GENETIC EVALUATION OF LINSEED (*Linum usitatissimum* L.) GERMPLASM FOR MORPHOLOGICAL CHARACTERS

THESIS

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Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
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By

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DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the thesis entitled **"GENETIC EVALUATION OF LINSEED (*Linum usitatissimum* L.) GERMPLASM FOR MORPHOLOGICAL CHARACTERS"** or part thereof has neither been submitted for any other Degree or Diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged.

Place: Nagpur **(BIJJAM CHANDRA VEERA KUMAR REDDY)**

Date: 17/10/2022 Enrolment No: OO/629

CERTIFICATE

This is to certify that thesis entitled **“GENETIC EVALUATION OF LINSEED (*Linum usitatissimum* L.) GERMPLASM FOR MORPHOLOGICAL CHARACTERS”** submitted in partial fulfilment of the requirement for the degree of **"Master of Science in Agriculture (Agricultural Botany)"** of Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola is a record of bonafide research work carried out by Bijjam Chandra Veera Kumar Reddy under my guidance and supervision.

The subject of the thesis has been approved by the Student's Advisory Committee.

Place: Nagpur

Date: 17/10/2022

Dr. Beena M. Nair
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THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE INCLUDING EXTERNAL EXAMINER (AFTER VIVA -VOCE)

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Place: Nagpur **(Bijjam Chandra Veera Kumar Reddy)**

Date: 17/10/2022

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(C) Abbreviations

%	:	Per cent
CAN	:	Agriculture College Nagpur
AGE	:	Agarose Gel Electrophoresis
AICRP	:	All India Coordinated Research Project
ALA	:	Alfa Linolenic Acid
C.D.	:	Critical difference
C.V	:	Coefficient of variation
cm	:	Centimeter
$\overline{D}$	:	Inter cluster distance mean
d.f	:	Degrees of freedom
D/W	:	Distilled Water
et al.	:	et alia (and associates)
etc.	:	Et cetera
g	:	Grams
Gy	:	gamma rays
h^2	:	Heritability
i.e.	:	that is
Kg ha^{-1}	:	Kilogram per hectare
LA	:	Linoleic Acid
m ha	:	million hectare

m t	:	million tones
MMT	:	Million Metric Tonnes
mm	:	millimetre
MY	:	Marketing Year
No. / no.	:	Number
PCV	:	Phenotypic coefficient of variation
$Plant^{-1}$	:	per plant
$Plot^{-1}$	:	per plot
RIL	:	Recombinant Inbred Line
S.D.	:	Standard Deviation
S.E (m)±	:	Standard error
viz.,	:	Namely
σ^2 g	:	Genotypic variance
σ^2 p	:	Phenotypic variance

(D) **THESIS ABSTRACT**

a) Title of the thesis	:	"GENETIC EVALUATION OF LINSEED (*Linum usitatissimum* L.) GERMPLASM FOR MORPHOLOGICAL CHARACTERS"
b) Full name of student	:	BIJJAM CHANDRA VEERA KUMAR REDDY
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ABSTRACT

One hundred and seventy eight genotypes were evaluated for genetic divergence to identify potential parents for linseed programme aimed for yield improvement in *rabi*. Mahalanobis D^2 statistics for eleven characters viz. days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1}, number of capsule plant^{-1}, seed yield plant^{-1} (g), 1000 seed weight (g), % bud fly infestation, % alternaria blight infestation, powdery mildew (score), flower size (mm), were used in this study for computing genetic divergence. The analysis of dispersion for eleven characters using Wilk's criterion, revealed highly significant difference between genotypes for all eleven characters. The one hundred seventy eight genotypes were grouped into thirteen clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster XII and XIII (D^2=40.20) and in between cluster VII and XII (D^2=37.76) whereas minimum inter cluster distance was found in between cluster V and cluster VI (D^2=7.39) .The canonical analysis revealed that differentiation for eleven characters among one hundred and seventy eight genotypes was completed in five phases indicated the importance of number of capsule plant^{-1}, days to 50% flowering, seed yield plant^{-1} for selecting parents . The canonical analysis and cluster means studied together revealed the importance of days to 50% flowering, number of capsule plant^{-1}, seed yield plant^{-1}, plant height, days to maturity as an important contributing characters towards the total divergence. Hence, these traits form the criteria for the selection of parents for hybridization programme.

The parents EC0041764, EC0041726, EC0001465, EC0001403, EC0541211, EC0541224, EC0041598, EC54225, EC41562, EC004140 are significantly superior over the checks for seed yield plant^{-1}. On the basis of the present study, It will be advisable to utilize all these parents in hybridization for improvement of bud fly resistance and seed yield in linseed.

CHAPTER I

INTRODUCTION

1.1 Background information

Linseed (*Linum usitatissimum* L.) belongs to genus *Linum* of the family Linaceae. The somatic chromosome number of the cultivated species is 2n=30. It is a multipurpose crop valued for its seed oil, fiber, probiotic and nutraceutical properties. It is a crop adopted to different environments and agro ecologies. *Linum* is the largest genus of family Linaceae with about 200 species displaying great diversity in Karyotype. Linnaeus in 1857 was first to give a botanical name *Linum usitatissimum* L**.** to the cultivated species. *Linum usitatissimum* L. is the only species with non-dehiscent or semi-dehiscent capsules suitable for modern cultivation of the family Linaceae (Getinet and Nigussie,1997). The origin of Indian type of linseed is traced to be in Ethiopia, though polyphyletic origin of the same is indicated. According to Vavilov linseed was probably native of Southwest Asia consisting of India, Afghanistan, and Turkey. Among the oilseed crops grown during rabi, Linseed (*Linum usitatissimum* L.) is next important to rapeseed and mustard in area as well as in production. *Linum usitatissimum* L. is an annual, self-pollinating and non-edible oil crop. It occupies a greater importance among oil seeds owing to its various uses and qualities.

India is the largest producer of oilseeds in the world and oilseed sector occupies an important position in the agricultural economy of the country. Oilseeds are among the major crops that are grown in the country apart from cereals. In terms of acreage, production and economic value, these crops are second only to food grains. India is the fifth largest vegetable oil economy in the world, next only to USA, China, Brazil, and Argentina. The diverse agro-ecological conditions in the country are favourable for growing eight annual oilseed crops, which include eight edible oilseeds (groundnut, rapeseed & mustard, soybean, sunflower, sesame, safflower, and Niger) and two Nonedible (Linseed and Castor). Linseed is an important industrial and edible oil and fiber producing crop.

All parts of plant have extensive and varied uses. Linseed oil is extensively used in the industry for the manufacturing of high quality paints and varnishes. It is also used for making oil cloth, printers' ink, soap, patent leather, antibiotic, and other products. Out of total linseed oil, 20% is used for edible and domestic purpose and rest of 80% goes for industrial utilization. The oil and protein per cent in the seed of linseed varies from 37.8 to 43.2 and 20.0 to 27.8, respectively. The residue cake, remaining after oil extraction, contains about 9.7 per cent oil, 32% carbohydrate and 32% protein. It is very rich proteinaceous feed for livestock and quick growing animals. Linseed oil is unique among oilseeds as it has high content of omega -3 fatty acids (57%) and omega -6 fatty acids (8%).

This crop is grown for fiber (fiber flax), seed oil (linseed) or both seed oil as well as fiber (example: dual purpose flax linseed). Linseed stem yields good quality fiber having strength and durability. Linseed is produced for natural textile fiber (Linen) or for oil for industrial application as well as for culinary purpose. Fiber diameter ranges from 10 to 12 cm. Fiber length ranges from 1 to 120 mm (Tamms, 1907). The fiber is lustrous and blends very well with wool, cotton, silk etc. The fiber extracted from straw is used in paper industry for high grade writing paper, stamp paper, parchment paper and cigarette paper. The fiber threads are strong and are used for sewing, linen fabrics, fish sieve lines and shoe threads. The coarse grades are used for making twines, ropes, geotextiles, canvas bags, decorative items, foot mat. Linseed is a good source of calcium and phosphorus with their contents as 170 and 370 mg/100 grains, respectively.

India has the greatest acreage under linseed than any other country in the world, but in respect of total production, it ranks third after Argentina and Canada due to its low productivity. In India the principal linseed growing states are Madhya Pradesh, Uttar Pradesh, Maharashtra, Chhattisgarh, Bihar and Orissa. The major causes behind low production are due to cultivation of linseed mainly in marginal / sub-marginal lands suffered with disease, insect-pests problem and also poor crop management. It is grown as an utera crop after paddy in Eastern Vidarbha with minimum or zero inputs.

India has largest area under linseed and stands first position followed by Canada, China, USA. India has third position in production.

Area, Production and Productivity of linseed during 2021

Season	Year/Region (2021)	Area (ha)	Production (tons)	Productivity (Kg/ha)
Rabi	**World**	30.6 lakh	31.56 lakh	1031
	India	183000	111000	605
	Maharashtra	5160	1499	267
	Vidarbha	4847	1292	323

(Anonymous 2021)

Around the globe this important crop occupies an area of 30.6 lakh ha yielding 31.56 lakh tones with an average productivity of 1031 kg hectare^{-1} in the world. In our country the crop occupies 183,000 ha with production of 111,000 tons culminating in low productivity of 605 kg hectare^{-1} in the committee of growing nations. (Annual Report, Linseed 2021). India contributes about 10.81 % and 5.3% to world area and production respectively. In Maharashtra it is cultivated mainly in Bandara, Gonidia, Chandrapur, Gadchiroli, Wardha, and some regions of Latur, Nagpur and Solapur districts with an area of 5160 hectares with production of 1499 tons and having productivity of 267 kg hectare^{-1}. In Vidarbha region it occupies 4847 hectares with production of 1292 tons and having productivity of 323 kg hectare^{-1}.

The study of diversity among the available germplasm is useful to plan Linseed breeding programme because success of breeding programme depends on selection of superior lines of diverse origin. The development of linseed varieties with high yield potential land high oil content assumes greater importance in linseed Improvement programme. Therefore, the information on genetic variation for yield and yield related agronomical characters is prerequisite to initiate the linseed breeding programme for development of varieties with high yield potential.

The productivity of linseed is very low in India because it acts as host to number of diseases and generally raised as a mixed crop in rainfed marginal lands. The significant yield losses occur in linseed due to bud fly (*Dasyneura lini*) (20-97%), alternaria blight (*Alternaria lini*) and powdery mildew (*Odium lini*) (up to 60%). Leaf infection causes 27 to 60 percent losses, bud infection causes losses up to 90 percent. The loss due to Alternaria is 28-60 %. Therefore, there is a need to develop varieties resistant to pests and diseases to stabilize the yield potentials of linseed varieties (Reddy *et al.* 2013).

Gene bank collections are sources of diverse germplasm collection such as land races, wild relative, commercial, obsolete and elite varieties, pure and breeding lines, mutants, polyploids and hybrids. The available germplasm serves as most valuable natural reservoir in providing donor parents for incorporating or imparting the characteristics by genetic reconstruction of plant for developing high yielding crop varieties (Hawkes, 1981). Therefore, collection, conservation and evaluation of germplasm is essential for present as well as for future crop improvement (Vavilov, 1951, Harlan, 1956). The proper evaluation of germplasm is essential for understanding its potential value as a breeding material, as the success of any breeding programme depends upon nature and extent of variability present in germplasm collection. Scientific studies needs to be done to identify donor germplasm for different traits which breeder can exploit to improve cultivars for future climatic adaptations.

It is revealed that in Linseed crop high estimates of phenotypic and genotypic coefficient of variations for number of capsules plant^{-1} also, high heritability estimates coupled with high genetic advance were recorded for fiber length and seed yield plant^{-1} .The result of the earlier studies on germplasm evaluation, variability, and genetic divergence in linseed are relevant only for materials and environments of the particular study due to their non-consistent nature and cannot be generalized. Linseed genotypes showed a wide fluctuation in their performance, when grown under varied agro-climatic conditions (Mathur *et al*.,1984; Reddy, 1982, Chiu,1981; Pandey *et al*., 1970; Negi and Kinga,1959 and Sahay,1957). Some of the genotypes perform well over wide range of environments, while others require specific environmental conditions to express their genetic potential, emphasizing immense use of screening a large number of genotypes.

The genetic improvement of linseed is expected through production breeding which requires precise information on the nature and degree of genetic variability present in linseed germplasm. Exploration from its principal areas of adaptation / cultivation which would help in understanding the evolutionary mechanism involved in intraspecific divergence and choice of desirable parents for evolving superior varieties are the major tasks before linseed breeders. Diverse germplasm is of digital importance and genetic improvement in yield and quality is possible only when there exists enough genetic variability which obviously reflects through phenotype of individual that have a sound base for the selection. Apart from it, the knowledge of most heritable traits and correlation are also helpful for increasing the yield. The identification of donor parent for important characters, assessment of genetic variation in the available germplasm and information about character association are required to device a successful breeding programme. Keeping these views, the present investigation has been planned to obtain information on genetic variation, and genetic divergence for yield and yield components in linseed.

1.2 Importance of study

Linseed oil plays a major role in catering edible oil as well as industrial demand of the country. In India farmers are still cultivating land races and local varieties of linseed which are highly susceptible to diseases and pests resulting in very poor yields, so there is a need of producing high yielding varieties with early maturity and high oil content. The aim of plant breeder is to achieve the high yielding, early maturity and disease resistant strains which are superior to those of existing strains. So, study of genetic evaluation, genetic diversity and multivariate analysis research are critical for successful evolution of genotypes having desirable characters.

1.3 Objectives of study

In view of all these facts large number of germplasm lines (178) was evaluated in the present investigation with the following objectives:

1) To assess the genetic diversity among the germplasms in linseed.
2) To study contribution of characters towards genetic diversity.
3) To identify genetically diverse genotypes.

1.4 Scope and limitations

This research work on genetic evaluation of linseed has wide scope in developing the new varieties of linseed with high yield. As existence of genetic variability in the population is prerequisite for planning any breeding programme. This study helps in estimation of extent of variability in the population. The study of genetic divergence among the set of available genotypes will be useful to plan hybridization program, because success of hybridization program depends upon the selection of suitable parents of diverse origin. The development of variety for higher seed yield and oil yield with resistance or tolerance against biotic or abiotic stress than the existing varieties is the main aim of linseed breeding.

The limitations faced during the implementation of this research work were

1. Genetic evaluation on large number of plants has to be handled.
2. Maintaining and recording of observations on such a large population was difficult

1.5 Hypothesis

D^2 Statistics will be helpful in grouping the genotypes into distinct clusters to enable the choice of parents for hybridization programme and further crop improvement. It will also be useful to quantify genetic diversity existing among genotypes and to identify genetically diverse genotypes.

CHAPTER II

REVIEW OF LITERATURE

Plant breeder is mainly concerned with quantitative characters showing continuous variation such as yield. As such inheritance of these have attracted the attention of biometricians. To breed better crops with higher yield, the breeder should select on the sliding scale of ever changing environment. Further, yield is a complex end product of action and interaction of vital activities of plant throughout the life cycle and is controlled by numerous factors shaped by genetical and environmental factors. Among these factors, most important is the inherent potential of the plants to produce higher yields, which depend up on the hereditary makeup of the plant. Therefore, for rational improvement of crop, understanding of the magnitude of genetic variability and extent to which the desirable characters are heritable becomes essential.

The relevant literature pertaining to these types of studies in respect of linseed is reviewed in this chapter. A brief account of the research work carried out and published by previous workers on genetic studies in *Linum usitatissimum* L. is reviewed as under.

Adugna and Labuschagne (2003) evaluated multivariate cluster and canonical variate analysis for 10 genotypes of linseed. Cluster analysis grouped the genotypes into 5 classes in accordance to their original sources. The six locations and eighteen environments were stratified in four and seven clusters, respectively. Days to flowering, maturity, oil content and lodging percent played major role in discriminating the genotypes. Comparison of the two methods showed clear differentiation by cluster analysis than canonical variate analysis. Canonical variate analysis also contributed information on how each variable discriminated the genotypes and their test environments. It is useful for efficient variety development programmes.

Negash *et al.* (2005) studied morphological studies of linseed (*Linum usitatissimum* L.) on 56 accessions collected from ten administrative regions (former regions) classified into seven altitude classes. The seeds were planted during 2001 in randomized complete block design (RCBD) with three replications with the aim of investigating the morphological diversity in the accessions. Over the entire accession, except seed number per boll, all the characters showed significant variation. However, regional groups of linseed accessions showed insignificant variations only for secondary branches number plant^{-1} (SBP), days to flowering (DTF) and days to maturity (DTM) among themselves, and altitudinal groups of linseed accessions only for seed number per boll (SNB) and days to flowering (DTF). Cluster analysis indicates that accessions collected from the two extremes of altitude classes have variations for the studied traits.

Begum *et al.* (2006) studied the D^2 analysis on the 36 genotypes / varieties of linseed grouped them into five distinct clusters. The cluster I included 11 genotypes that had medium mean values for 1000 seed weight (g) and seed yield plant^{-1}. The cluster II contained six genotypes, which had the highest mean values for number of seeds capsule^{-1}, number of branches plant^{-1} and seed yield plant^{-1}. They also showed the highest mean value for plant height. The cluster III had maximum number of genotypes 15, which had the highest mean value for 1000 seed weight (g). It is also related with medium mean values for rest of the characters. The cluster IV included three genotypes having the highest mean values for number of capsules plant^{-1} and days to maturity. The cluster V included single genotype, which had the lowest mean values for days to maturity and plant height. The highest inter cluster distance was observed among clusters V, IV and II, while the lowest between III and I. The highest intra cluster distance was observed in cluster III that revealed maximum variability within the clusters. In this study, two traits such as number of branches plant^{-1} and number of seeds capsule^{-1} contributed the maximum towards divergence in the existing germplasm.

Patial *et al.* (2011) studied the genetic diversity among 34 linseed (Linum usitatissimum L.) genotypes were studied using, 18 agro morphological traits as per the standard descriptors of DUS, UPOV 2011 at the experimental farm of the Department of Crop Improvement, CSKHPKV, Palampur. Six genotypes were found to be distinctive on the basis of morphological traits. Results revealed that sufficient genetic variability was observed for all the characters studied based on various genetic variability parameters. Principal component analysis (PCA) indicated that, out of total principal components, three PCs contributed 71.60% to the total variance amongst the genotypes assessed for nine agronomic traits. PC I contributed maximum towards the variability (36.91%) followed by PC II (22.15%) and PC III (12.54%). Cluster analysis clearly differentiated 34 genotypes into three clusters with cluster III having highest 15 genotypes. Sufficient variability was observed in the genotypes studied based on phenotypic and genotypic variance, principal component analysis and cluster analysis which could be utilized by researchers, in breeding programme and the genetic distinctiveness in the genotypes can be protected under PPVFRA.

Reddy *et al.* (2013) screened the genotypes on field conditions to evaluate genotypes for resistance to bud fly, alternaria blight and powdery mildew. The results revealed that the pest and diseases for parents ranged from 11.39 (EC544) to 59.54 (ES44) and 5.34 (Neelum) to 17.68 (ES44) for bud fly and alternaria blight. Among the hybrids Padmini x Ayogi and PKVNL - 260 X EC9825 were found to be resistant to bud fly infestation and Alternaria infestation. PKVNL - 260, PKDL18, KL178, LCK8605, A125, Karthika x Ayogi, Padmini x Ayogi, PKV-NL 260 x ACC NO4/47 and Padmini x ACC NO4/47 were found to be resistant to powdery mildew under field conditions and therefore, have the potential to reduce the yield losses because of these diseases and pest in the field.

Khan (2013) studied a set of 55 linseed accessions including a check variety (Chandni) under rainfed conditions during three crop seasons i.e., 2008-09, 2009-10 and 2010-11. Data were recorded for days to flower initiation, flower completion, maturity, reproductive period, plant height, branches plant-1, bolls per plant, plot biomass, harvest index and seed yield. Wide ranges between the mean values with high CV values were exhibited by plant height, bolls per plant, biomass and seed yield accompanied with maximum values of variances and standard deviation, revealed the existence of greater genetic diversity in the accessions for these traits. Dendrogram based on Euclidean distance coefficient using 10 quantitative traits, grouped all the linseed accessions into 13 clusters. Cluster II was the biggest and had 33 accessions followed by Cluster I having 11 accessions. For the development of high yielding varieties, best performing accessions of Clusters I and II could be used in hybridization programme by crossing with accessions of Clusters VII, VIII, IX and X followed by selection in segregating populations.

Ravindra *et al. (*2014) conducted experiment using 151 genotypes / varieties of diverse origin in randomized block design with two replications at Nawabganj, Research form of the Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *rabi* 2014-15. Observations were recorded on eleven characters namely, days to 50% flowering, size of corolla, number of primary branches plant^{-1}, plant height, capsule size, days to maturity, number of capsules plant^{-1}, number of seeds capsule^{-1}, 1000 seed weight, oil content and grain yield plant^{-1}. Genetic divergence suggested that cross between the genotypes of II and XIII clusters may give better results during hybridization programme. Based on magnitude of D^2 values, 151 genotypes of linseed were grouped into thirteen clusters. The distribution of genotypes in both the environments was different. Maximum genotypes (21) were present in cluster-XIII. The perusal of Table-1, 2, 3, 4 & 5 revealed that the maximum inter cluster distance was observed between cluster-II and cluster-XIII (271.45) indicated wide diversity between these groups.

Hybridization among the genotypes separated by high inter cluster distance will result in most heterotic crosses. The estimates of genetic divergence for most of the characters under study are in accordance with earlier reports. The maximum intra cluster distance was observed for cluster-XII (47.45) followed by cluster-II (45.80) and cluster-I (38.76). The maximum intra cluster value indicated maximum divergence among various genotypes within the cluster. A comparison of cluster means for eleven characters under study revealed considerable genetic differences between the clusters regarding one or more characters. The maximum character contribution towards divergence was observed for plant height (15.12 %) followed by days to 50 % flowering (14.69 %) and size of corolla (13.22).

Dikshit *et al.* (2015) studied 111 accessions of linseed germplasm belonging to 32 districts of six states (Bihar, Chhattisgarh, Himachal Pradesh, Jharkhand, Madhya Pradesh and Maharashtra) in India were characterized for five qualitative and six quantitative traits. Significant variability was observed in the agro morphological and qualitative traits in to two major clusters were formed when the characterization data was subjected to Ward's minimum variance method. DIVA-GI approaches for the analysis of the diversity in linseed germplasm were mapped for quantitative traits such as plant height, number of capsules plant^{-1} and seed oil content.

Dhirhi *et al.* (2016) concluded that the characterization and evaluation data is of greatest importance to realize the potential of flax in agriculture. In linseed, large number of germplasms are available with greater similarity for their plant structure as well as for blue flower so at this real use of DUS is very much applicable. Therefore, looking to these facts present study was based on DUS characterization of 150 diverse line including exotic and indigenous accessions of linseed, which were taken from AICRP on Linseed, Department of Genetics and Plant Breeding IGKV, Raipur (C.G.), India during *rabi* 2014-15. Observations were recorded as per DUS, UPOV 2011.The morphological traits were evaluated as per Distinctiveness, Uniformity and Stability (DUS) guidelines. Yield contributing characters like plant height, time of flowering, capsule size, seed size and 1000 seed weight showed variation and most of the lines comes under medium category as 79%, 43%, 52%, 77%, 43% respectively. The molecular descriptors developed here will be useful for genetic mapping and selection of breeding lines. The results showed the range of characters which can be exploited inbreeding lines appropriate for small holder and commercial farmers in, producing a sustainable, secure, high value crop meeting agricultural, economic and cultural needs.

Paul *et al.* (2016) analysed thirty two genotypes for nine morphological traits in RCBD replicated two times in two consecutive years (E-I, E-II) to investigate the genetic diversity pattern. Field data of two consecutive years were initially subjected to analysis of variance. There were highly significant ($p \leq 0.01$) differences among the genotypes for all the traits at both environments except for seeds capsule^{-1}, indicating the presence of adequate variability among the genotypes and the possibility to undertake cluster analysis. Moreover, genotypes responded differently to change in the environmental conditions at the two environments, as genotype × environment interaction mean squares were highly significant ($p \leq 0.01$) for all the traits. The phenotypic divergence and relative importance were estimated by multivariate analysis. The cluster analysis based on Tocher's method classified the genotypes into eight (E-I) and six (E-II) major groups of different sizes during both the years. The maximum distance was found between clusters V and VII (E-I) and between clusters IV and V (E-II). The genotypes from these clusters can be utilized for the improvement of linseed yield and obtaining good segregants in linseed breeding programs. In both the years, 1000 seed weight contribute maximum in E-I (93.55%) and E-II (91.33%) total genetic divergence between genotypes.

Riviz *et al*. (2016) studied 166 germplasm of linseed (*Linum usitatissimum* L.) including three checks, to assess the extent and pattern of genetic divergence. The experiment was conducted in Augmented Design II (AD-II) at Sam Higginbottom University of Agriculture, Technology and Sciences Allahabad (U.P) India during rabi 2016-2017. The genetic diversity was estimated by Mahalanobis D^2 statistics and the genotypes were grouped into 13 clusters using Tochers method each clusters having 15,3,11,20,4,11,14,17,16,19, 15,9 and 12 genotypes respectively. The highest intra-cluster distance was found in cluster III followed by in descending order cluster II, IV, I and V, suggesting possibility of easy trait manipulation between these genotypes for linseed improvement. Cluster IV, XIII, VII and VI showing the highest mean for primary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsule^{-1} and seed yield plant^{-1}, appears a desirable parent. Principle component analysis (PCA) showed the first four PCs had eigen value >1.00 and accounted more than 71.84% of total variation. The predominance nature of yield contributing traits like number of primary branches plant^{-1}, number of capsules plant^{-1} and number of seeds capsule^{-1}, indicated that these components were proven more important and crossing between and / or within cluster may give good recombinants for linseed improvement.

Choudhary *et al*. (2016) studied 160 linseed accessions and analysis of variance revealed significant difference among genotypes for all the twelve characters studied. Non-hierarchical Euclidean cluster analysis grouped germplasm into thirteen different clusters. Maximum inter cluster distance was observed between cluster XI and cluster IX (913.221) followed by clusters IX and IV (869.117) while, lowest divergence was noticed between cluster II and I (103.402). Among the twelve characters studied, number of capsules plant^{-1} contributed highest towards genetic divergence (35.76%), followed by plant height (26.84%). Cluster XI exhibited highest means for days to 50% flowering (90.97), plant height (65.778), test weight (8.686) and biological yield (16.123). Cluster IX exhibited lowest means for plant height (35.592), harvest index (17.256), and test weight (6.680). Greater genetic divergence was found between XI and IX followed by clusters IX and IV indicating superior and novel recombinants and explore the fullest range of variability for the characters and to realize good recombinant can be released by mating between the lines of these clusters in a definite fashion.

Bhajantri *et al*. (2017) found that the characters, days to 50% flowering, plant height, biological yield plant^{-1} and capsules plant^{-1} contributed more than 86% of the total genetic divergence. Mahalanobis D^2 statistics revealed considerable genetic diversity among the genotypes. The 35 genotypes grouped into six clusters. Genotypes belonging to cluster III (A-49, L-14, A-449, A-434 and 5620-A) exhibited maximum genetic diversity within the cluster as compared to the genotypes belonging to other clusters. Hence, hybridization could be taken up among these genotypes for obtaining desirable sergeants for the yield and yield component traits. On the basis of high inter cluster distance, hybridization programme could be taken up between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster IV (LC-185, A-385 and LC-2063) and also between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster VI (A-404, L-108, ARNY and NP-23K) for expecting the transgressive sergeants vice versa chance for selecting genetically variable genotypes for improvement in linseed.

Kumar *et al.* (2017) revealed that the characters like, days to 50% flowering, plant height, biological yield plant^{-1} and capsules plant^{-1} contributed more than 86% of the total genetic divergence. Mahalanobis D^2 statistics found that considerable genetic diversity among the genotypes. The 35 genotypes grouped into six clusters. This envisaged that the genotypes grouped within a particular cluster are more or less genetically similar to each other and apparent wide diversity is mainly due to the remaining genotypes distributed over rest of the other clusters. Genotypes belonging to cluster III (A-49, L-14, A-449, A-

434 and 5620-A) exhibited maximum genetic diversity within the cluster as compared to the genotypes belonging to other clusters. Hence, hybridization could be taken up among these genotypes for obtaining desirable segregants for the yield and yield component traits. On the basis of high inter cluster distance, hybridization programme could be taken up between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster IV (LC-185, A-385 and LC-2063) and also between the varieties of cluster II (A-210, Banner, A-10-2-2 and 191 RR 9/2) and cluster VI (A-404, L-108, ARNY and NP-23K) for expecting the transgressive sergeants visa-vis a chance for selecting genetically variable genotypes for improvement in linseed.

Bhajantri *et a*l. (2017) conducted experiment based on DUS characterization of thirteen diverse line including exotic and indigenous accessions of linseed. The seed materials were collected from AICRP on linseed, PC Unit, Kanpur. The genotypes used for the study were 1) Jeevan, 2) Ruchi, 3) Pratapalsi 4) Parvati, 5) Meera, 6) Rashmi, 7) Shikha, 8) Nagarkot, 9) Gaurav, 10) Jrf-1, 11) Jrf-3, 12) Jrf-4, 13) Pcl-16-2. Observations were recorded as per DUS, UPOV 2011.The morphological traits were evaluated as per Distinctiveness, Uniformity and Stability (DUS) guidelines. Yield contributing characters like plant height, time of flowering, capsule size, seed size and1000 seed weight showed variation and most of the lines come under medium category as 69.23%,76.92%,53.84%,100% and 69.23%, respectively. The results showed the range of characters which can be exploited in breeding lines appropriate for smallholder and commercial farmers in, producing a sustainable, secure, high value crop meeting agricultural, economic and cultural needs.

Chandrawati *et al.* (2017) was conducted research to evaluate genetic diversity and patterns of relationships among the 58 genotypes through ten morphological traits and twelve polymorphic microsatellite (SSR) markers. Euclidean analysis of agro-morphological traits grouped the 58 genotypes into four clusters of which cluster I was the largest with 20 accessions while clusters II and IV were most genetically diverse due to maximum inter cluster distance. The most diverse genotypes identified in this study can be used in breeding programs to broaden the genetic base of the linseed germplasm.

Satyendra *et al.* (2018) analysed 66 linseed genotypes, along with three check varieties (T-397, Mukta and Hira) were analysed for genetic diversity by Mahalanobis D2 statistics. Presence of diversity pave way for exploitation of genotypes in breeding programme intended to improve yield and yield attributing traits. The cluster analysis grouped 66 linseed genotypes into 9 distinct clusters. Genotypes group ed into cluster II were showed maximum intra cluster diversity while cluster V showed minimum intra-cluster diversity. The maximum inter cluster diversity was observed between cluster VIII and V while minimum inter cluster diversity was observed between cluster IV and III. From cluster mean value, genotypes in cluster VI, VII and IV deserve consideration for their direct use as parents in hybridization programs to develop high yielding linseed varieties. Thus, hybridization among these cluster pair recommended for getting high transgressive segregants in F_2 generation.

Paul and Kumari (2018) studied genetic variability and divergence studies among 18 genotypes of Linseed. The cluster analysis grouped the genotypes in to 2, 3 and 3 clusters in Env.I, Env.II and pooled over the environments, respectively indicating that clustering pattern was different in Env. I. Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and release of desirable recombination segregating generations. Therefore, in Env. I, parents should be selected from cluster combination from clusters I and II, in Env. II and in pooled over the environments from clusters I and III. The character 1000 seed weight contributed maximum towards total genetic divergence in Env.I, Env.II and in pooled over the environment among 18 genotypes under study.

Kaur *et a*l. (2018) evaluated 191 accessions of linseed germplasm in Augmented Block Design with three check varieties Rashmi, Surabhi, and RLC76 randomized in seven blocks consisting of 27 accessions each. Descriptive statistics, Principal component analysis (PCA) and Ward's agglomerative hierarchical clustering were done. Wide range of phenotypic expression for important agro morphological traits was observed in linseed germplasm. PCA identified days to flowering, plant height, thousand seed weight, seed weight and seed yield and seed size as the most important traits responsible for variation in the germplasm accessions. Custer analysis grouped the accessions under four major clusters which indicated fair association of genetic diversity and geographical diversity. Few traits specific promising accessions such as EC0718827 (tall, large corolla), and EC0718835 (high seed yield plant^{-1}) were identified with high estimates of heritability for the mentioned traits. The inter relationships between the traits suggested that accessions with short flowering and maturity duration, low plant height, large bolls and bold seeds should be given priority in breeding for enhanced yield. Donors for various traits were identified which may be used in future linseed breeding to target yield enhancement and diverse geographical adaptation.

Thakur *et.al* (2019) conducted experiment by using 30 genotypes of linseed germplasm in randomized block design with three replications during *rabi* 2019 to assess the extent of genetic diversity. As per the results obtained, cluster analysis grouped whole germplasm into VI clusters. Cluster II was the largest with ten linseed accessions and cluster I was smallest with single accession. The inter cluster distance was the farthest between cluster I and cluster VI (D2=7.143) followed by cluster I and III (D^2 =7.134) depicting greater genetic divergence among clusters. The intra-cluster distance ranged from 2.066 in cluster II to 2.776 in cluster IV. The contribution of days to maturity (11.08%), technical height (10.63%) and seed per capsule (9.66%) towards genetic divergence were higher.

Dinsa (2019) carried out to assess the genetic variability and association among quantitative traits of 36 linseed genotypes. The experiment was conducted in 2018 main cropping season by using simple lattice design. The analysis of variances revealed highly significant difference among the genotypes for most of traits considered in present study. Cluster analysis revealed that 36 linseed genotypes were grouped into two clusters and four genotypes remain ungrouped. The maximum inter cluster distance was observed between cluster II and the cluster I. The data set was reduced into four significant principal components (PCs) that comprise (80%) of the variance.

Thakur *et al.* (2019) conducted an experiment to study the nature and magnitude of genetic variability with a view to identify promising genotypes for yield and related traits in linseed. Eighteen diverse linseed (*Linum usitatissimum* L.) genotypes were evaluated in randomized block design in three replications during *rabi* 2019-20 for twelve agro morphological characters to assess the genetic parameters of variability. Analysis of variance indicated presence of a wide range of genetic variability among genotypes for all the traits.

Ankit *et al*. (2019) conducted studies to know the character association and genetic divergence analysis in linseed (*Linum usitatissimum* L.). The analysis of genetic divergence among 40 genotypes of linseed was carried out by Mahalanobis D^2 statistics. The clustering was done by Ward method. The forty genotypes of linseed were grouped into seven clusters. Cluster III was the largest, followed by cluster II, cluster V, cluster IV, cluster I and cluster VI and cluster VII respectively. The maximum intra cluster distance was observed in cluster VII followed by cluster VI, cluster V, cluster IV, cluster III, cluster I and the minimum intra cluster distance was observed in cluster II. Maximum genetic diversity within the cluster was observed in cluster VII (LCK-283 and LCK-206) as compared to the genotypes belonging to other clusters. The maximum inter cluster distance was observed between cluster I and VI having greater genetic divergence between the genotypes belonging to these clusters.

Patial *et al.* (2019) studied genetic diversity among 34 linseed genotypes using, 18 agro morphological traits. Cluster analysis showed 34 genotypes of linseed into three clusters. Each cluster contained genotypes that were highly similar. Cluster I consisted of 14 genotypes followed by cluster II (05), cluster III (15) genotypes. Cluster I had highest values for plant height followed by capsules per plant^{-1} and oil content, cluster II showed highest values for plant height followed by capsules plant^{-1} and technical height and cluster III showed highest value for capsule plant^{-1}, plant height, oil content and technical height. Cluster analysis revealed wide range of genetic divergence, which is useful for future hybridization programme for getting desirable transgressive segregants.

Singh *et al.* (2019) estimated the genetic diversity among the forty genotypes of linseed (*Linum usitatissimum* L.) during *rabi* season in Randomized Complete Block Design (RBD) with three replications. Each treatment was grown in 3 m long double row plot spaced 30 cm apart. The plant-to-plant distance was maintained at 10 cm through proper thinning. Based on D^2 value the forty entries were grouped into seven distinct clusters, indicating the presence of diversity for different traits. The highest number of genotypes appeared in cluster III, which possessed fourteen genotypes, followed by ten genotypes in cluster IV and five in cluster VI. Cluster I and cluster II comprised of four genotypes each. Cluster V has two and Cluster VII only one genotypes. The maximum intra cluster distance was obtained for cluster VI however the highest inter cluster D^2 values was observed between cluster V and cluster VII, indicating the existence of wide genetic variability.

Samantara *et al*. (2020) evaluated 55 linseed genotypes to determine genetic diversity by Mahalanobis D^2 statistics during *rabi* at the Department of Plant breeding and Genetics, Orissa University of

Agriculture and Technology, Odisha India. It revealed that 55 genotypes were grouped into eleven clusters. Result envisaged that genotypes grouped within a particular cluster are more or less genetically similar. Genotypes grouped into cluster I were showed maximum intra cluster diversity while maximum inter cluster diversity was observed between cluster XI and V followed by cluster XI and X. So, it could be suggested that hybridization program involving genotypes from the farthest diverse clusters (Cluster XI and V and cluster XI and X) are likely to achieve wider and desirable heterotic recombinants or even transgressive segregants.

Pallavi *et al.* (2021) carried out the present investigation with 60 genotypes including 4 checks (Kiran, Deepika, Padmini, and Indira Alsi) and 56 entries. The experiment was laid down in medium black soil under rainfed conditions during rabi season with augmented block design comprising seven blocks, each block consists of eight genotypes with four checks total of 12 plots. The linseed was classified into 5 clusters. Cluster I was the largest, containing of 18 genotypes followed by cluster IV comprising 17 genotypes, cluster V with 13 genotypes, cluster II comprising 7 genotypes, while cluster III with 5 genotypes. The highest intra cluster distance was recorded for cluster III (2123.64) (46.08), followed by cluster V (1640.66) (40.50), cluster II (1572.96) (36.66), cluster IV (1539.42) (39.23), while the lowest intra cluster distance was observed for cluster I (1411.20) (37.56). highest inter cluster distance was recorded between cluster II and III, followed by clusters III and V, cluster III and IV, cluster I and II, cluster I and V, cluster I and III, cluster II and IV, cluster I and IV, cluster II and V, while the lowest inter cluster distance was observed between cluster IV and V. Genotypes in cluster I demonstrate largest genetic diversity within the cluster be comparable to the genotypes be the member of other clusters. Thus, hybridization can be taken among all these genotypes to getting useful in F_2 generations for the yield and yield contributing characters.

Thakur *et al*. (2021) studied variability and genetic diversity to identify suitable and diverse parents for realizing high heterotic effects with transgressive segregants in later generations. Field experiment was conducted using 30 genotypes of linseed germplasm in randomized block design with three replications during *rabi* to assess the extent of genetic diversity. As per the results obtained, cluster analysis grouped whole germplasm into VI clusters. Cluster II was the largest with 10 linseed accessions and cluster I was smallest with single accession. The inter cluster distance was the farthest between cluster I and cluster VI (D^2 =7.143) followed by cluster I and III (D^2 =7.134) depicting greater genetic divergence among clusters. The intra-cluster distance ranged from 2.066 in cluster II to 2.776 in cluster IV. The contribution of days to maturity (11.08%), technical height (10.63%) and number of seeds capsule^{-1} (9.66%) towards genetic divergence were higher.

Hussain *et a*l. (2022) conducted experiment to assess the genetic variability in linseed germplasm and identify some promising lines of linseed. The study was designed with a total of 82 germplasm and a national check in RCBD for genetic variability for 11 agronomic traits. In this study, a considerable variation was observed for all the studied traits by using PCA analysis. It was also found that single plant yield, number of seeds capsule^{-1}, and number of capsules are ideal for linseed improvement through the selection in central India. Few high yielding accessions such as RL-10129 and Padmini showed maximum diversity with the popular variety T-397 and can be used in the hybridization program. Similarly, we identified a few potential accessions such as NDL-2013-03, EC-41741, Ruchi, EC-704, RL-10129 to be used as parents in the breeding program. A considerable variation in flowering time was observed (42 - 69 days) in the germplasms. Four genotypes showed early flowering than popular check variety T-397, which flowered in 51 days. The study found a considerable variation amongst the germplasms for number of capsules plant^{-1} was much higher in the germplasm (up to 66 capsules plant^{-1}, e.g., Rashmi) compared to T-397 (33 capsules plant^{-1}). The hierarchical cluster analysis following Ward's method resulted in 10 clusters (Table 3 and Figure 3). Cluster III was the largest cluster consisting of 25 lines, followed by cluster II (10 lines) and cluster V (10 lines). Cluster VI had only three genotypes, all high yielding lines, EC-41741, NDL-2013-03, and Shikha. All early flowering and maturing lines, e.g., EC-704, EX313-23, FRW-9, and RLC-140, were grouped into cluster VII (flowering 42.69 - 47.61 and maturity 85.7 - 104.5). Cluster IX had the highest cluster mean for seed yield plant^{-1} (2.76 g) followed by cluster VI (2.14 g) and cluster X (2.12 g), whereas cluster IX had the highest number of capsules plant^{-1} (57.16) followed by cluster X (47.13). Cluster IV exhibited the lowest means for seed yield plant^{-1} (~1.07 g) and number of capsules plant^{-1} (~29.84) (Table 3). The popular check variety (T-397) was grouped into cluster III. The Euclidean distance matrix identified the most diverse genotypes among the linseed germplasm and the most similar and diverse genotypes to the popular variety (T-397). Rashmi was the most diverse (8.6) than T-397, while SLS-95 (1.8) was the most similar genotype with T-397. Among the 82 genotypes, the most diverse pair of accessions was RL-10129 and Padmini, with 11.02. The top ten most diverse pairs of accessions.

Hanuman *et al.* (2022) studied morphological characters of linseed namely days to the first flower (33 to 40days), days to 50% flowering (first 50% flower from 46 to 52 days), height of plant (55 to 77.75 cm), number of primary branches plant^{-1} (branches varied from 2.00 to 7.00), number of capsules plant^{-1} (ranged from 26.5 to 67.50), number of seeds capsule^{-1} (ranged from 7.5 to 10.00 seeds per capsule), 1000 seeds weight (g) (from 5.52 to 8.68g), colour of flower (white and blue) were recorded. The dendrogram produced from linseed genotypes show three main cluster a limited number of entries comprising of the national check, zonal check, and local check. The eleven lines were grouped into 2 clusters and three out groups. The least similarity observed between genotype OL 10-2 and JLS 95 (ZC), NL 356 and T 397 (NC) was found to be only 12% similar and higher similarity observed between genotype SLS 122 and SLS 121 was found to be 88%

similar. Cluster I consisted of 14 genotypes, cluster II of 05 and cluster III of 15 genotypes. All these entries are evaluated in a randomized block design with three or four replications at the different locations.

CHAPTER III

MATERIAL AND METHODS

The present research work entitled “Genetic Evaluation of Linseed Germplasm for Morphological Characters" was conducted during *rabi* season at AICRP on Linseed and Mustard farm, College of Agriculture, Nagpur. The material used and methodology followed in this research work are described below:

3.1 Materials required

The material required in this experiment consisted of 178 germplasm of linseed. The list of which are given below.

Table 1: List of the germplasm

Sr. No.	Name of germplasm	Sr. No	Name of germplasm
1	EC1066	90	EC0012538
2	EC1386	91	EC0041762
3	EC1424	92	EC0541196
4	EC14539	93	EC0000526
5	EC1474	94	EC0115174
6	EC1588	95	EC0001437
7	EC1628	96	EC0399086
8	EC1645	97	EC0041687 – A
9	EC41623	98	EC0041672
10	EC45890	99	EC0541227
11	EC41659	100	EC0009827
12	EC41741	101	EC0541205
13	EC51904	102	EC0541212
14	EC 98994	103	EC0541223
15	EC 001457	104	EC0541226
16	EC 990017	105	EC541194
17	EC0041672 – 1	106	EC0541218
18	EC0001459	107	EC0541226

19	EC0041528	108	EC0001419
20	EC0520246	109	EC0022872
21	EC0001432	110	EC0000541 – A
22	EC0001550 -B	111	EC0041621
23	EC0041601 – A	112	EC054119
24	EC0110474	113	EC541196
25	EC0541213	114	EC0001388
26	EC0041753	115	EC0041650
27	EC0541215	116	EC0000522
28	EC0006160	117	EC0541210
29	EC0718850	118	EC0399082
30	EC0520247	119	EC0541220
31	EC0022388	120	EC041667
32	EC0041562	121	EC0041621 – B
33	EC41466	122	EC0041737
34	EC0541213	123	EC0041400
35	EC0541215	124	EC0001443
36	EC0541218	125	EC0000531 – A
37	EC0541202	126	EC0041467
38	EC0001005 – B	127	EC00414678 – B
39	EC0001395	128	EC0041700
40	EC0041547 – A	129	EC0041768
41	EC0541194	130	EC244634
42	EC0399084	131	EC0541211
43	EC0118743	132	EC0041653
44	EC000545	133	EC0001475
45	EC0001476	134	EC0023208
46	EC0041723	135	EC0399085
47	EC0041720	136	EC0022813 – B
48	EC0041646	137	EC0041755
49	EC0000543	138	EC0041478
50	EC0541195	139	EC0718852
51	EC0541198	140	EC0000538
52	EC0041735	141	EC0011748

53	EC0001403	142	EC0041647
54	EC0041601 – A	143	EC0541219
55	EC0001551	144	EC0001465
56	EC0041774 – A	145	EC0041726
57	EC0041469	146	EC054214
58	EC0041687	147	EC0455084
59	EC0041607 – 2	148	EC0718826
60	EC0718831	149	EC22648
61	EC0718825	150	EC0002711
62	EC0001395 – 1	151	EC0041535
63	EC0001433	152	EC0541201
64	EC0041615	153	EC0541217
65	EC0041649	154	EC0718823
66	EC0041622	155	EC718846
67	EC0541203	156	EC0541204
68	EC0041579	157	EC0718824
69	EC041643	158	EC0541216
70	EC0041764	159	EC22813
71	EC0718845	160	EC0718834
72	EC0115148	161	EC541206
73	EC0541207	162	EC718830
74	EC0041765	163	EC718835
75	EC000564	164	EC0718842
76	EC0041582	165	EC0718843
77	EC0041598	166	EC0718847
78	EC00411623	167	EC0001451
79	EC0041644	168	EC80490
80	EC0041758	169	EC0041734
81	EC0110289	170	EC0080490
82	EC0158985	171	EC0001396
83	EC0541224	172	EC0718827
84	EC541225	173	EC0718851
85	EC0041495 – 1	174	EC0541208
86	EC004181	175	EC0041619

87	EC0718828	176	EC0718848
88	EC0718829	177	TL 99 (Check)
89	EC0541213	178	PKV-NL-260 (Check)

3.2 Methods adopted

3.2.1 Experimental Detail

The above listed 178 germplasm of linseed were raised in augmented block design. The detailed of the experiment in *rabi* are as follows.

3.2.2 Treatment Details

Design of Experiment	Augmented block design
Number of germplasms	176 + 2 checks
Spacing	30cm X 5 cm
Number of rows	1
Number of plants /row	20
Number of observational plants	5
Checks used	TL 99, PKV -NL 260
Date of sowing	29/11/2021
Time of harvesting	As per maturity

All the recommended package of practices and plant protection measures were taken as per the schedule to raise a healthy crop.

3.2.2.1 Quantitative traits

1. Days to 50% flowering (plot wise)

The date on which 50% of the plants in each plot flowered was recorded and number of days required for 50%flowering from the date of sowing were calculated.

2. Days to maturity (plot wise)

Days to maturity was calculated by recording the dates taken by the plot to reach physiological maturity from the date of sowing.

3. Plant height at maturity (cm)

The height of plant from the base to the tip of the main stem was recorded in centimeters on randomly selected plants and mean plant height /plant calculated & plant height divided into 3 classes namely, long (>70cm), medium (51-70cm), short (<51).

4. Number of primary branches plant^{-1}

The number of primary branches were recorded on the main stem of the five randomly selected plants and mean primary branches plant^{-1} were calculated.

5. Number of capsules plant^{-1}

The number of capsules of five randomly selected plant were counted prior to harvest and mean number of capsules plant^{-1} was recorded.

6. Seed yield plant^{-1} (g)

The seed yield obtained from five randomly selected plants were weighed in gram separately on precision electronic balance and mean seed yield plant^{-1} was calculated.

7. 1000 seed weight (g)

Weight of 1000 well developed grains collected from the bulk of plants selected was recorded and expressed in grams. According to weight, it is grouped in 3 classes viz. high (>8g), medium (6-8g), low (<6g).

8. Bud fly infestation (%)

Individual plant was scored for bud fly infection. In each plant buds infected by bud fly (*Dasyneura lini*) were counted and percentage was taken from the total number of buds as follows (Anonymous, 2021).

$$\text{Bud fly \%} = \frac{\text{Infected buds}}{\text{Total no. of buds}} \times 100$$

9. Alternaria blight infestation (%)

Infected buds by *Alternaria lini* were counted in each plant and percentage was taken from the total number of buds (Anonymous, 2021).

$$\text{Alternaria blight \%} = \frac{\text{Infected buds}}{\text{Total no. of buds}} \times 100$$

10. Powdery mildew (Score)

Each plant was scored visually in the field and plants were rated in 0 to 5 scale as shown in the table. Based on the visual score of disease incidence the mean score was determined (Anonymous, 2021).

Score	Bud infection %	Disease reaction	
0	0%	immune	Free
1	0-10%	Resistant	R
2	10.1-25%	Medium Resistant	MR
3	25.1-50%	Medium susceptible	MS
4	50.1-75%	susceptible	S
5	above 75%	Highly susceptible	HS

11. Flower size (mm)

It is recorded in peak flowering, measured as the distance from petal to petal recorded in millimeter. This characters were categorized into 3 classes, viz. large (>20mm), medium (15-20mm), small (<15mm). [3- Small, 5- Medium, 7- Large]

3.2.2.2 Qualitative traits

Observations were also recorded for nine morphological qualitative traits by giving scores according to standard DUS descriptors of linseed as given in the parentheses. For the assessment of DUS descriptors.

1. Colour of corolla

It scored in fully opened flower by visual observation. It is classified into 6 groups as blue, tinge blue, lilac, white, light violet blue, red violet. [1- White, 2- Blue, 3- Violet, 4- Red violet]

2. Flower venation colour

It is recorded in fully developed flower. It is grouped into 3 classes as, blue, violet, white, light violet. [1- White, 2- Light violet, 3- Violet, 4- Blue]

3. Flower aestivation

It is recorded as arrangement of petals. According to this, it is grouped into 3 classes viz. semi twisted, twisted and valvate. [1- Twisted, 2- Semi-twisted, 3- Valvate]

4. Anther colour

Anther colour showed a continuous range of colour variation as, blue, violet, creamy, grey. [1- Cream, 2- Grey, 3- Violet, 4- Blue]

5. Stamen: colour of distal part of filament

It is recorded after flower opening. On the basis of distal part of filament colour, it is grouped into 3 categories viz. blue, violet, white. [1- White, 2- Violet, 3- Blue]

6. Flower shape

It must be recorded be forenoon. Flower shape are grouped in 4 groups namely, funnel, star, disk, tubular form. [1- Funnel, 2- Star, 3- Disc, 4- Tubular]

7. Capsule dehiscence

It is recorded at the maturity time. It is grouped into 3 classes as, Dehiscent, Semi Dehiscent and Non Dehiscent. [3- Semi Dehiscent, 5- Non-dehiscent]

8. Plant growth habit

It is recorded considering both the angle of the basal branching and the crop canopy. It is classified into 3 groups viz. erect, semi-erect and bushy. [3- Bushy, 5- Semi-erect, 7 - Erect]

9. Seed colour

It is recorded as visual observation. It is grouped in 4 categories viz. fawn, brown, dark brown, light brown and yellow. [1- Fawn, 2- Yellow, 3- Light brown, 4 - Brown, 5- Dark brown

3.3 Statistical analysis

The data were subjected to the following statistical and biometrical analysis.

1. Analysis of variance
2. Wilk's criterion
3. Estimation of D^2 values

4. Grouping of genotypes into different clusters
5. Canonical analysis
6. Average intra and inter cluster distance and mean
7. Selection of parents for hybridization programme

i) Analysis of variance

The analysis of variance for augmented design was carried as per the method suggested by Federer (1961). The generalized form of analysis of variance for an augmented design with one way elimination of heterogeneity is presented in table 3.2. For analysis of data generated from augmented design we obtain block totals, control treatment totals and means, block effects, general mean effect, control treatment effects and adjusted data for test treatments.

Table 2: Analysis of variance for Augmented design with one way elimination of heterogeneity

Source of variation	d.f	Sum of squares	Mean squares
Blocks (Ignoring treatments)	r – 1	SSB	--
Treatments eliminating blocks	(a+b) – 1	ASST	--
Checks	b – 1	SSc	--
Checks + Var vs. Var	A	SSn	--
Error	(b –1) x (r – 1)	SSE	MSE
Block eliminating (Check +Var)	r – 1	--	--
Entries (Ignoring blocks)	a + b – 1	SSB	--
Checks	b – 1	SSc	--
Varieties	a – 1	SSn	--
Checks vs Varieties	1	--	--
Error	(b –1) x (r – 1)	SSE	MSE

Where,

r = Number of blocks

a = Test treatments (recombinant lines)

b = Control treatments (Checks)

SSB (Block sum of squares) = Sum [(Block total)]^2 / No. of observations in a block – C.F.

TSS (Total sum of squares) = Sum of squares cell observation in raw data – C.F.

ASST (Treatments sum of squares) = m x grand total + sum of blocks effects and (eliminating blocks) totals + sum of test effects and observed values - sum [(block total)]^2 / No. of observations in a block]

Where,

m = adjusted general mean

SSE (Error sum of squares) = Total S.S – ASST-SSB

SSC (Control sum of squares) = Sum [(control)^2 / No. of rep.] – (control grand total)^2 /control No. x No. of rep.

Standard error:

Four kinds of standard errors for comparing mean difference are as follows.

1. Between two control treatment mean S.E. (1) = $\sqrt{\frac{2\ MSE}{r}}$
2. Between two test treatments in same block S.E. (2) = $\sqrt{2\ MSE}$
3. Between two test treatments not in same block S.E. (3) = $\sqrt{2\ MSE\ (1 + \frac{1}{b}})$

4. Between test treatments and a control treatment S.E. (4) = $\sqrt{MSE(1+\frac{1}{r}+\frac{1}{b}+\frac{1}{br})}$

ii) Wilk's criterion

Analysis of variance were carried out for all the characters X_1 to X_{11}. Estimates of variance and covariance components were provided by the linear functions of the mean squares and mean products. The phenotypic variance (σ^2p) was made up of genetic (σ^2g) and environmental (σ^2e) variance. By using this relationship, estimates of genetic and environmental components of phenotypic variance were obtained. The covariance analysis of data obtained for any two traits were carried out according to the same scheme as that of analysis of variance, which gives estimate of genetic and environmental components of phenotypic covariance. A matrix of 11 x 11 dispersion matrix (of genotypic variance and covariance) was used for the simultaneous test of significance for differences in the mean values of the nine characters (X_1 –X_{11}) based on Wilk's criterion as described by Rao (1952).

Where,

$$\wedge = \frac{\text{Determinant of error variance and covariance matrix}}{\text{Determinant of (genotype + error) variance and covariance matrix}}$$

The determinants were obtained by following the pivotal condensation method and multiplying each of the pivotal elements of the corresponding matrices further 'V' statistics will be calculated as below.

'V' (stat) = - m loge $\wedge$

$$m = \frac{n - (p + q + 1)}{2}$$

Where,

p = number of characters

q = number of genotypes – 1

n = df. for error + for genotypes

e = 2.7183

The calculated 'V' (stat) were tested at pq df. at 5 per cent level of significance.

iii) Estimation of D^2 values

The inverse matrix of original genotypic variance, covariance matrix were computed to derive the relationship by which the original character mean (X_1 – X_{11}) were to an uncorrelated set of variables Y_1 – Y_{11}. In terms of variance and covariance, the D^2 values were obtained as suggested by Mahalanobis, 1936.

$$pD^2 = \sum_{i=1}^{p} \sum_{j=1}^{p} W^{ij} \; (x_i^{-1} - x_i^{-2}) \; (x_j^{-1} - x_j^{-2})$$

Where,

X_i^{-1} and X_i^{-2} = The mean of i^{th} character for first and second genotype respectively.

X_j^{-1} and X_j^{-2} = The mean j^{th} character for first and second genotype respectively.

W^{ij} = inverse of variance and covariance matrix

The D^2 values obtained for a pair of populations were taken as the calculated value of x^2 and were tested against the tabulated value of x^2 for 'p' degree of freedom, where 'p' is the number of characters.

iv) Grouping of genotypes into different clusters

The grouping of genotypes were done by Tocher's method described by Rao (1952). The criteria used in clustering were belonging to same cluster should at least on an average show a smaller D^2 values than those belonging to different clusters.

v) Canonical analysis

Canonical root method suggested by Rao (1952) were followed. The matrix of variances and covariance (matrix A) were obtained by calculating between group of sum squares and sum of products from the transformed variables (Y_1, Y_2, ……. Y_{11}). Determination of the canonical variates were done by interaction starting with trial vectors (1, ……..., -1) each row of the matrix were multiplied and a derived vector which was a better approximation was obtained. This procedure were repeated until stable values of the vector were obtained. The highest value used in the last stage of division to obtain the final vector should be λ_1, the first canonical root The vector was standardized by dividing each element by square root of the sum of squares of all the elements. From the (i, jth) elements of the matrix A, the product λ_1, X_i^{th} element X_j^{th} element of the first vector were subtracted to obtain the reduced matrix (matrix B). The procedure followed in the case of matrix A were repeated to obtain the second and third canonical roots.

vi) Average intra and inter cluster distance and means

The average intra cluster distance (D^2) was obtained by using following formula.

Average intra cluster distance in $D^2 = \frac{\sum_{i=1}^{n} \mathbf{D_i^2}}{n}$

Where,

$\Sigma \mathrm{D_i}^2$ = the sum of distance between all possible combination (n) of genotypes involved in a cluster.

The average inter cluster distance between cluster i and j

$$D^2 = \frac{\sum D_i^2}{n_i \, X \, n_j}$$

Where,

$\sum D_i^2$ = Sum of distance between the genotypes.

n_i = no of genotypes in cluster i

n_j = no of genotypes in cluster j

vii) Selection of parents for hybridization programme

Selection of parents for hybridization from different clusters were done on the basis of mean statistical distance as suggested by Bhatt (1970).

$$\overline{D} = \frac{\sum n_i}{\frac{n(n+1)}{2}}$$

Where,

$\overline{D}$= mean statistical distance

n_i = sum of all D^2 values between all intra and inter cluster

n = no. of clusters

The crosses between parents belonging to different cluster having same or higher inter cluster distance than the mean statistical distance were selected for them in hybridization programme.

Implications

This study will be helpful in selecting potential and better parents in linseed for their use in hybridization programme.

CHAPTER IV

RESULTS AND DISCUSSION

The present investigation entitled "Genetic evaluation of linseed germplasm for morphological characters" was carried out to estimate the genetic diversity among 178 genotypes. The results obtained from this work are presented and discussed in this chapter under the following sub heads: -

4.1 Analysis of variance.

4.2 Mean performance of the genotypes.

4.3 Wilk's criterion and D^2 statistics.

4.4 Contribution of different characters towards diversion.

4.5 Grouping of genotypes into different clusters.

4.6 Canonical analysis.

4.7 Average intra and inter cluster distances and means

4.8 Selection of parents for hybridization programme

4.1 Analysis of variance for experimental design

The data were subjected to analysis of variance to study the genetic differences among 178 genotypes for eleven traits. The results are presented in Table 2.

Data from Table 2 shown that the analysis of variance for augmented design were highly significant for all eleven characters studied *i.e*. days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1}, number of capsule plant^{-1}, seed yield plant^{-1}(g), 1000 seed weight (g), bud fly infestation (%), alternaria blight infestation (%), powdery mildew infestation (%) , flower: corolla size (mm) indicating the presence of considerable genetic variation among the genotypes for the characters studied.

4.2 Mean performance of genotypes.

It is seen from Table 3 the mean squares due to the genotypes were highly significant for all eleven characters studied *i.e*. days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1}, number of capsule plant^{-1}, seed yield plant^{-1} (g), 1000 seed weight (g), bud fly infestation (%), alternaria blight infestation (%), Powdery mildew infestation (%),flower: corolla size (mm) indicating the presence of considerable genetic variation among the genotypes for the characters studied.

The data of 2021-22 indicated the presence of considerable genetic variation among the genotypes for character studied. This allows the further estimation in the experimental material. The wide variability for yield contributing characters in linseed were observed by the Dhirhi *et al*. (2016)

Choudhary *et al*. (2017) observed the analysis of variance due to genotypes for all characters studied were found to significant except number of seeds capsule^{-1} and number of primary branches plant^{-1}.

Bhajantri *et a*l. (2017) observed the analysis of variance was found highly significant for the yield contributing characters like capsule size, seed size,1000 seed weight, time of flowering.

Paul and Kumar (2018) observed the analysis of variance were highly significant among the genotypes for all the characters indicating sufficient variability in the present material selected thus indicated the scope for selection of suitable initial breeding material for crop improvement.

Thakur *et al*. (2019) observed the analysis of variance revealed highly significant among the treatments for all the characters studied.

Pallavi *et al*. (2021) from the analysis of variance in augmented block design observed highly significant and showed genetic diversity within the clusters.

Table 2: Analysis of variance for Augmented design with one way elimination of heterogeneity

Source of variation	d.f	Mean sum of squares				
		Plant height (cm)	No. of Capsules $Plant^{-1}$	No. of Branches $Plant^{-1}$	Flower size (mm)	Alternaria Infestation %
Blocks (Ignoring treatments)	7	84.78**	4918.16**	14.05**	522.04**	20.03**
Treatments (eliminating blocks)	177	52.77**	860.74**	3.56**	4.50**	2.85**
Checks	1	100**	2332.90**	14.06**	1.00	0.90
Checks + Var vs. Var	176	52.50**	852.37**	3.50**	4.52**	2.86**
Error	7	1.98	88.29	1.06	1.14	0.20
Block (eliminating (Check +Var)	7	17.12**	26.68	0.99	2.11	2.08**
Entries (Ignoring blocks)	177	55.45**	1054.19**	4.07**	7.37**	3.56**
Checks	1	100**	2332.90**	14.06**	1.00	0.90
Varieties	175	50.61**	1026.33**	4.01**	7.44**	3.42**
Checks vs Varieties	1	856.95**	4650.06**	5.411	1.05	30.14**
Error	7	1.98	88.29	1.06	1.14	0.20

Table 2: Continued….

Source of variation	d.f	Mean sum of squares					
		Bud Fly Infestation %	Powdery Mildew infestation %	Days to Maturity (days)	Days to 50% flowering (days)	1000 seed weight (g)	Seed yield $Plant^{-1}$ (g)
Blocks (Ignoring treatments)	7	465.83**	76.40**	229.86**	269.18**	3.40**	4.15**
Treatments (eliminating blocks)	177	41.11**	47.34**	18.11**	15.04**	0.91**	0.79**
Checks	1	13.51**	49**	36.30*	25**	7.43**	3.61**
Checks + Var vs. Var	176	41.27**	47.33**	18.01**	14.98**	0.87**	0.78**
Error	7	0.16	7.86	3.052	0.28	0.04	0.21
Block (eliminating (Check +Var)	7	1.2**	6.72	26.45**	9.00**	0.05	0.30
Entries (Ignoring blocks)	177	59.48**	50.09**	26.16**	25.32**	1.04**	0.95**
Checks	1	13.51**	49*	36.30*	25**	7.43**	3.61**
Varieties	175	54.94**	46.4**	26.02**	24.24**	0.85**	0.93**
Check vs Varieties	1	900.52**	697.13**	40.26**	216.18**	27.64**	1.19*
Error	7	0.16	7.86	3.05	0.28	0.04	0.21

* Significant at 5%

** Significant at 1%

4.2 Mean performance of the genotypes

1. Plant height at maturity (cm)

The data on mean value for plant height at maturity ranged from 40.38 cm to 76.58cm. The range for plant height (cm) at maturity was 36.20 cm. The genotype EC041643 (76.58 cm) was tallest followed by EC054214 (74.88 cm) and the genotype EC0001457 (40.38 cm) was shortest followed by EC0041753(41.58) cm.

2. Number of capsules plant^{-1}

The data on mean value for number of capsules plant^{-1} ranged from 28.03 to 183.03. The range for number of capsules plant^{-1} was 155.The genotype EC0041764 (183.03) was found to have maximum followed by EC0041598 (174.93) and the genotype EC0001457 (28.03) was minimum followed by EC0001432 (29.43).

3. Number of primary branches plant^{-1}

The data on mean value for number of branches plant^{-1} ranged from 3.01 to 14.41. The range for number of primary branches plant^{-1} was 11.4. The genotype EC0718848 (14.41) was maximum followed by EC0541227 (11.41) and the genotype EC0541213 (3.01) was minimum followed by EC0399086 (3.11).

4. Alternaria infestation %

The data on mean value for alternaria infestation % ranged from 0.26 % to 9.61 %. The range for alternaria blight infestation% was 9.35%. The genotype EC0041735 (9.61%) was maximum followed by EC0000541-A (7.76%). and the genotype EC0541215, EC0006160 (0.26%) was minimum followed by EC0041672-1 (1.16%) EC0541205 (1.56%).

5. Bud fly infestation %

The data on mean value for bud fly infestation % ranged from 3.56 % to 43.76%. The range for bud fly infestation % was 40.2%. The genotype EC0000543 (43.76%) was maximum followed by EC0541208 (40.46%). and the genotype EC0041562 (3.56%) was minimum followed by EC0541218 (4.06%) EC0041400 (4.96%).

6. Powdery mildew infestation %

The data on mean value for powdery mildew infestation % ranged from 4.05% to 43.45%. The range for powdery mildew infestation% was 39.4%. The genotype EC0718845 (43.45%) was maximum followed by EC0023208 (39.45%).and the genotype EC0541216 (4.05%) was minimum followed by EC0000541-A (6.05%) EC0718824 (8.05%).

7. Days to 50% flowering

The data on mean value for days to 50% flowering ranged from 47.00 to 73.80 days. The range for number of days to 50% flowering was 26.8 days. The genotype EC071885 (73.80 days) attained late flowering followed by EC0718828 (69.50).and the genotype EC054202 (47.0 days) attained earliest flowering followed by EC0399084 (49.0 days) EC0541215 (49.70 days), EC0541218 (49.70 days), EC0541223 (49.70 days).

8. Days to maturity

The data on mean value for days to maturity ranged from 99.51 to 123.46 days. The range for number of days to maturity was 23.95 days. The genotype EC0041755 (99.51 days) matured earliest followed by EC00000538, EC0023208, EC0022813-B (101.21 days), and the genotype EC0718829 (123.46 days) attained late maturity followed by EC0041619 (122.46 days).

9. 1000 seed weight (g)

The data on mean value for1000 seed weight ranged from 6.14 to 10.99 g. The range 1000 seed weight was 4.85g. The genotype EC0001403 (10.99 g) had maximum 1000 seed weight followed by PKV-NL 260 (10.83 g), EC0718824 (10.24 g).and the genotype EC0041753 (6.14 g) had minimum followed by EC000545 (6.54 g).

10. Seed yield plant^{-1} (g)

The data on mean value for seed yield plant^{-1} ranged from 0.60 to 5.85 g. The range for seed yield plant^{-1} was 5.25g. The genotype EC0041726 (5.85 g) was maximum followed by EC0041764 (5.65 g), EC0041400 (4.25 g). and the genotype EC80490 (0.60 g) was minimum followed by EC1588, EC 1628 (0.70 g).

11. Flower: size of corolla (mm)

The data on mean value for flower: size of corolla ranged from 10.9 mm to 27.9 mm. The range for flower: corolla size was 17mm. The genotype EC0541196 (27.9 mm) was largest flower size followed by EC45890, EC41659, EC41741 (25.9 mm) and the genotype EC0718829 (10.9 mm) was shortest followed by EC0718828 (11.9 mm), EC 0541207 (14.4 mm).

From above observations it is concluded that the genotype EC0541215 had shown minimum alternaria blight infestation% and earliest flowering, the genotype EC0718824 had shown less powdery mildew infestation% and maximum 1000 seed weight, the genotype EC0023208 shown early maturity and maximum powdery mildew infestation%, the genotype EC0718828 had shown shortest flower size and attained late flowering, the genotype EC0718829 had shown shortest flower size and late maturity, the genotype EC0001457 had shown shortest plant height and minimum number of capsules, the genotype EC0000541-A had shown less powdery infestation % and 7.06% alternaria blight infestation %.

Table 3: Adjusted mean performance of 176 genotypes and 2 checks for eleven quantitative characters

Sr. No	Name of the genotype	Plant height (cm)	No.of capsules plant^{-1}	No.of branches plant^{-1}	Alternaria infestation %	Bud fly infestation %
1	EC1066	60.88	70.93	4.91	2.36	16.66
2	EC1386	64.38	31.73	6.91	2.76	17.96
3	EC1424	66.18	46.53	5.71	2.86	8.76
4	EC14539	64.58	44.73	4.91	2.26	23.26
5	EC1474	61.08	55.13	4.91	2.06	15.86
6	EC1588	68.18	96.93	6.11	4.86	11.76
7	EC1628	71.58	63.13	5.91	3.96	10.66
8	EC1645	63.18	49.93	5.11	2.76	15.96
9	EC41623	64.88	43.73	9.31	2.06	12.26
10	EC45890	61.58	83.93	7.51	3.46	26.26
11	EC41659	63.58	57.33	4.91	3.76	13.96
12	EC41741	60.58	46.73	5.31	4.06	10.96
13	EC51904	61.88	44.13	4.11	4.36	14.26
14	EC98994	62.58	63.53	6.91	4.26	11.66
15	EC99001	60.18	74.93	5.71	3.26	16.06
16	EC0012538	51.08	60.33	4.91	2.86	16.16

17	EC0041762	62.38	37.53	4.71	2.86	16.66
18	EC0541196	47.68	48.73	6.11	4.66	16.46
19	EC0000526	44.68	43.73	4.51	4.06	17.26
20	EC0115174	53.88	55.13	4.91	4.96	15.96
21	EC0001437	44.68	75.53	6.11	3.66	16.66
22	EC0399086	54.88	32.13	3.11	4.26	18.26
23	EC0041687 – A	53.58	65.63	9.21	2.66	23.16
24	EC0041672	56.08	81.43	9.21	2.16	39.36
25	EC0541227	66.08	55.63	11.41	3.16	14.16
26	EC0009827	55.08	123.23	7.31	2.26	17.86
27	EC0541205	62.18	76.63	10.01	1.56	21.66
28	EC0541212	54.58	95.23	10.41	2.66	27.06
29	EC0001457	40.38	28.03	5.21	3.16	7.36
30	EC0041672 – 1	49.08	98.03	7.21	1.16	10.86
31	EC0001459	59.08	79.03	6.81	1.36	8.66
32	EC0041528	51.18	68.63	5.81	3.26	10.16
33	EC0520246	52.38	107.43	5.41	2.26	9.16
34	EC0001432	57.58	29.43	6.41	3.46	4.66
35	EC0001550 -B	52.18	75.63	6.21	1.56	9.56

36	EC0041601 – A	50.88	74.23	4.61	1.26	21.06
37	EC0110474	52.08	49.63	4.61	3.16	8.06
38	EC0541213	54.08	59.63	5.01	4.16	9.56
39	EC0041753	41.58	80.63	7.21	2.06	11.86
40	EC0541215	47.38	53.43	7.01	0.26	9.86
41	EC0006160	52.38	109.43	10.41	0.26	8.36
42	EC0718850	72.68	46.43	5.21	0.36	6.66
43	EC0520247	49.68	89.03	9.61	2.76	16.06
44	EC0022388	61.08	41.23	4.81	0.46	6.86
45	EC0041562	51.68	47.13	3.11	6.46	3.56
46	EC41466	51.38	61.33	4.51	6.26	10.36
47	EC0541213	57.38	98.53	4.11	2.36	11.66
48	EC0541215	59.08	105.73	7.71	3.16	10.16
49	EC0541218	73.18	129.73	4.11	2.16	4.06
50	EC0541223	64.08	85.73	5.11	4.16	11.16
51	EC0541226	51.08	105.13	6.11	4.26	9.86
52	EC541194	56.88	114.93	7.71	3.96	12.16
53	EC0541218	72.18	129.53	5.71	3.16	6.66
54	EC0541226	47.38	57.13	8.71	4.36	9.86

55	EC0001419	49.58	119.53	3.51	4.66	13.16
56	EC0022872	62.58	58.53	5.51	5.06	10.16
57	EC0000541 – A	58.38	67.73	4.31	7.76	19.06
58	EC0041621	51.18	99.93	7.11	3.36	6.86
59	EC054119	54.58	131.73	6.11	7.56	13.86
60	EC541196	51.18	99.93	7.51	4.06	13.16
61	EC0001388	47.18	117.13	5.11	7.66	8.06
62	EC0041650	54.68	84.53	5.31	6.76	17.36
63	EC0000522	45.18	89.73	4.11	5.06	15.06
64	EC0541210	46.38	89.93	4.51	4.06	13.16
65	EC0399082	67.18	100.13	5.11	5.06	16.86
66	EC0541220	57.08	105.53	7.11	3.06	12.06
67	EC041667	67.38	79.13	6.11	7.21	17.46
68	EC0041621 – B	58.18	103.73	5.11	5.21	12.56
69	EC0041737	68.68	106.13	6.91	3.41	18.56
70	EC0041400	64.68	50.73	4.11	3.31	4.96
71	EC0001443	56.38	56.53	6.31	2.41	8.46
72	EC0000531 – A	52.38	99.53	3.51	5.51	14.96
73	EC0541202	65.68	54.13	4.31	3.51	7.46

74	EC0001005 – B	59.38	96.33	5.11	3.51	13.96
75	EC0001395	64.18	111.93	6.51	5.01	27.06
76	EC0041547 – A	64.38	132.53	8.51	3.41	15.96
77	EC0541194	64.18	57.13	7.11	3.01	10.06
78	EC0399084	55.18	58.93	5.11	1.81	9.26
79	EC0118743	59.08	70.53	6.91	1.81	8.46
80	EC000545	65.58	93.73	7.11	1.41	19.96
81	EC0001476	62.18	39.13	4.11	3.31	17.96
82	EC0041723	52.68	42.33	5.31	5.31	15.76
83	EC0041720	59.38	60.53	4.11	4.31	16.76
84	EC0041646	59.88	91.63	5.11	3.41	10.26
85	EC0000543	56.68	76.13	8.51	2.51	43.76
86	EC0541195	58.68	89.73	8.71	3.41	23.06
87	EC0541198	58.18	49.13	6.11	3.91	14.26
88	EC0041735	67.18	79.93	6.31	9.61	16.56
89	EC0001403	52.68	70.33	5.01	6.71	18.51
90	EC0041601 – A	54.88	84.33	4.81	6.31	35.61
91	EC0001551	56.68	69.53	6.61	4.91	21.31
92	EC0041774 – A	46.18	95.53	5.01	3.41	22.31

93	EC0041469	55.88	56.73	4.41	3.31	14.81
94	EC0041687	55.08	89.73	3.41	6.81	13.81
95	EC0041607 – 2	54.38	28.73	3.61	1.91	16.31
96	EC0041467	57.38	64.93	4.61	2.31	20.81
97	EC00414678-B	63.18	59.33	4.41	5.41	17.81
98	EC0041700	49.18	38.73	5.41	3.31	16.01
99	EC0041768	51.18	56.93	7.41	5.31	21.31
100	EC244634	58.88	54.33	9.81	5.41	17.11
101	EC0541211	57.18	82.33	10.41	8.31	25.91
102	EC0041653	50.38	70.13	3.81	9.31	21.81
103	EC0001475	51.88	52.73	5.01	2.91	24.31
104	EC0023208	50.68	39.13	6.81	3.31	20.51
105	EC0399085	52.68	81.73	9.41	8.41	21.91
106	EC0022813 – B	64.38	65.13	7.61	8.61	22.81
107	EC0041755	57.88	61.33	4.41	7.81	22.81
108	EC0041478	52.68	45.73	6.41	5.31	21.81
109	EC0718852	58.08	59.53	6.21	7.91	21.51
110	EC0000538	58.58	43.13	5.01	6.41	20.01
111	EC0011748	54.68	90.63	4.61	5.71	22.06

112	EC0041647	46.08	38.63	4.61	0.91	20.06
113	EC0541219	51.68	68.43	9.61	1.41	14.66
114	EC0001465	56.08	71.53	9.61	1.91	17.56
115	EC0041726	51.08	85.23	10.41	3.01	18.16
116	EC054214	74.88	66.43	3.41	2.81	20.16
117	EC0455084	47.38	31.83	6.61	2.41	15.96
118	EC0718826	53.38	54.03	7.41	3.31	26.06
119	EC0718831	64.58	65.63	8.41	2.21	22.46
120	EC0718825	56.08	96.03	8.41	6.41	18.86
121	EC0001395 – 1	51.38	54.23	7.61	0.61	15.36
122	EC0001433	55.58	69.63	7.41	1.41	19.06
123	EC0041615	53.08	36.83	8.41	1.81	10.96
124	EC0041649	41.88	41.03	5.01	3.41	12.66
125	EC0041622	73.68	36.83	4.21	1.51	17.66
126	EC0541203	56.58	53.03	5.01	3.51	18.56
127	EC0041579	52.08	118.23	6.21	3.41	19.96
128	EC041643	76.58	124.43	6.41	8.01	35.86
129	EC0041764	61.88	183.03	6.61	4.31	25.86
130	EC0718845	60.08	86.83	10.01	4.41	29.66

131	EC0115148	59.38	54.83	4.61	5.41	20.46
132	EC0541207	59.18	88.03	6.61	4.41	15.66
133	EC0041765	68.88	109.33	8.21	6.41	15.66
134	EC000564	54.38	114.73	9.21	8.01	37.16
135	EC0041582	68.88	131.13	7.21	4.41	23.66
136	EC0041598	48.38	174.93	7.41	6.41	29.46
137	EC00411623	59.88	84.53	6.21	4.41	17.96
138	EC0041644	62.08	101.33	6.01	5.41	19.56
139	EC0041758	49.58	82.93	8.61	4.41	22.56
140	EC0110289	50.88	89.33	9.61	5.91	20.46
141	EC0158985	56.68	75.33	7.41	5.91	22.26
142	EC22648	64.08	77.73	6.21	5.41	18.96
143	EC0002711	50.08	77.13	7.61	6.01	19.26
144	EC0041535	66.58	96.33	7.41	8.01	20.46
145	EC0541201	60.88	93.53	10.61	6.81	19.66
146	EC0541217	47.88	113.33	10.41	9.01	26.46
147	EC0718823	56.38	152.53	6.61	6.81	24.66
148	EC718846	56.88	153.13	9.01	7.01	19.76
149	EC0541204	46.58	83.53	9.41	4.81	22.96

150	EC0718824	65.58	41.93	4.01	4.81	22.46
151	EC0541216	67.38	55.13	4.01	3.81	22.16
152	EC22813	57.68	113.53	10.61	5.81	26.96
153	EC0718834	52.18	60.33	7.41	4.81	17.96
154	EC541206	66.68	49.53	5.61	7.31	17.66
155	EC718830	59.38	78.73	4.41	1.06	21.86
156	EC718835	56.18	69.53	7.61	3.66	20.26
157	EC0718842	59.08	43.33	5.61	1.96	21.86
158	EC0718843	58.38	74.13	3.21	1.46	20.46
159	EC0718847	58.68	37.73	6.61	1.46	22.36
160	EC0001451	63.88	134.53	6.61	3.46	37.96
161	EC80490	59.38	33.53	3.81	2.46	13.96
162	EC0041734	62.38	60.53	5.61	1.46	21.46
163	EC0080490	61.68	51.53	8.81	1.46	26.96
164	EC0001396	61.88	88.93	7.41	1.46	20.36
165	EC0541224	64.38	199.13	7.21	2.46	25.86
166	EC541225	62.68	174.13	7.41	2.46	22.66
167	EC0041495 – 1	66.58	101.13	3.41	3.46	24.66
168	EC004181	73.88	150.33	6.01	2.46	33.66

169	EC0718828	62.18	78.93	6.41	3.46	29.36
170	EC0718829	48.08	90.73	8.21	5.46	30.96
171	EC0718827	60.68	76.33	7.61	1.46	12.36
172	EC0718851	58.68	99.33	7.41	2.46	28.66
173	EC0541208	73.38	58.73	7.01	4.46	40.46
174	EC0041619	58.38	96.53	7.01	6.16	21.96
175	EC0541213	68.58	55.13	3.01	2.46	23.46
176	EC0718848	41.88	61.73	14.41	6.46	19.16
177	PKV-NL 260	67.88	107.40	6.75	2.33	9.24
178	TL 99	62.88	83.25	4.88	2.80	11.08
CD	$(C_i - C_j)$	1.67	11.11	1.22	0.52	0.47
CD	$(B_i - B_j)$	4.71	31.42	3.45	1.48	1.32
CD	$(B_iV_i - B_jV_j)$	5.77	38.48	4.22	1.82	1.62
CD	$(C_i - V_i)$	4.33	28.86	3.17	1.36	1.22

Table 3: continued….

Sr. No	Name of the genotype	Powdery mildew infestation %	Days to 50% flowering (days)	Days to maturity (days)	Flower size (mm)	1000 seed weight (g)	Seed yield plant $^{-1}$ (g)
1	EC1066	10.05	50.00	107.76	15.90	9.34	1.70
2	EC1386	26.05	50.00	120.76	17.90	9.54	1.70
3	EC1424	10.05	61.00	118.76	18.90	9.04	1.20
4	EC14539	23.45	62.00	108.26	19.90	9.24	1.20
5	EC1474	14.05	49.00	112.76	20.90	8.04	1.20
6	EC1588	14.05	50.00	122.76	21.90	7.94	0.70
7	EC1628	10.05	58.00	112.76	22.90	8.34	0.70
8	EC1645	10.05	58.00	111.76	23.90	8.84	0.80
9	EC41623	27.45	62.00	114.76	22.90	9.94	1.40
10	EC45890	10.05	57.00	116.76	25.90	8.54	1.00
11	EC41659	23.45	50.00	118.76	25.90	8.84	0.80
12	EC41741	23.45	49.00	119.76	25.90	9.54	1.00
13	EC51904	23.45	57.00	112.16	25.90	9.14	0.70
14	EC98994	22.05	50.00	113.36	25.90	8.74	0.60

15	EC99001	11.45	53.00	113.06	23.90	8.64	0.90
16	EC0012538	11.45	49.00	108.96	25.90	9.94	2.90
17	EC0041762	15.45	56.00	117.76	25.90	10.14	2.30
18	EC0541196	15.45	50.00	120.76	27.90	8.04	1.30
19	EC0000526	15.45	55.00	121.76	25.90	5.94	0.70
20	EC0115174	19.45	61.00	122.86	25.90	6.24	0.70
21	EC0001437	14.05	50.00	111.76	22.90	7.94	1.40
22	EC0399086	27.45	61.00	109.76	22.90	8.34	1.00
23	EC0041687 – A	14.05	59.00	108.26	19.90	9.04	2.00
24	EC0041672	15.45	57.00	114.26	20.90	9.44	2.00
25	EC0541227	15.45	58.30	112.26	20.90	6.74	1.60
26	EC0009827	15.45	58.30	116.26	20.90	9.54	2.30
27	EC0541205	27.45	57.00	107.26	20.90	7.44	1.40
28	EC0541212	14.05	55.70	113.26	20.90	7.34	1.30
29	EC0001457	18.05	62.70	104.26	20.90	7.74	1.40
30	EC0041672 – 1	18.05	58.30	110.26	20.90	6.64	1.40
31	EC0001459	18.05	58.00	108.26	20.90	7.54	1.60
32	EC0041528	10.05	56.30	112.26	24.90	8.94	1.90

33	EC0520246	27.45	56.30	114.26	20.90	9.44	2.20
34	EC0001432	18.05	54.30	117.36	20.90	8.54	1.80
35	EC0001550 -B	23.45	58.30	115.26	20.90	8.54	2.00
36	EC0041601 – A	14.05	54.30	108.26	15.90	9.14	2.40
37	EC0110474	19.45	56.30	113.26	20.90	8.24	2.00
38	EC0541213	10.05	58.30	104.26	17.90	7.64	1.60
39	EC0041753	15.45	66.30	106.26	20.90	6.14	2.00
40	EC0541215	19.45	63.70	108.66	20.90	6.34	1.20
41	EC0006160	27.45	63.70	115.26	20.90	6.94	1.60
42	EC0718850	14.05	63.70	116.26	16.90	7.04	1.70
43	EC0520247	31.45	59.00	117.36	20.90	6.94	1.30
44	EC0022388	14.05	59.00	119.26	20.90	8.74	2.10
45	EC0041562	11.45	48.00	115.76	20.90	8.39	2.10
46	EC41466	10.05	48.00	117.76	19.90	9.29	2.70
47	EC0541213	11.45	50.00	118.76	19.90	7.69	1.50
48	EC0541215	10.05	49.70	113.76	19.90	7.49	1.90
49	EC0541218	10.05	49.70	109.76	20.90	10.19	2.40
50	EC0541223	10.05	49.70	110.76	19.90	9.69	2.80

51	EC0541226	11.45	50.30	118.76	19.90	8.19	2.20
52	EC541194	15.45	53.00	109.76	17.90	7.69	1.50
53	EC0541218	10.05	53.00	105.56	19.90	9.39	2.90
54	EC0541226	10.05	53.00	105.26	19.90	8.49	2.30
55	EC0001419	19.45	51.00	105.56	19.90	9.69	4.10
56	EC0022872	10.05	58.00	105.86	18.90	9.19	2.20
57	EC0000541 – A	6.05	54.00	106.26	19.90	8.69	2.50
58	EC0041621	23.45	61.00	117.76	19.90	9.39	3.10
59	EC054119	14.05	59.00	115.76	19.90	7.79	3.40
60	EC541196	19.45	55.00	105.26	19.90	7.79	1.60
61	EC0001388	10.05	55.00	109.76	19.90	7.29	1.50
62	EC0041650	11.45	55.00	119.76	19.90	9.29	1.80
63	EC0000522	11.45	57.00	109.76	19.90	8.79	1.60
64	EC0541210	11.45	54.00	108.76	19.90	8.39	3.20
65	EC0399082	11.45	54.00	111.76	19.90	8.49	2.70
66	EC0541220	11.45	55.00	113.76	19.90	8.09	1.90
67	EC041667	15.45	53.00	105.16	21.90	8.54	2.15
68	EC0041621 – B	19.45	58.00	106.36	20.90	8.24	2.65

69	EC0041737	14.05	54.30	106.06	21.90	9.14	3.35
70	EC0041400	23.45	53.00	101.96	21.90	8.34	4.25
71	EC0001443	19.45	54.00	110.76	21.90	6.74	1.45
72	EC0000531 – A	15.45	53.00	113.76	21.90	6.94	1.85
73	EC0541202	15.45	47.00	114.76	21.90	8.64	1.45
74	EC0001005 – B	15.45	54.00	115.86	23.90	7.74	1.75
75	EC0001395	15.45	53.00	104.76	21.90	7.74	1.65
76	EC0041547 - A	15.45	58.00	102.76	21.90	9.14	3.45
77	EC0541194	15.45	56.00	105.76	21.90	8.54	2.25
78	EC0399084	19.45	49.00	113.76	21.90	8.14	2.15
79	EC0118743	15.45	57.70	105.76	25.90	8.84	2.05
80	EC000545	15.45	58.30	111.76	21.90	6.54	1.95
81	EC0001476	15.45	56.00	109.76	22.90	10.04	1.45
82	EC0041723	15.45	54.00	113.76	21.90	9.54	1.45
83	EC0041720	27.45	57.00	104.76	21.90	6.94	1.75
84	EC0041646	19.45	58.30	110.76	23.90	9.34	3.45
85	EC0000543	31.45	60.00	101.76	21.90	9.34	3.65
86	EC0541195	11.45	58.30	107.76	21.90	8.54	1.95

87	EC0541198	10.05	51.00	105.76	21.90	8.24	1.65
88	EC0041735	15.45	53.00	109.76	21.90	8.44	2.35
89	EC0001403	9.45	52.00	111.71	20.90	10.99	3.90
90	EC0041601 - A	13.45	58.00	104.71	22.90	9.59	2.80
91	EC0001551	17.45	60.00	109.71	20.90	9.29	1.20
92	EC0041774 - A	13.45	59.00	100.71	20.90	9.39	1.40
93	EC0041469	17.45	59.00	102.71	20.90	8.69	1.00
94	EC0041687	13.45	59.00	105.11	19.90	8.39	1.40
95	EC0041607 - 2	13.45	59.00	111.71	22.90	9.69	1.90
96	EC0041467	17.45	59.00	112.71	22.90	8.39	1.80
97	EC00414678-B	13.45	59.00	113.81	22.90	8.39	3.00
98	EC0041700	21.45	54.00	115.71	20.90	8.59	1.20
99	EC0041768	13.45	58.00	104.71	22.90	10.09	0.80
100	EC244634	12.05	58.00	109.71	22.90	9.69	1.90
101	EC0541211	17.45	58.30	110.71	19.90	9.69	3.60
102	EC0041653	13.45	58.00	112.71	22.90	8.99	1.90
103	EC0001475	9.45	58.30	113.71	22.90	9.59	2.60
104	EC0023208	39.45	60.30	101.21	22.90	9.99	2.50

105	EC0399085	21.45	58.00	101.21	22.90	9.69	2.30
106	EC0022813 - B	17.45	58.30	101.51	22.90	9.49	3.40
107	EC0041755	13.45	52.00	99.51	20.90	9.59	2.50
108	EC0041478	13.45	59.30	100.81	20.90	8.69	0.90
109	EC0718852	9.45	61.00	101.51	20.90	8.59	1.50
110	EC0000538	17.45	51.50	101.21	20.90	10.39	3.30
111	EC0011748	17.45	56.00	110.46	21.40	9.94	3.45
112	EC0041647	17.45	59.00	109.46	20.40	10.04	1.65
113	EC0541219	17.45	66.00	110.06	19.40	8.54	1.65
114	EC0001465	17.45	63.00	109.46	19.40	9.54	5.75
115	EC0041726	17.45	63.00	109.76	19.40	8.64	5.85
116	EC054214	17.45	65.00	109.06	19.40	8.44	1.45
117	EC0455084	29.45	63.00	109.06	17.40	9.54	1.05
118	EC0718826	33.45	68.30	109.76	19.40	9.24	1.15
119	EC0718831	21.45	64.00	110.06	19.40	9.54	1.95
120	EC0718825	12.05	65.30	109.76	19.40	9.64	1.15
121	EC0001395 - 1	17.45	67.00	109.46	19.40	9.44	0.95
122	EC0001433	16.05	61.00	109.76	19.40	9.94	1.05

123	EC0041615	25.45	62.00	109.76	19.40	8.54	2.45
124	EC0041649	25.45	59.30	109.76	19.40	9.54	0.85
125	EC0041622	16.05	64.00	109.76	19.40	9.74	1.55
126	EC0541203	12.05	62.00	109.46	16.40	8.44	1.15
127	EC0041579	33.45	63.00	109.76	19.40	9.94	2.45
128	EC041643	12.05	64.00	110.46	19.40	9.74	1.35
129	EC0041764	17.45	65.00	110.76	19.40	8.54	5.65
130	EC0718845	43.45	62.00	109.76	19.40	10.34	4.15
131	EC0115148	17.45	61.00	110.76	19.40	8.54	2.55
132	EC0541207	16.05	61.00	109.46	14.40	8.44	1.45
133	EC0041765	33.45	61.50	108.46	20.40	8.14	1.00
134	EC000564	25.45	63.50	108.06	20.40	9.94	1.40
135	EC0041582	29.45	67.50	108.46	20.40	8.34	2.30
136	EC0041598	17.45	64.20	109.06	22.40	9.94	3.40
137	EC00411623	13.45	66.50	109.46	20.40	8.94	2.00
138	EC0041644	13.45	62.50	109.06	20.40	9.54	2.40
139	EC0041758	21.45	67.50	108.76	23.40	8.84	1.60
140	EC0110289	13.45	65.80	109.06	20.40	9.44	3.20

141	EC0158985	9.45	63.50	109.06	20.40	8.54	1.10
142	EC22648	29.45	62.50	108.76	20.40	8.24	0.90
143	EC0002711	25.45	62.50	109.76	20.40	9.94	3.30
144	EC0041535	13.45	63.50	109.06	20.40	9.74	1.10
145	EC0541201	13.45	60.50	108.76	25.40	10.54	3.00
146	EC0541217	13.45	61.50	108.76	20.40	9.94	2.30
147	EC0718823	9.45	64.20	108.46	20.40	8.54	2.30
148	EC718846	8.05	64.50	108.46	20.40	9.74	2.80
149	EC0541204	9.45	68.50	108.46	21.40	9.94	1.40
150	EC0718824	8.05	58.80	108.46	20.40	10.24	1.10
151	EC0541216	4.05	62.50	108.46	20.40	8.04	1.20
152	EC22813	33.45	67.50	108.46	20.40	7.94	2.10
153	EC0718834	17.45	62.50	108.06	20.40	9.84	2.00
154	EC541206	8.05	68.00	109.06	20.40	9.54	0.80
155	EC718830	27.45	62.50	110.26	21.90	9.39	2.30
156	EC718835	19.45	66.50	111.96	21.90	10.09	2.10
157	EC0718842	35.45	64.50	111.56	20.90	8.19	0.70
158	EC0718843	27.45	64.50	105.96	21.90	9.49	1.20

159	EC0718847	23.45	62.50	109.56	21.90	9.79	0.40
160	EC0001451	11.45	55.50	109.26	21.90	8.39	2.00
161	EC80490	15.45	59.50	109.96	21.90	9.19	0.60
162	EC0041734	10.05	58.50	108.56	21.90	9.09	0.80
163	EC0080490	23.45	59.50	108.56	16.90	8.09	0.90
164	EC0001396	27.45	60.50	108.96	17.90	8.39	1.50
165	EC0541224	14.05	63.50	109.26	15.90	8.79	1.60
166	EC541225	15.45	63.50	109.56	14.90	8.49	1.00
167	EC0041495 - 1	15.45	67.80	109.56	13.90	8.59	1.10
168	EC004181	23.45	67.50	109.46	12.90	8.79	1.10
169	EC0718828	27.45	69.50	121.46	11.90	7.59	1.20
170	EC0718829	27.45	68.80	123.46	10.90	8.89	1.00
171	EC0718827	39.45	73.80	110.26	11.90	8.79	2.50
172	EC0718851	27.45	58.50	110.26	12.90	8.09	0.80
173	EC0541208	31.45	69.20	121.46	13.90	7.49	2.20
174	EC0041619	14.05	68.80	122.46	14.90	8.59	3.20
175	EC0541213	19.45	69.50	116.46	15.90	9.19	1.20
176	EC0718848	27.45	68.80	113.46	19.90	8.19	0.70

177	PKV-NL 260	9	53.75	110.75	20.60	10.83	2.70
178	TL 99	12.5	56.25	113.76	21.10	9.46	1.70
CD	$(C_i - C_j)$	3.314	0.63	2.07	1.30	0.22	0.54
CD	$(B_i - B_j)$	9.373	1.78	5.84	3.60	0.63	1.54
CD	$(B_iV_i - B_jV_j)$	11.48	2.18	7.16	4.40	0.78	1.88
CD	$(C_i - V_i)$	8.61	1.64	5.37	3.30	0.58	1.41

4.2.2 Characterization of genotype based on morphological qualitative traits

The data on qualitative characters were presented in Table 4 shown that EC1424, EC14539, EC0041762, EC0041562, EC0041753, EC00541215, EC0006160, EC0041621, EC0041621-B, EC0041768, EC0718826, EC0718825, EC0041579, EC0001395-1, EC0115148, EC0541207, EC541255, EC993389, EC100951 (19 genotypes) had white flower colour, 16 genotypes had blue flower colour,143 genotypes had violet flower colour and none of the genotypes had red violet colour. 118 genotypes had shown funnel flower shape, 3 genotypes i.e., EC 1424, EC 41466, EC0541213 had star shape flowers, 56 genotypes had disc shape flowers, and 1 genotype i.e., EC0718846 had tubular shape flower. 81 genotypes had twisted aestivation, 51 genotypes had semi twisted aestivation, and 46 genotypes had valvate aestivation. 18 genotypes had white venation colour, 114 genotypes had violet colour,41 genotypes had blue colour venation, and 5 genotypes i.e., EC0041528, EC0520246, EC0541213, EC0541213-A, EC0541204 had light violet colour venation. 88 genotypes had white colour distal filament stamen, 63 genotypes had violet colour distal filament stamen, and 27 genotypes had blue colour distal filament stamen. 54 genotypes had cream colour anthers, 53 genotypes had grey colour anthers, 25 genotypes had violet colour anthers, and 46 genotypes had blue colour anthers. 60 genotypes had bushy growth habit, 80 genotypes had semi erect growth habit, and 38 genotypes had erect plant growth habit. 147 genotypes had non dehiscence capsule and 31 genotypes had semi dehiscence capsules. 9 genotypes i.e., EC0541208, EC0718827, EC0541211, EC0541195, EC0041720, EC0541210, EC054119 had fawn seed colour, 119 genotypes had light brown seed colour, 49 genotypes had brown seed colour, 1 genotype i.e., EC80490 had yellow seed colour and none of the genotypes had dark brown seed colour.

Table 4: Characterization of genotype based on qualitative traits

Sr. No	Name of genotype	Flower venation colour	Flower aestivation	Anther colour	Stamen: Filament colour	Capsule dehiscence	Plant growth habit	Flower shape	Flower colour	Seed colour
1	EC1066	4	3	4	1	5	7	1	3	4
2	EC1386	4	2	1	1	5	7	1	3	3
3	EC1424	1	1	1	1	5	5	1	1	4
4	EC14539	1	1	1	1	5	3	1	1	1
5	EC1474	4	3	1	2	5	5	1	3	3
6	EC1588	4	1	1	1	5	5	3	3	4
7	EC1628	3	3	3	1	3	5	1	3	3
8	EC1645	3	1	1	2	5	5	1	3	4
9	EC41623	3	1	3	1	5	5	3	3	3
10	EC45890	2	3	1	1	5	3	1	3	3
11	EC41659	3	3	1	1	5	5	1	3	3
12	EC41741	4	3	1	2	5	5	1	3	4
13	EC51904	3	1	3	1	5	5	3	3	4
14	EC98994	4	3	1	2	3	5	1	3	3
15	EC99001	3	2	3	3	5	5	1	3	3

16	EC0012538	4	3	4	2	5	7	1	3	4
17	EC0041762	1	3	1	1	3	7	1	1	3
18	EC0541196	4	3	1	3	5	5	1	3	4
19	EC0000526	4	3	3	2	3	5	1	3	3
20	EC0115174	4	3	1	1	5	5	1	2	3
21	EC0001437	3	1	1	3	5	5	1	3	3
22	EC0399086	4	1	1	2	5	7	3	2	4
23	EC0041687 - A	3	3	2	3	5	5	3	3	4
24	EC0041672	4	3	1	3	5	5	1	2	3
25	EC0541227	4	1	4	1	5	5	3	3	3
26	EC0009827	4	2	3	1	5	7	1	3	3
27	EC0541205	4	2	2	3	5	5	1	3	4
28	EC0541212	4	2	4	1	5	7	1	3	4
29	EC0001457	4	3	2	1	5	5	1	3	4
30	EC0041672 - 1	4	1	3	3	5	5	1	3	4
31	EC0001459	3	2	1	3	5	5	3	3	3
32	EC0041528	2	2	4	1	5	3	1	3	3
33	EC0520246	2	2	1	2	5	5	3	3	3
34	EC0001432	4	3	1	2	5	5	1	3	4

35	EC0001550 -B	4	3	4	2	5	7	1	3	3
36	EC0041601 - A	3	1	2	1	5	5	3	2	3
37	EC0110474	4	3	1	1	3	5	1	3	4
38	EC0541213	2	1	3	1	3	7	3	2	3
39	EC0041753	1	2	1	1	5	5	1	1	4
40	EC0541215	3	1	2	1	5	3	3	1	3
41	EC0006160	1	2	1	1	5	3	1	3	3
42	EC0718850	3	2	1	1	5	5	1	3	3
43	EC0520247	3	1	4	2	3	3	3	3	3
44	EC0022388	4	1	3	2	5	7	1	1	3
45	EC0041562	1	1	1	1	5	5	3	1	4
46	EC41466	1	2	1	1	3	7	1	1	3
47	EC0541213	2	3	1	1	5	5	1	3	3
48	EC0541215	3	1	4	1	5	7	1	3	3
49	EC0541218	3	1	4	3	3	7	1	3	3
50	EC0541223	3	3	1	2	3	7	1	3	3
51	EC0541226	4	1	1	1	3	5	1	3	3
52	EC541194	4	1	3	3	5	3	1	3	3
53	EC0541218-A	3	1	3	1	5	5	3	3	3

54	EC0541226-A	4	2	2	2	5	3	1	3	3
55	EC0001419	3	3	3	1	5	5	1	1	3
56	EC0022872	3	3	2	1	5	5	1	3	3
57	EC0000541 - A	4	1	4	2	5	5	3	1	3
58	EC0041621	1	1	1	1	3	3	3	3	3
59	EC054119	3	1	1	1	5	3	3	3	1
60	EC541196	4	1	1	1	5	7	1	3	3
61	EC0001388	3	1	2	1	5	5	3	3	3
62	EC0041650	3	2	2	2	5	5	1	3	3
63	EC0000522	4	1	2	1	5	5	3	3	1
64	EC0541210	4	1	2	1	5	5	3	3	3
65	EC0399082	3	1	1	1	5	7	3	3	3
66	EC0541220	4	1	2	2	5	5	1	3	3
67	EC041667	3	1	4	2	5	5	1	3	3
68	EC0041621 - B	1	2	1	1	5	5	1	1	3
69	EC0041737	3	1	2	2	5	5	3	3	4
70	EC0041400	4	1	1	2	3	5	1	2	3
71	EC0001443	4	2	3	1	3	7	1	3	3
72	EC0000531 - A	4	2	4	1	5	7	1	3	3

73	EC0541202	3	3	2	1	3	7	1	3	3
74	EC0001005 - B	3	1	4	1	5	7	3	3	3
75	EC0001395	3	2	4	1	5	5	3	3	3
76	EC0041547 - A	4	2	2	2	5	5	1	2	3
77	EC0541194	4	1	4	1	5	5	1	4	4
78	EC0399084	4	1	1	1	3	7	1	1	3
79	EC0118743	3	2	3	2	5	7	1	3	3
80	EC000545	2	3	4	1	5	5	1	4	3
81	EC0001476	4	3	4	2	3	7	1	4	3
82	EC0041723	3	1	4	2	5	7	1	4	3
83	EC0041720	3	2	2	1	5	7	3	2	1
84	EC0041646	3	2	2	1	5	7	1	2	3
85	EC0000543	2	1	4	1	3	3	3	4	3
86	EC0541195	2	3	1	2	5	3	1	1	1
87	EC0541198	4	1	2	1	5	3	1	2	1
88	EC0041735	2	1	1	1	5	7	3	1	3
89	EC0001403	3	1	1	3	5	5	3	1	3
90	EC0041601 - A	3	3	1	1	3	7	1	1	3
91	EC0001551	4	1	2	2	5	5	3	2	3

92	EC0041774 - A	3	1	1	1	5	3	1	1	3
93	EC0041469	3	1	2	2	5	3	3	2	3
94	EC0041687	4	1	3	1	5	5	3	3	4
95	EC0041607 - 2	3	1	3	2	5	7	1	3	3
96	EC0041467	4	1	2	3	5	7	3	2	3
97	EC00414678 -B	2	1	4	1	5	7	3	4	3
98	EC0041700	2	3	2	2	5	5	1	2	3
99	EC0041768	2	1	1	1	5	5	1	1	3
100	EC244634	3	1	2	1	5	3	3	2	1
101	EC0541211	3	2	2	2	5	5	1	2	3
102	EC0041653	3	2	4	2	5	5	3	3	4
103	EC0001475	2	1	2	2	5	5	3	3	4
104	EC0023208	3	2	2	1	5	3	1	3	4
105	EC0399085	4	1	1	1	5	3	3	3	3
106	EC0022813 -B	3	1	3	1	5	7	3	3	3
107	EC0041755	3	1	4	1	3	7	3	3	4
108	EC0041478	3	1	3	1	5	3	3	3	3
109	EC0718852	2	1	1	1	5	7	1	3	4
110	EC0000538	4	2	1	1	5	7	3	3	4

111	EC0011748	2	2	1	1	5	7	1	3	3
112	EC0041647	3	2	4	1	5	7	3	3	3
113	EC0541219	3	2	4	2	3	5	3	3	4
114	EC0001465	3	1	1	1	5	3	1	3	3
115	EC0041726	4	1	4	1	5	5	1	3	3
116	EC054214	4	1	2	2	5	3	1	3	3
117	EC0455084	4	3	1	1	5	3	1	3	3
118	EC0718826	3	2	2	1	5	3	3	3	4
119	EC0718831	3	2	1	1	5	3	3	1	4
120	EC0718825	2	3	4	1	5	3	1	1	3
121	EC0001395 - 1	2	1	2	2	5	5	3	3	3
122	EC0001433	3	3	4	1	5	3	3	3	3
123	EC0041615	3	1	2	1	5	3	1	3	3
124	EC0041649	2	3	2	2	5	7	1	3	3
125	EC0041622	3	2	2	1	5	7	1	3	3
126	EC0541203	3	1	1	2	5	5	1	1	4
127	EC0041579	1	1	1	1	5	3	3	3	3
128	EC041643	3	1	4	1	5	3	3	3	3
129	EC0041764	3	3	3	3	5	5	1	3	3

130	EC0718845	2	2	1	2	5	3	3	1	3
131	EC0115148	3	3	1	1	3	5	1	1	3
132	EC0541207	3	3	1	1	5	5	1	3	3
133	EC0041765	2	1	3	2	5	3	1	3	3
134	EC000564	3	2	4	1	5	3	3	3	3
135	EC0041582	3	3	2	2	5	7	1	3	4
136	EC0041598	3	3	2	2	5	3	2	3	3
137	EC00411623	2	2	3	1	5	3	3	3	3
138	EC0041644	2	2	4	2	5	5	3	3	3
139	EC0041758	3	2	2	2	5	3	3	3	4
140	EC0110289	3	2	3	2	5	3	1	3	4
141	EC0158985	2	3	2	1	5	5	1	3	3
142	EC22648	2	2	3	2	5	7	1	3	3
143	EC0002711	3	3	2	1	3	3	1	3	4
144	EC0041535	3	2	4	2	5	3	1	3	3
145	EC0541201	2	1	2	2	5	5	1	3	3
146	EC0541217	4	3	4	2	5	5	1	3	4
147	EC0718823	3	2	2	2	5	3	1	3	4
148	EC718846	3	1	4	2	5	5	4	3	3

149	EC0541204	2	3	4	2	5	5	1	3	3
150	EC0718824	3	1	2	1	5	5	1	3	3
151	EC0541216	2	1	2	2	5	7	3	3	4
152	EC22813	3	1	4	1	5	5	3	3	4
153	EC0718834	2	1	2	2	5	5	1	3	3
154	EC541206	3	1	1	1	5	3	3	3	4
155	EC718830	4	3	4	1	5	7	1	3	4
156	EC718835	3	1	2	1	5	3	3	3	4
157	EC0718842	2	3	4	3	5	3	1	3	4
158	EC0718843	4	3	4	3	5	5	1	3	3
159	EC0718847	4	3	4	2	5	7	1	3	3
160	EC0001451	4	2	4	2	5	5	1	3	3
161	EC80490	1	1	1	1	5	3	3	3	2
162	EC0041734	3	2	4	2	5	5	1	3	3
163	EC0080490	3	1	4	2	5	3	1	1	3
164	EC0001396	2	1	4	1	5	5	3	3	1
165	EC0541224	3	1	4	2	5	3	3	3	4
166	EC541225	1	2	2	2	5	3	1	3	3
167	EC0041495 - 1	3	2	2	1	5	3	3	3	3

168	EC004181	3	1	2	1	5	3	3	3	3
169	EC0718828	4	1	2	2	5	3	1	3	3
170	EC0718829	3	2	1	3	5	3	1	3	3
171	EC0718827	3	3	2	1	5	3	1	3	1
172	EC0718851	3	2	3	1	5	3	1	3	4
173	EC0541208	3	2	2	3	3	7	1	3	3
174	EC0041619	3	2	4	1	5	5	1	2	3
175	EC0541213	2	1	4	1	3	7	3	3	3
176	EC0718848	3	1	3	2	5	3	1	1	3
177	PKV-NL 260	3	1	3	2	5	3	1	1	3
178	TL99	3	1	3	2	5	3	1	1	3

4.3 Wilk's criterion and D^2 statistics

The results of analysis of dispersion are presented in Table 5. The analysis of dispersion for the test of significance of difference in the mean values based on the Wilk's criterion revealed highly significant difference among genotypes for eleven characters. Therefore, the data were further evaluated for D^2 and cluster analysis. The D^2 values obtained for 178 genotypes in all possible combinations were too large to be presented in thesis and hence not presented.

Table 5: Analysis of dispersion

Source of variations	df	Sum of squares	Mean squares
Varieties	177	1.4532E17	8.2103E14*
Error	353	1.1486E02	3.2540E-01
Total	530	1.4532E17	2.7419E14

*** Significant at 5% level**

4.4 Contribution of different characters towards divergence

The contribution of each character towards genetic divergence of 2021-22 data are presented in Table 6. Contribution of alternaria blight infestation % was maximum (24.52)% followed by number of capsule plant^{-1} (20.28%), seed yield plant^{-1} (17.39%), days to 50%flowering (10.00%), number of primary branches plant^{-1} (8.18%) powdery mildew infestation% (8.00%), flower size (5.53%), plant height (2.84%), 1000 seed weight (g)(1.76%), bud fly infestation % (1.49%), days to maturity (0.0%).This indicates that character like alternaria blight infestation %, by number of capsule plant^{-1}, seed yield plant^{-1}, days to 50%flowering were important traits contributing towards genetic divergence.

Table 6: Contribution of different characters towards divergence

Sr. No.	Characters	Time ranked 1st	Per cent Contribution
1	Plant height (cm)	448	2.84%
2	Number of capsules plant^{-1}	3195	20.28%
3	Number of branches plant^{-1}	1289	8.18%
4	Alternaria infestation %	3862	24.52%
5	Bud fly infestation%	235	1.49%
6	Powdery mildew infestation%	1261	8.00%
7	Days to maturity (days)	0	0.00%
8	1000 seed weight (g)	278	1.76%
9	Days to 50% flowering (days)	1575	10.00%
10	Seed yield plant^{-1}(g)	2739	17.39%
11	Flower: corolla size (cm)	871	5.53%
	Total	15753	
	Tochers cut-off value	271.75	

4.5 Grouping of genotypes into different clusters

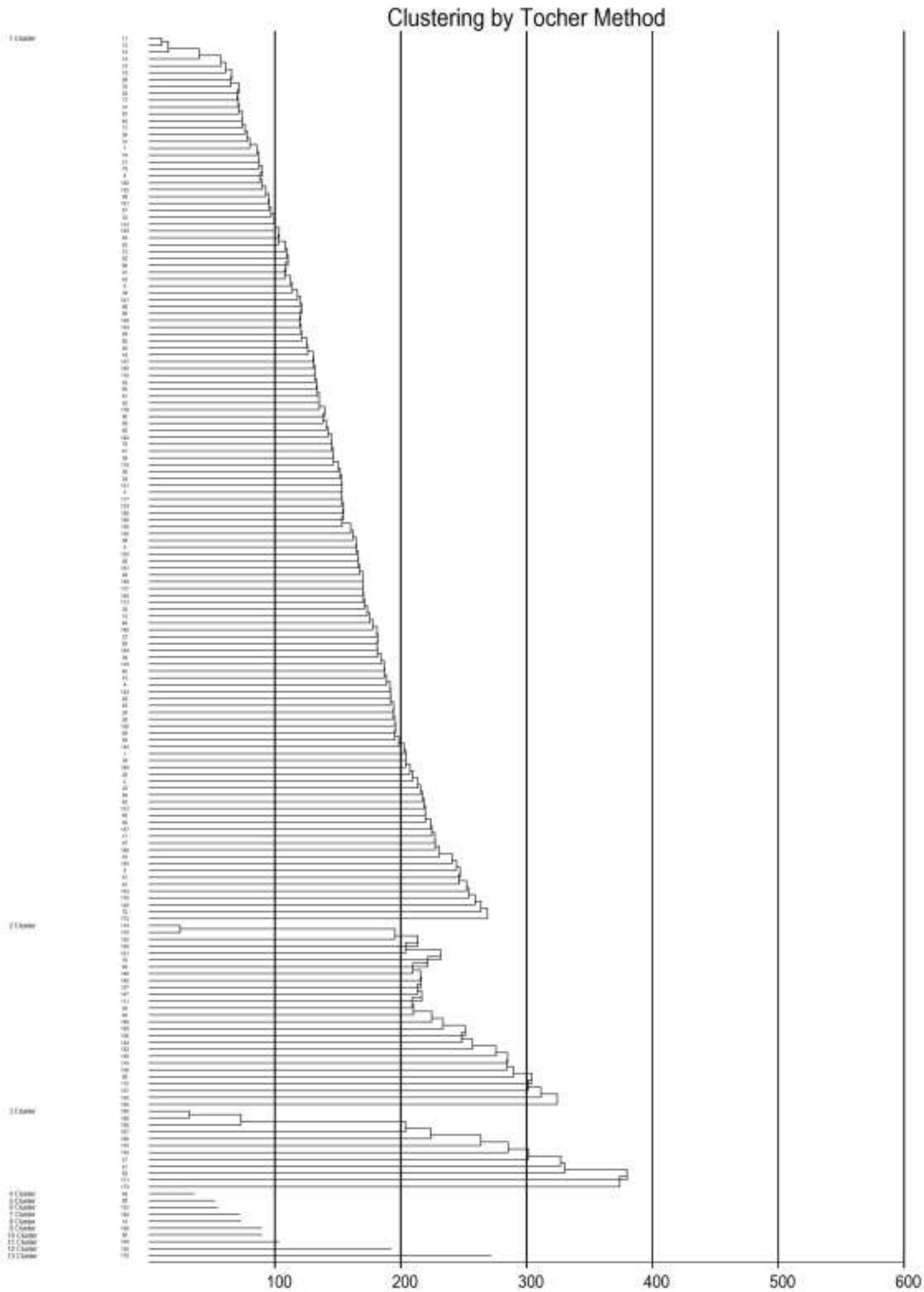
The grouping of 178 genotypes into different clusters were done by Tocher's method for 2021-22 are presented in Table 7 and Fig. 1.

Table 7: Grouping of genotypes into different clusters

Cluster	Number of genotypes	Name of the genotypes
I	130	EC41659, EC41741, EC98994, EC51904, EC0541202, EC99001, EC0041700, EC0399084, EC0041469, EC0541194, EC0110474, EC0541198, EC0022388, EC0001443, EC0001550-B, EC0001459, EC1628, EC0001437, EC0007005-B, EC0118743, EC1645, EC0041734, EC0001433, EC0041467, EC80490, EC0001476, EC0041720, EC0541195, EC1066, EC1386, EC1588, EC45890, EC0041687-A, EC41623, EC0041762, EC0541227, EC0520246, EC14539, EC0000526, EC0541205, EC0001457, EC1474, EC1424, EC0041672, EC541196, EC0115174, EC0399086, EC0041528, EC0001432, EC0520247, EC0041562, EC0718850, EC0541212, EC0009827 ,EC0041753, EC0041672-1, EC0041601-A, EC0541213, EC0541223, EC0541226, EC541194, EC0541226, EC0022872, EC0000541-A,EC0041621, EC0541215, EC41466, EC0541213, EC0541215, EC541196, EC0041650, EC0000522, EC0541210, EC0399082, EC0541220, EC041667, EC0041621-B, EC0041737, EC0041400, EC0000531-A ,EC0001395, EC0041723, EC0001551, EC0041774-A, EC0041687, EC0041607-2, EC00414678-B, EC0041768, EC244634, EC0001475, EC0041478, EC0041647, EC0541219, EC054214, EC0455084, EC0718826, EC0718831, EC0001395-1,EC0041615, EC0041649, EC0041622, EC0541203, EC0115148, EC0541207, EC00411623, EC0041644, EC0041758, EC0110289, EC0158985, EC22648, EC0002711, EC0041535, EC0541204, EC0541216, EC0718824, EC0718834, EC718830, EC718835, EC0718842, EC0718843, EC0718847, EC0080490, EC0001396, EC0718851,EC0541213, EC0041646,EC000545, PKV-NL-260,TL 99.
II	27	EC0041619, EC0001451, EC22813, EC718846, EC0541217, EC0541201, EC718823, EC0041582, EC000564, EC0041598, EC0718845, EC0041579, EC0718825, EC0041726, EC0001465, EC0011748, EC0000538,

		EC0718852, EC0041755, EC0022813-B, EC0399085, EC0541211, EC0041601-A, EC0001403, EC004154-A, EC054119, EC001419.
III	11	EC0006160, EC0541218-A, EC0001388,EC0041765, EC07188229, EC0718827, EC0541224, EC541225, EC0041495-1, EC004181, EC0718828.
IV	1	EC0541218
V	1	EC0041735
VI	1	EC0041653
VII	1	EC541206
VIII	1	EC0012538
IX	1	EC041643
X	1	EC0000543
XI	1	EC0023208
XII	1	EC0041764
XIII	1	EC0718848

Fig. No.1: Dendrogram showing clustering by Tocher's method



The entire genotypes (178) were grouped on the basis of D^2 statistics into thirteen clusters. The cluster I was largest comprising of 130 genotypes, followed by cluster II comprising of 27 genotypes, cluster III comprising of 11 genotypes, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X, cluster XI, cluster XII, cluster XIII comprising single genotypes in each cluster. The checks PKV NL 260, TL 99 grouped into cluster I along with 128 genotypes. This indicates that there are many germplasms which were highly diverse from the check and hence offers good scope for improvement.

4.6 Canonical analysis

The value of first five canonical vectors and canonical roots are presented in Table 8. The first five canonical roots accounted for 82.96 per cent of the observed variability in the material studied (λ_1= 31.53%, λ_2=18.65 %, λ_3=14.31 %, λ_4=11.39 %, λ_5=7.08 %). The overall contributions of the five canonical roots to the total variability among 178 genotypes were 82.96 per cent suggesting the major portion of differentiation in first five phases. This indicates that differentiations for eleven characters among 178 genotypes were completed in five phases.

Further coefficient in first five canonical vectors shows that out of eleven characters number of capsules plant^{-1}, alternaria blight infestation%, seed yield plant^{-1}, days to 50% flowering,1000 seed weight, powdery mildew infestation%, bud fly infestation%, number of branches plant^{-1}, plant height contributed in vector I accounting for 31.53% of total variation. characters number of capsules plant $^{-1,}$ number of branches plant^{-1}, days to 50% flowering, seed yield plant^{-1}, days to maturity, powdery mildew infestation% were important characters in vector II which accounted for 18.65% of total variation. Flower size, seed yield plant^{-1}, days to maturity, 1000 seed weight, plant height were important characters in vector III which accounted for 14.31% of total variation. The important characters in vector IV number of capsule plant^{-1}, alternaria blight infestation%, days to maturity are accounted for 11.39% of total variation. The important characters in vector V are 1000 seed weight, days to 50% flowering,1000 seed weight, number of capsules plant$^{-1,}$ plant height, seed yield plant^{-1} accounted for 7.08 % of total variation. This suggested that parent selected on the basis of number of capsule plant^{-1}, days to 50% flowering, alternaria blight infestation%, bud fly infestation% etc. may expected to be genetically diverse.

From the data it can observed that the parents selected on the basis of number of capsules plant $^{-1,}$ alternaria blight infestation%, seed yield plant^{-1}, days to 50% flowering,1000 seed weight, powdery mildew infestation%, bud fly infestation% may expected to be genetically diverse.

Table 8: Five canonical roots and their contribution expressed as per cent of the total variation

Root	Eigen value	Contribution in per cent
λ1	8333.82	31.53
λ2	4930.19	18.65
λ3	3780.96	14.31
λ4	3010.00	11.39
λ5	1871.35	7.08
Total	21926.32	82.96
Sum of all canonical roots	100	
Residual	17.04	

Table 9: Values of first five vectors

Sr. No	Characters	Vector I	Vector II	Vector III	Vector IV	Vector V
1	Plant height (cm)	0.04334	0.00538	0.04725	0.05943	0.39798
2	Number of capsules plant^{-1}	0.54752	0.42177	-0.00643	0.60411	0.10726
3	Number of branches plant^{-1}	0.28401	0.21298	-0.34286	-0.14649	-0.48986
4	Alternaria infestation %	0.49345	-0.74698	-0.23600	0.14944	-0.15912
5	Bud fly infestation %	0.08043	-0.08855	-0.11063	-0.23048	0.11313
6	Powdery mildew infestation%	0.09262	0.30127	-0.20161	-0.32967	-0.36487
7	Days to maturity (days)	-0.03188	0.22239	0.03688	0.03430	0.05820
8	1000 seed weight (g)	0.00987	-0.22705	0.20514	-0.18502	0.09381
9	Days to 50% flowering (days)	0.14634	0.10855	-0.49427	-0.43731	0.43473
10	Seed yield plant^{-1} (g)	0.57158	0.08239	0.60862	-0.44419	0.10213
11	Flower size (mm)	-0.09950	-0.02369	0.33679	-0.04435	-0.45529

4.7 Average intra and inter cluster distance

Average intra and inter cluster distance among eleven characters were worked out by Tocher's method and are presented in Table 10.

Data shows that inter cluster distance in most of the cases were higher than the intra cluster distance. The intra cluster distance range from 0.00 to 18.71. Cluster III possessed highest intra cluster distance (D^2=18.71) followed by cluster II (D^2=16.76) and cluster I (D^2=13.57). The average inter cluster distance was maximum between cluster XII and XIII (D^2=40.20), followed by cluster VII and cluster XII (D^2=37.76), cluster IV and cluster XIII (D^2=37.40) and cluster VIII and cluster XIII (D^2=35.91), cluster I and cluster XII (D^2=33.36) and cluster V and cluster XII (D^2=33.21) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter cluster distance was found to be minimum between cluster V and cluster VI (D^2=7.39).

From the data it can be observed that the average intra cluster distance was maximum in cluster III, cluster II, and cluster I and the average inter cluster distance was maximum between cluster XII and cluster XIII, cluster VII and cluster XII. Widely diverged clusters remain distinct in different environment. Therefore, the genotypes belonging to the distant clusters may be used in hybridization programmed for obtaining a wide spectrum of variation among the segregates. These findings are in confirmity with the finding of Begum *et al*. (2007) and Kanwar *et al*. (2013).

4.7.2 Cluster means

The cluster mean for all the eleven characters are presented in Table 11 and discussed below.

The comparison of cluster means for eleven characters under study marked considerable genetic difference between groups. Highest cluster mean for plant height was recorded by cluster IX (77.17) followed by cluster IV (76.33) and cluster VII (69.33) while cluster XIII (39.50) followed by cluster VIII (48.17) represented the lowest mean for plant height. Highest cluster mean for number of capsules plant^{-1} was recorded cluster XII (186.70) followed by cluster IX (128.17) and cluster IV (125.33) while cluster XI (38.13) followed by cluster VII (49.37) represented the lowest mean for number of capsules plant^{-1}. Highest cluster mean for number of branches plant^{-1} was recorded cluster XIII (15.50) followed by cluster X (8.17) and cluster III (7.64) while cluster VI (4.0) followed by cluster VIII (4.50) represented the lowest mean for number of branches plant^{-1}. For alternaria blight infestation % highest cluster mean was estimated by cluster V (9.50) followed by cluster VI (9.17) and cluster IX (8.87) and minimum cluster mean was estimated for cluster IV (1.40) followed by cluster VIII (1.60). For bud fly infestation % highest cluster mean was estimated by cluster X (43.00) followed by cluster IX (35.17) and cluster XII (25.17) and minimum cluster mean was estimated for cluster IV (4.67) followed by cluster I (16.09). For powdery mildew infestation % highest cluster mean was estimated by cluster XI (40.67) followed by cluster X (30.67) and cluster XIII (26.67) and minimum cluster mean was estimated for cluster VII (9.33) followed by cluster IV (13.33). For days to maturity highest cluster mean was estimated by cluster X and cluster XII (107.00) followed by cluster IX and cluster XI (106.67) and cluster III (106.39) and minimum cluster mean was estimated for cluster VIII (103.33) followed by cluster VI (105.00). For days to 50% flowering highest cluster mean was estimated by cluster XIII (70.33) followed by cluster VII (66.00) and cluster III (65.69) and minimum cluster mean was estimated for cluster VIII (50.00) followed by cluster IV (51.67). For 1000 seed weight highest cluster mean was estimated by cluster IV (10.30) followed by cluster VIII (10.20) and cluster XI (9.80) and minimum cluster mean was estimated for cluster XIII (7.40) followed by cluster XII (8.40). For seed yield plant^{-1} highest cluster mean was estimated by cluster XII (5.83) followed by cluster II (3.21) and cluster X (3.17) and minimum cluster mean was estimated for cluster VII (1.02) followed by cluster XIII (1.13). For flower size highest cluster mean was estimated by cluster VIII (25.88) followed by cluster XI and cluster VI (22.88) and cluster X (21.88) and minimum cluster mean was estimated for cluster III (15.59).

The variance for cluster means for all the characters indicated that the maximum variation was accounted for number of capsules plant^{-1} (1702.43) followed by plant height (114.36),bud fly infestation% (88.72), days to 50% flowering (32.12), powdery mildew infestation% (27.37),seed yield plant^{-1} (19.70), number of branches plant^{-1} (8.41), alternaria infestation% (8.24), flower size (5.72), days to maturity (0.94), 1000 seed weight (0.68).

Hence it is suggested that selection of parents for hybridization and subsequent genetic improvement may be made on the basis of the characters exhibiting maximum variation and expected to be genetically diverse. Thus, from this study it can be reported that parents may be selected for hybridization on the basis of seed yield plant$^{-1,}$ number of capsules plant^{-1},1000 seed weight, bud fly infestation%, alternaria blight infestation%. Since the % alternaria blight infestation was in resistant category, hence this character was not accounted in selection of plants for hybridization.

Table 10: Average intra and inter cluster distance D^2 values in linseed

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**13.57**	20.24	20.26	18.46	20.97	20.78	16.58	16.86	22.90	18.48	17.68	33.36	27.48
II		**16.76**	21.30	23.24	19.06	18.88	21.91	22.32	19.16	19.18	20.90	24.44	27.12
III			**18.71**	22.66	24.51	25.22	22.25	26.96	22.15	21.12	22.99	29.51	25.98
IV				**0.00**	27.13	28.69	25.16	17.80	26.25	23.21	23.77	29.36	37.40
V					**0.00**	7.39	15.71	26.14	12.05	27.29	25.38	33.21	25.31
VI						**0.00**	14.56	24.34	14.38	25.37	23.69	32.94	26.71
VII							**0.00**	23.54	16.97	24.31	22.49	37.76	26.22
VIII								**0.00**	29.44	18.07	18.00	32.33	35.91
IX									**0.00**	26.81	28.50	29.72	27.31
X										**0.00**	11.07	27.69	28.00
XI											**0.00**	33.08	27.61
XII												**0.00**	40.20
XIII													**0.00**

$\overline{D}$ = 10.56

Bold figures are average intra cluster distance

Table 11: Cluster means for eleven characters

Cluster	Plant height (cm)	No. of capsules plant^{-1}	No. of branches plant^{-1}	Alternaria infestation %	Bud fly infestati on%	Powdery mildew infestation %	Days to maturity	1000 seed weight (g)	Days to 50% flowering	Seed yield plant^{-1} (g)	Flower size (mm)
1	57.20	68.08	5.98	3.44	16.09	16.87	105.99	8.67	57.98	1.61	21.00
2	58.34	102.43	7.55	5.97	23.56	18.25	106.05	9.37	59.51	3.21	20.69
3	61.88	117.30	7.64	4.29	21.65	23.00	106.39	8.32	65.69	1.72	15.59
4	76.33	125.33	4.93	1.40	4.67	13.33	106.00	10.30	51.67	1.87	20.88
5	62.83	79.60	6.00	9.50	15.83	14.67	106.00	8.53	55.00	1.85	21.88
6	53.50	69.07	4.00	9.17	22.02	14.67	105.00	8.83	59.00	2.28	22.88
7	69.33	49.37	4.80	6.17	19.23	9.33	106.33	9.40	66.00	1.02	20.38
8	48.17	55.00	4.50	1.60	15.73	10.67	103.33	10.20	50.00	3.08	25.88
9	77.17	128.17	6.57	8.87	35.17	9.33	106.67	9.60	61.00	1.52	19.38
10	52.33	75.67	8.17	2.37	43.00	30.67	107.00	9.40	62.00	3.17	21.88
11	53.83	38.13	7.00	3.17	20.67	40.67	106.67	9.80	61.33	2.90	22.88
12	62.50	186.70	6.93	5.20	25.17	14.67	107.00	8.40	62.00	5.83	19.38
13	39.50	63.83	15.50	7.70	19.00	26.67	106.00	7.40	70.33	1.13	19.88
SD	**10.69**	**41.26**	**2.9**	**2.87**	**9.42**	**5.23**	**0.97**	**0.82**	**5.67**	**4.44**	**2.4**
VAR	**114.36**	**1702.43**	**8.41**	**8.24**	**88.72**	**27.37**	**0.94**	**0.68**	**32.12**	**19.70**	**5.72**

4.9 Selection of potential parents for use in breeding programme

Genetic divergence analysis was carried out to identify the superior parents for hybridization programme based on the mean performance, genetic distance, and clustering pattern. Genotypes grouped in the same cluster as that of the check show very little diversity between them as regards to the aggregates of eleven characters present in study. The practical significance of grouping the germplasm into different clusters and calculating the statistical distance between them and the check varieties are discussed here. In the present study, 178 genotypes including checks were grouped into different clusters. Checks (PKV NL 260, TL 99) were grouped in cluster I. Parents selected should be such that they belong to distant and away from the clusters involving checks. Therefore, the clusters having highest average inter cluster distance between themselves and the checks are expected to yield better. In present study selection of parents based on superiority over best check for seed yield plant^{-1} and number of capsules plant^{-1}, bud fly infestation % for 2021-22 are presented in Table 12.

All possible cluster combinations beyond the mean statistical distance $\overline{D}$ = 10.56 have been arranged in descending order in Table 10. The maximum inter cluster distance ($\overline{D}$ =33.36) was observed between the cluster I and cluster XII. The genotype showing highest mean superiority for seed yield plant^{-1}, number of capsules plant^{-1} are included in cluster XII is EC0041764. Check i.e., PKV NL 260 showing mean superiority in bud fly resistance included in cluster I. Other parents which showed bud fly resistance, number of capsules plant^{-1}, seed yield plant^{-1} are EC0541224, EC0541218-A, EC0006160, EC0001388, EC41765, EC07188299, EC0541225, EC004181, EC0718828, included in clusters III x XII ($\overline{D}$ =29.51), EC041643 in cluster IX x XII ($\overline{D}$ =27.31), EC0541218 in cluster IV x XII ($\overline{D}$ =29.36), EC0041735 in cluster V x XII ($\overline{D}$ =33.21).

Table 12: Selection of genotypes based on inter cluster distances and cluster means

Clusters	Distance between clusters	Selection based on Seed yield plant^{-1} and No. of capsules plant^{-1}
I & XII	33.36	PKV NL 260 X EC0041764
V & XII	33.21	EC0041735 X EC0041764
III & XII	29.51	EC0006160XEC0041764, EC541218-AXEC0041764, EC0541224XEC0041764, EC0001388XEC0041764, EC41765XEC0041764, EC07188229XEC0041764, EC0718828XEC0041764, EC541225XEC0041764, EC004181X EC0041764
IV & XII	29.36	EC0541218XEC0041764
IX & XII	27.31	EC041643XEC0041764

$\overline{D}$ = 10.56

CHAPTER V

SUMMARY AND CONCLUSIONS

The present investigation was undertaken during the *rabi* at AICRP on linseed and mustard farm, College of Agriculture, Nagpur with view to estimate the genetic divergence among 178 genotypes of linseed to identify the desirable and potential parents for hybridization. These 178 genotypes were grown in augmented block design. Data were recorded on five competitive plants for eleven quantitative characters and nine qualitative characters i.e. flower: corolla size (mm), days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1}, number of capsule plant^{-1}, seed yield plant^{-1} (g), 1000 seed weight (g), bud fly infestation%, alternaria blight infestation%, powdery mildew infestation%, flower venation colour, flower aestivation, anther colour, stamen: filament colour, capsule dehiscence, plant growth habit, flower shape, flower colour, seed colour. Mahalanobis D^2 statistics was used in this study for computing genetic divergence for quantitative characters studied.

The analysis of variance to test the significant differences in the mean values using Wilk's criterion revealed that highly significant differences existed among genotypes for all eleven quantitative characters. Analysis of variance was not done for nine qualitative characters. The genotypes EC054202 (47 days) and EC0399084 (49 days), EC0541215 (49.70 days), EC0541218, EC0541223 were the earliest to attained 50% flowering and EC 071885 (73.80 days), EC0718828 (69.50 days) attained late 50% flowering. The genotypes EC0041755 (99.51days), EC00000538, EC0023208, EC0022813-B (101.21days) matured earliest and the genotypes EC0718829 (123.46days), EC0041619 (122.46 days). The maximum plant height was showed by genotypes EC041643 (76.58cm), EC054214 (74.88 cm) and the genotypes EC0001457 (40.38cm), EC0718848 (41.88cm) showed minimum plant height. The genotypes showing maximum number of primary branches plant^{-1} were EC0718848 (14.41), EC0541227 (11.41) whereas the genotypes EC0541213 (3.01), EC0399086 (3.11), EC0041495-1 (3.41) recorded least number of branches plant^{-1}. The highest number of capsule plant^{-1} were recorded by the genotypes EC0041764 (183.03), EC0041598 (174.93) while the least was recorded by EC0001457 (28.03), EC0001432 (31.73). The largest flower size was showed by the genotypes EC0541196 (27.9mm), EC45890 (25.9 mm) , EC41659 (25.9 mm), EC41741(25.9 mm) and shortest flower size was recorded by EC0718829 (10.9 mm).The genotypes EC0041726 (5.85 g), EC0041764 (5.65 g) shown maximum seed yield plant^{-1} while the genotypes EC80490 (0.60 g), EC1588(0.70 g) shown minimum.1000 seed weight was observed to be maximum in genotypes EC0001403 (10.99 g), EC0041753 (6.14 g) while it was minimum in genotypes EC0041753 (6.14 g). The maximum bud fly infestation % was shown by genotypes EC0000543 (43.76%), EC0541208 (40.46%) and minimum was recorded by the genotypes EC0041562 (3.56%), EC0541218 (4.06%). The maximum alternaria blight infestation % was showed by genotypes EC0041735 (9.61%), EC0000541-A (7.76%) and minimum was recorded by EC0541215 (0.26%), EC0006160 (0.26%). The genotypes EC0718845 (43.45%), EC0023208 (39.345%) showed maximum powdery mildew infestation % while the genotypes EC0000541-A (6.05%), EC0718824 (8.05%) showed minimum powdery mildew infestation %.

The 178 genotypes were grouped into thirteen clusters considering eleven characters by Tocher's method. The cluster I was largest comprising of 130 genotypes, followed by cluster II comprising of 27 genotypes, cluster III comprising of 11 genotypes, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X, cluster XI, cluster XII, cluster XIII, each of comprising single genotypes. The checks PKV NL 260, TL 99 grouped into cluster I along with 128 genotypes. The maximum inter cluster distance was recorded between cluster XII and XIII (D^2=40.20) whereas minimum inter cluster distance was found in between cluster V and cluster VI (D^2=7.39) The highest intra cluster distance was observed for cluster III (D^2=18.71). It can be observed that the vector I accounted maximum canonical variation (31.53%) for characters number of capsule plant^{-1}, days to 50% flowering, seed yield plant^{-1},1000 seed weight, alternaria blight infestation %, bud fly infestation%, plant height, number of branches plant^{-1}, powdery mildew infestation%, days to 50% flowering. Overall study for cluster mean considering all the eleven characters indicated that cluster IX and cluster X possessed the highest cluster mean for plant height, days to 50% flowering, days to maturity, alternaria blight infestation%, bud fly infestation%, powdery mildew infestation%, and cluster XII for seed yield plant^{-1}. The canonical analysis and cluster means studied together revealed the importance of number of capsules plant^{-1}, seed yield plant^{-1},1000 seed weight, bud fly infestation% of as important contributors towards the total divergence. Hence, these traits form the criteria for the selection of parents for hybridization programme. It was noticed that the parents EC0041764, EC0541224, EC0541218-A, EC0006160, EC0001388, EC41765, EC07188299, EC0541225, EC004181, EC0718828, were significantly superior over the checks for number of capsules plant^{-1}, seed yield plant^{-1} and % bud fly infestation. It will be advisable to utilize all these parents in hybridization (as they have the maximum inter cluster distance with those clusters involving checks and also significantly superior mean performance for number of capsules plant^{-1}, seed yield plant^{-1} and lesser % bud fly infestation).

CHAPTER VI

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