59 (0.032), RW-85-59 × DRMR-15-16 (0.057), RW-85-59 × Giriraj (0.033), DRMR-15-16 × SKJM-05 (0.076), DRMR-15-16 × Kranti (0.048) and SKJM-05 × PHR-2 (0.034) while 3 cross combinations exhibited the significant and negative *sca* effects for this character are NPJ-194 × SKJM-05 (-0.065), NPJ-194 × Kranti (-0.061) and DRMR-15-16 × RNWR-09-3 (-0.068) and considered as having poor *sca*.

14.15.2.7 Chlorophyll b (mg/gm)

The value of *sca* effect for chlorophyll b ranged from -0.041 (NPJ-194 × SKJM-05) to 0.044 (DRMR-15-16 × RNWR-09-3). The total number of crosses with positive value was 16, out of which 6 were with positive significant *sca* effects whereas with negative value were 12, out of which only two cross combinations were expressing negatively significant value. The positive and significant value of specific combining ability effect for this character was obtained for the crosses, NPJ-194 × Giriraj (0.032), NPJ-194 × PHR-2 (0.031), RW-85-59 × Kranti (0.020), RW-85-59 × PHR-2 (0.026), DRMR-15-16 × RNWR-09-3 (0.044) and SKJM-05 × RNWR-09-3 (0.041). Crosses that showed negative significant *sca* effect were NPJ-194 × SKJM-05 (-0.041) and RW-85-59 × RNWR-09-3 (-0.019) which were measured as poor *sca* effect for chlorophyll b.

14.15.2.8 Total Chlorophyll (mg/gm)

For total chlorophyll *sca* effects varied from -0.248 (NPJ-194 × SKJM-05) to 0.318 (RW-85-59 × Kranti). The crosses NPJ-194 × Giriraj (0.292), NPJ-194 × PHR-2 (0.310), RW-85-59 × Kranti (0.318), RW-85-59 × PHR-2 (0.195), DRMR-15-16 × RNWR-09-3 (0.245) and Giriraj × PHR-2 (0.227) showed significant positive *sca* effects and were good specific combiners whereas the crosses DRMR-15-16 × SKJM-05 (-0.182), Giriraj × RNWR-09-3 (-0.218) and NPJ-194 × SKJM-05 (-0.248) showed significant negative *sca* effects and were poor specific combiners.

14.15.3 Estimation of specific combining ability (*sca*) effects for aphid related characters

The estimates of specific combining ability (*sca*) effects of 28 crosses for six aphid-related characters are presented in Table 4.27. The character-wise findings of *sca* effects are described as follows:

Table 4.26 Specific combining ability (sca) effects of crosses for physiological characters in Indian mustard (*Brassica juncea*)

S.No.	Crosses	Percentage of membrane stability index (%)	Percentage excised- leaf water loss (%)	Percentage relative water content (%)	Canopy temperature depression (°C)	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)
1	NPJ-194 × RW-85-59	0.043**	0.029	0.001	0.018	-0.375**	0.032**	0.003	0.080
2	NPJ-194 × DRMR-15-16	-0.015**	-0.103**	0.004	0.029	0.844**	0.008	0.009	0.085
3	NPJ-194 × SKJM-05	-0.031**	-0.182**	0.002	-0.031**	0.637**	-0.065**	-0.041**	-0.248**
4	NPJ-194 × Kranti	-0.020**	0.130**	-0.018**	0.013	-0.546**	-0.061**	0.002	0.107
5	NPJ-194 × Giriraj	0.003	-0.173**	0.000	0.009	-0.105	0.016	0.032**	0.292**
6	NPJ-194 × RNWR-09-3	0.013**	-0.070**	0.000	-0.003	-0.904**	0.026	0.003	0.102
7	NPJ-194 × PHR -2	-0.070**	0.147**	-0.009**	-0.019	0.562**	0.024	0.031**	0.310**
8	RW-85-59 × DRMR-15-16	-0.033**	-0.074**	-0.005	-0.052**	0.278**	0.057**	0.000	-0.017
9	RW-85-59 × SKJM-05	-0.003	0.193**	-0.010**	0.016	0.351**	0.001	-0.009	-0.037
10	RW-85-59 × Kranti	-0.005	0.052**	0.006	-0.004	0.315**	0.019	0.020**	0.318**
11	RW-85-59 × Giriraj	-0.009	-0.068**	-0.002	0.029	-0.484**	0.033**	0.007	0.040
12	RW-85-59 × RNWR-09-3	0.037**	-0.081**	-0.005	0.020	-0.674**	0.003	-0.019**	-0.030
13	RW-85-59 × PHR-2	0.002	-0.001	0.012**	0.004	-0.647**	-0.003	0.026**	0.195**
14	DRMR-15-16 × SKJM-05	0.003	0.128**	0.003	0.016	-0.097	0.076**	-0.017	-0.182**
15	DRMR-15-16 × Kranti	0.024**	-0.243**	0.006	0.026	-0.680**	0.048**	-0.001	-0.014
16	DRMR-15-16 × Giriraj	0.021**	0.147**	0.007	0.016	-0.152	0.008	-0.004	-0.019
17	DRMR-15-16 × RNWR-09-3	-0.033**	0.334**	-0.006	0.004	-0.195	-0.068**	0.044**	0.245**
18	DRMR-15-16 × PHR-2	0.008	-0.066**	0.008**	0.001	-0.468**	0.010	0.005	-0.017
19	SKJM-05 × Kranti	0.021**	0.148**	0.000	-0.016	-0.324**	0.022	0.000	-0.030
20	SKJM-05 × Giriraj	0.034**	0.091**	0.002	-0.066**	0.364**	-0.001	0.000	-0.081
21	SKJM-05 × RNWR-09-3	-0.023**	-0.182**	0.005	-0.016	-0.059	0.022	0.041**	0.019
22	SKJM-05 × PHR-2	0.008	-0.149**	0.006	0.035**	1.111**	0.034**	0.013	0.110
23	Kranti × Giriraj	-0.021**	0.113**	-0.009**	-0.010	1.171**	0.013	-0.004	-0.140
24	Kranti × RNWR-09-3	0.005	0.080**	0.002	0.028	0.499**	0.017	-0.007	0.000
25	Kranti × PHR-2	0.023**	-0.207**	0.002	0.002	-0.401**	0.008	-0.005	-0.105
26	Giriraj × RNWR-09-3	0.021**	-0.116**	-0.003	0.011	-0.087	-0.006	-0.016	-0.218**
27	Giriraj × PHR-2	-0.028**	-0.023	0.007	-0.005	-0.150	0.028	-0.018	0.227**
28	RNWR-09-3 × PHR-2	0.012	-0.147**	-0.016**	-0.027	0.414**	-0.028	-0.014	-0.036
	SE(sij))	0.007	0.034	0.005	0.021	0.138	0.021	0.013	0.111

*, ** Significant at 5% and 1% levels of probability, respectively

14.15.3.1 Water content of aphid probed twig (%)

Estimates of specific combining ability effect varied from -3.648 (NPJ-194 × RW-85-59) to 3.067 (RW-85-59 × Giriraj). The crosses NPJ-194 × DRMR-15-16 (1.597), NPJ-194 × Kranti (1.567), NPJ-194 × PHR-2 (2.083), RW-85-59 × DRMR-15-16 (0.015), RW-85-59 × Giriraj (3.067), RW-85-59 × RNWR-09-3 (0.532), DRMR-15-16 × Kranti (0.437), DRMR-15-16 × Giriraj (0.846), DRMR-15-16 × PHR-2 (0.830), SKJM-05 × Kranti (0.625), SKJM-05 × PHR-2 (0.378), Kranti × Giriraj (0.772) and RNWR-09-3 × PHR-2 (0.690) showed positive and significant specific combining ability effects and were good specific cross combinations for water content of aphid probed twig and the crosses NPJ-194 × RW-85-59 (-3.648), NPJ-194 × Giriraj (-1.334), NPJ-194 × RNWR-09-3 (-1.212), DRMR-15-16 × SKJM-05 (-2.638), Kranti × RNWR-09-3 (-1.596) and Kranti × PHR-2 (-1.421) observed negative and significant specific combining ability effects and were poor specific cross combinations for this character.

14.15.3.2 Water content of aphid uninfested twig (%)

Specific combining ability effect ranged from -5.785 (Kranti × PHR-2) to 4.610 (Kranti × Giriraj). Out of the 28 crosses, only two cross combinations exhibited significant and positive specific combining ability effects. The good combinations in order of merit were Kranti × Giriraj (4.610) and DRMR-15-16 × Giriraj (2.891) while significant negative specific combining ability effects were shown by seven crosses namely NPJ-194 × RW-85-59 (-2.460), NPJ-194 × Giriraj (-2.705), RW-85-59 × Giriraj (-2.131), DRMR-15-16 × SKJM-05 (-2.298), DRMR-15-16 × Kranti (-3.053), Kranti × RNWR-09-3 (-2.664) and Kranti × PHR-2 (-5.785) found to be poor specific cross combinations for the water content of aphid uninfested twig.

4.15.3.3 Water content of aphid (%)

The value of specific combining ability effects ranged from -0.072 (SKJM-05 × RNWR-09-3) to 0.148 (DRMR-15-16 × Kranti). The crosses *viz.*, NPJ-194 × Giriraj (-0.049),

NPJ-194 × RNWR-09-3(-0.062), RW-85-59 × SKJM-05 (-0.043), RW-85-59 × PHR-2 (-0.059), DRMR-15-16 × RNWR-09-3 (-0.048), SKJM-05 × Kranti (-0.059) and SKJM-05 × RNWR-09-3 (-0.072) showed significant negative specific combining ability effects were emerged to be best specific cross combinations for water content of aphid whereas seven crosses exhibited significant positive specific combining ability effects *i.e.* NPJ-194 × SKJM-05 (0.048), NPJ-194 × PHR-2 (0.041), RW-85-59 × Giriraj (0.127), DRMR-15-16 × SKJM-05 (0.085), DRMR-15-16 × Kranti (0.148), Giriraj × PHR-2 (0.061) and RNWR-09-3 × PHR-2 (0.138) were found to be poor specific cross combinations for this character.

14.15.3.4 Percentage of water differential between aphid probed twig and aphid itself (%)

Estimates of specific combining ability effect varied from -0.205 (DRMR-15-16 × Kranti) to 0.070 (RW-85-59 × PHR-2) and SKJM-05 × Kranti. The cross combinations NPJ-194 × Giriraj (0.055), NPJ-194 × RNWR-09-3 (0.054), RW-85-59 × SKJM-05 (0.046), RW-85-59 × PHR-2 (0.070), DRMR-15-16 × RNWR-09-3 (0.058), SKJM-05 × Kranti (0.070) and SKJM-05 × RNWR-09-3 (0.056) observed significant and positive *sca* effects for percentage of water differential between aphid probed twig and aphid itself. Six cross combinations revealed significant negative specific combining ability effects *i.e.* NPJ-194 × SKJM-05 (-0.049), RW-85-59 × Giriraj (-0.160), DRMR-15-16 × SKJM-05 (-0.149), DRMR-15-16 × SKJM-05 (-0.205), Giriraj × PHR-2 (-0.046) and RNWR-09-3 × PHR-2 (-0.140) were found to be poor specific cross combinations for this character.

14.15.3.5 Aphid count

The specific combining ability effect ranged from -0.211 (RW-85-59 × Giriraj) to 0.512 (RW-85-59 × DRMR-15-16). The crosses NPJ-194 × RW-85-59 (-0.171), NPJ-194 × DRMR-15-16 (-0.080), NPJ-194 × SKJM-05 (-0.054), RW-85-59 × SKJM-05 (-0.209), RW-85-59 × Giriraj (-0.211), DRMR-15-16 × Kranti (-0.176), DRMR-15-16 × RNWR-09-3 (-

0.053), DRMR-15-16 × PHR-2 (-0.113), SKJM-05 × Kranti (-0.093), SKJM-05 × RNWR-09-3 (-0.087), SKJM-05 × PHR-2 (-0.077), Giriraj × RNWR-09-3 (-0.143) and RNWR-09-3 × PHR-2 (-0.036) showed significant negative specific combining ability effects and were emerged to be best specific cross combinations for aphid count and twelve crosses exhibited significant positive specific combining ability effects which indicated poor performance for this character namely NPJ-194 × Giriraj (0.070), NPJ-194 × RNWR-09-3 (0.127), RW-85-59 × DRMR-15-16 (0.512), RW-85-59 × Kranti (0.050), RW-85-59 × RNWR-09-3 (0.209), RW-85-59 × PHR-2 (0.099), DRMR-15-16 × Giriraj (0.050), SKJM-05 × Giriraj (0.090), Kranti × Giriraj (0.138), Kranti × RNWR-09-3 (0.041), Kranti × PHR-2 (0.111) and Giriraj × PHR-2 (0.077).

4.15.3.6 Penetration force

Out of 28 crosses studied, for this character, 12 cross combinations in F_1 showed significant positive *sca* effects. The crosses based on their desirable *sca* values were NPJ-194 × RW-85-59 (4.837), NPJ-194 × SKJM-05 (4.246), NPJ-194 × Giriraj (3.691), NPJ-194 × RNWR-09-3 (13.952), RW-85-59 × DRMR-15-16 (10.188), RW-85-59 × RNWR-09-3 (0.534), DRMR-15-16 × Giriraj (10.403), SKJM-05 × Giriraj (7.036), Kranti × Giriraj (14.153), Kranti × PHR-2 (6.101), Giriraj × PHR-2 (4.453) and RNWR-09-3 × PHR-2 (10.050) while 11 crosses combinations exhibited the significant and negative *sca* effects for this character are NPJ-194 × PHR-2 (-10.644), RW-85-59 × Kranti (-7.174), RW-85-59 × Giriraj (-11.603), RW-85-59 × PHR-2 (-8.845), DRMR-15-16 × Kranti (-3.916), DRMR-15-16 × Giriraj (-3.475), DRMR-15-16 × PHR-2 (-3.880), SKJM-05 × RNWR-09-3 (-5.227), SKJM-05 × PHR-2 (-8.856), Kranti × RNWR-09-3 (-9.393) and Giriraj × PHR-2 (-7.505) and considered as having poor *sca* effect for this character.

Table 4.27 Specific combining ability (sca) effects of crosses for aphid related characters in Indian mustard (*Brassica juncea*)

S.No.	Crosses	Water content of aphid probed twig (%)	Water content of aphid uninfested twig (%)	Water content of aphid (%)	Percentage of water differential between aphid probed twig and aphid itself (%)	Aphid count	Penetration force (Kpascal)
1	NPJ-194 × RW-85-59	-3.648**	-2.460**	-0.029	-0.013	-0.171**	4.837**
2	NPJ-194 × DRMR-15-16	1.597**	1.285	0.028	0.012	-0.080**	0.452
3	NPJ-194 × SKJM-05	-0.088	-1.448	0.048**	-0.049**	-0.054**	4.246**
4	NPJ-194 × Kranti	1.567**	1.994	0.021	-0.005	0.011	-1.863
5	NPJ-194 × Giriraj	-1.334**	-2.705**	-0.049**	0.055**	0.070**	3.691**
6	NPJ-194 × RNWR-09-3	-1.212**	1.037	-0.062**	0.054**	0.127**	13.952**
7	NPJ-194 × PHR -2	2.083**	1.133	0.041**	-0.002	0.030	-10.644**
8	RW-85-59 × DRMR-15-16	0.015	1.386	0.014	0.011	0.512**	10.188**
9	RW-85-59 × SKJM-05	-1.137	0.963	-0.043**	0.046**	-0.209**	-2.322
10	RW-85-59 × Kranti	-0.049	-0.785	0.007	-0.006	0.050**	-7.174**
11	RW-85-59 × Giriraj	3.067**	-2.131**	0.127**	-0.160**	-0.211**	-11.603**
12	RW-85-59 × RNWR-09-3	0.532	-0.182	-0.016	0.013	0.209**	0.534
13	RW-85-59 × PHR-2	-0.773	1.783	-0.059**	0.070**	0.099**	-8.845**
14	DRMR-15-16 × SKJM-05	-2.638**	-2.298**	0.085**	-0.149**	-0.014	0.890
15	DRMR-15-16 × Kranti	0.437	-3.053**	0.148**	-0.205**	-0.176**	-3.916**
16	DRMR-15-16 × Giriraj	0.846	2.891**	-0.018	0.045	0.050**	-3.475**
17	DRMR-15-16 × RNWR-09-3	-0.802	-1.353	-0.048**	0.058**	-0.053**	10.403**
18	DRMR-15-16 × PHR-2	0.830	-1.901	0.022	0.008	-0.113**	-3.880**
19	SKJM-05 × Kranti	0.625	0.624	-0.059**	0.070**	-0.093**	-1.946
20	SKJM-05 × Giriraj	-0.409	0.995	-0.036	0.027	0.090**	7.036**
21	SKJM-05 × RNWR-09-3	-0.154	0.834	-0.072**	0.056**	-0.087**	-5.227**
22	SKJM-05 × PHR-2	0.378	-1.191	-0.016	0.027	-0.077**	-8.856**
23	Kranti × Giriraj	0.772	4.610**	0.008	0.021	0.138**	14.153**
24	Kranti × RNWR-09-3	-1.596**	-2.664**	0.018	-0.027	0.041**	-9.393**
25	Kranti × PHR-2	-1.421**	-5.785**	0.011	-0.016	0.111**	6.101**
26	Giriraj × RNWR-09-3	-0.850	0.220	-0.002	-0.003	-0.143**	-7.505**
327	Giriraj × PHR-2	-0.225	-0.548	0.061**	-0.046**	0.077**	4.453**
28	RNWR-09-3 × PHR-2	0.690	-0.696	0.138**	-0.140**	-0.036**	10.050**
	SE(sij)	0.807	1.422	0.027	0.031	0.023	1.880

*, ** Significant at 5% and 1% levels of probability, respectively

14.16 Estimation of Heterosis

4.16.1 Estimation of Heterosis for seed yield and its attributing characters

Heterosis over mid- parent (MP) and better parent (BP) for ten seed yield and its attributing characters are presented in Table 4.28.

4.16.1.1 Days to 50 % flowering

a) Heterosis over mid- parents

Relative heterosis was found to be significant for some of the characters in the 28 crosses. The number of crosses with negative relative heterosis was only eight, out of which only two were negatively significant. Significant and negative relative heterosis (desirable) was observed for DRMR-15-16 \times RNWR-09-3 (-7.370) and DRMR-15-16 \times PHR-2 (-3.930), whereas positive significant heterosis over mid-parent was observed in the crosses NPJ-194 \times DRMR-15-16 (12.310), NPJ-194 \times SKJM-05 (13.600), NPJ-194 \times Giriraj (6.820), NPJ-194 \times RNWR-09-3 (5.360), NPJ-194 \times PHR-2 (15.580), SKJM-05 \times Kranti (9.140).

b) Heterosis over better- parent

The heterosis over better parent ranged from -9.040 (DRMR-15-16 \times PHR-2 and RW-85-59 \times PHR-2) to 13.250 (NPJ-194 \times SKJM-05). Out of 28 crosses, 7 F₁s showed the heterosis over BP is highly significant and negative direction (desirable) for early flowering for crosses *i.e.* RW-85-59 \times DRMR-15-16 (-6.550), RW-85-59 \times SKJM-05 (-7.830), RW-85-59 \times Kranti (-5.200), RW-85-59 \times PHR-2 (-9.040), DRMR-15-16 \times Kranti (-6.360), DRMR-15-16 \times RNWR-09-3 (-8.190) and DRMR-15-16 \times PHR-2 (-9.040). Four crosses out of 28 F₁s crosses showed significant positive superiority over better parental values for late flowering types. The crosses showing positive significant heterosis are NPJ-194 \times DRMR-15-16 (11.310), NPJ-194 \times SKJM-05 (13.250), NPJ-194 \times PHR-2 (8.510) and SKJM-05 \times Kranti (6.940).

4.16.1.2 Primary branches per plant

a) Heterosis over mid- parent

In the case of primary branches per plant, heterosis over the mid parent varied from -17.330 (DRMR-15-16 × SKJM-05) to 36.430 (NPJ-194 × PHR-2). Total numbers of crosses with positive value were 17, out of these crosses only 3 were expressed positively significant, whereas with negative value were 11, and no one was negatively significant. The highest and significant positive values were recorded for crosses like NPJ-194 × PHR-2 (36.430), Kranti × PHR-2 (27.540) and Giriraj × PHR-2 (24.800).

b) Heterosis over better- parent

Heterosis over better- parent varied from -24.100 (NPJ-194 × RW-85-59) to 25.710 (NPJ-194 × PHR-2 and Kranti × PHR-2). Out of 28 crosses, only one hybrid *i.e.* NPJ-194 × PHR-2 (25.710) exhibited positive significant heterosis over better parent for primary branches per plant similarly one cross showed negative significant heterosis over better parent for this character *i.e.* NPJ-194 × RW-85-59 (-24.100).

4.16.1.3 Secondary branches plant⁻¹

a) Heterosis over mid- parent

Heterosis over the better parental ranged from -23.330 (DRMR-15-16 × RNWR-09-3) to 52.780 (Giriraj × PHR-2). Two crosses *viz.*, Giriraj × PHR-2 (52.780) and RW-85-59 × Kranti (41.800) observed positive significant heterosis to merit over mid parent for secondary branches plant-1. Eighteen hybrids exhibited negative heterosis over mid parent but none of the crosses showed significant negative heterosis, indicated poor performance for this character.

b) Heterosis over better- parent

Heterosis over better parent ranged from -34.460 (DRMR-15-16 × Giriraj) to 36.360 (Giriraj × PHR-2). Two crosses *viz.*, Giriraj × PHR-2 (36.360) and RW-85-59 × Kranti (33.680) revealed positive significant heterosis over better parent for secondary branches plant-1. Out of 28 crosses, only two crosses exhibited negative significant heterosis over better parent for this character *i.e.* DRMR-15-16 × Giriraj (-34.460) and NPJ-194 × RW-85-59 (-25.860)

4.16.1.4 Siliquae per plant

a) Heterosis over mid- parent

Heterosis over mid parent for siliquae per plant ranged from -6.880 (SKJM-05 × Kranti) to 9.900 (NPJ-194 × PHR-2). The hybrids with positive value were 12, out of which 11 were positively significant while with negative value were 16, out of which 14 were negatively significant. The highest positive and significant value were noted for NPJ-194 × DRMR-15-16 (5.060), NPJ-194 × SKJM-05 (2.490), NPJ-194 × Giriraj (2.930), NPJ-194 × RNWR-09-3 (9.810), NPJ-194 × PHR-2 (9.900), RW-85-59 × Kranti (0.970), DRMR-15-16 × Giriraj (3.350), DRMR-15-16 × PHR-2 (1.580), Kranti × Giriraj (4.580), Giriraj × RNWR-09-3 (2.220) and Giriraj × PHR-2 (4.170). The negative significant value were observed for crosses namely, NPJ-194 × RW-85-59 (-1.150), NPJ-194 × Kranti (-1.880), RW-85-59 × DRMR-15-16 (-6.130), RW-85-59 × SKJM-05 (-6.030), RW-85-59 × RNWR-09-3 (-2.370), RW-85-59 × PHR-2 (-6.280), DRMR-15-16 × SKJM-05 (-1.590), DRMR-15-16 × Kranti (-3.570), SKJM-05 × Kranti (-6.880), SKJM-05 × Giriraj (-2.540), SKJM-05 × RNWR-09-3 (-2.550), SKJM-05 × PHR-2 (-6.220), Kranti × RNWR-09-3 (-1.080) and Kranti × PHR-2 (-3.910).

b) Heterosis over better- parent

Heterosis over better parent varied from -8.850 (RW-85-59 × DRMR-15-16) to 9.080 (NPJ-194 × RNWR-09-3). Three crosses revealed significant positive heterosis over better parent namely, NPJ-194 × DRMR-15-16 (3.670), NPJ-194 × RNWR-09-3 (9.080) and NPJ-194 × PHR-2 (6.190) are best for this character. Whereas, 18 crosses had significant negative heterosis over mid parent namely, NPJ-194 × RW-85-59 (-5.260), NPJ-194 × Kranti (-5.830), RW-85-59 × DRMR-15-16 (-8.850), RW-85-59 × SKJM-05 (-7.330), RW-85-59 × Giriraj (-5.950), RW-85-59 × RNWR-09-3 (-5.810), RW-85-59 × PHR-2 (-7.050), DRMR-15-16 × SKJM-05 (-3.130), DRMR-15-16 × Kranti (-6.240), SKJM-05 × Kranti (-8.040), SKJM-05 ×

Giriraj (-7.400), SKJM-05 × RNWR-09-3 (-4.690), SKJM-05 × PHR-2 (-6.750), Kranti × Giriraj (-1.800), Kranti × RNWR-09-3 (-4.440), Kranti × PHR-2 (-4.580), Giriraj × PHR-2 (-1.550) and RNWR-09-3 × PHR-2 (-2.810).

4.16.1.5 Seed per siliquae

a) Heterosis over mid- parent

Heterosis over the mid parent for seed per siliquae was observed for all the crosses and varied from -30.100 (NPJ-194 × PHR-2) to 24.790 (DRMR-15-16 × Giriraj). Out of 28 crosses, 19 crosses showed positive value, out of which 4 were positively significant. The highest positive significant heterotic combinations were observed in the crosses DRMR-15-16 × Giriraj (24.790), DRMR-15-16 × RNWR-09-3 (20.000), RW-85-59 × Kranti (19.740) and RW-85-59 × Giriraj (19.160), respectively are considered as good for this character whereas negative significant heterosis over mid parent was observed in only one cross *i.e.* NPJ-194 × PHR-2 (-30.100).

b) Heterosis over better-parent

The magnitude of better parent heterosis varied from -36.570 (NPJ-194 × PHR-2) to 19.150 (DRMR-15-16 × Giriraj). Positive heterosis over better parent was shown by 16 crosses but none of the crosses were significantly contributed to the concerned character. Only two crosses exhibited significant negative heterosis out of 12 namely NPJ-194 × PHR-2 (-36.570) and RNWR-09-3 × PHR-2 (-21.760).

4.16.1.6 Height upto first fruiting branch

a) Heterosis over mid- parent

The heterosis over the mid-parent was estimated for all the crosses, in which the crosses with positive value were 11, out of which 5 were significantly contributed to the concerned character, while negative value was 17 and out of which 4 were negatively significant. The crosses showed the highest positive and significant value were observed for

height upto first fruiting branch are RW-85-59 × Kranti (7.410), SKJM-05 × Giriraj (4.390), RW-85-59 × DRMR-15-16 (3.110), Kranti × Giriraj (2.660), SKJM-05 × Kranti (2.520) and NPJ-194 × DRMR-15-16 (2.240) the crosses showed negative significant heterosis over mid parent was RW-85-59 × RNWR-09-3 (-2.630), RW-85-59 × PHR-2 (-4.470), DRMR-15-16 × SKJM-05 (-3.990) and Kranti × PHR-2 (-4.910).

b) Heterosis over better- parent

Crosses differed considerably in their heterotic response which ranged from -6.870 (Kranti × PHR-2) to 8.250 (RW-85-59 × PHR-2) over better parent. Out of 28 F₁s studied, only two F₁s expressed desirable positive significant heterosis over better parent namely RW-85-59 × Kranti (5.280) and RW-85-59 × PHR-2 (8.250). The crosses showed negative significant heterosis over better parent were NPJ-194 × RW-85-59 (-4.460), RW-85-59 × SKJM-05 (-3.960), RW-85-59 × Giriraj (-4.460), RW-85-59 × RNWR-09-3 (-5.450), DRMR-15-16 × SKJM-05 (-5.300), DRMR-15-16 × PHR-2 (-3.590), SKJM-05 × RNWR-09-3 (-3.330), Kranti × RNWR-09-3 (-2.580), Kranti × PHR-2 (-6.870).

4.16.1.7 Plant height**a) Heterosis over mid- parent**

The heterosis over the mid parent for plant height ranged from -0.800 (DRMR-15-16 × SKJM-05) to 5.880 (NPJ-194 × PHR-2). All most all the crosses were with positive values except six, out of which 17 were positively significant and rests were non-significant. The positive and significant values were observed for crosses like NPJ-194 × RW-85-59 (0.530), NPJ-194 × DRMR-15-16 (2.470), NPJ-194 × SKJM-05 (1.930), NPJ-194 × Kranti (2.000), NPJ-194 × Giriraj (2.770), NPJ-194 × RNWR-09-3 (4.240), NPJ-194 × PHR-2 (5.880), RW-85-59 × Giriraj (1.620), RW-85-59 × PHR-2 (1.170), DRMR-15-16 × Giriraj (2.790), SKJM-05 × Kranti (2.520), SKJM-05 × PHR-2 (1.080), Kranti × Giriraj (1.020), Kranti × PHR-2 (0.580), Giriraj × RNWR-09-3 (1.610), Giriraj × PHR-2 (3.950), RNWR-09-3 × PHR-2 (1.600)

whereas, with negative value were 6, out of which 3 were negatively significant. The crosses with significant negative significant values were RW-85-59 × SKJM-05 (-0.660), DRMR-15-16 × SKJM-05 (-0.800) and Kranti × RNWR-09-3 (-0.720).

b) Heterosis over better- parent

The estimates of heterosis over better parent ranged from -2.160 (RW-85-59 × SKJM-05) to 3.340 (NPJ-194 × PHR-2 and Giriraj × PHR-2). Out of all 28 crosses, 10 crosses showed significant and positive heterosis over better parent *viz.*, NPJ-194 × Giriraj (0.880), NPJ-194 × RNWR-09-3 (1.740), NPJ-194 × PHR-2 (3.340), RW-85-59 × Giriraj (1.180), DRMR-15-16 × Giriraj (2.640), SKJM-05 × Kranti (2.450), SKJM-05 × PHR-2 (0.580), Giriraj × RNWR-09-3 (1.020), Giriraj × PHR-2 (3.340) and RNWR-09-3 × PHR-2 (1.600) while the negative significant heterosis for this character was observed in crosses NPJ-194 × RW-85-59 (-0.890), NPJ-194 × SKJM-05 (-1.010), NPJ-194 × Kranti (-0.860), RW-85-59 × SKJM-05 (-2.160), RW-85-59 × Kranti (-1.730), RW-85-59 × RNWR-09-3 (-1.020), DRMR-15-16 × SKJM-05 (-1.730), DRMR-15-16 × Kranti (-0.860), SKJM-05 × Giriraj (-1.290), SKJM-05 × RNWR-09-3 (-0.580) and Kranti × RNWR-09-3 (-1.150).

4.16.1.8 Seed yield per plant

a) Heterosis over mid- parent

The crosses with significant positive heterosis are desirable for this character. The range of heterosis over the mid parent was -12.500 (SKJM-05 × Giriraj) to 10.910 (Kranti × PHR-2). The crosses with positive value were 12, out of which only 4 were positively significant NPJ-194 × SKJM-05 (10.820), NPJ-194 × PHR-2 (6.940), RW-85-59 × SKJM-05 (6.440), Kranti × PHR-2 (10.910) whereas, with negative value were 16, out of which 9 were negatively significant. The crosses with significant negative values were NPJ-194 × DRMR-15-16 (-7.690), RW-85-59 × Giriraj (-8.200), DRMR-15-16 × Giriraj (-9.960), SKJM-05 ×

Giriraj (-12.500), SKJM-05 × RNWR-09-3 (-5.580), Kranti × Giriraj (-6.920), Giriraj × RNWR-09-3 (-7.380) and Giriraj × PHR-2 (-7.280).

b) Heterosis over better- parent

The better parent heterosis varied from -16.220 (SKJM-05 × Giriraj) to 9.910 (Kranti × PHR-2). Only two crosses showed significant positive heterosis over better parent namely NPJ-194 × SKJM-05 (8.020) and Kranti × PHR-2 (9.910). Eleven crosses showed negative significant heterosis viz., NPJ-194 × DRMR-15-16 (-11.110), RW-85-59 × Giriraj (-13.510), DRMR-15-16 × Kranti (-9.050), DRMR-15-16 × Giriraj (-12.740), DRMR-15-16 × RNWR-09-3 (-7.410), DRMR-15-16 × PHR-2 (-4.940), SKJM-05 × Kranti (-16.220), SKJM-05 × RNWR-09-3 (-7.170), SKJM-05 × PHR-2 (-6.750), Kranti × Giriraj (-14.290), Kranti × RNWR-09-3 (-0.440), Giriraj × RNWR-09-3 (-12.740) and Giriraj × PHR-2 (-13.900).

4.16.1.9 1000 seed weight

a) Heterosis over mid- parent

A wide range of heterosis over mid parent was observed from -25.470 (Giriraj × RNWR-09-3) to 29.730 (RW-85-59 × DRMR-15-16). Total numbers of crosses with positive value were 16, out of which 15 were positively significant while with negative value were 11, and out of which only 4 were negatively significant. Positive and significant values were noted in order of merit for crosses like NPJ-194 × RW-85-59 (16.250), NPJ-194 × Kranti (21.250), NPJ-194 × Giriraj (5.730), NPJ-194 × RNWR-09-3 (15.880), NPJ-194 × PHR-2 (20.120), RW-85-59 × DRMR-15-16 (29.730), RW-85-59 × SKJM-05 (8.270), RW-85-59 × Kranti (7.520), RW-85-59 × Giriraj (8.220), DRMR-15-16 × SKJM-05 (18.970), DRMR-15-16 × PHR-2 (6.270), SKJM-05 × Kranti (8.020), Kranti × RNWR-09-3 (5.540), Giriraj × PHR-2 (13.480) and RNWR-09-3 × PHR-2 (4.210) while the negative significant crosses are RW-85-59 × RNWR-09-3 (-7.120), DRMR-15-16 × Giriraj (-17.180), SKJM-05 × Giriraj (-5.980) and Giriraj × RNWR-09-3 (-25.470).

b) Heterosis over better- parent

Heterobeltiosis for 1000 seed weight ranged from -30.150 (Giriraj × RNWR-09-3) to

20.000 (RW-85-59 × DRMR-15-16). Ten crosses expressed heterosis in positive direction (desirable) and ten crosses showed negative significant heterosis. Positive heterosis over better parent was exhibited by NPJ-194 × RW-85-59 (3.910), NPJ-194 × Kranti (8.380), NPJ-194 × PHR-2 (6.590), RW-85-59 × DRMR-15-16 (20.200), RW-85-59 × SKJM-05 (4.100), RW-85-59 × Kranti (7.220), RW-85-59 × Giriraj (6.110), DRMR-15-16 × SKJM-05 (6.150), SKJM-05 × Kranti (3.590) and Giriraj × PHR-2 (10.990) whereas negative significant heterosis was observed for the crosses NPJ-194 × DRMR-15-16 (-6.540), NPJ-194 × SKJM-05 (-14.870), NPJ-194 × Giriraj (-4.050), RW-85-59 × RNWR-09-3 (-11.560), DRMR-15-16 × Kranti (-8.940), DRMR-15-16 × Giriraj (-21.970), DRMR-15-16 × RNWR-09-3 (-14.070), SKJM-05 × Giriraj (-11.280), SKJM-05 × PHR-2 (-4.620) and Giriraj × RNWR-09-3 (-30.150).

4.16.1.10 Oil content

a) Heterosis over mid- parent

Relative heterosis varied from -11.510 (NPJ-194 × PHR-2) to 8.740 (RW-85-59 × PHR-2). The crosses namely NPJ-194 × RW-85-59 (2.450), NPJ-194 × DRMR-15-16 (4.460), NPJ-194 × Kranti (2.450), RW-85-59 × DRMR-15-16 (1.860), RW-85-59 × SKJM-05 (5.040), RW-85-59 × Kranti (3.410), RW-85-59 × Giriraj (7.480), RW-85-59 × PHR-2 (8.740), DRMR-15-16 × SKJM-05 (1.830), DRMR-15-16 × Giriraj (1.710), DRMR-15-16 × PHR-2 (3.990), SKJM-05 × PHR-2 (4.820) and RNWR-09-3 × PHR-2 (2.660) observed positive significant heterosis over mid parent for oil content. Out of 28 crosses, 14 crosses showed negative significant heterosis over mid parent viz., NPJ-194 × Giriraj (-5.590), NPJ-194 × RNWR-09-3 (-3.240), NPJ-194 × PHR-2 (-11.510), RW-85-59 × RNWR-09-3 (-2.000), DRMR-15-16 × Kranti (-1.890), DRMR-15-16 × RNWR-09-3 (-6.840), SKJM-05 × Kranti (-2.240), SKJM-05 × Giriraj (-2.760), SKJM-05 × RNWR-09-3 (-5.920), Kranti × Giriraj (-2.570), Kranti × RNWR-09-3 (-3.300), Kranti × PHR-2 (-9.780), Giriraj × RNWR-09-3 (-5.570) and Giriraj × PHR-2 (-4.910).

b) Heterosis over better- parent

Heterobeltiosis for oil content ranged from -31.000 (NPJ-194 × PHR-2) to 5.500 (RW-85-

59 × Giriraj). Five crosses expressed heterosis in positive direction (desirable) and 18 crosses showed negative significant heterosis. Positive heterosis over better parent was exhibited by RW-85-59 × SKJM-05 (3.460), RW-85-59 × Giriraj (5.500), RW-85-59 × PHR-2 (3.900), DRMR-15-16 × Giriraj (1.130) and SKJM-05 × PHR-2 (1.520) whereas negative significant heterosis was observed for the crosses NPJ-194 × RW-85-59 (-3.560), NPJ-194 × SKJM-05 (-5.450), NPJ-194 × Giriraj (-9.640), NPJ-194 × RNWR-09-3 (-3.540), NPJ-194 × PHR-2 (-13.000), RW-85-59 × Kranti (-1.090), RW-85-59 × RNWR-09-3 (-8.130), DRMR-15-16 × Kranti (-3.910), DRMR-15-16 × RNWR-09-3 (-10.630), DRMR-15-16 × PHR-2 (-6.070), SKJM-05 × Kranti (-5.220), SKJM-05 × Giriraj (-3.210), SKJM-05 × RNWR-09-3 (-10.630), Kranti × Giriraj (-5.010), Kranti × RNWR-09-3 (-5.420), Kranti × PHR-2 (-9.980), Giriraj × RNWR-09-3 (-10.000) and Giriraj × PHR-2 (-7.590).

4.16.2 Estimation of heterosis for physiological characters

Heterosis over mid- parent (MP) and better parent (BP) for nine physiological characters are presented in Table 4.29.

4.16.2.1 Percentage of membrane stability index (%)

a) Heterosis over mid- parent

Relative heterosis ranged from -5.650 (NPJ-194 × PHR-2) to 3.090 (RW-85-59 × RNWR-09-3). Eight crosses *viz.*, NPJ-194 × RW-85-59 (1.810), RW-85-59 × RNWR-09-3 (3.090), DRMR-15-16 × Kranti (1.430), DRMR-15-16 × Giriraj (1.140), SKJM-05 × Kranti (1.730), SKJM-05 ×

Giriraj (2.400), Kranti \times RNWR-09-3 (1.150) and Giriraj \times RNWR-09-3 (2.010) revealed positive significant heterosis over mid parent for percentage of membrane stability index. Out of 28 crosses, only seven crosses i.e. NPJ-194 \times DRMR-15-16 (-2.260), NPJ-194 \times SKJM-05 (-2.760), NPJ-194 \times Kranti (-1.800), NPJ-194 \times PHR-2 (-5.650), RW-85-59 \times DRMR-15-16 (-1.820), DRMR-15-16 \times RNWR-09-3 (-1.810) and Giriraj \times PHR-2 (-1.890) exhibited negative significant heterosis over mid parent for this character.

b) Heterosis over better- parent

Heterobeltiosis ranged from -5.650 (NPJ-194 \times PHR-2) to 2.900 (RW-85-59 \times RNWR-09-3). Five crosses *viz.*, RW-85-59 \times RNWR-09-3 (2.900), SKJM-05 \times Kranti (1.340), SKJM-05 \times Giriraj (1.710) and Giriraj \times PHR-2 (1.330) revealed positive significant heterosis over better parent for percentage of membrane stability index. Out of 28 crosses, nine crosses *i.e.* NPJ-194 \times DRMR-15-16 (-2.450), NPJ-194 \times SKJM-05 (-3.950), NPJ-194 \times Kranti (-2.640), NPJ-194 \times PHR-2 (-5.650), RW-85-59 \times SKJM-05 (-3.020), RW-85-59 \times PHR-2 (-1.510), DRMR-15-16 \times RNWR-09-3 (-2.840), SKJM-05 \times PHR-2 (-1.320), Giriraj \times PHR-2 (-2.450) revealed negative significant heterosis over better parent for this character.

4.16.2.2 Percentage of excised-leaf water (%)

a) Heterosis over mid- parent

Relative heterosis varied from -19.910 (RNWR-09-3 \times PHR-2) to 23.240 (DRMR-15-16 \times RNWR-09-3). 14 crosses revealed significant negative heterosis over mid parent *viz.*, NPJ-194 \times DRMR-15-16 (-9.070), NPJ-194 \times SKJM-05 (-16.280), NPJ-194 \times Giriraj (-16.380), NPJ-194 \times RNWR-09-3 (-11.810), RW-85-59 \times RNWR-09-3 (-8.060), RW-85-59 \times PHR-2 (-6.620), DRMR-15-16 \times Kranti (-14.010), DRMR-15-16 \times PHR-2 (-9.910), SKJM-05 \times RNWR-09-3 (-15.790), SKJM-05 \times PHR-2 (-16.950), Kranti \times PHR-2 (-19.650), Giriraj \times RNWR-09-3

Table 4.28 Heterosis (%) over mid-parent (MP) and better-parent (BP) for the seed yield and its attributing characters in Indian mustard (*Bassica juncea*)

S.No.	Crosses	Days to 50% flowering		Primary branches plant ⁻¹		Secondary branches Plant ⁻¹		Siliquae plant ⁻¹		Seed siliqua ⁻¹	
		MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	3.770	0.000	-11.270	-24.100*	-12.240	-25.860*	-1.150*	-5.260**	1.520	-1.340
2	NPJ-194 × DRMR-15-16	12.310**	11.310**	10.950	-2.560	0.000	-9.460	5.060**	3.670**	3.300	0.000
3	NPJ-194 × SKJM-05	13.600**	13.250**	14.500	4.170	-2.530	-14.010	2.490**	-0.430	-2.430	-7.180
4	NPJ-194 × Kranti	2.960	0.580	14.960	7.350	-2.190	-12.990	-1.880**	-5.830**	-2.130	-8.000
5	NPJ-194 × Giriraj	6.820**	4.650	8.770	5.080	-3.260	-7.500	2.930**	0.600	12.390	10.800
6	NPJ-194 × RNWR-09-3	5.360*	3.510	20.300	8.110	8.090	-3.290	9.810**	9.080**	3.910	2.200
7	NPJ-194 × PHR-2	15.580**	8.510**	36.430**	25.710*	29.460	28.930	9.900**	6.190**	-30.100**	-36.570**
8	RW-85-59 × DRMR-15-16	-2.180	-6.550*	10.560	7.230	-0.620	-8.050	-6.130**	-8.850**	10.550	10.110
9	RW-85-59 × SKJM-05	-4.080	-7.830**	3.230	-3.610	-14.800	-18.970	-6.030**	-7.330**	2.230	0.000
10	RW-85-59 × Kranti	0.610	-5.200*	5.960	-3.610	41.800**	33.680**	0.970*	0.830	19.740*	15.700
11	RW-85-59 × Giriraj	3.380	-2.330	0.000	-16.870	5.580	-18.390	0.290	-5.950**	19.160*	14.210
12	RW-85-59 × RNWR-09-3	3.700	-1.750	-8.280	-13.250	-9.200	-14.940	-2.370**	-5.810**	11.800	10.460
13	RW-85-59 × PHR-2	0.290	-9.040**	-12.420	-19.280	-5.760	-20.110	-6.280**	-7.050**	-1.370	-8.100
14	DRMR-15-16 × SKJM-05	-1.200	-1.790	-17.330	-20.510	-8.850	-11.460	-1.590**	-3.130**	12.270	10.260
15	DRMR-15-16 × Kranti	-4.990*	-6.360*	-10.960	-16.670	-13.250	-14.940	-3.570**	-6.240**	6.700	3.500
16	DRMR-15-16 × Giriraj	-1.760	-2.910	-8.270	-21.790	-20.160	-34.460*	3.350**	-0.290	24.790*	19.150
17	DRMR-15-16 × RNWR-09-3	-7.370**	-8.190**	-15.790	-17.950	-23.330	-24.340	-0.070	-0.730	20.000*	18.090
18	DRMR-15-16 × PHR-2	-3.930	-9.040**	-2.700	-7.690	4.090	-5.410	1.580**	-0.560	9.900	2.780
19	SKJM-05 × Kranti	9.140**	6.940**	12.860	9.720	0.320	-0.640	-6.880**	-8.040**	6.840	5.500
20	SKJM-05 × Giriraj	1.180	-0.580	2.360	-9.720	4.760	-15.920	-2.540**	-7.400**	15.300	8.210
21	SKJM-05 × RNWR-09-3	3.860	2.340	-12.330	-13.510	-15.210	-16.560	-2.550**	-4.690**	-2.920	-6.150
22	SKJM-05 × PHR-2	3.950	-2.130	-2.820	-4.170	-14.390	-24.200	-6.220**	-6.750**	2.680	-2.310
23	Kranti × Giriraj	2.030	1.730	17.070	5.880	-8.430	-25.970	4.580**	-1.800**	18.060	9.500
24	Kranti × RNWR-09-3	0.000	-0.580	-9.860	-13.510	-17.650	-18.180	-1.080*	-4.440**	-0.520	-5.000
25	Kranti × PHR-2	1.940	-2.130	27.540*	25.710	-21.450	8.440	-3.910**	-4.580**	-5.290	-8.800
26	Giriraj × RNWR-09-3	-0.290	-0.580	14.730	0.000	16.600	-5.260	2.220**	-0.740	0.850	-2.200
27	Giriraj × PHR-2	1.670	-2.660	24.800*	11.430	52.780**	36.360*	4.170**	-1.550**	-5.430	-15.280
28	RNWR-09-3 × PHR-2	3.620	-1.060	9.720	6.760	-2.560	-12.500	-0.070	-2.810**	-15.080	-21.760*
	SE (±)	0.902	1.042	0.350	0.404	0.892	1.030	0.007	0.008	0.794	0.917

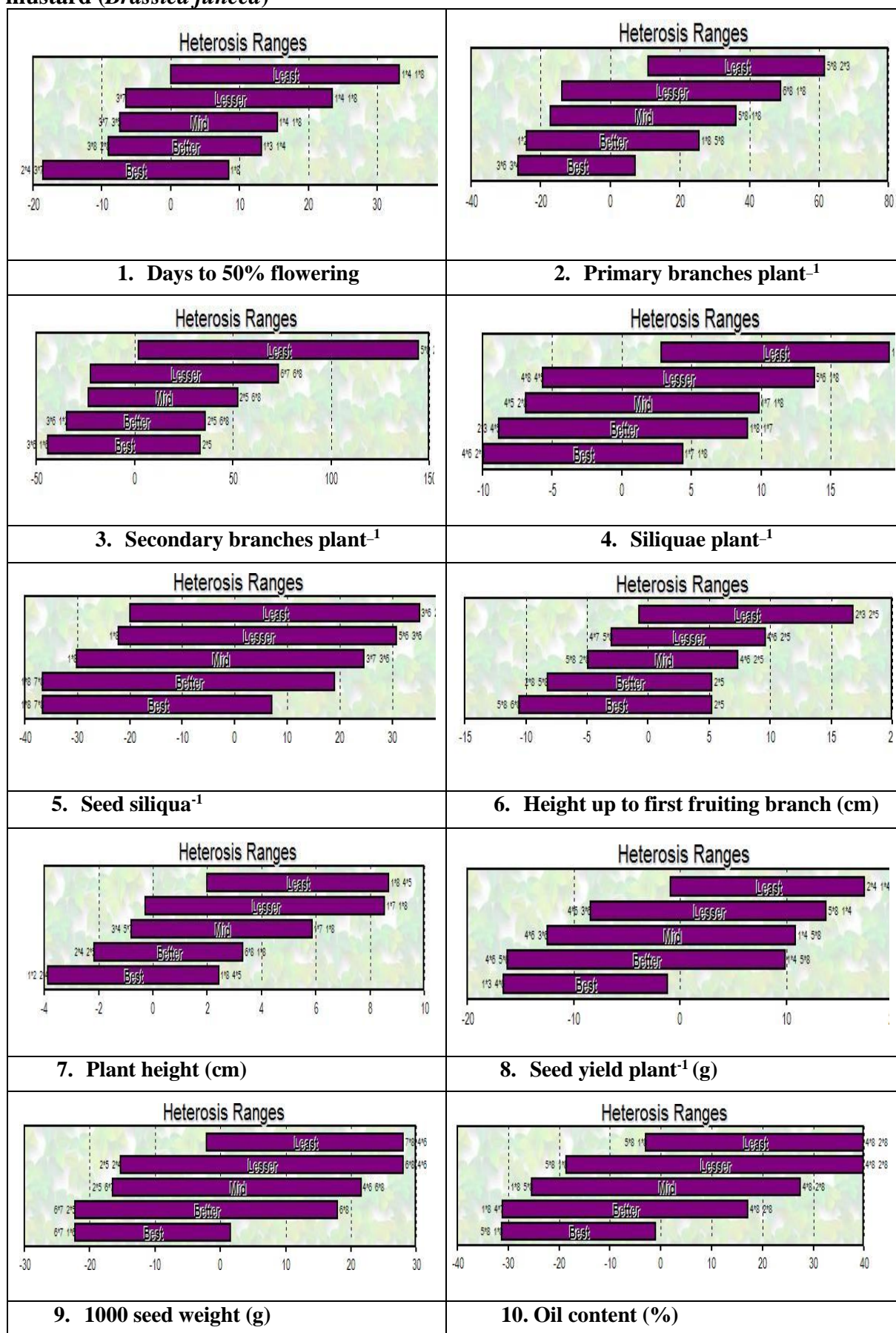
*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Table 4.28 (Continued)

S.No.	Crosses	Height up to first fruiting branch (cm)		Plant height (cm)		Seed yield plant ⁻¹ (g)		1000 seed weight (g)		Oil content (%)	
		MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	-1.950	-4.460**	0.530*	-0.890**	2.200	1.310	16.250**	3.910*	2.450**	-3.560**
2	NPJ-194 × DRMR-15-16	2.240*	1.370	2.470**	0.440	-7.690**	-11.110**	-2.720	-6.540**	4.460**	0.630
3	NPJ-194 × SKJM-05	0.520	0.000	1.930**	-1.010**	10.820**	8.020*	-1.190	-14.870**	-0.880	-5.450**
4	NPJ-194 × Kranti	-0.090	-0.690	2.000**	-0.860**	4.740	3.110	21.250**	8.380**	2.450**	0.630
5	NPJ-194 × Giriraj	0.090	-2.430	2.770**	0.880**	2.070	-4.630	5.730**	-4.050*	-5.590**	-9.640**
6	NPJ-194 × RNWR-09-3	-1.220	-1.570	4.240**	1.740**	-1.760	-2.620	15.880**	-1.010	-3.240**	-3.540**
7	NPJ-194 × PHR-2	-0.260	-1.740	5.880**	3.340**	6.940*	6.220	20.120**	6.590**	-11.510**	-13.000**
8	RW-85-59 × DRMR-15-16	3.110**	1.320	0.440	-0.150	1.270	1.650	29.730**	20.000**	1.860**	-0.680
9	RW-85-59 × SKJM-05	-0.940	-3.960**	-0.660**	-2.160**	6.440*	4.640	8.270**	4.100**	5.040**	3.460**
10	RW-85-59 × Kranti	7.410**	5.280**	-0.290	-1.730**	-2.010	-4.370	7.520**	7.220**	3.410**	-1.090*
11	RW-85-59 × Giriraj	0.520	-4.460**	1.620**	1.180**	-8.200**	-13.510**	8.220**	6.110**	7.480**	5.500**
12	RW-85-59 × RNWR-09-3	-2.630*	-5.450**	0.000	-1.020**	-2.620	-2.620	-7.120**	-11.560**	-2.000**	-8.130**
13	RW-85-59 × PHR-2	-4.470**	8.250**	1.170**	0.150	3.770	2.180	-1.100	-1.650	8.740**	3.900**
14	DRMR-15-16 × SKJM-05	-3.990**	-5.300**	-0.800**	-1.730**	0.000	-1.230	18.970**	6.150**	1.830**	0.910
15	DRMR-15-16 × Kranti	-1.290	-1.540	0.000	-0.860**	-4.120	-9.050**	-1.810	-8.940**	-1.890**	-3.910**
16	DRMR-15-16 × Giriraj	2.210	-1.200	2.790**	2.640**	-9.960**	-12.740**	-17.180**	-21.970**	1.710**	1.130*
17	DRMR-15-16 × RNWR-09-3	-0.350	-1.540	0.440	0.000	-4.660	-7.410*	-2.840	-14.070**	-	-
										6.840**	10.630**
18	DRMR-15-16 × PHR-2	-1.310	-3.590**	0.290	-0.150	-0.650	-4.940	6.270**	-2.200	3.990**	-6.070**
19	SKJM-05 × Kranti	2.520*	1.370	2.520**	2.450**	5.490	1.270	8.020**	3.590*	-2.240**	-5.220**
20	SKJM-05 × Giriraj	4.390**	2.280	-0.220	-1.290**	-12.500**	-16.220**	-5.980**	-11.280**	-2.760**	-3.210**
21	SKJM-05 × RNWR-09-3	-3.160	-3.330*	-0.070	-0.580*	-5.580*	-7.170*	-0.510	-1.510	-5.920**	-10.630**
22	SKJM-05 × PHR-2	-0.440	-1.410	1.080**	0.580*	-3.700	-6.750*	-1.330	-4.620**	4.820**	1.520**
23	Kranti × Giriraj	2.660*	-0.520	1.020**	0.000	-6.920*	-14.290**	0.280	-1.670	-2.570**	-5.010**
24	Kranti × RNWR-09-3	-1.650	-2.580*	-0.720**	-1.150**	2.010	-0.440	5.540**	0.500	-3.300**	-5.420**
25	Kranti × PHR-2	-4.910**	-6.870**	0.580*	0.140	10.910**	9.910**	-0.550	-1.100	-9.780**	-9.980**
26	Giriraj × RNWR-09-3	0.980	-1.230	1.610**	1.020**	-7.380**	-12.740**	-25.470**	-30.150**	-5.570**	-10.000**
27	Giriraj × PHR-2	-1.450	-2.510	3.950**	3.340**	-7.280**	-13.900**	13.480**	10.990**	-4.910**	-7.590**
28	RNWR-09-3 × PHR-2	-0.270	-1.400	1.600**	1.600**	-0.220	-1.750	4.210**	0.000	2.660**	0.630
	SE (±)	0.015	0.017	0.004	0.004	0.015	0.017	0.597	0.689	0.495	0.572

*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Fig 4 Heterosis range for the different seed yield and its attributing characters in Indian mustard (*Brassica juncea*)



(-11.900), Giriraj \times PHR-2 (-9.330) and RNWR-09-3 \times PHR-2 (-19.910) are considered as best for percentage of excised- leaf water loss whereas, eight crosses had significant positive heterosis over mid parental values namely NPJ-194 \times Kranti (6.470), RW-85-59 \times SKJM-05 (16.190), DRMR-15-16 \times Kranti (13.020), DRMR-15-16 \times Giriraj (12.520), DRMR-15-16 \times RNWR-09-3 (23.240), SKJM-05 \times Kranti (13.060), SKJM-05 \times Giriraj (7.130), Kranti \times Giriraj (8.810) for this character.

b) Heterosis over better- parent

The heterosis over better parent ranged from -25.200 (SKJM-05 \times PHR-2) to 19.480 (DRMR-15-16 \times RNWR-09-3). The negative significant heterosis was observed by crosses NPJ-194 \times DRMR-15-16 (-13.010), NPJ-194 \times SKJM-05 (-20.780), NPJ-194 \times Giriraj (-17.810), NPJ-194 \times RNWR-09-3 (-13.010), RW-85-59 \times RNWR-09-3 (-8.920), RW-85-59 \times PHR-2 (-13.320), DRMR-15-16 \times Kranti (-16.820), DRMR-15-16 \times PHR-2 (-18.030), SKJM-05 \times RNWR-09-3 (-19.250), SKJM-05 \times PHR-2 (-25.200), Kranti \times PHR-2 (-24.590), Giriraj \times RNWR-09-3 (-12.210), Giriraj \times PHR-2 (-15.370) and RNWR-09-3 \times PHR-2 (-25.000) and considered as good for this character. The significant positive heterosis was displayed by six crosses namely RW-85-59 \times SKJM-05 (12.440), DRMR-15-16 \times SKJM-05 (11.750), DRMR-15-16 \times Giriraj (9.460), DRMR-15-16 \times RNWR-09-3 (19.480), SKJM-05 \times Kranti (8.180), Kranti \times Giriraj (8.180) for percentage of excised- leaf water loss.

4.16.2.3 Percentage of relative water content (%)

a) Heterosis over mid- parent

Relative heterosis varied from -2.610 (NPJ-194 \times Kranti) to 2.010 (DRMR-15-16 \times PHR-2). The crosses *viz.*, RW-85-59 \times PHR-2 (1.830), DRMR-15-16 \times PHR-2 (2.010), SKJM-05 \times PHR-2 (1.500), Giriraj \times PHR-2 (1.490) and RNWR-09-3 \times PHR-2 (1.490) revealed significant positive heterosis over mid parent for percentage of relative water content whereas, out of 28 crosses, only one crosses observed negative significant heterosis over mid

parent *i.e.*, -2.610 (NPJ-194 × Kranti).

b) Heterosis over better- parent

Heterobeltiosis for percentage of relative water content values varied from -3.250 (NPJ-194 × Kranti) to 2.010 (DRMR-15-16 × PHR-2). Positive significant heterosis over better parent was observed for only one cross *i.e.* DRMR-15-16 × PHR-2 (2.010) while the negative significant heterosis was found in crosses NPJ-194 × Kranti (-3.250), NPJ-194 × PHR-2 (-1.640) and Kranti × Giriraj (-1.620).

14.16.2.4 Canopy temperature depression ($^{\circ}\text{C}$)

a) Heterosis over mid- parent

Relative heterosis ranged from -18.280 (SKJM-05 × Giriraj) to 11.020 (DRMR-15-16 × Kranti). None of the crosses showed significant positive heterosis over mid parent whereas one cross observed as significant negative heterosis over their mid parent *i.e.*, SKJM-05 × Giriraj (-18.280).

b) Heterosis over better- parent

Heterobeltiosis for crosses over their better parent values ranged from -11.030 (NPJ-194 × SKJM-05) to 7.630 (NPJ-194 × DRMR-15-16). None of the crosses showed significant positive heterosis over better parent for canopy temperature depression, whereas only one cross showed negative significant heterosis over better parent for this character *i.e.*, SKJM-05 × Giriraj (-20.280).

14.16.2.5 Proline content of leaf (mg/gm)

a) Heterosis over mid- parent

Relative heterosis ranged from -20.390 (RW-85-59 × RNWR-09-3) to 35.450 (SKJM-05 × PHR-2). Seven crosses revealed significant positive heterosis over mid parent namely NPJ-194 × DRMR-15-16 (13.880), NPJ-194 × SKJM-05 (24.150), NPJ-194 × PHR-2 (12.690), RW-85-59 × SKJM-05 (10.450), SKJM-05 × Giriraj (21.520), SKJM-05 × PHR-2 (35.450)

and Kranti × Giriraj (26.380) whereas, eight crosses observed significant negative heterosis over mid parent for proline content of leaf *i.e.*, NPJ-194 × RW-85-59 (-11.360), NPJ-194 × Kranti (-9.880), NPJ-194 × RNWR-09-3 (-19.700), RW-85-59 × Giriraj (-11.670), RW-85-59 × RNWR-09-3 (-20.390), RW-85-59 × PHR-2 (-14.670), DRMR-15-16 × Kranti (-15.370), DRMR-15-16 × RNWR-09-3 (-9.900) and DRMR-15-16 × PHR-2 (-8.840).

b) Heterosis over better- parent

The estimate heterobeltosis was recorded from -23.420 (NPJ-194 × RNWR-09-3) to 23.370 (Kranti × Giriraj). In all 28 crosses, six crosses showed significant and positive heterosis over better parent *viz.*, NPJ-194 × DRMR-15-16 (13.390), NPJ-194 × SKJM-05 (9.420), NPJ-194 × PHR-2 (12.180), SKJM-05 × Kranti (10.090), SKJM-05 × PHR-2 (18.910) and Kranti × Giriraj (23.370) while remaining 15 cross combinations namely NPJ-194 × RW-85-59 (-16.150), NPJ-194 × Kranti (-14.620), NPJ-194 × RNWR-09-3 (-23.420), RW-85-59 × DRMR-15-16 (-8.240), RW-85-59 × SKJM-05 (-7.200), RW-85-59 × Kranti (-9.870), RW-85-59 × Giriraj (-18.820), RW-85-59 × RNWR-09-3 (-21.060), RW-85-59 × PHR-2 (-18.930), DRMR-15-16 × Kranti (-19.490), DRMR-15-16 × RNWR-09-3 (-14.430), DRMR-15-16 × PHR-2 (-9.640), SKJM-05 × RNWR-09-3 (-12.320), Kranti × PHR-2 (-10.910) and Giriraj × RNWR-09-3 (-10.710) exhibiting significant negative heterosis .

14.16.2.6 Chlorophyll a (mg/gm)

a) Heterosis over mid- parent

Relative heterosis ranged from -33.730 (DRMR-15-16 × SKJM-05) to RW-85-59 × DRMR-15-16 (44.260). Crosses namely NPJ-194 × RW-85-59 (26.390), RW-85-59 × DRMR-15-16 (44.260), RW-85-59 × Kranti (36.750), RW-85-59 × Giriraj (44.000), DRMR-15-16 × Kranti (25.520) and Giriraj × PHR-2 (26.250) revealed positive significant heterosis over mid parent for this character whereas, only three crosses showed negative significant heterosis over mid parent for chlorophyll an *i.e.* NPJ-194 × SKJM-05 (-26.700), DRMR-15-16 × SKJM-05 (-

33.730) and DRMR-15-16 × RNWR-09-3 (-28.570).

b) Heterosis over better- parent

The estimate for heterobeltosis was recorded from -40.430 (DRMR-15-16 × SKJM-05) to 21.230 (DRMR-15-16 × Kranti). None of the crosses showed significant and positive heterosis over better parent for this character while four crosses namely NPJ-194 × SKJM-05 (-27.840), NPJ-194 × Kranti (-28.870), DRMR-15-16 × SKJM-05 (-40.430) and DRMR-15-16 × RNWR-09-3 (-35.480) exhibited significant negative heterosis for chlorophyll a.

14.16.2.7 Chlorophyll b (mg/gm)

a) Heterosis over mid- parent

Relative heterosis varied from -29.580 (NPJ-194 × SKJM-05) to 62.070 (DRMR-15-16 × RNWR-09-3). Crosses NPJ-194 × Giriraj (35.290), NPJ-194 × PHR-2 (42.860), RW-85-59 × PHR-2 (45.450), DRMR-15-16 × RNWR-09-3 (62.070) and SKJM-05 × RNWR-09-3 (38.030) exhibited significant positive heterosis over mid parent whereas, only one cross *i.e.*, NPJ-194 × SKJM-05 (-29.580) observed significant negative heterosis over mid parent for chlorophyll b.

b) Heterosis over better- parent

The estimate of all heterosis over better -30.560 (NPJ-194 × SKJM-05) to 38.890 (NPJ-194 × PHR-2). In all 28 crosses, only two crosses namely NPJ-194 × PHR-2 (38.890) and SKJM-05 × RNWR-09-3 (36.110) showed significant positive heterosis over better parent whereas none of the crosses showed significant negative heterosis over better parent for the character chlorophyll b.

14.16.2.8 Total chlorophyll b (mg/gm)

a) Heterosis over mid- parent

Relative heterosis ranged from -23.880 (DRMR-15-16 × SKJM-05) to 60.120 (NPJ-194 × PHR-2). Crosses namely NPJ-194 × RW-85-59 (42.400), NPJ-194 × Kranti (31.190),

NPJ-194 × Giriraj (46.300), NPJ-194 × RNWR-09-3 (25.310), NPJ-194 × PHR-2 (60.120), RW-85-59 × Kranti (55.260), RW-85-59 × PHR-2 (52.800) and Giriraj × PHR-2 (38.840) revealed positive significant heterosis while none of the crosses showed significant negative heterosis over mid parent for total chlorophyll.

b) Heterosis over better- parent

Heterobeltiosis for crosses varied from -34.090 (DRMR-15-16 × SKJM-05) to 58.680 (NPJ-194 × PHR-2). The crosses namely NPJ-194 × Giriraj (44.510), NPJ-194 × PHR-2 (58.680), RW-85-59 × Kranti (40.480), Giriraj × PHR-2 (35.930) exhibited positive significant heterosis over better parent. Only one cross *i.e.*, DRMR-15-16 × SKJM-05 (-34.090) showed negative significant heterosis over better parent, indicated poor performance for total chlorophyll.

14.16.3 Estimation of heterosis for aphid related characters

Heterosis over mid- parent (MP) and better parent (BP) for nine physiological characters are presented in Table 4.30.

14.16.3.1 Water content of aphid probed twig (%)

a) Heterosis over mid- parent

Relative heterosis varied from -7.050 (NPJ-194 × RW-85-59) to 5.020 (RW-85-59 × Giriraj). Crosses NPJ-194 × PHR-2 (3.590) and RW-85-59 × Giriraj (5.020) exhibited significant positive heterosis over mid parent whereas, NPJ-194 × RW-85-59 (-7.050), NPJ-194 × RNWR-09-3 (-3.650), RW-85-59 × SKJM-05 (-4.000) and DRMR-15-16 × SKJM-05 (-5.600) crosses observed significant negative heterosis over mid parent for water content of aphid probed twig.

b) Heterosis over better- parent

Heterobeltiosis for water content of aphid probed twig values ranged from -8.870 (NPJ-

194 × RW-85-59) to 3.540 (RW-85-59 × Giriraj). Out of 28 crosses, none of the crosses were found positive significant heterosis over better parent for water content of aphid probed twig whereas, seven crosses namely NPJ-194 × RW-85-59 (-8.660), NPJ-194 × Giriraj (-4.860), RW-85-59 × SKJM-05 (-5.470), DRMR-15-16 × Kranti (8.870), DRMR-15-16 × PHR-2 (-6.160), Kranti × RNWR-09-3 (-5.550) and Giriraj × RNWR-09-3 (-5.050) showed significant negative heterosis over better parent for this character.

14.16.3.2 Water content of aphid uninfested twig (%)

a) Heterosis over mid- parent

Relative heterosis ranged from -13.720 (Kranti × PHR-2) to 6.820 (Kranti × Giriraj). Kranti × Giriraj (6.820) crosses revealed significant positive heterosis over mid parental values whereas, crosses *viz.*, DRMR-15-16 × Kranti (-8.050), DRMR-15-16 × PHR-2 (-7.100), Kranti × RNWR-09-3 (-7.280) and Kranti × PHR-2 (-13.720) observed significant negative heterosis over mid parent for water content of aphid uninfested twig.

Table 4.29 Heterosis (%) over mid-parent (MP) and better-parent (BP) for physiological character Indian mustard (*Bassica juncea*)

S. No.	Crosses	Oil content (%)		Percentage of membrane stability index (%)		Percentage excised- leaf water loss (%)		Percentage relative water content (%)		Canopy temperature depression (°C)	
		MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	-1.650**	-15.950**	1.810**	0.380	-0.930	-3.200	-0.490	-0.660	6.870	6.870
2	NPJ-194 × DRMR-15-16	9.660**	-2.060**	-2.260**	-2.450**	-9.070**	-13.010**	0.330	-0.660	10.160	7.630
3	NPJ-194 × SKJM-05	-7.380**	-18.760**	-2.760**	-3.950**	-16.280**	-20.780**	-0.160	-0.330	-9.360	-11.030
4	NPJ-194 × Kranti	-1.630**	-9.190**	-1.800**	-2.640**	6.470*	5.250	-2.610**	-3.250**	6.150	5.340
5	NPJ-194 × Giriraj	-15.440**	-25.520**	-0.570	-1.130	-16.380**	-17.810**	-0.490	-0.660	2.190	-2.100
6	NPJ-194 × RNWR-09-3	-14.530**	-14.610**	0.100	-1.130	-11.810**	-13.010**	-0.490	-0.660	1.130	0.000
7	NPJ-194 × PHR-2	-25.410**	-31.140**	-5.650**	-5.650**	-1.300	-6.350	-0.660	-1.640*	-3.280	-3.820
8	RW-85-59 × DRMR-15-16	3.140**	-1.910**	-1.820**	-3.020**	-2.200	-4.310	-0.170	-0.990	-7.810	-9.920
9	RW-85-59 × SKJM-05	10.000**	6.720**	0.390	0.190	16.190**	12.440**	-0.990	-0.990	1.870	0.000
10	RW-85-59 × Kranti	6.630**	-2.000**	0.580	0.000	5.910	4.670	0.160	-0.650	3.080	2.200
11	RW-85-59 × Giriraj	14.290**	10.340**	0.290	-0.570	-4.400	-4.960	-0.330	-0.660	7.300	2.800
12	RW-85-59 × RNWR-09-3	-8.770**	-22.100**	3.090**	2.900**	-8.060*	-8.920*	-0.660	-0.980	7.170	5.970
13	RW-85-59 × PHR-2	27.620**	17.290**	-0.100	-1.510*	-6.620*	-13.320**	1.830**	0.990	2.290	2.290
14	DRMR-15-16 × SKJM-05	2.800**	0.720	-0.100	-1.130	13.020**	11.750**	0.830	0.000	2.680	-1.470
15	DRMR-15-16 × Kranti	-3.910**	-7.320**	1.430*	0.760	-14.010**	-16.820**	0.660	-0.970	11.020	9.300
16	DRMR-15-16 × Giriraj	3.030**	1.430*	1.140*	0.760	12.520**	9.460*	1.160	0.000	5.220	-1.400
17	DRMR-15-16 × RNWR-09-3	-17.940**	-26.780**	-1.810**	-2.840**	23.240**	19.480**	-0.170	-1.310	4.250	0.750
18	DRMR-15-16 × PHR-2	-8.050**	-11.310**	-0.570	-0.750	-9.910**	-18.030**	2.010**	2.010**	2.340	0.000
19	SKJM-05 × Kranti	-4.810**	-9.980**	1.730**	1.340*	13.060**	8.180*	-0.160	-0.970	-4.910	-7.350
20	SKJM-05 × Giriraj	-5.940**	-6.400**	2.400**	1.710**	7.130*	3.070	0.330	0.000	-18.280**	-20.280**
21	SKJM-05 × RNWR-09-3	-16.450**	-26.780**	0.770	-0.770	-15.790**	-19.250**	0.660	0.330	-5.930	-6.620
22	SKJM-05 × PHR-2	22.630**	15.960**	-0.100	-1.320*	-16.950**	-25.200**	1.500*	0.660	4.120	2.210
23	Kranti × Giriraj	-5.250**	-9.980**	-0.480	-0.760	8.810**	8.180*	-1.140	-1.620*	-0.740	-5.590
24	Kranti × RNWR-09-3	-11.070**	-17.980**	1.150*	0.770	3.750	3.500	-0.160	-0.650	9.510	7.460
25	Kranti × PHR-2	-18.630**	-18.630**	1.040	0.190	-19.650**	-24.590**	0.660	-0.970	2.310	1.530
26	Giriraj × RNWR-09-3	-14.890**	-25.090**	2.010**	1.330*	-11.900**	-12.210**	-0.330	-0.330	2.530	0.700
27	Giriraj × PHR-2	-9.680**	-14.190**	-1.890**	-2.450**	-9.330**	-15.370**	1.490*	0.330	-2.190	-6.290
28	RNWR-09-3 × PHR-2	-1.120**	-8.800**	0.480	-0.750	-19.910**	-25.000**	1.490*	0.330	-5.660	-6.720
	SE (±)	0.005	0.006	0.007	0.008	0.033	0.038	0.005	0.005	0.020	0.023

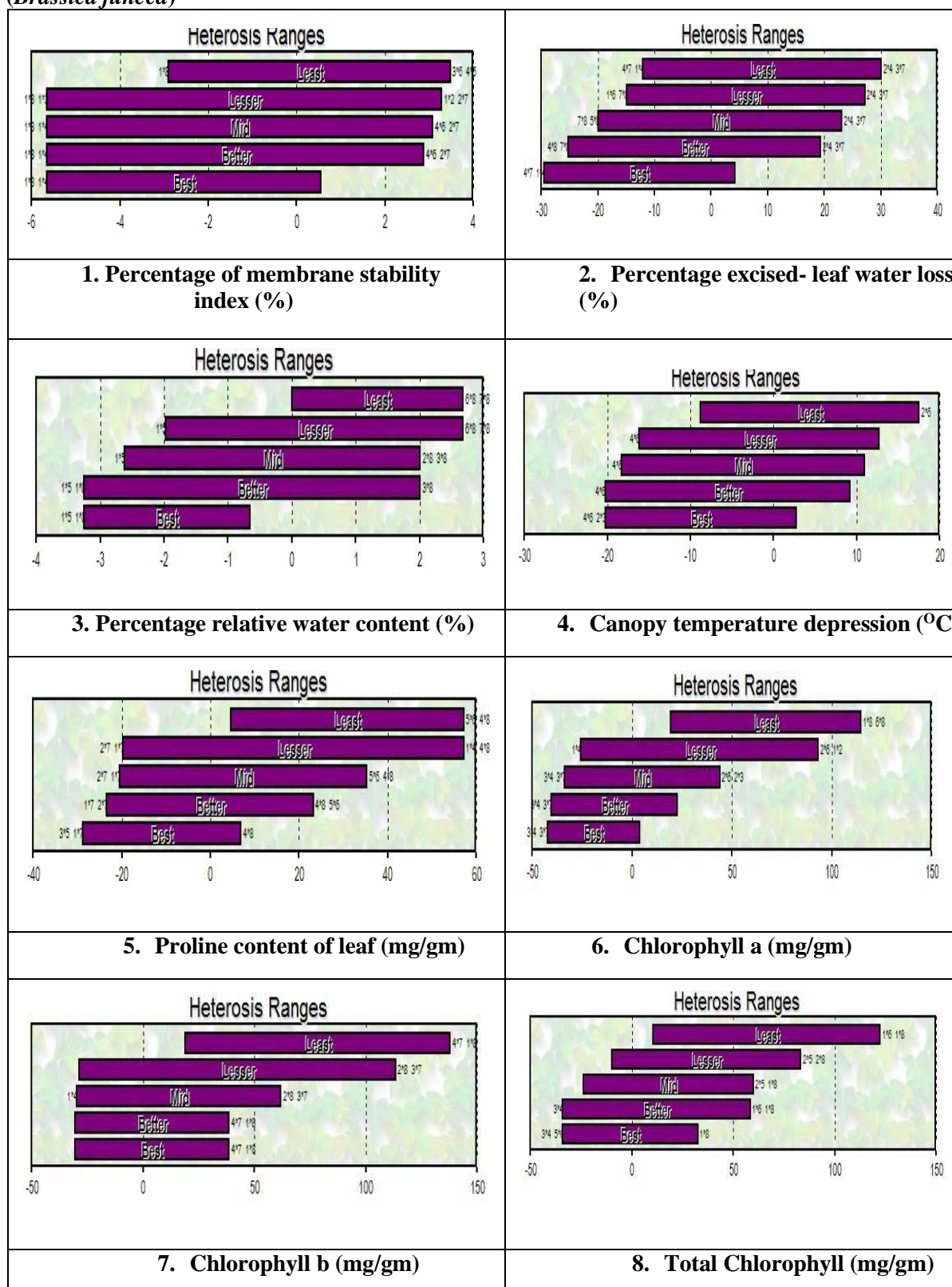
*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Table 4.29 (Continued)

S. No.	Crosses	Proline content of leaf (mg/gm)		Chlorophyll a (mg/gm)		Chlorophyll b (mg/gm)		Total Chlorophyll (mg/gm)	
		MP	BP	MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	-11.360**	-16.150**	26.390*	-6.190	19.300	-5.560	42.400**	22.870
2	NPJ-194 × DRMR-15-16	13.880**	13.390**	0.000	-11.340	27.590	2.780	27.740	20.730
3	NPJ-194 × SKJM-05	24.150**	9.420*	-26.700**	-27.840**	-29.580*	-30.560	-14.720	-22.310
4	NPJ-194 × Kranti	-9.880**	-14.620**	-17.370	-28.870**	11.110	-2.780	31.190*	24.390
5	NPJ-194 × Giriraj	1.170	-1.900	12.000	1.030	35.290*	27.780	46.300**	44.510**
6	NPJ-194 × RNWR-09-3	-19.700**	-23.420**	4.210	2.060	16.670	16.670	25.310*	14.680
7	NPJ-194 × PHR-2	12.690**	12.180**	12.850	4.120	42.860**	38.890*	60.120**	58.680**
8	RW-85-59 × DRMR-15-16	-2.610	-8.240*	44.260**	17.330	20.930	18.180	15.850	5.140
9	RW-85-59 × SKJM-05	10.450**	-7.200*	9.220	-18.090	-7.140	-25.710	-1.100	-21.050
10	RW-85-59 × Kranti	0.240	-9.870**	36.750*	14.290	33.330	18.520	55.260**	40.480*
11	RW-85-59 × Giriraj	-11.670**	-18.820**	44.000**	15.380	13.210	-6.250	21.860	6.250
12	RW-85-59 × RNWR-09-3	-20.390**	-21.060**	12.860	-15.050	-5.260	-25.000	12.160	-10.130
13	RW-85-59 × PHR-2	-14.670**	-18.930**	24.030	-2.440	45.450*	17.650	52.800**	30.840
14	DRMR-15-16 × SKJM-05	5.860	-6.350	-33.730**	-40.430**	-12.280	-28.570	-23.880	-34.090*
15	DRMR-15-16 × Kranti	-15.370**	-19.490**	25.520*	21.230	10.200	0.000	4.100	3.740
16	DRMR-15-16 × Giriraj	-2.500	-5.060	11.110	8.970	3.700	-12.500	2.610	-1.880
17	DRMR-15-16 × RNWR-09-3	-9.900**	-14.430**	-28.570**	-35.480**	62.070**	30.560	24.890	8.610
18	DRMR-15-16 × PHR-2	-8.840*	-9.640*	9.550	4.880	25.000	2.940	16.610	9.280
19	SKJM-05 × Kranti	3.990	-3.690	8.540	-5.320	-3.230	-14.290	-9.380	-21.300
20	SKJM-05 × Giriraj	21.520**	10.090*	2.330	-6.380	-4.480	-8.570	-14.050	-22.560
21	SKJM-05 × RNWR-09-3	3.640	-12.320**	-0.530	-1.060	38.030**	36.110*	-5.540	-6.020
22	SKJM-05 × PHR-2	35.450**	18.910**	12.500	5.320	15.940	14.290	13.780	4.510
23	Kranti × Giriraj	26.380**	23.370**	21.620	15.380	-5.080	-12.500	-7.820	-11.560
24	Kranti × RNWR-09-3	4.690	-5.160	9.200	-4.300	1.590	-11.110	4.790	-8.610
25	Kranti × PHR-2	-5.560	-10.910**	17.110	8.540	4.920	-5.880	9.550	2.990
26	Giriraj × RNWR-09-3	-3.590	-10.710**	2.920	-5.380	-8.820	-13.890	-14.410	-22.530
27	Giriraj × PHR-2	1.760	-1.760	26.250*	23.170	-9.090	-11.760	38.840**	35.930*
28	RNWR-09-3 × PHR-2	4.630	0.220	-6.290	-11.830	2.860	0.000	12.760	4.050
	SE (±)	0.132	0.152	0.021	0.024	0.012	0.014	0.106	0.122

*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Fig 5 Heterosis range for the different physiological characters in Indian mustard (*Brassica juncea*)



b) Heterosis over better- parent

Heterobeltiosis for water content of aphid uninfested twig values varied from -14.050 (Kranti × PHR-2) to 1.780 (DRMR-15-16 × Giriraj). None of the crosses exhibited positive significant heterosis over better parent whereas, crosses namely RW-85-59 × Kranti (-9.170), DRMR-15-16 × Kranti (-10.370), DRMR-15-16 × PHR-2 (-9.110), Kranti × RNWR-09-3 (-8.990), Kranti × PHR-2 (-14.050) and Giriraj × PHR-2 (-7.430) showed significant negative heterosis over better parent, which indicated poor performance for water content of aphid uninfested twig.

14.16.3.3 Water content of aphid (%)**a) Heterosis over mid- parent**

Relative heterosis varied from -6.720 (SKJM-05 × RNWR-09-3) to 16.550 (DRMR-15-16 × Kranti). NPJ-194 × RNWR-09-3 (-4.430) and SKJM-05 × RNWR-09-3 (-6.720) crosses recorded negative significant heterosis over mid parent for water content of aphid while, the crosses viz., NPJ-194 × DRMR-15-16 (5.450), NPJ-194 × PHR-2 (5.820), RW-85-59 × Giriraj (9.550), DRMR-15-16 × SKJM-05 (7.950), DRMR-15-16 × Kranti (16.550), DRMR-15-16 × PHR-2 (9.160), Kranti × PHR-2 (6.740), Giriraj × PHR-2 (9.240) and RNWR-09-3 × PHR-2 (11.780) exhibited positive significant heterosis over mid parent for this character.

b) Heterosis over better- parent

Heterobeltiosis for cross ranged from -8.320 (RW-85-59 × PHR-2) to 12.230 (DRMR-15-16 × Kranti). NPJ-194 × Giriraj (-7.630), NPJ-194 × RNWR-09-3 (-7.050), RW-85-59 × SKJM-05 (-6.490), RW-85-59 × PHR-2 (-8.320) and SKJM-05 × RNWR-09-3 (-8.070) crosses revealed negative significant heterosis over better parent

for water content of aphid, whereas crosses DRMR-15-16 × Kranti (12.230) and DRMR-15-16 × PHR-2 (8.250) showed positive significant heterosis over better parent for this character.

14.16.3.4 Percentage of water differential between aphid probed twig and aphid itself (%)

a) Heterosis over mid- parent

Relative heterosis ranged from -18.300 (DRMR-15-16 × Kranti) to 10.000 (RNWR-09-3 × PHR-2). RNWR-09-3 × PHR-2 (10.000) cross showed significant positive heterosis over mid parental values were found to be promising for percentage of water differential between aphid probed twig and aphid itself. Crosses namely RW-85-59 × Giriraj (-11.770), DRMR-15-16 × SKJM-05 (-11.940), DRMR-15-16 × Kranti (-18.300) and Giriraj × PHR-2 (-5.210) observed significant negative heterosis over their mid parental value.

b) Heterosis over better- parent

Heterobeltiosis for percentage of water differential between aphid probed twig and aphid itself values varied from -19.520 (DRMR-15-16 × Kranti) to 2.670 (SKJM-05 × Giriraj). None of the crosses revealed positive significant heterosis over better parent whereas, NPJ-194 × DRMR-15-16 (-8.960), NPJ-194 × SKJM-05 (-7.610), NPJ-194 × Kranti (-8.010), NPJ-194 × PHR-2 (-8.480), RW-85-59 × SKJM-05 (-8.170), RW-85-59 × Kranti (-7.190), RW-85-59 × Giriraj (-15.270), DRMR-15-16 × SKJM-05 (-13.350), DRMR-15-16 × Kranti (-19.520), Kranti × PHR-2 (-6.900), Giriraj × PHR-2 (-6.710) and RNWR-09-3 × PHR-2 (-13.020) showed significant negative heterosis for this character.

14.16.3.5 Aphid count

a) Heterosis over mid- parent

Relative heterosis varied from -14.680 (RW-85-59 × SKJM-05) to 39.230 (RW-85-59 × DRMR-15-16). Out of 28 crosses, crosses namely NPJ-194 × RW-85-59 (-6.690), NPJ-194 × DRMR-15-16 (-3.550), NPJ-194 × SKJM-05 (-9.210), RW-85-59 × SKJM-05 (-14.680), RW-85-59 × Giriraj (-7.270), DRMR-15-16 × SKJM-05 (-5.280), DRMR-15-16 × Giriraj (-7.440), SKJM-05 × Kranti (-10.200), SKJM-05 × RNWR-09-3 (-9.870), SKJM-05 × PHR-2 (-8.980) and Giriraj × RNWR-09-3 (-5.950) revealed negative significant heterosis over mid parent for aphid count. Crosses observed positive significant heterosis over mid parent for this character are NPJ-194 × Giriraj (3.650), NPJ-194 × RNWR-09-3 (6.500), RW-85-59 × DRMR-15-16 (39.230), RW-85-59 × Giriraj (8.790), RW-85-59 × RNWR-09-3 (17.740), RW-85-59 × PHR-2 (11.720), DRMR-15-16 × Giriraj (5.680), Kranti × Giriraj (9.870), Kranti × RNWR-09-3 (4.390), Kranti × PHR-2 (8.970) and Giriraj × PHR-2 (6.460).

b) Heterosis over better- parent

Heterobeltiosis for aphid count ranged from -23.780 (RW-85-59 × SKJM-05) to 33.810 (RW-85-59 × DRMR-15-16). The crosses namely NPJ-194 × RW-85-59 (-18.990), NPJ-194 × DRMR-15-16 (-13.260), NPJ-194 × SKJM-05 (-12.110), NPJ-194 × Kranti (-7.860), NPJ-194 × PHR-2 (-4.750), RW-85-59 × SKJM-05 (-23.780), RW-85-59 × Giriraj (-16.900), DRMR-15-16 × SKJM-05 (-12.240), DRMR-15-16 × Kranti (-9.090), DRMR-15-16 × RNWR-09-3 (-5.350), DRMR-15-16 × PHR-2 (-7.340), SKJM-05 × Kranti (-15.380), SKJM-05 × RNWR-09-3 (-12.240), SKJM-05 × PHR-2 (-12.240), Giriraj × RNWR-09-3 (-8.100) exhibited negative significant heterosis over better parent for aphid count, whereas crosses RW-85-59 × DRMR-15-16 (33.810), RW-85-59 × RNWR-09-3 (7.750), Kranti × Giriraj (3.870) and Kranti × PHR-2 (6.400) showed positive significant heterosis over better parent for aphid count.

4.16.3.6 Penetration force

a) Heterosis over mid- parent

Relative heterosis varied from -19.080 (RW-85-59 × PHR-2) to 27.590 (NPJ-194 × RNWR-09-3). NPJ-194 × DRMR-15-16 (8.550), NPJ-194 × SKJM-05 (7.830), NPJ-194 × Giriraj (12.470), NPJ-194 × RNWR-09-3 (27.590), RW-85-59 × SKJM-05 (11.090), DRMR-15-16 × RNWR-09-3 (20.740), SKJM-05 × Giriraj (9.270), Kranti × Giriraj (20.960) and RNWR-09-3 × PHR-2 (13.720) crosses noted positive significant heterosis over mid parent for penetration force and crosses namely NPJ-194 × PHR-2 (-12.950), RW-85-59 × SKJM-05 (-8.740), RW-85-59 × Kranti (-14.960), RW-85-59 × Giriraj (-17.620), RW-85-59 × SKJM-05 (-19.080), SKJM-05 × PHR-2 (-16.380) and Kranti × RNWR-09-3 (-9.770) exhibited positive significant heterosis over mid parent for this character.

b) Heterosis over better- parent

Heterobeltiosis ranged from -25.410 (RW-85-59 × Giriraj) to 26.090 (NPJ-194 × RNWR-09-3). Crosses viz., NPJ-194 × RNWR-09-3 (26.090), RW-85-59 × DRMR-15-16 (9.530), DRMR-15-16 × PHR-2 (15.070), Kranti × Giriraj (17.510) and RNWR-09-3 × PHR-2 (12.490) revealed positive significant heterosis over better parent for penetration force. Crosses recorded negative significant heterosis over better parent for this character are NPJ-194 × PHR-2 (-13.030), RW-85-59 × SKJM-05 (-9.540), RW-85-59 × Kranti (-20.900), RW-85-59 × Giriraj (-25.410), RW-85-59 × PHR-2 (-23.110), DRMR-15-16 × Kranti (-8.500), DRMR-15-16 × Giriraj (-7.220), DRMR-15-16 × PHR-2 (-8.700), SKJM-05 × Kranti (-12.970), SKJM-05 × RNWR-09-3 (-10.890), SKJM-05 × PHR-2 (-21.220), Kranti × RNWR-09-3 (-10.820).

4.17 Vr-Wr graph for the different characters in Indian Mustard (*Brassica juncea*)

4.17.1 Vr-Wr graph for the seed yield and its attributing characters in Indian Mustard (*Brassica juncea*)

Fig7 represents Vr-Wr graph for the different characters in Indian Mustard (*Brassica juncea*). Hayman's graphical analysis was done to assess the genetic relationship among the parents. Studies indicated variation in the mode of inheritance from additive to overdominance for the characters studied.

4.17.1.1 Days to 50% flowering

The regression analysis for days to 50% flowering (Fig.7.1) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. Giriraj (P6) had maximum dominant genes for it being nearest to the point of origin while NPJ-94 (P1), being farthest from the origin, possessed the maximum recessive genes.

4.17.1.2 Primary branches plant⁻¹

The regression analysis for days to primary branches plant⁻¹ (Fig.7.2) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. RNWR-09-03 (P7) had maximum dominant genes because of its proximity to the point of origin while NPJ-194 (P1), DRMR-15-16 (P3) and RW-85-89 (P2) possessed maximum recessive genes being farthest from origin.

4.17.1.3 Secondary branches plant⁻¹

The regression analysis for secondary branches plant⁻¹ (Fig.7.3) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. RNWR-09-03 (P7) followed by NPJ-194 (P1) and SKJM-05 (P4) had maximum dominant genes for it being nearest to the point of origin while Kranti (P5) possessed maximum recessive genes being farthest from origin.

4.17.1.4 Siliquae plant⁻¹

The regression analysis for siliquae plant-1 (Fig.7.4) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. RNWR-09-03 (P4) and DRMR-15-16 (P3) had maximum dominant genes because of its proximity to the point of origin while NPJ-194 (P1) possessed maximum recessive genes being farthest from origin.

4.17.1.5 Seeds siliqua⁻¹

The regression analysis for seeds siliquae⁻¹ (Fig.7.5) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. Kranti (P5) followed by RNWR-09-03 (P7), RW-85-89 (P2), DRMR-15-16 (P3) and SKJM-05 (P4) had maximum dominant genes because of its proximity to the point of origin while NPJ-194 (P1) possessed maximum recessive genes being farthest from origin.

4.17.1.6 Height upto first fruiting branch

The regression analysis for height upto first fruiting branch (Fig.7.6) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. PHR-2 (P8) followed by NPJ-194 (P1) and SKJM-05 (P4) had maximum dominant genes for it being nearest to the point of origin while NPJ-94 (P1) followed by Kranti (P5) and RW-85-89 (P2) possessed the maximum recessive genes for being farthest from origin.

4.17.1.7 Plant height (cm)

The regression analysis for plant height (Fig.7.7) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. DRMR-15-16 (P3) and RNWR-09-03 (P7) had maximum dominant genes because of its proximity to the point of origin while NPJ-194 (P1) possessed maximum recessive genes for being farthest from the origin.

Table 4.30 Heterosis (%) over mid-parent (MP) and better-parent (BP) for aphid related characters in Indian mustard (*Brassica juncea*)

S. No.	Crosses	Water content of aphid probed twig (%)		Water content of aphid uninfested twig (%)		Water content of aphid (%)	
		MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	-7.050**	-8.660**	-5.320	-6.420	-1.790	-3.520
2	NPJ-194 × DRMR-15-16	2.300	-1.430	0.390	-1.590	5.450*	-3.520
3	NPJ-194 × SKJM-05	-1.890	-2.090	-3.480	-6.330	1.430	-2.740
4	NPJ-194 × Kranti	2.230	0.380	0.710	-3.720	3.610	-1.760
5	NPJ-194 × Giriraj	-1.830	-4.860*	-3.700	-4.780	-1.670	-7.630**
6	NPJ-194 × RNWR-09-3	-3.650*	-3.670	0.070	-2.580	-4.430*	-7.050**
7	NPJ-194 × PHR-2	3.590*	0.580	-1.560	-5.540	5.820*	-3.910
8	RW-85-59 × DRMR-15-16	-0.680	-2.660	0.450	-2.650	4.690	-2.640
9	RW-85-59 × SKJM-05	-4.000*	-5.470**	0.370	-3.680	-4.160	-6.490*
10	RW-85-59 × Kranti	-0.760	-0.840	-3.930	-9.170**	2.840	-0.810
11	RW-85-59 × Giriraj	5.020**	3.540	-2.870	-2.910	9.550**	4.670
12	RW-85-59 × RNWR-09-3	-1.300	-3.040	-2.070	-5.740	-1.640	-2.640
13	RW-85-59 × PHR-2	-1.450	-2.660	-0.620	-5.700	-0.660	-8.320**
14	DRMR-15-16 × SKJM-05	-5.600**	-8.870**	-5.540	-6.500	7.950**	2.770
15	DRMR-15-16 × Kranti	0.980	-0.940	-8.050*	-10.370**	16.550**	12.230**
16	DRMR-15-16 × Giriraj	2.330	1.720	4.970	1.780	4.240	1.340
17	DRMR-15-16 × RNWR-09-3	-2.580	-6.160**	-4.550	-5.230	-0.110	-6.210*
18	DRMR-15-16 × PHR-2	2.180	1.370	-7.100*	-9.110*	9.160**	8.250**
19	SKJM-05 × Kranti	-0.240	-1.850	-1.600	-3.120	-2.910	-4.050
20	SKJM-05 × Giriraj	-1.300	-4.160	2.400	-1.690	-2.400	-4.480
21	SKJM-05 × RNWR-09-3	-2.930	-3.150	-0.400	-0.710	-6.720**	-8.070**
22	SKJM-05 × PHR-2	-0.140	-2.850	-5.310	-6.420	0.680	-4.900
23	Kranti × Giriraj	2.190	0.840	6.820*	1.030	4.520	3.490
24	Kranti × RNWR-09-3	-3.780	-5.550**	-7.280*	-8.990*	2.870	0.210
25	Kranti × PHR-2	-1.450	-2.680	-13.720**	-14.050**	6.740**	1.970
26	Giriraj × RNWR-09-3	-2.000	-5.050*	0.590	-3.150	0.640	-2.900
27	Giriraj × PHR-2	1.060	0.870	-2.490	-7.430*	9.240**	5.350
28	RNWR-09-3 PHR-2	0.380	-2.570	-5.050	-6.450	11.780**	4.140
	SE (±)	0.771	0.890	1.359	1.569	0.025	0.029

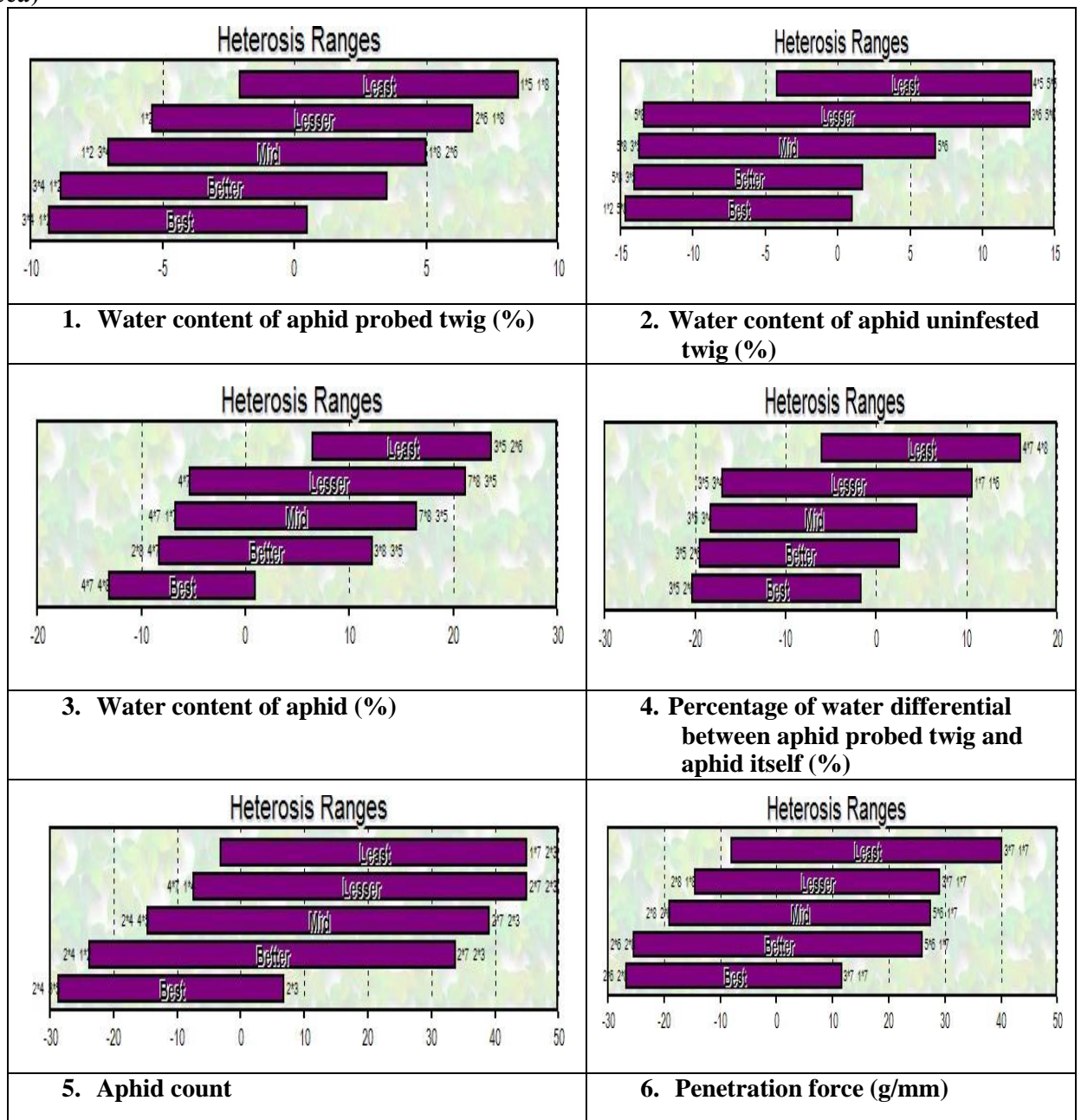
*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Table 4.30 (Continued)

S. No.	Crosses	Percentage of water differential between aphid probed twig and aphid itself (%)		Aphid count		Penetration force (Kpascal)	
		MP	BP	MP	BP	MP	BP
1	NPJ-194 × RW-85-59	-0.680	-3.100	-6.690**	-18.990**	6.100	0.890
2	NPJ-194 × DRMR-15-16	-1.930	-8.960**	-3.550*	-13.260**	8.550**	4.640
3	NPJ-194 × SKJM-05	-1.970	-7.610*	-9.210**	-12.110**	7.830*	1.690
4	NPJ-194 × Kranti	-2.290	-8.010**	0.810	-7.860**	1.070	-1.270
5	NPJ-194 × Giriraj	3.370	-3.050	3.650*	0.000	12.470**	6.800
6	NPJ-194 × RNWR-09-3	4.540	-0.210	6.500**	0.490	27.590**	26.090**
7	NPJ-194 × PHR -2	-0.960	-8.480**	1.930	-4.750**	-12.950**	-13.030**
8	RW-85-59 × DRMR-15-16	-3.350	-8.170**	39.230**	33.810**	11.090**	9.530**
9	RW-85-59 × SKJM-05	2.770	-0.820	-14.680**	-23.780**	-8.740**	-9.540**
10	RW-85-59 × Kranti	-3.730	-7.190*	8.790**	2.770	-14.960**	-20.900**
11	RW-85-59 × Giriraj	-11.770**	-15.270**	-7.270**	-16.900**	-17.620**	-25.410**
12	RW-85-59 × RNWR-09-3	0.320	-1.900	17.740**	7.750**	0.180	-5.800
13	RW-85-59 × PHR-2	2.190	-3.350	11.720**	3.200	-19.080**	-23.110**
14	DRMR-15-16 × SKJM-05	-11.940**	-13.350**	-5.280**	-12.240**	2.390	0.070
15	DRMR-15-16 × Kranti	-18.300**	-19.520**	-7.440**	-9.090**	-2.910	-8.500*
16	DRMR-15-16 × Giriraj	-1.510	-2.590	5.680**	-1.760	1.160	-7.220*
17	DRMR-15-16 × RNWR-09-3	0.310	-2.590	-0.390	-5.350**	20.740**	15.070**
18	DRMR-15-16 × PHR-2	-4.260	-4.730	-3.430	-7.340**	-5.200	-8.700*
19	SKJM-05 × Kranti	2.160	2.050	-10.200**	-15.380**	-5.660	-12.970**
20	SKJM-05 × Giriraj	1.130	0.610	-0.180	-0.520	9.270**	-1.840
21	SKJM-05 × RNWR-09-3	4.070	2.670	-9.870**	-12.240**	-4.440	-10.890**
22	SKJM-05 × PHR-2	0.500	-1.580	-8.980**	-12.240**	-16.380**	-21.220**
23	Kranti × Giriraj	-2.250	-2.650	9.870**	3.870*	20.960**	17.510**
24	Kranti × RNWR-09-3	-4.170	-5.540	4.390*	0.920	-9.770**	-10.820**
25	Kranti × PHR-2	-5.030	-6.900*	8.970**	6.400**	2.930	0.640
26	Giriraj × RNWR-09-3	-1.040	-2.850	-5.950**	-8.100**	-3.650	-7.460
27	Giriraj × PHR-2	-5.210*	-6.710*	6.460**	2.990	4.470	-0.710
28	RNWR-09-3 PHR-2	10.000**	-13.020**	0.090	-0.920	13.720**	12.490**
	SE (±)	0.030	0.035	0.022	0.025	1.795	2.073

*, ** Significant at 5% and 1% levels of probability, respectively; MP= Mid parent, BP= Better parent

Fig 6 Heterosis range for the different aphid related characters in Indian mustard (*Brassica juncea*)



4.17.1.8 Seed yield plant⁻¹ (g)

The regression analysis for seed yield plant⁻¹ (Fig.7.8) revealed negative intercepts of Wr/Vr regression line indicating overdominance gene action. RNWR-09-03 (P7) had maximum dominant genes because of its proximity to the point of origin while Giriraj (P6) possessed maximum recessive genes for being farthest from origin.

4.17.1.9 1000 seed weight (g)

The regression analysis for 1000 seed weight (Fig.7.9) revealed negative intercepts of Wr/Vr regression line indicating overdominance gene action. DRMR-15-16 (P3) followed by SKJM-05 (P4) and Kranti (P5) had maximum dominant genes because of its proximity to the point of origin while Giriraj (P6) possessed maximum recessive genes for being farthest from origin.

4.17.1.10 Oil content (%)

The regression analysis for percent oil content (Fig.7.10) exhibited positive intercepts of Wr/Vr regression line that supports an additive gene action with partial dominance. Kranti (P5) and DRMR-15-16 (P3) had maximum dominant genes for it being nearest to the point of origin while PHR-2 (P8) possessed the maximum recessive genes for being farthest from origin.

4.17.2 Vr-Wr graph for the physiological characters in Indian Mustard (*Brassica juncea*)

4.17.2.1 Percentage of membrane stability index (%)

The regression analysis for percentage of membrane stability index (Fig.7.11) exhibited positive intercepts of Wr/Vr regression line that supports an additive gene action with partial dominance. Kranti (P5) had maximum dominant genes for it being nearest to the point of origin while NPJ-94 (P1) possessed the maximum recessive genes for being farthest from the origin.

4.17.2.2 Percentage of excised leaf water loss (%)

The regression analysis for percentage of excised leaf water loss (Fig.7.12) exhibited positive intercepts of Wr/Vr regression line that supports an additive gene action with partial dominance. RW-85-89 (P2) had maximum dominant genes for it being nearest to the point of

origin while RNWR-09-03 (P7) followed by SKJM-05 (P4) possessed the maximum recessive genes for being farthest from the origin.

4.17.2.3 Percentage relative water content (%)

The regression analysis for percentage relative water content (Fig.7.13) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. Giriraj (P6) had maximum dominant genes because of its proximity to the point of origin while PHR-2 (P8) possessed maximum recessive genes for being farthest from origin.

4.17.2.4 Canopy temperature depression (°C)

The regression analysis for canopy temperature depression (Fig.7.14) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. PHR-2 (P8) had maximum dominant genes for it being nearest to the point of origin while Giriraj (P6) possessed the maximum recessive genes for being farthest from the origin.

4.17.2.5 Proline content of leaf (mg/gm)

The regression analysis for proline content of leaf (Fig.7.15) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. Giriraj (P6) had maximum dominant genes because of its proximity to the point of origin while SKJM-05 (P4) possessed maximum recessive genes for being farthest from the origin.

4.17.2.6 Chlorophyll a (mg/gm)

The regression analysis for chlorophyll a (Fig.7.16) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. Giriraj (P6) had maximum dominant genes for it being nearest to the point of origin while SKJM-05 (P4) and RW-85-89 (P2) possessed the maximum recessive genes for being farthest from the origin.

4.17.2.7 Chlorophyll b (mg/gm)

The regression analysis for chlorophyll b (Fig.7.17) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. Kranti

(P5) had maximum dominant genes because of its proximity to the point of origin while SKJM-05 (P4) and DRMR-15-16 (P3) possessed maximum recessive genes for being farthest from origin.

4.17.2.8 Total Chlorophyll (mg/gm)

The regression analysis for total Chlorophyll (Fig.7.18) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. None of the parents were revealed to lie near the point of origin indicating proportionate distribution of dominant and recessive genes while Giriraj (P6) followed by NPJ-194 (P1) possessed the maximum recessive genes for being farthest from origin.

4.17.2 Vr-Wr graph for the aphid related characters in Indian Mustard (*Brassica juncea*)

4.17.2.1 Water content of aphid probed twig

The regression analysis for water content of aphid probed twig (Fig.7.19) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. None of the parents were revealed to lie near the point of origin indicating proportionate distribution of dominant and recessive genes while NPJ-194 (P1) possessed the maximum recessive genes for being farthest from origin.

4.17.2.2 Water content of aphid uninfested twig (%)

The regression analysis for water content of aphid uninfested twig (Fig.7.20) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. RNWR-09-03 (P7) followed by SKJM-05 (P4) had maximum dominant genes because of its proximity to the point of origin while Giriraj (P6) followed by Kranti (P5) possessed maximum recessive genes for being farthest from the origin.

4.17.2.3 Water content of aphid (%)

The regression analysis for the percent water content of aphid (Fig.7.21) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. NPJ-94

(P1) had maximum dominant genes because of its proximity to the point of origin while DRMR-15-16 (P3) followed by PHR-2 (P8) possessed maximum recessive genes for being farthest from the origin.

4.17.2.4 Percentage of water differential between aphid probed twig and aphid itself (%)

The regression analysis for percent water differential between aphid probed twig and aphid itself (Fig.7.22) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. NPJ-194 (P1) had maximum dominant genes because of its proximity to the point of origin while DRMR-15-16 (P3) possessed maximum recessive genes for being farthest from origin.

4.17.2.5 Aphid count

The regression analysis for aphid count (Fig.7.23) exhibited positive intercepts of W_r/V_r regression line that supports an additive gene action with partial dominance. None of the parents were observed to lie near the point of origin indicating proportionate distribution of dominant and recessive genes while RW-85-89 (P2) possessed the maximum recessive genes for being farthest from origin.

4.17.2.6 Penetration force

The regression analysis for percent water content of aphid (Fig.7.22) revealed negative intercepts of W_r/V_r regression line indicating overdominance gene action. Kranti (P5) followed by PHR-2 (P8) had maximum dominant genes because of its proximity to the point of origin

while RW-85-89 (P2) followed by RNWR-09-03 (P7) possessed maximum recessive genes for being farthest from the origin.

4.18 Screening for aphid resistance

4.18.1 Analysis of variance of lab aphid count for both parents and crosses

Analysis of variance of lab aphid count for both parents and crosses are presented in Table 4.31 and Table 4.32. The analysis of variance (ANOVA) was estimated to test the

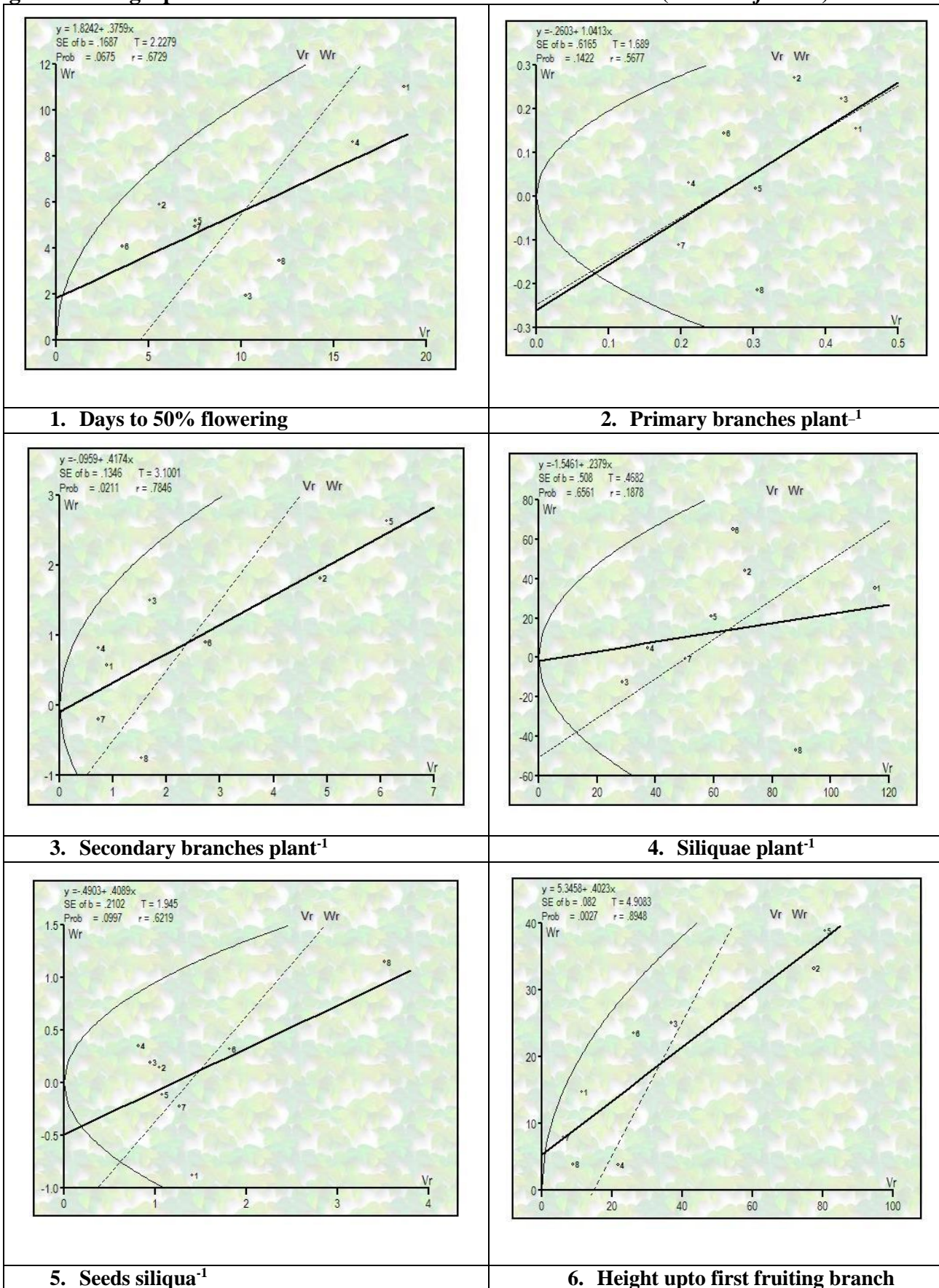
significance of variance among the eight diverse parents and F_1 s for the lab-based aphid count character at five different times (0, 12, 36, 60 and 84hrs). The mean sum of squares for the lab-based aphid count characters is given in Table 4.35. Analysis of variance of eight diverse parental genotypes of mustard revealed significant differences among the genotypes and five different times for all the three different numbers of aphid inoculated *i.e.*, A1, A5 and A10. Similarly, F_1 analysis of variance among 28 crosses of mustard revealed significant differences among the genotypes and five different times for A5 numbers of aphid artificially inoculated per plant. Here, A1 and A10 aphids were not taken into consideration as one aphid inoculated per plant, maybe migrated to other nearby plants in a box or may die and when 10 aphids were inoculated per plant, the growth of the aphid becomes fast which further hinder the proper aphid growth and counting become difficult at different time intervals. It leads to greater error while taking data. Therefore, five aphids were considered for the F_1 s study and addition to the above-mentioned reason, F_1 seeds were of the lesser amount and need to be utilized effectively.

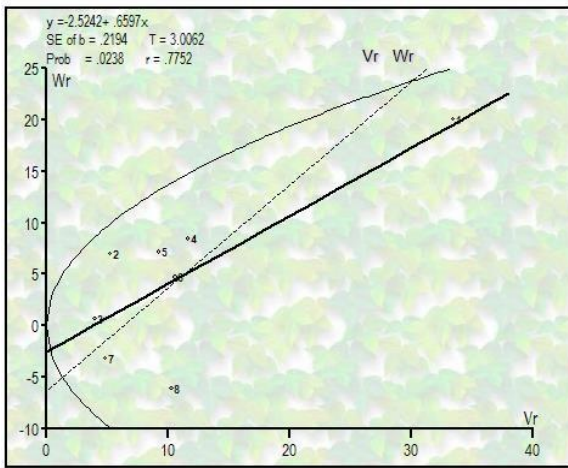
Fig 8 represents the DMRT grouping for lab-based aphid count of parents and F_1 s at different periods. When one aphid was inoculated per plant, the eight parental genotypes were grouped into five groups. Among all the groups, group 'a' showed the highest mean value (1.080) and the genotype fall in this group was Kranti while group 'c' showed the lowest mean value (0.449) and the genotype lie in this group was RW-85-59. Similarly, when five aphids were inoculated per plant, seven groups were formed. Group 'a' (2.456) again had the high meanvalue, comprising the genotype SKJM-05 and the low mean was observed in group 'f' (1.81). The genotype falls in-group 'f' was Giriraj. In case when ten aphids were inoculated per plant, five groups were formed. The genotype Kranti falls in group 'a' having the high mean (3.044) while the genotype RNWR-09-3 lie in-group 'd' consisting of the low mean (2.651). In the sameway, when five aphids were inoculated per plant of all the crosses, 18 groups were formed. Group 'a' (2.441) again had the high mean value, comprising the cross NPJ-194 ×

SKJM-05 and the low mean was observed in group 'f' (1.81) having the cross RW-85-59 × Giriraj.

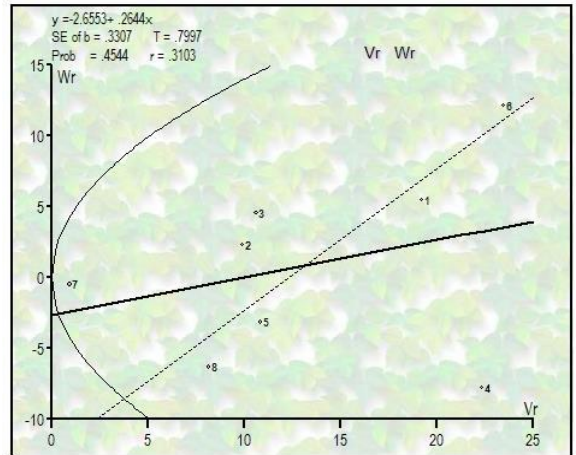
Fig 9 represents the regression analysis of aphid growth in parents and F₁. The regression coefficient represents the rate of growth of aphids. The higher regression coefficient higher is the rate of growth of aphids in that particular genotype which in turn means that the particular genotype is susceptible and vice versa. In case of parents, A1 aphid showed lesser slope for genotype RW-85-59 while higher slope was observed in genotype Kranti; for A5 aphid genotype Giriraj presented lesser slope compared to genotype SKJM-05 and for A10 higher slope was observed for Kranti and lower slope for genotype RNWR-09-3. In case of F₁s, A5 displayed lower slope for cross RW-85-59 × Giriraj while higher slope for NPJ-194 × SKJM-05.

Fig 7. Vr-Wr graph for the different characters in Indian Mustard (*Brassica juncea*)

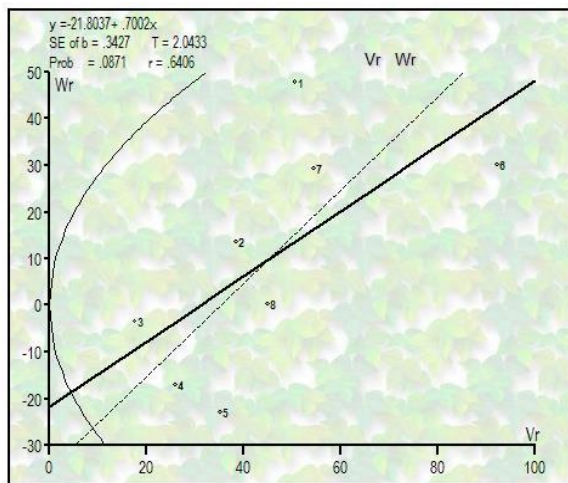




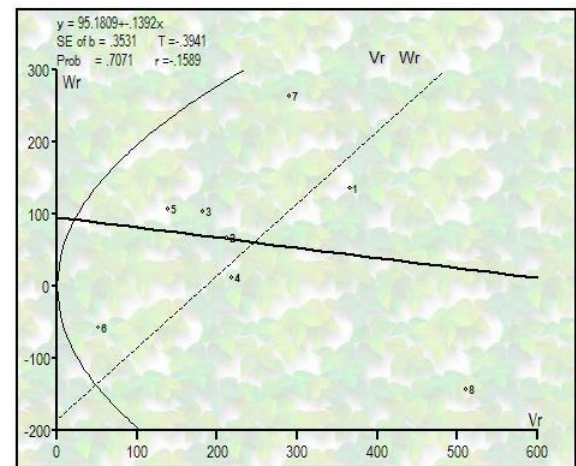
7. Plant height (cm)



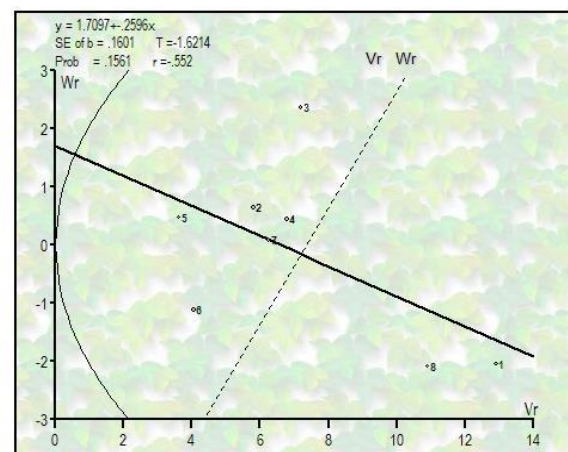
8. Seed yield plant⁻¹



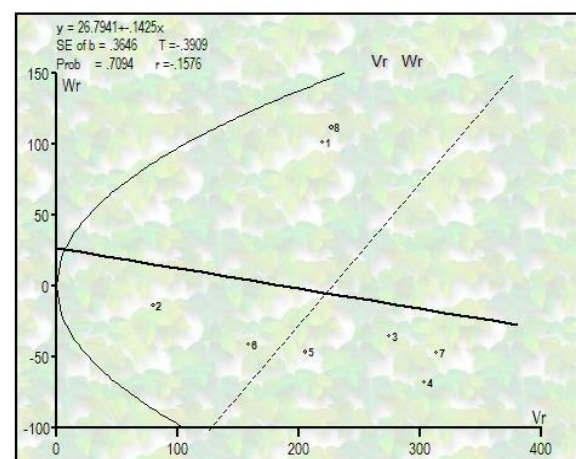
9. 1000 Seed weight



10. Oil content (%)

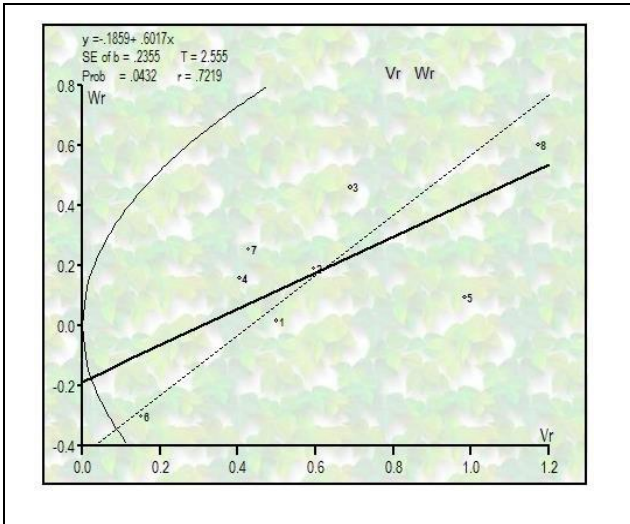


11. Percentage of membrane stability index (%)

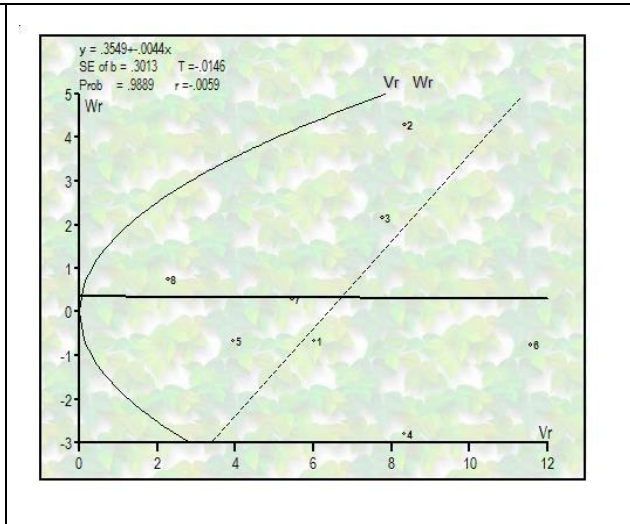


12. Percentage of excised leaf water loss (%)

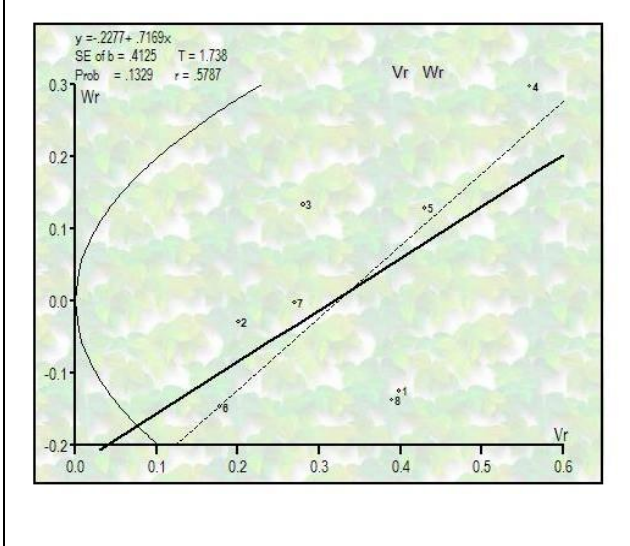
Fig 7 (Continued)



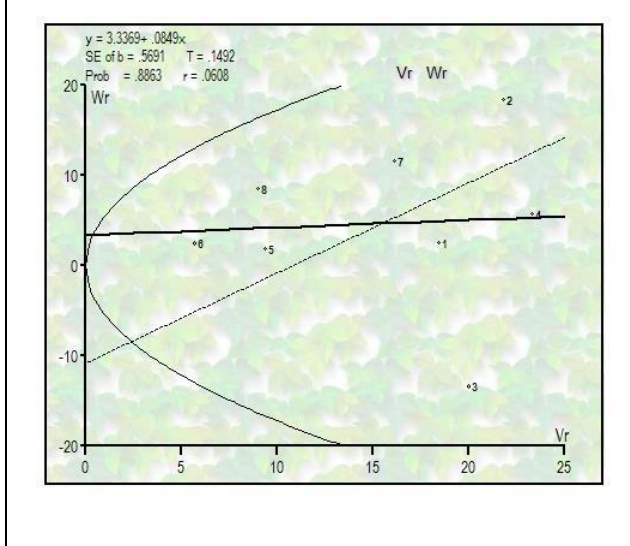
13. Percentage relative water content (%)



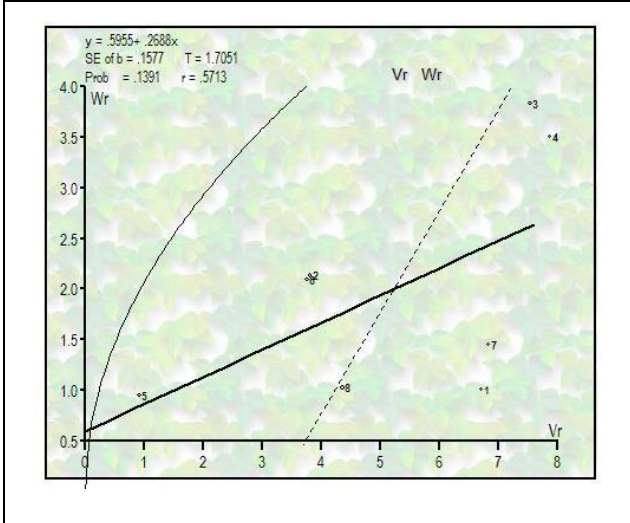
14. Canopy temperature depression (°C)



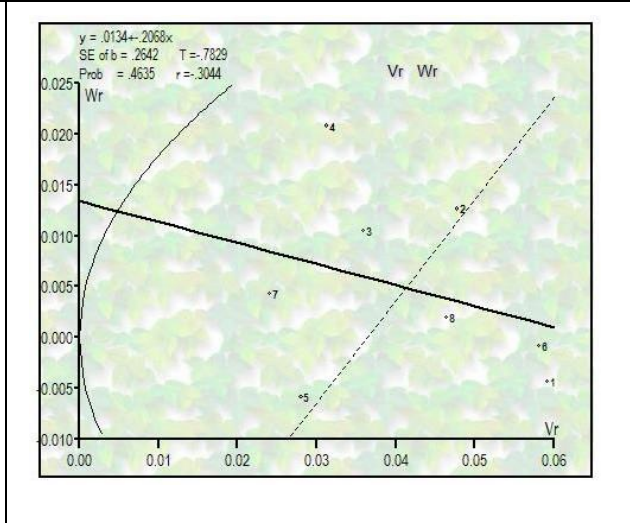
15. Proline content of leaf (mg/gm)



16. Chlorophyll a (mg/gm)

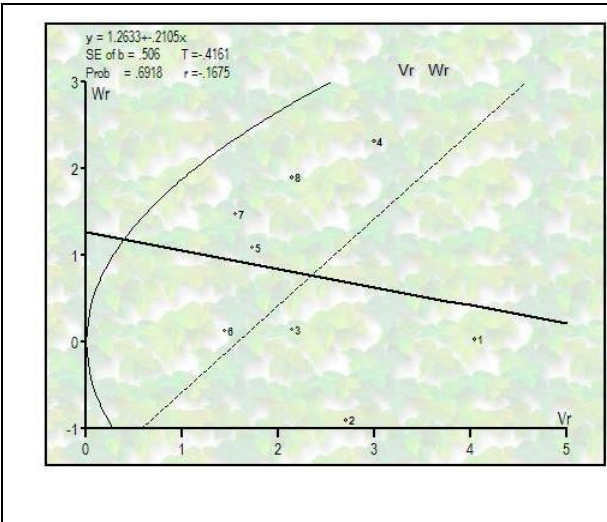


17. Chlorophyll b (mg/gm)

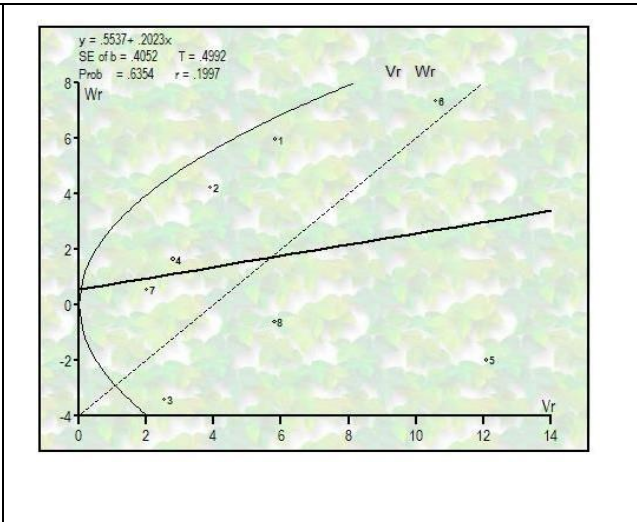


18. Total Chlorophyll (mg/gm)

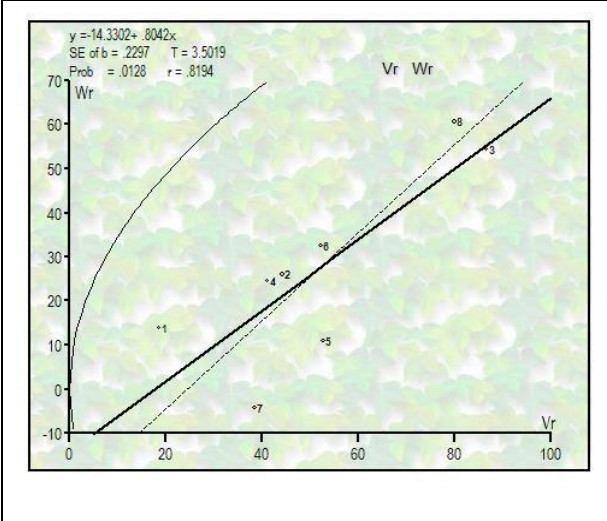
Fig 7 (Continued)



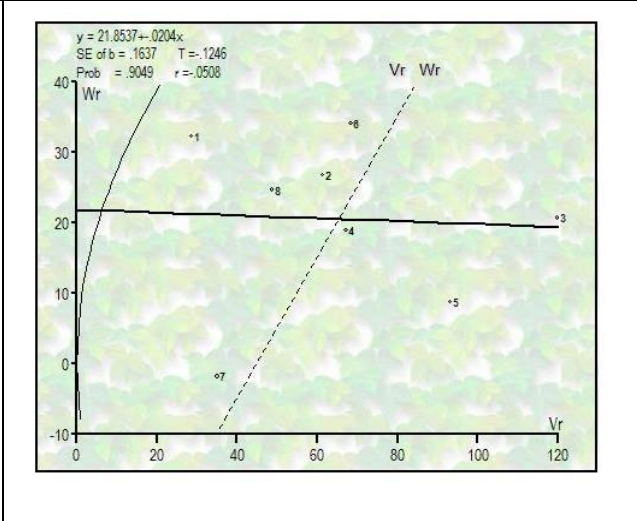
19. Water content of aphid probed twig (%)



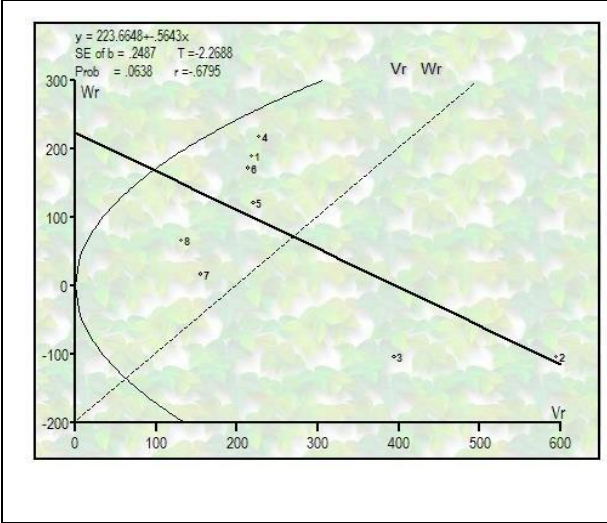
20. Water content of aphid uninfested twig (%)



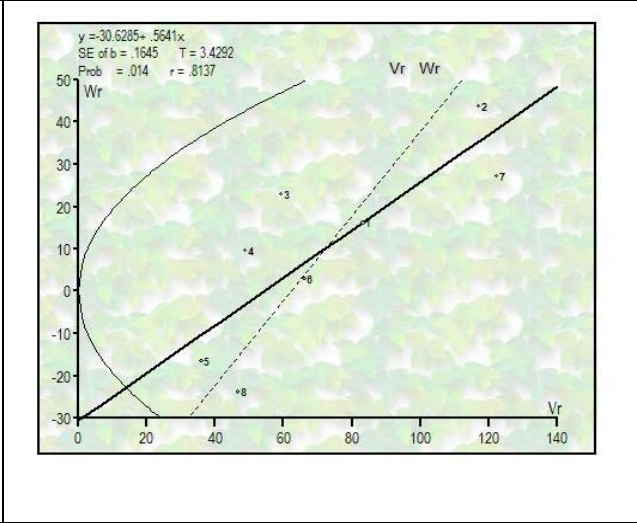
21. Water content of aphid (%)



22. Percentage of water differential between aphid probed twig and aphid itself (%)



23. Aphid count



24. Penetration force

Fig 7 (Continued)

Table 4.31 Analysis of variance (ANOVA) for lab aphid count for parents in Indian mustard (*Brassica juncea*)

Sources of variation	Df	A1-Parents (Lab Aphid count)	A5-Parents (Lab Aphid count)	A10- Parents (Lab Aphid count)
Time period	4	11.055**	6.001**	10.999**
Genotype	7	0.69*	0.739**	0.651**
Error	108	0.314	0.070	0.098

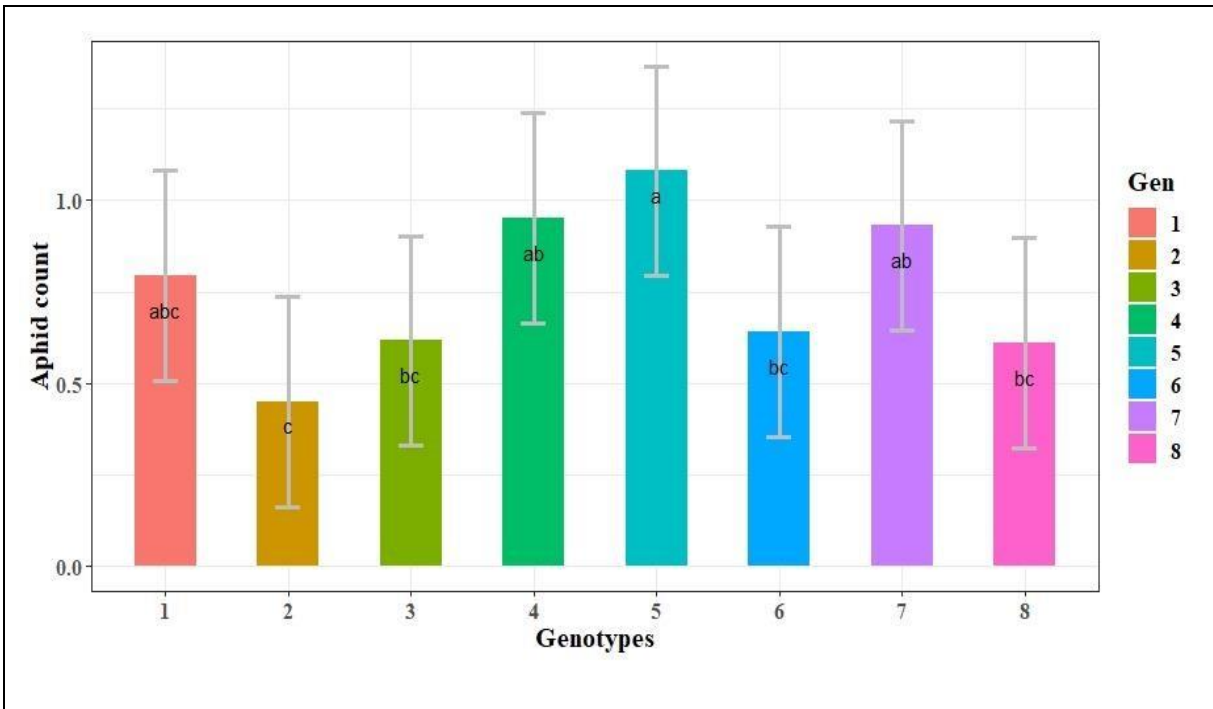
* significant at 5% and ** significant at 1% levels of probability; A1- one aphid inoculated per plant, A5- five aphids inoculated per plant and A10- ten aphids inoculated per plant

Table 4.32 Analysis of variance (ANOVA) for lab aphid count for F₁ in Indian mustard (*Brassica juncea*)

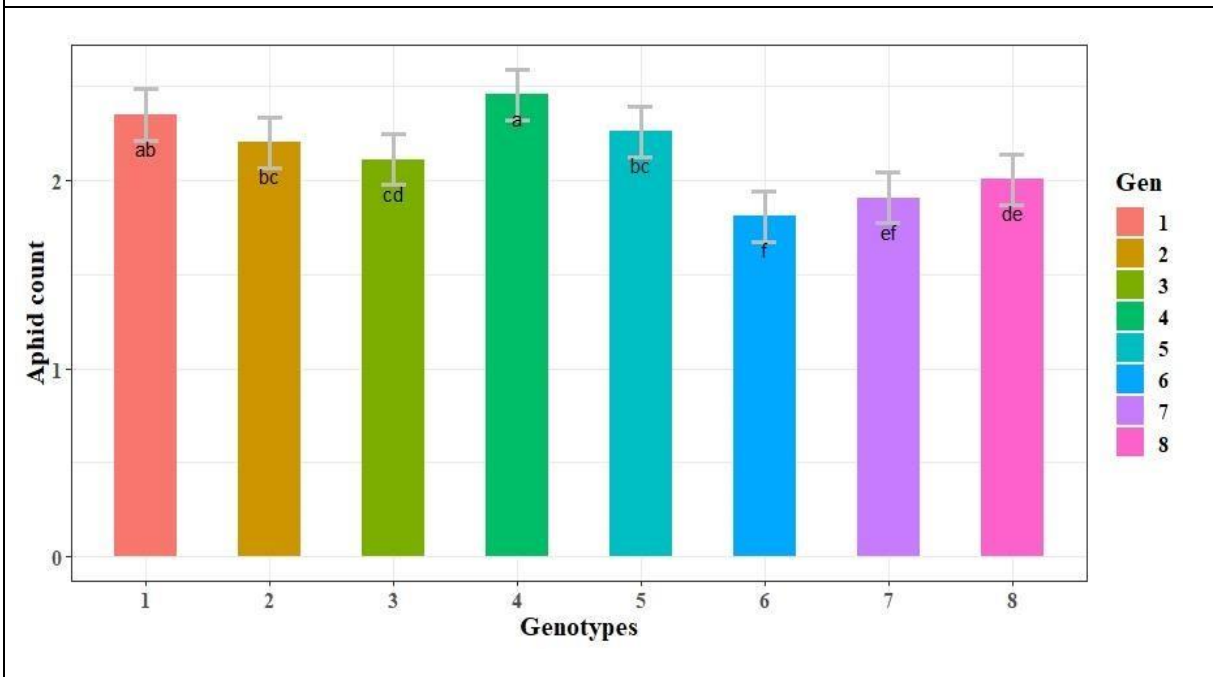
Sources of variation	Df	A5-F1s (Lab Aphid count)
Time period	4	27.497**
Genotype	27	0.254**
Error	388	0.062

* significant at 5% and ** significant at 1% levels of probability; A5- five aphids inoculated per plant

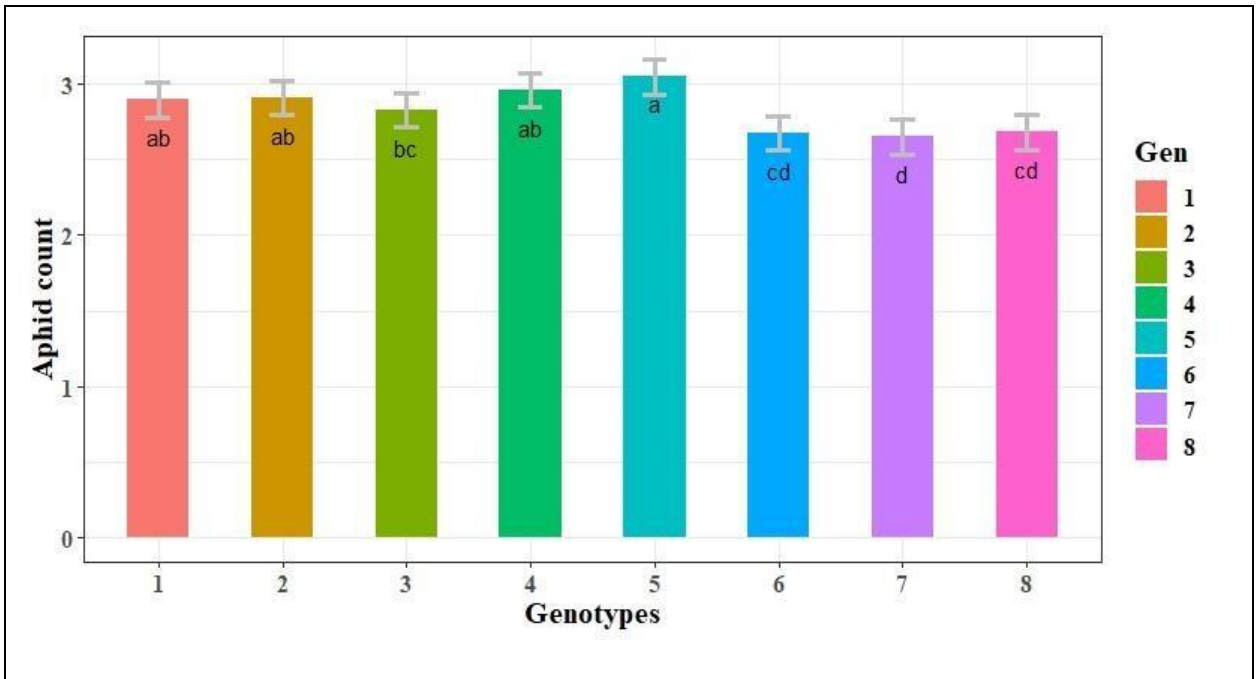
Fig 8 DMRT grouping for lab-based aphid count of parents and F1s at different periods



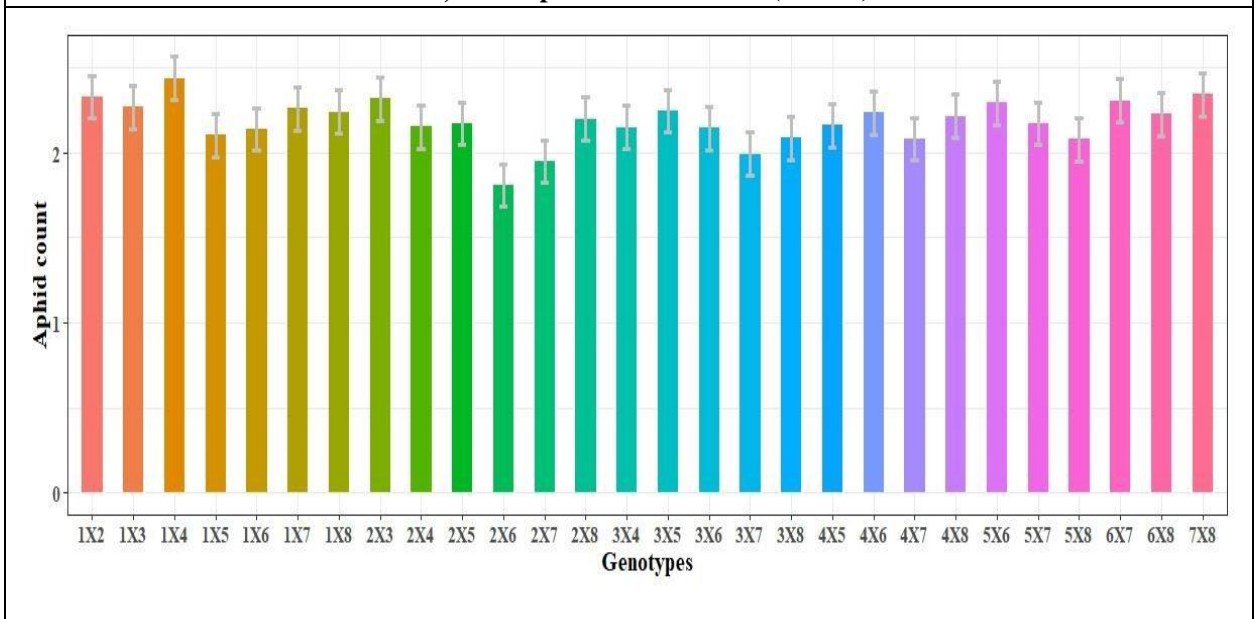
a) A1 Aphid Count-Parents (DMRT)



b) A5 Aphid Count-Parents (DMRT)



a) A10 Aphid Count-Parents (DMRT)



b) A5 Aphid count- F1 (DMRT)

Fig 8 (Continued)

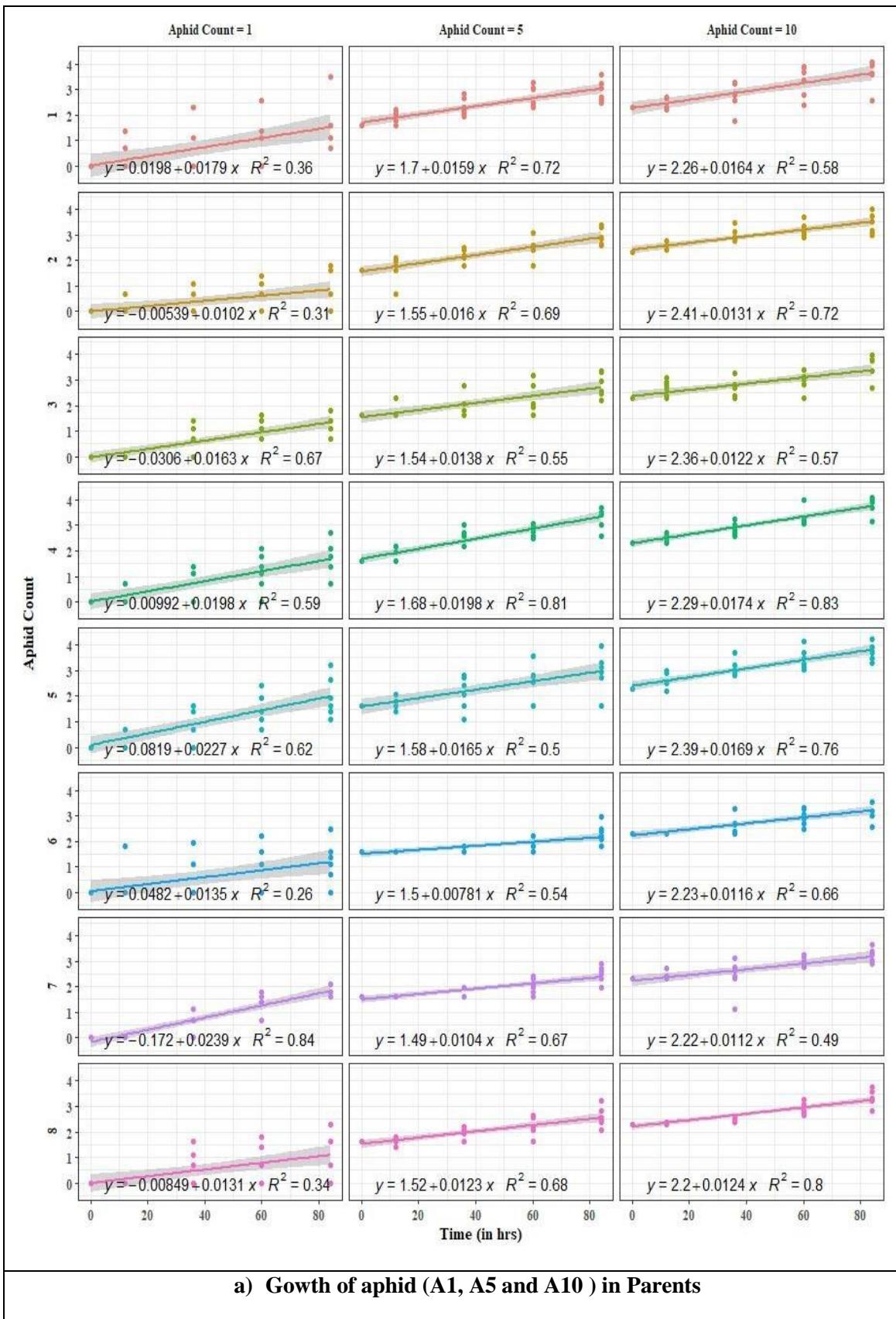
4.18.2 Ranking of parents and crosses concerning aphid count and its influencing characters

An overall ranking of eight parents and 28 crosses of Indian mustard was done for seven characters of aphid count and its influencing characters presented in Table 4.33. As per the rescaling index method suggested by Iyenger and Sudarshan (1982). It showed that based on all the nine characters, the genotype PHR-2 was the best and had the highest rescaled index value of 6.638 and ranked first followed by the cross DRMR-15-16 × RNWR-09-3 having rescaled index value of 5.774 (rank-2) which was closely followed by another genotype RNWR-09-3 which had rescaled index value of 5.656 (rank 3). In this way, all the parents and crosses were ranked according to their rescaled index values and the best among them could be selected.

4.18.3 Association between field aphid count and its influencing characters

Association between field aphid count and its influencing characters presented in Table 3.34. In the association between aphid count and its influencing characters at the genotypic level, it was revealed that proline content of leaf had no association with other characters namely chlorophyll a, chlorophyll b, total chlorophyll, water content of aphid probed twig, penetration force and field aphid count. Chlorophyll a content was found to be positively associated with chlorophyll b, total chlorophyll, water content of aphid probed twig and field aphid count. Chlorophyll b was found to be positively associated with total chlorophyll, water content of aphid probed twig and field aphid count. On the other hand, total chlorophyll was positively associated with water content of aphid probed twig and field aphid count.

Fig 9: Regression analysis of aphid growth in parents and F1



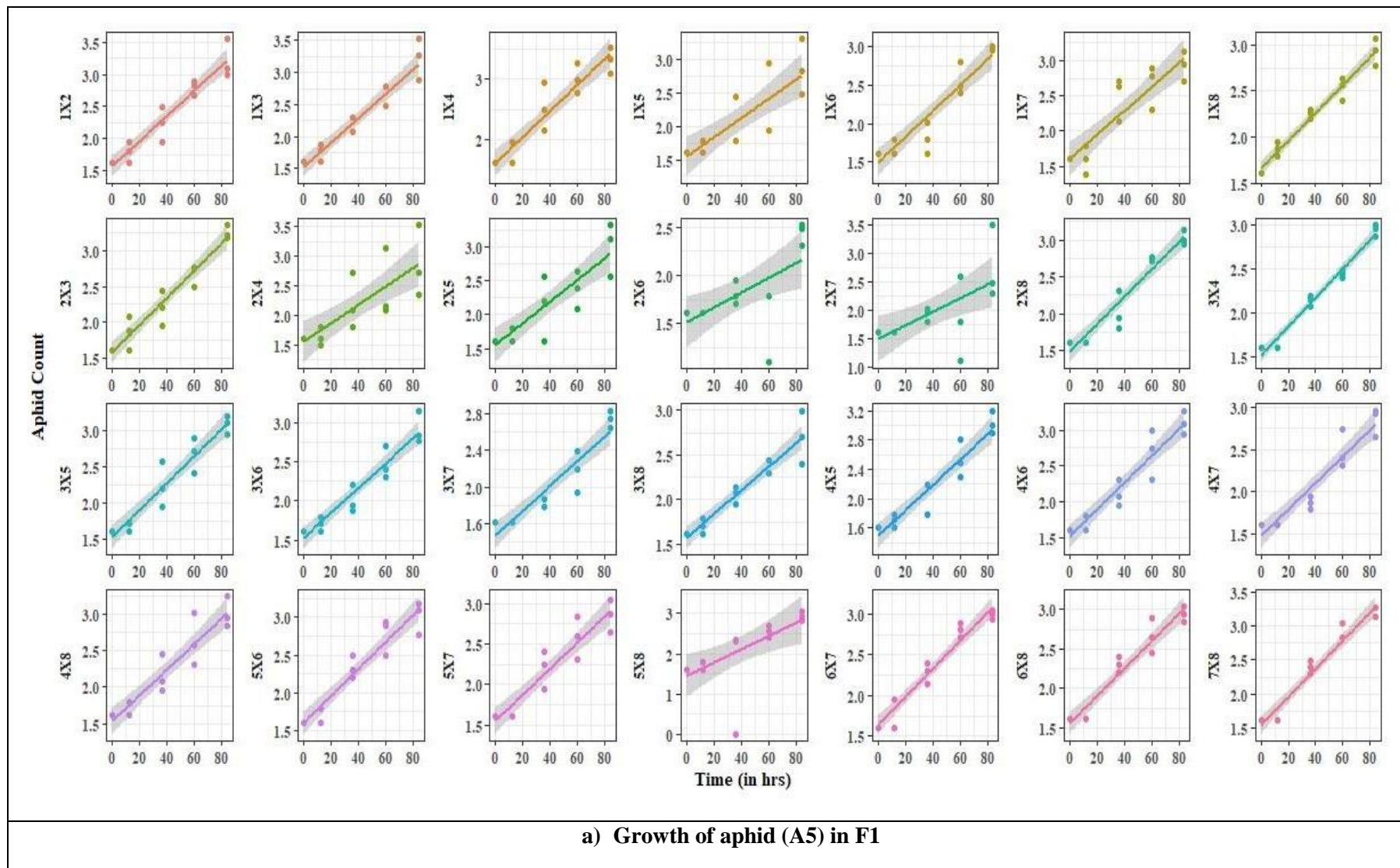


Fig 9 (Continued)

Table 4.33 Ranking of parents and crosses concerning aphid count and its influencing characters

S.No.	Genotype	Canopy temperature depression ($^{\circ}$ C) (A)	Rescaled Index value (A) = (Max-x)/(Max-Min)	Proline content of leaf (mg/gm) (B)	Rescaled Index value (B) = (x-Min)/(Max-Min)	Chlorophyll a (mg/gm) (C)	Rescaled Index value (C) = (x-Min)/(Max-Min)	Chlorophyll b (mg/gm) (D)	Rescaled Index value (D) = (x-Min)/(Max-Min)	Total Chlorophyll (mg/gm) (E)	Rescaled Index value (E) = (x-Min)/(Max-Min)	Water content of aphid probed twig (%) (F)	Rescaled Index value (F) = (x-Min)/(Max-Min)
		X		x		X		X		x		x	
1	NPJ-194	0.438	0.468	5.450	0.544	0.322	0.902	0.123	0.550	1.094	0.308	63.553	0.941
2	RW-85-59 (Sarma)	0.464	0.226	5.121	0.405	0.307	0.820	0.115	0.463	1.341	0.563	58.051	0.059
3	DRMR-15-16	0.472	0.145	6.181	0.851	0.287	0.713	0.123	0.552	1.320	0.541	62.643	0.795
4	SKJM-05	0.402	0.800	5.962	0.759	0.235	0.429	0.084	0.141	1.035	0.247	62.224	0.728
5	Kranti	0.460	0.256	4.653	0.209	0.229	0.399	0.116	0.478	1.360	0.582	63.791	0.979
6	Giriraj	0.469	0.179	5.349	0.501	0.327	0.931	0.157	0.902	1.581	0.809	60.469	0.446
7	RNWR-09-3	0.446	0.392	4.600	0.187	0.330	0.949	0.142	0.745	1.510	0.737	61.254	0.572
8	PHR 2	0.418	0.657	6.168	0.845	0.340	1.000	0.166	1.000	1.766	1.000	63.920	1.000
9	NPJ-194 \times RW-85-59	0.435	0.490	6.108	0.820	0.156	0.000	0.071	0.000	0.794	0.000	61.357	0.589
10	NPJ-194 \times DRMR-15-16	0.396	0.862	5.604	0.608	0.295	0.755	0.085	0.150	1.024	0.237	59.721	0.326
11	NPJ-194 \times SKJM-05	0.450	0.350	5.673	0.637	0.259	0.559	0.090	0.202	1.051	0.264	59.838	0.345
12	NPJ-194 \times Kranti	0.447	0.383	5.508	0.568	0.268	0.610	0.109	0.399	1.378	0.601	60.840	0.506
13	NPJ-194 \times Giriraj	0.488	0.000	4.961	0.338	0.299	0.779	0.100	0.306	1.133	0.348	63.531	0.938
14	NPJ-194 \times RNWR-09-3	0.475	0.123	4.824	0.281	0.263	0.581	0.090	0.206	1.185	0.402	61.661	0.638
15	NPJ-194 \times PHR -2	0.449	0.360	4.955	0.336	0.267	0.606	0.137	0.692	1.455	0.680	59.727	0.327
16	RW-85-59 \times DRMR-15-16	0.416	0.673	5.403	0.524	0.251	0.517	0.073	0.026	0.974	0.185	58.914	0.197
17	RW-85-59 \times SKJM-05	0.445	0.397	5.061	0.380	0.187	0.169	0.084	0.143	0.876	0.084	57.686	0.000
18	RW-85-59 \times Kranti	0.470	0.169	4.351	0.082	0.305	0.809	0.090	0.205	1.019	0.231	60.675	0.480

Table 4.33 (Continued)

S.No.	Genotype	Canopy temperature depression ($^{\circ}$ C) (A)	Rescaled Index value (A) = (Max-x)/(Max-Min)	Proline content of leaf (mg/gm) (B)	Rescaled Index value (B) = (x-Min)/(Max-Min)	Chlorophyll a (mg/gm) (C)	Rescaled Index value (C) = (x-Min)/(Max-Min)	Chlorophyll b (mg/gm) (D)	Rescaled Index value (D) = (x-Min)/(Max-Min)	Total Chlorophyll (mg/gm) (E)	Rescaled Index value (E) = (x-Min)/(Max-Min)	Water content of aphid probed twig (%) (F)	Rescaled Index value (F) = (x-Min)/(Max-Min)
		X		x		x		x		x		x	
19	RW-85-59 \times Giriraj	0.472	0.146	5.133	0.410	0.280	0.672	0.094	0.244	1.048	0.261	60.656	0.476
20	RW-85-59 \times RNWR-09-3	0.449	0.359	5.140	0.414	0.197	0.225	0.157	0.902	1.429	0.653	59.673	0.319
21	RW-85-59 \times PHR-2	0.437	0.474	4.970	0.342	0.284	0.696	0.116	0.473	1.214	0.432	60.676	0.480
22	DRMR-15-16 \times SKJM-05	0.453	0.327	4.155	0.000	0.313	0.853	0.117	0.486	1.332	0.553	63.296	0.900
23	DRMR-15-16 \times Kranti	0.422	0.620	4.698	0.228	0.294	0.749	0.102	0.324	1.048	0.262	62.128	0.713
24	DRMR-15-16 \times Giriraj	0.381	1.000	5.638	0.622	0.293	0.747	0.106	0.373	1.027	0.239	60.668	0.478
25	DRMR-15-16 \times RNWR-09-3	0.422	0.616	5.268	0.467	0.308	0.829	0.165	0.995	1.250	0.469	61.589	0.626
26	DRMR-15-16 \times PHR-2	0.462	0.241	6.537	1.000	0.326	0.923	0.133	0.652	1.395	0.618	61.490	0.610
27	SKJM-05 \times Kranti	0.430	0.545	4.878	0.303	0.233	0.418	0.092	0.220	0.979	0.191	61.249	0.571
28	SKJM-05 \times Giriraj	0.447	0.379	6.318	0.908	0.299	0.777	0.094	0.247	0.942	0.152	61.763	0.654
29	SKJM-05 \times RNWR-09-3	0.480	0.076	5.698	0.648	0.297	0.765	0.108	0.389	1.207	0.424	60.059	0.381
30	SKJM-05 \times PHR-2	0.445	0.402	4.900	0.313	0.294	0.753	0.106	0.374	1.148	0.364	59.603	0.308
31	Kranti \times Giriraj	0.477	0.097	5.123	0.406	0.260	0.567	0.106	0.369	1.066	0.280	59.634	0.312
32	Kranti \times RNWR-09-3	0.474	0.132	5.360	0.506	0.293	0.747	0.105	0.356	1.018	0.230	60.383	0.433
33	Kranti \times PHR-2	0.446	0.390	5.403	0.524	0.337	0.987	0.103	0.338	1.514	0.740	60.380	0.432
34	Giriraj \times RNWR-09-3	0.444	0.407	6.004	0.776	0.309	0.832	0.117	0.490	1.319	0.540	63.590	0.947
35	Giriraj \times PHR-2	0.416	0.677	6.020	0.783	0.276	0.652	0.120	0.513	1.369	0.592	61.958	0.685
36	RNWR-09-3 \times PHR-2	0.439	0.457	5.500	0.564	0.277	0.658	0.115	0.468	1.113	0.328	59.856	0.348

Table 4.33 (Continued)

		Penetration force (G)	Rescaled Index value (G) = (x- Min)/(Max- Min)	Field aphid count (H)	Rescaled Index value (H) = (Max- x)/(Max- Min)	Lab aphid count (I)	Rescaled Index value (I) = (Max-x)/(Max- Min)	Total of the rescaled values (J) J= A+B+C+D+E+ F+G+H+I	Ranking on the basis of the total rescaled value*
		x		x		x			
1	NPJ-194	76.372	0.399	2.035	0.196	1.301	0.365	4.673	11
2	RW-85-59 (Sarma)	85.433	0.672	1.652	0.725	1.278	0.424	4.358	15
3	DRMR-15-16	86.124	0.693	1.767	0.565	1.141	0.785	5.640	4
4	SKJM-05	87.652	0.739	1.788	0.537	1.439	0.003	4.384	14
5	Kranti	75.398	0.369	1.876	0.416	1.318	0.320	4.008	21
6	Giriraj	81.566	0.555	2.035	0.196	1.146	0.772	5.292	7
7	RNWR-09-3	96.294	1.000	2.047	0.180	1.099	0.894	5.656	3
8	PHR 2	66.416	0.098	1.942	0.325	1.168	0.714	6.638	1
9	NPJ-194 × RW-85-59	84.674	0.649	1.501	0.933	1.422	0.047	3.529	32
10	NPJ-194 × DRMR-15-16	92.750	0.893	2.177	0.000	1.401	0.104	3.936	24
11	NPJ-194 × SKJM-05	77.973	0.447	1.452	1.000	1.440	0.000	3.805	27
12	NPJ-194 × Kranti	66.970	0.115	1.735	0.610	1.250	0.500	4.291	19
13	NPJ-194 × Giriraj	63.163	0.000	1.571	0.836	1.290	0.394	3.941	23
14	NPJ-194 × RNWR-09-3	79.765	0.501	1.949	0.315	1.272	0.441	3.486	34
15	NPJ-194 × PHR -2	65.102	0.059	1.823	0.489	1.272	0.442	3.991	22
16	RW-85-59 × DRMR-15-16	82.306	0.578	1.628	0.757	1.414	0.070	3.527	33
17	RW-85-59 × SKJM-05	86.262	0.697	1.673	0.696	1.243	0.517	3.084	35
18	RW-85-59 × Kranti	75.309	0.367	1.537	0.883	1.304	0.356	3.582	30
19	RW-85-59 × Giriraj	76.367	0.399	1.862	0.436	1.059	1.000	4.044	20
20	RW-85-59 × RNWR-09-3	94.711	0.952	1.707	0.648	1.201	0.626	5.098	9
21	RW-85-59 × PHR-2	75.146	0.362	1.639	0.742	1.314	0.331	4.333	17
22	DRMR-15-16 × SKJM-05	86.199	0.695	1.906	0.375	1.274	0.435	4.624	12
23	DRMR-15-16 × Kranti	75.014	0.358	1.614	0.777	1.334	0.279	4.309	18

Table 4.33 (Continued)

		Penetration force (H)	Rescaled Index value (H) = (x- Min)/(Max- Min)	Field aphid count (I)	Rescaled Index value (I) = (Max- x)/(Max- Min)	Lab aphid count (J)	Rescaled Index value (J) = (Max- x)/(Max- Min)	Total of the rescaled values (K) K = A+B+C+D+E+F+G+H+I+J	Ranking on the basis of the total rescaled value*
		x		x		x			
24	DRMR-15-16 × Giriraj	84.613	0.647	1.894	0.390	1.269	0.450	4.948	10
25	DRMR-15-16 × RNWR-09-3	76.820	0.412	1.670	0.700	1.189	0.659	5.774	2
26	DRMR-15-16 × PHR-2	67.910	0.143	1.676	0.692	1.173	0.701	5.580	5
27	SKJM-05 × Kranti	72.835	0.292	1.689	0.673	1.315	0.328	3.542	31
28	SKJM-05 × Giriraj	85.582	0.677	1.965	0.293	1.345	0.249	4.335	16
29	SKJM-05 × RNWR-09-3	66.502	0.101	1.824	0.487	1.231	0.549	3.820	26
30	SKJM-05 × PHR-2	76.717	0.409	1.884	0.405	1.305	0.354	3.681	29
31	Kranti × Giriraj	68.669	0.166	1.890	0.396	1.309	0.344	2.937	36
32	Kranti × RNWR-09-3	69.008	0.176	1.742	0.600	1.237	0.532	3.712	28
33	Kranti × PHR-2	75.683	0.378	1.953	0.310	1.273	0.438	4.537	13
34	Giriraj × RNWR-09-3	74.570	0.344	1.807	0.510	1.301	0.366	5.214	8
35	Giriraj × PHR-2	85.746	0.682	1.788	0.537	1.277	0.428	5.548	6
36	RNWR-09-3 × PHR-2	76.226	0.394	1.773	0.558	1.379	0.160	3.936	25

x=Mean performance of the character; *Ranking has been done in descending order taking the highest rescaled value as 1 (first rank) followed by other lower rescaled values from rank 2 onwards. The formulas for the index value (rescaled value) are the same for all the characters except in the case of canopy temperature depression, field aphid count and lab aphid count.

4.18.4 Direct and indirect effects of field aphid count and its influencing characters

The direct and indirect effects of field aphid count and its influencing characters presented in Table 4.35. The path analysis evolving the six aphid count influencing characters exhibited that the highest direct effect on field aphid count was due to chlorophyll a (0.548) which was closely followed by penetration force (0.403) and total chlorophyll (0.338). among the three characters chlorophyll a, chlorophyll b and total chlorophyll which had a positive association with field aphid count. Only chlorophyll b had a negligible direct effect whereas chlorophyll a and total chlorophyll had a direct effect.

Table 4.34 Association (correlation) between field aphid count and its influencing characters at genotypic level in Indian mustard (*Brassica juncea*)

Characters	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)	Water content of aphid probed twig (%)	Penetration force (g/mm)	Field aphid count
Proline content of leaf (mg/gm)	0.002	0.055	0.012	0.204	-0.009	0.028
Chlorophyll a (mg/gm)		0.466**	0.536**	0.414**	-0.257	0.529**
Chlorophyll b (mg/gm)			0.878**	0.329*	-0.095	0.309*
Total Chlorophyll (mg/gm)				0.400**	-0.127	0.399**
Water content of aphid probed twig (%)					-0.232	0.207
Penetration force (g/mm)						0.239

* significant at 5% and ** significant at 1% level of probability

Table 4.35 Direct (diagonal) and indirect (off-diagonal) effects of field aphid count and its influencing characters in Indian mustard (*Brassica juncea*)

Characters	Proline content of leaf (mg/gm)	Chlorophyll a (mg/gm)	Chlorophyll b (mg/gm)	Total Chlorophyll (mg/gm)	Water content of aphid probed twig (%)	Penetration force (g/mm)	Correlation with field aphid count
Proline content of leaf (mg/gm)	0.038	0.001	-0.011	0.004	0.000	-0.004	0.028
Chlorophyll a (mg/gm)	0.000	0.548	-0.097	0.181	0.000	-0.104	0.529**
Chlorophyll b (mg/gm)	0.002	0.256	-0.207	0.297	0.000	-0.038	0.309*
Total Chlorophyll (mg/gm)	0.000	0.294	-0.182	0.338	0.000	-0.051	0.399**
Water content of aphid probed twig (%)	0.008	0.227	-0.068	0.135	-0.001	-0.094	0.207
Penetration force (g/mm)	0.000	-0.141	0.020	-0.043	0.000	0.403	0.239

* Significant at 5% and ** significant at 1% level of probability; Residual values = 0.745

DISCUSSION

5.1 Analysis of variance

The analysis of variance (ANOVA) was estimated to test the significance of variance among the 71 diversified genotypes of mustard for all the 11 characters presented in Table 4.1. Analysis of variance of 71 genotypes of mustard revealed significant differences among the genotypes for all the eleven characters studied *viz*; Plant height (cm), height upto first fruiting branch (cm), days to 50% flowering, primary branches per plant, secondary branches per plant, siliquae per plant (cm), seeds per siliqua, 1000 seed weight (g), penetration force (kpasal), aphid count (% incidence) and seed yield per plant (g). This indicated a wide spectrum of variation among the genotypes. Such significant difference was reported by Bibi (2016), Sandhu *et al.*, (2017), Devi (2018) and Tiwari (2019) for days to 50% flowering, primary branches per plant and seed yield per plant; Devi (2018), Sandhu *et al.*, (2017), Tiwari (2019) for 1000 seed weight; Meena (2017) for plant height, secondary branches per plant and number of seeds per siliqua.

5.2 Genetic parameters

5.2.1 Phenotypic coefficient of variation and genotypic coefficient of variation

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low (<10%) for plant height and seeds per siliqua presented in Table 4.2. These results are in agreement with Gangapur *et al.* (2011) and Islam *et al.*, (2015) for plant height; Rameeh *et al.*, (2016) and Synrem *et al.*, (2014) for seeds per siliqua.

Moderate GCV and PCV (10-25%) for days to 50% flowering, primary branches per plant, secondary branches per plant, siliquae per plant and 1000 seed weight. Such findings were observed by Gangapur *et al.*, (2011) and Singh *et al.*, (2011) in case of primary branches

per plant; Meena *et al.*, (2017) and Afrin *et al.*, (2011) in case of secondary branches per plant and siliquae per plant whereas Islam *et al.*, (2015) observed such finding in 1000 seed weight.

High GCV and PCV (>25%) for height up to first fruiting branch, aphid count and penetration force. This is in confirmation with the findings of Roy *et al.*, (2018) for height up to first fruiting branch. Seed yield per plant had moderate GCV and high PCV. PCV and GCV values for the different characters did not differ much which indicating the greater role of genetic factors influencing the expression of these characters. Few characters like seeds per siliqua, aphid count, penetration force and seed yield per plant showed a greater difference, which indicated the greater influence of the environment in the expression of these characters.

5.2.2 Heritability

Heritability of characters was represented in Table 4.2. The characters exhibiting high heritability for plant height, height up to first fruiting branch, days to 50% flowering, primary branches per plants, secondary branches per plant, siliquae per plant and 1000 seed weight. High heritability was observed by Sikarwar *et al.*, (2017) in case of plant height; Roy *et al.*, (2018) in case of height up to first fruiting branch; Afrin *et al.*, (2011) and Bindet *et al.*, (2014) in case of days to 50% flowering; Lodhi *et al.*, (2014) and Tiwari *et al.*, (2017) in primary branches per plants, secondary branches per plant and siliquae per plant; Lodhi *et al.*, (2014) and Bind *et al.*, (2014) for 1000 seed weight.

Moderate heritability for seeds per siliqua, aphid count, penetration force and seed yield per plant. Moderate heritability has been reported by Islam *et al.*, (2015) for seeds per siliqua and Gangapur *et al.*, (2011) for seed yield per plant. Most of the characters

expressed high heritability (>60%) except seeds per siliqua, aphid count, penetration force and seed yield per plant. None of the characters showed low heritability.

5.2.3 Genetic advance as a percentage of mean

Genetic advance as a percentage of mean presented in Table 4.2 was exhibited low (<10%) by seeds per siliquae. Low genetic advance for seeds per siliquae has been reported by Bind *et al.*, (2014); moderate (10- 20%) for plant height reported by Islam *et al.*, (2015); high (> 20%) for height up to first fruiting branch, days to 50% flowering, primary branches per plant, secondary branches per plant, siliquae per plant, 1000 seed weight, aphid count, penetration force and seed yield per plant. The high genetic advance was obtained by Sikarwar *et al.*, (2017) and Tiwari *et al.*, (2017) for primary branches per plant, secondary branches per plant and siliquae per plant; Lodhi *et al.*, (2014) for 1000 seed weight. Most of the characters expressed high genetic advance as percentage of mean except plant height which showed moderate genetic advance as percentage of mean and seeds per siliqua expressed the lowest genetic advance as percentage of mean. Any characters simultaneously expressing high heritability (h^2) and genetic advance as percentage of mean are under additive gene control and can be improved by appropriate selection.

The characters height up to first fruiting branch, primary branches per plant, secondary branches per plant, siliquae per plant and 1000 seed weight expressed high heritability along with high genetic advance as percentage of mean, indicating their additive gene control and the possibility of improvement through appropriate selection. Such high heritability with high genetic advance has been reported by Lodhi *et al.*, (2014) and Tiwari *et al.*, (2017) for primary branches per plant; Afrin *et al.*, (2011) and Sikarwar *et al.*, (2017) for secondary branches per plant; Mondal *et al.*, (2000) for 1000 seed weight.

5.3 Character association analysis

In the present investigation, the correlation coefficients were estimated among eleven characters at genotypic levels presented in Table 4.3. In genotypic correlation analysis, it was found that the significant positive correlation of seed yield was observed with secondary branches per plant and siliquae per plant while plant height had a positive association with height up to first fruiting branch, days to 50% flowering and primary branches per plant. Height up to first fruiting branch had a positive association with days to 50% flowering and primary branches per plant. Primary branches per plant were positively associated with only one character *i.e.* secondary branches per plant whereas secondary branches per plant were positively associated with siliquae per plant and seed yield per plant. The siliquae per plant had a positive association with seed yield per plant. Aphid count had a positive association with penetration force which is quite contradictory to the natural situation where the aphid count should decrease with increase in penetration force as increased penetration force reduces the suction of sap from the twigs. In the overall assessment of the character association analysis, it was found that secondary branches per plant and siliquae per plant had a positive association with seed yield per plant. This indicates that selection for these characters could yield higher productivity as they exhibited correlated response with seed yield. The positive association for secondary branches per plant and siliquae per plant with seed yield was observed by Afrin *et al.*, (2011), Uddin *et al.*, (2013), Helal *et al.*, (2014), Islam *et al.*, (2015), Rameeh *et al.*, (2016) and Roy *et al.*, (2018).

Plant height, height up to first fruiting branch and days to 50% flowering had a negative association with aphid count and penetration force. Secondary branches per plant showed a significant negative association with penetration force. Height up to first fruiting branch had a negative association with 1000 seed weight, aphid count, penetration force and seed yield per plant. Primary branches per plant were negatively associated with seeds per

siliqua, penetration force and seed yield per plant. Aphid count was negatively associated with seed yield per plant while seed yield itself was negatively correlated with height up to first fruiting branch, primary branches per plant and aphid count. It was observed that seed yield was negatively correlated with height up to first fruiting branch, primary branches per plant and aphid count. Such a negative correlation with seed yield was observed by Islam *et al.*, (2015) for primary branches per plant. From the correlation study involving the present set of 71 mustard genotypes, positive correlation (significant) with seed yield was observed only in case of secondary branches per plant and siliquae per plant.

5.4 Path coefficient analysis

Results on the genotypic path coefficient presented in Table 4.4 exhibited primary branches per plant had a negative correlation with seed yield per plant although its direct effect (0.086) was positive and low. But the direct effect was more than the coefficient of correlation. This indicates that the indirect negative effects through other attributes *i.e.* height up to first fruiting branch, siliquae per plant, 1000 seed weight, aphid count and penetration force have enhanced the negative relationship of primary branches per plant with seed yield per plant.

Association of siliquae per plant with seed yield per plant was positive and its direct effect was also high and positive. But the coefficient of correlation was more than the direct effect. This indicates that the indirect positive effects of siliquae per plant are supplemented through plant height, days to 50% flowering, secondary branches per plant, 1000 seed weight and aphid count, of which the via effect through plant height was highest.

The highest positive direct effect on yield was of penetration force followed by days to 50% flowering. The high positive direct effect was reported by Uddin *et al.*, (2013), Singh *et al.*, (2013) and Rameeh *et al.*, (2016) and Roy *et al.*, (2018) for days to 50%

flowering. However, penetration force had no association with seed yield and it was evident from the low coefficient of correlation with seed yield which was mainly due to the negative effects of penetration force as seed yield via plant height, days to 50% flowering, primary branches per plant, secondary branches per plant, siliquae per plant, seeds per siliqua, 1000 seed weight and aphid count. This negative effect could be the reason behind the positive correlation of penetration force with aphid count and subsequently not having any association with seed yield.

An interesting finding here is that the very high direct effect of penetration force is nullified by the negative effects via the other characters. Hence, for the present set of genotypes, the emphasis for selection cannot be laid on penetration force. Secondary branches per plant had a positive correlation with seed yield per plant and its direct effect was also positive, although low and was less than the coefficient of correlation. This indicated that the indirect positive effects are more than indirect negative effect and the former have supplemented to the positive association of secondary branches per plant with seed yield per plant. The indirect positive effect of secondary branches per plant on seed yield was observed via plant height, height upto first fruiting branch, primary branches per plant, siliquae per plant, seeds per siliqua and aphid count.

A perusal of the above results revealed that plant height, days to 50% flowering, secondary branches per plant siliquae per plant and penetration force had moderate to the high positive effect on seed yield. However, among these five characters, only secondary branches per plant and siliquae per plant were ultimately positively associated with seed yield and were controlled by additive genes, due to their high heritability and genetic advance. Therefore, to exercise a suitable selection programme it would be worth to concentrate on these characters for improvement in yield of mustard. Indirect contribution of the characters is mainly due to the indirect effects of the character through other

component characters. Indirect selection through such characters having a high or moderate positive effect on seed yield and would also be rewarding in yield improvement.

5.5 Clustering of genotypes

Based on D^2 values seventy-one genotypes of mustard were grouped into seven clusters Table 4.6. A total of thirty-one genotypes were grouped into cluster I; twenty-one genotypes in cluster IV; twelve genotypes in cluster V; two genotypes in cluster II, as well as in cluster III; two genotypes in cluster VI and one genotype in cluster VII.

Similarly, 19 diverse genotypes of Indian mustard were grouped into five clusters by Sinha and Singh (2004). Thirty-three diverse genotypes of Indian mustard were grouped into eight different clusters by Thul *et al.*, (2004). Monalisa *et al.*, (2005) carried out a similar type of genetic divergence study in nine genotypes of Indian mustard and grouped them into six clusters using Tocher's method. Malik *et al.*, (2006) studied 30 lines and cultivars of Indian mustard for 12 quantitative characters and grouped them into six clusters using Mahalanobis D^2 statistics. The clustering pattern of genotypes showed that the genotypes of different origin collected from Pulses and Oilseed Research Station, Berhampur, West Bengal, Banaras Hindu University and Directorate of Rapeseed- Mustard Research, Bharatpur were clubbed in one cluster, whereas the genotypes belonging to same-origin were grouped in different clusters indicating that the geographic distribution didn't consider to be the sole criterion of genetic diversity. A similar type of work was also reported by Alie *et al.*, (2011). The pattern of distribution of genotypes among various clusters reflected the considerable genetic diversity present in the genotypes under study.

5.6 Inter and intra-cluster distance

In the present investigation, the inter-cluster and intra cluster distance was estimated among eleven characters Table 4.7. The maximum intra cluster distance was

recorded in cluster VI followed by cluster, cluster IV, cluster I, cluster III, cluster II and cluster VII. The maximum intra cluster distance in cluster VI was because of wide genetic diversity among its genotypes. Similarly, Bind *et al.*, (2015) reported maximum intra cluster divergence was found in cluster III followed by cluster IV and cluster VI. Cluster III exhibited maximum intra cluster distance which indicated that genotype may be used to produce superior hybrid and transgressive segregants. Minimum intra cluster distance was observed for the cluster I reported by Gupta *et al.*, (2015). Earlier studied performed by Chandra *et al.*, (2018) reported cluster VI exhibited maximum intra cluster distance.

The maximum inter cluster distance was between cluster VII and V followed by cluster VII and VI, cluster VII and IV and cluster VII and I. Similarly, Doddabhimappa *et al.* (2012) Cluster I and II showed maximum inter cluster distance followed by between cluster II and VII and cluster I and V. Khan *et al.*, (2013) highest inter cluster distance between cluster I and V. Maximum inter cluster distance was found in cluster V and cluster VI by Bind *et al.*, (2015). The estimates of average intra and inter cluster distance value of seven clusters revealed that the genotypes belonging to the same cluster (intra cluster) have less genetic divergence as compared to genetic diversity between the genotypes of different clusters (inter cluster). The genotypes grouped into the same cluster displayed the lowest degree of divergence from one another and in case crosses are made between genotypes belonging to the same cluster, no transgressive segregant is expected from such combinations. Therefore, the hybridization program should always be formulated in such a way that the parents belonging to different clusters with maximum genetic distance divergence could be utilized to get desirable transgressive segregants.

5.7 Cluster mean and contribution percentage of various characters

The cluster mean and contribution percentage of various characters were presented in Table 4.9. The highest cluster mean value for plant height was recorded in case of cluster VII, for height upto first fruiting branch recorded in case of cluster VII, days to 50 % flowering in case of cluster VII, primary branches plant⁻¹ highest cluster mean value was recorded in case of cluster VII, secondary branches plant⁻¹ in case of cluster III, siliquae plant⁻¹ in case of cluster I, seeds per siliqua in case of cluster VI, 1000-seed weight in case of culture VI, aphid count in case of cluster V, penetration force in case of cluster V, seed yield plant⁻¹ in case of cluster III. The results obtained in the present study are in accordance with the findings of Khan *et al.*, (2013), Shekhawat *et al.*, (2014) and Singh *et al.*, (2018).

An interesting finding from the cluster mean for the seed yield is that the cluster III having the highest seed yield plant⁻¹ had not shown the highest genetic divergence from the other clusters. However, other clusters like cluster IV, cluster V, cluster VI and cluster VII showed higher genetic divergence amongst themselves.

For the characters like plant height, 1000 seed weight, penetration force, seed yield and aphid count contributing substantially high to the total genetic divergence, it was found that genetically divergent clusters namely IV, V, VI, and VII performed optimally and amongst these clusters only. Cluster VII was the poorest seed yielder. This reflected that the genetically divergent genotypes were distributed in the different clusters like cluster IV, V, VI, VII. This is in confirmation with our findings in this experiment with respect to the selection of genetically divergent genotypes from the clusters having the highest genetic divergent.

The percentage contribution of plant height has been maximum to divergence followed by 1000 seed weight as well as penetration force, aphid count, seed yield per plant

and days to 50 % flowering, contributed most towards genetic divergence, whereas remaining characters contributed very little towards genetic divergence *i.e.*, siliquae plant⁻¹, height up to first fruiting branch, secondary branches plant⁻¹, primary branches plant⁻¹ and seeds per siliqua.

In contrast, Shalini (1998) and Somu (2001) indicated that the siliquae plant⁻¹ followed by plant height and days to 50% flowering were the major contributors towards genetic divergence. Jahan *et al.*, (2013) observed primary branches plant⁻¹, number of secondary branches plant⁻¹ and days to 50% flowering contributed maximum towards divergence. Similarly, Devi *et al.*, (2017) observed the highest contribution percentage for the number of siliquae per plant followed by 1000 seed weight.

A proper follow up of this experiment would be justifiable if a suitable crossing programme is carried out using the eight most genetically divergent mustard genotypes identified based on the inter-cluster distance, intra cluster distance and the D2 distance between the individual genotypes, namely PHR 2, RNWR-09-3, Giriraj, Kranti, SKJM-05, DRMR-15-16, RW-85-59 (Sarna) and NPJ-194.

5.8 Combining ability

Breeding system of Indian mustard is principally the gathering or creating variabilities and choosing predominant genotypes from the germplasm. For using the previously mentioned step, assessment of genetic variability, heritability, genetic advance, general and specific combining ability, genetic variance, mechanism of gene action involved and the extent of heterotic vigour are of most extreme significance. Yield is the unpredictable attribute being administered by the huge number of cumulative dominant genes which is profoundly affected by the climate. Thus, the importance of the selection of appropriate parental material and suitable breeding methodology has to be emphasized more comprehensively. The regular methodology of choosing the parental material for

hybridization-based on its *per se* performance and local adaptation may not prompt productive outcome and henceforth the decision of parental material based on previously mentioned standards is a pre-essential for the plant breeder.

The critical step in the breeding programme is the selection of parents. One of the integral assets in the possession of plant breeder is combining ability which helps in the selection of suitable parents for hybridization, isolation of promising F₁ hybrids and understanding the inheritance of the characters for further exploitation in the breeding programme. The interactions among genes and between genotypes and environments decide the ability of parents to combine well with other desirable parents. The good general combiner can be recognized and used for hybridization in self-pollinated species for gaining superior segregants in the further generations. The selection of parents should be based on *per se* performance in respect of yield and other economic traits are important was suggested by Joshi (1979). To carry out the improvement in required directions for various quantitative traits requires the knowledge of the relative magnitude of additive and non-additive action of genes actions. Previously, the basis of selection of parents for hybridization in crop improvement was *per se* performance but this is the chief cause of misdeed within the crosses. Gene action helps in the selection of parents for use in hybridization programmes and also the choice of suitable breeding procedure for genetic improvement. Spargue and Tatum (1942) in maize first suggested the use of combining ability as a measure of the type of gene action. It refers to the ability of the genotype to transmit a superior performance to its crosses. It helps in categorizing superior cross combinations that may be used for commercial exploitation of heterosis.

Conferring to Malik *et al.*, (2004), general combining ability is owing to genes, which are chiefly additive in their effects and specific combining ability is due to the genes with dominance or epistatic effect. In mustard, the evaluations of general combining

ability (GCA) are very beneficial, as (Rashid *et al.*, 2007) proposed that the variance due to general combining ability is attributable to additive gene actions, while the variance due to specific combining ability (SCA) is attributable to non-additive gene actions. The objective of the current investigation was to estimate the general combining ability of parents and specific combining ability of crosses for yield and its components to determine the potential of hybrid production in mustard.

5.8.1 Analysis of variance for parents and crosses

5.8.1.1 Analysis of variance for parents and crosses for seed yield and its attributing characters

Analysis of variance for parents and crosses for seed yield and its attributing characters presented in Table 4.10. In the present investigation, the analysis of variance revealed a significant difference among the parents for the majority of characters apart from seed siliqua⁻¹ indicating a considerable amount of variability among the parents. Mean squares due to crosses were significant for all the characters. This revealed existence of considerable variability in the plant material used. Comparison of mean squares due to parent vs crosses was found significant for days to 50% flowering, plant height, 1000 seed weight and oil content indicating the presence of a substantial difference between parents and crosses. Vaghela *et al.*, (2011) earlier reported that the analysis of variance showed highly significant differences existed among genotypes for all the characters studied. Arifullah *et al.*, (2013) revealed that there were highly significant differences among the treatments for all the characters studied also supports the experimental results of the analysis of variance.

5.8.1.2 Analysis of variance for parents and crosses for physiological characters

Analysis of variance for parents and crosses for physiological characters presented in Table 4.11. Analysis of variance showed highly significant parental mean squares value

for all the character excluding total chlorophyll indicating significant variability among all the parents studied for physiological characters. Among the crosses, the mean sum of squares revealed significant variance for all the physiological characters indicating the presence of genetic variability in the crosses. Mean squares due to parent vs crosses were also significant for most of the traits *viz.*, percentage of excised - leaf water loss, chlorophyll a, chlorophyll b and total chlorophyll which depicted the presence of heterosis for these characters in the series of the crosses.

5.8.1.3 Analysis of variance for parents and crosses for aphid related characters

Analysis of variance for parents and crosses for aphid related characters presented in Table 4.12. Mean squares revealed that parental genotypes had a significant difference for all the aphid related characters providing that the parents are comprising the diverse genetic background. Analysis of variance showed a highly significant difference among the crosses for all the characters representing considerable genetic variability among the crosses. Parent vs crosses mean squares were found significant for all the characters except for water content of aphid probed twig, for percentage of water differential between aphid probed twig and aphid itself and penetration force indicated that mean value of the hybrids were significantly different from that of the parents as a group for these characters thereby, suggesting the presence of heterosis for most of these characters.

5.8.2 Mean performance of parents and crosses

5.8.2.1 Mean performance of parents and crosses for seed yield and its attributing characters

Mean performance of parents and crosses for seed yield and its attributing characters presented in Table 4.13. Mean performances of crosses were comparatively

higher than the parents for most of the characters *viz.*, secondary branches plant⁻¹, seeds per siliquae⁻¹, height upto first fruiting branch, plant height and 1000 seed weight revealed superiority and the presence of sufficient amount of heterosis in the crosses. The superiority of F₁s was also reported by Karthikeyan *et al.* (2009), Shanthi *et al.*, (2011) in rice and Vaghela *et al.*, (2011) and Arifullah (2013) in mustard. The parent PHR-2 showed good performance for the majority of characters namely primary branches plant⁻¹, secondary branches plant⁻¹, siliquae per plant⁻¹ and seeds per siliqua⁻¹ whereas DRMR-15-16 performed better for height upto first fruiting branches and oil content. Early flowering and short stature were showed by the parental genotypes NPJ-194 and RW-85-59 while for seed yield SKJM-05 parent was best performed. Among the crosses, NPJ-194 × Kranti showed the best performance for secondary branches plant⁻¹, siliquae plant⁻¹, seed siliquae⁻¹ and height upto first fruiting branch. Cross NPJ-194 × RW-85-59 showed early flowering and dwarf stature while Kranti × Giriraj had high mean value for seed yield and NPJ-194 × DRMR-15-16 for primary branches per plant.

5.8.2.2 Mean performance of parents and crosses for physiological characters

Mean performance of parents and crosses for physiological characters presented in Table 4.14. The mean performance of crosses was higher than the parents for certain attributes namely percentage of membrane stability index, percentage of excised leaf water loss, percentage of relative water content, canopy temperature depression, proline content of leaf, chlorophyll a, chlorophyll b and total chlorophyll. Crosses showed high mean value than parents uncovered predominance and the presence of adequate measure of heterosis in crosses. The parent NPJ-194 showed highest average value for percentage of relative water content; RW-85-59 for percentage of membrane stability index; SKJM-05 for percentage of excised leaf water loss and canopy temperature depression; DRMR-15-16 for proline content of leaf; PHR-2 showed highest mean value for chlorophyll a,

chlorophyll b and total chlorophyll.

The crosses DRMR-15-16 × Giriraj represented the best performance for percentage of membrane stability index and canopy temperature depression; DRMR-15-16 × RNWR-09-3 exhibited the best execution for percentage of excised leaf water loss and chlorophyll b; Kranti × PHR-2 indicated high mean value for chlorophyll a and total chlorophyll; SKJM-05 × Kranti for percentage of relative water content and DRMR-15-16 × PHR-2 for proline content of the leaf.

5.8.2.3 Mean performance of parents and crosses for aphid related characters

Mean performance of parents and crosses for aphid related characters presented in Table 4.15. Out of six aphid related attributes only two characters indicated higher mean value for the crosses than the parental genotypes, revealed transcendence and presence of sufficient proportion of heterosis for the traits water content of aphid uninfested twig (%) and percentage of water differential between aphid probed twig and aphid itself (%) in crosses. Parent Giriraj indicated best performance for water content of aphid (%) and percentage of water differential between aphid probed twig and aphid itself (%); PHR-2 demonstrated high average value for water content of aphid probed twig (%) and penetration force; Kranti for water content of aphid uninfested twig (%) and RW-85-59 for aphid count.

The crosses RNWR-09-3 × PHR-2 appeared as best performer for water content of aphid (%) and percentage of water differential between aphid probed twig and aphid itself (%); Giriraj × RNWR-09-3 for water content of aphid probed twig (%); SKJM-05 × Giriraj for water content of aphid uninfested twig (%); NPJ-194 × SKJM-05 for aphid count and NPJ-194 × Giriraj for penetration force.

5.8.3 Analysis of variance for combining ability

5.8.3.1 Analysis of variance for combining ability for seed yield and its attributing characters

Analysis of variance for combining ability for seed yield and its attributing characters presented in Table 4.16. Analysis of combining ability indicated that the mean sum of squares due to general combining ability and specific combining ability were significant for all the characters except seed siliqua⁻¹ which showed non-significant specific combining ability. Subsequently, we can infer that there was a significant difference among the GCA of eight parents and SCA of twenty-eight crosses, recommending the significance of both additive and non-additive gene effect in the inheritance of the characters. Similarly, Teklewold and Becker (2005) and Noshin *et al.*, (2007) Singh *et al.*, (2008), Singh and Dixit (2006) also reported significant mean squares due to GCA and SCA for various morphological and seed yield traits in brown mustard. Ghosh *et al.*, (2002) believed that for most of the major traits including seed yield had both additive and non-additive gene action of prime importance in Indian mustard. However, other researchers Cheema and Sadaqat (2004), Larik and Rajput (2000) and Rameah *et al.*, (2003) have emphasized the importance of additive genetic effects for some characters such as the number of branches and number of pod per plant in this crop. Present results are supported by earlier findings of Fray *et al.*, (1997) who reported that mean squares due to general and specific combining ability were significant for yield and its components for oil content. These results exhibited the importance of additive and non-additive type of variance in the inheritance of most of the traits studied, similar findings were reported by Labana *et al.*, (1978) and Tamber *et al.*, (1991), Chaurasiya *et al.*, (2018) in Indian mustard.

5.8.3.2 Analysis of variance for combining ability for physiological characters

Analysis of variance for combining ability for physiological characters presented in Table 4.17. Estimates of GCA and SCA variance were significant for all the characters aside from the canopy temperature depression signifying the operation of both additive and non-additive components of gene action for the inheritance of the character studied.

5.8.3.3 Analysis of variance for combining ability for aphid related characters

Analysis of variance for combining ability for aphid related characters presented in Table 4.18. The mean squares due to general combining ability and specific combining ability were significant for all the characters. Hence, we can presume that there are significant differences among the GCA of parents and SCA of crosses. Significance of mean square suggested that additive genetic variance is responsible and non-additive variance is also involved in the inheritance of the attributes.

5.8.4 Estimation of genetic components of variances

5.8.4.1 Genetic component of the variance for seed yield and its attributing characters

The genetic component of the variance for seed yield and its attributing characters presented in Table 4.19. The specific combining ability component of variance (σ^2_{sca}) were higher than the general combining ability component of variance (σ^2_{gca}) for all the ten seed yield and its attributing characters studied *viz.*, days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliqua⁻¹, height up to first fruiting branch, plant height, seed yield plant⁻¹, 1000 seed weight and oil content. It indicated, the control of the non-additive type of gene action. These results are in agreement with the results of Rao and Gulati (2002), Patel *et al.*, (2003) and Singh *et al.*, (2008). The proportion of GCA and SCA variance ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was less than 1 for all the characters showed the greater association of non-additive gene action for these

characters (Yadav, 1996). In this manner, the choice may be productive for the improvement of the characters in the later generation in genotypes, which had profoundly high genotypic mean squares. The similar findings conform with Yadav *et al.*, (1992), Chaudhary *et al.*, (1997), Khulbe *et al.*, (1998), Ghosh *et al.*, (2002), Katiyar *et al.*, (2004), Verma *et al.*, (2011), Ali and Pant (2013) and Chaurasiya *et al.*, (2019).

The mean degree of dominance $(\sigma_{sca}^2/\sigma_{gca}^2)^{0.5}$ was found to be greater than 1 for all the characters, which indicated that the involvement of over dominance for these characters. Estimates of components of variances revealed that the values of dominant variance (σ_D^2) were higher than additive variance (σ_A^2) for all the characters except days to 50% flowering which showed that there was a higher role of dominant component of variance as compared to the additive component of variance in the expression of character under investigation.

Since the ratio of additive genetic variance and dominance genetic variance (σ_A^2/σ_D^2) is less than unity (one) for all the seed yield and its attributing characters except days to 50% flowering which means, majority of characters were governed by dominance gene action. Baker (1978) suggested the predictability ratio ($\sigma_A^2/\sigma_A^2+\sigma_D^2$) understand the importance of general combining ability and specific combining ability for deciding the progeny performance. Closer the proportion to unity, more prominent will be the predictability dependent on general combining ability. In the current study, the ratio is more than 0.50 in all the cases recommending preponderance of additive genetic effects in the characters.

The result obtained in the present study expressing the nature and magnitude of gene effects for different characters has also been reported by several workers engaged in the improvement of oilseed as a whole and mustard in particular. Sheikh and Singh (1998) and Kumar *et al.* (2002) also reported a preponderance of non-additive gene action in

most of the character they studied. However, Sheikh and Singh (1998) and Monalisa *et al.*, (2005) reported additive genetic variance to be more important for plant height.

5.8.4.2 Genetic component of the variance for physiological characters

The genetic component of the variance for physiological characters presented in Table 4.20. The magnitude of specific combining ability component of variance (σ^2_{sca}) was higher than the general combining ability component of variance (σ^2_{gca}) and the ratio of general combining ability to that of specific combining ability variance ($\sigma^2_{gca}/\sigma^2_{sca}$) was less than unity for all the eight physiological characters studied *i.e.*, percentage of membrane stability index, percentage of excised leaf water loss, percentage of relative water content, canopy temperature depression, proline content of leaf, chlorophyll a, chlorophyll b and total chlorophyll. It was subsequently inferred that; non-additive genetic component gives more priority than the additive genetic component in deciding the inheritance of these attributes.

The estimates of mean degree of dominance ($(\sigma^2_{sca}/\sigma^2_{gca})^{0.5}$) was found to be greater than one for majority of the characters, which indicated that the involvement of over dominance for these characters under study. The dominance genetic variance (σ^2_D) was higher than additive variance (σ^2_A) and the ratio of additive genetic variance and dominance genetic variance (σ^2_A/σ^2_D) is less than unity (one) for all the physiological characters involved in study implied the characters were governed by dominance gene action. The estimates of predictability ratio ($\sigma^2_A/\sigma^2_A+\sigma^2_D$) were higher than 0.50 for all the characters indicating additive genetic effect.

5.8.4.3 Genetic component of the variance for aphid related characters

The genetic component of the variance for aphid related characters presented in Table 4.21. Estimates of general combining ability effect of the parents and specific combining ability effect of the crosses revealed that specific component of variance (σ^2_{sca}) were higher than the general combining ability component of variance (σ^2_{gca}) and the ratio of general combining ability to that of specific combining ability variance ($\sigma^2_{gca}/\sigma^2_{sca}$) was less than unity for all the aphid related characters studied *i.e.*, water content of aphid probed twig (%), water content of aphid uninfested twig (%), water content of aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force which indicated the preponderance of non-additive variance of gene action in these characters.

The value of mean degree of dominance ($\sigma^2_{sca}/\sigma^2_{gca}$)^{0.5} was found greater than unity indicated the over dominance. Estimates of dominance variance (σ^2_D) were larger in magnitude than the additive variance (σ^2_A) and the ratio of additive genetic variance and dominance genetic variance (σ^2_A/σ^2_D) is lower than unity (one) for all the aphid related characters indicates that the characters were governed by dominance gene action. The evaluations of predictability ratio ($\sigma^2_A/\sigma^2_A+\sigma^2_D$) were higher than 0.50 for all the characters and much higher for penetration force indicating additive genetic effect.

5.8.5 Estimation of general combining ability (gca) effects

5.8.5.1 Estimation of general combining ability (gca) effects for seed yield and its attributing characters

Estimation of general combining ability (gca) effects for seed yield and its attributing characters are presented in Table 4.22.

The general combining ability effect revealed that none of the parents was found as a good general combiner for all the ten seed yield and its attributing characters, however, the

parent RW-85-59 was good combiner for days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, height up to first fruiting branch and plant height whereas Kranti was noted as good general combiner for secondary branches plant⁻¹, siliquae plant⁻¹ and height up to first fruiting branch. Genotype NPJ-194 was recorded as a good general combiner for siliquae plant⁻¹ plant height and oil content, PHR-2 for siliquae plant⁻¹, SKJM-05 for seed yield and 1000 seed weight.

Based on gca effect RW-85-59 was found to be best general combiner for six characters followed by DRMR-15-16 for four characters, Kranti for three characters, NPJ-194 for three characters whereas PHR-2, SKJM-05 for two characters. RW-85-59, DRMR-15-16, Kranti and NPJ-194 seemed to be a good general combiner for most of the characters. These parents have desirable alleles for most of the characters and fixable component of gene action, additive and additive × additive type of epistasis, these could be successfully exploited by developing a homozygous line for the improvement of characters. These parental lines might be utilized for producing the intermating population to get desirable recombinants in Indian mustard. These results conform with Singh *et al.*, (1985), Badwal and Labana (1987), Wani and Srivastava (1989), Gupta *et al.*, (1991), Patel *et al.*, (1996), Basudev *et al.*, (2001), Nashim *et al.*, (2007), Vaghela *et al.*, (2011), Gami and Chauhan (2013), Patel *et al.*, (2013) and Dholu *et al.*, (2014).

5.8.5.2 Estimation of general combining ability (gca) effects for physiological characters

Estimation of general combining ability (gca) effects for physiological characters presented in Table 4.23.

The estimates of gca effects of the parental lines for various physiological characters revealed that four genotypes PHR-2, NPJ-194, RNWR-09-3 and Kranti were good general combiner. Based on gca effect was seen that none of the parents was found as an acceptable general combiner for all the physiological characters studied. Parent PHR-

2 was good general combiner for proline content, chlorophyll a, chlorophyll b and total chlorophyll; NPJ-194 for oil content, chlorophyll a, chlorophyll b and total chlorophyll; RNWR-09-3 for oil content, percentage of excised leaf water loss, chlorophyll b and total chlorophyll while Kranti showed good general combiner for the percentage of membrane stability index and percentage of relative water content. Two parental lines Giriraj and SKJM-05 recorded as good general combiner for only one character each *i.e.*, percentage of membrane stability index and percentage of excised leaf water loss respectively.

PHR-2, NPJ-194, RNWR-09-3 and Kranti appeared to be good general combiner for most of the characters. These parents showed significant *gca* effect, which revealed that they are fixable and are responsible for additive or additive \times additive gene effects for the inheritance of the characters. Adaptation of simple selection these characters can be improved in Indian mustard and the parents which showed good general combiners for these physiological characters could be used in further crossing programme. General combining ability helps to identify the parent with the highest proportion of positive additive alleles associated with trait of interest. Similar results are observed by Dabholkar (2006), Kadkol *et al.*, (1984) and Skoric (1992).

5.8.5.3 Estimation of general combining ability (*gca*) effects for aphid related characters

Estimation of general combining ability (*gca*) effects for aphid related characters presented in Table 4.24.

A perusal of *gca* effects of parents indicated that none of the parents was found to be a good general combiner for all the characters. However, one of the parents SKJM-05 was found to be a good general combiner for five aphid related characters *viz.*, water content of aphid probed twig (%), water content of aphid uninfested twig (%), water content of

aphid (%), percentage of water differential between aphid probed twig and aphid itself (%), aphid count and penetration force; DRMR-15-16 showed good general combiner for water content of aphid (%), aphid count and penetration force; Kranti for water content of aphid unfested twig (%) and aphid count; NPJ-194 for water content of aphid probed twig (%) and penetration force and Giriraj for the percentage of water differential between aphid probed twig and aphid itself (%) and penetration force. Parental lines RNWR-09-3 and RW-85-59 was found to be a good general combiner for one character each *i.e.* aphid count and penetration force respectively.

It can be concluded that SKJM-05, DRMR-15-16, Kranti, NPJ-194, PHR-2 and Giriraj possesses desirable alleles for most of the aphid related characters. The parents examined above had high gca effect and the fixable segment of gene action *i.e.*, additive and additive \times additive interaction effects and are liable for the inheritance of the specific attributes. The parents which showed a good general combiner for the aphid related attributes could be further utilized in the breeding programme.

5.8.6 Estimation of specific combining ability (sca) effects

5.8.6.1 Estimation of specific combining ability (sca) effects for seed yield and its attributing characters

Estimation of specific combining ability (sca) effects for seed yield and its attributing characters presented in Table 4.25. In the present investigation, out of 28 F₁s, none of the crosses exhibited good specific combiner for all the characters under study. Out of 28 F₁s, five crosses exhibited negative significant sca effect while six crosses showed positive significance for days to 50% flowering; six crosses were positively significant and four crosses were negatively significant for primary branches plant⁻¹; four positively significant while five negatively significant crosses for secondary branches plant⁻¹; siliquae plant⁻¹ showed eleven crosses as positively significant whereas negatively

significant by sixteen crosses; seeds siliqua⁻¹ exhibited three crosses as positively significant; six crosses were positively significant for height up to first fruiting branch; fifteen crosses displayed positively significance for plant height; seed yield plant⁻¹ revealed seven crosses positively significant; fourteen crosses were positively significant for 1000 seed weight and ten crosses were positively significant for oil content. The hybrids which recorded positively significant specific combining ability effect are recommended for heterosis breeding except for days 50% flowering and plant height whereas negatively significant specific combining ability effect was desirable.

Some of the cross combinations namely NPJ-194 × SKJM-05, NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, SKJM-05 × Kranti and Kranti × PHR-2 showed positive significant specific combining ability effect for seed yield per plant and also expressed significant specific combining ability effect for some important yield attributing characters. For instance, the cross NPJ-194 × SKJM-05 expressed desirable specific combining ability effect for siliquae plant⁻¹. NPJ-194 × PHR-2 for primary branches plant⁻¹, secondary branches plant⁻¹ siliquae plant⁻¹ and 1000 seed weight. RW-85-59 × DRMR-15-16 for primary branches plant⁻¹, height up to first fruiting branch and 1000 seed weight. RW-85-59 × SKJM-05 for days to 50% flowering, plant height, 1000 seed weight and oil content and Kranti × PHR-2 for primary branches plant⁻¹ and plant height. These findings were supported by Chander *et al.*, (1985), Badwal and Labana (1987), Thakur *et al.*, (1989), Dhillion *et al.*, (1990), Diwakar and Singh (1993), Bhatia *et al.*, (1995), Khulbe *et al.*, (1998), Basudev *et al.*, (2001), Katiyar *et al.*, (2004), Gupta *et al.*, (2010), Verma *et al.*, (2011), Gami and Chauhan (2013) and Dholu *et al.*, (2014).

The three best performing crosses showed high specific combining ability effect in the order of merit were DRMR-15-16 × RNWR-09-3, RW-85-59 × SKJM-05 and DRMR-

15-16 × PHR-2 for days to 50% flowering; NPJ-194 × PHR-2, RW-85-59 × DRMR-15-16 and Kranti × PHR-2 for primary branches plant⁻¹; RW-85-59 × Kranti, Giriraj × PHR-2 and NPJ-194 × PHR-2 for secondary branches plant⁻¹; NPJ-194 × PHR-2, NPJ-194 × RNWR-09-3 and RW-85-59 × Kranti for siliquae plant⁻¹; RW-85-59 × Kranti, DRMR-15-16 × RNWR-09-3 and DRMR-15-16 × Giriraj for seeds siliqua⁻¹; RW-85-59 × Kranti, SKJM-05 × Giriraj and RW-85-59 × DRMR-15-16 for height up to first fruiting branch; Kranti × RNWR-09-3, SKJM-05 × Giriraj and DRMR-15-16 × SKJM-05 for plant height; NPJ-194 × SKJM-05, Kranti × PHR-2 and RW-85-59 × SKJM-05 for seed yield plant⁻¹; RW-85-59 × DRMR-15-16, DRMR-15-16 × SKJM-05 and Giriraj × PHR-2 for 1000 seed weight and RW-85-59 × PHR-2, RNWR-09-3 × PHR-2 and NPJ-194 × DRMR-15-16 for oil content.

Best general combiners and a few specific combiners for seed yield and its attributing characters in Indian mustard (*Brassica juncea*) presented in Table 4.36. SKJM-05 considered as a best general combiner and showed positive significant specific combining ability effect for seed yield plant⁻¹ and the crosses involving this parent were SKJM-05 × Kranti, RW-85-59 × SKJM-05 and NPJ-194 × SKJM-05 showed positively significant specific combining ability effect and their *per se* performance is also good. Crosses RW-85-59 × DRMR-15-16, NPJ-194 × PHR-2, NPJ-194 × Giriraj and Kranti × PHR-2 showed non-significant general combining ability effect for both the parents and positively significant specific combining ability effect.

In case of secondary branches plant⁻¹ RW-85-59 and Kranti were the best general combiner and showed the positively significant general combining effect. One cross comprising these parents *i.e.*, RW-85-59 × Kranti showed significant specific combining ability effect whereas other crosses Giriraj × PHR-2, NPJ-194 × PHR-2 and Giriraj × RNWR-09-3 expressed non-significant gca effect and significant specific combining ability effect.

Five parents were showed positively significant gca effect in case of 1000 seed weight *i.e.*, SKJM-05, RW-85-59, PHR-2, RNWR-09-3 and Kranti and the sca effect of NPJ-194 \times RW-85-59, NPJ-194 \times Kranti, NPJ-194 \times RNWR-09-3, NPJ-194 \times PHR-2, RW-85-59 \times DRMR-15-16, RW-85-59 \times SKJM-05, RW-85-59 \times Giriraj, DRMR-15-16 \times SKJM-05, DRMR-15-16 \times PHR-2, SKJM-05 \times Kranti, Kranti \times RNWR-09-3, Giriraj \times PHR-2 and RNWR-09-3 \times PHR-2 were also significant whereas the cross namely NPJ-194 \times Giriraj showed significant sca effect but both the parents showed the non-significant effect.

The four parents PHR-2, NPJ-194, RW-85-59 and Kranti recorded positively significant gca effect. Hence, these four parents can be used in breeding programmes to improve siliquae plant⁻¹. The hybrids comprising these parents are NPJ-194 \times PHR-2, NPJ-194 \times RNWR-09-3, RW-85-59 \times Kranti, Kranti \times Giriraj, Giriraj \times PHR-2, NPJ-194 \times DRMR-15-16, NPJ-194 \times SKJM-05, DRMR-15-16 \times PHR-2 and RW-85-59 \times Giriraj also showed significant desirable sca effect whereas the hybrids DRMR-15-16 \times Giriraj and DRMR-15-16 \times SKJM-05 showed significant sca effect but non-significant gca effect. A cross combination exhibiting high specific combining ability effects as well as high *per se* performance involving at least one parent as good general combiner for a particular character, is expected to throw desirable segregants in the segregating generations. Hence, it could be concluded from here that the seed yield per plant and all the major yield attributing characters *i.e.*, siliquae plant⁻¹, secondary branches plant⁻¹ and 1000 seed weight comprises of hybrid which showed significant gca effect and significant sca effect.

Table 4.36 Best general combiners and a few specific combiners for yield and its attributing characters in Indian mustard (*Brassica juncea*)

Characters	Best general combiners	gca effects	<i>Per se</i> performance of theparent	Best specific combiners	sca effects	<i>Per se</i> performance ofcrosses	gca status of parents	
Seed yield (g)	SKJM-05	0.013*	6.133	RW-85-59 × DRMR-15-16	0.025**	5.507	NS × NS	M × M
				NPJ-194 × PHR-2	0.026**	5.090	NS × NS	M × L
				SKJM-05 × Kranti	0.029**	4.327	S × NS	M × L
				NPJ-194 × Giriraj	0.039**	4.587	NS × NS	M × M
				RW-85-59 × SKJM-05	0.044**	5.313	NS × S	M × M
				Kranti × PHR-2	0.061**	4.527	NS × NS	M × L
				NPJ-194 × SKJM-05	0.065**	5.733	NS × S	M × M
Secondary branches plant ⁻¹	RW-85-59	1.200**	8.60	RW-85-59 × Kranti	4.250**	8.730	S × S	H × M
	Kranti	0.726*	8.93	Giriraj × PHR-2	2.758**	8.870	NS × NS	L × M
				NPJ-194 × PHR-2	1.551**	9.270	NS × NS	L × M
				Giriraj × RNWR-09-3	1.445**	10.130	NS × NS	L × L
1000 Seed weight (g)	SKJM-05	3.158*	2.570	NPJ-194 × RW-85-59	2.511**	2.953	NS × S	L × H
	RW-85-59	2.458*	3.173	NPJ-194 × Kranti	6.344**	3.430	NS × S	L × H
	PHR-2	1.758*	16.853	NPJ-194 × Giriraj	1.611**	3.343	NS × NS	L × L
	RNWR-09-3	1.558*	32.963	NPJ-194 × RNWR-09-3	7.078**	2.850	NS × S	L × H
	Kranti	1.292*	40.980	NPJ-194 × PHR -2	5.878**	2.967	NS × S	L × H
				RW-85-59 × DRMR-15-16	12.878**	2.220	S × NS	H × L
				RW-85-59 × SKJM-05	1.744**	3.893	S × S	H × H
				RW-85-59 × Giriraj	4.211**	1.820	S × NS	H × L
				DRMR-15-16 × SKJM-05	9.178**	3.463	NS × S	L × H
				DRMR-15-16 × PHR-2	0.911**	3.183	NS × S	L × H
				SKJM-05 × Kranti	2.578**	2.957	S × S	H × H
				Kranti × RNWR-09-3	3.511**	1.900	S × S	H × H
				Giriraj × PHR-2	8.578**	3.573	NS × S	L × H
				RNWR-09-3 × PHR-2	2.378**	3.060	S × S	H × H
	Siliquae plant ⁻¹	PHR 2	0.038***	329.800	NPJ-194 × PHR -2	0.166**	173.733	S × S
NPJ-194		0.023**	162.13	NPJ-194 × RNWR-09-3	0.141**	185.600	S × NS	M × L
RW-85-59		0.013**	192.00	RW-85-59 × Kranti	0.097**	178.333	S × S	M × M
Kranti		0.030**	184.27	Kranti × Giriraj	0.095**	128.800	S × NS	M × L
				Giriraj × PHR-2	0.060**	201.000	NS × S	L × M
				NPJ-194 × DRMR-15-16	0.053**	158.200	S × NS	M × L
				NPJ-194 × SKJM-05	0.047**	172.067	S × NS	M × L
				DRMR-15-16 × PHR-2	0.041**	162.467	NS × S	L × M
				DRMR-15-16 × Giriraj	0.041**	148.267	NS × NS	L × L
				DRMR-15-16 × SKJM-05	0.019**	220.800	NS × NS	L × L
				RW-85-59 × Giriraj	0.019**	183.267	S × NS	M × L

*, ** Significant at 5% and 1% levels of probability, respectively; H= high gca effect, M= medium gca effect and L= low gca effect; S= significant parent, NS= non-significant parent

Most of the hybrids were having one parent as positively significant gca effect, recommended for recombination breeding. However, since the sca effect of the hybrids is significant therefore selection of superior plants should be postponed to a later generation. The hybrids showed non-significant gca effect and significant sca effect so the heterosis breeding is recommended in these hybrids.

5.8.6.2 Estimation of specific combining ability (sca) effects for physiological characters

Estimation of specific combining ability (sca) effects for physiological character presented in Table 4.26. The sca effect exhibited that, the number of crosses that had desirable significant effects were ten for oil content, nine for percentage of membrane stability index, fourteen for percentage of excised leaf water loss, two for percentage of relative water content, three for canopy temperature depression, eleven for proline content, six for chlorophyll a, six for chlorophyll b and six for total chlorophyll.

The three best performing crosses showed high desirable sca effect in the order of merit were SKJM-05 \times PHR-2, NPJ-194 \times DRMR-15-16 and RW-85-59 \times Giriraj for oil content; NPJ-194 \times RW-85-59, RW-85-59 \times RNWR-09-3 and SKJM-05 \times Giriraj for percentage of membrane stability index; DRMR-15-16 \times Kranti , Kranti \times PHR-2 and SKJM-05 \times RNWR-09-3 for percentage of excised leaf water loss; RW-85-59 \times PHR-2 and DRMR-15-16 for percentage of relative water content; SKJM-05 \times Giriraj, RW-85-59 \times DRMR-15-16 and NPJ-194 \times SKJM-05 for canopy temperature depression; Kranti \times Giriraj, SKJM-05 \times PHR-2 and NPJ-194 \times DRMR-15-16 for proline content; DRMR-15-16 \times SKJM-05, RW-85-59 \times DRMR-15-16 and DRMR-15-16 \times Kranti for chlorophyll a; DRMR-15-16 \times RNWR-09-3, SKJM-05 \times RNWR-09-3 and NPJ-194 \times Giriraj for chlorophyll b and RW-85-59 \times Kranti, NPJ-194 \times PHR-2 and NPJ-194 \times Giriraj for total

chlorophyll. Similar results recorded by Sankar *et al.*, (2008). Thirumeni *et al.*, (2000). Shanthi *et al.*, (2011), Mohan *et al.*, (2000) and Babu *et al.*, (2005).

Best general combiners and a few specific combiners for physiological characters in Indian mustard (*Brassica juncea*) presented in Table 4.37. NPJ-194, DRMR-15-16, RNWR-09-3 and PHR-2 was considered as good general combiner having positive significant general combining ability effect and hybrids from such parents are NPJ-194 × PHR-2, NPJ-194 × Giriraj, DRMR-15-16 × RNWR-09-3, Giriraj × PHR-2 and RW-85-59 × PHR-2 showed positively significant specific combining ability effect for total chlorophyll whereas the hybrids namely RW-85-59 × Kranti showed non-significant general combining ability effect for either of the parents while their specific combining ability effect was significant.

In case of proline content of a leaf, the significant gca effect was expressed by only one parent i.e. PHR-2 and the significant specific combining ability effect was showed by SKJM-05 × PHR-2, NPJ-194 × PHR-2 and RNWR-09-3 × PHR-2 while the crosses Kranti × Giriraj, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, SKJM-05 × Giriraj, RW-85-59 × SKJM-05, RW-85-59 × Kranti, Kranti × RNWR-09-3 and RW-85-59 × DRMR-15-16 expressed significant specific combining ability effect but the parents involved were non-significant general combining ability effect.

Two parents Giriraj and Kranti were the best general combiner and showed positively significant gca effect for percentage of membrane stability index and the hybrids from these parents namely SKJM-05 × Giriraj, DRMR-15-16 × Kranti, Kranti × PHR-2, DRMR-15-16 × Giriraj, SKJM-05 × Kranti and Giriraj × RNWR-09-3 showed positively significant specific combining ability effect. However, the crosses which were positively significant specific combining ability effect but the general combining ability effect was not significant were NPJ-194 × RW-85-59, RW-85-59 × RNWR-09-3 and NPJ-194 ×

RNWR-09-3. The hybrid which had at least one of the parents had positively significant general combining ability effects and the other parent with non-significant general combining ability effects could be used in recombination breeding. However, the specific combining ability effects of these hybrids is significant therefore selection of superior plant should be postponed to the later generations. The hybrids which recorded positively significant specific combining ability effects and non-significant general combining ability effect for parents are recommended for heterosis breeding for the improvement of that particular traits.

5.8.6.3 Estimation of specific combining ability (sca) effects for aphid related character

Estimation of specific combining ability (sca) effects for aphid related character presented in Table 4.27. In the present investigation, out of 28 F_{1s} , thirteen crosses were positively significant and six crosses showed negatively significant for water content of aphid probed twig; two crosses were positively significant and seven crosses, negatively significant for water content of aphid uninfested twig; seven crosses, negatively significant for water content of aphid; seven crosses were positively significant and six crosses, negatively significant for percentage of water differential between aphid probed twig and aphid itself; thirteen crosses, negatively significant *sca* effects for aphid count and twelve crosses, positively significant *sca* effects for penetration force.

The three best performing crosses showed high desirable *sca* effect in the order of merit were RW-85-59 x Giriraj, NPJ-194 x PHR-2 and NPJ-194 x DRMR-15-16 for water content of aphid probed twig; Kranti x Giriraj (4.610) and DRMR-15-16 x Giriraj (2.891) for water content of aphid uninfested twig; SKJM-05 x RNWR-09-3, NPJ-194 x RNWR-09-3 and RW-85-59 x PHR-2 for water content of aphid; SKJM-05 x Kranti, RW-85-59 x PHR-2 and DRMR-15-16 x RNWR-09-3 for the percentage of water differential between aphid probed twig and aphid itself; RW-85-59 x Giriraj, RW-85-59 x SKJM-05 and

DRMR-15-16 x Kranti for aphid count and Kranti x Giriraj, NPJ-194 x RNWR-09-3 and DRMR-15-16 x Giriraj for penetration force.

Best general combiners and a few specific combiners for aphid related characters in Indian mustard (*Brassica juncea*) presented in Table 4.38. The best general combiners for aphid count were RW-85-59, DRMR-15-16, SKJM-05 and Kranti showed negative significant general combining ability effect. The hybrids including these parents *i.e.*, RW-85-59 x Giriraj, RW-85-59 x SKJM-05, DRMR-15-16 x Kranti, NPJ-194 x RW-85-59, DRMR-15-16 x PHR-2, SKJM-05 x Kranti, SKJM-05 x RNWR-09-3, NPJ-194 x DRMR-15-16, SKJM-05 x PHR-2, NPJ-194 x SKJM-05, DRMR-15-16 x RNWR-09-3 appeared significant specific combining ability effect. The parent RNWR-09-3 x PHR-2 and Giriraj x RNWR-09-3 indicated non-significant general combining ability effect for both the parents and critical specific combining ability effect.

The penetration force demonstrated significant general combining ability effect for DRMR-15-16, NPJ-194, SKJM-05, Giriraj and RNWR-09-3 and the hybrids including these parents additionally indicated significant specific combining ability effect *viz.*, Kranti x Giriraj, NPJ-194 x RNWR-09-3, DRMR-15-16 x RNWR-09-3, RW-85-59 x DRMR-15-16, RNWR-09-3 x PHR-2, SKJM-05 x Giriraj, NPJ-194 x RW-85-59, Giriraj x PHR-2, SKJM-05 x Giriraj, NPJ-194 x RW-85-59, Giriraj x PHR-2, NPJ-194 x SKJM-05, NPJ-194 x Giriraj. The crosses Kranti x Giriraj and Kranti x PHR-2 showed significant specific combining ability effect but their parents were non-significant.

The crosses which had one of the parents having significant general combining ability effect and the other parent with non-significant could be utilized in transgressive breeding while the specific combining ability impact of the hybrids is significant and subsequently, the choice of the better plant ought to be delayed to the further generation. The crosses which recorded positively significant specific combining ability effect and non-

significant general combining ability effect for parents are suggested for heterosis breeding for the development of those specific characters.

The good specific combiners included all the three potential blends between the parents with high and low general combining ability impacts *viz.*, high \times high, high \times low and low \times low. A desirable cross combination doesn't generally happen because of crosses between high \times high or high \times low combiners. Low \times low combiners were additionally liable to be a superior cross combination for the exploitation of such crosses, recombination breeding through various crosses would be valuable. If two good combiners engaged with a cross which turned out to be hereditary dissimilar, the position would be especially beneficial for reasonable breeding. Subsequently, a good cross combination isn't generally the aftereffect of high \times high GCA parents, rather it can likewise result from high \times medium or high \times low GCA parents. High GCA status of one of the parents and normal or poor of the other in heterotic crosses showed that additive gene effects of good general combiner and epistatic impact of poor combiner acted in a correlative way, prompting a high expression of the attributes. Such crosses are agreeable to progress through biparental mating as well as heterosis breeding.

5.9 Estimation of heterosis over mid parent (relative heterosis) and better parent (heterobeltiosis)

Heterosis breeding assumes a significant role in yield improvement for getting higher production. Heterosis has been abused in both self-and cross-pollinated crops for acquiring better yield. In self-pollinated plant-like mustard, the scope of utilization of heterosis depends upon the direction and magnitude of heterosis, feasibility and the types of gene action involved. To recognize the true heterotic cross combinations, assessment of heterosis over mid parent (relative heterosis) and over better parent (heterobeltiosis) may be beneficial.

Table 4.38 Best general combiners and a few specific combiners for aphid related characters in Indian mustard (*Brassica juncea*)

Characters	Best general combiners	gca effects	<i>Per se</i> performance of parents	Best specific combiners	sca effects	<i>Per se</i> performance of crosses	gca status of parents		
Aphid count	RW-85-59	-0.076**	45.110	RW-85-59 × Giriraj	-0.211**	73.557	S × NS	H × M	
	(Sarma)			RW-85-59 × SKJM-05	-0.209**	47.333	S × S	H × H	
	DRMR-15-16	-0.050**	59.00	DRMR-15-16 × Kranti	-0.176**	41.333	S × S	H × H	
	SKJM-05	-0.053**	61.67	NPJ-194 × RW-85-59	-0.171**	32.000	NS × S	M × H	
	Kranti	-0.031**	75.22	Giriraj × RNWR-09-3	-0.143**	64.220	NS × NS	M × M	
				DRMR-15-16 × PHR-2	-0.113**	47.443	S × NS	H × M	
				SKJM-05 × Kranti	-0.093**	49.113	S × S	H × H	
				SKJM-05 × RNWR-09-3	-0.087**	66.780	S × NS	H × M	
				NPJ-194 × DRMR-15-16	-0.080**	150.441	NS × S	M × H	
				SKJM-05 × PHR-2	-0.077**	76.557	S × NS	H × M	
				NPJ-194 × SKJM-05	-0.054**	28.667	NS × S	M × H	
				DRMR-15-16 × RNWR-09-3	-0.053**	47.000	S × NS	H × M	
				RNWR-09-3 × PHR-2	-0.036**	59.333	S × NS	M × M	
	Penetration force (Kpascal)	DRMR-15-16	4.682**	86.123	Kranti × Giriraj	14.153**	68.670	NS × S	L × M
		NPJ-194	2.716**	76.37	NPJ-194 × RNWR-09-3	13.952**	79.763	NS × S	M × M
		SKJM-05	2.418**	87.65	DRMR-15-16 × RNWR-09-3	10.403**	76.817	S × S	M × M
Giriraj		3.114**	81.57	RW-85-59 × DRMR-15-16	10.188**	82.307	NS × S	L × M	
RNWR-09-3		1.352*	96.29	RNWR-09-3 × PHR-2	10.050**	76.227	S × NS	M × M	
				SKJM-05 × Giriraj	7.036**	85.583	S × S	M × M	
				Kranti × PHR-2	6.101**	75.683	NS × NS	L × M	
				NPJ-194 × RW-85-59	4.837**	84.673	S × NS	M × L	
				Giriraj × PHR-2	4.453**	85.747	S × NS	M × M	
				NPJ-194 × SKJM-05	4.246**	77.973	S × S	M × M	
				NPJ-194 × Giriraj	3.691**	63.160	S × S	M × M	

** Significant at 1% levels of probability; H= high gca effect, M= medium gca effect and L= low gca effect; S= significant parent, NS= non significant parent

Heterosis measured as mean superiority of F_1 s over their better parent or mid parent and thus, it is rated to be an important parameter in such studies.

5.9.1 Estimation of heterosis (relative and heterobeltiosis) for seed yield and its attributing characters

The manifestation of heterosis was found in both positive and negative direction for all the morphological traits Table 4.28. The manifestation of heterosis was found in both positive and negative direction for days to 50% flowering. Out of 28 F_1 s, eight hybrids showed significant heterotic values over mid parent in which two crosses were significant negative heterosis while seven F_1 s showed negative significant heterosis over better parent. Significant negative heterosis was desirable for the selection of hybrids for a short duration. For evolving early flowering varieties the crosses exhibited negative significant heterosis over mid and better parent were desirable. Similar results on the importance of negative heterosis for days to 50% flowering has been reported by Singh *et al.*, (1983), Verma *et al.*, (1989), Hirve and Tiwari (1991) and Sheikh and Singh (2001).

Three crosses expressed positively significant over mid parent and one hybrid over better parent in case of primary branches per plant. These results are somewhat in accordance with the findings of Singh *et al.*, (1985), Lefort Buson *et al.*, (1987), Chauhan *et al.*, (2000), Singh *et al.*, (2003), Singh *et al.*, (2009) and Gami and Chauhan (2013). Relative heterosis for the number of secondary branches per plant over the mid parent ranged from -23.330 (DRMR-15-16 \times RNWR-09-3) to 52.780 (Giriraj \times PHR-2). Two crosses observed positive significant heterosis in order of merit whereas heterosis over the better parent ranged from -34.460 (DRMR-15-16 \times Giriraj) to 36.360 (Giriraj \times PHR-2). Here also two crosses revealed positively significant heterosis over better parent. In our study, these hybrids could be considered for further study to develop heterotic hybrids. Such types of findings were reported by Tyagi *et al.*, (2001), Singh *et al.*, (2003), Singh *et*

al., (2009), Gupta *et al.*, (2010), Vaghela *et al.*, (2011), Patel *et al.*, (2013), Dholu *et al.*, (2014).

The mid parent heterosis for seed per siliqua the crosses varied from -30.100 (NPJ-194 × PHR-2) to 24.790 (DRMR-15-16 × Giriraj). Four crosses were positively significant for heterosis over the mid parent whereas none of the crosses showed positively significant heterosis over the better parent. Thus, only four combinations having significant positive heterosis over mid parent could be considered for further evaluation in developing new parents. Heterosis of similar magnitude has been reported by Banga and Labana (1984), Singh *et al.*, (1985), Lefort Buson *et al.*, (1987), Rai (1993), Khulbe *et al.*, (1998), Chauhan *et al.*, (2000), Kumar *et al.*, (2002), Singh and Lallu (2004), Singh *et al.* (2007) and Verma *et al.*, (2011).

The highly significant and positive mid parent heterosis for height upto first fruiting branch was found in five hybrids while only two hybrids showed desirable significant heterosis over the better parent. Heterosis for plant height, three crosses showed negatively significant heterosis over the mid parent and eleven crosses showed significant and negative heterosis over better parent for this trait. Improvement of significant negative heterosis for this character, short stature plant avoiding lodging could be expected. The present study in agreement with Singh *et al.*, (1983), Verma *et al.*, (1989), Hirve and Tiwari (1991), Agarwal and Badwal (1998), Tyagi *et al.*, (2001), Sheikh and Singh (2001) and Vaghela *et al.*, (2011).

Production of yield by different variety might be due to the contribution of cumulative favourable effects of the crop characteristics. Four hybrids showed significant positive heterosis over mid- parent while two crosses were significantly positive over better parent for seed yield plant⁻¹ character. This was aligned with the findings of Singh *et al.*, (1983), Banga and Labana (1984), Singh *et al.*, (1985), Lefort Buson *et al.* (1987),

Verma *et al.*, (1989), Kumar *et al.*, (1990), Rai (1993), Patel and Sharma (1993), Rai and Singh (1994), Singh *et al.*, (1996), Khulbe *et al.*, (1998), Chauhan *et al.*, (2000), Tyagi *et al.*, (2001), Kumar *et al.* (2002), Singh *et al.*, (2003), Singh and Lallu (2004), Singh *et al.*, (2007) and Singh *et al.*, (2009), Gupta *et al.*, (2010), Vaghela *et al.*, (2011), Gami and Chauhan (2013) and Dholu *et al.*, (2014). Heterosis in 1000 seed weight, 15 hybrids out of 16 were significantly positive heterosis over mid parent while with negative value were 11 and out of which only 4 were negatively significant. Ten crosses expressed heterosis in positive direction (desirable) and ten crosses showed negative significant heterosis over better parent. The expression of heterosis of similar magnitude for this trait has also been reported by Singh *et al.*, (1985), Kumar *et al.*, (1990), Rai (1993), Agarwal and Badwal (1998), Khulbe *et al.*, (1998), Tyagi *et al.*, (2001), Singh and Lallu (2004), Gupta *et al.*, (2010), Vaghela *et al.*, (2011) and Saheed *et al.*, (2013). The estimates of heterosis revealed that, out of 28 F₁s, 13 crosses showed positively significant heterosis over mid parent while 5 crosses expressed heterosis over better parent in positive direction for oil content. These results are in general agreement with the findings of Lefort Buson *et al.*, (1987), Verma *et al.*, (1989), Kumar *et al.*, (1990), Rai (1993), Singh *et al.*, (1996), Khulbe *et al.*, (1998), Tyagi *et al.*, (2001), Singh *et al.*, (2007) and Singh *et al.*, (2009).

5.9.2 Estimation of heterosis (relative and heterobeltiosis) for physiological characters

Estimation of heterosis (relative and heterobeltiosis) for physiological characters was presented in Table 4.29. Eight crosses *viz.*, NPJ-194 × RW-85-59, RW-85-59 × RNWR-09-3, DRMR-15-16 × Kranti, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × Giriraj, Kranti × RNWR-09-3 and Giriraj × RNWR-09-3 revealed positive significant heterosis over mid parent and five crosses *viz.*, RW-85-59 × RNWR-09-3, SKJM-05 × Kranti, SKJM-05 × Giriraj and Giriraj × PHR-2 revealed positive significant heterosis over better parent for percentage of membrane stability index.

In the case of percentage of excised leaf water loss, 14 crosses revealed significant negative heterosis over mid parent and better parent heterosis. Moreover, five crosses revealed significant positive heterosis over mid parent and one cross showed significant positive heterosis over better parent for percentage of relative water content. Further, one cross showed negative significant heterosis over better and mid parent for canopy temperature depression.

Seven crosses out of 28 F₁s revealed significant positive heterosis over mid parent while six crosses showed significant and positive heterosis over better parent for proline content of the leaf. In case of chlorophyll a, six crosses revealed positive significant heterosis over mid parent and none of the crosses showed significant and positive heterosis over better parent. Five crosses exhibited significant positive heterosis over mid parent, whereas only two crosses namely NPJ-194 × PHR-2 and SKJM-05 × RNWR-09-3 showed significant positive heterosis over better parent. Eight crosses revealed positive significant heterosis over mid parent while four crosses showed significant negative heterosis over better parent for total chlorophyll.

5.9.3 Estimation of heterosis (relative and heterobeltiosis) for aphid related characters

Estimation of heterosis (relative and heterobeltiosis) for aphid related characters was presented in Table 4.30. Manifestation of heterosis was found in both positive and negative directions for water content of aphid probed twig. Out of 28 crosses, only two F₁s showed the heterosis over mid parent is highly significant and positive direction (desirable) while none of the crosses was found positive significant heterosis over better parent for water content of aphid probed twig. Kranti × Giriraj crosses revealed significant positive heterosis over mid parental values and none of the crosses exhibited positive significant heterosis over better parent for water content of aphid uninfested twig. Relative heterosis varied from -6.720 (SKJM-05 × RNWR-09-3) to 16.550 (DMR-15-16 × Kranti). NPJ-194

× RNWR-09-3 and SKJM-05 × RNWR-09-3 crosses recorded negative significant heterosis over mid parent while five crosses revealed negative significant heterosis over better parent for water content of aphid.

Percentage of water differential between aphid probed twig and aphid itself showed the relative heterosis (MP) ranged from -18.300 (DMR-15-16 × Kranti) to 10.000 (RNWR-09-3 × PHR-2). RNWR-09-3 × PHR-2 (10.000) cross showed significant positive heterosis over mid parental values were found to be promising for this character but none of the crosses revealed positive significant heterosis over better parent. In case of aphid count, out of 28 crosses combinations, eleven crosses showed the significant and negative heterosis over mid parent and fifteen crosses exhibited negative significant heterosis over better parent for aphid count. Further, the estimates of heterosis for penetration force over mid parent ranged from -19.080 (RW-85-59 × PHR-2) to 27.590 (NPJ-194 × RNWR-09-3). In all nine crosses showed significant and positive heterosis over mid parent and five crosses displayed significant and positive heterosis over better parent.

5.10 Ranking of three best hybrids and their parents based on specific combining ability and *per se* performance

An overall positioning of three best hybrids and their parents based on specific combining ability and *per se* performance for seed yield and its attributing characters, physiological and aphid related characters in Indian mustard (*Brassica juncea*) was done Table 4.39, four were seed yield and its attributing characters, three were physiological characters and the two were aphid related characters, according to rescaling index method recommended by Iyenger and Sudarshan (1982). From the rescaling index value, the cross Kranti × PHR-2 ranked the highest followed by NPJ-194 × SKJM-05 and RW-85-59 × SKJM-05, when the ranking of three best crosses and their parents was done based on sca for seed yield plant⁻¹.

In case of 1000 seed weight, crosses NPJ-194 × Kranti showed highest followed by RW-85-59 × DRMR-15-16 and NPJ-194 × RNWR-09-3; for siliquae plant⁻¹ three best crosses were NPJ-194 × RNWR-09-3 followed by RW-85-59 × Kranti and NPJ-194 × PHR-2. Similarly, for secondary branches plant⁻¹, NPJ-194 × PHR-2 showed highest followed by Giriraj × PHR-2 and RW-85-59 × Kranti. When the ranking of three best crosses and their parents was done for total chlorophyll NPJ-194 × Giriraj followed by NPJ-194 × PHR-2 and RW-85-59 × Kranti; for proline content of leaf, cross Kranti × Giriraj, SKJM-05 × PHR-2 and Kranti × Giriraj; for percentage of membrane stability index, NPJ-194 × RW-85-59 followed by SKJM-05 × Giriraj and RW-85-59 × RNWR-09-3; for aphid count DRMR-15-16 × PHR-2 followed RW-85-59 × RNWR-09-3 and RW-85-59 × Giriraj and for penetration force Kranti × Giriraj followed by RW-85-59 × DRMR-15-16 followed by NPJ-194 × RNWR-09-3 and Kranti × Giriraj.

5.11 Screening for aphid resistance

5.11.1 Analysis of variance of lab aphid count for both parents and crosses

Analysis of variance of lab aphid count for both parents and crosses are presented in Table 4.35 and Table 4.36. Analysis of variance of eight diverse parental genotypes of mustard revealed significant differences among the genotypes and five different times for all the three different numbers of aphid inoculated *i.e.* A1, A5 and A10. Similarly, analysis of variance among the crosses of mustard revealed significant differences among the genotypes and five different times for A5 numbers of aphid inoculated indicating there are significant variation among the parents, F₁s and different periods.

Table 4.39 Ranking of three best hybrids and their parents based on specific combining ability and *per se* performance for seed yield and its attributing characters, physiological characters and aphid related characters in Indian mustard (*Brassica juncea*)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		A		B		C		D	
		X	Rescaled Index value (A) = (Max-x)/(Max-Min)	x	Rescaled Index value (B) = (x-Min)/(Max-Min)	X	Rescaled Index value (C) = (x-Min)/(Max-Min)	x	Rescaled Index value (D) = (x-Min)/(Max-Min)
Hybrids	Seed yield plant⁻¹ (g)								
NPJ-194 × SKJM-05	0.065**	51.000	1.000	5.333	1.000	9.400	0.077	172.067	0.000
Kranti × PHR 2	0.061**	61.000	0.000	5.200	0.889	11.000	1.000	214.600	1.000
RW-85-59 × SKJM-05	0.044**	55.000	0.600	4.133	0.000	9.267	0.000	186.000	0.328
Parents									
NPJ-194	0.006	55.000	1.000	3.933	0.000	8.000	0.000	162.133	0.000
RW-85-59	0.000	55.000	1.000	4.200	0.138	8.600	0.250	192.000	0.178
SKJM-05	0.013*	62.667	0.410	5.000	1.000	9.000	0.417	215.600	0.319
Kranti	-0.011*	58.000	0.769	4.867	0.483	8.933	0.389	184.267	0.132
PHR 2	-0.005	68.000	0.000	5.867	1.000	10.400	1.000	329.800	1.000
Hybrids	1000 seed weight (g)								
RW-85-59 × DRMR-15-16	12.878**	56.000	0.000	5.200	0.750	9.867	0.000	186.000	0.005
NPJ-194 × RNWR-09-3	7.078**	56.000	0.000	4.800	0.000	9.867	0.000	185.600	0.000
NPJ-194 × Kranti	6.344**	54.667	1.000	5.333	1.000	15.507	1.000	268.390	1.000
Parents									
RW-85-59	2.458*	55.000	1.000	4.200	0.191	8.600	0.333	192.000	0.257
RNWR-09-3	1.558*	59.000	0.455	5.333	1.000	9.800	1.000	278.533	1.000
Kranti	1.292*	58.000	0.591	4.867	0.667	8.933	0.518	184.267	0.190
DRMR-15-16	-3.642*	62.333	0.000	5.067	0.810	8.933	0.518	225.333	1.000
NPJ-194	-3.275*	55.000	1.000	3.933	0.000	8.000	0.000	162.133	0.000
Hybrids	Siliquae plant⁻¹								
NPJ-194 × PHR-2	0.166**	57.000	0.000	4.467	0.287	9.267	0.471	173.733	0.000
NPJ-194 × RNWR-09-3	0.141**	56.000	0.333	4.800	1.000	9.867	1.000	185.600	2.580
RW-85-59 × Kranti	0.097**	54.000	1.000	4.333	0.000	8.733	0.000	178.333	0.388
Parents									
NPJ-194	0.023**	55.000	1.000	3.933	0.000	8.000	0.000	162.133	0.000
RW-85-59	0.013**	55.000	1.000	4.200	0.191	8.600	0.333	192.000	0.257
Kranti	0.030**	58.000	0.250	4.867	0.667	8.933	0.518	184.267	0.190
RNWR-09-3	-0.011**	59.000	0.000	5.333	1.000	9.800	1.000	278.533	1.000

		A		B		C		D	
		X	Rescaled Index value (A) = (Max-x)/(Max-Min)	x	Rescaled Index value (B) = (x-Min)/(Max-Min)	x	Rescaled Index value (C) = (x-Min)/(Max-Min)	x	Rescaled Index value (D) = (x-Min)/(Max-Min)
Secondary branches plant⁻¹									
Hybrids									
RW-85-59 × Kranti	4.250**	54.000	1.000	4.330	0.000	8.730	0.000	178.330	0.169
Giriraj × PHR-2	2.758**	62.000	0.000	5.270	1.000	8.870	0.259	201.000	1.000
NPJ-194 × PHR-2	1.551**	57.000	0.625	4.470	0.149	9.270	1.000	173.730	0.000
Parents									
NPJ-194	-0.491	55.000	1.000	3.930	0.000	8.000	0.200	162.130	0.000
RW-85-59	1.200**	55.000	1.000	4.200	0.139	8.600	0.400	192.000	0.178
Kranti	0.726*	58.000	0.769	4.870	0.485	8.930	0.510	184.270	0.132
Giriraj	-1.098**	60.000	0.615	4.130	0.103	7.400	0.000	167.330	0.031
PHR-2	0.009	68.000	0.000	5.870	1.000	10.400	1.000	329.800	1.000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; A= Days to 50% flowering, B= Primary branches plant⁻¹, C=Secondary branches plant⁻¹ and D= Siliquae plant

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based <i>per se</i> performance on									
		E		F		G		H		I	
		X	Rescaled Index	x	Rescaled Index	x	Rescaled Index	x	Rescaled Index	x	Rescaled Index
			value (E) =		value (F) =		value (G) =		value (H) =		value (I) =
			(x-Min)/(Max-Min)		(x-Min)/(Max-Min)		(Max-x)/(Max-Min)		(x-Min)/(Max-Min)		(x-Min)/(Max-Min)
Hybrids	Seed yield plant⁻¹ (g)										
NPJ-194 × SKJM-05	0.065**	13.000	0.375	86.933	1.000	185.200	1.000	5.733	1.000	6.420	0.015
Kranti × PHR 2	0.061**	12.200	0.000	64.933	0.000	234.733	0.000	4.527	0.000	8.633	1.000
RW-85-59 × SKJM-05	0.044**	14.333	1.000	70.400	0.249	188.800	0.927	5.313	0.652	6.387	0.000
Parents											
NPJ-194	0.006	11.733	0.830	82.467	0.648	153.000	1.000	4.587	0.000	5.270	0.000
RW-85-59	0.000	12.267	1.000	85.733	1.000	167.800	0.820	4.970	0.248	6.127	0.329
SKJM-05	0.013*	12.067	0.936	82.733	0.676	196.067	0.476	6.133	1.000	7.877	1.000
Kranti	-0.011*	12.267	1.000	84.267	0.842	196.933	0.465	4.953	0.237	7.720	0.940
PHR 2	-0.005	9.133	0.000	76.467	0.000	235.133	0.000	5.270	0.442	6.670	0.537
Hybrids	1000 seed weight (g)										
RW-85-59 × DRMR-15-16	12.878**	12.533	0.000	88.667	0.132	187.933	0.000	5.507	1.000	2.220	0.000
NPJ-194 × RNWR-09-3	7.078**	13.733	0.415	81.800	0.000	186.133	1.000	4.587	0.176	2.850	0.521
NPJ-194 × Kranti	6.344**	15.427	1.000	133.750	1.000	186.167	0.981	4.390	0.000	3.430	1.000
Parents											
RW-85-59	2.458*	12.267	0.668	85.733	0.466	167.800	0.762	4.970	1.000	3.173	0.758
RNWR-09-3	1.558*	12.400	0.834	77.533	0.000	215.200	0.000	4.517	0.388	3.557	1.000
Kranti	1.292*	12.267	0.668	84.267	0.383	196.933	0.294	4.953	0.977	3.450	0.933
DRMR-15-16	-3.642*	12.533	1.000	95.133	1.000	192.733	0.361	4.230	0.000	2.000	0.017
NPJ-194	-3.275*	11.733	0.000	82.467	0.280	153.000	1.000	4.587	0.482	1.973	0.000
Hybrids	Siliquae plant⁻¹										
NPJ-194 × PHR-2		13.233	0.000	71.200	0.000	198.467	0.000	5.090	1.000	5.970	0.000
NPJ-194 × RNWR-09-3	0.141**	13.733	0.882	81.800	0.864	186.133	1.000	4.587	0.257	8.383	1.000
RW-85-59 × Kranti	0.097**	13.800	1.000	83.467	1.000	196.667	1.000	4.413	0.000	6.437	0.194
Parents											
NPJ-194	0.023**	11.733	0.000	82.467	1.511	153.000	1.000	4.587	0.155	5.270	0.000
RW-85-59	0.013**	12.267	1.000	85.733	1.000	167.800	0.762	4.970	1.000	6.127	0.295
Kranti	0.030**	12.267	0.801	84.267	0.821	196.933	0.294	4.953	0.962	7.720	0.843
RNWR-09-3	-0.011**	12.400	1.249	77.533	0.000	215.200	0.000	4.517	0.000	8.177	1.000

		E		F		G		H		I		
		X	Rescaled Index value (E) = (x-Min)/(Max-Min)	x	Rescaled Index value (F) = (x-Min)/(Max-Min)	x	Rescaled Index value (G) = (Max-x)/(Max-Min)	x	Rescaled Index value (H) = (x-Min)/(Max-Min)	x	Rescaled Index value (I) = (x-Min)/(Max-Min)	
Hybrids		Secondary branches plant⁻¹										
RW-85-59 × Kranti	4.250**	13.800	1.000	83.470	1.000	196.670	1.000	4.410	0.000	6.440	0.155	
Giriraj × PHR-2	2.758**	11.270	0.000	75.870	0.381	214.670	0.000	4.600	0.279	9.000	1.000	
NPJ-194 × PHR-2	1.551**	13.230	0.775	71.200	0.000	198.470	0.900	5.090	1.000	5.970	0.000	
Parents												
NPJ-194	-0.491	11.730	0.672	82.470	0.722	153.000	1.000	4.590	0.000	5.270	0.000	
RW-85-59	1.200**	12.270	0.811	85.730	1.000	167.800	0.820	4.970	0.373	6.130	0.351	
Kranti	0.726*	12.270	0.811	84.270	0.876	196.930	0.465	4.950	0.353	7.720	1.000	
Giriraj	-1.098**	13.000	1.000	74.000	0.000	194.130	0.499	5.610	1.000	5.450	0.073	
PHR-2	0.009	9.130	0.000	76.470	0.211	235.130	0.000	5.270	0.667	6.670	0.571	

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; E=Seed siliqua⁻¹, F= Height up to first fruiting branch (cm), G= Plant height (cm), H= Seed yield plant⁻¹(g) and I= 1000 Seed weight (g)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance									
		J		K		L		M		N	
		x	Rescaled Index value (J) = (x - Min)/(Max - Min)	x	Rescaled Index value (K) = (x - Min)/(Max - Min)	x	Rescaled Index value (L) = (Max - x)/(Max - Min)	x	Rescaled Index value (M) = (x - Min)/(Max - Min)	x	Rescaled Index value (N) = (Max - x)/(Max - Min)
Hybrids	Seed yield plant⁻¹ (g)										
NPJ-194 × SKJM-05	0.065**	26.923	1.000	65.117	0.276	36.663	0.000	82.460	0.000	1.820	0.000
Kranti × PHR 2	0.061**	19.573	0.000	64.103	0.000	23.933	1.000	90.887	1.000	1.797	0.767
RW-85-59 × SKJM-05	0.044**	25.443	0.799	67.783	1.000	32.527	0.325	85.210	0.326	1.790	1.000
Parents											
NPJ-194	0.006	60.027	1.000	74.133	1.000	29.030	0.280	86.350	1.000	1.747	0.441
RW-85-59	0.000	31.383	0.337	73.957	0.992	26.163	0.422	85.563	0.892	1.910	0.000
SKJM-05	0.013*	27.840	0.254	58.767	0.272	14.460	1.000	84.407	0.733	1.540	1.000
Kranti	-0.011*	40.980	0.559	63.820	0.511	34.693	0.000	79.060	0.000	1.887	0.062
PHR 2	-0.005	16.853	0.000	53.030	0.000	33.377	0.065	80.820	0.241	1.623	0.776
	1000 seed weight (g)										
Hybrids											
RW-85-59 × DRMR-15-16	12.878**	24.963	0.127	72.540	0.750	21.567	1.000	79.010	0.000	1.613	1.000
NPJ-194 × RNWR-09-3	7.078**	24.307	0.000	74.500	1.000	21.690	1.000	84.417	0.490	1.990	0.000
NPJ-194 × Kranti	6.344**	29.493	7.899	66.673	0.000	31.120	0.000	90.037	1.000	1.800	0.504
Parents											
RW-85-59	2.458*	31.383	0.000	73.957	0.983	26.163	0.278	85.563	0.109	1.910	0.279
RNWR-09-3	1.558*	32.963	0.155	69.237	0.525	18.713	1.000	85.293	0.855	1.793	0.796
Kranti	1.292*	40.980	0.943	63.820	0.000	34.693	0.000	79.060	0.000	1.887	0.381
DRMR-15-16	-3.642*	41.560	1.060	63.887	0.006	18.810	0.994	84.770	0.783	1.973	0.000
NPJ-194	-3.275*	40.027	0.849	74.133	1.000	29.030	0.354	86.350	1.000	1.747	1.000
Hybrids	Siliqueae plant⁻¹										
NPJ-194 × PHR-2	0.166**	58.107	1.000	68.093	0.000	26.257	0.000	89.790	1.000	1.813	1.000
NPJ-194 × RNWR-09-3	0.141**	24.307	0.000	74.500	0.977	21.690	0.421	84.417	0.000	1.990	0.000
RW-85-59 × Kranti	0.097**	24.780	0.014	74.650	1.000	15.403	1.000	88.067	0.679	1.950	0.226
Parents											
NPJ-194	0.023**	60.027	1.000	74.133	1.000	29.030	0.354	86.350	1.000	1.747	1.000
RW-85-59	0.013**	31.383	0.000	73.957	0.983	26.163	0.534	85.563	0.892	1.910	0.000
Kranti	0.030**	40.980	0.335	63.820	0.000	34.693	0.000	79.060	0.000	1.887	0.141
RNWR-09-3	-0.011**	32.963	0.055	69.237	0.525	18.713	1.000	85.293	0.855	1.793	0.718

Discussion

		J		K		L		M		N	
		x	Rescaled Index value (J) = (x- Min)/(Max- Min)	x	Rescaled Index value (K) = (x-Min)/(Max- Min)	x	Rescaled Index value (L) = (Max-x)/(Max- Min)	x	Rescaled Index value (M) = (x- Min)/(Max- Min)	x	Rescaled Index value (N) = (Max- x)/(Max- Min)
Secondary branches plant⁻¹											
Hybrids											
RW-85-59 × Kranti	4.250**	24.78	0.000	74.650	1.000	15.400	1.000	88.070	0.000	1.950	0.067
Giriraj × PHR-2	2.758**	42.02	0.517	69.840	0.267	16.780	0.873	88.920	0.494	1.960	0.000
NPJ-194 × PHR-2	1.551**	58.11	1.000	68.090	0.000	26.260	0.000	89.790	1.000	1.810	1.000
Parents											
NPJ-194	-0.491	60.03	1.000	74.130	1.000	29.030	0.304	86.350	1.000	1.750	0.594
RW-85-59	1.200**	31.38	0.336	73.960	0.992	26.160	0.459	85.560	0.892	1.910	0.094
Kranti	0.726*	40.98	0.559	63.820	0.511	34.690	0.000	79.060	0.000	1.890	0.156
Giriraj	-1.098**	21.09	0.098	68.960	0.755	16.100	1.000	84.630	0.764	1.940	0.000
PHR-2	0.009	16.85	0.000	53.030	0.000	33.380	0.070	80.820	0.241	1.620	1.000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; J= Oil content (%), K= Percentage of membrane stability index (%), L= Percentage of excised leaf water loss (%), M= Percentage of relative water content (%) and N= Canopy temperature depression (°C)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		O		P		Q		R	
		x	Rescaled Index value (O) = (x-Min)/(Max-Min)	X	Rescaled Index value (P) = (x-Min)/(Max-Min)	x	Rescaled Index value (Q) = (x-Min)/(Max-Min)	x	Rescaled Index value (R) = (x-Min)/(Max-Min)
Hybrids	Seed yield plant⁻¹(g)								
NPJ-194 × SKJM-05	0.065**	5.670	1.000	0.820	0.435	0.230	0.213	1.050	0.272
Kranti × PHR 2	0.061**	5.403	0.562	1.180	1.000	0.267	1.000	1.513	1.000
RW-85-59 × SKJM-05	0.044**	5.060	0.000	0.543	0.000	0.220	0.000	0.877	0.000
Parents									
NPJ-194	0.006	5.450	0.525	1.097	0.785	0.330	0.461	1.093	0.082
RW-85-59	0.000	5.123	0.310	1.040	0.667	0.303	0.354	1.343	0.731
SKJM-05	0.013*	5.963	0.864	0.720	0.000	0.213	0.000	1.033	0.000
Kranti	-0.011*	4.653	0.000	0.737	0.035	0.307	0.370	1.360	0.446
PHR 2	-0.005	6.170	1.000	1.200	1.000	0.467	1.000	1.767	1.000
Hybrids	1000 seed weight (g)								
RW-85-59 × DRMR-15-16	12.878**	5.403	0.848	0.790	0.000	0.183	0.000	0.973	0.000
NPJ-194 × RNWR-09-3	7.078**	4.823	0.000	0.837	0.587	0.233	0.481	1.183	0.520
NPJ-194 × Kranti	6.344**	5.507	1.000	0.870	1.000	0.287	1.000	1.377	1.000
Parents									
RW-85-59	2.458*	5.123	0.331	1.040	0.842	0.303	0.000	1.343	0.600
RNWR-09-3	1.558*	4.600	0.000	1.143	1.128	0.387	1.000	1.510	1.000
Kranti	1.292*	4.653	0.034	0.737	0.000	0.307	0.048	1.360	0.640
DRMR-15-16	-3.642*	6.180	1.000	0.943	0.572	0.327	1.000	1.320	0.544
NPJ-194	-3.275*	5.450	0.538	1.097	1.000	0.330	0.321	1.093	0.000
Hybrids	Siliquae plant⁻¹								
NPJ-194 × PHR-2	0.166**	4.953	1.000	0.867	0.164	0.367	1.000	1.457	1.000
NPJ-194 × RNWR-09-3	0.141**	4.823	0.784	0.837	0.000	0.233	0.000	1.183	0.377
RW-85-59 × Kranti	0.097**	4.350	0.000	1.020	1.000	0.237	0.030	1.017	0.000
Parents									
NPJ-194	0.023**	5.450	1.000	1.097	0.887	0.330	0.321	1.093	0.000
RW-85-59	0.013**	5.123	0.615	1.040	0.747	0.303	0.000	1.343	0.600
Kranti	0.030**	4.653	0.062	0.737	0.000	0.307	0.048	1.360	0.640
RNWR-09-3	-0.011**	4.600	0.000	1.143	1.000	0.387	1.000	1.510	1.000

		O	P	Q	R					
		x	Rescaled Index value (O) = (x-Min)/(Max-Min)	X	Rescaled Index value (P) = (x-Min)/(Max-Min)	x	Rescaled Index value (Q) = (x-Min)/(Max-Min)	x	Rescaled Index value (R) = (x-Min)/(Max-Min)	
Hybrids		Secondary branches plant⁻¹								
RW-85-59 × Kranti	4.250**	4.350	0.000	1.020	1.000	0.240	0.000	1.020	0.000	
Giriraj × PHR-2	2.758**	6.020	1.000	0.900	0.200	0.320	0.615	1.370	0.795	
NPJ-194 × PHR-2	1.551**	4.950	0.359	0.870	0.000	0.370	1.000	1.460	1.000	
Parents										
NPJ-194	-0.491	5.450	0.526	1.100	0.923	0.330	0.176	1.090	0.000	
RW-85-59	1.200**	5.120	0.309	1.040	0.769	0.300	0.000	1.340	0.368	
Kranti	0.726*	4.650	0.000	0.740	0.000	0.310	0.059	1.360	0.397	
Giriraj	-1.098**	5.350	0.461	1.130	1.000	0.440	0.824	1.580	0.721	
PHR-2	0.009	6.170	1.000	1.200	1.179	0.470	1.000	1.770	1.000	

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; O= Proline content of leaf (mg/gm), P= Chlorophyll a (mg/gm), Q= Chlorophyll b (mg/gm) and R= Total chlorophyll (mg/gm)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		S		T		U		V	
		x	Rescaled Index value (S) = (x-Min)/(Max-Min)	x	Rescaled Index value (T) = (x-Min)/(Max-Min)	x	Rescaled Index value (U) = (Max-x)/(Max-Min)	x	Rescaled Index value (V) = (x-Min)/(Max-Min)
Hybrids	Seed yield plant⁻¹ (g)								
NPJ-194 × SKJM-05	0.065**	74.740	0.802	75.663	1.000	32.613	1.000	42.127	1.000
Kranti × PHR 2	0.061**	75.563	1.000	74.200	0.459	37.783	0.570	37.783	0.717
RW-85-59 × SKJM-05	0.044**	71.397	0.000	72.957	0.000	44.623	0.000	26.773	0.000
Parents									
NPJ-194	0.006	80.110	0.938	73.540	0.554	59.130	0.000	20.983	0.000
RW-85-59	0.000	71.990	0.000	67.530	0.000	48.310	0.884	23.680	0.211
SKJM-05	0.013*	78.267	0.725	73.120	0.515	51.180	0.650	27.090	0.478
Kranti	-0.011*	80.453	0.978	78.380	1.000	53.430	0.466	27.023	0.473
PHR 2	-0.005	80.647	1.000	75.990	0.780	46.893	1.000	33.760	2.092
Hybrids	1000 seed weight (g)								
RW-85-59 × DRMR-15-16	12.878**	73.297	0.000	77.150	0.972	19.527	1.000	53.767	1.000
NPJ-194 × RNWR-09-3	7.078**	77.437	1.000	73.137	0.028	42.150	0.175	35.287	0.325
NPJ-194 × Kranti	6.344**	76.243	0.712	73.023	0.000	46.960	0.000	29.283	0.000
Parents									
RW-85-59	2.458*	71.990	0.000	67.530	0.000	48.310	0.541	23.680	0.161
RNWR-09-3	1.558*	76.853	0.575	76.110	0.791	39.127	1.000	37.723	1.000
Kranti	1.292*	80.453	1.000	78.380	1.000	53.430	0.285	27.023	0.361
DRMR-15-16	-3.642*	78.873	0.813	75.703	0.753	48.127	1.000	30.753	0.584
NPJ-194	-3.275*	80.110	0.959	73.540	0.554	59.130	0.000	20.983	0.000
Hybrids	Siliquae plant⁻¹								
NPJ-194 × PHR-2	0.166**	74.563	0.000	75.737	1.000	28.160	1.000	46.400	1.000
NPJ-194 × RNWR-09-3	0.141**	77.437	1.000	73.137	0.311	42.150	0.580	35.287	0.652
RW-85-59 × Kranti	0.097**	76.003	1.004	71.963	0.000	61.497	1.000	14.507	0.000
Parents									
NPJ-194	0.023**	80.110	0.959	73.540	0.554	59.130	0.000	20.983	0.000
RW-85-59	0.013**	71.990	0.000	67.530	0.000	48.310	0.541	23.680	0.161
Kranti	0.030**	80.453	1.000	78.380	1.000	53.430	1.000	27.023	0.361
RNWR-09-3	-0.011**	76.853	0.575	76.110	0.791	39.127	1.000	37.723	1.000

		S		T		U		V	
		X	Rescaled Index value (S) = (x-Min)/(Max-Min)	x	Rescaled Index value (T) = (x-Min)/(Max-Min)	x	Rescaled Index value (U) = (Max-x)/(Max-Min)	x	Rescaled Index value (V) = (x-Min)/(Max-Min)
Hybrids	Secondary branches per plant								
RW-85-59 × Kranti		76.000	0.434	71.960	0.000	61.500	0.000	14.510	0.000
Giriraj × PHR-2	2.758**	77.880	1.000	75.110	0.833	53.920	0.227	23.950	0.296
NPJ-194 × PHR-2	1.551**	74.560	0.000	75.740	1.000	28.160	1.000	46.400	1.000
Parents									
NPJ-194	-0.491	80.110	0.938	73.540	0.554	59.130	0.000	20.980	0.000
RW-85-59	1.200**	71.990	0.000	67.530	0.000	48.310	0.489	23.680	0.152
Kranti	0.726*	80.450	0.977	78.380	1.000	53.430	0.258	27.020	0.341
Giriraj	-1.098**	75.700	0.428	69.110	0.146	37.010	1.000	38.690	1.000
PHR-2	0.009	80.650	1.000	75.990	0.780	46.890	0.553	33.760	0.722

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; S= Water content of aphid probed twig (%), T= Water content of aphid unfested twig (%), U= Water content of aphid (%) and V= Percentage of water differential between aphid probed twig and aphid itself (%)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance					
		W X	Rescaled Index value (W) = (Max-x)/(Max-Min)	X	Rescaled Index value (X) = (x-Min)/(Max-Min)	Total of the rescaled values (Y) L=(A+B+C+D+E+F +G+H+I+J+K+L+M +N+O+P+Q+R+S+T +U+V+W+X)	Ranking on the basis of the total rescaled value*
Hybrids	Seed yield plant⁻¹ (g)						
NPJ-194 × SKJM-05	0.065**	28.667	1.000	77.973	0.216	13.681	2
Kranti × PHR 2	0.061**	90.000	1.000	75.683	0.000	13.964	1
RW-85-59 × SKJM-05	0.044**	47.333	0.696	86.263	1.000	8.901	3
Parents							
NPJ-194	0.006	108.443	0.000	76.370	0.469	11.011	5
RW-85-59	0.000	45.110	1.000	85.430	0.895	12.657	3
SKJM-05	0.013*	61.667	0.739	87.653	1.000	14.464	1
Kranti	-0.011*	75.223	0.525	75.397	0.423	11.103	4
PHR 2	-0.005	87.667	0.328	66.417	0.000	14.261	2
Hybrids	1000 seed weight (g)						
RW-85-59 × DRMR-15-16	12.878**	42.557	1.000	82.307	1.000	10.584	2
NPJ-194 × RNWR-09-3	7.078**	89.223	0.000	79.763	0.813	8.531	3
NPJ-194 × Kranti	6.344**	66.973	0.477	68.670	0.000	22.573	1
Parents							
RW-85-59	2.458*	45.110	1.000	85.430	0.065	10.621	3
RNWR-09-3	1.558*	111.333	0.000	96.293	1.000	16.501	1
Kranti	1.292*	75.223	0.545	75.397	1.000	11.456	4
DRMR-15-16	-3.642*	59.000	0.790	86.123	0.000	14.608	2
NPJ-194	-3.275*	108.443	0.044	76.370	0.909	11.292	5
Hybrids	Siliqueae plant⁻¹						
NPJ-194 × PHR-2	0.166**	66.553	0.414	65.103	0.000	11.335	3
NPJ-194 × RNWR-09-3	0.141**	89.223	0.000	79.763	1.000	15.019	1
RW-85-59 × Kranti	0.097**	34.443	1.000	75.310	0.696	12.231	2
Parents							
NPJ-194	0.023**	108.443	1.000	76.370	0.047	12.788	2
RW-85-59	0.013**	45.110	1.000	85.430	0.480	12.390	3
Kranti	0.030**	75.223	0.545	75.397	0.000	10.479	4
RNWR-09-3	-0.011**	111.333	1.000	96.293	1.000	16.768	1

		W		X			
		X	Rescaled Index value (W) = (Max-x)/(Max-Min)	X	Rescaled Index value (X) = (x-Min)/(Max-Min)	Total of the rescaled values (Y) Y=(A+B+C+D+E+F +G+H+I+J+K+L+M +N+O+P+Q+R+S+T +U+V+W+X)	Ranking on the basis of the total rescaled value*
Hybrids	Secondary branches plant⁻¹						
RW-85-59 × Kranti	4.250**	34.440	1.000	75.310	0.494	9.319	3
Giriraj × PHR-2	2.758**	61.670	0.152	85.750	1.000	12.190	2
NPJ-194 × PHR-2	1.551**	66.550	0.000	65.100	0.000	12.808	1
Parents							
NPJ-194	-0.491	108.440	0.004	76.370	1.000	11.613	4
RW-85-59	1.200**	45.110	1.000	85.430	1.000	11.932	3
Kranti	0.726*	75.220	0.526	75.380	0.471	10.656	5
Giriraj	-1.098**	108.670	1.000	81.570	0.797	13.315	2
PHR-2	0.009	87.670	0.330	66.420	0.000	13.325	1

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; W=Aphid count and X= Penetration force (Kpascal)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		A		B		C		D	
		x	Rescaled Index value (A) = (Max-x)/(Max-Min)	X	Rescaled Index value (B) = (x-Min)/(Max-Min)	x	Rescaled Index value (C) = (x-Min)/(Max-Min)	X	Rescaled Index value (D) = (x-Min)/(Max-Min)
Hybrids	Total chlorophyll (mg/gm)								
NPJ -194 × PHR 2	0.310**	57.000	0.000	4.467	0.502	9.267	0.728	173.732	0.000
RW-85-59 × Kranti	0.318**	54.000	1.000	4.333	0.000	8.733	0.000	178.332	0.401
NPJ-194 × Giriraj	0.292**	56.000	0.333	4.600	1.000	9.467	1.000	185.202	1.000
Parents									
NPJ -194	0.127**	55.000	1.000	3.933	0.000	8.000	0.391	162.131	0.000
RW-85-59	-0.067	55.000	1.000	4.200	0.286	8.600	0.783	192.001	1.000
Kranti	-0.077*	58.000	0.400	4.867	1.000	8.933	1.000	184.262	0.741
Giriraj	-0.043	60.000	0.000	4.133	0.214	7.400	0.000	167.332	0.174
	Proline content of leaf (mg/gm)								
Hybrids									
Kranti × Giriraj	1.171**	57.333	0.444	3.667	0.000	6.333	0.000	128.802	0.000
SKJM-05 × PHR 2	1.111**	61.333	0.000	5.867	0.971	11.133	1.000	195.862	1.000
NPJ-194 × DRMR -15-16	0.844**	52.333	1.000	5.933	1.000	10.667	0.903	158.202	0.438
Parents									
NPJ- 194	0.077	55.000	1.000	3.933	0.000	8.000	0.200	162.131	0.000
DRMR-15-16	-0.092*	62.33	0.436	5.067	0.586	8.933	0.511	225.331	0.377
SKJM-05	-0.102*	62.66	0.411	5.000	0.552	9.000	1.000	215.601	0.319
Kranti	-0.229**	58.00	0.769	4.867	0.483	8.933	0.511	184.262	0.132
Giriraj	0.023	60.00	0.615	4.133	0.103	7.400	0.000	167.332	0.031
PHR 2	0.179**	68.00	0.000	5.867	1.000	10.400	1.000	329.801	1.000
	Percentage of membrane stability index (%)								
Hybrids									
NPJ-194 × RW-85-59	0.043	51.000	1.000	5.533	1.000	11.600	1.000	257.201	1.000
RW-85-59 × RNWR-09-3	0.037	52.333	0.826	4.267	0.000	7.667	0.017	178.867	0.000
SKJM-05 × Giriraj	0.034	58.667	0.000	4.800	0.421	7.600	0.000	229.533	0.647
Parents									
NPJ-194	-0.006*	55.000	1.000	3.933	0.000	8.000	0.250	162.133	0.000
RW-85-59	-0.004	55.000	1.000	4.200	0.191	8.600	0.500	192.000	0.257
RNWR-09-3	-0.001	59.000	0.478	5.333	1.000	9.800	1.000	278.533	1.000
SKJM-05	-0.007**	62.667	0.000	5.000	0.762	9.000	0.667	215.600	0.459
Giriraj	0.008**	60.000	0.348	4.133	0.143	7.400	0.000	167.333	0.045

** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; A= Days to 50% flowering, B= Primary branches plant⁻¹, C=Secondary branches plant⁻¹ and D= Siliquae plant⁻¹

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects		Rank based on <i>per se</i> performance														
			E			F			G			H			I		
	x	Rescaled Index value (E) = (x-Min)/(Max-Min)	x	Rescaled Index value (F) = (x-Min)/(Max-Min)	x	Rescaled Index value (G) = (Max-x)/(Max-Min)	x	Rescaled Index value (H) = (x-Min)/(Max-Min)	X	Rescaled Index value (I) = (x-Min)/(Max-Min)							
Hybrids		Total chlorophyll (mg/gm)															
NPJ -194 × PHR 2	0.310**	13.233	0.000	71.200	0.000	198.461	0.000	5.090	1.000	5.970	0.000						
RW-85-59 × Kranti	0.318**	13.800	0.586	83.467	0.836	196.661	0.796	4.413	0.000	6.437	0.267						
NPJ-194 × Giriraj	0.292**	14.200	1.000	85.867	1.000	196.201	1.000	4.587	0.257	7.717	1.000						
Parents																	
NPJ -194	0.127**	11.733	0.000	82.467	0.722	153.002	1.000	4.587	0.000	5.270	0.000						
RW-85-59	-0.067	12.267	0.421	85.733	1.000	167.802	0.663	4.970	0.375	6.127	0.350						
Kranti	-0.077*	12.267	0.421	84.267	0.875	196.931	0.000	4.953	0.359	7.720	1.000						
Giriraj	-0.043	13.000	1.000	74.000	0.000	194.131	0.064	5.607	1.000	5.453	0.115						
Hybrids		Proline content of leaf (mg/gm)															
Kranti × Giriraj	1.171**	11.400	0.000	65.733	0.039	185.061	0.994	6.330	1.000	5.130	0.000						
SKJM-05 × PHR 2	1.111**	13.133	0.722	63.867	0.000	207.131	0.000	5.530	0.240	8.437	1.000						
NPJ-194 × DRMR -15-16	0.844**	13.800	1.000	111.664	1.000	184.931	1.000	5.277	0.000	6.873	0.527						
Parents																	
NPJ- 194	0.077	11.733	0.672	82.467	0.454	153.002	1.000	4.587	0.259	5.270	0.000						
DRMR-15-16	-0.092*	12.533	0.879	95.133	1.000	192.732	0.516	4.230	0.000	8.437	1.000						
SKJM-05	-0.102*	12.067	0.759	82.733	0.413	196.062	0.476	6.133	1.000	7.877	0.823						
Kranti	-0.229**	12.267	0.810	84.267	0.486	196.931	0.465	4.953	0.380	7.720	0.774						
Giriraj	0.023	13.000	1.137	74.000	0.000	194.131	0.499	5.607	0.724	5.453	0.058						
PHR 2	0.179**	9.133	0.000	76.467	0.117	235.132	0.000	5.270	0.547	6.670	0.442						
Hybrids		Percentage of membrane stability index (%)															
NPJ-194 × RW-85-59	0.043	12.433	0.000	104.66	1.000	175.933	1.000	4.830	1.000	8.657	1.000						
RW-85-59 × RNWR-09-3	0.037	14.800	1.000	83.200	0.000	195.400	0.347	4.610	0.426	7.850	0.000						
SKJM-05 × Giriraj	0.034	14.600	0.916	84.867	0.078	205.733	1.000	4.447	0.000	8.500	0.805						
Parents																	
NPJ-194	-0.006*	11.733	0.000	82.467	0.722	153.000	1.000	4.587	0.043	5.270	0.000						
RW-85-59	-0.004	12.267	0.421	85.733	1.000	167.800	1.000	4.970	0.280	6.127	0.295						
RNWR-09-3	-0.001	12.400	0.526	77.533	0.301	215.200	0.000	4.517	0.000	8.177	1.000						
SKJM-05	-0.007**	12.067	0.264	82.733	0.744	196.067	0.308	6.133	1.000	7.877	0.897						
Giriraj	0.008**	13.000	1.000	74.000	0.000	194.133	0.339	5.607	0.675	5.453	0.063						

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; E=Seed siliqua⁻¹, F= Height up to first fruiting branch (cm), G= Plant height (cm), H= Seed yield plant⁻¹(g) and I= 1000 Seed weight (g)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects		Rank based on <i>per se</i> performance								
	J	K	L	M	N	Rescaled Index value (J) = (x-Min)/(Max-Min)	Rescaled Index value (K) = (x-Min)/(Max-Min)	Rescaled Index value (L) = (Max-x)/(Max-Min)	Rescaled Index value (M) = (x-Min)/(Max-Min)	Rescaled Index value (N) = (Max-x)/(Max-Min)	
Total chlorophyll (mg/gm)											
Hybrids											
NPJ -194 × PHR 2		58.107	1.000	68.093	0.066	26.257	0.000	89.790	1.000	1.813	1.000
RW-85-59 × Kranti	0.318**	24.780	0.000	74.650	1.000	15.403	1.000	88.067	0.567	1.950	0.481
NPJ-194 × Giriraj	0.292**	31.297	0.196	67.633	0.000	21.950	0.397	85.810	0.000	2.077	0.000
Parents											
NPJ -194	0.127**	60.027	1.000	74.133	1.000	29.030	0.305	86.350	1.000	1.747	1.000
RW-85-59	-0.067	31.383	0.264	73.957	0.983	26.163	0.459	85.563	0.892	1.910	0.168
Kranti	-0.077*	40.980	0.511	63.820	0.000	34.693	0.000	79.060	0.000	1.887	0.286
Giriraj	-0.043	21.090	0.000	68.963	0.499	16.103	1.000	84.633	0.764	1.943	0.000
Proline content of leaf (mg/gm)											
Hybrids											
Kranti × Giriraj	1.171**	22.533	0.855	68.433	0.571	25.793	0.000	88.970	1.000	2.003	0.000
SKJM-05 × PHR 2	1.111**	16.873	0.000	74.390	1.000	16.993	1.000	87.673	0.828	1.793	0.409
NPJ-194 × DRMR -15-16	0.844**	23.493	1.000	60.513	0.000	21.593	1.000	81.450	0.000	1.490	1.000
Parents											
NPJ- 194	0.077	60.027	1.000	74.133	1.000	29.030	0.389	86.350	1.000	1.747	
DRMR-15-16	-0.092*	54.893	0.881	63.887	0.514	18.810	0.785	84.770	0.783	1.973	0.522
SKJM-05	-0.102*	27.840	0.254	58.767	0.272	14.460	1.000	84.407	0.733	1.540	0.000
Kranti	-0.229**	40.980	0.559	63.820	0.511	34.693	0.000	79.060	0.000	1.887	1.000
Giriraj	0.023	21.090	0.098	68.963	0.755	16.103	0.919	84.633	0.764	1.943	0.199
PHR 2	0.179**	16.853	0.000	53.030	0.000	33.377	0.065	80.820	0.241	1.623	0.069
Hybrids											
Percentage of membrane stability index (%)											
NPJ-194 × RW-85-59	0.043	18.333	0.000	63.103	0.336	25.080	1.000	84.127	0.883	1.727	1.000
RW-85-59 × RNWR-09-3	0.037	20.333	0.875	61.627	0.000	49.960	0.000	82.950	0.000	1.817	0.000
SKJM-05 × Giriraj	0.034	22.620	1.000	66.020	1.000	34.747	0.611	84.283	1.000	1.803	0.156
Parents											
NPJ-194	-0.006*	60.027	1.000	74.133	1.000	29.030	0.000	86.350	1.000	1.747	0.486
RW-85-59	-0.004	31.383	0.264	73.957	0.989	26.163	0.197	85.563	0.595	1.910	0.082
RNWR-09-3	-0.001	32.963	0.305	69.237	0.681	18.713	0.708	85.293	0.456	1.793	0.372
SKJM-05	-0.007**	27.840	0.173	58.767	0.000	14.460	1.000	84.407	0.000	1.540	1.000
Giriraj	0.008**	21.090	0.000	68.963	1.972	16.103	0.887	84.633	0.116	1.943	1.000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; J= Oil content (%), K= Percentage of membrane stability index (%), L= Percentage of excised leaf water loss (%), M= Percentage of relative water content (%) and N= Canopy temperature depression (°C)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects		Rank based on <i>per se</i> performance						
			P		Q		R		
	O		x		X		x		
		Rescaled Index value (O) = (x-Min)/(Max-Min)		Rescaled Index value (JP) = (x-Min)/(Max-Min)		Rescaled Index value (Q) = (x-Min)/(Max-Min)		Rescaled Index value (R) = (x-Min)/(Max-Min)	
Hybrids	Total chlorophyll (mg/gm)								
NPJ -194 × PHR 2	0.310**	4.953	0.989	0.867	0.000	0.367	1.000	1.457	1.000
RW-85-59 × Kranti	0.318**	4.350	0.000	1.020	1.000	0.237	0.000	1.017	0.000
NPJ-194 × Giriraj	0.292**	4.960	1.000	1.003	0.889	0.260	0.003	1.133	0.264
Parents									
NPJ -194	0.127**	5.450	0.000	1.097	0.916	0.330	0.201	1.093	0.000
RW-85-59	-0.067	5.123	0.590	1.040	0.771	0.303	0.000	1.343	0.513
Kranti	-0.077*	4.653	1.000	0.737	0.000	0.307	0.030	1.360	0.548
Giriraj	-0.043	5.347	0.871	1.130	1.000	0.437	1.000	1.580	1.000
Hybrids	Proline content of leaf (mg/gm)								
Kranti × Giriraj	1.171**	5.120	0.311	0.823	0.000	0.277	1.000	1.067	0.550
SKJM-05 × PHR 2	1.111**	4.900	0.000	0.970	0.980	0.277	1.000	1.147	1.000
NPJ-194 × DRMR -15-16	0.844**	5.607	1.000	0.973	1.000	0.217	0.000	1.023	0.000
Parents									
NPJ- 194	0.077	5.450	0.522	1.097	0.785	0.330	0.461	1.093	0.082
DRMR-15-16	-0.092*	6.180	1.000	0.943	0.465	0.327	0.449	1.320	0.391
SKJM-05	-0.102*	5.963	0.858	0.720	0.000	0.213	0.000	1.033	0.000
Kranti	-0.229**	4.653	0.000	0.737	0.035	0.307	0.370	1.360	0.446
Giriraj	0.023	5.347	0.454	1.130	0.854	0.437	0.882	1.580	0.745
PHR 2	0.179**	6.170	0.993	1.200	1.000	0.467	1.000	1.767	1.000
Hybrids	Percentage of membrane stability index (%)								
NPJ-194 × RW-85-59	0.043	6.110	0.824	0.433	0.000	0.177	0.000	0.793	0.000
RW-85-59 × RNWR-09-3	0.037	5.140	0.000	0.580	0.264	0.437	1.000	1.430	1.000
SKJM-05 × Giriraj	0.034	6.317	1.000	0.990	1.000	0.243	0.340	0.943	0.235
Parents									
NPJ-194	-0.006*	5.450	0.624	1.097	0.891	0.330	0.522	1.093	0.110
RW-85-59	-0.004	5.123	0.384	1.040	0.757	0.303	0.402	1.343	0.567
RNWR-09-3	-0.001	4.600	0.000	1.143	1.000	0.387	0.777	1.510	0.872
SKJM-05	-0.007**	5.963	1.000	0.720	0.000	0.213	0.000	1.033	0.000
Giriraj	0.008**	5.347	0.548	1.130	0.969	0.437	1.000	1.580	1.000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; O= Proline content of leaf (mg/gm), P= Chlorophyll a (mg/gm), Q= Chlorophyll b (mg/gm) and R=Total chlorophyll (mg/gm)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		S		T		U		V	
		X	Rescaled Index value (S) = (x-Min)/(Max-Min)	x	Rescaled Index value (T) = (x-Min)/(Max-Min)	x	Rescaled Index value (U) = (Max-x)/(Max-Min)	x	Rescaled Index value (V) = (x-Min)/(Max-Min)
Hybrids									
Total chlorophyll (mg/gm)									
NPJ-194 × PHR 2	0.310**	74.563	0.000	75.737	1.000	28.160	1.000	46.400	1.000
RW-85-59 × Kranti	0.318**	76.003	0.261	71.963	0.454	61.497	0.038	14.507	0.000
NPJ-194 × Giriraj	0.292**	80.087	1.000	68.820	0.000	62.803	0.000	17.283	0.087
Parents									
NPJ-194	0.127**	80.110	0.959	73.540	0.554	59.130	0.000	20.983	0.000
RW-85-59	-0.067	71.990	0.000	67.530	0.000	48.310	0.489	23.680	0.152
Kranti	-0.077*	80.453	1.000	78.380	1.000	53.430	0.258	27.023	0.341
Giriraj	-0.043	75.700	0.438	69.107	0.145	37.007	1.000	38.693	1.000
Proline content of leaf (mg/gm)									
Hybrids									
Kranti × Giriraj	1.171**	74.407	0.182	71.450	0.503	27.127	1.000	47.280	1.000
SKJM-05 × PHR 2	1.111**	74.387	0.000	68.150	0.000	35.503	0.426	38.883	0.421
NPJ-194 × DRMR-15-16	0.844**	74.497	1.000	74.713	1.000	41.72	1.000	32.773	0.000
Parents									
NPJ-194	0.077	80.110	0.891	73.540	0.478	59.130	1.000	20.983	0.000
DRMR-15-16	-0.092*	78.873	0.641	75.703	0.711	48.127	0.497	30.753	0.552
SKJM-05	-0.102*	78.267	0.519	73.120	0.433	51.180	1.000	27.090	0.345
Kranti	-0.229**	80.453	0.961	78.380	1.000	53.430	0.258	27.023	0.341
Giriraj	0.023	75.700	0.000	69.107	0.000	37.007	1.000	38.693	1.000
PHR 2	0.179**	80.647	1.000	75.990	0.742	46.893	0.553	33.760	0.721
Percentage of membrane stability index (%)									
Hybrids									
NPJ-194 × RW-85-59	0.043	76.987	0.802	71.433	0.000	48.093	0.000	28.897	0.000
RW-85-59 × RNWR-09-3	0.037	74.477	0.000	73.007	0.140	28.810	1.000	45.670	1.000
SKJM-05 × Giriraj	0.034	77.607	1.000	82.677	1.000	37.990	0.524	39.617	0.639
Parents									
NPJ-194	-0.006*	80.110	1.000	73.540	0.700	59.130	1.000	20.983	0.000
RW-85-59	-0.004	71.990	0.000	67.530	0.000	48.310	0.489	23.680	0.152
RNWR-09-3	-0.001	76.853	0.599	76.110	1.000	39.127	0.904	37.723	0.945
SKJM-05	-0.007**	78.262	0.772	73.120	0.652	51.180	0.359	27.090	0.345
Giriraj	0.008**	75.700	0.457	69.107	0.527	37.007	1.000	38.693	1.000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; S= Water content of aphid probed twig (%), T= Water content of aphid unfested twig (%), U= Water content of aphid (%) and V= Percentage of water differential between aphid probed twig and aphid itself (%)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects		Rank based on <i>per se</i> performance				
	W	X	Rescaled Index value (W) = (Max-x)/(Max-Min)	x	Rescaled Index value (X) = (x-Min)/(Max-Min)	Total of the rescaled values (Y) Y=(A+B+C+D+E+F+G+H+I+J+K+L+M+N+O+P+Q+R+S+T+U+V+W+X)	Ranking on the basis of the total rescaled value*
Hybrids	Total chlorophyll (mg/gm)						
NPJ -194 × PHR 2	0.310**	66.553	0.000	65.103	0.160	11.443	2
RW-85-59 × Kranti	0.318**	34.443	1.000	75.310	1.000	10.688	3
NPJ-194 × Giriraj	0.292**	37.447	1.000	63.160	0.000	12.425	1
Parents							
NPJ -194	0.127**	108.443	1.000	76.370	11.146	11.146	4
RW-85-59	-0.067	45.110	1.000	85.430	13.160	13.160	1
Kranti	-0.077*	75.223	0.526	75.397	11.296	11.296	3
Giriraj	-0.043	108.667	0.000	81.567	11.899	11.899	2
Hybrids	Proline content of leaf (mg/gm)						
Kranti × Giriraj	1.171**	77.777	0.983	68.670	0.000	10.433	3
SKJM-05 × PHR 2	1.111**	76.557	1.000	76.717	0.334	13.332	2
NPJ-194 × DRMR -15-16	0.844**	150.441	0.000	92.747	1.000	15.868	1
Parents							
NPJ- 194	0.077	108.443	0.005	76.370	0.469	12.188	4
DRMR-15-16	-0.092*	59.000	1.000	86.123	0.928	14.904	1
SKJM-05	-0.102*	61.667	1.000	87.653	1.000	14.166	2
Kranti	-0.229**	75.223	0.673	75.397	0.423	10.586	6
Giriraj	0.023	108.667	0.000	81.567	0.713	11.423	5
PHR 2	0.179**	87.667	0.423	66.417	0.000	12.653	3
Hybrids	Percentage of membrane stability index (%)						
NPJ-194 × RW-85-59	0.043	32.000	1.000	84.673	0.000	13.845	1
RW-85-59 × RNWR-09-3	0.037	51.113	0.690	94.710	1.000	9.583	3
SKJM-05 × Giriraj	0.034	93.557	0.000	85.583	0.091	13.463	2
Parents							
NPJ-194	-0.006*	108.443	0.000	76.370	0.000	11.349	4
RW-85-59	-0.004	45.110	1.000	85.430	0.455	11.275	5
RNWR-09-3	-0.001	111.333	0.000	96.293	1.000	14.926	1
SKJM-05	-0.007**	61.667	1.000	87.653	0.566	11.968	3
Giriraj	0.008**	108.667	0.040	81.567	0.261	13.390	2

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; W=Aphid count and X= Penetration force (Kpasacal)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects		Rank based on <i>per se</i> performance						
	A		B		C		D		
	x	Rescaled Index value (A) = (Max-x)/(Max-Min)	x	Rescaled Index value (B) = (x-Min)/(Max-Min)	x	Rescaled Index value (C) = (x-Min)/(Max-Min)	x	Rescaled Index value (D) = (x-Min)/(Max-Min)	
Hybrids	Aphid count								
RW-85-59 × Giriraj	-0.211**	55.667	0.6296	4.067	0.0000	6.467	0.0000	183.267	1.0000
RW-85-59 × RNWR-09-3	-0.209**	52.333	1.0000	4.267	0.3752	7.667	0.8186	178.867	0.7885
DRMR-15-16 × PHR 2	-0.113**	61.333	0.0000	4.600	1.0000	7.933	1.0000	162.467	0.0000
Parents									
RW-85-59	-0.396	55.000	1.0000	4.200	0.0558	8.600	0.5000	192.000	0.2218
RNWR-09-3	1.352*	59.000	0.4545	5.333	1.0000	9.800	1.0000	278.533	1.0000
DRMR-15-16	4.682**	62.333	0.0000	5.067	0.7783	8.933	0.6388	225.333	0.5216
Giriraj	3.114**	60.000	0.3182	4.133	0.0000	7.400	0.0000	167.333	0.0000
	Penetration force (g/mm)								
Hybrids									
Kranti × Giriraj	14.153**	57.333	0.0000	3.667	0.0000	6.333	0.0000	128.800	0.0000
NPJ-194 × RNWR-09-3	13.952**	56.000	1.0000	4.800	0.7391	9.867	1.0000	185.600	0.9930
RW-85-59 × DRMR-15-16	10.403**	56.000	1.0000	5.200	1.0000	9.867	1.0000	186.000	1.0000
Parents									
NPJ-194	2.716**	55.000	1.0000	3.933	0.0000	8.000	0.2500	162.133	0.0000
RW-85-59	-0.396	55.000	1.0000	4.200	0.1907	8.600	0.5000	192.000	0.2566
DRMR-15-16	4.682**	62.333	1.0000	5.067	0.8100	8.933	0.6388	225.333	0.5430
Kranti	-3.729**	58.000	0.5909	4.867	0.6671	8.933	0.6388	184.267	0.1902
Giriraj	3.114**	60.000	0.3182	4.133	0.1429	7.400	0.0000	167.333	0.0447
RNWR-09-3	1.352*	59.000	0.4545	5.333	1.0000	9.800	1.0000	278.533	1.0000

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; A= Days to 50% flowering, B= Primary branches plant⁻¹, C=Secondary branches plant⁻¹ and D= Siliquae plant⁻¹

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance									
		E		F		G		H		I	
		x	Rescaled Index value (E) = (x-Min)/(Max-Min)	x	Rescaled Index value (F) = (x-Min)/(Max-Min)	x	Rescaled Index value (G) = (Max-x)/(Max-Min)	x	Rescaled Index value (H) = (x-Min)/(Max-Min)	x	Rescaled Index value (I) = (x-Min)/(Max-Min)
Hybrids	Aphid count										
RW-85-59 × Giriraj	-0.211**	14.933	1.0000	85.067	1.0000	215.133	0.0000	4.653	1.0000	6.657	0.1010
RW-85-59 × RNWR-09-3	-0.209**	14.800	0.8464	83.200	0.8323	195.400	1.0000	4.610	0.8097	7.850	1.0000
DRMR-15-16 × PHR 2	-0.113**	14.067	0.0000	73.933	0.0000	213.933	0.0608	4.427	0.0000	6.523	0.0000
Parents											
RW-85-59	-0.396	12.267	0.0000	85.733	0.5552	167.800	1.0000	4.970	0.5374	6.127	0.2259
RNWR-09-3	1.352*	12.400	0.1814	77.533	0.1672	215.200	0.0000	4.517	0.2084	8.177	0.9129
DRMR-15-16	4.682**	12.533	0.3629	95.133	1.0000	192.733	1.0000	4.230	0.0000	8.437	1.0000
Giriraj	3.114**	13.000	1.0000	74.000	0.0000	194.133	1.0000	5.607	1.0000	5.453	0.0000
	Penetration force (g/mm)										
Hybrids											
Kranti × Giriraj	14.153**	11.400	0.0000	65.733	0.0000	185.067	1.0000	6.330	1.0000	5.130	0.0000
NPJ-194 × RNWR-09-3	13.952**	13.733	1.0000	81.800	0.7006	186.133	0.6281	4.587	0.0000	8.383	1.0000
RW-85-59 × DRMR-15-16	10.403**	12.533	0.4856	88.667	1.0000	187.933	0.0000	5.507	0.5278	7.827	0.0000
Parents											
NPJ-194	2.716**	11.733	0.0000	82.467	0.4007	153.000	1.0000	4.587	0.2593	5.270	0.0000
RW-85-59	-0.396	12.267	0.4215	85.733	0.5552	167.800	0.7621	4.970	0.5374	6.127	0.2706
DRMR-15-16	4.682**	12.533	0.6314	95.133	1.0000	192.733	0.3612	4.230	0.0000	8.437	1.0000
Kranti	-3.729**	12.267	0.4215	84.267	0.4858	196.933	0.2937	4.953	0.5251	7.720	0.7736
Giriraj	3.114**	13.000	1.0000	74.000	0.0000	194.133	0.3387	5.607	1.0000	5.453	0.0578
RNWR-09-3	1.352*	12.400	0.5264	77.533	0.1672	215.200	0.0000	4.517	0.2084	8.177	0.9179

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; E=Seed siliqua⁻¹, F= Height up to first fruiting branch (cm), G= Plant height (cm), H= Seed yield plant⁻¹(g) and I= 1000 Seed weight (g)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance									
		J		K		L		M		N	
		x	Rescaled Index value (J) = (x-Min)/(Max-Min)	x	Rescaled Index value (K) = (x-Min)/(Max-Min)	x	Rescaled Index value (L) = (Max-x)/(Max-Min)	x	Rescaled Index value (M) = (x-Min)/(Max-Min)	x	Rescaled Index value (N) = (Max-x)/(Max-Min)
Hybrids	Aphid count										
RW-85-59 × Giriraj	-0.211**	26.123	0.8344	74.563	1.0000	34.943	0.4497	87.790	0.9597	1.963	0.0000
RW-85-59 × RNWR-09-3	-0.209**	20.333	1.0000	61.627	0.0000	49.960	0.0000	82.950	0.0000	1.817	1.0000
DRMR-15-16 × PHR 2	-0.113**	55.287	0.0000	68.500	0.5313	16.570	1.0000	87.993	1.0000	1.897	0.4521
Parents											
RW-85-59	-0.396	31.383	0.6955	73.957	1.0000	26.163	0.0000	85.563	1.0000	1.910	0.3500
RNWR-09-3	1.352*	32.963	0.6488	69.237	0.5313	18.713	0.7406	85.293	0.7097	1.793	1.0000
DRMR-15-16	4.682**	54.893	0.0000	63.887	0.0000	18.810	0.7309	84.770	0.1473	1.973	0.0000
Giriraj	3.114**	21.090	1.0000	68.963	1.0164	16.103	1.0000	84.633	0.0000	1.943	0.1667
	Penetration force (g/mm)										
Hybrids											
Kranti × Giriraj	14.153**	22.533	1.0000	68.433	0.0000	25.793	0.0000	88.970	1.0000	2.003	0.0000
NPJ-194 × RNWR-09-3	13.952**	24.307	0.2700	74.500	1.0000	21.690	0.9709	84.417	0.5429	1.990	0.0333
RW-85-59 × DRMR-15-16	10.403**	24.963	0.0000	72.540	0.6769	21.567	1.0000	79.010	0.0000	1.613	1.0000
Parents											
NPJ-194	2.716**	60.027	0.0000	74.133	1.0000	29.030	0.3046	86.350	1.0000	1.747	1.0000
RW-85-59	-0.396	31.383	0.7356	73.957	0.9829	26.163	0.4588	85.563	0.8920	1.910	0.2788
DRMR-15-16	4.682**	54.893	0.1319	63.887	0.0065	18.810	0.8544	84.770	0.7833	1.973	0.0000
Kranti	-3.729**	40.980	0.4892	63.820	0.0000	34.693	0.0000	79.060	0.0000	1.887	0.3805
Giriraj	3.114**	21.090	1.0000	68.963	0.4987	16.103	1.0000	84.633	0.7645	1.943	0.1327
RNWR-09-3	1.352*	32.963	0.6951	69.237	0.5253	18.713	0.8596	85.293	0.8550	1.793	0.7965

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; J= Oil content (%), K= Percentage of membrane stability index (%), L= Percentage of excised leaf water loss (%), M= Percentage of relative water content (%) and N= Canopy temperature depression (°C)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		O		P		Q		R	
		x	Rescaled Index value (O) = (x-Min)/(Max-Min)	x	Rescaled Index value (P) = (x-Min)/(Max-Min)	x	Rescaled Index value (Q) = (x-Min)/(Max-Min)	x	Rescaled Index value (R) = (x-Min)/(Max-Min)
Hybrids	Aphid count								
RW-85-59 × Giriraj	-0.211**	5.130	0.0000	0.907	0.3944	0.240	0.0000	1.047	0.0000
RW-85-59 × RNWR-09-3	-0.209**	5.140	0.0071	0.580	1.0000	0.437	1.0000	1.430	1.0000
DRMR-15-16 × PHR 2	-0.113**	6.540	1.0000	1.120	0.0000	0.360	0.6091	1.390	0.8958
Parents									
RW-85-59	-0.396	5.123	0.3310	1.040	0.5150	0.303	0.0000	1.343	0.0882
RNWR-09-3	1.352*	4.600	0.0000	1.143	0.0000	0.387	0.6269	1.510	0.7308
DRMR-15-16	4.682**	6.180	1.0000	0.943	1.0000	0.327	0.1791	1.320	0.0000
Giriraj	3.114**	5.347	0.4728	1.130	0.0650	0.437	1.0000	1.580	1.0000
	Penetration force (g/mm)								
Hybrids									
Kranti × Giriraj	14.153**	5.120	0.5121	0.823	0.2979	0.277	1.0000	1.067	0.4476
NPJ-194 × RNWR-09-3	13.952**	4.823	0.0000	0.837	0.0000	0.233	0.5319	1.183	1.0000
RW-85-59 × DRMR-15-16	10.403**	5.403	1.0000	0.790	1.0000	0.183	0.0000	0.973	0.0000
Parents									
NPJ-194	2.716**	5.450	0.5380	1.097	0.1133	0.330	0.2015	1.093	0.0000
RW-85-59	-0.396	5.123	0.3310	1.040	0.2537	0.303	0.0000	1.343	0.5135
DRMR-15-16	4.682**	6.180	1.0000	0.943	0.4926	0.327	0.1791	1.320	0.4664
Kranti	-3.729**	4.653	0.0335	0.737	1.0000	0.307	0.0299	1.360	0.5482
Giriraj	3.114**	5.347	0.4728	1.130	0.0320	0.437	1.0000	1.580	1.0000
RNWR-09-3	1.352*	4.600	0.0000	1.143	0.0000	0.387	0.6269	1.510	0.8563

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; O= Proline content of leaf (mg/gm), P= Chlorophyll a (mg/gm), Q= Chlorophyll b (mg/gm) and R=Total chlorophyll (mg/gm)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance							
		S		T		U		V	
		x	Rescaled Index value (S) = (x-Min)/(Max-Min)	x	Rescaled Index value (T) = (x-Min)/(Max-Min)	x	Rescaled Index value (U) = (Max-x)/(Max-Min)	x	Rescaled Index value (V) = (x-Min)/(Max-Min)
Hybrids	Aphid count								
RW-85-59 × Giriraj	4.250**	75.963	0.5463	78.767	1.0000	29.690	0.0000	46.267	0.1067
RW-85-59 × RNWR-09-3	-0.209**	74.477	0.0000	73.007	0.0000	28.810	0.2340	45.670	0.0000
DRMR-15-16 × PHR 2	-0.113**	77.197	1.0000	75.143	0.3708	25.930	1.0000	51.267	9.3752
Parents									
RW-85-59	-0.396	71.990	0.0000	67.530	0.0000	48.310	0.0000	23.680	0.0000
RNWR-09-3	1.352*	76.853	0.7065	76.110	1.0000	39.127	0.8124	37.723	0.9354
DRMR-15-16	4.682**	78.873	1.0000	75.703	0.9526	48.127	0.0162	30.753	0.4711
Giriraj	3.114**	75.700	0.5390	69.107	0.1838	37.007	1.0000	38.693	1.0000
	Penetration force (g/mm)								
Hybrids									
Kranti × Giriraj	14.153**	74.407	0.2681	71.450	0.0000	27.127	0.6641	47.280	0.6490
NPJ-194 × RNWR-09-3	13.952**	77.437	1.0000	73.137	0.2960	42.150	0.0000	35.287	0.0000
RW-85-59 × DRMR-15-16	10.403**	73.297	0.0000	77.150	1.0000	19.527	1.0000	53.767	1.0000
Parents									
NPJ-194	2.716**	80.110	0.9595	73.540	0.5539	59.130	0.0000	20.983	0.0000
RW-85-59	-0.396	71.990	0.0000	67.530	0.0000	48.310	0.4891	23.680	0.1523
DRMR-15-16	4.682**	78.873	0.8133	75.703	0.7533	48.127	0.4974	30.753	0.5836
Kranti	-3.729**	80.453	1.0000	78.380	1.0000	53.430	0.2577	27.023	0.3608
Giriraj	3.114**	75.700	0.4384	69.107	0.1453	37.007	1.0000	38.693	1.0579
RNWR-09-3	1.352*	76.853	0.5746	76.110	0.7908	39.127	0.9042	37.723	0.9452

Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; S= Water content of aphid probed twig (%), T= Water content of aphid uninfested twig (%), U= Water content of aphid (%) and V= Percentage of water differential between aphid probed twig and aphid itself (%)

Table 4.39 (Continued)

Hybrids/Parents	SCA/GCA effects	Rank based on <i>per se</i> performance					Total of the rescaled values (Y) Y=(A+B+C+D+E+F+G+H+I+J+K+L+ M+N+O+P+Q+R+S+T+U+V+W+X)	Ranking on the basis of the total rescaled value*
		W	Rescaled Index value (W) = (Max-x)/(Max-Min)		X	Rescaled Index value (X) = (x-Min)/(Max-Min)		
		x		x				
Hybrids	Aphid count							
RW-85-59 × Giriraj	-0.211**	73.557	0.0000	76.367	0.3156	10.3374	3	
RW-85-59 × RNWR-09-3	-0.209**	51.113	0.8595	94.710	1.0000	14.5713	2	
DRMR-15-16 × PHR 2	-0.113**	47.443	1.0000	67.907	0.0000	20.2951	1	
Parents								
RW-85-59	-0.396	45.110	1.0000	85.430	0.2623	9.3381	4	
RNWR-09-3	1.352*	111.333	1.0000	96.293	1.0000	15.3668	1	
DRMR-15-16	4.682**	59.000	0.7903	86.123	0.3094	11.8984	2	
Giriraj	3.114**	108.667	0.0403	81.567	0.0000	11.8021	3	
	Penetration force (Kpascal)							
Hybrids								
Kranti × Giriraj	14.153**	77.777	0.2453	68.670	0.0000	8.0839	3	
NPJ-194 × RNWR-09-3	13.952**	89.223	0.0000	79.763	0.8134	13.5191	2	
RW-85-59 × DRMR-15-16	10.403**	42.557	1.0000	82.307	1.0000	15.6904	1	
Parents								
NPJ-194	2.716**	108.443	0.0436	76.370	0.0466	8.6709	5	
RW-85-59	-0.396	45.110	1.0000	85.430	0.5036	11.0854	4	
DRMR-15-16	4.682**	59.000	0.7903	86.123	0.5133	13.8496	2	
Kranti	-3.729**	75.223	0.5453	75.397	0.0000	10.2316	5	
Giriraj	3.114**	108.667	0.0403	81.567	0.2953	11.7801	3	
RNWR-09-3	1.352*	111.333	0.0000	96.293	1.0000	14.7039	1	

*, ** Significant at 5% and 1% levels of probability, respectively; Values in superscript indicate respective ranks within the group; W=Aphid count and X= Penetration force (Kpascal)

In Fig 8, when one aphid was inoculated per plant, group 'a' showed the highest mean value and the genotype fall in this group was Kranti while the group 'c' showed the lowest mean value and the genotype lie in this group was RW-85-59. Similarly, when five aphids were inoculated per plant, group 'a' again had the high mean value, comprising the genotype SKJM-05 and the low mean was observed in group 'f'. The genotype falls in-group 'f' was Giriraj. In case when ten aphids were inoculated per plant. The genotype Kranti fall in-group 'a' having the high meanwhile the genotype RNWR-09-3 lie in-group 'd' consisting of the low mean. In the same way, when five aphids were inoculated per plant of all the crosses, 18 groups were formed. Group 'a' again had the high mean value, comprising the cross NPJ-194 × SKJM-05 and the low mean was observed in group 'f' having the cross RW-85-59 × Giriraj. This indicated that genotype RW-85-59, Giriraj and RNWR-09-3 were resistant for A1, A5 and A10 aphid number respectively while the genotype Kranti and SKJM-05 were considered susceptible for A1, A10 and A5 respectively. In crosses, genotype RW-85-59 × Giriraj was resistant and the susceptible cross was NPJ-194 × SKJM-05.

Fig 9 represents the regression analysis of aphid growth in parents and F₁. Genotype RW-85-59 was resistant while genotype Kranti was susceptible for A1 aphid ;for A5 aphid genotype Giriraj was resistant whereas genotype SKJM-05 was susceptible and for A10 genotype Kranti was susceptible and lower slope for genotype RNWR-09-3 considered as resistant. In case of F₁s, A5 displayed cross RW-85-59 × Giriraj was resistant while higher slope for NPJ-194 × SKJM-05 indicating susceptible cross. Similar reports observed by Pawar *et al.*, (2009), Sarwar (2013) and Chaudhary and Patel (2016).

5.11.2 Association between field aphid count and its influencing characters

Association between field aphid count and its influencing characters presented in Table 3.38. It was observed that chlorophyll a, chlorophyll b and total chlorophyll were instrumental in increase the aphid attack as evidenced by their positive association with field aphid count which was due to the fact the higher chlorophyll content was increasing the water content of the plant and thereby making it more succulent and attractive to the aphids. This was further confirmed by the positive association of chlorophyll a, chlorophyll b and total chlorophyll with the water content of aphid probed twig. The variation in the chlorophyll content had no impact on penetration force which made the mustard plants an easy prey for aphids.

5.11.3 Direct and indirect effects of field aphid count and its influencing characters

The direct and indirect effects of field aphid count and its influencing characters presented in Table 4.39. The correlation coefficient between chlorophyll a and field aphid count (0.529) was found to be lower than the direct effect of chlorophyll a (0.548) which showed that there were certain characters like chlorophyll b and penetration force which were reducing the direct effect of chlorophyll a. The correlation coefficient between chlorophyll b and field aphid count (0.309) was found to be much higher than the direct effect of chlorophyll b (-0.207). However, the indirect effect of chlorophyll b on field aphid count *via* chlorophyll a (0.256) and total chlorophyll (0.297) was quite high.

The correlation between total chlorophyll and field aphid count (0.399) was partially higher than the direct effect of total chlorophyll (0.338) indicating that the indirect effect of total chlorophyll on field aphid count via other characters like chlorophyll a (0.294) and chlorophyll b (-0.182) and penetration force (-0.051) were cancelling the effects of one over the other. An interesting fact was that the penetration force despite having the highest direct

effect (0.403) did not have a significant correlation with field aphid count. This was due to the fact that the indirect effect of the penetration force on field aphid count *via* chlorophyll a (-0.141) and total chlorophyll (-0.043) had a negative impact on the direct effect on penetration force thereby, reducing it substantially and causing the correlation between penetration force and field aphid count to be non-significant.



**SUMMARY AND
CONCLUSION**

The current study entitled “Studies on combining ability for seed yield along with its attributing characters and aphid resistance in mustard [*Brassica juncea* (L.) Czern & Coss.]” was carried out with 8 parent and 28 F₁s developed from half diallel mating (excluding reciprocals). Seed yield and its attributing characters taken into consideration for diversity study were plant height, height up to first fruiting branch, days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliquae⁻¹, 1000 seed weight, aphid count, penetration force and seed yield plant⁻¹. Data was recorded for ten yield attributing characters namely days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹, seed siliquae⁻¹, height up to first fruiting branch, plant height, seed yield plant⁻¹, 1000 seed weight and oil content; eight physiological characters namely percentage of membrane stability index, percentage of excised leaf water loss, percentage of relative water content, canopy temperature depression, proline content, chlorophyll a, chlorophyll b and total chlorophyll and six aphid related characters *viz.*, water content of aphid probed twig, water content of aphid uninfested twig, water content of aphid itself, percentage of water differential between aphid probed twig and aphid itself, aphid count and penetration force were recorded.

Summary

Analysis of variance of 71 genotypes of mustard revealed significant differences among the genotypes for all the eleven characters studied *viz*; Plant height (cm), height up to first fruiting branch (cm), days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹ (cm), seeds siliqua⁻¹, 1000 seed weight (g), penetration force (kpascal), aphid count (% incidence) and seed yield plant⁻¹ (g).

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low (<10%) for plant height and seeds per siliqua. Moderate GCV and PCV (10-25%) for days to 50% flowering, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae per plant and 1000 seed weight. High GCV and PCV (>25%) for height up to first fruiting branch, aphid count and penetration force. Seed yield plant⁻¹ had moderate GCV and high PCV.

The characters height up to first fruiting branch, primary branches plant⁻¹, secondary branches plant⁻¹, siliquae plant⁻¹ and 1000 seed weight expressed high heritability along with high genetic advance as percentage of the mean.

In genotypic correlation analysis, it was found that the significant positive correlation of seed yield was observed with secondary branches plant⁻¹ and siliquae plant⁻¹. The siliquae plant⁻¹ had a positive association with seed yield plant⁻¹.

Correlation of height up to first fruiting branch with seed yield plant⁻¹ was negative and its direct effect was also negative. Primary branches plant⁻¹ had a negative correlation with seed yield plant⁻¹ although its direct effect was positive and low. Association of siliquae plant⁻¹ with seed yield plant⁻¹ was positive and its direct effect was also high and positive. The highest positive direct effect on yield was of penetration force followed by days to 50% flowering. Secondary branches plant⁻¹ had a positive correlation with seed yield plant⁻¹ and its direct effect was also positive. The highest direct negative effect was of the height up to first fruiting branch followed by aphid count.

It showed that based on all the eleven characters including aphid count, the genotype PRD-2013-9 was the best and had the highest rescaled index value and ranked first followed by the genotypes RH-0923 (rank-2) which was closely followed by another genotype RGN-389 (rank 3).

Based on D^2 values seventy-one genotypes of mustard were grouped into seven clusters. A total of thirty-one genotypes were grouped into cluster I; twenty-one genotypes in cluster IV; twelve genotypes in cluster V; two genotypes in cluster II; two genotypes in cluster VI and one genotype in cluster VII. The maximum intra cluster distance was recorded in cluster VI followed by cluster V, cluster IV, cluster I, cluster III, cluster II and cluster VII. The maximum inter-cluster distance was between cluster VII and V followed by cluster VII and VI, cluster VII and IV and cluster VII and I. The highest cluster mean value for plant height was recorded in case of cluster VII, for height up to first fruiting branch recorded in case of cluster VII, days to 50 % flowering in case of cluster VII, primary branches plant⁻¹ highest cluster mean value was recorded in case of cluster VII, secondary branches plant⁻¹ in case of cluster III, siliquae plant⁻¹ in case of cluster I, seeds per siliqua in case of cluster VI, 1000-seed weight in case of culture VI, aphid count in case of cluster V, penetration force in case of cluster V, seed yield plant⁻¹ in case of cluster III. The percentage contribution of plant height has been maximum to divergence followed by 1000 seed weight as well as penetration force, aphid count, seed yield per plant and days to 50 % flowering.

The results of the present study showed significant differences among the treatments, parental lines and crosses for all the seed yield and its attributing characters. Days to 50% flowering, plant height, 1000 seed weight and oil content exhibited significant variance for parents vs crosses. The analysis of variance of treatment and parents and crosses revealed significant differences for all eight physiological characters except total chlorophyll for parents and crosses. Parents vs crosses showed significance for percentage of excised leaf water loss, chlorophyll a, chlorophyll b, total chlorophyll. The mean square for six aphid related characters indicated that significant differences were recorded

among the treatments and parents and crosses for all the characters. Significant differences were recorded among the parent Vs crosses for all the characters studied.

The mean sum of squares due to GCA and SCA was significant for all the ten seed yield and its attributing characters except seed siliqua⁻¹ in case of SCA. The results for combining ability analysis revealed that the mean square for GCA and SCA was significant for all the physiological characters. It was observed that the mean square of both GCA and SCA were significant for all six aphid related characters. Significance of mean square suggested that additive genetic variance is responsible and non-additive variance is also involved in the inheritance of the attributes.

The contribution of SCA component of variance (σ^2_{sca}) was higher than the GCA component of variance (σ^2_{gca}) indicated the control of the non-additive type of gene action. The GCA and SCA variance ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was less than 1 showed the greater association of non-additive gene action for these characters. The mean degree of dominance ($\sigma^2_{sca}/\sigma^2_{gca}$)^{0.5} was found to be greater than 1 which indicated that the involvement of over dominance for these characters. The estimates of variance due to dominance (σ^2_D) were higher than corresponding additive genetic variance (σ^2_A) for all the seed yield and its attributing characters which showed that there was a higher role of dominant component of variance as compared to the additive component of variance in the expression of character under investigation.

The ratio of additive variance to dominance variance (σ^2_A/σ^2_D) was lower than unity for all the characters except days to 50% flowering which means, the majority of characters were governed by dominance gene action. The estimates of predictability ratio ($\sigma^2_A/\sigma^2_A+\sigma^2_D$) were higher than 0.05 for all the characters under study recommending, the preponderance of additive genetic effects in the characters.

The magnitude of SCA variance (σ^2_{sca}) was higher than GCA variance (σ^2_{gca}). The GCA and SCA variance ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was less than 1. The value of the degree of dominance was low ($\sigma^2_{sca}/\sigma^2_{gca}$)^{0.5} for all the characters. The dominance of genetic variation (σ^2_D) was higher than the additive genetic variance (σ^2_A). The ratio of additive variance to dominance variance (σ^2_A/σ^2_D) was lower than unity. The predictability ratio ($\sigma^2_A/\sigma^2_A+\sigma^2_D$) was higher than 0.50 for all the characters.

The SCA component of variance (σ^2_{sca}) was higher than GCA variance (σ^2_{gca}). The GCA and SCA variance ratio ($\sigma^2_{gca}/\sigma^2_{sca}$) was lesser than one. The mean degree of dominance was found greater than unity. Estimates of dominance variance (σ^2_D) were larger in magnitude than the additive variance for all the aphid characters under study. The additive and non-additive ratio (σ^2_A/σ^2_D) was lower than unity. The estimates of predictability ratios ($\sigma^2_A/\sigma^2_A+\sigma^2_D$) higher than 0.50 in all the aphid related characters and much higher in case of penetration force.

Among the parental genotypes, RW-85-59 and DRMR-15-16 exhibited significant negative general combining ability effects and were found to be good general combiners for early flowering. Genotype RW-85-59 showed significant positive general combining ability effects and were found to be good general combiner for primary branches plant⁻¹. The genotypes RW-85-59 and Kranti emerged as good general combiners for secondary branches plant⁻¹ which revealed significant positive general combining ability effects. Parents NPJ-194, RW-85-59, Kranti and PHR-2 were found good general combiners for siliquae plant⁻¹ by exhibiting significant positive general combining ability effects. Out of all parental lines, only one genotype DRMR-15-16 revealed significant positive general combining ability effect and was found to be the best general combiner for seeds per siliqua. The significant and desirable general combining ability effects were marked for height up to first fruiting branch in the genotypes RW-85-59, DRMR-15-16 and Kranti are best general

combiners. In the case of plant height genotypes NPJ-194, RW-85-59 and DRMR-15-16 were good general combiners for dwarfness and exhibited significant negative general combining ability effects. Out of all parental lines, one genotype SKJM-05 showed significant and positive general combining ability effects and were found to be good general combiner for seed yield per plant. The parents namely NPJ-194, Kranti, RNWR-09-3 and PHR-2 showed positive and significant gca effects which may be considered as good general combiners for oil content.

Good general combiners for percentage of membrane stability index with significant positive gca effects were observed in Kranti and Giriraj. Only two parents namely SKJM-05 and RNWR-09-3 were found as a good general combiner for percentage of excised -leaf water loss by exhibiting significant negative gca effects. Good general combiners for percentage of relative water content with significant positive gca effects were observed one genotype *i.e.*, *Kranti*. No parents showed to be a good combiner of the canopy temperature depression. The proline content of leaf with significant positive gca effects was observed only in PHR-2 and this genotype was considered as a good general combiner. The parents namely NPJ-194 and PHR-2 showed positive and significant gca effects which may be considered as good general combiners for chlorophyll a. Significant positive gca effects for chlorophyll b, was exhibited by NPJ-194, RNWR-09-3 and PHR-2. Positive and significant gca effect was observed in the parental genotypes *viz.*, NPJ-194, DRMR-15-16, RNWR-09-3 and PHR-2, resulting these genotypes were good general combiners for total chlorophyll.

In the case of water content of aphid probed twig, positive and significant gca effects were recorded for only one parent *i.e.*, NPJ-194 and considered as excellent general combiners. Significant positive GCA effects for water content of aphid uninfested twig were possessed by two parental genotypes *i.e.*, SKJM-05 and Kranti. The parents, DRMR-

15-16, SKJM-05 and PHR-2 showed negative and significant gca effects and considered as a best general combiner for water content of aphid. Among parents, significant and positive gca effects were recorded by SKJM-05, Giriraj and PHR-2 were found as a good general combiner for percentage of water differential between aphid probed twig and aphid itself. Only two parents *viz.*, RW-85-59, DRMR-15-16, SKJM-05 and Kranti was found as a good general combiner for aphid count by exhibiting significant negative gca effects. Significant and positive gca effects were showed by NPJ-194, DRMR-15-16, SKJM-05, Giriraj and RNWR-09-3 considered as good general combiner for penetration force. These parents have desirable alleles for most of the characters and fixable component of gene action, additive and additive \times additive type of epistasis, these could be successfully exploited by developing a homozygous line for the improvement of characters. These parental lines might be utilized for producing the intermating population to get desirable recombinants in Indian mustard.

Five crosses exhibited negative significant sca effects namely NPJ-194 \times Kranti, RW-85-59 \times SKJM-05, DRMR-15-16 \times Kranti, DRMR-15-16 \times RNWR-09-3 and DRMR-15-16 \times PHR-2 were considered desirable as they were early flower types. In case of primary branches plant⁻¹ six crosses expressed positively significant sca effects *viz.*, NPJ-194 \times RNWR-09-3, NPJ-194 \times PHR-2, RW-85-59 \times DRMR-15-16, Kranti \times PHR-2, Giriraj \times RNWR-09-3 and Giriraj \times PHR-2 and were considered as desirable specific combiners. For this character, four cross combinations showed significant positive sca effects *i.e.* NPJ-194 \times PHR-2, RW-85-59 \times Kranti, Giriraj \times RNWR-09-3 and Giriraj \times PHR-2 was found as a good specific combiner for secondary branches plant⁻¹. Ten crosses exhibited positive and significant sca effects for siliquae plant⁻¹ character namely NPJ-194 \times DRMR-15-16, NPJ-194 \times SKJM-05, NPJ-194 \times RNWR-09-3, NPJ-194 \times PHR-2, RW-85-59 \times Kranti, RW-85-59 \times Giriraj, DRMR-15-16 \times SKJM-05, DRMR-15-16 \times Giriraj, DRMR-15-16 \times PHR-2,

Kranti × Giriraj and Giriraj × PHR-2 was found as a good specific combiner. Based on sca effects of the crosses showed positive significant sca effect namely RW-85-59 × Kranti, DRMR-15-16 × Giriraj and DRMR-15-16 × RNWR-09-3 were good cross combinations for seeds siliquae⁻¹. Out of 28 crosses, only 6 combinations showed significant and positive sca effects viz., NPJ-194 × DRMR-15-16, RW-85-59 × DRMR-15-16, RW-85-59 × Kranti, SKJM-05 × Kranti, SKJM-05 × Giriraj and RNWR-09-3 × PHR-2 and recorded as excellent specific combiners for height up to first fruiting branch. Negative significant and best specific combining ability effects were shown in crosses NPJ-194 × RW-85-59, RW-85-59 × SKJM-05, RW-85-59 × Kranti, DRMR- 15-16 × SKJM-05, DRMR- 15-16 × Kranti, DRMR- 15-16 × PHR-2, SKJM-05 × Giriraj, SKJM-05 × RNWR-09-3, Kranti × RNWR-09-3 and Kranti × PHR-2 for plant height. The positive and significant value of sca for seed yield plant⁻¹ was obtained by the crosses namely, NPJ-194 × SKJM-05, NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, SKJM-05 × Kranti and Kranti × PHR-2. The crosses namely NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR -2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, Kranti × RNWR-09-3, Giriraj × PHR-2 and RNWR-09-3 × PHR-2 were having the positive and significant value of sca effects for 1000 seed weight.

The crosses NPJ-194 × DRMR-15-16, NPJ-194 × Kranti, RW-85-59 × SKJM-05, RW-85-59 × Kranti, RW-85-59 × Giriraj, RW-85-59 × PHR-2, DRMR-15-16 × SKJM-05, DRMR-15-16 × Giriraj, SKJM-05 × PHR-2 and RNWR-09-3 × PHR-2 showed significant positive sca effects for oil content.

In order of merit in NPJ-194 × RW-85-59, NPJ-194 × RNWR-09-3, RW-85-59 × RNWR-09-3, DRMR-15-16 × Kranti, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × Giriraj, Kranti × PHR-2 and Giriraj × RNWR-09-3 which were considered as good specific combiners for percentage membrane stability index. The most promising crosses

which exhibited negative and significant sca effects for percentage of excised leaf water loss were NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, RW-85-59 × DRMR-15-16, RW-85-59 × Giriraj, RW-85-59 × RNWR-09-3, DRMR-15-16 × Kranti, DRMR-15-16 × PHR-2, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Kranti × PHR-2, Giriraj × RNWR-09-3 and RNWR-09-3 × PHR-2. Two crosses expressing high significant sca effects in a positive direction were RW-85-59 × PHR-2 and DRMR-15-16 × PHR-2 for percentage of relative water content. The high significant and negative specific combining ability effects were observed in the cross, *i.e.* NPJ-194 × SKJM-05, RW-85-59 × DRMR-15-16 and SKJM-05 × Giriraj for canopy temperature depression. The cross combination like NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × PHR-2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, RW-85-59 × Kranti, SKJM-05 × Giriraj, SKJM-05 × PHR-2, Kranti × Giriraj, Kranti × RNWR-09-3 and RNWR-09-3 × PHR-2 were identified as good specific combiners these were exhibiting high positive significant sca effects for proline content of the leaf. Six cross combinations in F₁ showed significant positive sca effects namely NPJ-194 × RW-85-59, RW-85-59 × DRMR-15-16, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Kranti and SKJM-05 × PHR-2. The positive and significant value of specific combining ability effect for chlorophyll b was obtained for the crosses, NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × Kranti, RW-85-59 × PHR-2, DRMR-15-16 × RNWR-09-3 and SKJM-05 × RNWR-09-3. The crosses NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × Kranti, RW-85-59 × PHR-2, DRMR-15-16 × RNWR-09-3 and Giriraj × PHR-2 showed significant positive sca effects and were good specific combiners total chlorophyll.

The crosses NPJ-194 × DRMR-15-16, NPJ-194 × Kranti, NPJ-194 × PHR-2, RW-85-59 × DRMR-15-16, RW-85-59 × Giriraj, RW-85-59 × RNWR-09-3, DRMR-15-16 × Kranti, DRMR-15-16 × Giriraj, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × PHR-2, Kranti × Giriraj and RNWR-09-3 × PHR-2 showed positive and significant specific

combining ability effects and were good specific cross combinations for water content of aphid probed twig. Only two crosses combinations exhibited significant and positive specific combining ability effects. The good combinations in order of merit were Kranti \times Giriraj and DRMR-15-16 \times Giriraj. The crosses *viz.*, NPJ-194 \times Giriraj, NPJ-194 \times RNWR-09-3, RW-85-59 \times SKJM-05, RW-85-59 \times PHR-2, DRMR-15-16 \times RNWR-09-3, SKJM-05 \times Kranti and SKJM-05 \times RNWR-09-3 showed significant negative specific combining ability effects were emerged to be best specific cross combinations for water content of aphid. The cross combinations NPJ-194 \times Giriraj, NPJ-194 \times RNWR-09-3, RW-85-59 \times SKJM-05, RW-85-59 \times PHR-2, DRMR-15-16 \times RNWR-09-3, SKJM-05 \times Kranti and SKJM-05 \times RNWR-09-3 observed significant and positive sca effects for percentage of water differential between aphid probed twig and aphid itself. The crosses NPJ-194 \times RW-85-59, NPJ-194 \times DRMR-15-16, NPJ-194 \times SKJM-05, RW-85-59 \times SKJM-05, RW-85-59 \times Giriraj, DRMR-15-16 \times Kranti, DRMR-15-16 \times RNWR-09-3, DRMR-15-16 \times PHR-2, SKJM-05 \times Kranti, SKJM-05 \times RNWR-09-3, SKJM-05 \times PHR-2, Giriraj \times RNWR-09-3 and RNWR-09-3 \times PHR-2 showed significant negative specific combining ability effects and were emerged to be best specific cross combinations for aphid count. The crosses based on their desirable sca values for penetration force were NPJ-194 \times RW-85-59, NPJ-194 \times SKJM-05, NPJ-194 \times Giriraj, NPJ-194 \times RNWR-09-3, RW-85-59 \times DRMR-15-16, RW-85-59 \times RNWR-09-3, DRMR-15-16 \times Giriraj, SKJM-05 \times Giriraj, Kranti \times Giriraj, Kranti \times PHR-2, Giriraj \times PHR-2 and RNWR-09-3 \times PHR-2.

Significant and negative relative heterosis over mid parent was observed for DRMR-15-16 \times RNWR-09-3 and DRMR-15-16 \times PHR-2 in case of days to 50% flowering whereas, seven F_1 s showed the heterosis over BP for crosses *i.e.* RW-85-59 \times DRMR-15-16, RW-85-59 \times SKJM-05, RW-85-59 \times Kranti, RW-85-59 \times PHR-2, DRMR-15-16 \times Kranti, DRMR-15-16 \times RNWR-09-3 and DRMR-15-16 \times PHR-2. In case of primary

branches per plant, heterosis over the mid parent the highest and significant positive value was recorded for crosses like NPJ-194 × PHR-2, Kranti × PHR-2 and Giriraj × PHR-2 while, only one hybrid *i.e.* NPJ-194 × PHR-2 exhibited positive significant heterosis over better parent. Two crosses *viz.*, Giriraj × PHR-2 and RW-85-59 × Kranti observed positive significant heterosis to merit over mid parent for secondary branches plant⁻¹ and two crosses *viz.*, Giriraj × PHR-2 and RW-85-59 × Kranti revealed positive significant heterosis over better parent for secondary branches plant⁻¹. The highest positive and significant value for siliquae plant⁻¹ over mid parent were noted for NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Kranti, DRMR-15-16 × Giriraj, DRMR-15-16 × PHR-2, Kranti × Giriraj, Giriraj × RNWR-09-3 and Giriraj × PHR-2 while, three crosses revealed significant positive heterosis over better parent namely, NPJ-194 × DRMR-15-16, NPJ-194 × RNWR-09-3 and NPJ-194 × PHR-2 are best for this character. The highest positive significant heterotic combinations were observed in the crosses DRMR-15-16 × Giriraj, DRMR-15-16 × RNWR-09-3, RW-85-59 × Kranti and RW-85-59 × Giriraj are considered as good for seed siliqua⁻¹ whereas, none of the crosses was significantly contributed over better parent. The crosses showed highest positive and significant value was observed for height up to first fruiting branch over mid parent were RW-85-59 × Kranti, SKJM-05 × Giriraj, RW-85-59 × DRMR-15-16, Kranti × Giriraj, SKJM-05 × Kranti and NPJ-194 × DRMR-15-16 while, only two F₁s expressed desirable heterosis over better parent namely RW-85-59 × Kranti and RW-85-59 × PHR-2. The crosses showed negative and significant values were observed for plant height over mid parent were NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Giriraj, RW-85-59 × PHR-2, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × PHR-2, Kranti × Giriraj, Kranti × PHR-2, Giriraj × RNWR-09-3, Giriraj × PHR-2, RNWR-09-3 ×

PHR-2 whereas, 10 crosses showed significant and positive heterosis over better parent *viz.*, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Giriraj, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × PHR-2, Giriraj × RNWR-09-3, Giriraj × PHR-2 and RNWR-09-3 × PHR-2. Four crosses were positively significant for seed yield over mid parent namely NPJ-194 × SKJM-05, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, Kranti × PHR-2 whereas, only two crosses showed significant positive heterosis over better parent namely NPJ-194 × SKJM-05 and Kranti × PHR-2. Positive and significant values were noted for 1000 seed weight over mid parent for crosses like NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR -2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, RW-85-59 × Kranti, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, Kranti × RNWR-09-3, Giriraj × PHR-2 and RNWR-09-3 × PHR-2 while, the F₁s expressed desirable positive significant heterosis over better parent are NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × PHR -2, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, RW-85-59 × Kranti, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, SKJM-05 × Kranti and Giriraj × PHR-2. The crosses NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × Kranti, RW-85-59 × DRMR-15-16, RW-85-59 × SKJM-05, RW-85-59 × Kranti, RW-85-59 × Giriraj, RW-85-59 × PHR-2, DRMR-15-16 × SKJM-05, DRMR-15-16 × Giriraj, DRMR-15-16 × PHR-2, SKJM-05 × PHR-2 and RNWR-09-3 × PHR-2 observed positive significant heterosis over mid parent while significant heterosis over better parent for oil content was exhibited by RW-85-59 × SKJM-05, RW-85-59 × Giriraj, RW-85-59 × PHR-2, DRMR-15-16 × Giriraj and SKJM-05 × PHR-2.

Five crosses *viz.*, RW-85-59 × RNWR-09-3, SKJM-05 × Kranti, SKJM-05 × Giriraj and Giriraj × PHR-2 revealed positive significant heterosis over better parent for percentage of membrane stability index. 14 crosses revealed significant negative heterosis over mid parent *viz.*, NPJ- 194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Giriraj,

NPJ-194 × RNWR-09-3, RW-85-59 × RNWR-09-3, RW-85-59 × PHR-2 , DRMR-15-16 × Kranti, DRMR-15-16 × PHR-2, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Kranti × PHR-2, Giriraj × RNWR- 09-3, Giriraj × PHR-2 and RNWR-09-3 × PHR-2 are considered as best for percentage of excised- leaf water loss whereas, the negative significant heterosis over better parent was observed by crosses NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Giriraj , NPJ-194 × RNWR-09- 3, RW-85-59 × RNWR-09-3, RW-85-59 × PHR-2, DRMR-15-16 × Kranti, DRMR-15-16 × PHR-2, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Kranti × PHR-2, Giriraj × RNWR-09-3, Giriraj × PHR-2 and RNWR-09-3 × PHR-2 were considered as good for this character. The crosses *viz.*, RW-85-59 × PHR-2, DRMR-15-16 × PHR-2, SKJM-05 × PHR-2, Giriraj × PHR-2 and RNWR-09-3 × PHR-2 revealed significant positive heterosis over mid parent for percentage of relative water content whereas, positive significant heterosis over better parent was observed for only one cross *i.e.* DRMR-15-16 × PHR-2. One cross observed as significant negative heterosis over mid parent and better parent for canopy temperature depression *i.e.* SKJM-05 × Giriraj. Seven crosses revealed significant positive heterosis over mid parent namely, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, SKJM-05 × Giriraj, SKJM-05 × PHR-2 and Kranti × Giriraj whereas, six crosses showed significant and positive heterosis over better parent *viz.*, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × PHR-2, SKJM-05 × Kranti, SKJM-05 × PHR-2 and Kranti × Giriraj for proline content. Crosses namely NPJ-194 × RW-85-59, RW-85-59 × DRMR-15-16, RW-85-59 × Kranti, RW-85-59 × Giriraj, DRMR-15-16 × Kranti and Giriraj × PHR-2 revealed positive significant heterosis over mid parent whereas, none of the crosses showed significant and positive heterosis over better parent for chlorophyll a. Crosses NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × PHR-2, DRMR-15-16 × RNWR-09-3 and SKJM-05 × RNWR-09-3 exhibited significant positive heterosis over mid parent whereas, only two crosses namely NPJ-194 × PHR-2 and SKJM- 05 × RNWR-09-3 showed significant

positive heterosis over better parent for chlorophyll b. Crosses namely NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Kranti, RW-85-59 × PHR-2 and Giriraj × PHR-2 revealed positive significant heterosis while, the crosses namely NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × Kranti, Giriraj × PHR-2 exhibited positive significant heterosis over better parent for total chlorophyll.

Crosses NPJ-194 × PHR-2 and RW-85-59 × Giriraj exhibited significant positive heterosis over mid parent whereas, none of the crosses was found positive significant heterosis over better parent for water content of aphid probed twig. Kranti × Giriraj revealed significant positive heterosis over mid parental values whereas, none of the crosses exhibited positive significant heterosis over better parent for water content of aphid uninfested twig. NPJ-194 × RNWR-09-3 and SKJM-05 × RNWR-09-3 crosses recorded negative significant heterosis over mid parent while, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, RW-85-59 × SKJM-05, RW-85-59 × PHR-2 and SKJM-05 × RNWR-09-3 crosses revealed negative significant heterosis over better parent for water content of aphid. RNWR-09-3 × PHR-2 cross showed significant positive heterosis over mid parental values were found to be promising whereas none of the crosses revealed positive significant heterosis over better parent for percentage of water differential between aphid probed twig and aphid itself. Crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2 and Giriraj × RNWR-09-3 revealed negative significant heterosis over mid parent while the crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Kranti, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Kranti, DRMR-15-16 × RNWR-09-3, DRMR-

15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Giriraj × RNWR-09-3 exhibited negative significant heterosis over better parent for aphid count. NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, RW-85-59 × SKJM-05, DRMR-15-16 × RNWR-09-3, SKJM-05 × Giriraj, Kranti × Giriraj and RNWR-09-3 × PHR-2 crosses noted positive significant heterosis over mid parent and crosses *viz.*, NPJ-194 × RNWR-09-3, RW-85-59 × DRMR-15-16, DRMR-15-16 × PHR-2, Kranti × Giriraj and RNWR-09-3 × PHR-2 revealed positive significant heterosis over better parent for penetration force.

From the rescaling index value, the cross Kranti × PHR-2 ranked the highest followed by NPJ-194 × SKJM-05 and RW-85-59 × SKJM-05, when the ranking of three best crosses and their parents was done based on sca for seed yield plant⁻¹. In case of 1000 seed weight, crosses NPJ-194 × Kranti showed highest followed by RW-85-59 × DRMR-15-16 and NPJ-194 × RNWR-09-3; for siliquae plant⁻¹ three best crosses were NPJ-194 × RNWR-09-3 followed by RW-85-59 × Kranti and NPJ-194 × PHR-2. Similarly, for secondary branches plant⁻¹, NPJ-194 × PHR-2 showed highest sca followed by Giriraj × PHR-2 and RW-85-59 × Kranti. When the ranking of three best crosses and their parents was done on the basis of sca for total chlorophyll NPJ-194 × Giriraj followed by NPJ-194 × PHR-2 and RW-85-59 × Kranti; for proline content of leaf, cross Kranti × Giriraj, SKJM-05 × PHR-2 and Kranti × Giriraj; for percentage of membrane stability index, NPJ-194 × RW-85-59 followed by SKJM-05 × Giriraj and RW-85-59 × RNWR-09-3; for aphid count DRMR-15-16 × PHR-2 followed RW-85-59 × RNWR-09-3 and RW-85-59 × Giriraj and for penetration force Kranti × Giriraj followed by RW-85-59 × DRMR-15-16 followed by NPJ-194 × RNWR-09-3 and Kranti × Giriraj.

Analysis of variance of eight diverse parental genotypes of mustard revealed significant differences among the genotypes and five different times for all the three different numbers of aphid inoculated *i.e.* A1, A5 and A10. Similarly, analysis of variance among 28

crosses of mustard revealed significant differences among the genotypes and five different times for A5 numbers of aphid inoculated indicating there are significant variation among the parents, F₁s and different periods.

When one aphid was inoculated per plant, group 'a' showed the highest mean value and the genotype fall in this group was Kranti while the group 'c' showed the lowest mean value and the genotype lie in this group was RW-85-59. Similarly, when five aphids were inoculated per plant, group 'a' again had the high mean value, comprising the genotype SKJM-05 and the low mean was observed in group 'f'. The genotype falls in-group 'f' was Giriraj. In case when ten aphids were inoculated per plant. The genotype Kranti fall in-group 'a' having the high meanwhile the genotype RNWR-09-3 lie in-group 'd' consisting of the low mean. In the same way, when five aphids were inoculated per plant of all the crosses, 18 groups were formed. Group 'a' again had the high mean value, comprising the cross NPJ-194 × SKJM-05 and the low mean was observed in group 'f' having the cross RW-85-59 × Giriraj. This indicated that genotype RW-85-59, Giriraj and RNWR-09-3 were resistant for A1, A5 and A10 aphid number respectively while the genotype Kranti and SKJM-05 were considered susceptible for A1, A10 and A5 respectively. In crosses, genotype RW-85-59 × Giriraj was resistant and the susceptible cross was NPJ-194 × SKJM-05.

Chlorophyll a, chlorophyll b and total chlorophyll were instrumental in increase the aphid attack as evidenced by their positive association with field aphid count. This was further confirmed by the positive association of chlorophyll a, chlorophyll b and total chlorophyll with water content of aphid probed twig. The variation in the chlorophyll content had no impact on penetration force which made the mustard plants an easy prey for aphids.

The correlation coefficient between chlorophyll a and field aphid count was found to be lower than the direct effect of chlorophyll a which showed that there were certain characters like chlorophyll b and penetration force which were reducing the direct effect of

chlorophyll a. The correlation coefficient between chlorophyll b and field aphid count was found to be much higher than the direct effect of chlorophyll b. However, the indirect effect of chlorophyll b on field aphid count *via* chlorophyll a and total chlorophyll was quite high. The correlation between total chlorophyll and field aphid count was partially higher than the direct effect of total chlorophyll indicating that the indirect effect of total chlorophyll on field aphid count via other characters like chlorophyll a and chlorophyll b and penetration force were cancelling the effects of one over the other.

Conclusion

Secondary branches plant⁻¹ and siliquae plant⁻¹ were ultimately positively associated with seed yield and were controlled by additive genes, due to their high heritability and genetic advance. Therefore, to exercise a suitable selection programme it would be worth to concentrate on these traits for improvement in yield of mustard.

A proper follow up of this experiment would be justifiable if a suitable crossing programme is carried out using the eight most genetically divergent mustard genotypes identified on the basis of the inter-cluster distance, intra cluster distance and the D² distance between the individual genotypes, namely PHR 2, RNWR-09-3, Giriraj, Kranti, SKJM-05, DRMR-15-16, RW-85-59 (Sarna) and NPJ-194.

RW-85-59, DRMR-15-16, Kranti and NPJ-194 seemed to be a good general combiner for most of the seed yield and its attributing characters; PHR-2, NPJ-194, RNWR-09-3 and Kranti appeared to be good general combiner for most of the physiological characters and SKJM-05, DRMR-15-16, Kranti, NPJ-194, PHR-2 and Giriraj possesses desirable alleles formost of the aphid related characters.

SKJM-05 × Kranti, RW-85-59 × SKJM-05 and NPJ-194 × SKJM-05 showed positively significant specific combining ability effect and *per se* performance is also good

for seed yield plant¹. NPJ-194 × PHR-2, NPJ-194 × Giriraj, DRMR-15-16 × RNWR-09-3, Giriraj × PHR-2 and RW-85-59 × PHR-2 showed positively significant specific combining ability effect for total chlorophyll. The hybrids including these parents *i.e.* RW-85-59 × Giriraj, RW-85-59 × SKJM-05, DRMR-15-16 × Kranti, NPJ-194 × RW-85-59, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, NPJ-194 × DRMR-15-16, SKJM-05 × PHR-2, NPJ-194 × SKJM-05, DRMR-15-16 × RNWR-09-3 appeared significant specific combining ability effect for aphid count.

Positively significant heterosis for seed yield over mid parent namely NPJ-194 × SKJM-05, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, Kranti × PHR-2 whereas, only two crosses showed significant positive heterosis over better parent namely NPJ-194 × SKJM-05 and Kranti × PHR-2.

Crosses namely NPJ-194 × RW-85-59, NPJ-194 × Kranti, NPJ-194 × Giriraj, NPJ-194 × RNWR-09-3, NPJ-194 × PHR-2, RW-85-59 × Kranti, RW-85-59 × PHR-2 and Giriraj × PHR-2 revealed positive significant heterosis while, the crosses namely NPJ-194 × Giriraj, NPJ-194 × PHR-2, RW-85-59 × Kranti, Giriraj × PHR-2 exhibited positive significant heterosis over better parent for total chlorophyll.

Crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Giriraj, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2 and Giriraj × RNWR-09-3 revealed negative significant heterosis over mid parent while the crosses namely NPJ-194 × RW-85-59, NPJ-194 × DRMR-15-16, NPJ-194 × SKJM-05, NPJ-194 × Kranti, NPJ-194 × PHR-2, RW-85-59 × SKJM-05, RW-85-59 × Giriraj, DRMR-15-16 × SKJM-05, DRMR-15-16 × Kranti, DRMR-15-16 × RNWR-09-3, DRMR-15-16 × PHR-2, SKJM-05 × Kranti, SKJM-05 × RNWR-09-3, SKJM-05 × PHR-2, Giriraj × RNWR-09-3 exhibited negative significant heterosis over better parent for aphid count.

Significant variation among the parental genotypes and different periods was observed for all the three different numbers of aphid inoculated *i.e.* A1, A5 and A10 whereas for F₁ significant variability was observed for A5 aphid number.

Genotype RW-85-59, Giriraj and RNWR-09-3 were resistant for A1, A5 and A10 aphid number respectively while the genotype Kranti and SKJM-05 were considered susceptible for A1, A10 and A5 respectively. In crosses, genotype RW-85-59 × Giriraj was resistant and the susceptible cross was NPJ-194 × SKJM-05.



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