GENETIC ANALYSIS OF SEED YIELD AND RELATED TRAITS IN DOUBLED HAPLOIDS AND RESPONSE TO ANTHER CULTURE IN ETHIOPIAN MUSTARD (Brassica carinata A. Braun)

THESIS

By

SHITOLE AJIT MOHANRAO
(A-2010-30-37)

Submitted to

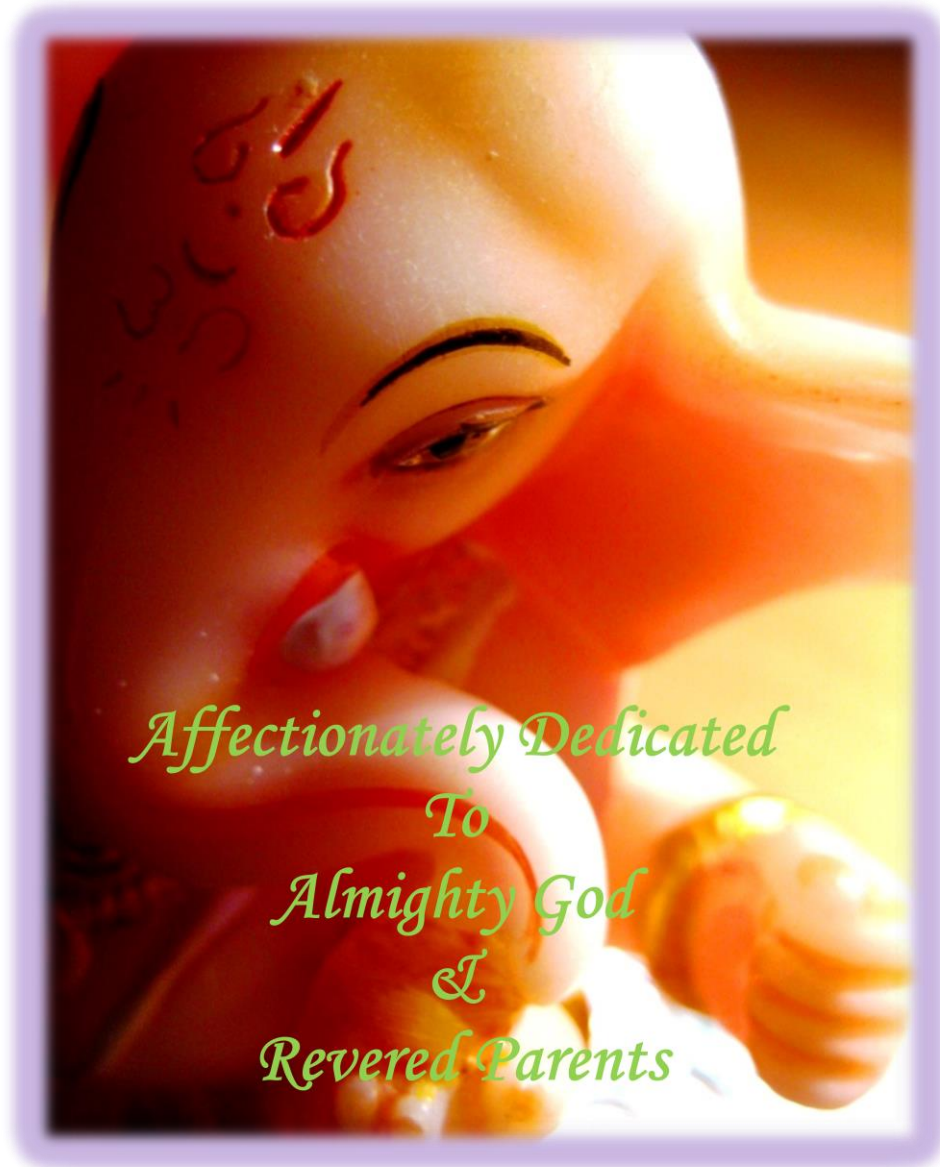## CHAUDHARY SARWAN KUMAR HIMACHAL PRADESH KRISHI VISHVAVIDYALAYA PALAMPUR – 176 062 (H.P.) INDIA

in

partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE IN AGRICULTURE
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Affectionately Dedicated

To

Almighty God

&

Revered Parents

Dr. Vedna Kumari   Department of Crop Improvement
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CERTIFICATE – I

This is to certify that the thesis entitled "**Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)"** submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics** of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Mr. Shitole Ajit Mohanrao (A-2010-30-37)** son of **Shri Shitole Mohan Aanandrao** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

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

                                                            (Dr. Vedna Kumari)
Place: Palampur   Major Advisor
Dated: 19th July, 2012

CERTIFICATE- II

This is to certify that the thesis entitled **"Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)"** submitted by **Shitole Ajit Mohanrao (Admission No. A-2010-30-37)** son of **Shri Shitole Mohan Aanandrao** to the CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in the discipline of **Plant Breeding and Genetics** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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Place : Palampur
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LIST OF ABBREVIATIONS USED

Sr. No.	Abbreviation	Meaning
1	*et al.*	et alii (and other)
2	*i.e.*	Id (that is)
3	*viz.*	Vi delicet (namely)
4	p	page
5	pp	particular pages
6	^{0}C	degree Celsius
7	g	gram
8	kg	Kilogram
9	ha	hectare
10	Fig	figure
11	amsl	above mean sea level
12	dm	decimeter
13	cm	centimeter
14	l	liter
15	ml	milliliter
16	mm	millimeter
17	Env	environment
18	df	degree of freedom
19	HM	hormonal combination

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ABSTRACT

The present investigation entitled "Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)" was undertaken to assess the nature of genetic variability, extent of genetic diversity and association of various characters with seed yield and their direct and indirect effects for effective selection under two different environments during *rabi* 2010-11. In addition, androgenesis-mediated responsiveness of genotypes and their crosses was also studied through anther culture. Data were recorded on seed yield and their component characters and reaction to *Alternaria* blight. The data analysis was done as per standard statistical procedures. The data recorded on anther culture studies were analysed using CPCS software. Sufficient genetic variability was observed for most of the characters in Env.I, Env.II and pooled over the environments. High heritability coupled with high genetic advance was observed for 1000-seed weight, plant height and number of secondary branches per plant in Env.I which indicated the predominance of additive gene action. The multivariate analysis revealed that grouping of the genotypes was almost similar in Env.I, Env.II and pooled over the environments. The clustering pattern of karan rai and mustard genotypes indicated the parallelism between genetic divergence and species-wise geographical distribution. Maximum contribution towards genetic divergence was due to plant height in Env.I, days to 50 per cent flowering in Env.II and days to 75 per cent maturity in pooled over the environments. Based upon the correlation and path coefficient analysis, harvest index and biological yield per plant were observed to be the best selection parameters because of their high positive direct and indirect contributions towards seed yield per plant. In androgenesis-mediated response, the genotype P-51 performed better in B$_5$ medium supplemented with HM$_2$ (0.2mg/l BAP + 2.0 mg/l NAA) and 3 per cent sucrose concentration for high callus induction frequency and calli index.

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1. INTRODUCTION

Oilseed crops are the backbone of Indian agricultural economy and occupy an important position in daily diet, being a rich source of fats and vitamins. India is the second largest rapeseed-mustard growing country and accounts for 21.7% area in the world after China. Among oilseeds, rapeseed-mustard is the second most important oilseed crop of the country after groundnut and plays a significant role in Indian oil economy by contributing about 27.8% to the total oilseed production (Anonymous 2010).

Under rapeseed-mustard group, seven annual oilseeds belonging to the family *Brassicaceae (Cruciferae)* are grown in India *viz.,* Indian mustard [*Brassica juncea* (L.) Czern. & Coss.], three ecotypes of Indian rape *viz.,* toria, brown sarson and yellow sarson (*Brassica campestris* L. ssp. *oleifera*), gobhi sarson (*Brassica napus* L.), Ethiopian mustard or karan rai (*Brassica carinata* A. Braun) and taramira (*Eruca sativa* Mill.). Rapeseed-mustard is primarily used for human consumption as desirable edible oil. The oil and fats serve as important raw material for manufacture of paints, soaps, varnishes, hair oil, lubricants, textile auxiliaries and pharmaceuticals. The cake is used as cattle feed.

Brassica carinata A. Braun is a self pollinated crop believed to have been originated in Ethiopia and its cultivation is thought to have started about 4000 years B.C. (Alemayehu and Becker 2002; Schippers 2002). It has been cultivated there as oilseed and leafy vegetable crop.

Present day evidence indicates that *B. carinata* is an amphidiploid species (2n =34, BBCC) evolved from the hybridization of *Brassica nigra* (BB, 2n=16) and *Brassica oleracea* (CC, 2n=18) in the highlands of Ethiopia and the adjacent areas of East Africa and the Mediterranean coast where both the parental species exist (Gomez-Campo and Prakash 1999). The crop has gained popularity because of its high resistance to biotic and abiotic stresses under semi-arid conditions (Teklewold and Becher 2006).

Rapeseed-mustard is the third important oilseed crop in the world after soybean (*Glycine max*) and palm (*Elaeis guineensis* Jacq.). The crop occupies an area of 30.74

million hectares with a total annual production of 59.93 million tonnes and productivity 1950 kg/ha. In production, India ranks third after China (22.9%) and Canada (19.7%). The global production of rapeseed-mustard oil is around 12-14 million tonnes. In India, it is grown over an area of 5.53 million hectares (23.7% of the total oilseed crops) and produces 6.41 million tonnes (26.0% of the total oilseed crops). In India, it is cultivated as a winter season crop mainly in Rajasthan, Uttar Pradesh, Haryana, Gujarat, West Bengal, Assam and Bihar. In Himachal Pradesh, the crop is grown over an area of 8.4 thousand hectares with a total production of 3.6 thousand metric tonnes. The average productivity of the state is 430 kg/ha as compared to 1157 kg/ha in India and 1950 kg/ha world over (Anonymous 2010).

Rapeseed-mustard in general, has shown a declining trend both in acreage and production largely due to lack of suitable cultivars for different ecosystems, fluctuations in weather conditions, cultivation in marginal and sub marginal lands and prevalence of various biotic and abiotic stresses. The present day varieties are more susceptible to *Alternaria* blight caused by *Alternaria brassicae* (Berk.) Sacc. It is one of the most important limiting factors causing yield losses up to 35-45% in Ethiopian mustard (Kolte 2002). Hence, the most suitable alternate way to increase productivity is by adoption of high yielding, input responsive genotypes having resistance against various biotic and abiotic stresses with high stability index. Therefore, concerted efforts are needed to increase the productivity through conventional and non conventional breeding techniques to evolve improved varieties.

The success of any breeding programme depends upon the nature and magnitude of variability present in the germplasm stock which provides better chances of selecting desirable types (Vavilov 1951). The chances of initiating an effective breeding programme are greater if more genetic variability is available with the plant breeder. Thus, studies on parameters of genetic variability *viz.,* phenotypic and genotypic coefficients of variation, heritability and genetic advance, are of paramount importance. Studies on genetic diversity are useful as a general guide for the choice of parents for future hybridization programme in order to obtain high heterotic response and superior transgressants. Estimation of degree of divergence within biological population and computation of relevant contribution of different components to the total divergence is

done through Mahalanobis's generalized distance (D^2-statistic) method. Correlation studies provide the degree, but, not the cause of associations whereas the path coefficient analysis permits a critical examination of specific forces acting to produce a given correlation and measures the relative importance of each factor contributing towards seed yield or any other final product. Thus, knowledge of associations among seed yield and its related traits and their direct and indirect contributions towards seed yield being a polygenic trait, is of prime importance in formulating suitable breeding methodology.

Genetic parameters may vary from one environment to another due to differential gene expression (Jatassara and Paroda 1978). As most of cultivated area (nearly 80%) of the state is rainfed and due to changing climatic conditions, the normal sowing is important to utilize the *kharif* residual moisture. However, late sowing is important when the fields are not vacated by second fortnight of October or useful for contingent crop planning when normal sown crop fails under aberrant climatic conditions. Moreover, genetic studies under different sowing dates (limited in Ethiopian mustard) are of utmost importance for the development of varieties for varied situations.

Conventional methods for breeding crop plants require more than six to seven years of continuous efforts to get true breeding lines after following hybridization approach. Hence, biotechnological tools including anther culture, hold a great promise in accelerating the pace of breeding programme (Guha and Maheshwari 1964). *In vitro* technique of anther culture helps to achieve homozygosity very quickly (Snape 1989). Anther culture of potential F_1 generation genotypes can be used to facilitate regeneration of stable recombinant inbreds in one to two years thereby saving time and resources for their further use directly as commercial cultivars and/or in structural and functional genomics.

In view of above, the present study entitled "Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)" was undertaken with the following objectives:

i.   To estimate the nature and extent of genetic divergence & character associations for seed yield, related traits and identify suitable donors and

ii.   investigate the androgenesis-mediated response of different genotypes & their cross combinations.

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2. REVIEW OF LITERATURE

In both evolution and plant breeding, populations are constantly being shifted for superior types. In this constant shifting, the primary force is selection in which individuals with certain characteristics are favoured in reproduction. Selection can lead to improvement in crop plants only if sufficient genetic variability is present in the population. For developing superior varieties with high yield potential and other desirable characters, the knowledge of genetic parameters is helpful. Besides, association of yield with its component traits and their partitioning into direct and indirect effects is very essential. To decide about the combinations of parents in hybridization, the knowledge of genetic divergence among the different populations plays a significant role. Presence of genotype x environment (g x e) interactions also poses a problem in getting the precised information on parameters of genetic variability, genetic divergence and nature of associations among traits and in realizing the predicted genetic advance.

A review of literature pertaining to various aspects included in the present study has been divided under following sub-heads:

2.1   Genetic variability studies

2.2   Genetic divergence studies

2.3   Correlation and Path coefficient analysis

2.4   Anther culture studies

2.1   Genetic variability studies

The nature and extent of genetic variability in any population is important for the breeder and it depends to a large extent upon the nature of reproduction in that population. The most important step in initiation of any breeding programme is to choose more potential genotypes. Fisher (1918) partitioned the continuous variation exhibited by a quantitative character into heritable and non heritable components, the former being a consequence of genotype while the later, a result of environmental factors. Since phenotype is the result of interaction between genotype and environment, it is the phenotype on which selection pressure is exercised. Therefore, it becomes necessary to score the phenotypic variability expressed in population especially in respect of yield and

major yield contributing characters. It is the heritable component which is transferred from generation to generation, thus, heritability of the different characters gains importance. Wright (1921) reported that the heritability component comprised of additive and non-additive portion and it was the former which responds to selection. However, high heritability alone does not necessarily mean high genetic gain, therefore, is not sufficient to make improvement through selection. The heritability estimates indicate only the effectiveness of selection with the genotypes on the basis of their phenotypic performance, but, fail to indicate the real progress. Lush (1940) classified heritability into broad sense and narrow sense. Heritability in broad sense is the proportion of genetic variance to the total variance whereas the narrow sense heritability is the proportion of additive genetic variance to total variance.

Vavilov (1951) was the first to realize that a wide range of variability in any crop provides chances of selecting the desirable types. High amount of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) along with *per se* performance of individual genotypes are the indicators of desirable genetic variability. However, these estimates alone are not much helpful in determining the heritable portion, therefore, the further estimates *i.e.* heritability along with genetic advance together with PCV and GCV would be essential for crop improvement. According to Burton (1952), the GCV, heritability and genetic advance would give better information about efficiency of selection. Burton and De Vane (1953) also suggested that a combination of genetic gain and heritability estimates give a reliable indication of amount of improvement to be expected from selection and further remarked that expected genetic advance under particular system provides practical information that is needed by a breeder. Johnson *et al.* (1955) suggested that heritability considered together with genetic advance is more reliable in predicting the effect of selection than heritability alone. The relevant literature in this aspect is reviewed here under:

Panse and Kharagonkar (1957) reported high heritability coupled with low genetic advance for days to maturity and oil content and suggested the presence of non-additive gene action for these characters.

Mehrotra *et al.* (1976) recorded considerable variation for harvest index in their experiments which varied between 25 and 35 per cent in early maturing varieties and 26 to 40 per cent in late maturing varieties of Indian mustard.

The harvest index of the range between 11.6 and 31.6 per cent was reported by Hodgson (1979).

Singh *et al.* (1987) recorded medium heritability for number of primary branches per plant, number of siliquae per plant, number of seeds per siliqua and seed yield per plant and high heritability for number of secondary branches per plant in Indian mustard.

Kumar *et al.* (1988) observed higher heritability for all the traits studied except seed yield. The maximum genetic advance was observed for the secondary branches and siliquae per plant.

Nagaraja (1990) reported higher genotypic coefficient of variation and phenotypic coefficient of variation for number of siliquae per plant. The broadsense heritability was high for days to maturity, days to flowering, oil content, plant height and number of siliquae per plant whereas heritability estimates were moderate for length of main shoot, seed yield per plant, siliquae on main shoot, number of primary branches per plant, number of seeds per siliqua, siliquae per plant and biological yield per plant. The expected genetic advance was highest for number of siliquae per plant.

Chowdhary and Goswami (1991) observed highest genotypic coefficient of variation and phenotypic coefficient of variation for seed yield per plant followed by number of siliquae per plant. Highest heritability and genetic advance were observed for number of siliquae per plant followed by plant height in Indian mustard.

Gupta *et al.* (1992) highlighted the importance of combined analysis over environments for taking care of the effect of genotype x environment interaction on classification of genotypes.

Diwakar and Singh (1993) conducted a study on heritability and genetic advance in segregating populations of yellow seeded Indian mustard and revealed that the narrow sense heritability and genetic advance were high for days to flowering and plant height.

Gowda (1993) reported the highest genotypic coefficient of variation, phenotypic coefficient of variation and genetic advance for seed yield per plant followed by number of racemes per plant and number of siliquae per plant in mustard. The broad sense

heritability was higher for all the characters except length of siliqua where it was moderate.

Uddin *et al.* (1995) reported high PCV and GCV for 1000-seed weight, seed yield per plant, primary branches per plant and siliquae per plant. High heritability values were observed for 1000-seed weight and moderately high for other characteristics except primary branches per plant. The expected genetic advance values were also observed to be high for 1000-seed weight and siliquae per plant.

Das *et al.* (1998) observed high estimates of PCV and GCV for siliquae per plant and number of secondary branches per plant. High heritability coupled with high genetic advance was observed for siliquae per plant, number of secondary branches per plant, 1000-seed weight and plant height indicating predominance of additive gene action in inheritance of these traits.

Shalini (1998) indicated high PCV and GCV for number of siliquae per plant and 1000-seed weight while number of secondary branches per plant showed moderate heritability with moderate genetic advance. Days to 50 per cent flowering showed high heritability coupled with low genetic advance in Indian mustard.

Khulbe *et al.* (2000) conducted genetic variability, heritability and genetic advance studies for seed yield and its components in Indian mustard and revealed maximum variability for seed yield. All the characters except percent oil content exhibited high heritability with high or moderate genetic advance suggesting the role of additive gene action in conditioning the traits. Non-additive gene action appeared to influence the expression of days to maturity while environment had a major influence on per cent oil content.

Shalini *et al.* (2000) studied genetic variation in 81 diverse Indian mustard genotypes. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all ten characters studied. They also observed moderate to high genotypic coefficient of variation, heritability and genetic gain for 1000-seed weight, number of siliquae per plant and number of secondary branches per plant indicating the higher response to selection for these characters. Low coefficient of variation, medium to low heritability and low genetic gain were observed for the remaining characters.

Sikarwar *et al.* (2000) studied 30 varieties of mustard to measure heritability and genetic advance. The heritability estimates for number of siliquae per plant, 1000-grain

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weight, number of secondary branches, plant height and seed yield per plant were found genetically more variable than rest of the characters.

Ghosh and Gulati (2001) conducted studies on genetic variability and heritability on 36 genotypes of Indian mustard. Both genotypic and phenotypic coefficients of variability were high in magnitude for all the characters except plant height. The differences between the PCV and GCV were narrow for all the characters studied. This coupled with high heritability except plant height, indicated the usefulness of phenotypic selection in improving these traits. High heritability coupled with high genetic advance was observed for oil content, harvest index, number of primary branches, number of siliquae on main shoot, main shoot length and number of seeds per siliqua. This suggested the importance of additive gene action for their inheritance and improvement could be brought about by simple phenotypic selection.

Lalta *et al.* (2001) conducted heritability and genetic advance studies using 21 F_1 Indian mustard hybrids and their parents for yield and its components. High heritability was observed for days to flowering, days to maturity, length of main raceme and test weight. The genetic advance was also high for days to flowering, length of main raceme, number of secondary branches and yield. Low to medium estimates of expected genetic advance were observed for days to maturity, test weight and oil content.

Mahto (2001) reported high genotypic and phenotypic variances in Indian mustard for number of secondary branches per plant, number of siliquae per plant and seed yield per plant. Heritability, genetic gain and genetic gain per cent of mean were high for seed yield per plant.

Pant and Singh (2001) while studying genetic variability for nine traits in 25 genotypes of Indian mustard, observed highly significant genotypic differences for all traits studied except days to flower. All traits showed high heritability, with the highest value estimated for seed yield per plant. The estimates of genetic advance were comparatively low for oil content and days to flower. The genotypic coefficients of variation and heritability estimates for oil content and days to flower suggested that these traits can not be improved effectively merely by phenotypic selection.

Vijaykumar *et al.* (2001) evaluated four species of *Brassica viz., Brassica juncea*, *Brassica napus*, *Brassica carinata* and *Brassica campestris* for two years for plant type

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traits including basal branching. In *Brassica juncea,* there was greater variation for plant height, but, not for seed yield. It was only next to *Brassica campestris* followed by *Brassica napus* for variation in basal branching trait. In *Brassica campestris,* there was no genetic variation for basal branching trait, but, it showed greater variation for days to flowering and total number of primary and secondary branches.

Mahto and Haider (2002) conducted variability studies in nine lines of Indian mustard and observed highly significant differences between the genotypes for most of the yield contributing characters.

Khan and Khan (2003) observed highly significant differences among 8 genotypes of Indian mustard for various traits *viz.,* plant height, number of primary branches, number of secondary branches and number of pods per plant.

Mahla *et al.* (2003) conducted genetic variability studies in 55 Indian mustard genotypes. They observed significant variation among the genotypes for all the traits except number of seeds per pod. The phenotypic coefficient of variation was slightly higher than the genetic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was observed for days to flowering followed by 1000-seed weight, days to maturity and plant height indicating that the heritability of these traits was attributed to additive gene effects. High heritability along with medium to low genetic advance was recorded for plant height, length of main branch and number of days to flowering indicating the presence of non-additive gene action for these characters.

Naazar *et al.* (2003) studied 25 winter type rapeseed varieties introduced from diverse sources of the world for variability, heritability and genetic advance for seed yield and yield components. Significant differences among genotypes for most of the traits indicated that there was sufficient variability available for effective selection. Genotypic and phenotypic variances were highest for pods per plant followed by plant height whereas the maximum genotypic and phenotypic coefficients of variability were found for seed yield per plant and pods per plant, respectively. Maximum heritability (90.3 %) was obtained for days to maturity followed by flower duration (66.2 %), seed weight (54.8 %) and seed yield (47.7 %). High heritability for flower duration, seed weight and seed yield coupled with high genetic advance indicated that these traits could be improved through mass selection.

Singh *et al.* (2003) while studying variability, heritability and genetic advance in 40 Indian mustard cultivars, reported that varietal differences were highly significant for

plant height, days to 50 per cent flowering, siliquae per plant, seeds per siliqua, days to maturity, 1000-seed weight and seed yield per plot. The coefficients of genotypic and phenotypic variation were highest for 1000-seed weight and lowest for days to maturity. The highest genetic advance was obtained for 1000-seed weight followed by seed yield per plot, days to 50 per cent flowering and siliquae per plant.

Mahak *et al.* (2004) studied genetic variability, heritability and genetic advance in twenty one F_1 hybrids of Indian mustard and their seven parents. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters studied. High heritability coupled with high genetic advance was observed for days to flowering followed by 1000-seed weight, days to maturity and plant height.

Singh and Singh (2004) studied variability, heritability and genetic advance in forty Indian mustard cultivars and the varietal differences were highly significant for plant height, days to 50 per cent flowering, siliquae per plant, seeds per siliqua, days to maturity, 1000-seed weight and seed yield per plot. The coefficients of genotypic and phenotypic variation were highest for 1000-seed weight and minimum for days to maturity. The highest genetic advance was obtained for 1000-seed weight followed by seed yield per plot, days to 50 per cent flowering and siliquae per plant.

Monalisa *et al.* (2005) observed highly significant differences among all the genotypes of Indian mustard for various traits *viz.,* plant height, days to 50 per cent flowering, days to maturity, primary branches per plant, siliquae per plant, seeds per siliquae, 100-seed weight, seed yield per plant and oil content.

Rai *et al.* (2005) observed higher estimates of phenotypic coefficient of variation and genotypic coefficient of variation for 1000-seed weight, seed yield per plant, number of primary branches, seeds per siliquae and number of siliquae on main raceme. They also reported moderate to higher estimates of genetic advance coupled with high heritability for all the characters except days to maturity, days to 50 per cent flowering and oil content.

Kumar and Mishra (2006) evaluated fifteen varieties of mustard and toria genotypes for comparative account of genetic variability, heritability and genetic advance for eight quantitative and two qualitative characters. They concluded that performance of mustard cultivars was considerably better than that of toria varieties. In general,

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phenotypic coefficients of variation were higher than genotypic coefficients of variation indicating the influence of environment for all the traits under study.

Patel and Patel (2006) conducted variability studies on 40 genotypes of Indian mustard for days to 50 per cent flowering and maturity, plant height, length of main branch, primary and secondary branches per plant, siliquae per plant, seeds per siliqua, length of siliqua, seed yield per plant, 1000-seed weight, oil content and harvest index. The analysis of variance showed highly significant differences among the genotypes for all the characters studied.

Kumar and Mishra (2007) observed significant differences among all the genotypes for days to flowering and maturity, plant height, siliquae per branch and seed yield per plant. The estimates of phenotypic variances were higher than their corresponding genotypic variances. Plant height, siliquae per branch and seed yield per plant had high heritability estimates along with high genetic advance indicating the improvement for these characters through simple phenotypic selection.

Muhammad *et al.* (2007) while studying genetic variability in 10 genotypes of *Brassica juncea,* reported siliquae per plant to be the strong trait for seed yield improvement because of its higher genotypic coefficient of variability, broad sense heritability and genetic advance.

Mukesh *et al.* (2007) conducted pooled analysis of variance studies for days to 50 per cent flowering, days to 50 per cent maturity, plant height, number of primary branches, number of secondary branches, length of the main shoot, number of pods on the main shoot, number of pods on primary branches, number of pods on secondary branches, seed filling period, pod length, number of seeds per pod and 1000-seed weight in Indian mustard. The study revealed significant variation among the genotypes for all traits except pod length.

Abebe (2008) conducted variability studies on 60 Ethiopian mustard genotypes. The analysis of variance showed highly significant difference for all characters *viz.,* days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plot, seed yield per plant, biomass per plot, oil content and oil yield per plot. High phenotypic coefficients of variation (PCV) were recorded for seed yield per plot, oil yield per plot,

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biomass per plot, seed yield per plant and number of pods per plant. The magnitudes of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for seed yield per plot, oil yield per plot, biomass per plot and secondary branches per plant. Heritability estimates were high for days to maturity, days to flowering, 1000-seed weight, plant height, primary branches per plant, biomass per plot, seed yield per plot, oil content and oil yield per plot.

Acharya and Pati (2008) reported high heritability estimates coupled with high genetic advance for plant height, number of secondary branches per plant and number of siliquae per plant in 15 genotypes of Indian mustard.

Bhuiyan *et al.* (2008) observed significant variations due to different planting dates in Indian mustard for days to flowering, days to maturity, plant height, number of primary branches per plant, siliquae per plant, seeds per siliqua, 1000-seed weight, seed yield per plant and seed yield per hectare. Results showed that the highest seed yield (1.86 t/ha) was obtained from the second planting (October 30) and it was significantly different from the yields of all other dates of planting. The seed yield (1.47 t/ha) of last planting (November 30) was also satisfactory because of the prolonged winter season prevailing in the northern part of the country.

Verma *et al.* (2008) observed higher significant genotypic differences in pooled analysis of variance for all the characters *viz.,* days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of seeds per siliqua, length of siliqua, 1000-seed weight and seed yield per plant in Indian mustard. The genotypes showed different responses in different years.

Zehra and Gulcan (2009) evaluated 10 winter rapeseed genotypes for genetic variation and broad sense heritability for plant height, number of branches per plant, number of pods per plant, pods per main stem, pod length, 1000-seed weight, seed yield per plant and per cent oil content for two years. The results revealed significant differences for all yield and quality characters which indicated the presence of sufficient genetic variability for effective selection. Variability, broad sense heritability and genetic advance were maximum for oil yield and seed yield followed by protein yield.

Dilara *et al.* (2011) conducted a field experiment with 25 mustard (*Brassica* ssp. L.) genotypes to study the genetic diversity present among the genotypes. Eleven quantitative characteristics such as plant height, days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, diameter of siliqua, length of siliqua, number of seeds per siliqua, 100-seed weight and yield per plant were taken into consideration. The analysis of variance revealed a remarkable variability among the genotypes in terms of the specified characteristics.

Rameeh (2011) studied genetic variation in 36 rapeseed genotypes including four cultivars and 32 advanced lines. The analysis of variance indicated significant genetic variation for different seed yield contributing characters. Much variation among the genotypes was observed for seeds per siliqua and siliquae on main raceme. Heritability estimates were high for siliquae on main raceme, seeds per siliqua and siliquae per plant.

Saad *et al.* (2011) conducted two field experiments for canola (*Brassica napus* L.) during two successive winter seasons in order to find out the effect of sowing dates on the growth, yield and quality of canola cultivars. The results indicated that the second planting date (15th October) gave the highest number of primary branches, leaf area index, number of siliquae per plant, dry weight per plant, number of seeds per siliqua, 1000-seed weight, total yield and oil yield while the first planting date (10th October) gave the highest percentage of oil in seeds in both seasons.

Yared *et al.* (2012) observed significant differences among the genotypes for days to flowering, days to maturity and per cent oil content. The highest heritability values were exhibited by per cent oil content followed by days to flowering and days to maturity. High heritability along with high genetic advance (as per cent of mean) was recorded for days to flowering and per cent oil content. Days to flowering, days to maturity and per cent oil content appeared to be important traits to be considered for further varietal development programme.

2.2   Genetic divergence studies

Several statistical procedures have been developed for measuring the divergence among genotypes. Multivariate analysis based on Mahalanobis (1936) D^2-statistic serve

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as important tool in quantifying the degree of genetic divergence among all possible pairs of populations at genotypic level (Rao 1952).

Anand and Rawat (1984) grouped 50 geographically diverse *Brassica 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.

Yadav *et al.* (1985) studied seed yield per plant along with ten related characters in seven varieties of *Brassica juncea* and their 21 F_1 hybrids. The parents and hybrids were assigned to 5 clusters.

Gupta *et al.* (1991) classified 48 apparently diverse genotypes of Indian mustard into 5 clusters 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.

Rao *et al.* (1993) stressed the importance of interspecific hybridization to create genetic variability in rapeseed-mustard and successfully developed short statured plants in the back cross progeny of *Brassica napus* x *Brassica carinata.*

Shalini (1998) reported that considerable amount of genetic diversity was prevalent among 81 genotypes representing diverse eco-geographical region of the country which were randomly distributed into 11 clusters. The ranking of characters indicated that number of siliquae per plant followed by plant height and days to 50 per cent flowering were the major contributors towards genetic divergence. The investigation also revealed that the clusters XI, X, IX, II and VI possessed the potential genotypes which had the superiority in economic traits which needs to be considered in the genetic improvement of mustard.

Choudhary *et al.* (2000) studied the crossability between *Brassica carinata* (BBCC, 2n=34) and *Brassica rapa* (AA, 2n=20) and the cytomorphology of their F_1 hybrids. Hybrids between these two species were only obtained when *Brassica carinata* was used as the female parent. The hybrid plants exhibited intermediate leaf and flower morphology and were found to be free from white rust and *Alternaria* blight diseases. Meiotic analysis of F_1 hybrids indicated that traits of economic importance, such as

disease resistance, could be transferred from *Brassica carinata* to *Brassica rapa* through interspecific crosses.

Srivastav and Singh (2000) conducted genetic divergence studies on 26 cultivars of Indian mustard using Mahalanobis D^2-statistic. All the cultivars were grouped into 6 clusters. Cluster I was the biggest with 18 cultivars followed by clusters III and II with 3 and 2 cultivars, respectively. Clusters IV, V and VI had only 1 cultivar each. Cluster I had the lowest intra-cluster D-value (7.56). The highest inter-cluster D-value was observed between clusters III and V (20.51) while the lowest inter-cluster D-value was observed between clusters I and II. Based on average cluster means for the characters studied, cultivars in cluster III had the highest number of primary (6) and secondary branches (22), oil percentage (40.79 per cent) and mean seed yield per plant.

Verma and Sachan (2000) studied 64 genotypes of Indian mustard for genetic divergence using Mahalanobis D^2-statistic. All the genotypes were grouped into 12 clusters. Clusters I was largest comprising 57.8 per cent genotypes while clusters VII, VIII, IX, X, XI and XII were monogenotypic. No parallelism was observed between geographic diversity and genetic diversity.

Sinha and Singh (2004) studied genetic divergence in Indian mustard and grouped 19 genotypes into 5 clusters with cluster I having the highest number of genotypes (11). The intra-cluster distance was highest in cluster II while inter-cluster divergence was highest between clusters IV and V. Genotypes in cluster IV recorded highest main shoot length, number of pods per main shoot and seed yield per plant whereas genotypes in cluster V had tallest plants.

Thul *et al.* (2004) grouped 33 Indian mustard genotypes into eight different clusters. Cluster III was the biggest with 11 genotypes followed by cluster I with 9 genotypes while clusters V and VI consisted of 4 and 3 genotypes, respectively. Clusters II and VII included two genotypes each and clusters IV and VIII included one genotype each.

Monalisa *et al*. (2005) grouped 19 Indian mustard genotypes into 6 clusters and observed wide range of genetic diversity in the material. The highest number of genotypes were included in cluster III (9). The maximum intra-cluster distance was recorded in cluster III whereas the maximum inter-cluster distance was observed between clusters II and V. The lowest inter-cluster distance was observed between cluster I and II.

Siliquae per plant had the highest contribution towards total genetic divergence followed by days to maturity and plant height.

Goswami and Behl (2006) studied genetic divergence among 43 genotypes of Indian mustard using D^2-statistic in two environments. All the genotypes were grouped into 6 and 15 clusters in environment I and environment II, respectively. Plant height contributed maximum towards total genetic divergence followed by days to maturity, main shoot length, days to 50 per cent flowering, siliquae on main shoot, oil content and seed yield per plant in both environments. The characters such as primary branches, siliqua length and 1000-seed weight contributed very less towards total genetic divergence in both environments.

Malik *et al.* (2006) conducted genetic divergence studies among 30 cultivars of Indian mustard using Mahalanobis D^2-statistic. All genotypes could be grouped into 6 clusters. Cluster IV had the highest number of genotypes (8). The inter-cluster distance was highest between clusters V and VI followed by clusters I and VI. Based on cluster means, cluster VI was observed to be important for seed yield, days to 50 per cent flowering, number of secondary branches, days to maturity, number of siliquae per plant, length of siliqua and 1000-seed weight and cluster III for biological yield, number of primary branches and number of seeds per siliqua.

Patel and Patel (2006) grouped 40 genotypes of Indian mustard into 4 clusters. Cluster I was the largest consisting of 28 genotypes while cluster IV comprised only one genotype suggesting that genotype Zem 2 diverged most from others. The intra-cluster distance was maximum in cluster II and minimum in cluster IV. The maximum inter-cluster distance appeared between clusters III and IV followed by clusters I and IV suggesting wide diversity between two clusters. An examination of cluster mean values showed the importance of cluster IV for number of primary and secondary branches per plant, number of siliquae per plant, seeds per siliqua and seed yield and that of cluster III for early flowering, dwarf plant type, high oil content and high harvest index.

Mukesh *et al.* (2007) studied genetic divergence in Indian mustard and grouped 25 genotypes into seven clusters. The cluster I was the largest with 6 genotypes followed by cluster II (5), clusters IV and V (4 genotypes each), cluster III (3), cluster VI (2) and cluster VII (1). The inter cluster distance was highest between clusters VI and VII.

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Cluster VII exhibited the highest seed yield per plant, 1000-seed weight, number of secondary branches, length of the main shoot, number of pods on the main shoot and number of pods on secondary branches. Cluster VI showed the highest mean values for days to 50 per cent flowering and maturity, seed filling period, number of secondary branches, length of the main shoot and number of pods on primary branches.

Singh *et al.* (2007) grouped 81 genotypes of Indian mustard into 13 clusters. Cluster I was the largest, comprising of 25 genotypes followed by clusters II, III, IV, V, VI, VII, VIII and IX which had 16, 13, 7, 5, 4, 3, 2 and 2 genotypes, respectively and clusters X, XI, XII and XIII had one genotype each. Cluster analysis revealed that the geographical distribution of the cultivars did not significantly contribute to genetic divergence. The intra-cluster distances ranged from 52.33 to 89.52 for clusters III and VII, respectively. Clusters XI and XII were the most diverse while the inter-cluster proximity was maximum between clusters I and III.

Mahmuda *et al.* (2008) studied genetic divergence and grouped 22 rapeseed genotypes into four clusters based on the mean performance and clustering pattern. Cluster II contained the maximum number of genotypes (9) and cluster III contained the lowest (2). The highest inter-cluster distance was found between clusters I and III. The highest intra-cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and 1000-seed weight. Cluster III had the lowest cluster mean values for number of days to 50 per cent flowering and the number of days to maturity.

Kumari (2010) conducted genetic divergence studies on 31 genotypes of Indian mustard using Mahalanobis D^2-statistic. All cultivars were grouped into 11 clusters in Env.I, 5 clusters in Env.II and 6 clusters in pooled over the environments. Maximum genotypes were grouped in cluster I in Env.I, Env.II and pooled over the environments. Maximum intra-cluster distance was observed for cluster I in Env.I and pooled over the environments and cluster II in Env.II. Maximum inter-cluster distance existed among clusters X and XI in Env.I, III and IV in Env.II and III and V in pooled over the environments. Highest cluster means for seeds per siliqua and harvest index were observed in cluster VII in Env.I. in Env.II, highest cluster means for siliquae per plant, siliquae on main shoot, seed yield per plant, biological yield per plant and harvest index

were observed while in pooled over the environments, cluster III had maximum values for length of main shoot, 1000-seed weight and seed yield per plant.

Sheikh *et al.* (2010[a]) used interspecific hybridization to successfully introgress genes for morphological traits from the quality lines of *Brassica juncea* (AABB, 2n=36) into *Brassica carinata* (BBCC, 2n=34). Plant height recorded a significant decrease in the progenies over both parents indicating successful introgression of genes for short stature from *Brassica juncea* to *Brassica carinata.* In addition, an increase in primary branches and secondary branches per plant was also recorded.

Sheikh *et al.* (2010[b]) again used interspecific hybridization to successfully introgress genetic variability into *Brassica carinata* (BBCC, 2n=34) for morphological traits from quality lines of *Brassica napus* (AACC, 2n=38). The assessment of morphological trait of BC_1 F_2 progeny revealed excellent variability. A significant reduction in the plant height and days to maturity in the progeny was observed. Besides, siliquae on main shoot and length of main shoot also showed significant increase.

Singh *et al.* (2010) derived three lines of *Brassica carinata viz.,* 08–304, 08–312 and 08–316 from interspecific hybridization and evaluated for morphological traits during 2007–08 and 2008–09. These lines showed significant increase in shoot length, 1000-seed weight and significant decrease in maturity duration. Development of these lines is important for Karan rai improvement programme in India.

NRCKR 304 (INGR 10049), an early maturing bold seeded line with long main shoot derived from the cross of Varuna (*Brassica juncea*) x BPKR 13 (*Brassica carinata*) has been developed and registered with NBPGR, New Delhi (Anonymous 2010-2011).

Singh *et al.* (2012) studied genetic divergence in Indian mustard and grouped 50 genotypes into 6 clusters. The cluster I was largest and had 30 genotypes followed by cluster II (10) and cluster III (6) whereas remaining clusters comprised only one genotype each. The Intra-cluster values were found to be zero for clusters IV, V and VI. The highest Intra-cluster D-value was observed for cluster I followed by II and III. The average Inter-cluster values were obtained to be highest between clusters V and VI followed by Clusters IV and VI.

2.3   Correlation and Path coefficient analysis

The correlation coefficient is a measure of the degree of association between two characters. To raise the genetic potential of a crop, the knowledge of nature and magnitude of association among different characters is of immense value to any breeding programme and forms basis for selection. For selection of several characters simultaneously, the knowledge of character association is helpful to avoid undesirable correlated changes in other characters. Johnson *et al.* (1955) have stressed the importance of both phenotypic and genotypic correlations among the characters in planning and evaluating breeding programmes. Correlation coefficients for a given trait vary with the genotypes studied and the environment where the test is carried out.

In correlation studies, when more variables are included, the associations between various characters do not give the clear picture because these give the degree, but, not the cause. For finding a suitable and reliable selection index, these correlations must be analysed further and partitioned into direct and indirect effects through path analysis. Path coefficient analysis as originally proposed by Wright (1921) measures the direct influence of one variable upon the other and permits the partitioning of the correlation coefficients into components of direct and indirect effects. Dewey and Lu (1959) have opened the way for plant breeders by using first time, path coefficient analysis in breeding programme.

Mehrotra *et al.* (1976) observed that seed yield per plant had significant positive association with biological yield, harvest index and pod production per plant in Indian mustard.

Hari *et al.* (1985) while studying 38 genotypes of Indian mustard revealed that total siliquae number per plant, harvest index, secondary branches per plant and 1000-seed weight were significantly and positively correlated with yield and total siliquae number per plant, harvest index and 1000- seed weight had the greatest direct effects on seed yield.

Thakur and Zerger (1989) studied genotypic and phenotypic correlations between seed yield and eight other characters in 63 genotypes of Indian mustard. They observed that the three characters *viz.,* primary branches, secondary branches and siliquae per plant had significant and positive correlation with seed yield. Primary and secondary branches, seeds per siliqua and 1000-seed weight influenced seed yield directly while siliquae per plant and days to maturity contributed *via* secondary branches.

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Reddy (1991) reported that seed yield per plant had significant and positive correlation with primary and secondary branches per plant, siliquae per plant and seeds per siliqua in Indian mustard.

Joshi *et al.* (1992) observed significant positive correlation of seed yield per plant with plant height, number of siliquae per plant and number of seeds per siliqua.

Uddin *et al.* (1995) observed highly significant correlations of plant height, primary branches per plant and 1000-seed weight with seed yield per plant, but, high negative and significant correlation with seeds per siliqua at both genotypic and phenotypic levels in Indian mustard.

Yadav *et al.* (1996) conducted path analysis studies on 25 genotypes of Indian mustard and revealed that number of siliquae per plant had the highest positive direct effect on seed yield per plot.

Major and Gyanendra (1997) while studying 52 genotypes of Indian mustard observed that seed yield exhibited significant and positive association with branches per plant, siliquae per plant, seeds per siliqua and 100-seed weight. Path analysis revealed that siliquae per plant, seeds per siliqua and 100-seed weight had the greatest direct and positive effect on seed yield.

Khulbe and Pant (1999) conducted correlation studies on twelve yield related traits in 8 Indian mustard parents and their 28 F_1 hybrids and revealed that grain yield was positively associated with siliquae per plant, siliqua length, seeds per siliqua and 1000-seed weight. Path coefficient analysis revealed that harvest index, siliquae per plant, siliqua length, 1000-seed weight, seeds per siliqua and days to initial flowering were the major characters influencing grain yield both directly and indirectly.

Niraj and Srivastava (2000) while studying the association analysis in Indian mustard, observed that seed and oil yields were significantly and positively associated with plant height and primary branches. Path analysis suggested that seed and oil yields mutually contributed considerably towards each other. Days to flowering and maturity, plant height and seed oil content were the other characters which contributed directly towards both the parameters of economic yield whereas 1000-seed weight and primary branches contributed directly to seed yield only.

Shalini *et al.* (2000) conducted correlation and path coefficient studies on 81 Indian mustard genotypes and revealed that number of siliquae, number of primary

branches per plant, number of secondary branches per plant, seeds per siliqua and plant height had highly significant and positive association with seed yield. The number of siliquae per plant had the highest direct effect on seed yield followed by 1000-seed weight, number of primary branches per plant and plant height. Most of the characters had an indirect effect on seed yield.

Ghosh and Gulati (2001) reported that seed yield per plant had significant positive association with days to 50 per cent flowering, days to maturity, plant height, number of secondary branches, number of siliquae on main shoot and oil content. These components in turn, exhibited significant positive correlation with each other. The results indicated that selection for one of these characters might automatically combine the other variables and these appeared to be the most important selection criteria for increasing seed yield in Indian mustard.

Patel *et al.* (2001) observed that at genotypic level, seed yield per plant had highly significant positive correlation with days to flowering, days to maturity, plant height, branches per plant, length of siliquae, number of siliquae per plant and 1000-seed weight except number of seeds per siliqua. The number of siliqua per plant exhibited the strongest genotypic association and highest direct effect towards seed yield. Days to flowering, 1000-seed weight, length of siliqua and branches per plant had positive direct and indirect effect on seed yield. In contrast, days to maturity and plant height had negative direct and indirect effects on seed yield.

Shah *et al.* (2002) observed that genotypic correlation coefficients were higher than their respective phenotypic correlation coefficients for most of the characters. At both levels, seed yield per plant had the strongest positive and significant correlation with number of siliquae per plant.

Pant *et al.* (2002) while studying 25 genotypes of Indian mustard, revealed that seed yield per plant was positively and significantly correlated with days to flower, plant height, number of primary and secondary branches, number of siliquae on main raceme and oil content at the genotypic level, but, was negatively correlated with siliqua length and 1000-seed weight.

Srivastava and Singh (2002) conducted correlation and path coefficient studies on 26 genotypes of Indian mustard and observed that seed yield per plant had significant

positive association with number of primary branches, number of secondary branches, 1000-seed weight and oil content. Path coefficient analysis showed that these characters had strong direct effect on seed yield except oil content.

Beena and Charjan (2003) and Chaudhary *et al.* (2003) while studying correlation and path analysis on 28 genotypes of Indian mustard, observed that seed yield per plant had highly significant and positive correlation with days to maturity, length of main axis, primary branches per plant, secondary branches per plant, number of siliquae per plant, siliqua length, number of seeds per siliqua and 1000-seed weight. Path analysis revealed that secondary branches per plant, number of siliquae per plant and siliqua length were the most important characters having high direct effect on seed yield per plant.

Mahak *et al.* (2003) reported that seed yield per plant had significant positive association with days to flowering, days to maturity, number of primary and secondary branches per plant, length of main fruiting branch, plant height and number of seeds per siliqua.

Mahla *et al.* (2003) while studying correlation in 55 Indian mustard genotypes, revealed that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Seed yield per plant was positively and significantly associated with number of branches per plant, number of siliquae on main branch, plant height, number of seeds per siliqua and length of main branch. Oil content was negatively and significantly correlated with test weight. Path analysis revealed that the number of branches per plant had the greatest direct and indirect effects on seed yield per plant.

Nazaar *et al.* (2003) while studying 25 winter type rapeseed genotypes, revealed that seed yield per plant had positive and significant correlation with harvest index, seed weight and flower duration. Significant positive correlation of seed weight with harvest index, flower duration and seed yield indicated that improvement in seed weight will give higher harvest index resulting in high seed yield. Harvest index, seed weight and pods per plant recorded a considerable direct positive effect on seed yield. The results indicated that seed weight, pods per plant and harvest index may be good selection criteria to improve seed yield.

Mahak *et al.* (2004) studied correlation in 21 F_1 hybrids of Indian mustard along with 7 parents and observed that the seed yield per plant had positive and significant

correlation with number of branches, length of main raceme, 1000-seed weight and oil content.

Sheikh *et al.* (2004) observed that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for all characters studied. Seed yield had significant positive association with plant height, siliquae per plant and seeds per siliqua. Plant height, siliquae per plant and seeds per siliqua had positive direct effect on seed yield.

Singh and Singh (2004) conducted path coefficient studies on 40 Indian mustard lines and observed that the plant height had the highest positive direct effect followed by number of seeds per siliqua on seed yield. On the other hand, the number of primary branches per plant, siliquae per plant and days to maturity had low and negative direct effects on seed yield.

Sirohi *et al.* (2004) studied correlation and path analysis in 30 Indian mustard genotypes and reported that seed yield had significant and positive association with biological yield, harvest index and number of siliquae per plant. Path coefficient analysis showed that biological yield and harvest index had high, positive and direct effects on seed yield. Harvest index had major indirect contribution towards seed yield.

Sudan *et al.* (2004) while studying correlation and path coefficient analysis in 10 genotypes of Indian mustard, observed that seed yield per plant showed significant and positive association with number of primary branches per plant, number of secondary branches per plant and 1000-seed weight. Path analysis indicated that number of primary branches exhibited the highest direct effect on seed yield per plant.

Kardam and Singh (2005) reported that phenotypic correlation coefficients were higher in magnitude compared to genotypic correlation coefficients for most of the characters studied. Seed yield per plant was significantly and positively correlated with plant height, primary branches per plant, number of siliquae per plant, number of seeds per siliqua and 1000-seed weight. The number of siliquae per plant had the highest direct contribution to seed yield followed by primary branches per plant, 1000-seed weight, number of siliquae on main shoot and number of seeds per siliqua.

Rai *et al.* (2005) observed that at phenotypic level, seed yield per plant had significant positive correlation with plant height, number of primary branches per plant, days to 50 per ecnt flowering and number of siliquae on main raceme.

Sharad and Basudeo (2005) evaluated 100 germplasm lines of Indian mustard and found that seed yield per plant had significant and positive correlation with number of secondary branches per plant, length of main shoot, length of siliqua, siliquae on main shoot and 1000-seed weight. Oil content had negative and significant correlation with seed yield. Length of siliqua had the highest positive direct effect on seed yield per plant followed by 1000-seed weight, plant height, number of secondary branches per plant and length of main shoot.

Verma and Mahto (2005) observed that seed yield per plant had positive and significant correlation with days to first flowering, days to 50 per cent flowering, plant height, number of primary branches, number of secondary branches, number of siliquae per plant, number of seeds per siliqua, days to maturity and 1000-seed weight. Partitioning of correlation coefficients revealed the highest positive direct effect of days to 50 per cent flowering followed by number of siliquae per plant, plant height and number of primary branches per plant on seed yield per plant at the genotypic level. High residual effects were observed both at phenotypic (0.473) and genotypic (0.418) levels.

Tusar *et al.* (2006) conducted correlation and path coefficient studies on 5 Indian mustard genotypes for eleven yield related characters and revealed that seed yield was positively and significantly associated with plant height, number of siliquae per plant, 1000-seed weight and number of branches per plant. Path coefficient analysis revealed that the number of siliquae per plant had the greatest direct contribution on seed yield followed by 1000-seed weight.

Muhammad *et al.* (2007) while studying 10 genotypes of Indian mustard, revealed that siliquae per plant showed highly significant positive correlation and maximum direct contribution towards seed yield.

Acharya and Pati (2008) observed that seed yield per plant had significant and positive association with days to 50 per cent flowering, days to maturity, plant height, number of seeds per siliqua and 1000-seed weight. Number of seeds per siliqua, days to 50 per cent flowering and day to maturity recorded highest positive direct effect on seed yield per plant followed by number of secondary branches per plant. The studies suggested that selection for number of seeds per siliqua, number of secondary branches

per plant, days to maturity and seed yield was important to develop high yielding cultivars in mustard.

Verma *et al.* (2008) observed that genotypic correlation coefficients were higher in magnitude than the phenotypic correlation coefficients for most of the characters suggesting that the association between various characters, in general, was genetically controlled. Seed yield per plant showed highly significant and positive correlation with plant height, number of primary branches per plant, number of secondary branches and number of seeds per siliqua. Path coefficient analysis indicated that high positive direct effects on seed yield were observed for plant height, number of primary branches per plant, number of seeds per siliqua and 1000-seed weight. On the other hand, days to maturity and length of siliqua showed high negative direct effects on seed yield.

Sirohi *et al.* (2008) studied correlation and path coefficients for twelve characters using 30 Indian mustard genotypes. Genotypic correlations, in general, were higher than phenotypic correlations. Seed yield showed significant and positive association with harvest index and biological yield. The path coefficient analysis revealed that biological yield and harvest index had high and positive direct effects on seed yield. Among the 11 independent contributing traits, the harvest index had the major indirect contributions towards seed yield.

Rameeh (2011) reported that siliquae per plant had significant positive correlation with seed yield per plant and also had high positive direct effect on seed yield per plant, thus, any change for this trait will have considerable effect on seed yield.

Kumari and Kumari (2012) conducted correlation and path coefficients studies on 31 genotypes of Indian mustard. Both the phenotypic and genotypic correlation coefficients revealed significant positive associations of number of primary branches per plant, siliquae on main shoot, biological yield per plant and harvest index with seed yield per plant. The path coefficient analysis revealed that biological yield per plant and harvest index exhibited positive and high phenotypic and genotypic direct effects on seed yield per plant. Therefore, these characters could be considered as the best selection parameters for the improvement of seed yield in Indian mustard.

Singh *et al*. (2012) studied correlation and path coefficients for 200 genotypes of Indian mustard. Seed yield per plant recorded positive and significant correlations with main shoot length, siliqua length, number of seeds per siliqua and 1000-seed weight

whereas it was negative with days to first flowering and days to 50 per cent flowering. Path analysis indicated that days to 50 per cent flowering exhibited maximum positive direct effect on seed yield followed by siliquae on main shoot, seeds per siliqua, oil content, 1000-seed weight, main shoot length and days to maturity. Maximum indirect effects on seed yield were also observed *via* days to 50 per cent flowering and number of siliquae on main shoot.

2.4   Anther culture studies

Male reproductive processes take place in the stamens of flowering plants. The diploid cells (microspore mother cells) undergo meiosis and produce haploid male spores or microspores. In general, microspores divide mitotically and differentiate into multicellular male gametophytes or pollen grains. The principle of androgenesis is to arrest the development of the pollen grains (male gametophytes) and force them towards a somatic pathway. *In vitro* androgenesis can be achieved from the microspores leading to the formation of haploids either by direct embryogenesis or *via* callus formation.

The term haploid refers to the plant containing the gametic chromosome number (n) or half the somatic number of chromosomes (2n). By doubling the haploid complement, the normal number of chromosome is restored. Doubled haploids offer the fastest possible approach to homozygosity for research purposes or cultivar release. The employment of haploid production techniques greatly shorten the breeding cycle to develop cultivars (Chu 1982 and Jain *et al.* 1996). Doubled haploids can effectively be utilized for developing linkage maps using molecular markers, in mutation breeding as well as genetic engineering. Doubled haploids are most reliable for developing homozygous genotypes in *Brassica* (Yadav *et al*. 2012).

The first report of haploids was published by Blakeslee *et al.* (1922) in *Datura stramonium*. Subsequently, haploids were reported in many species. Guha and Maheshwari (1964) developed an *in vitro* anther culture technique for the production of haploids. A rapid expansion in research ensued with further development of chromosome doubling techniques (n→2n) that converted sterile haploids (H) into fertile, homozygous doubled haploid (DH) plants.

Anther culture of *Datura innoxia* (Guha and Maheshwari 1964) appears to be the first successful application of this technique. This technique has been refined and

extended to induce haploids by several workers in other crops like tobacco (Tanaka and Nakata 1969; Burk 1970) and lotus (Niizeki and Grant 1971). Since then, the technique has been successfully used to produce pollen plants in many species including crop plants such as *Oryza sativa* (Niizeki and Oono 1968), *Hordeum vulgare* (Clapham 1971; 1973; Malepszy and Grunewaldt 1974), *Solanum tuberosum* (Dunwell and Sunderland 1973), *Triticum aestivum* (Ouyang *et al.* 1973; Craig 1974), *Triticale* (Wang *et al.* 1973) and *Secale cereale* (Thomas and Wenzel 1975). In *Brassica,* androgenesis was first reported by Kameya and Hinata (1970) in *Brassica oleracea*. This was followed by microspore embryogenesis reports in *Brassica napus* and *Brassica campestris*. After this, due to refinement in the technique, haploids from several *Brassica* species were reported through anther culture (Jain *et al*. 1989; Keller and Armstrong 1978; 1979; Sharma and Bhojwani 1985). Roy and Saha (1997) have reported higher percentage of callus induction on a medium with 2 mg/l 2, 4-D and NAA each.

2.4.1 Androgenesis- a supplementary technique to conventional breeding

Production of doubled haploids through anther culture technique is a rapid method to achieve homozygosity essential to develop varieties in self pollinated crops. Genetic recombinants as a consequence of hybridization in F_1 gametes can be instantly fixed in one generation through androgenesis reducing the time of homozygous line development to one generation from 6-7 generations of selfing required, in general. The saving of time and resources are more in long duration than short duration crop species (Baenziger *et al.* 1984).

In addition, doubled haploids are increasingly being used for the rapid development of mapping populations and construction of genetic linkage maps. The haploids have been used to express several recessive traits in *Brassica napus* by Henderson and Pauls (1992). Simultaneously, haploids can also be useful to detect and fix desirable recessive traits induced through mutation or hybridization and also provide an opportunity to fix rare gene combinations which otherwise may not be possible to isolate in the segregating population through conventional means (Gosal *et al.* 1997).

Philem and Chadha (2010) conducted studies to develop doubled haploids through anther culture and identify suitable medium for androgenesis in Ethiopian

mustard by using B_5, N_6 and KA media, supplemented with eight hormonal combinations with 2, 4 and 6 days of pretreatment at 35°C and revealed that 2 days pre-treatment at 35°C in the callusing medium B_5 supplemented with 0.5 mg/l 2, 4-D + 1.0 mg/l NAA was most suitable for production of induced doubled haploids. The doubled haploids regenerated from a diverse intraspecific cross of *Brassica carinata* in the present study will help in identifying the potential doubled haploids containing desired combinations of traits for exploitation as a cultivar or in breeding programme.

2.4.2 Factors affecting *in vitro* anther culture response

Enormous factors have been shown to affect androgenic response of *in vitro* cultured anthers in different crops. These include genotype (Gresshoff and Doy 1972; Guha-Mukherjee 1973; Dunwell 1996; Xu *et al*. 2007), physiological status of the donor plant (Sunderland 1971; 1974), developmental stage of microspores (Clapham 1971; Sunderland and Wick 1971; Ouyang *et al*. 1973), culture medium (Sharp *et al*. 1971; Clapham 1973), growth regulators and sucrose. The relevant literature pertaining to these factors in *Brassica* species is presented below:

2.4.2.1 Plant genotype

Genetic make up of donor plants decisively influences induced androgenesis. The genotypic effect of embryogenic response has been observed in most *Brassica* species where development of haploids through microspore and anther culture has been attempted (Arnison and Keller 1990; Baillie *et al*. 1992; Thurling and Chay 1984; Wang *et al*. 2004; Lichter 1989; Phippen and Ockendon 1990; Ferrie *et al.* 1995; Seguin-Swartz *et al*. 1983). In *Brassica carinata*, significant effect of genotype on the response of *in vitro* anther/microspore culture has been reported by Barro and Martin (1999), Chuong and Beversdorf (1985), Yadav *et al.* (1988) and Arora and Bhojwani (1988).

2.4.2.2 Physiological status of the donor plants

The physiological state of the parent plant and its age also play a crucial role in the success of haploid plant regeneration. Success in haploid induction is dependent on the physiology of the pollen yielding plants. In various plant species, it has also been shown that the frequency of androgenesis is higher in anthers harvested at the beginning of the flowering period and declines with plant age. Generally, the buds from the first flush of flowering show better androgenic response than those borne subsequently. The

most appropriate stage of anthers for induction of embryogenesis/callusing was when anther colour was yellowish green. The lower frequency of induction of haploids in anthers taken from older plants may also be associated with a decline in pollen viability. Seasonal variation, physical treatment and application of hormones and salt to the plant also alter its physiological status which is reflected in a change in anther culture response.

Studies on the effect of the physiological status of the donor plants on anther/pollen culture in *Brassica juncea* showed improved androgenic response from three per cent to 16 per cent by late sowing of the donor plants which probably act as stress on the plants (Agarwal and Bhojwani 1993). In contrast, Roulund *et al.* (1990) reported better embryo formation from anthers of field grown donor plants of head cabbage (*Brassica oleracea* L. convar. *capitata* (L.)) than plants grown in the green house. In *Brassica napus*, the most responsive pollen stage ranges between early uninucleate to late binucleate stage, though, late uninucleate stage is considered to be best (Kott *et al*. 1988). However, in some studies, mid-late to very late uninucleate stage is considered to be optimum for microspore culture (Guo and Pulli 1996).

2.4.2.3 Developmental stage of microspore

Microspore developmental stage is most critical factor affecting frequency of pollen embryos/ calli formation in anther/microspore culture. Generally, bud size is used as an index of pollen stage. However, size of the bud enclosing pollen at optimum stage may vary with growing conditions and age of the plants (Takahata *et al.* 1993). Therefore, success of anther /microspore culture depends upon the accuracy in selection of floral buds containing the appropriate stage of the microspore. Barro and Martin (1999) evaluated lines of *Brassica carinata* and found the highest cell division and embryo yields from the bud size between 2.5 to 3.5 mm long. In *Brassica oleracea*, best results of pollen embryogenesis were reported when majority of cultured microspores were at late uninucleate to binucleate stage (Vyvadilova *et al*. 1998; Zhang *et al*. 1998). In *Brassica napus,* most of the embryos were formed from late uninucleate to early binucleate stage (Pechan and Keller 1988; Hansen and Svinnset 1993). Kieffer *et al.* (1993) reported that late uninucleate to late binucleate stages were more responsive to anther culture in *Brassica olerecea*. Singh and Sachan (1999), in a study on embryogenesis of 3 *Brassica* species including *Brassica juncea,* obtained best response of flower buds (1 to 1.5 mm size) at uninucleate stage of microspores whereas Prem *et al.*

(2005) obtained highest frequency of microspore embryogenesis in *Brassica juncea* from late uninucleated microspores in bud size of 3.1 to 3.5 mm.

2.4.2.4 Culture medium

Composition of the culture medium plays an important role for induction of embryos/ callus from *in vitro* anthers/microspore culture. It is critical to change the composition of the media or replenish them to keep the balance of micronutrients and maintain the pH. The pH of the medium changes drastically with time of onset of embryo/callus development. Water, carbohydrates, minerals, vitamins, amino acids and growth regulators comprising the *in vitro* culture medium, can be manipulated to influence the embryogenesis/callusing response of *in vitro* cultured anthers.

2.4.2.4.1 Basal medium

Murashige and Skoog's (MS), Gamborg's medium (B_5), Nitsch and Nitsch (N&N) and Keller's medium have been successfully used to induced *in vitro* anther culture for induction of embryo/callus in *Brassica carinata* (Chuong and Beversdorf 1985; Sharma and Bhojwani 1985; Narasimhulu and Chopra 1987). Most of the studies reported successful use of MS media for *in vitro* callusing/embryogenesis in cultured anthers of *Brassica* species.

In *Brassica carinata*, modification of Nitsch and Nitsch (N&N) medium resulted in high embryo yield and plantlet formation during anther culture (Chuong and Beversdorf 1985). Zhang *et al.* (1996) observed successful embryogenesis and callusing in *Brassica carinata* and *Brassica napus* on modified B_5 medium. Arora and Bhojwani (1988) reported the occurrence of pollen embryogenesis in anther culture of *Brassica carinata* on KA medium.

Successful embyrogenic response has been reported on Keller's medium (Gwag *et al.* 1987) and Gamborg's medium (Kwon *et al.* 1989) in *Brassica napus* anther culture. Isolated microspores of *Brassica juncea* have been reported to be cultured successfully on NLN medium (Prem *et al.* 2005). Purnima and Rawat (1997) also reported successful culture of the isolated microspores of *Brassica juncea* on NLN medium and achieved development of embryos.

Significant effect of media, hormones and their interaction on callus induction frequency (%) was also reported by earlier workers. Keller's medium with 0.2 mg/l NAA, 0.2 mg/l 2, 4-D and 11 per cent sucrose was reported to be best for anther culture

in *Brassica juncea* by Singh (2006). However, Devi (2009) observed that the callusing medium B_5 supplemented with 0.5 mg/l 2,4-D + 1.0mg/l NAA was most suitable for androgenesis in *Brassica carinata.* In *Brassica juncea,* B_5 medium supplemented with 1.0 mg/l 2, 4-D gave better callus induction frequency (Kumari 2010).

2.4.2.4.2   Growth regulators

In addition to basal salt and vitamins, hormones in the medium are critical factors for embryos or calli induction. In solanaceous plants, pollen embryogenesis does not require any growth regulator, but, low levels of auxins, cytokinins and even GA appear beneficial. In *Hyoscyamus niger*, 2 mg/l 2, 4-D enhanced the frequency of callus induction, but, had no effect on the number of embryogenic pollen. In contrast, cytokinins (0.01-10 mg/l) reduced the number of embryogenic pollen grains most likely by interfering with cell division.

Arora and Bhojwani (1988) reported the occurrence of pollen embryogenesis in anther of *Brassica carinata* on growth regulator free KA medium. However, most *Brassica* species are reported to require an auxin and a cytokinin for the regeneration of plants from pollen calli (George and Rao 1982; Lillo and Hansen 1987; Goel *et al.* 1990; Paksoy *et al.* 1995; Chang *et al.* 1996; Purnima and Rawat 1997). George and Rao (1982) obtained *in vitro* shoot bud formation from cultured anthers on the medium supplemented with NAA and BA. Narasimhulu and Chopra (1987) reported the production of one to three shoots per anther directly on MS medium supplemented with IAA whereas callus formation was reported in 2, 4-D supplemented medium.

In *Brassica juncea*, microspores responded better on modified B_5 medium supplemented with 2 mg/l 2, 4-D or NAA. The plantlets regeneration efficiency in calli induced on 2, 4-D was reported to be less as compared to that of NAA supplemented medium containing both auxins as well as cytokinins (Chang *et al.* 1996).

Zhang *et al.* (2006) showed the best response when the embryos were cultured on medium 1/2 MS + 2.0 mg dm-3 BAP and when the embryos were cultured on 1/2 MS + 0.1 mg dm-3 GA_3, poor responses of plant development were observed in *Brassica napus*.

2.4.2.4.3   Carbon source and levels

Sucrose is considered the most effective carbohydrate source which cannot be

substituted by other disaccharides. It not only acts as a source of carbon, but, is also involved in osmo-regulation. The concentration of sucrose also plays an important role in induction of pollen plants. Studies conducted by Arora and Bhojwani (1988) in *Brassica carinata* revealed that only 5 per cent glucose as the sole source of carbohydrate did not induce androgenesis. However, the combination of 5 per cent sucrose and 2.5 per cent glucose led to increased frequency of androgenesis even higher than with 10 per cent sucrose alone. Dunwell and Thurling (1985) found that a higher concentration of sucrose was beneficial for initial growth and development, but, further development required a lower sucrose concentration. In *Brassica campestris*, microspores cultured using 17 per cent sucrose in NLN media for two days and thereafter on 10 per cent sucrose improved androgenic response (Baillie *et al*. 1992). Narasimhulu and Chopra (1987) reported the induction of shoots when sucrose was supplemented at 2 per cent in *Brassica carinata*. In *Brassica napus*, comparatively low sucrose content (8 %) has been reported to be optimum for anther/microspore culture (Lichter 1981; Singh and Sachan 1999).

3. MATERIALS AND METHODS

The present investigation entitled "Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)" was carried out at the experimental farm of the Department of Crop Improvement and Molecular Cytogenetics and Tissue Culture Laboratory of the Department, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during *rabi,* 2010-11 under two different environments. The details of materials used and methods employed are described under the following sub-heads:

3.1 **General description of the experimental site**

3.2 **Materials**

3.3 **Methods**

    3.3.1   Field evaluation of experimental material

    3.3.2   Observations recorded

    3.3.3   Reaction to *Alternaria* blight

    3.3.4   Statistical analysis

    3.3.5   Genetic variability analysis

    3.3.6   Genetic diversity analysis

    3.3.7   Correlation coefficient analysis

    3.3.8   Path coefficient analysis

    3.3.9   Anther culture studies

3.1 **Experimental site**

The experimental farm of Department of Crop Improvement is situated at an elevation of 1290.8 m above mean sea level with latitude 32°6´ N and 76°3´ E longitude which represents the mid hill zone of Himachal Pradesh. The experimental site at Shivalik Agricultural Research and Extension Centre, (SAREC) Kangra, is located in the historic town of Kangra (32^0 05" N latitude, 75^0 18" E longitude and 700 m above mean sea level). Weather data is presented in Appendix V.

3.2   Materials

The materials for the present investigation comprised of thirty three genotypes including twenty eight doubled haploids obtained through anther culture technique, one advanced breeding line (P-138) and four check varieties *viz.,* Nav Gold, Jayanti, Pusa Jaikisan and RCC-4. The doubled haploids were obtained from the cross Jayanti x RCC-6-1 developed in the Department of Agricultural Biotechnology, CSK HPKV, Palampur. Details of materials used are presented in Table 3.1.

Table 3.1 List of thirty three genotypes used in present study

Sr. No.	Genotype	Crop species	Source
1.	P-12	*Brassica carinata*	CSKHPKV, Palampur
2.	P-17	*Brassica carinata*	CSKHPKV, Palampur
3.	P-23	*Brassica carinata*	CSKHPKV, Palampur
4.	P-24	*Brassica carinata*	CSKHPKV, Palampur
5.	P-26	*Brassica carinata*	CSKHPKV, Palampur
6.	P-31	*Brassica carinata*	CSKHPKV, Palampur
7.	P-33	*Brassica carinata*	CSKHPKV, Palampur
8.	P-34	*Brassica carinata*	CSKHPKV, Palampur
9.	P-39	*Brassica carinata*	CSKHPKV, Palampur
10.	P-43	*Brassica carinata*	CSKHPKV, Palampur
11.	P-45	*Brassica carinata*	CSKHPKV, Palampur
12.	P-51	*Brassica carinata*	CSKHPKV, Palampur
13.	P-56	*Brassica carinata*	CSKHPKV, Palampur
14.	P-62	*Brassica carinata*	CSKHPKV, Palampur
15.	P-63	*Brassica carinata*	CSKHPKV, Palampur
16.	P-64	*Brassica carinata*	CSKHPKV, Palampur
17.	P-74	*Brassica carinata*	CSKHPKV, Palampur
18.	P-75	*Brassica carinata*	CSKHPKV, Palampur
19.	P-77	*Brassica carinata*	CSKHPKV, Palampur
20.	P-89	*Brassica carinata*	CSKHPKV, Palampur
21.	P-92	*Brassica carinata*	CSKHPKV, Palampur
22.	P-96	*Brassica carinata*	CSKHPKV, Palampur
23.	P-101	*Brassica carinata*	CSKHPKV, Palampur
24.	P-103	*Brassica carinata*	CSKHPKV, Palampur
25.	P-117	*Brassica carinata*	CSKHPKV, Palampur
26.	P-122	*Brassica carinata*	CSKHPKV, Palampur
27.	P-133	*Brassica carinata*	CSKHPKV, Palampur
28.	P-137	*Brassica carinata*	CSKHPKV, Palampur
29.	P-138	*Brassica carinata*	CSKHPKV, Palampur
30.	Nav Gold (c)	*Brassica juncea*	Rajasthan
31.	Jayanti (c)	*Brassica carinata*	H.P.
32.	Pusa Jaikisan (c)	*Brassica juncea*	New Delhi
33.	RCC-4 (c)	*Brassica juncea*	H.P.

3.3   Methods

3.3.1   Field evaluation of experimental material

All the genotypes were raised at the experimental farm of Department of Crop Improvement, CSK HPKV, Palampur in randomized complete block design with three replications in the plot size of 3.0×0.60 m^2 on two different environments *viz.*, 12th October, 2010 (Env.I) and 29th October, 2010 (Env.II). The row to row and plant to plant spacings were kept at 30cm and 15cm, respectively. Each genotype was raised in two rows. The recommended cultural practices were followed to raise the crop (Plate I). All the genotypes were also raised in the field at Shivalik Agricultural Research and Extension Centre (SAREC), Kangra, for scoring disease reaction during *rabi,* 2011-12 (Plate II).

3.3.2   Observations recorded

Observations for the following traits were recorded on the basis of five randomly selected plants from each genotype in each replication and their average was worked out. The observations on days to flower initiation, days to 50 per cent flowering and days to 75 per cent maturity were recorded on plot basis.

1. **Days to flower initiation:** The total number of days taken from date of sowing to first flower initiation were recorded.

2. **Days to 50 % flowering:** The total number of days taken from date of sowing to the period when nearly half of the plants in a plot showed flowering, were recorded.

3. **Days to 75 % maturity:** The total number of days taken from the date of sowing to the period when nearly 75 per cent of the plants in a plot matured, were recorded.

4. **Plant height (cm):** The height of selected plants was measured at the time of maturity from ground surface to the apex of main stem with meter rod.

5. **Number of primary branches per plant:** The total number of branches emerging directly from the main stem were counted for each selected plant.

6. **Number of secondary branches per plant:** The total number of branches arising from primary branches in selected plants of each genotype were recorded.

7. **Siliquae per plant:** At the time of harvest, total number of siliquae produced on individual plant were recorded.

8. **Length of main shoot (cm):** At the time of the harvest, length of the main shoot was measured with the help of the meter rod.

9. **Siliquae on main shoot:** At the time of harvest, total number of siliquae produced on the main shoot were recorded.

10. **Siliqua length (cm):** Five mature and insect attack free siliquae were randomly selected from each plant and their lengths were measured with meter rod.

11. **Seeds per siliqua:** Five mature and effective siliquae were randomly selected from each plant. These were threshed manually and average number of seeds per siliqua was worked out.

12. **1000-seed weight (g):** Weight of one thousand dry and well filled seeds was recorded.

13. **Seed yield per plant (g):** Five randomly selected plants were harvested together, threshed and weight of seeds was recorded.

14. **Biological yield per plant (g):** Five randomly selected plants were sun dried and weighed together to get biological yield per plant.

15. **Harvest Index (%):** Harvest Index was calculated as the ratio of seed yield to the total biological yield.

$$\text{HI (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

16. **Oil content (%):** Oil content of each genotype was determined by Nuclear Magnetic Resonance (NMR) method at Oilseed section, Department of Plant Breeding, Punjab Agricultural University, Ludhiana.

3.3.3   Reaction to *Alternaria* blight (*Alternaria brassicae*)

All the genotypes were screened for reaction to *Alternaria brassicae* under natural epiphytotic field conditions and observations on disease severity were recorded on the basis of visual observations.

3.3.3.1   Disease assessment

Data on disease severity of *Alternaria* blight on leaves was recorded on about 100 days after sowing on 10 leaves sampled randomly from each plot. Disease severity on

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Plate I   Field view of the experiment cunducted at CSK HPKV, Palampur
(*Rabi,* 2010-11)

Plate II   Field view of the experiment cunducted at CSK HPKV,
SAREC, Kangra (*Rabi,* 2011-12)

Available online at http://www.ijart.info/

pods was recorded 15 days before the crop harvest. For recording of *Alternaria* blight on pods, 10 pods per plot were sampled randomly and disease scoring was done as per the scale of Conn *et al.* (1990) as followed under AICRP (Rapeseed-mustard).

Table 3.2   Scale (0-9) for rating of genotypes for reaction to *Alternaria* blight

Rating	Symptoms	
	AB on leaf	**AB on pod**
0	No infection	No infection
1	Up to 5% leaf area covered	Up to 5% pod area covered
3	>5-10% leaf area covered	>5-10% pod area covered
5	>11-25% leaf area covered	>11-25% pod area covered
7	>26-50% leaf area covered	>26-50% pod area covered
9	>50% leaf area covered	>50% pod area covered

Table 3.3   Categorization scale for reaction to *Alternaria* blight

Sr. No.	Category	Area infected (%)
1.	Resistant	0-10%
2.	Moderately resistant	11-25%
3.	Moderately susceptible	26-50%
4.	Susceptible	51-75%
5.	Highly susceptible	>75%

Per cent Disease Intensity (PDI) was calculated by using the formula of McKinney (1923).

$$PDI = \frac{\text{Total sum of all numerical rating}}{\text{Number of observations taken} \times \text{maximum disease score}} \times 100$$

3.3.4 Statistical Analysis

The statistical analysis for various characters recorded was carried out under the followed sub heads:

Analysis of Variance

Data were statistically analysed as per the procedure given by Panse and Sukhatme (1985). The analysis of variance was based on the following linear model:

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

Where

Y_{ij} = phenotypic observation of the ith genotype in the jth replication

m = general population 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 with zero mean and σ^2 variance

Analysis of variance

Source of variation	Degree of freedom	Mean Sum of Squares	F- value	Expected Mean Squares
Replications	r-1	Mr	Mr/Me	$\sigma^2e + g\sigma^2r$
Genotypes	g-1	Mg	Mg/Me	$\sigma^2e + r\sigma^2g$
Error	(r-1)(g-1)	Me	----	σ^2e
Total	(rg-1)			

Where

r = number of replications
g = number of genotypes
σ^2r = variance due to replication
σ^2g = variance due to genotypes
σ^2e = error variance

The replication and genotypic mean squares were tested against error mean square by 'F' test for (r-1), (r-1)(g-1) and (g-1), (r-1)(g-1) degrees of freedom, respectively at 5 per cent level of significance (P ≤ 0.05) and 1 per cent level of significance (P ≤ 0.01).

The genotypic and phenotypic variances were calculated as below:

Genotypic variance ($\sigma^2 g$) = (Mg- Me)/r

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Error variance   ($\sigma^2 e$) = Me

The Standard Error of mean (SE(m)), Standard Error of difference (SE(d)) and Critical Difference (CD) for comparing the means of any two genotypes were computed as below:

SE (m) = $\pm$ (Me/r)$^{1/2}$

SE (d) = $\pm$ (2 Me/r)$^{1/2}$

CD = SE (d) $\times$ 't' value at error degree of freedom

Where 'Me' is the error mean square and 't' is the table value at error degree of freedom at 5 per cent level of significance.

Coefficient of Variation (CV %) was calculated as per the following formula:

CV (%) = [(Me)$^{1/2}$ / $\overline{x}$] $\times$ 100

Where $\overline{x}$ = grand mean

3.3.5   Genetic variability analysis

Components of variability and genetic parameters in individual environments

These were calculated as suggested by Burton and De Vane (1953) and Johnson *et al.* (1955).

Phenotypic Coefficient of Variation (PCV%) = (σp/ $\overline{x}$) $\times$100

Genotypic Coefficient of Variation (GCV%) = (σg/ $\overline{x}$) $\times$100

Environmental Coefficient of Variation (ECV%) = (σe/ $\overline{x}$) $\times$100

Where

σp = phenotypic standard deviation

σg = genotypic standard deviation

σe = environmental standard deviation

$\overline{x}$ = grand mean

Heritability in broad sense ($h^2{}_{bs}$)

$$\text{Heritability } [h^2{}_{bs}\%] = \frac{\sigma^2 g}{(\sigma^2 g + \sigma^2 e)} \times 100$$

Expected Genetic advance

$$\text{Genetic advance (GA)} = K \times \sigma p \times h^2{}_{(bs)}$$

Where

      K   = selection differential at 5% selection intensity *i.e.* 2.06

      σp = phenotypic standard deviation

      $h^2{}_{(bs)}$ = heritability in broad sense

Genetic advance expressed as per cent of mean

$$= (GA/\bar{x}) \times 100$$

Analysis of variance combined over environments

      The analysis of variance combined over the environments was computed as per the procedure given by Verma *et al.* (1987).

      The analysis was based on the following linear model:

$$Y_{ijk} = m + \alpha_i + \beta_j + \alpha\beta_{ij} + r_k + e_{ijk}$$

Where

      Y_{ijk} =   phenotype of the ith genotype grown in j^{th} environment in the kth block

      m   =   general population mean

      α_i =   effect of ith genotype

      β_j =   effect of jth environment

      $\alpha\beta_{ij}$ =   effect of interaction of ith genotype with j^{th} environment

      rk   = k^{th} replication effect

      e_{ijk} =   random error

Analysis of variance combined over the environments

Source of variation	Degree of freedom	Mean Sum of Squares	F- value	Expected Mean Squares
Replications	(r-1)	Mr	Mr/Me	$\sigma^2e + gy\sigma^2r$
Environments	(y-1)	My	My/Me	$\sigma^2e + rg\sigma^2e + r\sigma^2gy$
Replications × environments	(r-1)(y-1)	Mry	Mry/Me	$\sigma^2e + g\sigma^2ry$
Genotypes	(g-1)	Mg	Mg/Me	$\sigma^2e + r\sigma^2gy + yr\sigma^2g$
Genotypes × environments	(g-1)(y-1)	Mgy	Mgy/Me	$\sigma^2e + r\sigma^2gy$
Pooled error	y(r-1)(g-1)	Me	----	σ^2e

Where

r = number of replications

g = number of genotypes

y = number of environments

σ^2e = error variance = Me

σ^2g = variance due to genotypes = Mg

σ^2r = variance due to replication = Mr

σ^2y = variance due to environments = My

σ^2ry = variance due to replication x environments = Mry

σ^2gy = variance due to genotype x environments = Mgy

Standard errors

Standard error of mean SE (m) = $\pm$ (Me/ry)$^{1/2}$

Standard error of difference between two genotypic means SE (d) = $\pm$ (2 Me/ry)$^{1/2}$

Critical Difference

For comparing the means of any two genotypes

CD = SE (d) × 't' value at 5 per cent level of significance at combined error degrees of freedom.

Coefficient of Variation

CV (%) = [(Me)$^{1/2}$ / $\bar{x}$] ×100

Estimation of parameters of variability in combined over environments

Phenotypic Coefficient of Variation (PCV %) = [($\sigma g + \sigma gy + \sigma e$) / $\bar{x}$] × 100

Genotypic Coefficient of Variation (GCV %) = ($\sigma g/\bar{x}$) × 100

Heritability (h^2_{bs}) in broad sense (%) = [$\sigma^2 g/ (\sigma^2 g + \sigma^2 gy + \sigma^2 e)$] × 100

Genetic advance (GA) at 5 % selection intensity = K ($\sigma g + \sigma gy + \sigma e$) × $h^2_{(bs)}$

Genetic advance expressed as per cent of mean (GA%) = (GA/ $\bar{x}$) × 100

Where

σg = genotypic standard deviation

σgy = genotypic environmental standard deviation

σg = error standard deviation

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

PCV and GCV:	>30% - high; 10 - 30% - moderate; <10% – low
Heritability in broad sense:	>60% - high; 30 - 60% - moderate; <30% - low
Genetic advance:	>30% - high; 10 - 30% - moderate; <10% - low

Test of significance

The F - test (Test of Homogeneity) or the 'variance ratio' test was used to test the significance whether error variances are homogeneous or not. In order to carry out the test of significance, F- ratio was calculated as:

$$F = \frac{S_1^2}{S_2^2}$$

Where

S_1^2 = Large estimate of variance

S_2^2 = Smaller estimate of variance

and $S_1^2 > S_2^2$

at $v_1 = n_1 - 1$ and $v_2 = n_2 - 1$ degrees of freedom

Where

v_1 = degrees of freedom for sample having larger variance

v_2 = degrees of freedom for sample having smaller variance

The calculated value of F was compared with the table value for v_1 and v_2 degrees of freedom at 5 per cent level of significance. If calculated value of F was greater than the tabulated value, the F- ratio was considered as significant. If the calculated value of F

was less than the table value, F- ratio was considered as non significant and it was inferred that both the samples have come from the population having same variance.

3.3.6 Genetic diversity analysis

A measure of group distance based on multiple characters was given by Mahalanobis (1936) and Rao (1952).

With x_1, x_2, x_3 ……………. x_p as the multiple measurements available on each individual and d_1, d_2, d_3 …….. d_p as $x_1^{-1} - x_1^{-2}$, $x_2^{-1} - x_2^{-2}$ ………$x_p^{-1} - x_p^{-2}$, respectively, being the difference in the means of two populations, Mahalanobis D^2 statistic is defined as:

$$pD^2 = b_1d_1 + b_2d_2 + ……………. b_pd_p$$

Here, the b_i values are to be estimated such that the ratio of variance between the populations to the variance within the populations is maximized. In terms of variances and covariances, the D^2 value is obtained as follows:

$$pD^2 = W_{ij} (x_i^{-1} - x_i^{-2}) (x_j^{-1} - x_j^{-2})$$

Where

W_{ij} is the inverse of estimated variance covariance matrix.

Test of significance

Using 'V' statistic which, in turn, utilizes Wilk's criteria, simultaneous test of differences between mean values of a number of correlated variables/ characters at 'pq' d.f. (where p = number of characters and q = number of germplasm-1) was done as suggested by Rao (1952).

3.3.6.1 Grouping of genotypes into various clusters

Using D^2 values, different genotypes were grouped into various clusters following Tocher's method as suggested by Rao (1952).

3.3.6.2 Average intra - and inter- cluster distances

Average intra- cluster $D^2 = \sum D_i^2/n$

Where

$\sum D_i^2$ = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

Average inter- cluster distance $D^2 = \sum D_{ij}^2/n_i.n_j$

Where

$\sum D_{ij}^2$ = sum of all distances between all possible combinations ($n_i.n_j$) of the genotypes between the clusters.

n_i = number of genotypes in ith cluster

n_j = number of genotypes in jth cluster

3.3.6.3 Cluster mean

Character means of all *Brassica* genotypes falling under different clusters were calculated.

3.3.6.4 Contribution of individual character towards divergence

In all combinations, each character was ranked on the basis of $d_i = Y_i^j - Y_i^k$ values. Rank 1 was given to the highest mean difference and rank 'p' to the lowest mean difference where 'p' is the total number of characters. The contribution of individual character to the divergence was worked out in terms of 'n' number of times it appeared first.

3.3.7 Correlation coefficient analysis

Phenotypic, genotypic and environmental coefficients of correlation were worked out following Analysis of covariance involving all possible paired combinations among the characters studied.

Analysis of covariance

Source of variation	Degree of freedom	Mean Sum of Products	F- value	Expected Mean Sum of Products
Replications	r-1	Mr_{xy}	Mr_{xy}/Me_{xy}	$\sigma e_{xy} + g\sigma r_{xy}$
Genotypes	g-1	Mg_{xy}	Mg_{xy}/Me_{xy}	$\sigma e_{xy} + r\sigma g_{xy}$
Error	(r-1)(g-1)	Me_{xy}	----	σe_{xy}

The genotypic, phenotypic and environmental covariances were calculated as follows:

$$\sigma p_{xy} = \sigma g_{xy} + \sigma e_{xy}$$

$$\sigma g_{xy} = (Mg_{xy} - Me_{xy})/r$$

$$\sigma e_{xy} = Me_{xy}$$

Where

r = number of replications

g = number of genotypes

σg_{xy} = genotypic covariance between characters x and y

σp_{xy} = phenotypic covariance between characters x and y

σe_{xy} = environmental covariance between characters x and y

Mg_{xy} = mean sum of products due to genotypes from the analysis of covariance between characters x and y

Me_{xy} = mean sum of products due to error from the analysis of covariance between characters x and y

The phenotypic, genotypic and environmental correlation coefficients were computed as per the methods suggested by Al-Jibouri *et al*. (1958) as under.

Phenotypic coefficient of correlation (rp $_{xy}$)

$$rp_{xy} = \frac{\sigma p_{xy}}{(\sigma^2 p_x \times \sigma^2 p_y)^{\frac{1}{2}}}$$

Where

σp_{xy} =   phenotypic covariance between characters x and y

$\sigma^2 p_x$ =   phenotypic variance of character x

$\sigma^2 p_y$ =   phenotypic variance of character y

Genotypic coefficient of correlation (rg$_{xy}$)

$$rg_{xy} = \frac{\sigma g_{xy}}{(\sigma^2 g_x \times \sigma^2 g_y)^{\frac{1}{2}}}$$

Where

σg_{xy} =   genotypic covariance between characters x and y

$\sigma^2 g_x$ =   genotypic variance of character x

$\sigma^2 g_y$ =   genotypic variance of character y

Environmental coefficient of correlation (re$_{xy}$)

$$re_{xy} = \frac{\sigma e_{xy}}{(\sigma^2 e_x \times \sigma^2 e_y)^{\frac{1}{2}}}$$

Where

σe_{xy} =   environmental covariance between characters x and y

$\sigma^2 e_x$ =   environmental variance of character x

$\sigma^2 e_y$ =   environmental variance of character y

Test of significance

The significance of phenotypic coefficient of correlation at (g-2) df where, 'g' is the number of genotypes and environmental coefficient of correlation at [(r-1)(g-1)-1] df, where, 'r' and 'g' stand for number of replications and genotypes, respectively, were tested at 5 per cent level of significance against the table values of correlation coefficient (Fisher and Yates 1963).

To test the significance of genotypic coefficient of correlation, the F-value was calculated as below:

$$F = [(g-2)r^2]/(1-r^2)$$

And compared with the F-distribution at 1 and (g-2) degrees of freedom where g and r represent number of genotypes and genotypic coefficient of correlation, respectively (Mead and Curnow 1983).

3.3.8 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient which permits the partitioning of correlations into direct and indirect effects. The path coefficients of yield and other characters including percent oil content with seed yield were worked out following Dewey and Lu (1959) as under:

$Py_1 + Py_2. r_{12} + Py_3. r_{13} + \text{.......................} \text{.............................}+ Py_n. r_{1n} = ry_1$

$Py_1. r_{12} + Py_2 + Py_3. r_{23} + \text{..} + Py_n. r_{2n} = ry_2$

$Py_1. r_{13} + Py_2. r_{23} + Py_3 + \text{..}+ Py_n. r_{3n} = ry_3$

$:$ $:$

$:$ $:$

$Py_1. r_{n1} + Py_2. r_{n2} + Py_3 r_{n3} + \text{..} + Py_n = ry_n$

Where

$Py_1, Py_2, Py_3, \text{................}, Py_n$ are the direct path effects of 1, 2, 3, ..., n variables on the dependent variable 'y'.

$r_{12}, r_{13}, \text{...........}, r_{(n-1)n}$ are the possible coefficients of correlation between various independent variables and $ry_1, ry_2, ry_{3,...........}, ry_n$ are the coefficients of correlation of independent variables with dependent variable 'y'.

The variation in the dependant variable which remained undetermined by including all the variables, was assumed to be due to variable/variables not included in

the present study. The degree of determination of such variable/variables on dependant variable was calculated as below:

Residual effect $= (1-R^2)^{1/2}$

where

$R^2 = Py_1ry_1 + Py_2\,ry_2 + ... + Py_n\,ry_n$

R^2 is the squared multiple correlation coefficient and is the amount of variation in yield that can be attributed to the variable/variables not included in present study.

3.3.9 Anther culture studies

The anther culture work was carried out in the Molecular Cytogenetics and Tissue culture Laboratory of Department of Crop Improvement, CSK HPKV, Palampur. The material used and methodology adopted to achieve the objectives of the investigation are given below.

3.3.9.1 Experimental material

The material used for anther culture studies comprised of four elite genotypes and their 3 cross combinations (Table 3.4).

Table 3.4   List of genotypes and their cross combinations under anther culture study

Sr. No	Genotype	Parentage	Salient features
1	Jayanti	Developed through irradiation from the parent variety HC-1	Moderately susceptible to *A. brassicae*, Tall
2	P-18	Advanced generation mutant obtained through treatment of Jayanti seeds with 0.3% EMS (Pre-Soaked)	Moderately resistant to *A. brassicae*, Dwarf
3	P-51	Advanced generation mutant obtained through treatment of Jayanti seeds with 0.3% EMS (Pre-Soaked)	Moderately resistant to *A. brassicae*, Dwarf
4	P$_{(2)2}$	Advanced generation mutant obtained through treatment of Jayanti seeds with 90 kR dose of gamma radiations	Moderately resistant to *A. brassicae*
5	Jayanti x P-18	-	-
6	Jayanti x P-51	-	-
7	Jayanti x P$_{(2)2}$	-	-

3.3.9.2 Methods

3.3.9.2.1   Plant material for anther culture

Sufficient numbers of plants of aforementioned four genotypes and their cross combinations were raised in the pots. In order to have availability of anthers over a long period of time, plants were raised in five lots at an interval of 15 days each.

3.3.9.2.2   Stage of explants

For anther culture, florets from plants were clipped off when the size of bud was about 2-4 mm. The bud size was earlier established on the basis of presence of majority of the microspores at late uninuclate to early binucleate stage as studied by squashing of anthers in a drop of 1 per cent acetocarmine. The florets of appropriate size were collected in 50 ml test tubes containing distilled water.

3.3.9.2.3 Plating of anthers in callus induction media

The florets collected at aforementioned stages were treated with 70 per cent ethanol for 10-15 seconds under aseptic conditions in a laminar air flow chamber. The florets were then surface sterilized with 0.1 per cent $HgCl_2$ for 3-5 minutes with intermittent shaking followed by three washings with sterile distilled water. Florets were blot dried and opened under aseptic conditions with the help of sterile forceps and the six anthers were clipped off from each floret without damaging the anther wall. About 60 anthers were cultured in each pre-sterilized petri plate containing about 25 ml of culture medium.

Two basal media *viz.*, B_5 (Gamborg *et al.* 1968) and MS (Murashige and Skoog 1962) were used for callus induction. Each of these medium was supplemented with two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose and each of these sucrose concentrated media was also supplemented with three combinations of hormones *viz.*, HM_1, HM_2 and HM_3 (Table 3.5). All the media were supplemented with 0.8 per cent agar based upon the earlier studies (Kumari 2010). The basal compositions of B_5 and MS media are given in Appendix IV.

The experiments on different callus induction media were replicated thrice involving different media and plant growth hormones. Anthers of all four genotypes and their crosses were plated in a replicated fashion. If there was any contamination, replating

of the particular treatment was done to complete the experiment under uniform conditions. All the cultured plates were sealed with parafilm wax and kept under dark at $25 \pm 1°C$ until calli were developed.

3.3.9.3 Statistical analysis

The Callus induction frequency (%), Days to calli appearance and Calli Index were calculated as follows:

1. Callus induction frequency (%) $\quad = \quad \dfrac{\text{Number of calli forming anthers}}{\text{Number of anthers plated}} \times 100$

2. Days to calli appearance $\quad = \quad$ Number of days taken for calli appearance from the day of culturing of anthers

3. Calli Index = Growth score x per cent callus induction frequency

3.3.9.4   Data analysis

The data pertaining to different parameters were subjected to appropriate transformation using arc sine transformation wherever necessary. Data on callus induction frequency, days to calli appearance and calli index were analyzed in Factorial Completely Randomized Design (CRD) to obtain the effect of various treatments and their interactions using statistical CPCS software.

Table 3.5   Different media, hormones and sucroe concentration used for callus induction

Medium	Sucrose concentration	Hormone	
		Designation	Name and Concentration
B_5	3%	HM_1	NAA (1.0 mg/l)
B_5	3%	HM_2	BAP (2.0 mg/l) + NAA (2.0 mg/l)
B_5	3%	HM_3	2, 4-D (0.5 mg/l) + NAA (1.0 mg/l)
B_5	4%	HM_1	NAA (1.0 mg/l)
B_5	4%	HM_2	BAP (2.0 mg/l) + NAA (2.0 mg/l)
B_5	4%	HM_3	2, 4-D (0.5 mg/l) + NAA (1.0 mg/l)
MS	3%	HM_1	NAA (1.0 mg/l)

MS	3%	HM_2	BAP (2.0 mg/l) + NAA (2.0 mg/l)
MS	3%	HM_3	2, 4-D (0.5 mg/l) + NAA (1.0 mg/l)
MS	4%	HM_1	NAA (1.0 mg/l)
MS	4%	HM_2	BAP (2.0 mg/l) + NAA (2.0 mg/l)
MS	4%	HM_3	2, 4-D (0.5 mg/l) + NAA (1.0 mg/l)

4. RESULTS AND DISCUSSION

The present investigation entitled "Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)" was undertaken during *rabi,* 2010-11 under two environments *viz.,* Env.I and Env.II. The experiments were conducted in randomized complete block design with three replications at the Experimental farm of the Department of Crop Improvement, CSKHPKV Palampur, with a view to assess genetic variability, genetic divergence through D^2 analysis, associations between yield and its components and their causes in order to identify the potential parents for future breeding programme. The evaluation for resistance to *Alternaria* blight was carried out at CSK HPKV, SAREC, Kangra, during *rabi,* 2011-12 under natural epiphytotic field conditions. The androgenesis-mediated responsiveness of *Alternaria* blight susceptible and moderately resistance genotypes and their cross combinations with respect to haploid production were carried out in Molecular Cytogenetics and Tissue Culture Laboratory of the Department. The results on various aspects of present study are presented and discussed below:

4.1 Nature and magnitude of variation for seed yield and related traits under different environments

The success of any crop improvement programme lies in the careful management of genetic variability, techniques to be employed and clear understanding of the extent and nature of genetic variability which is important for effective selection. Selection is the basis of any breeding programme and operates only on heritable variation that is genetic in nature. A wide range of variability in any crop species provides a better chance of selecting the desired types (Vavilov 1951). Most of the characters of interest to plant breeders are quantitative in nature and thus, exhibit continuous variation which is composed of both heritable and non-heritable components (Fisher 1918). The heritable component is a consequence of genotypic and non-heritable of environmental factors. It is very difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression (which is an outcome of genotype and environmental interaction) in the existing material. Therefore, the study of various characters under investigation is of great importance.

4.1.1 Analysis of variance

The analysis of variance (ANOVA) for Env.I and Env.II is presented in Table 4.1. In Env.I, analysis of variance revealed that mean squares due to genotypes were significant for all characters except siliqua length and percent oil content. On the other hand in Env.II, the mean squares due to genotypes were significant for days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, 1000-seed weight, seed yield per plant and harvest index indicating thereby a wide range of genetic variability and scope for selection for these traits.

On the basis of analysis of variance, the genotypic differences existed for most of the morphological and yield contributing characters. Abebe (2008) observed significance differences for days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, seed yield per plant and oil content. Zehra and Gulcan (2009) also observed significant differences for plant height, number of branches per plant, number of pods per plant, pods per main stem, pod length, 1000-seed weight, seed yield per plant and percent oil content in two environments. Yared *et al.* (2012) also observed highly significant differences for days to flower initiation and days to maturity. Mahto and Haider (2002), Naazar *et al.* (2003), Dilara *et al.* (2011) and Rameeh (2011) also observed significant differences among genotypes for seed yield contributing characters. High amount of genetic variability for many of these characters has also been reported by some earlier workers *viz.,* Mehrotra *et al.* (1976), Hodgson (1979), Vijaykumar *et al.* (2001), Khan and Khan (2003), Mahla *et al.* (2003), Singh *et al.* (2003) and Kumar and Mishra (2007). Monalisa *et al*. (2005) and Patel and Patel (2006) also observed highly significant differences for days to 50 per cent flowering, days to maturity, primary branches per plant, plant height, siliquae per plant, seeds per siliqua, 1000-seed weight, seed yield per plant and oil content.

The pooled analysis of variance over the environments (Table 4.2) exhibited that mean squares due to genotypes when tested against mean squares due to g x e interactions, were significant for days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, 1000 seed weight and percent oil content. Likewise, the

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mean squares due to environments were significant for days to flower initiation, days to
50 per cent flowering, plant height, number of primary branches per plant, number of

**Table 4.1 Analysis of variance for different characters of *Brassica carinata* in Env.I
and Env.II**

Sr. No.	Characters	Env.I		Env.II	
		Mean Squares			
	Source	Genotypes	Error	Genotypes	Error
	df	32	64	32	64
1	Days to flower initiation	153.08**	10.87	203.82**	37.03
2	Days to 50% flowering	68.91**	8.33	198.81**	8.43
3	Days to 75% maturity	189.79**	8.94	119.96**	44.47
4	Plant height (cm)	2318.26**	207.41	226.03*	117.46
5	Number of primary branches /plant	2.60**	0.57	2.19**	1.08
6	Number of secondary branches /plant	7.44**	0.97	7.8**	3.92
7	Siliquae /plant	3703.66**	666.21	8929.05**	2579.37
8	Length of main shoot (cm)	127.24**	23.73	48.36	37.67
9	Siliquae on main shoot	180.78**	35.26	45.55	41.95
10	Siliqua length (cm)	0.263	0.217	0.23	0.160
11	Seeds /siliqua	2.36*	0.87	2.43	2.08
12	1000-seed weight (g)	1.15**	0.10	0.20*	0.11
13	Seed yield /plant (g)	7.36**	1.42	3.54**	1.47
14	Biological yield /plant (g)	140.18**	34.49	68.41	64.92
15	Harvest index (%)	44.47**	19.81	71.77*	39.51
16	Oil content (%)	11.54	12.56	12.75	15.50

* Significance at $P \leq 0.05$; ** Significance at $P \leq 0.01$

Table 4.2 Analysis of variance for different characters of *Brassica carinata* in pooled over the environments

Sr. No.	Characters Source		Mean Squares			
			Genotypes	Environments	Genotype x Environment (g x e)	Pooled error
		df	32	1	32	128
1	Days to flower initiation		337.18**	255.68**	17.72	23.95
2	Days to 50% flowering		235.09**	147.68**	32.63**	8.38
3	Days to 75% maturity		264.37**	6.55	45.38**	10.21
4	Plant height (cm)		1322.76	15254.73**	1221.53**	162.43
5	Number of primary branches / plant		1.52	20.97**	3.27**	0.82
6	Number of secondary branches / plant		7.57	250.26**	7.67**	2.44
7	Siliquae /plant		7940.97	1426.19	4691.74**	1622.49
8	Length of main shoot (cm)		90.82	955.68**	84.79**	30.70
9	Siliquae on main shoot		93.19	3224.25**	133.14**	38.60
10	Siliqua length (cm)		0.23	0.44	0.323*	0.20
11	Seeds /siliqua		2.21	52.08**	2.58**	1.47
12	1000-seed weight (g)		0.86*	0.19	0.48**	0.11
13	Seed yield /plant (g)		3.64	0.05	7.25**	1.44
14	Biological yield /plant (g)		105.19	251.16	103.41**	46.70
15	Harvest index (%)		47.92	199.20	68.29**	29.70
16	Oil content (%)		18.31**	81.08**	6.10	13.62

* Significance at $P \leq 0.05$; ** Significance at $P \leq 0.01$

secondary branches per plant, length of main shoot, siliquae on main shoot and percent oil content indicating that the environments were diverse. Mukesh *et al.* (2007) observed significant variation among the genotypes for days to 50 per cent flowering, days to 50 per cent maturity, 1000-seed weight and other yield contributing characters except pod length. Similar results were also reported by Verma *et al.* (2008) in pooled analysis of variance over the environments.

The g x e interactions were significant for all characters except days to flower initiation and percent oil content. The presence of g x e interaction has greatly influenced the variation due to genotypes to the extent that genotypic differences recorded in individual environments have vanished for these characters. Gupta *et al.* (1992) also stressed the importance of g x e interactions while pooling the data over environments.

4.1.2 Estimates of mean performance

Estimates of mean values for 33 genotypes in Env.I, Env.II and pooled over the environments are given in Appendix-I, II and III, respectively. The salient features of mean estimates are described environment wise and pooled over the environments as below:

4.1.2.1 Days to flower initiation

Days to flower initiation of different genotypes in Env.I varied between 68.0-99.7 with an average of 89.6 days. None of genotypes could initiate flowering earlier than the earliest flowering mustard checks *viz.,* Nav Gold and RCC-4 (68.0 days each). However, the genotype P-138 flowered earlier (87.0 days) among different DH lines and the parent Jayanti (92 days) while P-26 was significantly late and took 99.7 days to show flower initiation. In Env.II, the range of different genotypes varied between 60.0-94.7 with an average of 87.3 days. None of genotypes exhibited flowering earlier than the earliest flowering mustard check Nav Gold (60.0 days) while the genotype P-101 was last to initiate flowering (94.7 days) though, statistically at par with the parent Jayanti (85.7 days). In pooled over the environments, days to flower initiation varied between 64.0-94.0 days with an average value of 88.5 days. Among mustard checks, Nav Gold appeared as earliest flowering variety and none of genotypes could exhibit flowering earlier than Nav Gold (64.0 days). All the doubled haploid lines were statistically at par with the parent Jayanti (88.8 days) to initiate flowering.

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4.1.2.2 Days to 50 percent flowering

In Env.I, days to 50 percent flowering varied between 114.3-135.0 with mean value of 128.7 days. None of the genotypes showed significant earliness for this character in comparison to the best mustard checks Nav Gold and Pusa jaikisan (114.3 days each). The genotype P-77 took maximum days to exhibit 50 percent flowering and appeared as significantly late in comparison to the parent Jayanti (128.7 days). In Env.II, the range varied between 102.7 to 137.0 with an average of 127.0 days. The genotype P-92 (137.0 days) was last to exhibit 50 per cent flowering though, remained statistically at par with the parent Jayanti (136.3 days). In pooled over the environments, range for days to 50 percent flowering varied from 108.5 to 134.0 with an average of 127.8 days. None of the genotypes was found to be significantly earlier for days to 50 per cent flowering than the earliest flowering mustard check Nav Gold in Env.II and pooled over the environments. The genotypes such as P-23, P-26, P-39, P-56, P-62, P-74, P-75, P-96, P-137 and P-138 took significantly lesser days to 50 per cent flowering as compared to the parent Jayanti (132.5 days) while the genotype P-77 took maximum days to 50 per cent flowering (134.0 days).

4.1.2.3 Days to 75 per cent maturity

Days to 75 per cent maturity of different genotypes varied between 144.7 and 178.0 with grand mean of 167.5 days in Env.I. None of the genotypes was found to be significantly earlier in maturity than the earliest maturing mustard check RCC-4 which took 144.7 days to mature. Five genotypes *viz.,* P-17, P-23, P-26, P-31 and P-34 matured significantly earlier than the parent Jayanti which took 170 days while P-24, P-75 and P-133 matured significantly late than the parent Jayanti. On the other hand in Env.II, the maturity duration varied from 149.3 to 178.3 with the mean value of 167.9 days. The mustard check Nav Gold was the earliest to mature (149.3 days) followed by RCC-4 (150.7 days). Three genotypes *viz.,* P-26, P-75 and P-117 appeared to be significantly late in maturity while rest of the genotypes remained statistically at par with the late maturing check Jayanti (168 days). In pooled over the environments, the range varied from 147.7 to 176.0 with an average value of 167.7 days. None of the genotypes exhibited maturity earlier than the earliest maturing mustard checks *viz.,* RCC-4 and Nav Gold which took 147.7 and 148.8 days, respectively. The genotype P-34 exhibited significantly earliness while P-75 and P-117 were significantly late in maturity in comparison to the late maturing check Jayanti (169.0 days).

4.1.2.4 Plant height

In Env.I, the range of different genotypes for plant height varied from 81.6-191.3 with an average value of 122.4 cm. The genotypes P-51 and P-56 exhibited significantly less plant height than the most dwarf mustard check Pusa jaikisan (107.4 cm). The genotype P-64 (191.3 cm) was observed to be significantly taller followed by P-31, P-39, P-138, P-92 and P-17 than the tallest mustard check Nav Gold (117.5 cm). On the other hand in Env.II, plant height of different genotypes ranged from 83.7-121.8 with mean value of 104.3 cm. The genotype P-12 (121.8 cm) was observed to be tallest followed by P-43, P-117, P-133, P-92, P-17, P-56, P-45, P-33 and P-31, though, remained statistically at par with the tallest check Pusa Jaikisan (107.0 cm). The minimum value for plant height was recorded by P-62 (83.7 cm) statistically at par with the parental check Jayanti (85.9 cm). In pooled over the environments, range varied between 93.7 and 147.9 with mean value of 113.4 cm. The four genotypes *viz.,* P-31, P-39, P-138 and P-64 exhibited significantly higher plant height than the tallest mustard check Nav Gold (111.6 cm) while the genotype P-51 recorded lowest plant height (93.7 cm) statistically at par with the most dwarf parental check Jayanti (101.3 cm).

4.1.2.5 Number of primary branches per plant

In Env.I, range for this character varied from 4.0-7.4 branches per plant with an average value of 5.2. The genotype P-138 showed maximum branches per plant (7.4) and was found to be significantly superior to the best check Jayanti (5.9). In Env.II, the range varied from 2.7-7.0 with an average value of 4.5. The genotype P-12 showed maximum number of primary branches per plant (7.0) and appeared to be significantly superior to the best check Pusa Jaikisan (5.0). In pooled over the environments, the values varied from 3.8-5.8 with an average value of 4.9. The genotype P-138 showed maximum number of primary branches per plant (5.8) followed by P-12, P-24, P-56 and P-133, though, statistically at par with the best check Jayanti (5.3).

4.1.2.6 Number of secondary branches per plant

In Env.I, the range for this character varied from 4.2-10.9 with an average value of 7.0. The genotype P-12 showed maximum number of secondary branches per plant (10.9) and was found to be significantly superior to the best check RCC-4 (8.5). On the other hand in Env.II, the range for this character varied from 5.4-12.5 with an average

value of 9.2. Highest number of secondary branches per plant was recorded by P-12 (12.5) followed by P-39 (11.7), though, remained statistically at par with the best check Jayanti (10.9). In pooled over the environments, range varied between 6.2-11.7 with an average value of 8.1. The genotype P-12 showed maximum number of secondary branches per plant (11.7) and appeared significantly superior to the best check RCC-4 (9.1).

4.1.2.7 Siliquae per plant

In Env.I, range for this character varied between 117.6-284.6 with an average value of 172.7. The highest siliquae per plant were exhibited by the genotype P-31 (284.6) followed by P-12, P-39 and P-17 and were found to be significantly superior to the best check RCC-4 (167.5). In Env.II, range varied between 132.2-394.0 with an average value of 178.1. Highest siliquae per plant was recorded by P-12 (394.0) followed by P-23 (335.3) and were significantly superior to best check Jayanti (175.1). In pooled over the environments, the range varied between 141.0-329.4 with an average value of 175.4. The highest siliquae per plant were exhibited by the genotype P-12 (329.4) followed by P-23 (246.9) and were found to be significantly superior to the best check Jayanti (168.1).

4.1.2.8 Length of main shoot

Length of main shoot of different genotypes in Env.I varied between 31.0-57.3 with an average of 44.7 cm. The genotype P-133 showed maximum and significantly higher length of main shoot (57.3 cm) than the best check RCC-4 (49.3 cm). On the other hand in Env.II, range varied between 33.0-52.3 with an average value of 40.3 cm. The genotype P-12 recorded maximum length of main shoot (52.3 cm) followed by P-26, though, remained statistically at par with the best check RCC-4 (44.0 cm). However, in pooled over the environments, range varied between 34.5-52.3 with an average value of 42.5 cm. The genotype P-12 showed maximum length of main shoot (52.3 cm) followed by P-26 (50.0 cm) and were found to be statistically at par with the best check RCC-4 (46.7 cm).

4.1.2.9 Siliquae on main shoot

In Env.I, the range for this character varied from 20.0-50.3 with an average value of 35.0. Significantly highest siliquae on main shoot were recorded by the genotype P-

137 (50.3) in comparison to the best check Jayanti (39.3). On the other hand in Env.II, the range varied from 18.0-34.0 with an average value of 26.9. None of the genotypes surpassed the best check RCC-4 (34.0) significantly for this character. In pooled over the environments, the range varied from 22.7-37.5 with an average value of 30.9. Highest siliquae on main shoot were recorded by P-33 (37.5) followed by P-137 (37.0) and both were statistically at par with best check RCC-4 (31.2).

4.1.2.10 Siliqua length

In Env.I, range for this character varied from 3.4-4.4 with an average value of 3.7 cm. None of the genotypes had significantly higher siliqua length than the best checks RCC-4 and Nav Gold (4.4 cm each). In Env.II, range for this character varied from 3.2-4.2 with an average value of 3.6 cm. Highest siliqua length was recorded by the genotypes P-77 and P-137 (4.2 cm each) and both were statistically at par with best check Pusa Jaikisan (4.0 cm). However, in pooled over the environments, range for this character varied from 3.4-4.1 with an average value of 3.7. None of the genotypes had significantly higher siliqua length than the best checks Nav Gold and RCC-4 (4.1 cm each).

4.1.2.11 Seeds per siliqua

In Env.I, seeds per siliqua for various genotypes ranged from 9.5-13.5 with an average of 11.0. The genotype P-39 (13.5) was found to be significantly superior to best check Nav Gold (11.7). Minimum seed per siliqua were recorded by P-12 (9.5). In Env.II, range varied between 8.2-11.6 with an average value of 10.0. None of the genotypes had significantly higher seeds per siliqua than the best check Nav Gold (11.6). However, in pooled over environments, range varied between 9.3-11.8 with an average value of 10.5. Highest seeds per siliqua were recorded for P-63 (11.8) and found statistically at par with the best mustard check Nav Gold (11.6).

4.1.2.12 1000-seed weight

In Env.I, 1000-seed weight for various genotypes ranged from 2.1-5.0 with an average of 2.7 g. In Env.II, range for this character varied between 2.2-3.2 with an average of 2.6 g. In pooled over environments, 1000-seed weight ranged from 2.3-4.0 with an average of 2.7 g. None of the genotypes was found to be significantly superior to the best check Nav Gold (5.0 g) in Env.I, Pusa Jaikisan (3.2 g) in Env.II and Nav Gold (4.0 g) in pooled over the environments. However, P-33 (2.9 g) in Env.I, P-26 (3.1 g) and

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P-101 (2.9 g) in Env.II and P-24 and P-137 (2.8 g each) in pooled over the environments exhibited higher 1000-seed weight than the parental check Jayanti.

4.1.2.13 Seed yield per plant

In Env.I, seed yield per plant varied from 4.1-8.8 with an average of 6.2 g. The genotypes P-31 and P-138 (8.8 g each) exhibited the highest seed yield per plant followed by P-26 (8.7 g), P-63 (8.7 g) and P-43 (8.0 g) which were statistically at par with the best mustard check Nav Gold (7.8 g). However, the nine genotypes *viz.,* P-12, P-26, P-31, P-33, P-34, P-43, P-63, P-64 and P-138 exhibited significantly higher seed yield per plant in comparison to the parental check Jayanti (5.3 g). In Env.II, seed yield per plant varied from 4.5-8.6 with an average of 6.2 g. The genotypes P-51 and P-117 (8.6 g each) recorded the highest seed yield per plant followed by P-103, P-92, P-34, P-39 and P-77 and were statistically at par with the best mustard somaclonal check Pusa Jaikisan (7.0 g). Out of these, three genotypes *viz.,* P-51, P-117 and P-103 recorded significantly higher seed yield per plant than the karan rai parental check Jayanti (5.9 g). However, in pooled over the environments, seed yield per plant for various genotypes ranged from 4.6-7.4 with an average of 6.2 g. The genotype P-34 recorded the highest seed yield per plant (7.4 g) followed by P-117, P-138, P-63 and P-64 which were statistically at par with the best mustard check Pusa Jaikisan (6.6 g) and parental check Jayanti (5.6 g). Significant variations due to different planting dates were also observed earlier by Bhuiyan *et al.* (2008) in Indian mustard for seed yield per plant and other component characters.

4.1.2.14 Biological yield per plant

In Env.I, biological yield per plant varied from 13.0-53.7 with an average of 36.4 g. The highest biological yield per plant was recorded for P-31 (53.7 g) followed by P-64 (49.0 g) and were found to be statistically at par with the best check Nav Gold (45.0 g) but, significantly higher than karan rai parental check Jayanti (33.7g). In Env.II, range for this character varied between 25.7-43.7 with an average of 34.1 g. The significantly highest biological yield per plant was recorded for P-33 (43.7 g) followed by P-23 (42.0 g) in comparison to best karan rai check Jayanti (28.0 g) but, were found to be statistically at par with the best mustard check RCC-4 (38.7 g). However, in pooled over the environments, range for this character varied between 27.8-44.3 with an average of 35.2 g. The genotypes P-31 showed the significantly highest biological yield per plant

(44.3 g) followed by P-33 (42.2 g), P-64 (42.0 g) and P-137 (40.2 g) in comparison to karan rai check Jayanti (30.8 g) but, remained statistically at par with the best mustard check RCC-4 (39.8 g).

4.1.2.15 Harvest index

In Env.I, harvest index for various genotypes ranged from 11.1-27.7 with an average of 17.4%. The genotype P-63 (27.7 %) was found to be significantly superior to best mustard check Nav Gold (17.5 %) and karan rai check Jayanti (17.4 %). On the other hand in Env.II, range for this character varied between 13.1-29.8 with an average of 19.4 %. The genotype P-117 showed the highest harvest index (29.8 %) followed by P-77, P-74 and P-34 and all were found to be statistically at par with the best karan rai check Jayanti (21.9 %). In pooled over the environments, range for this character varied from 12.5-25.0 with an average of 18.4 %. The genotype P-34 showed the highest harvest index (25.0 %) followed by P-77, P-138 and P-63, though, remained statistically at par with the best karan rai check Jayanti (19.7 %).

4.1.2.16 Oil content

In Env.I, oil content of different genotypes ranged between 33.1-41.8 with an average value of 37.4 %. The highest oil content was recorded for P-75 (41.8 %) which was found to be statistically at par with the best check Jayanti (40.3 %). The genotype P-89 recorded the lowest percent oil content (33.1 %). On the other hand in Env.II, range for this character varied between 32.4-40.0 with an average of 36.2 %. The genotype P-12 (40.0 %) showed the highest oil content followed by P-24 (39.1 %), P-75 (39.1 %), P-138 (39.0 %) and P-133 (38.9 %) and were found to be statistically at par with the best check Jayanti (38.5 %). In pooled over the environments, the range varied between 33.6-40.4 with an average of 36.8 %. The genotype P-75 (40.4 %) recorded the highest percent oil content followed by P-12 (40.0 %) and were statistically at par with the best check Jayanti (39.4 %). None of the genotypes exhibited significantly higher percent oil content than the best check Jayanti in Env.I, Env.ll and pooled over the environments. Earlier, Saad *et al.* (2011) also stressed the importance of sowing date to realize better percent oil content and oil yield in *Brassica napus.*

4.1.3 Estimates of parameters of variability

The estimates of parameters of variability *viz.,* phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad sense and expected genetic advance expressed as percent of mean for the characters studied in Env.I, Env.II and pooled over the environments are presented in Tables 4.3 and 4.4, respectively and described here under environment-wise and combined over environments:

4.1.3.1 Estimates of parameters of variability in Env.I

The estimates of PCV were higher than their corresponding GCV for all characters studied which indicated that the apparent variation is not only due to genotypes, but, also due to the influence of environment. Therefore, caution has to be exercised in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. Similar findings with respect to PCV and GCV have been reported by Mahla *et al.* (2003), Mahak *et al.* (2004), Kumar and Mishra (2006) and Kumar and Mishra (2007).

A wide range of variability was observed for all the characters studied. Phenotypic coefficient of variation was high (>30%) for harvest index while moderate estimates (10-30 %) of PCV were recorded for the characters such as seed yield per plant, siliquae on main shoot, number of secondary branches per plant, 1000-seed weight, plant height, siliquae per plant, biological yield per plant, number of primary branches per plant, length of main shoot, siliqua length and seeds per siliqua. Low PCV values (<10 %) were recorded for the remaining traits.

The moderate GCV (10-30 %) was observed for seed yield per plant, 1000-seed weight, plant height, number of secondary branches per plant, siliquae on main shoot, siliquae per plant, harvest index, biological yield per plant, number of primary branches per plant and length of main shoot while the estimates of GCV were low (<10 %) for the remaining characters. The lower estimates of PCV and GCV were observed for days to 75 per cent maturity. The result is in confirmation to the earlier findings of Singh *et al.* (2003).

A useful measure of considering the ratio of genetic variance to the total phenotypic variance is heritability. The information on heritability estimates are helpful in studying the inheritance of quantitative characters as well as for planning breeding

programmes with desired degree of expected genetic progress. In the present study, the heritability estimates were high (>60 %) for days to 75 per cent maturity followed by days to flower initiation, 1000-seed weight, plant height, days to 50 per cent flowering, number of secondary branches per plant and siliquae per plant. High heritability estimates indicated the dependency of phenotypic expression which reflects the genotypic ability of cultivars to transmit the genes to their off springs. High heritability estimates for siliquae per plant and days to 75 per cent maturity were also observed by Kumar *et al.* (1988), Nagaraja (1990), Chowdhary and Goswami (1991) and Diwakar and Singh (1993). Singh *et al.* (1987) recorded high heritability for number of secondary branches per plant only. Sikarwar *et al.* (2000) recorded high heritability for number of siliquae per plant, 1000-grain weight and plant height. Muhammad *et al.* (2007) also recorded high heritability for number of siliquae per plant. Mahla *et al.* (2003) and Mahak *et al.* (2004) recorded high heritability for days to flowering, days to maturity, 1000-seed weight and plant height. Kumar and Mishra (2007) observed high heritability for plant height and siliquae per plant. Lalta *et al.* (2001), Abebe (2008) and Yared *et al.* (2012) also reported high heritability for days to flowering, days to maturity, length of main raceme, plant height and test weight. High heritability estimates for yield contributing characters were observed by Khulbe *et al.* (2000), Ghosh and Gulati (2001) and Pant and Singh (2001). The estimates were moderate (30-60 %) for the characters *viz.*, length of main shoot followed by seed yield per plant, siliquae on main shoot, number of primary branches per plant, biological yield per plant and seeds per siliqua while rest of the characters exhibited low heritability (<10 %). Similar results were also observed by Nagaraja (1990). Singh *et al.* (1987) observed medium heritability for number of primary branches per plant and seeds per siliqua. Low heritability estimates indicated that the character is highly influenced by environmental factors and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects.

For an effective selection programme, knowledge of estimates of heritability alone is not sufficient and genetic advance, if studied along with heritability is more useful. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high heritability and high genetic variability are important to obtain higher genetic gain.

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In the present study, the results revealed that the response to selection for different characters which showed high heritability need to be given due emphasis for effective selection and suggested that these characters were under genetic control. However, the high heritability does not necessarily mean high genetic gain and alone is not sufficient to

Table 4.3 Estimates of different parameters of variability for various characters in Env.I and Env.II

Characters	Env.I				Env.II			
	PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance (%) of mean	PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance (%) of mean)
Days to flower initiation	8.52	7.68	81.3	14.30	11.02	8.54	60.0	13.63
Days to 50% flowering	4.15	3.49	70.3	6.05	6.68	6.27	88.3	12.14
Days to 75% maturity	4.96	4.64	87.1	8.91	4.11	3.58	75.9	6.43
Plant height (cm)	24.65	21.67	77.2	39.23	11.88	5.77	23.6	5.77
No. of primary branches /plant	21.54	15.91	54.5	24.19	26.58	13.44	25.6	14.01
No. of secondary branches /plant	25.35	21.07	69.1	36.08	24.76	12.32	24.8	12.65
Siliquae /plant	23.72	18.42	60.3	29.47	38.47	25.83	45.1	35.72
Length of main shoot (cm)	17.05	13.13	59.3	20.82	15.92	4.68	8.6	2.83
Siliquae on main shoot	26.17	19.92	57.9	31.22	24.42	4.07	2.8	1.40
Siliqua length (cm)	12.89	3.22	6.2	1.70	11.70	4.09	12.2	2.95
Seeds /siliqua	10.58	6.39	36.5	7.95	14.81	3.40	5.3	1.61
1000-seed weight (g)	24.75	21.80	77.6	39.56	14.16	6.30	19.8	5.77
Seed yield /plant (g)	29.91	22.82	58.2	35.86	23.71	13.40	31.9	15.60
Biological yield /plant (g)	22.95	16.32	50.5	23.90	23.82	3.16	1.8	0.87
Harvest index (%)	30.44	16.48	29.3	18.36	36.57	16.90	21.4	16.11
Oil content (%)	9.34	1.57	-	-	10.54	2.66	-	-

PCV: Phenotypic Coefficient of variation; GCV: Genotypic Coefficient of Variation; h^2_{bs} (%): Heritability in broad sense; GA: Genetic Advance (%) of mean

- Not estimated due to negative variances

make improvement through simple phenotypic selection. The heritability estimates become more beneficial when used to estimate genetic advance (Johnson *et al.* 1955). Thus, the genetic advance has an added edge over heritability as a guiding factor to breeders in various selection programmes.

The high expected genetic advance (>30 %), expressed as percentage of mean was observed for 1000-seed weight followed by plant height, number of secondary branches per plant, seed yield per plant and siliquae on main shoot. Diwakar and Singh (1993) and Kumar and Mishra (2007) also reported high genetic advance for plant height. Mahto (2001) reported high genetic advance for seed yield per plant. Mahla *et al.* (2003) and Mahak *et al.* (2004) also reported high genetic advance for 1000-seed weight and plant height. Singh *et al.* (2003) also reported highest genetic advance for 1000-seed weight followed by seed yield per plot, days to 50 per cent flowering and siliquae per plant.

Expected genetic advance was moderate (10-30 %) for siliquae per plant followed by number of primary branches per plant, biological yield per plant, length of main shoot, harvest index and days to flower initiation, all the remaining characters exhibited low estimates (<10 %) for genetic advance. Shalini (1998) indicated that days to 50 per cent flowering had high heritability coupled with low genetic advance in mustard. Lalta *et al.* (2001) also reported low to medium estimates of expected genetic advance for days to maturity, test weight and oil content.

Based on the present study, high heritability coupled with high genetic advance was observed for 1000-seed weight, plant height and number of secondary branches per plant. The results suggested the importance of additive gene action for their inheritance and improvement could be brought about by phenotypic selection. Uddin *et al.* (1995) reported high heritability coupled with high genetic advance for 1000-seed weight. Das *et al.* (1998) and Acharya and pati (2008) also observed high heritability coupled with high genetic advance for siliquae per plant, number of secondary branches per plant, plant height and 1000-seed weight indicating predominance of additive gene action in inheritance of these characters. High heritability coupled with high genetic advance for 1000 seed weight, plant height and other characters has also been reported earlier (Mahla *et al.* 2003; Mahak *et al.* 2004; Rai *et al.* 2005; Kumar and Mishra 2007).

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4.1.3. Estimates of parameters of variability in Env.II

In the present study, PCV values were higher than their corresponding GCV values for all the characters studied. Similar findings with respect to PCV and GCV have also been reported earlier by Mahla *et al.* (2003), Mahak *et al.* (2004), Kumar and Mishra (2006) and Kumar and Mishra (2007). The high PCV (>30 %) values were observed for siliquae per plant followed by harvest index. Similar result was also observed by Mahto (2001). The estimates were moderate (10-30 %) for number of primary branches per plant followed by number of secondary branches per plant, siliquae on main shoot, biological yield per plant, seed yield per plant, length of main shoot, seeds per siliqua, 1000-seed weight, plant height, siliqua length, days to flower initiation, and percent oil content. The low estimates of PCV (<10 %) were recorded for the remaining characters.

The moderate GCV (10-30 %) was recorded for siliquae per plant followed by harvest index, number of primary branches per plant, seed yield per plant and number of secondary branches per plant while remaining characters exhibited low estimates (<10 %). Chowdhary and Goswami (1991) and Shalini (1998) observed high PCV for siliquae per plant. Ghosh and Gulati (2001) also observed high estimates of PCV and GCV for all characters except plant height.

Heritability estimates were high (>60 %) for days to 50 per cent flowering followed by days to 75 per cent maturity and days to flower initiation. High heritability estimates for days to flower initiation and days to 75 per cent maturity were also observed by Kumar *et al.* (1988), Nagaraja (1990), Gowda (1993), Khulbe *et al.* (2000), Lalta *et al.* (2001) and Pant and Singh (2001). The estimates were moderate (30-60%) for siliquae per plant and seed yield per plant. similar results were also observed by Nagaraja (1990). The heritability estimates were low for the remaining characters.

High expected genetic advance (>30 %) was observed for siliquae per plant. Uddin *et al.* (1995) observed high genetic advance for siliquae per plant. It was moderate (10-30 %) for harvest index followed by seed yield per plant, number of primary branches per plant, days to flower initiation, number of secondary branches per plant and days to 50 per cent flowering. Shalini (1998) observed moderate genetic advance for number of secondary branches per plant. The values were low for the remaining characters. Panse and Kharagonkar (1957) and Lalta *et al.* (2001) reported high

heritability coupled with low genetic advance for days to maturity and oil content. For percent oil content, the estimates of heritability and genetic advance could not be estimated due to negative variances both in Env.I and Env.II.

4.1.3.3 Estimates of parameters of variability in pooled over the environments

A wide range of variability was observed for all the characters studied. The high estimates of PCV (>30 %) were recorded for harvest index followed by siliquae per plant. Moderate estimates (10-30 %) were observed for seed yield per plant followed by siliquae on main shoot, number of secondary branches per plant, biological yield per plant, number of primary branches per plant, plant height, 1000-seed weight, length of main shoot, seeds per siliqua and siliqua length. However, PCV estimates were low for the remaining characters.

Moderate GCV (10-30 %) estimates were recorded for siliquae per plant followed by 1000-seed weight, plant height and number of secondary branches. The GCV estimates were observed to be low for the remaining characters. Chowdhary and Goswami (1991) and Shalini (1998) observed high PCV for siliquae per plant. Ghosh and Gulati (2001) observed high estimates of PCV and GCV for all characters except plant height. The lower estimates of PCV and GCV were observed for days to 75 per cent maturity. This result is in confirmation to the earlier findings of Shalini *et al.* (2000), Singh *et al.* (2003) and Singh and Singh (2004).

Heritability estimates were high (>60 %) for days to 50 per cent flowering followed by days to 75 per cent maturity and days to flower initiation. High heritability estimates for days to 75 per cent maturity were also observed by Kumar *et al.* (1988), Nagaraja (1990), Khulbe *et al.* (2000) and Pant and Singh (2001). Moderate (30-60%) heritability estimates were observed for 1000-seed weight. Similar results have also been observed earlier (Shalini 2000).

Expected genetic advance expressed as percent of mean was moderate (10-30%) for siliquae per plant followed by 1000-seed weight, days to flower initiation and plant height. All the remaining characters exhibited low estimates of expected genetic advance. High heritability coupled with low genetic advance was observed for days 50 per cent flowering and days to 75 per cent maturity. Panse and Kharagonkar (1957) and Lalta *et*

al. (2001) also reported high heritability coupled with low genetic advance for days to maturity.

Table 4.4 Estimates of different parameters of variability for various characters in pooled over the environments

Characters	PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance (%) of mean
Days to flower initiation	9.82	8.18	69.4	14.03
Days to 50% flowering	5.54	4.76	73.6	8.41
Days to 75% maturity	4.56	3.83	70.5	6.62
Plant height (cm)	20.35	11.09	29.7	12.45
No. of primary branches /plant	20.91	3.84	2.6	1.27
No. of secondary branches /plant	25.21	10.18	16.3	8.47
Siliquae /plant	32.18	17.58	29.8	19.78
Length of main shoot (cm)	16.58	6.74	16.5	5.64
Siliquae on main shoot	25.75	7.88	9.4	4.97
Siliqua length (cm)	12.33	2.02	2.7	0.68
Seeds /siliqua	12.68	2.79	4.8	1.26
1000-seed weight (g)	20.28	12.61	38.7	16.16
Seed yield /plant (g)	26.97	6.72	6.2	3.45
Biological yield /plant (g)	23.38	7.75	11.0	5.30
Harvest index (%)	34.01	7.19	4.5	3.14
Oil content (%)	9.94	2.69	7.3	1.50

PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variation; h^2_{bs} (%): Heriatibility in broad sense; GA: Genetic Advance (%) of mean

4.1.4 Genetic divergence studies

The selection of suitable diverse parents for hybridization programme is an important feature of any crop improvement strategy for getting desired recombinants or transgressive segregants. Genetic divergence helps in quantifying the degree of divergence between biological populations at genotypic level and also to assess the relative contribution of different components to the total divergence both at inter- and intra-cluster level (Mischer and Sokal 1957; Morashima and Oka 1960; Nair and Mukherjee 1960; Murthy and Quadri 1966). The importance of intra-specific divergence in plant breeding has also been emphasized by several scientists (Griffing and Lindstorm 1954; Moll *et al.* 1962; De Pace *et al.* 1978; Arunachalam 1981; Hawkes 1981). Assessment of genetic divergence helps in reducing the number of breeding lines to be maintained and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide a greater scope for isolating superior recombinants/segregants. D^2-statistic is a powerful tool for measuring genetic diversity between genotypes.

4.1.4.1 Test of significance

The technique of multivariate analysis was used for grouping of genotypes into clusters. Simultaneous test of significance based on Wilk's criterion and D^2 values obtained for each pair of populations were observed to be significant in Env.I, Env.II and pooled over the environments suggesting that the populations in each environment differed significantly in respect of means.

4.1.4.2 Grouping of genotypes into clusters

On the basis of D^2 values for all possible pairs, 33 genotypes of *Brassica* species were grouped into different clusters using Tocher's procedure (Rao 1952) and dendrogram was constructed. The composition of clusters both for Env.I and II as well as pooled over the environments are presented in Tables 4.5, 4.6, 4.7 and figures 1, 2 and 3, respectively. The cluster analysis revealed that all the genotypes could be grouped into eight, three and three clusters in Env.I, Env.II and pooled over the environments, respectively. Different clustering pattern in rapeseed-mustard was also reported by earlier workers (Yadav *et al.* 1985; Srivastav and Singh 2000; Verma and Sachan 2000; Thul *et al.* 2004; Patel and Patel 2006; Mukesh *et al.* 2007; Singh *et al.* 2007; Mahmuda *et al.*

2008). Different clustering pattern in different environments has also been reported by Goswami and Behl (2006) and Kumari (2010).

In all the environments, cluster I was largest one. Srivastav and Singh (2000), Verma and Sachan (2000), Sinha and Singh (2004), Patel and Patel (2006), Mukesh *et al.* (2007), Singh *et al.* (2007), Kumari (2010) and Singh *et al.* (2012) also grouped genotypes into different clusters and reported that cluster I was the largest one. On the other hand, Monalisa *et al*. (2005) and Malik *et al.* (2006) reported that cluster III and IV were largest, respectively.

In Env.I, all the genotypes were grouped into eight clusters, six of which contained only one genotype each. Cluster I was largest consisting of 24 genotypes *viz.,* P-24, P-96, P-122, P-51, P-62, P-101, P-74, P-77, P-45, P-43, P-56, P-137, P-117, P-103, Jayanti, P-33, P-89, P-34, P-23, P-133, P-75, P-64, P-138 and P-39. Cluster II contained three genotypes as checks each of which belonged to *Brassica juncea viz.,* Nav Gold, Pusa Jaikisan and RCC-4. Clusters III, IV, V, VI, VII and VIII had one genotype each *viz.,* P-26, P-17, P-92, P-31, P-63 and P-12, respectively.

On the other hand in Env.II and pooled over the environments, all the genotypes were grouped into three clusters each. Cluster I was the largest and contained 29 genotypes such as P-45, P-64, P-43, P-96, P-63, P-75, P-34, P-31, P-56, P-74, P-89, P-133, P-101, P-77, P-17, P-24, P-51, P-103, P-122, P-33, P-39, Jayanti, P-117, P-92, P-62, P-138, P-137, P-26 and P-23. Cluster II had three genotypes each *viz.,* RCC-4, Nav Gold and Pusa Jaikisan while cluster III had only one genotype *viz.,* P-12 each.

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Table 4.5 Cluster composition in *Brassica carinata* following multivariate analysis in Env.I

Cluster number	Number of Genotypes	Genotypes
I	24	P-24, P-96, P-122, P-51, P-62, P-101, P-74, P-77, P-45, P-43, P-56, P-137, P-117, P-103, Jayanti, P-33, P-89, P-34, P-23, P-133, P-75, P-64, P-138, P-39
II	3	Nav Gold, Pusa Jaikisan, RCC-4
III	1	P-26
IV	1	P-17
V	1	P-92
VI	1	P-31
VII	1	P-63
VIII	1	P-12

Table 4.6 Cluster composition in *Brassica carinata* following multivariate analysis in Env.II

Cluster number	Number of Genotypes	Genotypes
I	29	P-45, P-64, P-43, P-96, P-63, P-75, P-34, P-31, P-56, P-74, P-89, P-133, P-101, P-77, P-17, P-24, P-51, P-103, P-122, P-33, P-39, Jayanti, P-117, P-92, P-62, P-138, P-137, P-26, P-23
II	3	RCC-4, Pusa Jaikisan, Nav Gold
III	1	P-12

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Table 4.7 Cluster composition in *Brassica carinata* following multivariate analysis in pooled over the environments

Cluster number	Number of genotypes	Genotypes
I	29	P-43, P-45, P-51, P-103, P-122, P-96, P-62, P-26, P-74, P-101, P-89, Jayanti, P-33, P-133, P-24, P-63, P-77, P- 56, P-137, P-39, P-34, P-75, P-138, P-64, P-117, P-17, P-92, P-31, P-23,
II	3	RCC-4, Nav Gold, Pusa Jaikisan
III	1	P-12
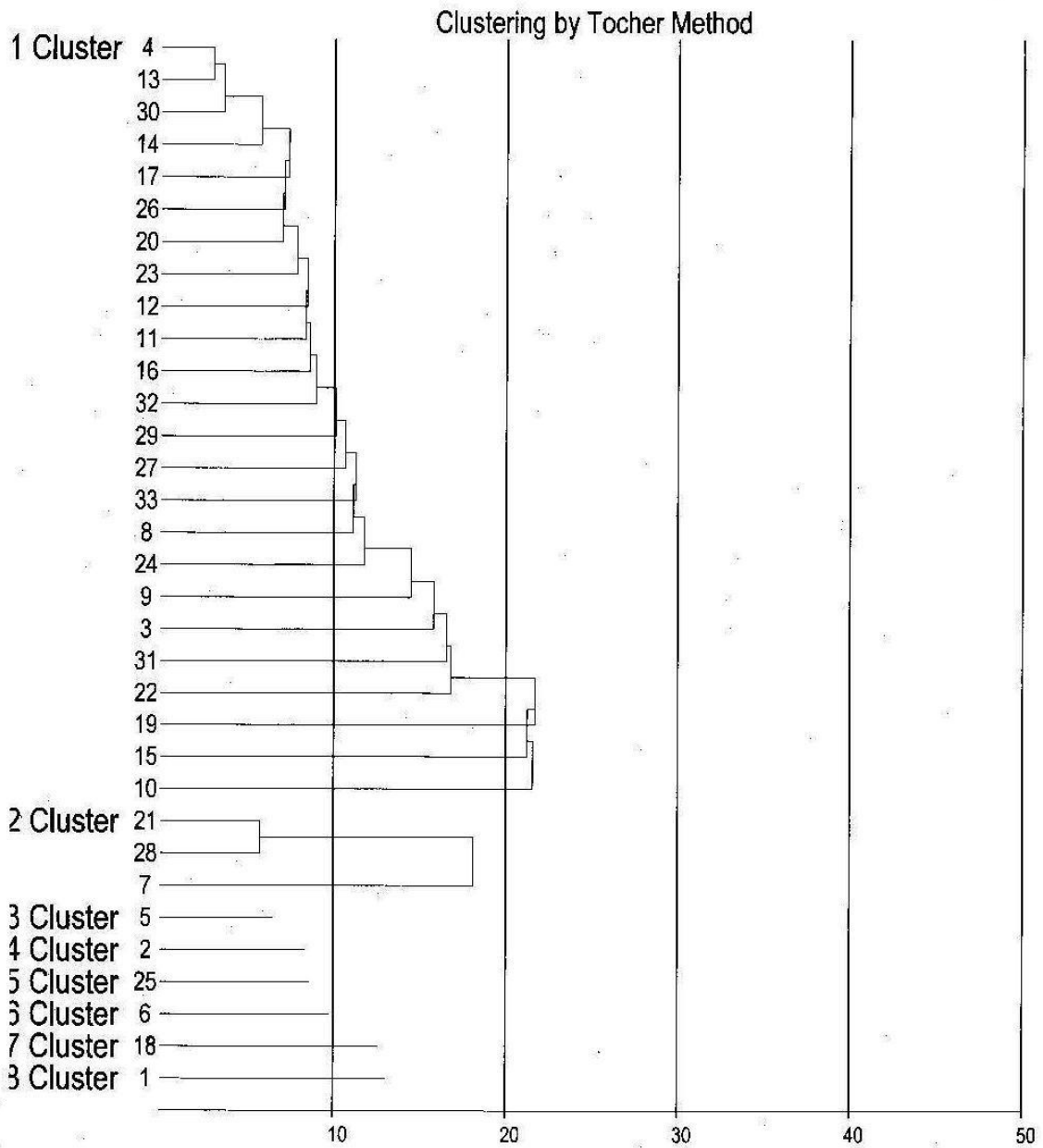
Fig.1 **Dendrogram showing grouping of 33 *Brassica carinata* genotypes generated using D^2 multivariate analysis (Tocher's method) in Env.I**

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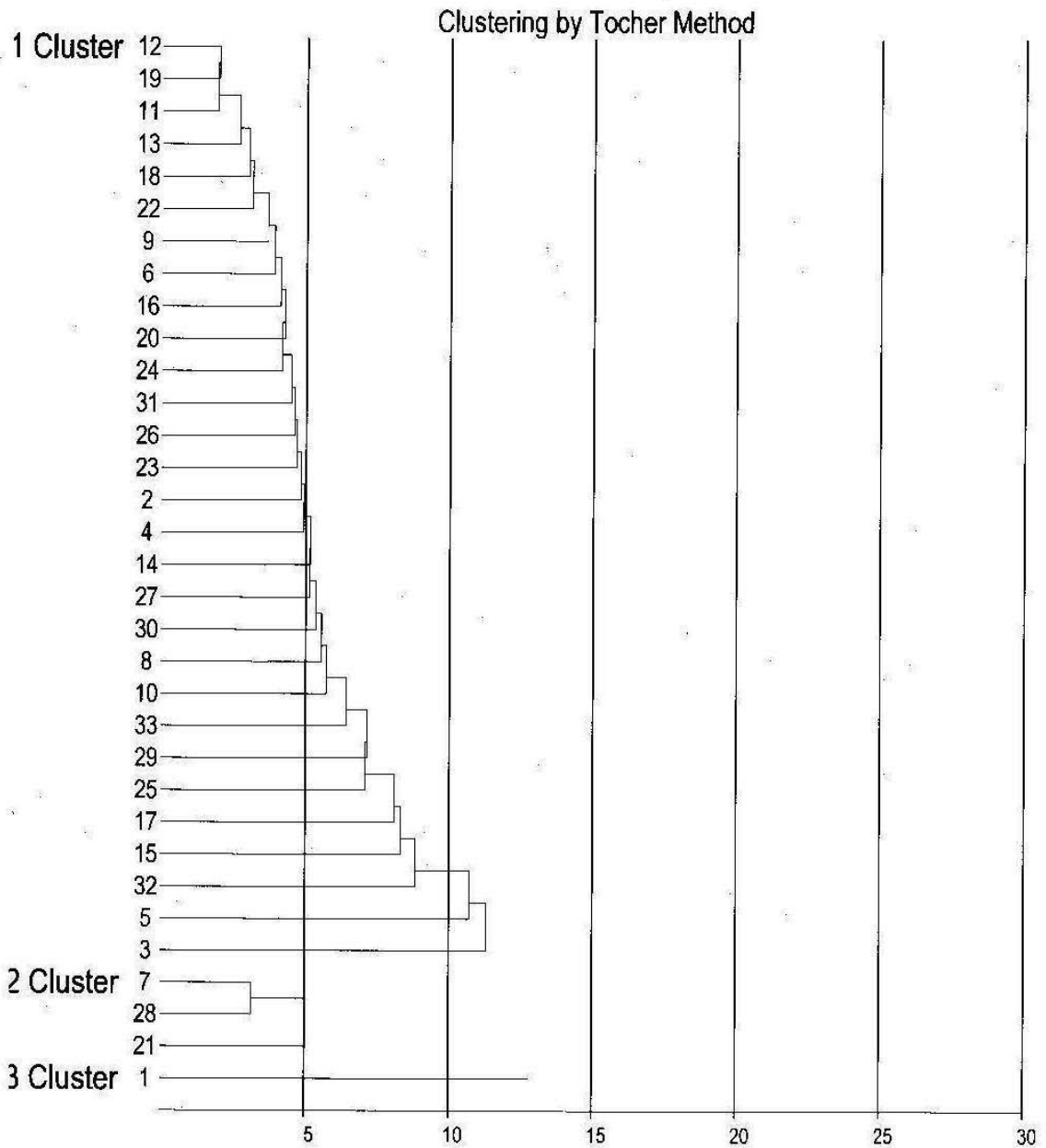
Fig.2   Dendrogram showing grouping of 33 *Brassica carinata* genotypes generated using D^2 multivariate analysis (Tocher's method) in Env.II
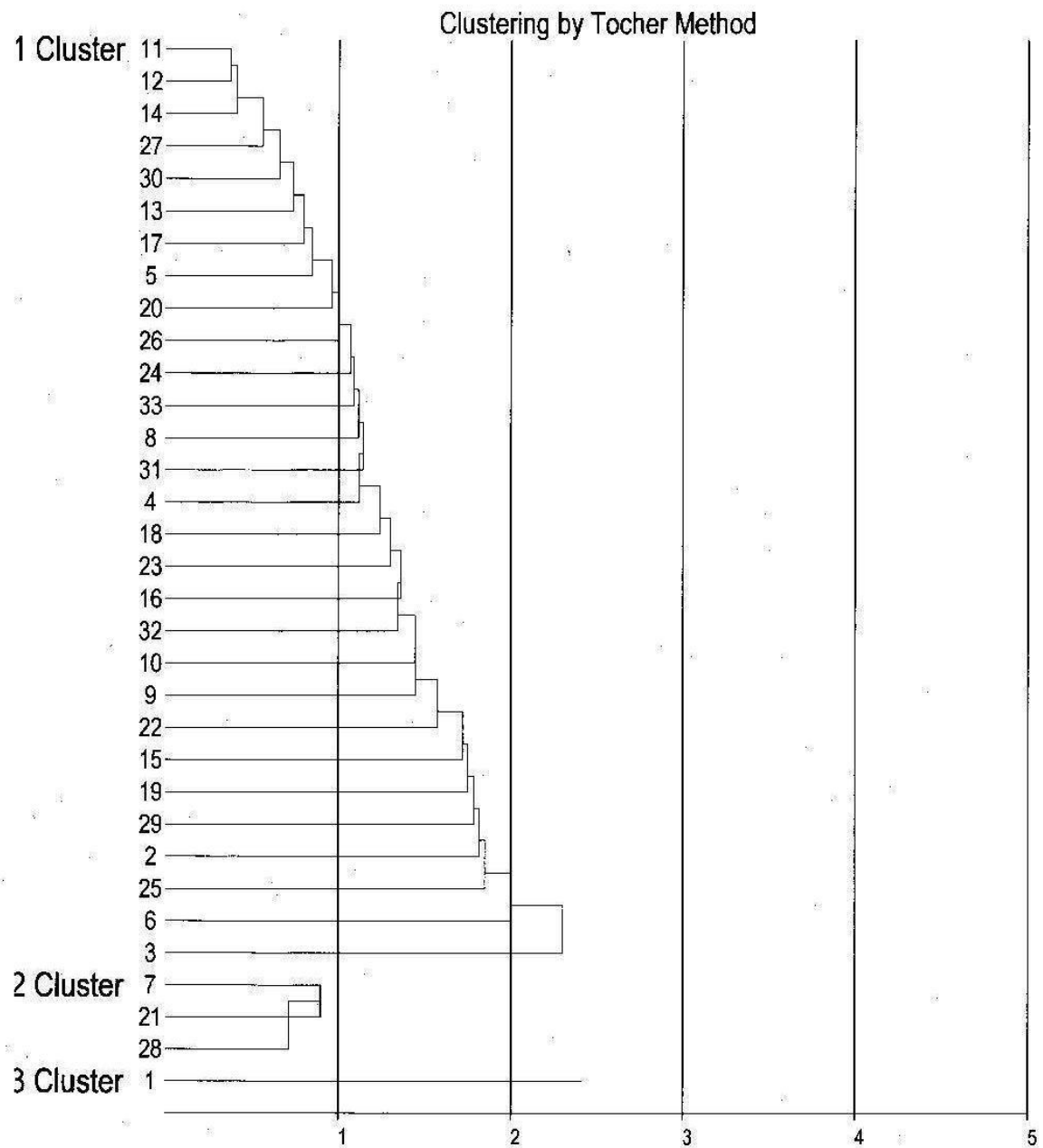
Fig.3   Dendrogram showing grouping of 33 *Brassica carinata* genotypes generated using D^2 multivariate analysis (Tocher's method) in pooled over the environments

On the overall comparison of the clusters in Env.I, Env.II and pooled over the environments, three clusters exhibited overlapping of the genotypes. The genotypes which were found to be common for both the environments and the pooled over environment in cluster I were 24 in number *viz.,* P-24, P-96, P-122, P-51, P-62, P-101, P-74, P-77, P-45, P-43, P-56, P-137, P-117, P-103, Jayanti, P-33, P-89, P-34, P-23, P-133, P-75, P-64, P-138 and P-39. For cluster II, three genotypes *viz.,* Nav Gold, Pusa Jaikisan and RCC-4 and one genotype *i.e.* P-12 in cluster VIII in Env.I and III in Env.II and pooled over the environments were common which indicated that the D^2-statistic is not much influenced by environmental variation resulting in consistent clustering of genotypes in these environments. Further, the clustering pattern indicated that all the mustard checks formed separate clusters while all doubled haploids appeared in separate clusters in Env.I, Env.II and pooled over environments. This further supported that Indian mustard (AABB, 2n=36) has been originated in china by hybridization between *Brassica campestris* (AA) and *Brassica nigra* (BB) in nature while Ethiopian mustard (BBCC, 2n=34) has been originated in Ethiopia by hybridization between *Brassica oleracea* (CC) and *Brassica nigra* (BB), though, one genome is common in both species. These results therefore, emphasized that the parents should be selected on the basis of total divergence for the traits used for an overall improvement in the yield.

4.1.4.3 Average intra- and inter-cluster distances

Average intra- and inter-cluster distances for Env.I, Env.II and pooled over the environments are presented in Tables 4.8, 4.9 and 4.10, respectively. In Env.I, the intra-cluster distances were comparable in clusters I (1.96) and II (2.11) while for clusters III, IV, V, VI, VII and VIII, the values were zero as these clusters were constituted by a single genotype each. In Env.II, the intra-cluster distances were almost of the same order and comparable in clusters I (1.62) and II (1.56) while for cluster III, the intra-cluster distance was zero since this cluster contained only a single genotype. In the analysis of genetic divergence pooled over the environments, the intra-cluster distances were comparable for clusters I (1.12) and II (1.00) while for cluster III, intra-cluster distance was zero. Since the intra-cluster distance was low, the chances of developing good segregants by hybridization among parents within clusters would be low, therefore, it is logical to attempt crosses between the genotypes falling in different clusters based on

inter-cluster distances. Srivastav and Singh (2000) reported that cluster I had the lowest intra-cluster D-value. Sinha and Singh (2004) and Patel and Patel (2006) reported highest intra-cluster distance in cluster II in Indian mustard.

In Env.I, maximum genetic divergence based on inter-cluster distances was recorded between clusters II and VIII (3.46) followed by the distance between II and VI (3.26) and II and V (3.23) while the minimum inter-cluster distance was observed between clusters III and IV (1.70). Monalisa *et al*. (2005) also reported maximum inter-cluster distance between clusters II and V while the lowest inter-cluster distance was observed between clusters I and II.

On the other hand in Env.II, the maximum inter-cluster distance was observed between clusters I and II (2.95) followed by clusters II and III (2.94) while the lowest inter-cluster distance was recorded between clusters I and III (2.05). The analysis of genetic divergence pooled over the environments indicated the highest inter-cluster distance between clusters II and III (2.34) followed by distance between clusters I and II (2.21). The lowest inter-cluster distance was observed between clusters I and III (1.42). This clearly indicates that the genotypes included in these clusters are having sufficient genetic diversity and parents from diverse clusters could be used in hybridization programme for improving seed yield. Further, the clustering pattern in Env.I, Env.II and pooled over the environments suggested the parallelism between the genetic divergence and species-wise geographical distribution. However, Anand and Rawat (1984) and Gupta *et al.* (1991) suggested that geographical diversity of line does not necessarily reflect on index of its genetic diversity. No parallelism between geographical diversity and genetic diversity was reported by Verma and Sachan (2000) in Indian mustard. Geographical distribution of the cultivars did not significantly contribute to genetic divergence (Singh *et al.* 2007).

Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and release of desirable recombinants in segregating generations. Therefore, the parents should be selected from cluster combinations between clusters II and VIII, I and II and II and III in Env.I, Env.II and pooled over the environments, respectively. In the remaining clusters, the inter-cluster distance was low

in all the environments which indicated that the genotypes of these clusters had close relationship and hence, may not be emphasized for hybridization programme.

Table 4.8 Average intra- and inter-cluster distance in Env.I

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**3.88** **(1.96)**	10.12 (3.18)	5.10 (2.25)	5.11 (2.26)	4.87 (2.20)	5.85 (2.41)	5.13 (2.26)	5.30 (2.30)
II		**4.47** **(2.11)**	9.61 (3.1)	10.18 (3.19)	10.49 (3.23)	10.63 (3.26)	8.89 (2.98)	11.98 (3.46)
III			**0.00** **(0.00)**	2.89 (1.7)	7.68 (2.77)	4.43 (2.10)	6.54 (2.55)	4.39 (2.09)
IV				**0.00** **(0.00)**	7.40 (2.72)	4.10 (2.02)	7.09 (2.66)	3.99 (1.99)
V					**0.00** **(0.00)**	6.65 (2.57)	4.30 (2.07)	7.02 (6.64)
VI						**0.00** **(0.00)**	6.74 (2.59)	4.24 (2.05)
VII							**0.00** **(0.00)**	7.24 (2.69)
VIII								**0.00** **(0.00)**

Values in bold letters are intra-cluster distances
Values in parenthesis are $\sqrt{D^2}$ = D values

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Table 4.9 Average intra- and inter-cluster distance in Env.II

Clusters	I	II	III
I	**2.64** **(1.62)**	8.71 (2.95)	4.21 (2.05)
II		**2.46** **(1.56)**	8.65 (2.94)
III			**0.00** **(0.00)**

Values in bold letters are intra-cluster distances
Values in parenthesis are $\sqrt{D^2}$ = D values

Table 4.10 Average intra- and inter-cluster distance in pooled over the environments

Clusters	I	II	III
I	**1.26** **(1.12)**	4.90 (2.21)	2.03 (1.42)
II		**1.01** **(1.00)**	5.48 (2.34)
III			**0.00** **(0.00)**

Values in bold letters are intra-cluster distances
Values in parenthesis are $\sqrt{D^2}$ = D values

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4.1.4.4 Cluster means and contribution of individual character towards divergence

Cluster means of different characters for Env.I, Env.II and pooled over the environments are presented in Tables 4.11, 4.12 and 4.13, respectively. Based on the comparison of cluster means of different characters for both environments and pooled over the environments, it was observed that substantial differences existed among the cluster means for each character.

Based on cluster means in Env.I, cluster II was characterized by maximum siliqua length (4.27 cm) and 1000-seed weight (4.53 g) and minimum days to flower initiation (68.56 days), days to 50 per cent flowering (114.56 days) and days to 75 per cent maturity (146.67 days). This cluster showed moderate to low values for remaining characters. Cluster III was characterized by minimum plant height (108.47 cm) while it showed moderate to low values for all the remaining characters studied. Patel and Patel (2006) also reported dwarf plants in cluster III. Highest cluster mean was recorded by cluster IV for siliquae on main shoot (44.67). Sinha and Singh (2004) observed that genotypes in cluster IV recorded highest main shoot length, number of pods per main shoot and seed yield per plant. Patel and Patel (2006) reported highest values for number of primary and secondary branches per plant, number of siliquae per plant, seeds per siliqua and seed yield per plant in cluster IV in Indian mustard. Cluster VI showed maximum values for number of primary branches per plant (5.60), siliquae per plant (284.57), seed yield per plant (8.76 g) and biological yield per plant (53.67 g). The genotype in cluster VII was characterized by maximum seeds per siliqua (12.67) and harvest index (27.73 %). Kumari (2010) also observed that genotypes in cluster VII had highest cluster means for seeds per siliqua and harvest index. The cluster VIII showed highest cluster mean for number of secondary branches per plant (10.90), length of main shoot (52.33 cm) and percent oil content (40.00 %).

In Env.II, the highest cluster mean was recorded by cluster I for seed yield per plant (6.22 g) and harvest index (19.65 %). The genotypes in cluster II were characterized by maximum 1000-seed weight (3.05 g) and minimum days to flower initiation (63.33 days), days to 50 per cent flowering (104.33 days), days to 75 per cent maturity (150.33 days) and plant height (102.4 cm). Cluster III was represented by genotype having maximum number of primary branches per plant (7.00), number of secondary branches per plant (12.50), siliquae per plant (394.00), length of main shoot (52.33 cm), siliquae on

Table 4.11 Cluster means for different characters in Env.I

Clusters / Characters	I	II	III	IV	V	VI	VII	VIII	Mean	Minimum	Maximum
Days to flower initiation	91.64	68.56	90.67	87.67	90.67	92.00	94.67	96.00	88.99	68.56	96.00
Days to 50% flowering	130.00	114.56	130.67	129.00	130.67	131.33	130.00	132.00	128.53	114.56	132.00
Days to 75% maturity	170.32	146.67	159.33	162.67	174.00	163.67	171.33	168.67	164.58	146.67	174.00
Plant height (cm)	120.48	113.59	108.47	141.6	148.13	184.47	109.07	115.8	130.20	108.47	184.47
No. of primary branches/ plant	5.36	4.14	5.47	5.07	3.93	5.60	5.23	4.43	4.90	3.93	5.60
No. of secondary branches/ plant	6.86	5.81	8.60	10.07	4.20	9.20	5.10	10.90	7.59	4.20	10.90
Siliquae / plant	163.88	151.38	206.5	210.6	157.43	284.57	189.47	264.73	203.57	151.38	284.57
Length of main shoot (cm)	45.68	39.56	50.67	39.00	42.67	45.67	31.00	52.33	43.32	31.00	52.33
Siliquae on main shoot	36.90	26.44	39.33	44.67	20.00	29.67	22.67	32.67	31.54	20.00	44.67
Siliqua length (cm)	3.65	4.27	3.77	3.60	3.73	4.10	4.00	3.63	3.84	3.60	4.27
Seeds/ siliqua	10.98	11.54	11.07	10.07	11.07	11.44	12.67	9.53	11.05	9.53	12.67
1000- seed weight (g)	2.53	4.53	2.32	2.38	2.58	2.69	2.62	2.37	2.75	2.32	4.53
Seed yield / plant	5.75	6.79	8.73	6.63	4.48	8.76	8.74	7.65	7.19	4.48	8.76
Biological yield / plant (g)	34.82	41.67	42.00	39.33	41.00	53.67	32.00	31.67	39.52	31.67	53.67
Harvest index (%)	16.92	16.37	21.43	17.30	11.10	16.77	27.73	24.53	19.02	11.10	27.73

Oil content (%)	37.12	36.74	38.8	39.87	38.87	38.27	38.33	40.00	38.50	36.74	40.00

Table 4.12 Cluster means for different characters in Env.II

Clusters / Characters	I	II	III	Mean	Minimum	Maximum
Days to flower initiation	89.79	63.33	87.67	80.26	63.33	89.79
Days to 50% flowering	129.29	104.33	128.00	120.54	104.33	129.29
Days to 75% maturity	169.76	150.33	165.33	161.81	150.33	169.29
Plant height (cm)	103.89	102.42	121.80	109.37	102.42	121.80
No. of primary branches/ plant	4.51	3.86	7.00	5.12	3.86	7.00
No. of secondary branches/ plant	9.02	10.10	12.50	10.54	9.02	12.50
Siliquae / plant	172.39	161.44	394.00	242.61	161.44	394.00
Length of main shoot (cm)	39.85	41.11	52.33	44.43	39.85	52.33
Siliquae on main shoot	26.49	28.67	33.33	29.50	26.49	33.33
Siliqua length (cm)	3.61	3.84	4.03	3.83	3.61	4.03
Seeds/ siliqua	9.95	10.03	11.37	10.45	9.95	11.37
1000- seed weight (g)	2.60	3.05	2.76	2.80	2.60	3.05
Seed yield / plant	6.22	5.99	6.17	6.13	5.99	6.22
Biological yield / plant (g)	33.90	34.11	40.67	36.23	33.90	40.67
Harvest index (%)	19.65	18.19	15.7	17.85	15.70	19.65
Oil content (%)	35.92	37.98	40.00	37.97	35.92	40.00

Table 4.13 Cluster means for different characters in pooled over the environments

Clusters / Characters	I	II	III	Mean	Minimum	Maximum
Days to flower initiation	90.67	65.94	91.83	82.81	65.94	91.83
Days to 50% flowering	129.67	109.44	130.00	123.04	109.44	130.00
Days to 75% maturity	169.68	148.50	167.00	161.73	148.50	169.68
Plant height (cm)	113.73	108.01	118.80	113.51	108.01	118.80
No. of primary branches/ plant	4.91	4.00	5.72	4.88	4.00	5.72
No. of secondary branches/ plant	7.99	7.96	11.70	9.22	7.96	11.70
Siliquae / plant	172.09	156.41	329.37	219.29	156.41	329.37
Length of main shoot (cm)	42.43	40.33	52.33	45.03	40.33	52.33
Siliquae on main shoot	31.21	27.56	33.00	30.59	27.56	33.00
Siliqua length (cm)	3.64	4.06	3.83	3.84	3.64	4.06
Seeds/ siliqua	10.49	10.79	10.45	10.58	10.45	10.79
1000- seed weight (g)	2.56	3.79	2.57	2.97	2.56	3.79
Seed yield / plant	6.13	6.39	6.91	6.48	6.13	6.91
Biological yield / plant (g)	34.94	37.89	36.17	36.33	34.94	37.89
Harvest index (%)	18.45	12.28	20.12	16.95	12.28	20.12
Oil content (%)	36.67	37.36	40.00	38.01	36.67	40.00

main shoot (33.33), siliqua length (4.03 cm), seeds persiliqua (11.37) and biological yield per plant (40.67 g). Srivastav and Singh (2000) reported that cluster III had the highest number of primary branches per plant, number of secondary branches per plant, oil percentage and mean seed yield per plant. Kumari (2010) also observed that genotypes in cluster III had highest cluster means for siliquae per plant, siliquae on main shoot, seed yield per plant, biological yield per plant and harvest index. Therefore, the crosses involving genotypes of cluster I and P-12 as one of the parent are expected to give desirable transgressants.

In pooled over the environments, genotypes in cluster I had moderate values for all the characters studied. Cluster II revealed maximum cluster means for siliqua length (4.06 cm), seeds per siliqua (10.79), 1000-seed weight (3.79 g) and biological yield per plant (37.89 g) and the genotypes recorded minimum days to flower initiation (65.94 days), days to 50 per cent flowering (109.44 days), days to 75 per cent maturity (148.50 days) and plant height (108.01 cm). Likewise, cluster III was characterized by maximum number of primary branches per plant (5.72), number of secondary branches per plant (11.70), siliquae per plant (329.37), length of main shoot (52.33 cm), siliquae on main shoot (33.00), seed yield per plant (6.91 g), harvest index (20.12 %) and percent oil content (40.00 %). Kumari (2010) observed that genotypes in cluster III had maximum cluster means for length of main shoot, 1000-seed weight and seed yield per plant. The characters such as length of main shoot (52.33 cm) and per cent oil content (40.00 %) showed constant value in all the clusters both in Env.I, Env.II and pooled over the environments. Based upon the inter-cluster distances and cluster means, the crosses among the genotypes belonging to clusters II and VIII, I and II and II and III in Env.I, Env.II and pooled over the environments, respectively, may give transgressants for higher seed yield, dwarf plant type, earliness in flowering and maturity, high biological yield and harvest index. Earlier workers have also attempted interspecific hybridization between *Brassica napus* x *Brassica carinata* (Rao *et al.* 1993; Sheikh *et al.* 2010[b]), *Brassica carinata* x *Brassica rapa* (Chaudhary *et al.* 2000), *Brassica juncea* x *Brassica carinata* (Sheikh *et al.* 2010[a]; Anonymous 2010-11) and derived desirable transgressive segregants in the progeny by introgressing the desirable genes in Ethiopian mustard. Singh *et al.* (2010) also reported significant increase in shoot length, 1000-seed weight and significant decrease in maturity duration through interspecific hybridization in *Brassica carinata.*

Table 4.14   Contribution of individual characters to the divergence among 33 genotypes of *Brassica carinata* in Env.I, Env.II and environments and pooled over the environments

Characters	Env.I		Env.II		Poolaed over the environments	
	Times ranked Ist	Contribution (%)	Times ranked Ist	Contribution (%)	Times ranked Ist	Contribution (%)
Days to flower initiation	8	1.52	1	0.19*	9	1.70*
Days to 50% flowering	2	0.38	174	32.95**	67	12.69
Days to 75% maturity	64	12.12	39	7.39	95	17.99**
Plant height	99	18.75**	19	3.60	92	17.42
Number of primary branches / plant	26	4.92	25	4.73	11	2.08
Number of secondary branches/ plant	65	12.31	32	6.06	24	4.55
Siliquae / plant	17	3.22	54	10.23	38	7.20
Length of main shoot	57	10.80	8	1.52	31	5.87
Siliquae on main shoot	52	9.85	25	4.73	27	5.11
Siliqua length	2	0.38	10	1.89	15	2.84
Seeds/ siliqua	19	3.60	12	2.27	20	3.79
1000-seed weight	57	10.80	29	5.49	12	2.27
Seed yield / plant	40	7.58	84	15.91	25	4.73
Biological yield / plant	14	2.65	10	1.89	19	3.60
Harvest index	1	0.19*	1	0.19*	17	3.22
Oil content	5	0.95	5	0.95	26	4.92

**** Maximum contribution;   * Minimum contribution**

The contribution of individual characters to divergence has been worked out in terms of number of times it appeared first (Table 4.14). In Env.I, plant height contributed maximum (18.75 %) towards total genetic divergence followed by number of secondary branches per plant (12.31 %) and days to 75 per cent maturity (12.12 %). Similar results have also been reported earlier by Goswami and behl (2006). In Env.II, days to 50 per cent flowering contributed maximum (32.95 %) towards total genetic divergence followed by seed yield per plant (15.91 %) and siliquae per plant (10.23 %). Days to 75 per cent maturity contributed maximum (17.99 %) towards total genetic divergence followed by plant height (17.42 %) in pooled over the environments among 33 genotypes studied. Shalini (1998) reported that that number of siliquae per plant contributed maximum towards total genetic divergence followed by plant height and days to 50 per cent flowering. On the other hand, siliquae per plant had the maximum contribution towards total genetic divergence followed by days to maturity and plant height (Monalisa *et al.* 2005).

4.1.5 Studies on correlation and path coefficients under different environments

After understanding the nature of variation for seed yield and other traits, it would be desirable to know the nature and magnitude of associations among these traits in order to bring about improvement in a complex trait like yield. Grafius (1956) also opined that the improvement of a complex character such as seed yield may be accomplished better through component breeding. Thus, the correlation studies help in better understanding of the contribution of each trait towards the genetic make-up of the crop.

In the present study, in order to understand the nature and magnitude of correlations among seed yield and other traits along with their causal factors, estimates of correlation coefficients at phenotypic, genotypic and environmental levels and their direct and indirect effects through path coefficient analysis were computed under Env.I, Env.II and pooled over the environments and results obtained are discussed as under:

4.1.5.1 Estimates of correlation coefficients at phenotypic and genotypic levels

The effectiveness of any breeding or selection programme depends upon the nature and magnitude of associations between yield and other component characters. More directly and positively a character is associated with seed yield, the more will be the success of the selection programme. Therefore, besides getting information on the

nature and magnitude of variation, it is also imperative to have knowledge on the associations of seed yield with other traits and among themselves and their causation to identify characters for defining an ideal plant type as well as for increasing the efficiency of both direct and indirect selection through it by other traits. Estimates of phenotypic and genotypic coefficients of correlation and that of direct and indirect effects provide the base necessary for identification of traits for an ideal plant type and effective selection. Based on the estimates of genotypic and phenotypic correlations, the breeder can decide the method of breeding to be followed to exploit the useful correlation.

The results on correlations computed at phenotypic and genotypic levels for all possible paired combinations in Env.I, Env.II and pooled over environments are presented in Tables 4.15, 4.16 and 4.17, respectively.

4.1.5.1.1 Estimates of correlation coefficients at phenotypic and genotypic levels in Env.I

At phenotypic level, significant positive correlation of seed yield per plant was observed with plant height, number of secondary branches per plant, siliquae per plant, siliqua length, biological yield per plant and harvest index. On the other hand, seed yield per plant showed significant negative correlation with days to 75 per cent maturity which is a desirable correlation and therefore, should be exploited directly through simple phenotypic selection. Significant positive association of seed yield with biological yield per plant, harvest index and pods per plant was earlier observed by Mehrotra *et al.* (1976). Significant and positive association with secondary branches per plant and siliquae per plant was reported by Hari *et al.* (1985), Thakur and Zerger (1989), Reddy (1991), Major and Gyanendra (1997), Shalini *et al.* (2000) and Patel *et al.* (2001). Srivastava and Singh (2002) also reported significant and positive association with secondary branches per plant. Significant positive correlation of seed yield per plant was observed with number of secondary branches per plant, siliquae per plant and siliqua length by Beena and Charjan (2003) and Chaudhary *et al.* (2003). Sirohi *et al.* (2004) reported that seed yield had significant and positive association with biological yield, harvest index and number of siliquae per plant. Mahak *et al.* (2004) and Sudan *et al.* (2004) also observed that seed yield per plant showed significant and positive association with number of secondary branches per plant. Similarly, Shalini *et al.* (2000), Pant *et al.* (2002), Mahak *et al.* (2003), Verma and Mahto (2005) and Verma *et al.* (2008) also reported significant positive correlation of seed yield with plant height and number of

Table 4.15 Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different characters in Env.I

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	Siliquae/ plant	Length of main shoot	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Biological yield/ plant	Harvest index	Oil content
Seed yield /plant	P	-0.092	-0.089	-0.281*	0.329*	0.083	0.194*	0.440*	-0.128	-0.094	0.221*	-0.012	0.115	0.397*	0.681*	0.024
	G	-0.218	-0.154	-0.456	0.431	0.148	0.243	0.750	-0.226	-0.151	1.175	-0.069	0.228	0.687	0.718	-0.509
Days to flower initiation	P		0.795*	0.759*	0.029	0.236*	0.162	0.178	0.181	0.247*	-0.304*	-0.073	-0.776*	-0.280*	0.143	0.057
	G		0.997	0.897	0.061	0.246	0.211	0.289	0.343	0.325	-1.244	-0.184	-0.975	-0.384	0.126	-0.714
Days to 50% flowering	P			0.706*	0.073	0.307*	0.148	0.159	0.264*	0.118	-0.354*	-0.140	-0.712*	-0.174	0.053	0.044
	G			0.859	0.139	0.449	0.260	0.292	0.351	0.328	-1.486	-0.193	-1.034	-0.331	0.144	-0.270
Days to 75% maturity	P				0.026	0.216*	0.055	-0.087	0.051	0.176	-0.298*	-0.075	-0.669*	-0.287*	-0.053	0.087
	G				0.038	0.322	-0.007	-0.125	0.181	0.195	-1.181	-0.171	0.799	-0.485	-0.120	-0.470
Plant height	P					0.324*	-0.040	0.418*	-0.020	-0.226*	0.122	0.225*	0.007	0.370*	0.050	0.086
	G					0.405	-0.085	0.609	0.002	0.282	0.517	0.192	-0.027	0.576	0.029	-0.979
No. of primary branches/ plant	P						0.004	0.066	0.116	-0.086	-0.076	0.163	-0.147	-0.016	0.076	-0.027
	G						-0.068	0.051	0.217	-0.025	-0.434	0.038	-0.330	0.097	0.114	1.033
No. of secondary branches/ plant	P							0.368*	0.205*	0.234*	0.013	-0.276*	-0.206*	-0.008	0.216*	0.163
	G							0.425	0.477	0.388	-0.277	-0.721	-0.383	0.030	0.303	-0.882
Siliquae/ plant	P								0.027	-0.032	0.240*	-0.041	-0.161	0.209*	0.300*	0.142
	G								0.016	-0.097	0.197	-0.113	-0.258	0.499	0.563	0.799
Length of main shoot	P									0.155	-0.161	-0.132	-0.252*	-0.155	-0.009	-0.025
	G									0.436	-0.777	-0.116	-0.381	-0.279	-0.043	-0.012
Siliquae on main shoot	P										-0.164	-0.260*	-0.354*	-0.049	-0.094	-0.019
	G										-0.902	-0.335	-0.483	-0.070	-0.163	-0.037
Siliqua length	P											0.202*	0.310*	0.018	0.202*	0.123
	G											0.728	1.567	1.262	0.353	0.392
Seeds/ siliqua	P												0.185	-0.072	0.060	-0.042
	G												0.237	0.114	-0.243	0.985
1000- seed weight	P													0.182	-0.033	-0.036
	G													0.354	-0.073	0.515
Biological yield/ plant	P														-0.374*	-0.089
	G														-0.026	0.306
Harvest index	P															0.095
	G															-1.336

* Significance at P ≤ 0.05

secondary branches per plant. Sharad and Basudeo (2005) also observed significant positive correlation of seed yield with number of secondary branches per plant and length of siliqua. Tusar *et al.* (2006) observed that seed yield per plant had significant and positive association with plant height, number of siliquae per plant, 1000-seed weight and number of branches per plant. Yadav *et al.* (1996), Muhammad *et al.* (2007) and Rameeh (2011) showed significant positive correlation of seed yield with siliquae per plant only. Uddin *et al.* (1995), Niraj and Srivastava (2000), Singh and Singh (2004), Rai *et al.* (2005) and Acharya and Pati (2008) observed significant positive association of seed yield with plant height. Singh *et al.* (2012) observed significant positive association of seed yield with siliqua length. Among other traits, significantly positive correlations were observed for days to flower initiation with days to 50 per cent flowering, days to 75 per cent maturity, number of primary branches per plant and siliquae on main shoot while it showed significant negative association with siliqua length, 1000-seed weight and biological yield per plant. Days to 50 per cent flowering exhibited significantly positive correlation with days to 75 per cent maturity, number of primary branches per plant and length of main shoot and significant negative correlation with siliqua length and 1000-seed weight. Days to 75 per cent maturity also showed significant positive correlation with number of primary branches per plant while significant negative correlation with siliqua length, 1000-seed weight and biological yield per plant were observed. Significant positive correlation of plant height was recorded with number of primary branches per plant, siliquae per plant, seeds per siliqua and biological yield per plant whereas it exhibited significant negative correlation with siliquae on main shoot. Number of secondary branches per plant exhibited significantly positive correlation with siliquae per plant, length of main shoot, siliquae on main shoot and harvest index while significant negative associations were observed with seeds per siliqua and 1000-seed weight. Siliquae per plant were significantly and positively correlated with siliqua length, biological yield per plant and harvest index while length of main shoot exhibited significantly negative correlation with 1000-seed weight. Siliquae on main shoot exhibited significantly negative correlation with seeds per siliqua and 1000-seed weight while siliqua length was positively and significantly associated with seeds per siliqua, 1000-seed weight and harvest index. Biological yield per plant and harvest index were significantly and negatively correlated with each other.

In general, genotypic correlation coefficients were higher than their corresponding phenotypic ones indicating the inherent association among the various traits studied. Similar results have also been reported by earlier workers (Shah *et al.* 2002; Mahla *et al.* 2003; Sheikh *et al.* 2004; Verma *et al.* 2008; Sirohi *et al.* 2008).

However, Kardam and Singh (2005) reported that phenotypic correlation coefficients were higher in magnitude compared to genotypic correlation coefficients for most of the characters studied.

4.1.5.1.2 Estimates of correlation coefficients at phenotypic and genotypic levels in Env.II

At phenotypic level, seed yield per plant had significant positive association with harvest index. The significant positive association of seed yield per plant with harvest index has also been reported by Mehrotra *et al.* (1976), Hari *et al.* (1985), Sirohi *et al.* (2004) and Sirohi *et al.* (2008). Among other traits, significantly positive correlations were observed for days to flower initiation with days to 50 per cent flowering, days to 75 per cent maturity and number of primary branches per plant while it showed significant negative association with 1000-seed weight. Days to 50 per cent flowering exhibited significantly positive correlation with days to 75 per cent maturity while significant negative correlation with siliquae on main shoot and 1000-seed weight was observed. The character days to 75 per cent maturity exhibited significantly negative correlation with siliqua length and 1000-seed weight. Number of primary branches per plant exhibited significantly positive correlation with siliquae per plant. Number of secondary branches per plant also exhibited significantly positive correlation with siliquae per plant and 1000-seed weight while length of main shoot recorded significantly positive correlation with siliquae on main shoot. Siliqua length and 1000 seed weight were significantly and positively correlated with each other while harvest index exhibited significantly negative correlation with seeds per siliqua and biological yield per plant. 1000-seed weight was positively and significantly correlated with percent oil content.

At genotypic level, the estimates of correlation coefficients were generally similar to those observed at phenotypic level for most of the characters. However, the magnitude of correlation coefficients was higher than their corresponding phenotypic ones indicating the inherent association among the various characters studied. The results are in

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conformity with the earlier findings (Shah *et al.* 2002; Mahla *et al.* 2003; Sheikh *et al.* 2004; Verma *et al.* 2008; Sirohi *et al.* 2008).

4.1.5.1.3 Estimates of correlation coefficients at phenotypic and genotypic levels in pooled over the environments

At phenotypic level, significant positive correlation of seed yield per plant was observed with plant height, number of secondary branches per plant, siliquae per plant, biological yield per plant and harvest index. On the other hand, seed yield per plant showed significant negative correlation with days to 75 per cent maturity which is a desirable association to be exploited directly through phenotypic selection. Significant positive correlations for seed yield with various characters have also been reported earlier by different workers such as biological yield per plant, siliquae per plant and harvest index (Mehrotra *et al.* 1976), plant height and siliquae per plant (Joshi *et al.* 1992), plant height and number of secondary branches per plant (Ghosh and Gulati 2001; Pant *et al.* 2002), plant height and siliquae per plant (Patel *et al*. 2001; Kardam and Singh 2005; Verma and Mahto 2005), number of secondary branches per plant and siliqua per plant (Reddy 1991; Beena and Charjan 2003; Chaudhary *et al.* 2003) and biological yield per plant and harvest index (Sirohi *et al.* 2004 and Sirohi *et al.* 2008). Among other traits, significantly positive correlations were observed for days to flower initiation with days to 50 per cent flowering, days to 75 per cent maturity and number of primary branches per plant while it showed significant negative association with siliqua length and 1000-seed weight. Days to 50 per cent flowering exhibited significantly positive correlation with days to 75 per cent maturity and number of primary branches per plant and significant negative correlation with siliqua length and 1000-seed weight. Days to 75 per cent maturity recorded significant positive correlation with number of primary branches per plant and significant negative correlations with siliqua length, 1000-seed weight and biological yield per plant were observed. Significant positive associations of plant height were observed with number of primary branches per plant, siliquae per plant, seeds per siliqua and biological yield per plant whereas it showed significant negative correlation with siliquae on main shoot. Number of primary branches per plant exhibited significantly positive correlation with siliquae per plant. Number of secondary branches per plant also showed significant positive correlation with siliquae per plant and percent

Table 4.16 Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different characters in Env.II

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	No. of primary branches/plant	No. of secondary branches/plant	Siliquae/plant	Length of main shoot	Siliquae on main shoot	Siliqua length	Seeds/siliqua	1000-seed weight	Biological yield/plant	Harvest index	Oil content
Seed yield /plant	P	0.035	0.122	-0.029	0.019	-0.004	0.120	-0.069	-0.007	-0.023	-0.023	-0.139	-0.084	-0.074	0.668*	-0.158
	G	0.077	0.264	-0.007	0.356	0.293	0.002	-0.086	-1.304	-1.630	0.292	-0.555	-0.084	-0.074	0.668	-0.158
Days to flower initiation	P		0.658*	0.671*	0.043	0.229*	-0.106	-0.035	-0.015	-0.101	-0.040	0.028	-0.237*	0.052	0.034	-0.017
	G		0.946	0.992	0.209	0.396	-0.323	0.144	-0.290	-0.586	-0.396	0.342	-0.797	0.222	0.071	1.018
Days to 50% flowering	P			0.631*	0.122	0.129	-0.044	-0.024	-0.118	-0.207*	-0.105	-0.006	-0.348*	0.115	0.180	-0.192
	G			0.811	0.264	0.304	-0.205	-0.028	-0.346	-0.762	-0.357	-0.040	-0.855	-0.439	0.351	0.493
Days to 75% maturity	P				0.036	0.145	-0.142	0.035	0.001	-0.033	-0.213*	-0.094	-0.226*	0.032	-0.024	-0.193
	G				0.039	0.152	-0.346	0.003	-0.071	-0.569	-0.564	-0.207	-0.449	0.170	0.039	0.647
Plant height	P					0.152	0.034	0.145	0.055	0.090	0.029	0.101	-0.023	0.003	0.024	0.020
	G					0.117	-0.087	0.596	-0.200	-0.995	0.251	0.234	-0.459	1.061	0.045	0.000
No. of primary branches/plant	P						0.055	0.215*	0.058	0.037	0.055	-0.039	-0.012	0.086	-0.105	0.152
	G						0.336	0.5928	1.168	1.162	0.565	0.309	0.318	2.140	-0.145	-0.189
No. of secondary branches/plant	P							0.218*	0.031	0.015	-0.020	-0.066	0.202*	-0.013	0.092	0.147
	G							0.296	-0.351	0.234	0.049	0.132	0.002	1.493	-0.308	-0.068
Siliquae/plant	P								0.117	0.010	0.047	0.141	0.016	0.166	-0.167	-0.002
	G								0.765	0.668	0.186	0.321	0.058	1.754	-0.400	-0.662
Length of main shoot	P									0.752*	0.016	0.160	0.133	0.085	-0.421	0.153
	G									0.585	-0.076	1.550	0.229	0.827	-1.510	-3.452
Siliquae on main shoot	P										-0.091	0.125	0.059	0.165	-0.124	0.099
	G										-0.317	-0.775	0.213	1.464	-1.510	-3.452
Siliqua length	P											-0.079	0.204*	-0.083	0.114	0.152
	G											0.327	0.461	-1.580	0.560	-0.447
Seeds/ silique	P												-0.143	0.192	-0.209*	-0.043
	G												0.246	-1.407	-0.152	-1.409
1000- seed weight	P													-0.052	-0.006	0.242*
	G													0.108	-0.618	-0.677
Biological yield/ plant	P														-0.752*	-0.004
	G														-1.065	0.670
Harvest index	P															-0.096
	G															0.444

* Significance at P ≤ 0.05

Table 4.17 Estimates of correlation coefficients at phenotypic (P) and genotypic (G) levels among different characters in pooled over the environments

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	Siliquae/ plant	Length of main shoot	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000-seed weight	Biological yield/ plant	Harvest index	Oil content
Seed yield /plant	P	-0.028	0.028	-0.181*	0.242*	0.042	0.152*	0.140*	-0.079	-0.068	0.120	-0.074	0.053	0.190*	0.652*	-0.060
	G	-0.213	-0.203	-0.322	0.542	0.431	-0.187	0.521	0.427	0.565	0.120	0.214	-0.234	0.596	0.339	-0.107
Days to flower initiation	P		0.699*	0.699*	0.030	0.231*	-0.004	0.033	0.078	0.078	-0.162*	-0.011	-0.511*	-0.096	0.074	0.014
	G		0.973	0.970	0.038	1.369	0.111	0.236	0.316	0.569	-1.500	-0.251	-1.089	-0.365	0.289	-0.151
Days to 50% flowering	P			0.631*	0.075	0.191*	0.019	0.026	0.044	-0.051	-0.200*	-0.050	-0.475*	-0.135	0.139	-0.104
	G			0.937	0.182	1.175	0.047	0.160	0.134	0.270	-1.581	-0.302	-1.102	-0.334	0.312	-0.053
Days to 75% maturity	P				0.027	0.181*	-0.046	-0.015	0.030	0.095	-0.262*	-0.083	-0.520*	-0.144*	-0.036	-0.045
	G				0.099	1.313	-0.025	0.014	0.165	0.396	-1.247	-0.368	-0.962	0.389	0.062	0.439
Plant height	P					0.246*	-0.012	0.246*	-0.001	-0.150*	0.097	0.159*	0.001	0.246*	0.035	0.059
	G					-0.429	0.352	0.432	0.155	-0.104	-0.537	-0.086	-0.196	0.389	0.062	0.439
No. of primary branches/ plant	P						0.034	0.158*	0.877	-0.032	-0.012	0.046	-0.092	0.036	-0.031	0.070
	G						1.518	0.945	0.835	1.335	-0.619	-2.182	-1.405	-0.947	1.798	-0.008
No. of secondary branches/ plant	P							0.263*	0.112	0.123	-0.005	-0.146*	-0.032	-0.011	0.137	0.153*
	G							0.842	0.756	0.279	-0.386	-0.295	-0.026	0.516	-0.768	0.522
Siliquae/ plant	P								0.075	-0.010	0.119	0.082	-0.065	0.176*	-0.023	0.048
	G								0.725	0.249	-0.726	-0.238	-0.242	0.286	0.168	0.405
Length of main shoot	P									0.379*	-0.082	0.016	-0.126	-0.047	-0.026	0.060
	G									0.359	0.030	-0.070	-0.180	0.104	0.256	0.453
Siliquae on main shoot	P										-0.135	-0.074	-0.234*	0.039	-0.104	0.032
	G										-0.396	-0.857	-0.358	0.589	-0.182	-0.185
Silique length	P											0.053	0.268*	0.029	0.151*	0.136
	G											1.056	1.546	0.249	-0.175	0.384
Seeds/ silique	P												0.005	0.074	-0.109	-0.043
	G												0.362	-0.203	0.382	0.108
1000-seed weight	P													0.097	-0.020	0.066
	G													0.222	-0.583	0.432
Biological yield/ plant	P														-0.581*	-0.045
	G														-0.573	-0.419
Harvest index	P															-0.018
	G															0.301

* Significance at P ≤ 0.05

oil content while significant negative association was observed with seeds per siliqua. Siliquae per plant were significantly and positively correlated with biological yield per plant while biological yield per plant exhibited significantly negative correlation with harvest index. Length of main shoot was positively and significantly correlated with siliquae on main shoot whereas siliquae on main shoot exhibited significantly negative correlation with 1000-seed weight. Siliqua length was positively and significantly correlated with 1000-seed weight and harvest index. At genotypic level, the estimates of correlation coefficients were generally higher to those observed at the phenotypic level for most of the traits. This indicated that phenotypic estimates of correlation coefficients represent the genotypic correlation coefficients, therefore, yield improvement through the traits which were significantly and positively correlated, would be effective. Genotypic correlation provides measures of genetic association between traits and is more reliable than phenotypic correlation and these along with observed correlations help to identify the traits to be considered in breeding programmes. Similar results have also been reported by earlier workers (Shah *et al.* 2002; Mahla *et al.* 2003; Sheikh *et al.* 2004; Verma *et al.* 2008; Sirohi *et al.* 2008). On the other hand, Kardam and Singh (2005) reported the phenotypic correlation coefficients to be higher in magnitude compared to genotypic correlation coefficients for most of the characters studied.

4.1.6 Estimates of direct and indirect effects

In order to find out the direct and indirect contribution of different characters towards seed yield per plant, the path coefficient analysis was done separately for Env.I, Env.II as well as pooled over the environments and the results are presented in Tables 4.18, 4.19 and 4.20, respectively.

4.1.6.1 Estimates of direct and indirect effects at phenotypic (P) and genotypic (G) levels in Env.I

At phenotypic level, seed yield per plant showed significant positive correlations with six traits *viz.,* plant height, number of secondary branches per plant, siliquae per plant, siliqua length, biological yield par plant and harvest index while it showed significantly negative association with days to 75 per cent maturity.

Highest positive direct effects on seed yield per plant were recorded by harvest index followed by biological yield per plant. So, the seed yield can be improved through the direct selection for harvest index and biological yield per plant. The results are similar to earlier findings (Sirohi *et al.* 2004; Sirohi *et al.* 2008; Kumari and Kumari 2012). The high positive direct effect of harvest index on seed yield per plant was also reported by Hari *et al.* (1985), Khulbe and Pant (1999) and Nazaar *et al.* (2003). The direct effects of remaining traits on seed yield per plant were observed to be low.

The significant negative correlation of seed yield per plant with days to 75 per cent maturity was mainly due to its highest negative indirect effects *via* biological yield per plant followed by harvest index. Likewise, the significant positive correlation of plant height with seed yield per plant was due to its highest positive indirect effects *via* biological yield per plant followed by harvest index. The significant positive association of number of secondary branches per plant with seed yield per plant was only due to its high positive indirect effect *via* harvest index, though, counter balanced by its own direct effect to a lesser extent. The significant positive correlation of siliquae per plant with seed yield per plant was mainly due to its highest positive indirect effects *via* harvest index followed by biological yield per plant. Significant positive correlation of siliqua length with seed yield per plant was mainly contributed by its high positive and indirect effect *via* harvest index, though, its own direct effect also contributed to a smaller extent followed by indirect effects *via* days to flower initiation and biological yield per plant.

4.1.6.2 Estimates of direct and indirect effects at phenotypic (P) and genotypic (G) levels in Env.II

At phenotypic level, seed yield per plant showed significant positive correlation with harvest index. Estimates of direct and indirect effects indicated that the harvest index contributed through its own high positive direct effect only. The high positive direct effect was counter balanced by biological yield per plant to some extent. So, the seed yield can be increased through the direct selection for harvest index. Sirohi *et al.* (2004), Sirohi *et al.* (2008) and Kumari and Kumari (2012) also reported that harvest index had high and positive direct effect on seed yield per plant.

4.1.6.3 Estimates of direct and indirect effects at phenotypic (P) and genotypic

(G) Levels in pooled over the environments

At phenotypic level, seed yield per plant showed significant positive correlation with five traits *viz.,* plant height, number of secondary branches per plant, siliquae per plant, biological yield par plant and harvest index while it showed significantly negative association with days to 75 per cent maturity.

High positive direct effects on seed yield per plant were recorded by biological yield per plant followed by harvest index. So, the seed yield can be increased through the direct selection for biological yield per plant and harvest index. The results are in conformity with the earlier findings of Sirohi *et al.* (2004), Sirohi *et al.* (2008) and Kumari and Kumari (2012). The direct effects of remaining traits on seed yield per plant were observed to be less. The significant negative correlation of seed yield per plant with days to 75 per cent maturity was mainly due to its highest negative indirect effects *via* biological yield per plant followed by harvest index and days to flower initiation, counter balanced by number of primary branches per plant and 1000-seed weight to a lesser extent.

Significant positive correlation of plant height with seed yield per plant was mainly contributed by its high positive indirect effect *via* biological yield per plant followed by harvest index, though, its own direct effect counter balanced the indirect effects to a lesser extent. The significant positive correlation of number of secondary branches per plant with seed yield per plant was only due to its positive indirect effect *via* harvest index, though, counter balanced by its own direct effect to a lesser extent. The significant positive association of siliquae per plant with seed yield per plant was mainly due to its highest positive indirect effects *via* biological yield per plant, though, its own direct effect was counter balanced by harvest index to a lesser extent.

The estimates of direct and indirect effects at genotypic levels were generally higher in magnitude than their phenotypic ones for different characters on seed yield in Env.I, Env.II and pooled over the environments.

Therefore, the results from present study indicated that biological yield per plant and harvest index would be the best selection indices for increasing seed yield per plant in *Brassica carinata.* The residual effects *viz.,* 0.20 (Env.I), 0.32 (Env.II) and 0.28

(pooled over the environments) are low which indicated that some additional imperative traits should also be included as 80 % (Env.I), 68 % (Env.II) and 72 % (pooled over the environments) of the variability has been explained by the traits studied in present investigation. Associations and their direct and indirect effects, though, vary in nature

Table 4.18 Estimates of direct and indirect effects at phenotypic (P) and genotypic (G) levels of different characters on seed yield in Env.I

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Siliquae/ plant	Length of main shoot	Silique on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Biological yield/ plant	Harvest index	Oil content
Days to flower	P	**-0.045**	-0.036	-0.034	-0.001	-0.011	-0.007	-0.008	-0.008	-0.011	0.014	0.003	0.035	0.013	-0.006	-0.003
initiation	G	**-0.126**	-0.125	-0.113	-0.008	-0.031	-0.027	-0.036	-0.043	-0.041	0.156	0.023	0.123	0.048	-0.016	0.090
Days to 50%	P	0.025	**0.031**	0.022	0.002	0.010	0.005	0.005	0.008	0.004	-0.011	-0.004	-0.022	-0.005	0.002	0.001
flowering	G	1.532	**1.537**	1.320	0.214	0.691	0.400	0.449	0.540	0.504	-2.285	0.297	-1.589	0.508	0.221	-0.415
Days to 75%	P	-0.012	-0.011	**-0.016**	0.000	-0.003	-0.001	0.001	-0.001	-0.003	0.005	0.001	0.010	0.004	0.001	-0.001
maturity	G	-1.956	-1.873	**-2.181**	-0.083	-0.701	0.015	0.272	-0.394	-0.425	2.576	0.374	1.742	1.057	0.262	1.025
Plant height	P	0.000	0.001	0.000	**0.010**	0.003	0.000	0.004	0.000	-0.002	0.001	0.002	0.000	0.004	0.001	0.001
	G	0.011	0.026	0.007	**0.187**	0.076	-0.016	0.114	0.000	-0.053	0.097	0.036	-0.005	0.108	0.005	-0.183
Number of	P	0.008	0.011	0.007	0.011	**0.034**	0.000	0.002	0.004	-0.003	-0.003	0.006	-0.005	-0.001	0.003	-0.001
primary branches/ plant	G	-0.197	-0.360	-0.258	-0.324	**-0.801**	0.055	-0.041	-0.174	0.020	0.347	-0.030	0.261	-0.078	-0.091	-0.827
Number of	P	-0.003	-0.003	-0.001	0.001	0.000	**-0.021**	-0.008	-0.004	-0.005	0.000	0.006	0.004	0.000	-0.004	-0.003
secondary branches/ plant	G	-0.228	-0.280	0.007	0.092	0.074	**-1.078**	-0.458	-0.515	-0.418	0.622	0.777	0.412	0.033	-0.326	0.950
Siliquae/ plant	P	-0.001	-0.001	0.001	-0.003	0.000	-0.002	**-0.006**	0.000	0.000	-0.002	0.000	0.001	-0.001	-0.002	-0.001
	G	-0.627	-0.632	0.270	-1.318	-0.111	-0.920	**-2.166**	-0.036	0.209	-0.427	0.244	0.560	-1.081	-1.220	1.730
Length of main	P	-0.002	-0.003	-0.001	0.000	-0.001	-0.002	0.000	**-0.011**	-0.002	0.002	0.001	0.003	0.002	0.000	0.000
shoot	G	0.240	0.246	0.126	0.002	0.152	0.334	0.012	**0.699**	0.305	-0.544	-0.081	-0.267	-0.195	-0.030	-0.009
Siliquae on main	P	0.001	0.006	0.010	-0.012	-0.005	0.013	-0.002	0.008	**0.054**	-0.009	-0.014	-0.019	-0.003	-0.005	-0.001
shoot	G	-0.364	-0.367	-0.219	0.316	0.029	-0.434	0.108	-0.489	**-1.121**	1.011	0.376	0.542	0.079	0.182	0.041
Siliqua length	P	-0.005	-0.006	-0.005	0.002	-0.001	0.000	0.004	-0.003	-0.003	**0.018**	0.004	0.006	0.000	0.004	0.002
	G	0.018	0.022	0.017	-0.008	0.006	0.008	-0.003	0.012	0.013	**-0.015**	-0.011	-0.023	-0.018	-0.005	0.006
Seeds/ siliqua	P	0.002	0.003	0.002	-0.005	-0.004	0.006	0.001	0.003	0.006	-0.004	**-0.022**	-0.004	0.002	-0.001	0.001
	G	0.146	0.154	0.136	-0.152	-0.030	0.573	0.089	0.092	0.266	-0.579	**-0.794**	-0.188	-0.090	0.193	-0.782
1000-seed weight	P	-0.002	-0.002	-0.001	0.000	0.000	0.000	0.000	-0.001	-0.001	0.001	0.000	**0.002**	0.000	0.000	0.000
	G	1.879	1.993	1.540	0.052	0.636	0.738	0.498	0.735	0.932	-3.020	-0.456	**-1.928**	-0.683	0.140	-0.992
Biological yield/	P	-0.208	-0.130	-0.214	0.275	-0.012	-0.006	0.155	-0.115	-0.036	0.013	-0.053	0.136	**0.744**	-0.278	-0.067
plant	G	-0.832	-0.717	-1.051	1.248	0.210	0.066	1.081	-0.604	-0.152	2.735	0.247	0.768	**2.168**	-0.056	0.662
Harvest index	P	0.0.1381	0.051	-0.051	0.048	0.074	0.209	0.291	-0.008	-0.092	0.196	0.058	-0.032	-0.362	**0.969**	0.092
	G	0.153	0.175	-0.146	0.035	0.138	0.368	0.684	-0.052	-0.198	0.429	-0.295	0.088	-0.032	**1.215**	-1.623
Oil content	P	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.003**
	G	0.131	0.049	0.086	0.179	-0.189	0.161	0.146	0.002	0.007	0.072	-0.180	-0.094	-0.056	0.245	**-0.183**
Correlation with	P	-0.092	-0.089	-0.281*	0.329*	0.083	0.194*	0.440*	-0.128	-0.094	0.221*	-0.012	-0.115	0.397*	0.681*	0.024
Seed yield /plant	G	-0.218	-0.154	-0.456	0.431	0.148	0.243	0.750	-0.226	-0.151	1.175	-0.069	0.228	0.687	0.718	-0.509

Residual effects (P) = 0.20; G) =0.28   *Significant at 5 per cent level   **The bold values indicates direct effects**

Table 4.19 Estimates of direct and indirect effects at phenotypic (P) and genotypic (G) levels of different characters on seed yield in Env.II

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	Siliquae/ plant	Length of main shoot	Silique on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Biological yield/ plant	Harvest index (%)	Oil content (%)
Days to flower initiation	P	**-0.094**	-0.062	-0.063	-0.004	-0.022	0.010	0.003	0.001	0.010	0.004	-0.003	0.022	-0.005	-0.003	0.002
	G	**-0.296**	-0.280	-0.294	-0.062	-0.117	0.095	-0.043	0.086	0.174	0.117	-0.101	0.236	-0.066	-0.021	-0.301
Days to 50% flowering	P	0.018	**0.027**	0.017	0.003	0.004	-0.001	-0.001	-0.003	-0.006	-0.003	0.000	-0.010	-0.003	0.005	-0.005
	G	-0.655	**-0.692**	-0.562	-0.183	-0.211	0.142	0.019	0.239	0.528	0.247	0.028	0.592	0.304	-0.243	-0.342
Days to 75% maturity	P	-0.019	-0.018	**-0.029**	-0.001	-0.004	0.004	-0.001	0.000	0.001	0.006	0.003	0.007	-0.001	0.001	0.006
	G	0.836	0.683	**0.842**	0.033	0.128	-0.291	0.002	-0.060	-0.479	-0.475	-0.174	-0.378	0.143	0.032	0.545
Plant height	P	-0.001	-0.003	-0.001	**-0.023**	-0.003	-0.001	-0.003	-0.001	-0.002	-0.001	-0.002	0.001	0.000	-0.001	0.000
	G	0.093	0.117	0.017	**0.443**	0.052	-0.038	0.264	-0.089	-0.441	0.111	0.103	-0.203	0.470	0.020	0.000
Number of primary branches/ plant	P	0.022	0.012	0.014	0.014	**0.094**	0.005	0.020	0.005	0.003	0.005	-0.004	-0.001	0.008	-0.010	0.014
	G	0.050	0.039	0.019	0.015	**0.127**	0.043	0.075	0.148	0.148	0.072	0.039	0.040	0.272	-0.019	-0.024
Number of secondary branches/ plant	P	0.002	0.001	0.003	-0.001	-0.001	**-0.017**	-0.004	-0.001	0.000	0.000	0.001	-0.004	0.000	-0.002	-0.003
	G	-0.085	-0.054	-0.091	-0.023	0.089	**0.264**	0.078	-0.093	0.062	0.013	0.035	0.001	0.394	-0.081	-0.018
Siliquae/ plant	P	0.000	0.000	0.000	0.000	0.001	0.001	**0.003**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	G	0.093	0.018	-0.002	-0.386	-0.384	-0.191	**-0.647**	-0.495	-0.432	-0.121	-0.208	-0.037	-1.135	0.259	0.429
Length of main shoot	P	0.000	0.002	0.000	-0.001	-0.001	-0.001	-0.002	**-0.019**	-0.014	0.000	-0.003	-0.003	-0.002	0.001	-0.003
	G	-0.050	-0.060	-0.012	-0.035	0.203	-0.061	0.133	**0.174**	0.102	-0.013	0.270	0.040	0.144	-0.203	-0.484
Siliquae on main shoot	P	0.001	0.002	0.000	-0.001	0.000	0.000	0.000	0.005	**-0.007**	0.001	-0.001	0.000	-0.001	0.001	-0.001
	G	-0.007	-0.009	-0.007	-0.012	0.014	0.003	0.008	0.007	**0.012**	-0.004	-0.010	0.003	0.018	-0.018	-0.042
Siliqua length	P	0.005	0.012	0.024	-0.003	-0.006	0.002	-0.005	-0.002	0.010	**-0.114**	0.009	-0.023	0.010	-0.013	-0.017
	G	-0.138	-0.124	-0.196	0.087	0.197	0.017	0.065	-0.027	-0.111	**0.348**	0.114	0.161	-0.551	0.195	-0.156
Seeds/ siliqua	P	-0.001	0.000	0.003	-0.004	0.001	0.002	-0.005	-0.006	-0.004	0.003	**-0.035**	0.005	-0.007	0.007	0.002
	G	-0.028	0.003	0.017	-0.019	-0.025	-0.011	-0.026	-0.127	0.064	-0.027	**-0.082**	-0.020	0.116	0.013	0.116
1000-seed weight	P	0.004	0.005	0.003	0.000	0.000	-0.003	0.000	-0.002	-0.001	-0.003	0.002	**-0.015**	0.001	0.000	-0.004
	G	0.345	0.371	0.195	0.199	-0.138	-0.001	-0.025	-0.099	-0.093	-0.200	-0.107	**-0.434**	-0.047	0.268	0.293
Biological yield/ plant	P	0.052	-0.116	0.032	0.003	0.087	-0.013	0.167	0.084	0.166	-0.084	0.194	-0.053	**0.807**	-0.195	-0.004
	G	0.053	-0.104	0.040	0.251	0.506	0.353	0.415	0.196	0.346	-0.374	-0.333	0.026	**0.237**	-0.252	0.159
Harvest index	P	0.048	0.259	-0.034	0.035	-0.152	0.132	-0.240	-0.061	-0.018	0.164	-0.300	-0.009	-0.807	**0.876**	-0.138
	G	0.075	0.368	0.040	0.048	-0.152	-0.322	-0.420	-1.224	-1.582	0.587	-0.159	-0.647	-1.116	**1.048**	0.465
Oil content	P	0.000	0.001	0.001	0.000	-0.001	-0.001	0.000	-0.001	-0.001	-0.001	0.000	-0.001	0.000	0.001	**-0.005**
	G	-0.022	-0.011	-0.014	0.000	0.004	0.001	0.014	0.059	0.074	0.010	0.030	0.014	-0.014	-0.009	**-0.021**
Correlation with Seed yield /plant	P	0.035	0.122	-0.029	0.019	-0.004	0.120	-0.062	-0.007	-0.023	-0.023	-0.139	-0.084	-0.074	0.668*	-0.158
	G	0.077	0.007	0.086	1.304	1.630	0.555	0.608	0.832	0.077	0.007	0.086	1.304	1.630	0.988	0.988

Residual effects (P) = 0.32; G) =(1-1.0294)   *Significant at 5 per cent level   **The bold values indicates direct effects**

Table 4.20 Estimates of direct and indirect effects at phenotypic (P) and genotypic (G) levels of different characters on seed yield in pooled over the environments

Characters		Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Siliquae/ plant	Length of main shoot	Silique on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Biological yield/ plant	Harvest index	Oil content
Days to flower initiation	P	**-0.058**	-0.040	-0.040	-0.002	-0.013	0.000	-0.002	-0.005	-0.005	0.009	0.001	0.030	0.006	-0.004	-0.001
	G	**1.972**	1.919	1.913	0.074	2.700	0.219	0.465	0.624	1.121	-2.958	-0.495	-2.147	-0.720	0.570	-0.297
Days to 50% flowering	P	0.001	**0.002**	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000
	G	0.054	**0.055**	0.052	0.010	0.065	0.003	0.009	0.007	0.015	-0.088	-0.017	-0.061	-0.019	0.017	-0.003
Days to 75% maturity	P	-0.007	-0.006	**-0.010**	0.000	-0.002	0.001	0.000	0.000	-0.001	0.003	0.001	0.005	0.001	0.000	0.000
	G	-2.535	-2.450	**-2.614**	-0.258	-3.432	0.066	-0.037	-0.430	-1.035	3.258	0.962	2.515	0.869	-0.439	-0.077
Plant height	P	-0.007	-0.002	-0.001	**-0.021**	-0.005	0.000	-0.005	0.000	0.003	-0.002	-0.003	0.000	-0.005	-0.001	-0.001
	G	0.038	0.184	0.100	**1.007**	-0.432	0.354	0.435	0.156	-0.105	-0.541	-0.087	-0.198	0.392	0.062	0.443
Number of primary branches/ plant	P	0.015	0.012	0.012	0.016	**0.065**	0.002	0.010	0.006	-0.002	-0.001	0.003	-0.006	0.002	-0.002	0.015
	G	-0.138	-0.118	-0.132	0.043	**-0.101**	-0.153	-0.095	-0.084	-0.134	0.062	0.219	0.141	0.095	-0.181	0.001
Number of secondary branches/ plant	P	0.000	0.000	0.001	0.000	0.000	**-0.011**	-0.003	-0.001	-0.001	0.000	0.002	0.000	0.000	-0.002	0.000
	G	-0.012	-0.005	0.003	-0.038	-0.162	**-0.107**	-0.090	-0.081	-0.030	0.041	0.032	0.003	-0.055	0.082	-0.056
Siliquae/ plant	P	0.001	0.001	0.000	0.005	0.003	0.005	**0.020**	0.002	0.000	0.002	0.002	-0.001	0.004	-0.001	0.001
	G	-0.211	-0.144	-0.013	-0.387	-0.846	-0.754	**-0.895**	-0.650	-0.223	0.650	0.213	0.217	-0.256	-0.151	-0.362
Length of main shoot	P	-0.002	-0.001	-0.001	0.000	-0.002	-0.003	-0.002	**-0.026**	-0.010	0.002	0.000	0.003	0.001	0.001	-0.002
	G	0.169	0.072	0.088	0.083	0.446	0.404	0.387	**0.534**	0.192	0.016	-0.037	-0.096	0.056	0.137	0.242
Siliquae on main shoot	P	0.002	-0.001	0.003	-0.004	-0.001	0.003	0.000	0.010	**0.025**	-0.003	-0.002	-0.006	0.001	-0.003	0.001
	G	0.370	0.176	0.258	-0.068	0.868	0.182	0.162	0.233	**0.651**	-0.258	-0.557	-0.233	0.383	-0.118	-0.120
Siliqua length	P	0.006	0.007	0.009	-0.003	0.000	0.000	-0.004	0.003	0.005	**-0.036**	-0.002	-0.010	0.001	-0.005	-0.005
	G	0.140	0.147	0.116	0.050	0.058	0.036	0.068	-0.003	0.037	**-0.093**	-0.098	-0.144	-0.023	0.016	-0.036
Seeds/ siliqua	P	0.000	0.000	0.001	-0.001	0.000	0.001	-0.001	0.000	0.001	-0.001	**-0.009**	0.000	-0.001	0.001	0.000
	G	0.061	0.073	0.089	0.021	0.526	0.071	0.057	0.017	0.206	-0.254	**-0.241**	-0.087	0.049	-0.092	-0.026
1000-seed weight	P	0.011	0.010	0.011	0.000	0.002	0.001	0.001	0.003	0.005	-0.006	-0.001	**-0.022**	-0.002	0.000	-0.001
	G	-0.284	-0.288	-0.251	-0.051	-0.367	-0.007	-0.063	-0.047	-0.094	0.404	0.095	**0.261**	0.058	-0.152	0.113
Biological yield/ plant	P	-0.083	-0.116	-0.124	0.211	0.031	-0.009	0.151	-0.040	0.033	-0.025	0.063	0.083	**0.859**	-0.188	-0.039
	G	-0.045	-0.041	-0.041	0.048	-0.118	0.064	0.036	0.013	0.073	0.031	-0.025	0.028	**0.124**	-0.071	-0.052
Harvest index	P	0.086	0.162	-0.042	0.041	-0.036	0.160	-0.026	-0.030	-0.121	0.176	-0.127	-0.023	-0.677	**0.855**	-0.021
	G	0.197	0.213	0.115	0.042	1.226	-0.524	0.115	0.175	-0.124	-0.119	0.260	-0.397	-0.391	**0.682**	0.205
Oil content	P	0.000	-0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	**0.005**
	G	0.012	0.004	-0.002	-0.036	0.001	-0.042	-0.033	-0.037	0.015	-0.031	-0.009	-0.035	0.034	-0.024	**-0.081**
Correlation with Seed yield /plant	P	-0.028	0.028	-0.181*	0.242*	0.042	0.152*	0.140*	-0.079	-0.068	0.120	-0.074	0.053	0.190*	0.652*	-0.060
	G	0.213	0.203	0.322	0.542	0.187	0.542	0.521	0.521	0.521	0.521	0.214	0.234	0.214	0.339	0.107

Residual effects (P) = 0.28; (G)= (1-1.2498)   *Significant at 5 per cent level   The bold values indicates direct effect

and magnitude in both the environments as well as pooled over the environments, however, the traits which showed significant positive correlations and direct and indirect effects are almost similar in Env.I and pooled over the environments.

4.1.7 Disease reaction for *Alternaria* blight

The screening of 33 genotypes including four checks *viz.,* Nav Gold, Jayanti, Pusa Jaikisan and RCC-4 against *Alternaria* blight was carried out during *rabi,* 2011-12 at SAREC, Kangra under natural epiphytotic field conditions as Kangra is considered as one of the hot spots for the development of *Alternaria* blight.

4.1.7.1 Reaction to *Alternaria* blight on leaves

Data on field reaction of 33 genotypes for *Alternaria* is presented in Table 4.21. The reaction to *Alternaria* revealed that only one genotype *viz.,* Pusa Jaikisan was found to be moderately resistant as the per cent disease severity ranged between 11-25 per cent. Twenty six genotypes *viz.,* P-12, P-23, P-24, P-26, P-31, P-33, P-34, P-39, P-43, P-45, P-62, P-63, P-74, P-75, P-77, P-89, P-92, P-96, P-101, P-103, P-117, P-133, P-137, P-138, Nav Gold and Jayanti were found to be moderately susceptible as the per cent disease severity ranged between 26-50 per cent. Six genotypes *viz.,* P-17, P-51, P-56, P-64, P-122 and RCC-4 were found to be susceptible as the per cent disease severity ranged between 51-75 per cent (Table 4.22, Plate III).

4.1.7.1 Reaction to *Alternaria* blight on pods

Of the 33 genotypes screened for disease reaction, twenty eight genotypes *viz.,* P-12, P-17, P-23, P-24, P-31, RCC-4, P-33, P-39, P-43, P-45, P-51, P-56, P-63, P-64, P-74, P-75, P-77, P-92, P-96, P-101, P-103, P-117, P-122, P-133, P-137, P-138, Nav Gold and Jayanti were found to be moderately resistant as the per cent disease severity ranged between 11-25 per cent. Three genotypes *viz.,* P-89, P-62 and Pusa Jaikisan were found to be moderately susceptible as the per cent disease severity ranged between 26-50 per cent (Table 4.23) and only two genotypes *viz.,* P-26 and P-34 appeard to be resistant as the percent disease severity ranged between 0-10 per cent.
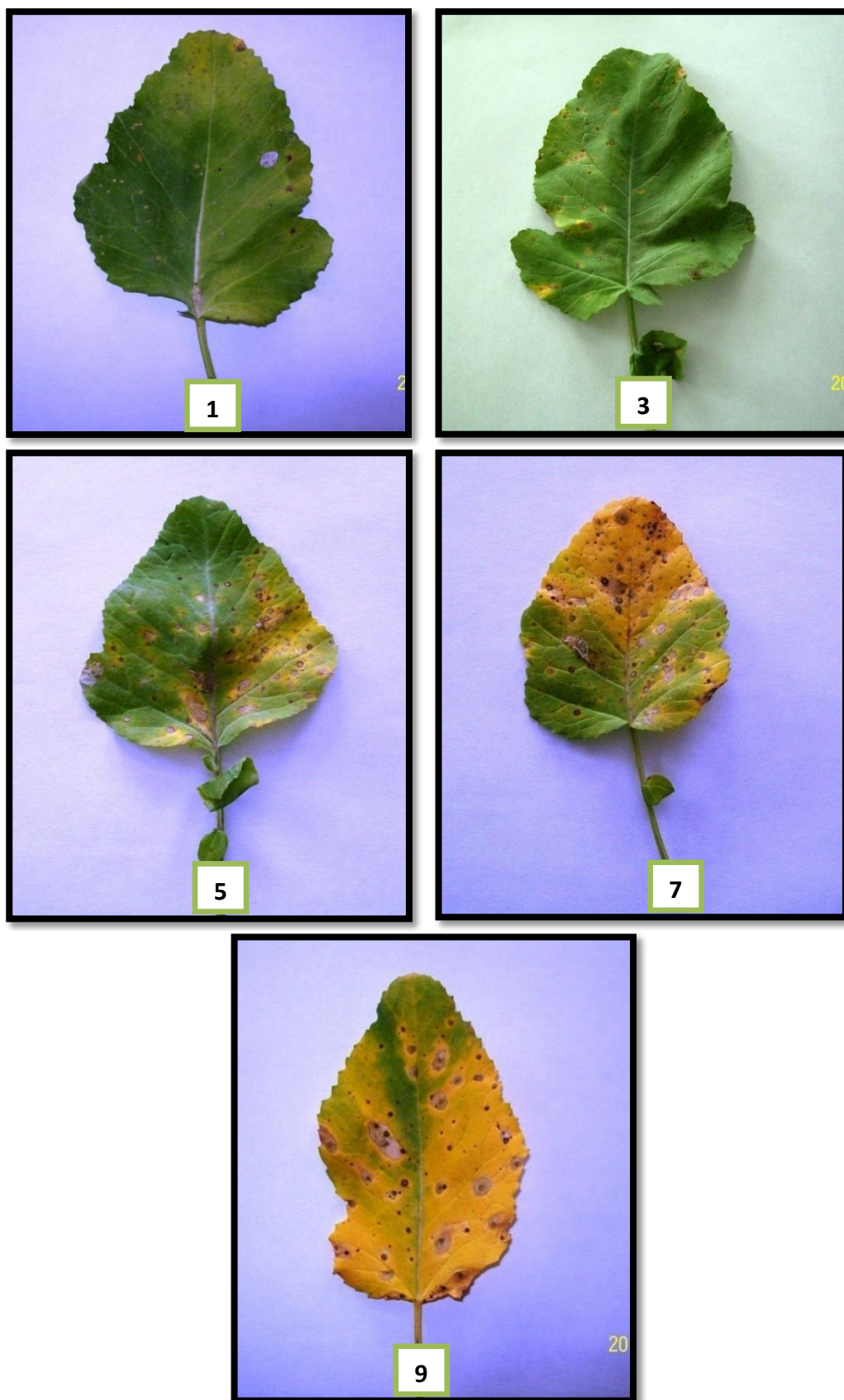
Plate III   *Alteranaria* **blight reaction on a scale of 0-9**

Available online at http://www.ijart.info/

Table 4.21 Per cent disease intensity and reaction of 33 genotypes of *Brassica carinata* against *Alternaria* blight under artificial field conditions

Sr. No.	Genotypes	AB on leaves		AB on pods	
		% disease intensity	Reaction	% disease intensity	Reaction
1.	P-12	42.22	MS	13.33	MR
2.	P-17	57.78	S	13.33	MR
3.	P-23	42.22	MS	13.33	MR
4.	P-24	44.44	MS	14.44	MR
5.	P-26	40.00	MS	10.00	R
6.	P-31	40.00	MS	12.22	MR
7.	P-33	40.00	MS	24.44	MR
8.	P-34	42.22	MS	10.00	R
9.	P-39	40.00	MS	13.33	MR
10.	P-43	42.22	MS	13.33	MR
11.	P-45	42.22	MS	17.78	MR
12.	P-51	57.78	S	15.56	MR
13.	P-56	53.33	S	15.56	MR
14.	P-62	37.78	MS	26.67	MS
15.	P-63	35.56	MS	24.44	MR
16.	P-64	53.33	S	17.78	MR
17.	P-74	35.56	MS	17.78	MR
18.	P-75	46.67	MS	15.56	MR
19.	P-77	42.22	MS	14.44	MR
20.	P-89	33.33	MS	31.11	MS
21.	P-92	40.74	MS	24.44	MR
22.	P-96	40.00	MS	15.56	MR
23.	P-101	40.74	MS	13.33	MR
24.	P-103	37.04	MS	17.46	MR
25.	P-117	45.68	MS	20.00	MR
26.	P-122	59.26	S	14.29	MR
27.	P-133	40.00	MS	15.56	MR
28.	P-137	40.00	MS	20.00	MR
29.	P-138	42.22	MS	17.78	MR
30.	Nav Gold	28.89	MS	24.44	MR
31.	Jayanti	42.22	MS	12.22	MR
32.	Pusa Jaikisan	24.44	MR	33.33	MS
33.	RCC-4	55.56	S	21.11	MR

MR: Moderately resistant; MS: Moderately susceptible; S: Susceptible; R: Resistant

AB: *Alternaria* blight

Table 4.22 Reaction of various genotypes of *Brassica carinata* to *Alternaria* blight on leaves

Sr. No.	% Leaf area covered	Reaction	No. of genotypes	Genotypes
1.	11-25%	Moderately resistant	1	Pusa Jaikisan
2.	26-50%	Moderately susceptible	26	P-12, P-23, P-24, P-26, P-31, P-33, P-34, P-39, P-43, P-45, P-62, P-63, P-74, P-75, P-77, P-89, P-92, P-96, P-101, P-103, P-117, P-133, P-137, P-138, Nav Gold and Jayanti
3.	51-75%	Susceptible	6	P-17, P-51, P-56, P-64, P-122 and RCC-4

Table 4.23 Reaction of various genotypes of *Brassica carinata* to *Alternaria* blight on pods

Sr. No.	% Pod area covered	Reaction	No. of genotypes	Genotypes
1.	0-10%	Resistant	2	P-26 and P-34
2.	11-25%	Moderately resistant	28	P-12, P-17, P-23, P-24, P-31, RCC-4, P-33, P-39, P-43, P-45, P-51, P-56, P-63, P-64, P-74, P-75, P-77, P-92, P-96, P-101, P-103, P-117, P-122, P-133, P-137, P-138, Nav Gold and Jayanti
3.	26-50%	Moderately susceptible	3	P-89, P-62 and Pusa Jaikisan

Based upon the present study, the potential genotypes for seed yield per plant and other characters over Env.I, Env.II and pooled over the environments are presented bolow:

Potential genotypes for seed yield and other characters in Env.I, Env.II and pooled over the environments

	Genotypes	Characters
Env.I	P-26 (MS)	Earliness
	P-31 (MS)	Earliness, siliquae per plant and biological yield per plant
	P-138 (MS)	Number of primary branches per plant
Env.II	P-51 (S)	Days to 75 per cent maturity, primary branches per plant, siliquae on main shoot and seeds per siliqua
	P-103 (MS)	Day to 50 per cent flowering, number of primary branches per plant, number of secondary branches per plant, siliquae on main shoot, biological yield per plant and harvest index.
Pooled over the enninronments	P-33 (MS)	Days to flower initiation, number of secondary branches per plant, siliquae on main shoot and seeds per siliqua
	P-34 (MS)	Days to 75 per cent maturity
	P-63 (MS)	Plant height, siliquae per plant, seeds per siliqua and harvest index
	P-138 (MS)	Days to 50 per cent flowering and number of primary branches per plant

MS: Moderately Susceptible

Based upon Env.I, Env.II and pooled over the environments, the genotype P-12 had the excellent potential for secondary branches per plant and siliquae per plant, P-34 for seed yield per plant and P-75 for per cent oil content. Therefore, these three genotypes can be utilized for the introgression of desirable genes in *Brassica carinata* improvement programme.

4.2   Anther culture studies

Induction of haploid plants from anther culture of *Datura innoxia* was first reported by two Indian scientists, Guha and Maheshwari (1964) and became a major breakthrough in haploid breeding of higher plants. As a result of haploid induction followed by chromosome doubling, homozygosity can be achieved in the quickest possible way making genetic and breeding research much easier. This technique has been extended to many other crop plants of commercial importance. Application of anther culture technique in *Brassicas* was first reported by Kameya and Hinata (1970) who reported induction of callus and haploid plants from cultured anthers of *Brassica oleracea*. Further, with improvement in protocols, induction of haploids through anther culture has also been reported in *Brassica carinata* (Chuong and Beversdorf 1985; Arora and Bhojwani 1988; Zhang *et al,* 1996; Barro and Martin 1999).

Improvement of various agronomically important qualitative and quantitative characters, nutritional profile, oil quality and disease resistance are some of the main breeding objectives of *Brassica carinata* crop improvement programme. By conventional breeding method, improvement of qualitative and quantitative characters requires long period of time (6-7 years) to obtain homozygous lines. However, induced androgenesis in F_1 enables the breeder to obtain completely homozygous genotypes from heterozygous parents in a single generation and allow fixing the recombinant gametes directly as fertile homozygous lines.

In order to study the androgenesis-mediated responsiveness, the anthers of four elite genotypes *viz.,* Jayanti, P-18, P-51 and $P_{(2)2}$ and their hybrids *viz.,* Jayanti x P-18, Jayanti x P-51 and Jayanti x $P_{(2)2}$ were cultured on B_5 and MS media. Each of these medium was supplemented with two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose and each of these sucrose concentrated media was also supplemented with three combinations of hormones *viz.*, HM_1, HM_2 and HM_3. All the media were supplemented with 0.8 per cent agar to know their effect on androgenic callus induction frequency, days to callus appearance and calli index based upon the earlier studies (Kumari 2010).

4.2.1 Effects of different parameters on callus induction frequency

Analysis of variance for callus induction frequency in anthers of seven genotypes cultured *in vitro* on two media supplemented with two different sucrose

concentrations and each of these sucrose concentrated media supplemented with three combinations of hormones, is presented in Table 4.24 and Plate IV. Mean sum of squares due to all factors were significant revealing thereby significant effects of genotypes, media, hormones, sucrose and their interactions on callus induction frequency. The results are in conformity with the finding of Singh (2006), Devi (2009) and Kumari (2010) in respect of media, hormones and hormones x media whereas contrary to the finding of Singh (2006) and Kumari (2010) for genotypes x media interactions.

4.2.1.1 Effects of media and genotypes on callus induction frequency

The data pertaining to effects of media and genotypes on callus induction frequency is presented in Table 4.25. Out of two media tested, B_5 gave highest callus induction frequency (77.50 %) and was found significantly superior than MS medium. Out of the seven genotypes used for anther culture, P-51 gave highest mean callusing (75.80 %) and was statistically at par with Jayanti x P-18. On the other hand, Jayanti and Jayanti x $P_{(2)2}$ showed least callus induction frequency (71.20 % each). In genotypes x media interaction, the highest callus induction frequency was recorded in P-51 (87.30 %) on B_5 medium followed by P-18 (81.40 %) and Jayanti x $P_{(2)2}$ on B_5 medium (77.40 %) whereas P-51 exhibited lowest callus induction frequency on MS medium (64.30 %). Overall B_5 medium was best for callus induction frequency. Zhang *et al.* (1996) reported successful embryogenesis and callusing in *Brassica carinata* and *Brassica napus* on modified B_5 medium. Devi (2009) and Kumari (2010) also reported successful embryogenesis and callusing in *Brassica carinata and Brassica juncea* on modified B_5 medium, respectively. Apart from B_5 medium, KA and N_6 media have also been successfully used to induce *in vitro* callusing in anther culture of *Brassica carinata* by various workers (Sharma and Bhojwani 1985; Arora and Bhojwani 1988).

4.2.1.2 Effects of hormones and genotypes on callus induction frequency

The perusal of data presented in Table 4.26 indicated that out of the three hormonal combinations tested, HM_2 gave the highest mean callusing (81.80 %) and was found to be significantly superior to HM_1 and HM_3. Hormonal combination HM_1 showed the least callus induction frequency (59.70 %). Out of the seven genotypes, P-

51 gave highest callus induction (75.80 %) followed by Jayanti x P-18 (75.60 %) and both were found to be statistically at par with each other. Jayanti and Jayanti x P$_{(2)2}$ exhibited lowest callus induction frequency (71.20 % each). The interaction

Table 4.24 ANOVA for Callus induction frequency (%) in different genotypes of *Brassica carinata* and their hybrids involving different media, hormones and sucrose concentration

Source of variation	df	Mean Squares	CD (5%)	CV (%)
Genotypes	6	146.91**	2.96	8.7
Hormones	2	3375.03**	1.94	
Genotypes x Hormones	12	826.23**	5.13	
Media	1	10768.06**	1.58	
Genotypes x Media	6	824.45**	4.18	
Hormones x Media	2	576.26**	2.74	
Genotypes x Hormones x Media	12	198.70**	7.25	
Sucrose	1	2483.36**	1.58	
Genotypes x Sucrose	6	156.31**	4.18	
Hormones x Sucrose	2	3901.22**	2.74	
Genotypes x Hormones x Sucrose	12	283.26**	7.25	
Media x Sucrose	1	2410.23**	2.24	
Genotypes x Media x Sucrose	6	913.80**	5.92	
Hormones x Media x Sucrose	2	17017.98**	3.87	
Genotypes x Hormones x Media x Sucrose	12	339.16**	10.25	
Error	168	40.01		

** Significant at P ≤ 0.01

Table 4.25   Effects of media and genotypes on callus induction frequency (%)

Media	Genotypes								
	Jayanti	P$_{(2)2}$	P-51	P-18	Jayanti x P$_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
MS	67.50 (55.24)	78.30 (62.24)	64.30 (53.31)	64.50 (53.43)	64.90 (53.67)	65.70 (57.15)	75.90 (60.60)	68.70 (55.98)	1.58 (Media)
B$_5$	74.90 (59.93)	69.30 (65.35)	87.30 (69.12)	81.40 (64.45)	77.40 (61.61)	77.00 (61.34)	75.30 (60.20)	77.50 (61.68)	
Mean	71.20 (57.54)	73.80 (59.21)	75.80 (60.53)	72.90 (58.63)	71.20 (57.54)	71.40 (57.67)	75.60 (60.40)		

CD (P≤0.05) = 2.96 (Genotypes)
CD interaction= 4.18 (Genotypes x Media)
Values in parentheses are arc sine transformed values

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Plate IV Effects of different media, hormones and sucrose concentration on callus induction frequency
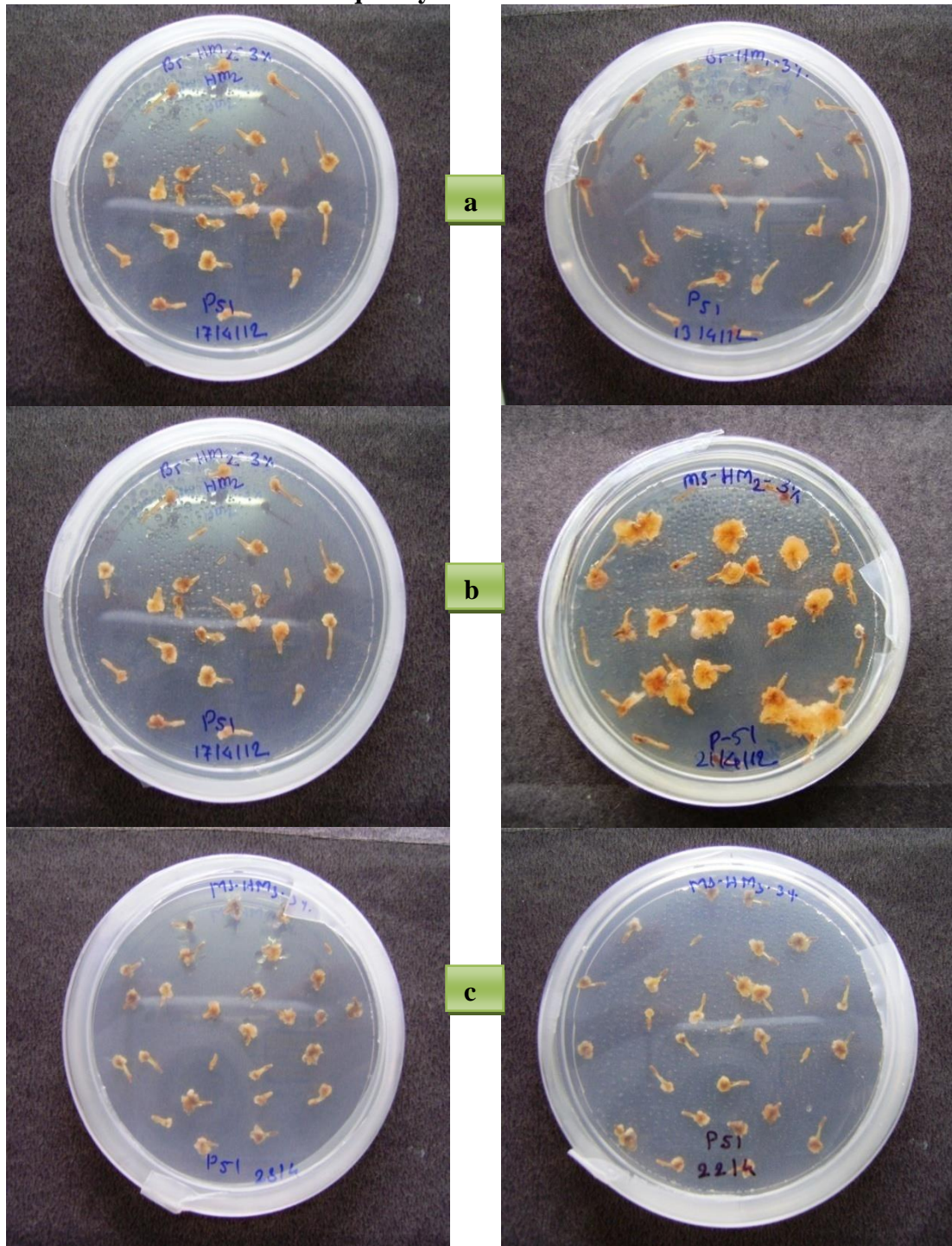
a) B₅ + P-51

b) P-51 + HM₂

c) 3 % sucrose + P-51
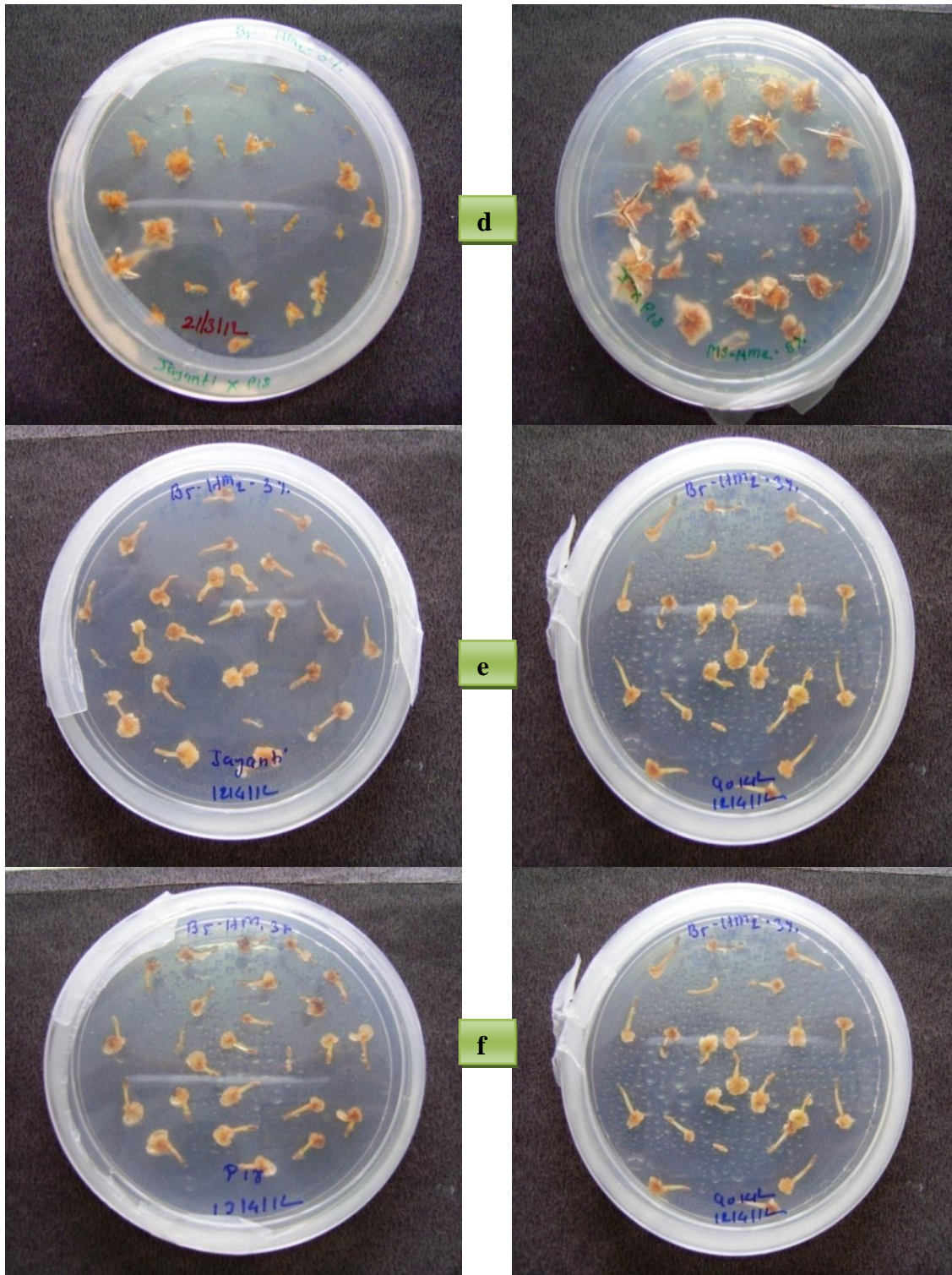
d) 3 % sucrose + HM₂

e) HM₂ + B₅

f) B₅ + 3 % sucrose

genotypes x hormones had significant effect on the callus induction frequency. Considering interaction between these two factors, the highest callus induction frequency was observed for genotype P-51 with HM_2 (86.20 %) and was statistically at par with Jayanti on HM_2 (84.30 %) and Jayanti x P-51 on HM_2 (84.00 %). Overall, the genotype P-51 and hormone HM_2 (0.2 mg/l BAP+2.0mg/l NAA) appeared to be best for callus induction frequency. Roy and Saha (1997) have reported higher percentage of callus induction on a medium with 2 mg/l 2, 4-D and NAA each.

4.2.1.3 Effects of sucrose and genotypes on callus induction frequency

The data pertaining to effects of sucrose and genotypes on callus induction frequency is presented in Table 4.27. Out of two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose tested, 3 per cent sucrose gave highest callus induction frequency (74.27 %) and was found significantly superior than 4 per cent sucrose. Out of the seven genotypes, P-51 gave highest callus induction frequency (75.77 %) followed by Jayanti x P-18 (75.64 %), both were found to be statistically at par with each other while Jayanti showed least callus induction frequency (71.17 %). In Genotypes x Sucrose interaction, the highest callus induction frequency was recorded for $P_{(2)2}$ (78.46 %) followed by Jayanti x P-18 (77.89 %) on 3 per cent sucrose whereas Jayanti x P-51 exhibited lowest callus induction frequency on 4 per cent sucrose (69.00 %). Overall, 3 per cent sucrose and the genotype P-51 was best for callus induction frequency.

Sucrose is considered the most effective carbohydrate source which cannot be substituted by other disaccharides. The concentration of sucrose also plays an important role in induction of pollen plants. Studies conducted by Arora and Bhojwani (1988) in *Brassica carinata* revealed that only five per cent glucose as the sole source of carbohydrate did not induce androgenesis. However, the combination of 5 per cent sucrose and 2.5 per cent glucose led to increased frequency of androgenesis even higher than with 10 per cent sucrose alone. Dunwell and Thurling (1985) found that a higher concentration of sucrose was beneficial for initial growth and development. Narasimhulu and Chopra (1987) reported the induction of shoots when sucrose was supplemented at two per cent in *Brassica carinata*.

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Table 4.26 Effects of hormones and genotypes on callus induction frequency (%)

| Hormonal Combination	Genotypes								
	Jayanti	P$_{(2)2}$	P-51	P-18	Jayanti x P$_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
HM$_1$	57.70 (49.43)	69.70 (56.60)	63.40 (52.77)	64.30 (53.31)	56.80 (48.91)	45.10 (42.19)	60.50 (51.06)	59.70 (50.59)	1.94 (Hormones)
HM$_2$	84.30 (66.66)	80.90 (64.09)	86.20 (68.19)	78.00 (62.03)	78.10 (62.10)	84.00 (66.42)	81.00 (64.16)	81.80 (64.75)	
HM$_3$	71.50 (57.73)	70.80 (57.29)	77.70 (61.82)	76.40 (60.94)	78.60 (62.44)	85.00 (67.21)	85.50 (67.62)	77.90 (61.96)	
Mean	71.20 (57.54)	73.80 (59.21)	75.80 (60.53)	72.90 (58.63)	71.20 (57.54)	71.40 (57.67)	75.60 (60.40)		

CD (P≤0.05) = 2.96 (Genotypes)
CD interaction= 5.13 (Genotypes x Hormone)
Values in parentheses are arc sine transformed values

Table 4.27 Effects of sucrose and genotypes on callus induction frequency (%)

Sucrose	Genotypes								
	Jayanti	P$_{(2)2}$	P-51	P-18	Jayanti x P$_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
3%	72.29 (58.24)	78.46 (62.35)	74.09 (59.40)	73.68 (59.13)	69.69 (56.60)	73.76 (59.19)	77.89 (61.95)	74.27 (59.52)	1.58 (Sucrose)
4%	70.05 (56.82)	69.15 (56.26)	77.46 (61.66)	72.17 (58.16)	72.67 (58.48)	69.00 (56.17)	73.39 (58.95)	71.98 (58.04)	
Mean	71.17 (57.52)	73.81 (59.22)	75.77 (60.51)	72.93 (58.65)	71.18 (57.53)	71.38 (57.66)	75.64 (60.43)		

CD (P≤0.05) = 2.96 (Genotypes)
CD interaction = 4.18 (Genotypes x Sucrose)
Values in parentheses are arc sine transformed values

4.2.1.4 Effects of sucrose and hormones on callus induction frequency

The perusal of data presented in Table 4.28 indicated that out of two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose tested, the former gave highest callus induction frequency (74.27 %) and was found significantly superior than the latter. Out of the three hormonal combinations, HM$_2$ (0.2 mg/l BAP+2.0 mg/l NAA) gave significantly highest callus induction frequency (81.79 %) than HM$_1$ and HM$_3$. The interaction between two factors *i.e.* sucrose x hormones had significant effect on the callus induction frequency. Considering interaction, the highest callus induction

frequency was observed in 3 per cent sucrose supplemented with HM_2 (88.22 %) followed by 4 per cent sucrose supplemented with HM_3 (75.55 %).

Table 4.28 Effects of sucrose and hormones on callus induction frequency (%)

Sucrose	Hormonal combination				
	HM_1	HM_2	HM_3	Mean	CD (P≤0.05)
3 %	54.26 (47.44)	88.22 (69.93)	80.32 (63.66)	74.27 (59.52)	1.58 (Sucrose)
4 %	65.04 (53.75)	75.36 (60.24)	75.55 (60.37)	71.98 (58.04)	
Mean	59.65 (50.56)	81.79 (64.74)	77.94 (61.99)		

CD (P≤0.05) = 1.94 (Hormone)
CD interaction= 2.74 (Hormone x Sucrose)
Values in parentheses are arc sine transformed values

4.2.1.5 Effects of hormones and media on callus induction frequency

The data pertaining to effect of hormones and media on callus induction frequency is presented in Table 4.29. Out of the three hormonal combinations tested, HM_2 (0.2 mg/l BAP+2.0 mg/l NAA) gave highest callus induction frequency to (81.80 %) and was found to be significantly superior than HM_3 and HM_1. Out of two media, B_5 medium gave highest callus induction (77.50 %) and was found to be significantly superior to the MS medium. The interaction between two factors *i.e.* hormones x media had significant effect on the callus induction frequency. Considering interaction, the highest callus induction frequency was observed in MS medium supplemented with HM_2 (82.90 %) followed by B_5 medium supplemented with HM_2 (80.70 %). Kumari (2010) reported highest callus induction frequency in B_5 medium (59.74 %) when supplemented with HM_2 (1.0 mg/l 2, 4- D). Devi (2009) also reported highest callus induction in B_5 medium (24.94 %) when supplemented with HM_5 (0.5 mg/l 2, 4-D + 1.0 mg/l NAA).

4.2.1.6 Effects of media and sucrose on callus induction frequency

The perusal of data presented in Table 4.30 revealed that out of two media tested, B_5 gave highest callus induction frequency (77.60 %) and was found significantly superior than MS medium. Out of two different sucrose concentrations tested, 3 per cent sucrose gave highest callus induction frequency (74.30 %) and was found to be significantly superior than 4 per cent sucrose. The interaction between two factors *i.e.*

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media x sucrose had significant effect on the callus induction frequency. Considering interaction, the highest callus induction frequency was observed in B_5 medium supplemented with 3 per cent sucrose (82.30 %) followed by B_5 medium supplemented with 4 per cent sucrose (72.80 %).

Table 4.29 Effects of hormones and media on callus induction frequency (%)

Hormonal Combination	Callusing Media			
	MS	B_5	Mean	CD (P≤0.05)
HM_1	43.70 (41.38)	72.20 (58.18)	58.00 (49.60)	1.94 (Hormones)
HM_2	82.90 (65.57)	80.70 (63.94)	81.80 (64.75)	
HM_3	76.20 (60.80)	79.60 (63.15)	77.90 (61.96)	
Mean	67.60 (55.30)	77.50 (61.68)		

CD (P≤0.05) = 1.58 (Media)
CD interaction = 2.74 (Media x Hormone)
Values in parentheses are arc sine transformed values

Table 4.30 Effects of media and sucrose on callus induction frequency (%)

Media	Sucrose			
	3%	4%	Mean	CD (P≤0.05)
MS	66.30 (54.51)	71.20 (57.54)	68.80 (56.04)	1.58 (Media)
B_5	82.30 (65.12)	72.80 (58.56)	77.60 (61.75)	
Mean	74.30 (59.54)	72.00 (58.05)		

CD (P≤0.05) = 1.58 (Sucrose)
CD interaction = 2.24 (Sucrose x Media)

Values in parentheses are arc sine transformed values

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4.2.2   Effects of different parameters on days to calli appearance

Analysis of variance for days to calli appearance involving different parameters is presented in Table 4.31. Out of four factors, only genotypes had significant effect on days to calli appearance. Nine out of eleven interactions *viz.,* genotypes x hormones, genotypes x media, hormones x media, genotypes x hormones x media, hormones x sucrose, genotypes x hormones x sucrose, genotypes x media x sucrose, hormones x media x sucrose and genotypes x hormones x media x sucrose showed significant effect on days to calli appearance.

Table 4.31 ANOVA for days to calli appearance in different genotypes of *Brassica carinata* and their hybrids involving different media, hormones and sucrose concentration

Source of variation	df	Mean Squares	CD (5%)	CV (%)
Genotypes	6	28.23**	0.47	11.00
Hormones	2	1.38	NS	
Genotypes x Hormones	12	5.17**	0.82	
Media	1	0.25	NS	
Genotypes x Media	6	4.67**	0.67	
Hormones x Media	2	21.60**	0.44	
Genotypes x Hormones x Media	12	5.04**	1.16	
Sucrose	1	0.25	NS	
Genotypes x Sucrose	6	0.93	NS	
Hormones x Sucrose	2	63.65**	0.44	
Genotypes x Hormones x Sucrose	12	5.21**	1.16	
Media x Sucrose	1	1.02	NS	
Genotypes x Media x Sucrose	6	12.06**	0.94	
Hormones x Media x Sucrose	2	113.34**	0.62	
Genotypes x Hormones x Media x Sucrose	12	7.19**	1.64	
Error	168	1.02		

** Significant at $P \leq 0.01$

From the Tables 4.32, 4.33 and 4.34, it is pertinent that the effects of media, hormones and sucrose were found to be non-significant on all seven genotypes which indicated that different genotypes behaved similar in different media, hormonal combinations and sucrose concentrations for days to calli appearance. However, the genotype Jayanti x $P_{(2)2}$ recorded lowest days to calli appearance on different media and sucrose concentrations. Likewise, the genotype P-51 took lowest days to calli appearance on different hormonal combinations.

Table 4.32 Effects of media and genotypes on days to calli appearance

Media	Genotypes								
	Jayanti	$P_{(2)2}$	P-51	P-18	Jayanti x $P_{(2)2}$	Jayanti x P-51	Jayanti X P-18	Mean	CD (P≤0.05)
MS	10.50	8.39	9.39	8.44	8.39	9.50	8.44	9.01	NS (Media)
B_5	11.44	11.06	8.56	8.83	8.44	8.89	8.83	9.44	
Mean	10.97	9.72	8.97	8.64	8.42	9.19	8.64		

CD (P≤0.05) = 0.47 (Genotypes)
CD interaction = 0.67 (Genotypes x Media)

Table 4.33 Effects of hormones and genotypes on days to calli appearance

Hormonal combination	Genotypes								
	Jayanti	$P_{(2)2}$	P-51	P-18	Jayanti x $P_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
HM_1	13.08	9.75	10.00	10.75	9.33	10.50	10.75	10.60	NS (Hormones)
HM_2	9.67	9.42	7.17	6.67	7.25	7.08	6.67	7.70	
HM_3	10.17	10.00	7.17	8.50	8.67	10.00	8.50	9.00	
Mean	10.97	9.72	8.11	8.64	8.42	9.19	8.64		

CD (P≤0.05) = 0.47 (Genotypes)
CD interaction= 0.82 (Genotypes x Hormones)

Table 4.34 Effects of sucrose and genotypes on days to calli appearance

Sucrose	Genotypes								
	Jayanti	$P_{(2)2}$	P-51	P-18	Jayanti x $P_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
3 %	10.17	10.39	8.72	8.56	8.78	9.00	8.56	9.17	NS (Sucrose)
4 %	11.78	9.06	9.22	8.72	8.06	9.39	8.72	9.28	
Mean	10.97	9.72	8.97	8.64	8.42	9.19	8.64		

CD (P≤0.05) = 0.47 (Genotypes)
CD interaction = NS (Genotypes x Sucrose)

The effects of sucrose and hormones, hormones and media and media and sucrose on days to calli appearance are presented in Tables 4.35, 4.36 and 4.37, respectively. The results revealed that the effects of sucrose and hormones, hormones and media and media and sucrose were found to be non-significant which indicated that days to calli appearance were not affected significantly by different media, hormonal combinations and sucrose concentrations.

Table 4.35 Effects of sucrose and hormones on days to calli appearance

Sucrose	Hormonal Combination				
	HM_1	HM_2	HM_3	Mean	CD (P≤0.05)
3 %	10.88	7.67	8.95	9.17	NS (Sucrose)
4 %	10.31	7.74	9.79	9.28	
Mean	10.60	7.70	9.37		

CD (P≤0.05) = NS (Hormones)
CD interaction = 0.44 (Hormones x Sucrose)

Table 4.36 Effects of hormones and media on days to calli appearance

Hormonal combination	Callusing Media			
	MS	B_5	Mean	CD (P≤0.05)
HM_1	10.05	10.95	10.50	NS (Hormones)
HM_2	7.40	8.00	7.70	
HM_3	9.38	9.36	9.37	
Mean	8.94	9.44		

CD (P≤0.05) = NS (Media)
CD interaction = 0.44 (Media x Hormones)

Table 4.37 Effect of media and sucrose on days to calli appearance

Media	Sucrose			
	3%	4%	Mean	CD (P≤0.05)
MS	8.98	9.03	9.01	NS (Media)
B_5	9.35	9.52	9.44	
Mean	9.17	9.28		

CD (P≤0.05) = NS (Sucrose)

CD interaction = NS (Sucrose x Media)

4.2.3 Effects of different parameters on calli index

Analysis of variance for calli index in anthers of seven genotypes cultured *in vitro* on two media supplemented with three hormonal combinations and two different sucrose concentrations, is presented in Table 4.38. Mean sum of squares due to all factors were significant revealing thereby significant effects of genotypes, hormones, media, sucrose and their interactions on calli index.

4.2.3.1 Effects of media and genotypes on calli Index

Effects of media and genotypes on calli index are presented in Table 4.39. Out of the two media tested, the anthers plated on B_5 medium recorded significantly highest calli index (62.01) than MS medium. Out of the seven genotypes tested, P-51 recorded highest calli index (62.50) and was statistically at par with Jayanti x P-18. On the other hand Jayanti x $P_{(2)2}$ recorded least calli index (55.11). The calli index was also significantly affected by the genotype x media interaction. Best calli index of cultured anthers was recorded for P-51 on B_5 medium (76.64) followed by P-18 (66.91) and Jayanti x $P_{(2)2}$ (60.93). Overall, culturing anthers of genotype P-51 on B_5 medium exhibited significantly better calli index.

4.2.3.2 Effects of hormones and genotypes on calli Index

The perusal of data presented in Table 4.40 indicated that out of three hormonal combinations tested, HM_2 gave significantly highest calli index (68.18) in comparison to HM_1 and HM_3. Out of seven genotypes used for anther culture, P-51 gave highest calli index (62.50) followed by Jayanti x P-18 (59.27) being statistically at par with each other. Jayanti x $P_{(2)2}$ gave lowest calli index (55.11). The interaction genotypes x hormones had significant effect on calli index. Best calli index of cultured anthers was recorded for P-51 on HM_2 (74.86). Overall, culturing anthers of P-51 in HM_2 (0.2mg/l BAP+2.0mg/l NAA) exhibited significantly better calli index.

4.2.3.3 Effects of sucrose and genotypes on calli Index

The data pertaining to effects of sucrose and genotypes on callus induction frequency is presented in Table 4.41. Out of two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose tested, 3 per cent sucrose gave highest calli index (58.52 %) and was statistically at par with 4 per cent sucrose. Out of the seven genotypes tested,

P-51 recorded highest mean calli index (63.88). On the other hand Jayanti x $P_{(2)2}$ recorded least calli index (55.67). The calli index was also significantly affected by the sucrose x

Table 4.38 ANOVA for calli index in different genotypes of *Brassica carinata* and their hybrids involving different media, hormones and sucrose concentrations

Source of variation	df	Mean Squares	CD (5%)	CV (%)
Genotypes	6	233.54*	4.22	15.6
Hormones	2	2029.45**	2.76	
Genotypes x Hormones	12	1080.43**	7.30	
Media	1	16382.76**	2.25	
Genotypes x Media	6	1127.07**	5.96	
Hormones x Media	2	407.57**	3.90	
Genotypes x Hormones x Media	12	434.24**	10.33	
Sucrose	1	2277.56**	2.25	
Genotypes x Sucrose	6	250.43**	5.96	
Hormones x Sucrose	2	3453.60**	3.90	
Genotypes x Hormones x Sucrose	12	446.90**	10.33	
Media x Sucrose	1	1669.55**	3.19	
Genotypes x Media x Sucrose	6	1552.63**	8.43	
Hormones x Media x Sucrose	2	25199.98**	5.52	
Genotypes x Hormones x Media x Sucrose	12	507.45**	14.61	
Error	168	81.23		

*Significant at $P \leq 0.05$;   ** Significant at $P \leq 0.01$

Table 4.39 Effect of media and genotypes on calli index

Media	Genotypes								
	Jayanti	$P_{(2)2}$	P-51	P-18	Jayanti x $P_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
MS	50.81	63.90	48.37	47.78	49.28	55.84	59.52	53.64	2.25 (Media)
B_5	59.68	50.31	76.64	66.91	60.93	60.60	59.03	62.01	
Mean	55.24	57.11	62.50	57.34	55.11	58.22	59.27		

CD (P≤0.05) = 4.22 (Genotypes)
CD interaction= 5.96 (Genotypes x Media)

Table 4.40   Effects of hormones and genotypes on calli index

Hormonal combination	Genotypes								
	Jayanti	P$_{(2)2}$	P-51	P-18	Jayanti x P$_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
HM$_1$	41.34	52.38	51.28	48.89	39.74	32.08	37.01	43.25	2.76 (Hormones)
HM$_2$	72.00	68.02	74.86	63.52	62.13	69.48	67.25	68.18	
HM$_3$	52.39	50.92	61.37	59.62	63.44	73.10	73.56	62.06	
Mean	55.24	57.11	62.50	57.34	55.11	58.22	59.27		

CD (P≤0.05) = 4.22 (Genotypes)
CD interaction = 7.30 (Genotypes x Hormones)

Table 4.41 Effect of sucrose and genotypes on calli index

Sucrose	Genotypes								
	Jayanti	P$_{(2)2}$	P-51	P-18	Jayanti x P$_{(2)2}$	Jayanti x P-51	Jayanti x P-18	Mean	CD (P≤0.05)
3 %	55.98	55.97	64.86	58.94	56.08	58.62	59.23	58.52	2.25
4 %	55.37	56.92	62.90	57.61	55.27	58.29	59.27	57.94	(Sucrose)
Mean	55.68	56.44	63.88	58.27	55.67	58.45	59.25		

CD (P≤0.05) = 4.22 (Genotypes);
CD interaction = 5.96 (Genotypes x Sucrose)

genotype interaction. Best calli index of cultured anthers was recorded for P-51 on 3 per cent sucrose (64.86) followed by 4 per cent sucrose concentrations (62.90). Overall, culturing anthers of genotype P-51 on 3 per cent sucrose concentration exhibited better calli index.

4.2.3.4 Effects of sucrose and hormones on calli index

The perusal of data presented in Table 4.42 indicated that out of two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose tested, 4 per cent sucrose gave highest calli index (9.28) than 3 per cent sucrose and both were statistically at par with each other. Out of three hormonal combinations tested, HM$_1$ (1.0 mg/l NAA) gave

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highest calli index (10.60) and was statistically at par with HM_3. The interaction between two factors *i.e.* sucrose x hormones had significant effect on the calli index. Considering interaction, the highest calli index was observed in 3 per cent sucrose supplemented with HM_1 (10.88) followed by 4 per cent sucrose supplemented with HM_1 (10.31).

4.2.3.5 Effects of hormones and media on calli index

The data pertaining to effects of hormones and media on calli index is presented in Table 4.43. Out of the three hormonal combinations used for anther culture, HM_2 gave significantly highest calli index (68.18) than HM_3 and HM_1. Out of two media tested, B_5 medium gave significantly highest calli index (62.01) in comparison to MS medium. The calli index was also significantly affected by media x hormones interaction. Significantly higher calli index of cultured anthers were recorded in MS medium supplemented with HM_2 (70.12) followed by B_5 medium also supplemented with HM_2 (66.24). Overall, B_5 medium supplemented with HM_2 (0.2mg/l BAP+2.0mg/l NAA) was best for calli index.

Table 4.42 Effects of sucrose and hormones on calli index

Sucrose	Hormonal combination				
	HM_1	HM_2	HM_3	Mean	CD (P≤0.05)
3 %	10.88	7.67	8.95	9.17	2.25
4 %	10.31	7.74	9.79	9.28	(Sucrose)
Mean	10.60	7.70	9.37		

CD (P≤0.05) = 2.76 (Hormone)
CD interaction = 3.90 (Hormone x Sucrose)

Table 4.43 Effects of hormones and media on calli index

Hormonal combination	Callusing Media			
	MS	B_5	Mean	CD (P≤0.05)
HM_1	30.86	55.63	43.25	2.76
HM_2	70.12	66.24	68.18	(Hormone)
HM_3	59.95	64.17	62.06	
Mean	53.64	62.01		

CD (P≤0.05) = 2.25 (Media)
CD interaction = 3.90 (Media x Hormone)

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4.2.3.6 Effects of media and sucrose on calli index

The perusal of data presented in Table 4.44 indicated that out of two media tested, B_5 gave highest calli index (62.79) and was found to significantly superior than MS medium. Out of two different sucrose concentrations, 3 per cent sucrose gave highest calli index (60.91) and was found to significantly superior than 4 per cent sucrose. The interaction between two factors *i.e.* media x sucrose had significant effect on the calli index. Considering interaction, the highest calli index was observed in B_5 medium supplemented with 3 per cent sucrose (67.47).

Table 4.44 Effects of media and sucrose on calli index

Media	Sucrose			
	3%	**4%**	**Mean**	**CD (P≤0.05)**
MS	54.35	52.94	53.64	2.25
B_5	67.47	58.10	62.79	(Media)
Mean	60.91	55.52		

CD (P≤0.05) = 2.25 (Sucrose)

CD interaction = 3.19 (Sucrose x Media)

5. SUMMARY AND CONCLUSIONS

The present investigation entitled "Genetic analysis of seed yield and related traits in doubled haploids and response to anther culture in Ethiopian mustard (*Brassica carinata* A. Braun)" was undertaken to assess the nature of genetic variability, extent of genetic diversity among genotypes through multivariate analysis and association of various characters with seed yield and their direct and indirect effects for effective selection under two different environments *viz*., Env.I and Env.II. In addition, the androgenesis-mediated responsiveness of four genotypes and their three crosses was also studied through anther culture.

The experimental material was comprised of 33 genotypes of Ethiopian mustard including four checks *viz.,* Nav Gold, Jayanti, Pusa Jaikisan and RCC-4. All the genotypes were raised in randomized complete block design with three replications, at the experimental farm of Department of Crop Improvement, CSK HPKV, Palampur, during *rabi,* 2010-11. The disease reaction studies were conducted at Shivalik Agricultural Research and Extension Centre (SAREC), Kangra during *rabi,* 2011-12. Data were recorded on five randomly selected plants for various traits *viz.,* days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, length of main shoot, siliquae on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant, biological yield per plant, harvest index and percent oil content. In addition, all genotypes were also scored for reaction to *Alternaria brassicae* under natural epiphytotic field conditions. Anther culture studies were carried out in the Molecular Cytogenetics and Tissue Culture Laboratory, Department of Crop Improvement, CSK HPKV, Palampur.

The data analysis for seed yield and other related characters was done as per the standard statistical procedures for parameters of genetic variability, genetic diversity,

correlations and path coefficients in Env.I, Env.II and pooled over the environments. Grouping of genotypes into different categories for disease reaction to *Alternaria* blight was done using 0-9 scale. The data recorded on three parameters in anther culture studies *viz.,* callus induction frequency, days to calli appearance and calli index were analysed using factorial completely randomized design.

Analysis of variance indicated the presence of sufficient genetic variability for all characters except siliqua length and percent oil content in Env.I. On the other hand in Env.II, the presence of sufficient genetic variability for days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, 1000-seed weight, seed yield per plant and harvest index was observed. Pooled analysis over environments revealed the presence of g x e interactions for all characters except days to flower initiation and percent oil content. The presence of g x e interaction has greatly influenced the variation due to genotypes to the extent that genotypic differences recorded in individual environments have vanished for these characters.

On the basis of mean performance, Env.I exhibited its excellent potential for the characters *viz.,* days to 75 per cent maturity, number of primary branches per plant, length of main shoot, siliquae on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, biological yield per plant and per cent oil content. For days to flower initiation, days to 50 per cent flowering, plant height, number of secondary branches per plant, siliquae per plant and harvest index, excellent potential was recorded in Env.II. However, both Env.I and II exhibited excellent potential for seed yield per plant.

Three genotypes *viz.,* P-26, P-31 and P-138 in Env.I, while two genotypes *viz.,* P-51 and P-103 in Env.II and four genotypes *viz.,* P-33, P-34, P-63 and P-138 in pooled over the environments were found to be superior for seed yield per plant and other characters over the parental check Jayanti.

The estimates of PCV were higher than their corresponding GCV for all characters in all the environments. In Env.I, the PCV values were found to be high for harvest index while in Env.II and pooled over the environments, high PCV values were observed for siliquae per plant and harvest index. The estimates of GCV were moderate in Env.I, Env.II and pooled over the environments. In Env.I, high heritability values were observed for 75 per cent maturity followed by days to flower initiation, 1000-seed

weight, plant height, days to 50 per cent flowering, number of secondary branches per plant and siliquae per plant whereas in Env.II and pooled over the environments, high heritability values were observed for days to 50 per cent flowering followed by days to 75 per cent maturity and days to flower initiation. High heritability coupled with high genetic advance was observed for 1000-seed weight, plant height and number of secondary branches per plant in Env.I indicating the predominance of additive gene action for these characters. This would be useful for effective selection in early segregating generations due to their high breeding values.

The multivariate analysis revealed considerable genetic diversity present in the genotypes studied. All the 33 genotypes could be grouped into eight, three and three clusters in Env.I, Env.II and pooled over the environments, respectively. Grouping of the genotypes was almost similar in both the environments as well as pooled over the environments. Maximum genotypes were placed in cluster I in Env.I, Env.II as well as pooled over the environments. However, the three genotypes *viz.,* Nav Gold, Pusa Jaikisan and RCC-4 formed a separate cluster and showed consistency in clustering pattern in all the environments while the genotype P-12 showed uniformity on the basis of monogenotypic cluster in all the environments. Further, the clustering pattern indicated that all the mustard genotypes as checks formed separate clusters while all doubled haploids appeared in separate clusters in Env.I, Env.II and pooled over the environments. The clustering pattern of karan rai and mustard genotypes indicated the parallelism between genetic divergence and species-wise geographical distribution. In Env.I, maximum intra-cluster distance was observed in cluster II while in Env.II and pooled over the environments, maximum intra-cluster distance was observed in cluster I. Maximum inter-cluster distance existed among clusters II and VIII in Env.I, I and II in Env.II and II and III in pooled over the environments. Maximum contribution towards genetic divergence was due to plant height in Env.I, days to 50 per cent flowering in Env.II and days to 75 per cent maturity in pooled over the environments. Selection of genotypes as superior and diverse parents for hybridization programme should be based on diverse clusters *viz.,* II (Nav Gold, Pusa Jaikisan and RCC-4) and VIII (P-12) in Env.I, I (P-51 and P-103) and II (Nav Gold, Pusa Jaikisan and RCC-4) in Env.II and II (Nav

Gold, Pusa Jaikisan and RCC-4) and III (P-12) in pooled over the environments to get heterotic crosses for getting superior recombinants in early segregating generations.

Correlation studies indicated the higher magnitude of genotypic correlations than their corresponding phenotypic correlations for most of the characters studied indicating the inherent association among the various characters. Seed yield per plant exhibited significant positive correlation with plant height, number of secondary branches per plant, siliquae per plant, siliqua length, biological yield per plant and harvest index while seed yield per plant showed significant negative correlation with days to 75 per cent maturity in Env.I. In Env.II, seed yield per plant had significant positive correlation with harvest index only. In pooled over the environments, seed yield per plant had significant positive correlation with plant height, number of secondary branches per plant, siliquae per plant, biological yield per plant and harvest index. On the other hand, seed yield per plant showed significant negative correlation with days to 75 per cent maturity which is a desirable association to be exploited directly through phenotypic selection.

Path coefficient analysis revealed the high positive direct effects of biological yield per plant and harvest index on seed yield per plant in Env.I and pooled over the environments and harvest index only in Env.II. The characters such as plant height and siliquae per plant showed negligible direct effect but, their indirect contribution was through biological yield per plant and harvest index. Therefore, biological yield per plant and harvest index could be considered as the best selection parameters for the improvement of seed yield per plant due to their high direct and indirect contributions.

Based on disease reaction to *Alternaria brassicae,* only one genotype *viz.,* Pusa Jaikisan appeared to be moderately resistant while all remaining 32 genotypes exhibited susceptible to moderately susceptible reaction on leaves. Based upon disease reaction on pods, two genotypes *viz.,* P-26 and P-34 appeared to be resistant while 28 genotypes exhibited moderately resistant reaction. Only 3 genotypes *viz.,* P-89, P-62 and Pusa Jaikisan were found to be susceptible.

Anthers of four genotypes and their hybrids were cultured on two different media *viz.,* B_5 and MS, each of these media was supplemented with two different sucrose concentrations *i.e.* 3 per cent and 4 per cent sucrose and each of these sucrose concentrated media was also supplemented with three different combinations of

hormones. The observations were recorded for callus induction frequency (%), days to calli appearance and calli index. Significant effects of all 4 factors *viz.,* genotypes, media, hormones, sucrose and their interactions on the callus induction frequency (%) and calli index were observed. The highest callusing and calli index were observed in B_5 medium supplemented with HM_2 (0.2mg/l BAP + 2.0 mg/l NAA) and 3 per cent sucrose concentration. The factors such as media, hormones, sucrose, genotypes x sucrose and media x sucrose had non-significant effect on days to calli appearance.

Conclusions

Sufficient genetic variability was observed for most of the characters studied in Env.I, II and pooled over the environments. High heritability coupled with high genetic advance was observed for 1000-seed weight, plant height and number of secondary branches per plant in Env.I which indicated the predominance of additive gene action, important for effective selection in early segregating generations. The multivariate analysis revealed the presence of considerable genetic diversity in the 33 genotypes studied. The three mustard genotypes *viz.,* Nav Gold, Pusa Jaikisan and RCC-4 formed a separate cluster and showed consistency in clustering pattern while the genotype P-12 showed uniformity on the basis of monogenotypic cluster in all the environments. The clustering pattern of karan rai and mustard genotypes indicated the parallelism between genetic divergence and species-wise geographical distribution. Based upon correlation and path coefficient analysis, biological yield per plant and harvest index in Env.I and pooled over the environments and harvest index in Env.II were observed to be the best selection parameters because of their high positive direct and indirect contributions towards seed yield per plant. In androgenesis-mediated response, the genotype P-51 performed better in B_5 medium supplemented with HM_2 (0.2mg/l BAP + 2.0 mg/l NAA) and 3 per cent sucrose concentration for high callus induction frequency and calli index. The factors such as media, hormones, sucrose and their interactions *viz.,* genotypes x sucrose and media x sucrose had non-significant effects on days to calli appearance which indicated that the genotypes behaved similar in different media, hormonal combinations and sucrose concentrations.

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Appendix -I Estimates of mean values for 33 genotypes of *Brassica carinata* in Env.I

Characters / Genotypes	Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Siliquae/ plant	Length of main shoot
P-12	96.0	132.0	168.7	115.8	4.4	10.9	264.7	52.3
P-17	87.7	129.0	162.7	141.6	5.1	10.1	210.6	39.0
P-23	91.7	129.3	159.3	109.0	5.8	7.5	158.4	56.7
P-24	91.0	129.7	175.3	113.7	5.7	8.6	117.6	51.3
P-26	99.7	130.7	159.3	108.5	5.5	8.6	206.5	50.7
P-31	92.0	131.3	163.7	187.5	5.6	9.2	284.6	45.7
P-33	90.7	130.3	170.7	130.5	6.6	7.2	135.2	43.7
P-34	92.0	128.0	162.0	108.5	3.5	7.5	197.5	46.0
P-39	92.7	127.7	167.0	186.0	6.3	4.8	217.1	45.7
P-43	89.7	130.0	168.7	99.3	4.3	8.1	158.8	44.7
P-45	91.7	131.3	170.0	104.3	4.5	7.0	174.4	37.3
P-51	90.0	131.3	170.0	82.4	4.8	7.0	127.4	48.7
P-56	90.3	125.7	170.7	81.6	4.8	7.9	151.4	42.3
P-62	91.3	130.7	171.0	95.7	4.7	6.9	168.4	39.3
P-63	94.7	130.0	171.3	109.1	5.2	5.1	189.5	31.0
P-64	90.7	130.0	169.0	191.3	5.1	7.0	194.7	41.0
P-74	94.3	129.7	172.7	97.1	5.1	6.6	166.9	37.3
P-75	96.0	130.3	178.0	132.0	4.6	6.8	155.8	42.7
P-77	94.0	135.0	166.7	115.5	6.2	5.5	173.9	51.3
P-89	88.7	130.7	171.0	122.0	7.1	7.2	157.3	42.3
P-92	90.7	130.7	174.0	148.1	3.9	4.2	157.4	42.7
P-96	91.0	129.7	171.7	117.7	4.7	8.3	142.5	51.0
P-101	88.7	130.7	168.7	126.9	5.7	5.2	159.8	43.3
P-103	97.0	131.7	172.7	114.6	4.5	5.8	176.2	52.0
P-117	93.3	129.0	174.3	132.9	4.8	7.0	167.2	45.0
P-122	90.7	130.7	171.7	114.0	6.2	7.1	145.6	49.7
P-133	94.3	129.7	175.0	120.1	5.8	6.8	156.2	57.3
P-137	90.7	126.3	171.7	99.4	4.6	5.9	143.9	47.3
P-138	87.0	131.0	170.0	180.3	7.4	6.2	195.9	46.0
Nav Gold (c)	68.0	114.3	148.3	117.5	4.7	4.5	129.4	37.3
Jayanti (c)	92.0	128.7	170.0	116.7	5.9	6.7	161.1	34.7
Pusa Jaikisan (c)	69.7	114.3	147.0	107.4	3.8	4.5	157.2	32.0
RCC-4 (c)	68.0	115.0	144.7	115.9	4.0	8.5	167.5	49.3
Range	68.0-99.7	114.3-135.0	144.7-178.0	81.6-191.3	4.0-7.4	4.2-10.9	117.6-284.6	31.0-57.3
Grand mean ($\bar{x}$)	89.6	128.7	167.5	122.4	5.2	7.0	172.7	44.7
SE (m) ±	1.9	1.7	1.7	8.3	0.4	0.6	14.9	2.8
CD at $P \leq 0.05$	5.4	4.7	4.9	23.5	1.2	1.6	42.1	7.9
CV (%)	3.7	2.2	1.8	11.8	14.5	14.1	14.9	10.9

Characters / Genotypes	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Seed yield/ plant	Biological yield/ plant	Harvest index	Oil content
P-12	32.7	3.6	9.5	2.4	7.7	31.7	24.5	40.0
P-17	44.7	3.6	10.1	2.4	6.6	39.3	17.3	39.9
P-23	43.3	3.4	10.9	2.5	5.9	37.0	16.7	35.3
P-24	31.3	3.4	11.5	2.7	4.7	27.0	18.2	39.3
P-26	39.3	3.8	11.1	2.3	8.7	42.0	21.4	38.8
P-31	29.7	4.1	11.4	2.7	8.8	53.7	16.8	38.3
P-33	42.3	3.8	9.8	2.9	7.6	40.7	18.9	38.8
P-34	40.7	3.7	10.1	2.4	7.6	32.3	23.8	37.6
P-39	36.7	4.0	13.5	2.7	7.0	38.0	18.7	36.6
P-43	36.3	3.6	10.0	2.6	8.0	33.7	23.6	38.2
P-45	47.3	3.7	10.3	2.5	6.3	38.3	16.3	34.9
P-51	45.7	3.4	11.6	2.3	4.1	27.0	15.0	36.2
P-56	43.3	4.2	10.5	2.5	6.1	39.0	15.8	35.2
P-62	30.0	3.5	10.6	2.5	4.3	27.3	16.2	36.5
P-63	22.7	4.0	12.7	2.6	8.7	32.0	27.7	38.3
P-64	30.0	3.7	11.6	2.6	7.9	49.0	16.3	38.7
P-74	35.7	3.7	12.1	2.6	4.8	32.0	15.2	34.9
P-75	32.0	4.2	11.6	2.6	4.5	27.0	17.2	41.8
P-77	29.3	3.8	11.9	2.4	5.8	33.0	18.7	36.8
P-89	24.7	3.5	10.2	2.6	5.7	43.3	13.0	33.1
P-92	20.0	3.7	11.1	2.6	4.5	41.0	11.1	38.9
P-96	38.0	3.4	10.6	2.7	4.8	32.3	15.1	37.2
P-101	35.3	3.4	11.5	2.3	3.9	31.7	12.4	37.4
P-103	33.3	3.4	10.5	2.7	4.9	33.7	14.3	35.3
P-117	47.3	3.5	10.1	2.1	6.0	43.3	13.9	39.1
P-122	32.0	3.4	11.9	2.4	5.5	33.7	16.5	33.6
P-133	39.7	3.8	10.5	2.5	3.9	22.3	18.1	39.4
P-137	50.3	3.4	11.5	2.5	4.2	13.0	11.5	37.1
P-138	31.7	3.9	10.6	2.7	8.8	37.3	23.7	36.5
Nav gold (c)	25.3	4.4	11.7	5.0	7.8	45.0	17.5	36.1
Jayanti (c)	39.3	3.5	10.1	2.7	5.3	33.7	17.4	40.3
Pusa Jaikisan (c)	25.7	4.0	11.4	4.5	6.1	39.0	15.8	36.7
RCC-4 (c)	28.3	4.4	11.6	4.1	6.5	41.0	15.9	37.4
Range	20.0-50.3	3.4-4.4	9.5-13.5	2.1-5.0	4.1-8.8	13.0-53.7	11.1-27.7	33.1-41.8
Grand mean ($\overline{x}$)	35.0	3.7	11.0	2.7	6.2	36.4	17.4	37.4
SE (m) ±	3.4	2.3	0.5	0.2	0.7	3.4	2.6	2.0
CD at $P \leq 0.05$	9.7	0.8	1.5	0.5	1.9	9.6	7.3	5.8
CV (%)	17.0	12.5	8.4	11.7	19.3	16.1	25.6	9.5

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Appendix –II Estimates of mean values for 33 genotypes of *Brassica carinata* in Env.II

Characters / Genotypes	Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Siliquae/ plant	Length of main shoot
P-12	87.7	128.0	165.3	121.8	7.0	12.5	394.0	52.3
P-17	89.3	134.0	172.0	114.5	4.5	9.9	221.0	33.0
P-23	91.7	120.3	172.3	103.8	4.5	9.9	335.3	37.7
P-24	85.7	130.7	167.7	107.3	5.5	10.7	173.7	41.3
P-26	88.0	126.0	178.3	101.4	4.5	6.8	132.2	49.3
P-31	92.3	129.7	170.7	108.2	4.3	10.8	146.6	42.3
P-33	92.7	127.3	170.0	108.7	3.8	11.6	143.0	41.3
P-34	93.0	129.0	165.3	104.0	5.3	7.6	143.8	43.3
P-39	84.0	127.3	169.0	97.2	4.1	11.7	149.9	37.3
P-43	90.7	132.0	166.3	117.4	4.9	6.9	164.8	40.0
P-45	89.0	130.3	168.7	109.0	4.9	5.4	178.0	43.3
P-51	93.0	130.7	167.0	105.1	4.8	7.7	164.6	37.0
P-56	92.0	127.7	170.0	109.7	6.0	8.1	145.2	37.3
P-62	88.7	125.0	166.7	83.7	5.6	9.7	160.7	40.3
P-63	91.7	129.7	170.7	91.9	4.9	9.3	178.5	43.7
P-64	85.7	130.7	168.3	104.5	4.3	8.5	175.7	43.0
P-74	89.7	127.0	172.7	99.7	4.5	7.5	144.4	40.3
P-75	92.0	126.3	174.0	104.6	4.1	8.9	159.3	43.0
P-77	92.3	133.0	166.3	103.7	4.2	9.8	148.8	39.7
P-89	88.7	132.0	171.3	103.2	3.5	8.0	155.0	38.0
P-92	85.7	137.0	167.0	114.9	3.9	8.7	196.3	36.3
P-96	92.0	126.3	171.3	104.1	4.1	7.7	240.3	42.0
P-101	94.7	132.0	167.3	105.5	3.5	9.1	146.4	35.7
P-103	90.3	132.7	167.7	104.1	4.9	11.2	164.8	35.7
P-117	91.0	133.3	174.7	116.3	4.6	9.3	163.5	41.0
P-122	83.7	127.3	169.0	102.2	2.7	8.5	152.1	35.0
P-133	92.0	128.0	170.3	115.2	4.9	10.0	177.5	37.0
P-137	92.0	126.3	172.7	90.4	5.3	9.8	138.1	37.7
P-138	87.0	121.3	167.7	96.5	4.1	7.4	224.5	43.0
Nav Gold (c)	60.0	102.7	149.3	105.7	3.0	10.2	156.1	42.3
Jayanti (c)	85.7	136.3	168.0	85.9	4.6	10.9	175.1	41.0
Pusa Jaikisan (c)	65.7	105.7	151.0	107.0	5.0	10.5	174.4	37.0
RCC-4 (c)	64.3	104.7	150.7	94.5	3.6	9.6	153.8	44.0
Range	60.0-94.7	102.7-137.0	149.3-178.3	83.7-121.8	2.7-7.0	5.4-12.5	132.2-394.0	33.0-52.3
Grand mean ($\bar{x}$)	87.3	127.0	167.9	104.3	4.5	9.2	178.1	40.3
SE (m) ±	3.6	1.7	2.0	6.3	0.6	1.1	29.3	3.5
CD at P ≤ 0.05	9.9	4.7	5.5	17.7	1.7	3.2	82.8	10.0
CV (%)	7.0	2.3	2.0	10.4	22.9	21.5	28.5	15.2

Characters / Genotypes	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Seed yield/ plant	Biological yield/ plant	Harvest index	Oil content
P-12	33.3	4.0	11.4	2.8	6.2	40.7	15.7	40.0
P-17	20.7	3.3	10.2	2.6	5.5	33.7	17.6	32.4
P-23	25.3	3.4	9.7	2.7	5.8	42.0	13.8	33.1
P-24	32.7	3.7	8.7	2.9	5.6	31.3	18.9	39.1
P-26	31.7	3.2	10.3	3.1	5.4	35.0	16.1	36.1
P-31	29.3	3.2	10.8	2.5	4.6	35.0	13.1	33.9
P-33	32.7	3.5	10.6	2.2	5.7	43.7	13.3	37.0
P-34	30.3	3.4	10.6	2.4	7.1	28.0	26.2	36.2
P-39	28.0	3.2	8.3	2.5	7.1	32.0	22.6	34.1
P-43	29.0	3.9	9.5	2.5	4.5	35.3	13.5	37.1
P-45	25.7	3.6	9.8	2.4	5.2	38.7	13.6	35.9
P-51	23.3	3.8	10.5	2.5	8.6	38.7	23.3	33.3
P-56	25.3	3.7	9.9	2.6	7.0	37.3	18.9	33.8
P-62	26.7	3.5	10.4	2.8	6.2	38.7	15.9	36.5
P-63	30.7	3.5	10.9	2.5	5.5	36.7	16.3	37.4
P-64	27.0	3.5	10.5	2.3	6.2	35.0	18.5	37.8
P-74	27.7	3.9	10.4	2.5	7.0	25.7	28.2	35.5
P-75	30.0	3.3	9.7	2.8	5.3	37.0	14.9	39.1
P-77	24.3	4.2	10.3	2.3	7.1	26.0	29.7	34.2
P-89	25.3	4.0	9.0	2.4	6.4	27.3	25.1	34.1
P-92	25.3	3.5	11.1	2.5	7.5	34.7	25.5	35.8
P-96	25.7	3.6	10.5	2.6	5.3	36.0	15.2	36.7
P-101	22.0	3.6	11.5	2.9	5.4	27.7	20.7	37.0
P-103	23.7	3.4	9.9	2.4	8.3	35.7	24.8	34.5
P-117	26.3	3.6	8.6	2.7	8.6	30.3	29.8	35.9
P-122	23.0	3.4	8.5	2.4	6.6	35.0	20.0	33.8
P-133	18.0	3.9	10.1	2.7	6.7	33.3	20.8	38.9
P-137	23.7	4.2	9.6	3.2	4.8	37.3	13.8	34.9
P-138	32.0	3.8	9.6	2.7	5.6	28.0	20.9	39.0
Nav Gold (c)	24.7	3.8	11.6	3.0	5.2	28.0	19.6	38.3
Jayanti (c)	23.0	3.6	9.1	2.6	5.9	28.0	21.9	38.5
Pusa Jaikisan (c)	27.3	4.0	8.2	3.2	7.0	35.7	20.0	38.3
RCC-4 (c)	34.0	3.8	10.3	3.0	5.8	38.7	15.0	37.3
Range	18.0-34.0	3.2-4.2	8.2-11.6	2.2-3.2	4.5-8.6	25.7-43.7	13.1-29.8	32.4-40.0
Grand mean ($\bar{x}$)	26.9	3.6	10.0	2.6	6.2	34.1	19.4	36.2
SE (m) ±	3.7	0.2	0.8	0.2	0.7	4.7	3.6	2.3
CD at P ≤ 0.05	10.6	0.7	2.4	0.5	2.0	13.1	10.3	6.4
CV (%)	24.1	1.4	14.4	12.7	19.6	23.6	32.4	10.9

Appendix –III Estimates of mean values for 33 genotypes of *Brassica carinata* in pooled over the environments

Characters / Genotypes	Days to flower initiation	Days to 50% flowering	Days to 75% maturity	Plant height	Number of primary branches/ plant	Number of secondary branches/ plant	Siliquae/ plant	Length of main shoot
P-12	91.8	130.0	167.0	118.8	5.7	11.7	329.4	52.3
P-17	88.5	131.5	167.3	128.0	4.8	10.0	215.8	36.0
P-23	91.7	124.8	165.8	106.4	5.1	8.7	246.9	47.2
P-24	88.3	130.2	171.5	110.5	5.6	9.7	145.6	46.2
P-26	89.3	128.3	168.8	104.9	5.0	7.7	169.4	50.0
P-31	92.2	130.5	167.2	146.4	5.0	10.0	215.6	44.0
P-33	91.7	128.8	170.3	119.6	5.2	9.4	154.1	42.5
P-34	92.5	128.5	163.7	106.2	4.4	7.5	170.7	44.7
P-39	88.3	127.5	168.0	141.6	5.2	8.3	183.5	41.5
P-43	90.2	131.0	167.5	108.4	4.6	7.5	161.8	42.3
P-45	90.3	130.8	169.3	106.7	4.7	6.2	176.2	40.3
P-51	91.5	131.0	168.5	93.7	4.8	7.3	146.0	42.8
P-56	91.2	126.7	170.3	95.6	5.4	8.0	148.3	39.8
P-62	90.0	127.8	168.8	89.7	5.2	8.3	164.5	39.8
P-63	93.2	129.8	171.0	100.5	5.1	7.2	184.0	37.3
P-64	88.2	130.3	168.7	147.9	4.7	7.8	185.2	42.0
P-74	92.0	128.3	172.7	98.4	4.8	7.1	155.7	38.8
P-75	94.0	128.3	176.0	118.3	4.3	7.9	157.6	42.8
P-77	93.2	134.0	166.5	109.6	5.2	7.7	161.4	45.5
P-89	88.7	131.3	171.2	112.6	5.3	7.6	156.2	40.2
P-92	88.2	133.8	170.5	131.5	3.9	6.4	176.9	39.5
P-96	91.5	128.0	171.5	110.9	4.4	8.0	191.4	46.5
P-101	91.7	131.3	168.0	116.2	4.6	7.2	153.1	39.5
P-103	93.7	132.2	170.2	109.4	4.7	8.5	170.5	43.8
P-117	92.2	131.2	174.5	124.6	4.7	8.1	165.4	43.0
P-122	87.2	129.0	170.3	108.1	4.4	7.8	148.8	42.3
P-133	93.2	128.8	172.7	117.7	5.4	8.4	166.9	47.2
P-137	91.3	127.8	172.2	94.9	5.0	7.9	141.0	42.5
P-138	87.0	126.2	168.8	138.4	5.8	6.8	210.2	44.5
Nav Gold (c)	64.0	108.5	148.8	111.6	3.8	7.3	142.8	39.8
Jayanti (c)	88.8	132.5	169.0	101.3	5.3	8.8	168.1	37.8
Pusa Jaikisan (c)	67.7	110.0	149.0	107.2	4.4	7.5	165.8	34.5
RCC-4 (c)	66.2	109.8	147.7	105.2	3.8	9.1	160.7	46.7
Range	64.0-94.0	108.5-134.0	147.7-176.0	93.7-147.9	3.8-5.8	6.2-11.7	141.0-329.4	34.5-52.3
Grand mean (x̄)	88.5	127.8	167.7	113.4	4.9	8.1	175.4	42.5
SE (m) ±	2.0	1.5	1.7	7.9	0.5	0.8	19.9	2.6
CD at P ≤ 0.05	5.5	4.1	4.7	22.1	1.3	2.1	53.9	7.3
CV (%)	5.4	2.8	2.5	17.1	23.6	23.1	27.0	15.1

Characters / Genotypes	Siliquae on main shoot	Siliqua length	Seeds/ siliqua	1000- seed weight	Seed yield/ plant	Biological yield/ plant	Harvest index	Oil content
P-12	33.0	3.8	10.5	2.6	6.9	36.2	20.1	40.0
P-17	32.7	3.5	10.1	2.5	6.1	36.5	17.5	36.1
P-23	34.3	3.4	10.3	2.6	5.8	39.5	15.3	34.2
P-24	32.0	3.5	10.1	2.8	5.2	29.2	18.6	39.2
P-26	35.5	3.5	10.7	2.7	7.0	38.5	18.8	37.5
P-31	29.5	3.7	11.1	2.6	6.7	44.3	15.0	36.1
P-33	37.5	3.7	10.2	2.5	6.6	42.2	16.1	37.9
P-34	35.5	3.5	10.3	2.3	7.4	30.2	25.0	36.9
P-39	32.3	3.6	10.9	2.6	7.0	35.0	20.7	35.3
P-43	32.7	3.8	9.8	2.5	6.2	34.5	18.6	37.7
P-45	36.5	3.6	10.1	2.5	5.7	38.5	14.9	35.4
P-51	34.5	3.6	11.1	2.4	6.3	32.8	19.1	34.8
P-56	34.3	4.0	10.2	2.5	6.5	38.2	17.3	35.0
P-62	28.3	3.5	10.5	2.6	5.3	33.0	16.0	36.5
P-63	26.7	3.8	11.8	2.5	7.1	34.3	22.0	37.9
P-64	28.5	3.6	11.1	2.4	7.1	42.0	17.4	38.2
P-74	31.7	3.8	11.3	2.6	5.9	28.8	21.7	35.2
P-75	31.0	3.8	10.6	2.7	4.9	32.0	16.1	40.4
P-77	26.8	4.0	11.1	2.5	6.5	29.5	24.2	35.5
P-89	25.0	3.8	9.6	2.5	6.1	35.3	19.0	33.6
P-92	22.7	3.6	11.1	2.6	6.0	37.8	16.8	37.2
P-96	31.8	3.5	10.6	2.7	5.0	34.2	15.2	36.9
P-101	28.7	3.5	11.5	2.6	4.6	29.7	16.6	37.2
P-103	28.5	3.4	10.2	2.5	6.6	34.7	19.6	34.9
P-117	36.8	3.6	9.3	2.4	7.3	36.8	21.9	37.5
P-122	27.5	3.4	10.2	2.4	6.0	34.3	18.3	33.7
P-133	28.8	3.9	10.3	2.6	5.3	27.8	19.5	39.2
P-137	37.0	3.8	10.6	2.8	4.8	40.2	12.5	36.0
P-138	31.8	3.8	10.1	2.7	7.2	32.7	22.3	37.7
Nav Gold (c)	25.0	4.1	11.6	4.0	6.5	36.5	18.5	37.2
Jayanti (c)	26.2	3.6	9.6	2.6	5.6	30.8	19.7	39.4
Pusa Jaikisan (c)	26.5	4.0	9.8	3.8	6.6	37.3	17.9	37.5
RCC-4 (c)	31.2	4.1	11.0	3.5	6.1	39.8	15.5	37.4
Range	22.7-37.5	3.4-4.1	9.3-11.8	2.3-4.0	4.6-7.4	27.8-44.3	12.5-25.0	33.6-40.4
Grand mean ($\bar{x}$)	30.9	3.7	10.5	2.7	6.2	35.2	18.4	36.8
SE (m) ±	3.1	0.1	0.5	0.2	0.7	3.2	2.5	1.4
CD at P ≤ 0.05	8.6	0.5	0.5	0.5	1.8	8.9	7.0	4.0
CV (%)	24.5	12.2	12.4	15.9	26.1	22.1	33.2	9.6

Appendix IV

Composition of basal medium

Compounds	Concentration (mg/l)	
	MS	B$_5$
Inorganic		
NH_4NO_3	1650	-------
KH_2PO_4	170	-------
KNO_3	1900	2527.5
$MgSO_4.7H_2O$	370	246.5
$(NH_4)_2SO_4$	-------	134
KCl	-------	150
$CaCl_2.2H_2O$	440	150
KI	0.83	0.75
H_3BO_4	6.2	3.0
$MnSO_4.4H_2O$	22.3	-------
$MnSO_4.H_2O$	-------	10
$ZnSO_4.7H_2O$	8.6	2
$Na_2MoO_4.2H_2O$	0.25	0.25
$CuSO_4.5H_2O$	0.025	0.025
$CoCl_2.6H_2O$	0.025	0.025
$FeSO_4.7H_2O$	27.8	-------
$Na_2.EDTA.2H_2O$	37.3	-------
Sequestrene 330 Fe$_4$	-------	28
Organic		
a) Vitamins		
Inositol	100	100
Nicotinic acid	0.5	1.0
Pyridoxine HCl	0.5	1
Thiamine HCl	0.1	10
b) Amino acid		
Glycine	2	-------
L-Glutamine	-------	-------
L-Serine	-------	-------

- MS- Murashige, T. and Skoog, F. 1962. Plant Physiology. 15: 473-497.
- B$_5$- Gamburg,O.L., Miller, R.A. and Ojima, K. 1968. Experimental Cell Res. 50: 151-158.

Appendix V

Weather data during *rabi,* 2010-2011 at Palampur

Parameters	Month	Oct., 2010	Nov., 2010	Dec., 2010	Jan., 2011	Feb., 2011	Mar., 2011	Apr., 2011
Temperature	Max. (^{0}C)	25.6	22.9	18.3	15.2	16.9	22.6	25.2
	Min. (^{0}C)	13.3	9.4	4.8	3.5	6.6	10.2	13.1
Relative Humidity (%)		79-59	74-48	71-47	71-51	74-58	66-44	69-46
Rainfall (mm)		32.9	5.2	91.2	65.0	139.4	45.3	90.7

Weather data during *rabi,* 2011-2012 at SAREC, Kangra

Parameters	Month	Oct., 2011	Nov., 2011	Dec., 2011	Jan., 2012	Feb., 2012	Mar., 2012	Apr., 2012
Temperature	Max. (^{0}C)	29.8	25.8	21.8	16.8	18.2	25.8	30.7
	Min. (^{0}C)	15.7	10.1	5.0	4.0	6.8	10.0	16.0
Relative Humidity (%)		90-48	91-49	92-41	93-60	93-74	91-73	83-43
Rainfall (mm)		7.3	0.0	0.0	191.6	46.0	33.5	54.0

Brief Biodata of the Student

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Academic Qualifications:

Examination passed	Year	School/Board/ University	Major Subjects
10th	2003	Shri Bhanoba Vidyalaya, Kusegaon.	Marathi, Hindi, English, Maths, Science, Social Sciences
10+2	2005	Gopinath Vidyalaya, Varavand.	English, Marathi, Geography, Physics, Chemistry, Biology
B.Sc. (Agriculture)	2009	Late Dadasaheb Patil College of Agriculture, Dahegaon.	All Agriculture and Allied subjects
M.Sc. (Agri.) Plant Breeding and Genetics	2012	CSK Himachal Pradesh Agriculture University, Palampur (H.P.), India	Major Discipline: Plant Breeding and Genetics Minor Discipline: Plant Pathology