

**“Generation Mean Analysis for Yield
and Quality Components in Greengram
[*Vigna radiata* (L.) Wilczek]”**

THESIS

Submitted to

Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

**In partial fulfilment of the requirements for
the Degree of**

DOCTOR OF PHILOSOPHY

In

**AGRICULTURE
(GENETICS AND PLANT BREEDING)**

By

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2021

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All the assistance and help received during the course of the investigation has been acknowledged by him.

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(Tasphiya Elahi)

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LIST OF SYMBOLS

Sr. No.	Abbreviations	Stand for
1	%	- Percentage
2	$\sqrt{\quad}$	- Square root
3	Σ	- Summation
4	't' test	- Student 't' test
5	Cm	- Centimeter
6	et al.	- And co-workers
7	G	- Gram
8	Ha	- Hectare
9	SE	- Standard error
10	viz.	- Namely
11	ANOVA	- Analysis of Variance
12	AOAC	- Association of Official Agricultural Chemists
13	B ₁	- Backcross generation of parent one
14	B ₂	- Backcross generation of parent two
15	CD	- Critical Difference
16	Cov. (F.S)	- Covariance of Full Sibs
17	Cov. (H.S)	- Covariance of Half Sibs
18	CV	- Co-efficient of Variation
19	F ₁	- First filial generation
20	F ₂	- Second filial generation
21	$h^2_{(b)}$	- Heritability in broad sense
22	K	- Selection differential
23	L x T	- Line x Tester
24	MP	- Mid parent
25	MS	- Mean Sum of Squares
26	No.	- Number

Sr. No.	Abbreviations	Stand for
27	P ₁	- Parent one/ female parent
28	P ₂	- Parent two/ male parent
29	<i>Per se</i>	- As such with mean
30	PCV	- Phenotypic coefficient of variation
31	GCV	- Genotypic coefficient of variation
32	±	- Plus or minus
33	>	- More than
34	<	- Less than
35	-	- Hyphen
36	()	- Parenthesis
37	:	- Colon
38	;	- Semicolon
39	,	- Coma
40	/	- Oblique
41	.	- Full stop
42	Fig.	- Figure
43	i.e.	- That is
44	SD	- Standard Deviation
45	mha	- Million hectare
46	ml	- Milliliter
47	Mt	- Million ton
48	<i>gca</i>	- General Combining Ability
49	<i>sca</i>	- Specific Combining Ability
50	r _p	- Phenotypic correlation coefficient

Chapter – I

INTRODUCTION

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is a short duration legume crop which belongs to the family leguminosae and sub family Papilionaceae. The word legume is derived from the word Terge' which means 'to gather' because the pods have to be gathered or picked by hands, as distinct from reaping the cereal crops. This crop is also known as moong, green gram, chickasaw pea and oregon pea. Mungbean is self-pollinating diploid legume with the chromosome number $2n=2x=22$ Karpechenko (1925) with the genome size of 494 to 579 Mb. Mungbean probably originated in India De Candole (1886) or the Indo-Burmese region Vavilov (1951). The primary gene center of diversity for mungbean was suggested to be the central Asian region Vavilov (1951) with India as the gene center and probable center of domestication Smartt (1985). Mungbean has the ability to fix atmospheric nitrogen in symbiotic association with Rhizobium bacteria, which enables it to meet its own nitrogen requirement and also benefit the succeeding crops. This crop has also been reported to smother weed flora appreciably (20–45%) when intercropped with tall cereals and consequently, reduce the cost incurred on weed control. On account of short duration and photo-thermo insensitivity, this crop is considered as excellent crop for crop intensification and diversification.

Nutritional Composition

Green gram is considered as rich source of protein with higher digestibility and can serve to convalescing babies or malnutrition people. The important nutrients are not distributed uniformly in major components such as seed coat, cotyledon and embryo of the mungbean seed. The protein and lipids are found to be high in embryo, whereas the starch and crude fiber are concentrated in cotyledons and seed coats respectively. The average moisture content present in the whole mungbean seed is 10.6 g/100 g of whole green gram with high protein (22.9 g), fat (1.2 g), total carbohydrate (61.8 g), crude fiber (4.4 g) and ash (3.5 g) per 100 g of sample Adsule et al. (1986). The presence of anti nutritional factors such as tannins (366.6 mg/100 mg), phytic acid (441.5 mg/100 g), hemagglutinin, trypsin inhibitors, proteinase inhibitors and polyphenols (462.5 mg/100 g) were reported in

mungbean, which affects the digestion and bioavailability of full nutrition Mubarak (2005).

India is the largest producer and consumer of pulses in the world contributing around 25-28 per cent of the total global production. In India, total production of pulses during 2020-21 was 25.57 million tonnes and Madhya Pradesh produced 4.36 million tonnes (Anonymous 2021). As per the 3rd DES Advance estimates of 2020, total green gram production in India during 2019-20 was 2.34 million tons.

Botany

Green gram belongs to family leguminosae and sub family Papilionaceae. Its chromosome number is $2n=2x=22$. Over 2000 different types have been reported in this crop. There are three subgroups of *Vigna radiata*: one is cultivated (*Vigna radiata* subsp. *radiata*), and two are wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). Green gram is rapidly growing erect or sub-erect, annual, usually 30 to 90 cm in height and showing considerable variation in form and adaptation. It is frequently branched and only few cultivars are having spreading habit. Sometimes the tips of the branches are vining. The stems are usually green but sometimes found splashed with purple. The branches emerge out from the base and are angular. The leaves are trifoliate with large ovate, entirely or rarely lobed, membranous leaflets 5 to 10 cm long with scattered hairs on both sides and light to dark green in color.

Floral biology

Flowers are hermaphrodite, zygomorphic, either lighter yellowish olive/olive yellow and are in an axillary or terminal raceme, peduncle up to 13 cm in length with clusters of 10 to 20 flowers. Corolla is yellow in color and papilionaceous, sometimes curved and 5-10 cm long. Small flowers are borne in capitate clusters on the end of long hairy peduncles. Petals are five in numbers and having three kinds of petals: 1 standard, 2 wings and 2 keels. Male reproductive part stamen has got two parts: anther and filament. Female reproductive part made up of stigma, style and ovary. Gynoecium is monocarpellary with a superior unilocular ovary. The stigma is hairy and placentation is marginal. Greengram is a self pollinated crop, sometimes cleistogamy is prevalent with a cross pollination of 0.5-3%.

Seed Morphology

The seeds enclosed within the pods are small and nearly globular. The three major components of dicotyledonous green gram seed are seed coat, cotyledon, and embryo accounting 12.1%, 85.6%, and 2.3% of the whole seed, respectively. Seed coat or testa is an outer covering which protects the embryo. The embryonic shoot above the cotyledon is epicotyl, and the embryonic root below the cotyledon is hypocotyl. Micropyle is a small pore on the seed that allows water absorption, and the hilum is a mark left on the seed coat by the stalk which attached the ovule to the ovary wall before it became a seed Sefa-Dedeh and Stanley (1979).

Research Priorities

The mungbean plant passes through nine distinct phenological stages of growth. Any kind of stress at these phases may result in low yield. However, generally the yield of pulses is comparatively less than most of the cereals and millets as these were the neglected crops considering their genetic improvement in term of seed yield and attributing traits. Green gram suffered a little bit more in this regard due to various associated features of the crop including susceptibility to insect, pest and diseases (fungal, bacterial and viral). Salinity and water limitations also pulled the crop towards survival mechanism instead of promoting genes for higher yield Sahoo and Jaiwal (2008). Water stress during floral initiation, boost the rate of floral abscission, if prevailed for longer time may decrease the seed yield as well. Water stress just prior to initiation of reproductive phases, prominently increases the abortion rate of earlier developed flowers. Non stress pistils may give satisfactory pod yield compared to water stressed pistils, irrespective of the fact if pollinated with stress developed pollens or otherwise. The same highlighted that female portion of flower is sensitive to drought conditions and ultimately effect the pod setting percentage Kokubun *et al* (2001). A little attention was paid on the genetic improvement until the recent past by developing resistance against biotic stresses. A major hurdle in attaining higher yield in mungbean was scarcity of adequate genetic variation, lack of ideal ideotypes for different cropping schemes.

The genetic variation which was already available in nature in the form of germplasm which could respond to inputs (fertilizer, irrigation, organic matters etc.) has vanished in the form of genetic erosion. The main reason for this was consecutive cultivation of the crop under rain fed conditions on comparatively less productive soils and subsequently selection of genotypes favoring that particular environment. That selection pressure actually eliminated the genotypes which were input reactive. Selection favoring the survival of crop under adverse soil and environmental conditions resulted in elimination of most productive genes. This created a narrow genetic base, resulted in low productivity of the crop and lack of suitable plant types for different cropping situations.

The pedigree of the most popular mungbean lines grown worldwide are based on only few dozen parental sources Yang (1996). Loss of variation in crops may be linked with modernization of agriculture. Two stages leading to genetic erosion are recognized: the initial replacement of landraces by modern cultivars and further trends in diversity as a consequence of modern breeding practices. It may occur at three levels of integration: crop, variety and allele Rogers (2004) and is often magnified or accelerated by human activities. This trend in turn gave birth to number of negative linked attributes including low harvest index due to excessive leafiness or vegetative growth, photo and thermo period sensitivity, low pod setting during first flower flush, less concentration of pod cluster at the top, pod shattering, slow initial growth, limited and short pod size with few seeds. These are some sort of genotype $\times$ environmental interaction. Sensitive/delicate nature of the flower, a plant associated attribute damaged the crop significantly as a result the hybridization work was not initiated as earlier in this crop as it was commenced in cereals and other economically vibrant crops, which restricted the exploitation of natural variation already available in the crop. Flower shedding is a big obstacle in the way of attaining higher seed yield in mungbean Kumari and Varma (1983) may be influenced by high temperature, precipitation and desiccating winds Sinha (1977), Rainey and Griffiths (2005). Lack of proper attention of the breeders, obviously due to less economic importance of the crop and paucity of developed commercial varieties thrown this crop in the darks.

To achieve the goals regarding improvement for the genetic architecture of the mungbean crop, some of the important points might be considered for the development of high yielding and disease/ insect resistant varieties by studying the nature and magnitude of genetic variability present in the available stocks for different traits. Morphological characterization is first step to start the journey of the genetic improvement programme. Characterization of germplasm helps to form trait specific groups and gives the idea about those traits, which may be used to distinguish the genotypes from each other. Lee *et al.* (2004) and Piyada *et al.* (2010) also gave the emphasis on morphological characterization to assess the variability and classify the crop germplasm. Some of the agro-morphological traits may be used as morphological marker in crop improvement. Morphological characterization also provides some of the important ideas to identify the unique trait discovery for the utilization and development of new ideotypes required in the modern cultivation technology and also provides information to improve genetic gain of the crops.

The adequate information on extent of variability parameters may be helpful in the development of promising varieties through the identification of yield determinants. Genetic parameters for yield components worked out on the nature of variability, heritability and character associations by different researchers are inconsistent and highly variable. Therefore, knowledge on the precise nature of genetic variability in the germplasm of any crop species is considered to be critical for making further genetic improvement in yield as well as other economically important traits. Estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection.

Direct selection may not provide accurate information on all the yield and yield contributing traits and their association. The indirect selection is more effective than the direct selection. Association analysis helps to determine the contribution of yield component traits towards seed yield. So correlation coefficient helps to validate/ confer the importance of the yield component traits. Therefore, the knowledge of correlation between yield and yield component traits is essential. Under the complex situation, correlation

coefficient doesn't give the clear cut information. For such situation, path analysis gives the information on establishment of cause-effect relationship.

To breed a genotype with high yielding potential, information on the genetic mechanism controlling various traits in the material being handled, is a prerequisite. The estimates of combining ability along with *per se* performance of genotypes in a plant improvement programme have a direct bearing upon the choice of breeding methodology to be followed. The Line $\times$ Tester mating design suggested by Kempthorne (1957) is the modified form of top cross is an appropriate method to assess the combining ability of parents and crosses for different quantitative characters as well as to study the extent of heterosis and nature of gene actions for yield and yield contributing characters. The information generated in this process on the magnitude of heterosis provides the basis for genetic diversity and guide the choice of desirable parents to exploit hybrid vigor and/or for building better gene pool. However, it does not provide information on the nature of epistatic interactions which are an integral component of genetic architecture of the population.

The detection and estimation of epistasis in the inheritance of various quantitative traits are utmost important to understand the genetic cause of heterosis with greater reliability and to frame an efficient breeding plan leading to rapid improvement. Generation mean analysis Hayman (1958) has been considered to be one of the best methods for estimating the different components of genetic variance and testing the presence or absence of epistasis using the scaling test, which measures epistasis accurately whether it is complimentary (Additive $\times$ Additive) or duplicate (Additive $\times$ Dominance) and (Dominance $\times$ Dominance) at the digenic level. In this method a set of segregating and non segregating generations belonging to a common ancestry is subjected to analysis simultaneously for extracting a comprehensive picture of gene action controlling the trait. Whereas, such vital information which helps in formulation of an effective and sound breeding programme for improvement of various metrical traits in green gram is scanty, very few attempts were made to do research in this direction, since it involves more number of generations and meticulous planning of experiment.

Keeping the above points in consideration, the present investigation entitled “**Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]**” was carried out to understand the genetic behavior and advancement with the following objectives:

- Morphological characterization of parental lines and their progenies.
- Estimation of parameter of genetic variability, assessment of phenotypic and genotypic correlation and estimation of direct and indirect effects.
- Assessment of heterosis over better and mid parent values.
- To estimate the general combining ability (*gca*) effects of parents and specific combining ability (*sca*) of crosses for seed yield and its attributing characters.
- To elucidate the nature and magnitude of gene action for seed yield and its attributing characters.

Chapter - II

REVIEW OF LITERATURE

REVIEW OF LITERATURE

The present investigation entitled “Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]” was carried out at at Seed Breeding Farm, Department of Plant Breeding & Genetics, College of Agriculture, JNKVV, Jabalpur, during summer 2020, kharif 2020 & summer 2021. Literature in respect of the work aimed for research prospects in this research programme has been reviewed and presented in this chapter.

The available relevant literature related to present investigation has been furnished under the following heads:

- 2.1 Morphological character study
- 2.2 Genetic variability
- 2.3 Heritability and genetic advance
- 2.4 Correlation coefficient analysis
- 2.5 Path coefficient analysis
- 2.6 Heterosis
- 2.7 Combining ability analysis
- 2.8 Generation mean analysis

2.1 Morphological character study

Germplasm provides the base material for crop improvement. A need for germplasm collection, evaluation and cataloguing is of utmost importance to have a dynamic crop improvement programme. Character study of cultivars is based on different agro-morphological traits, which is the most important step in the genetic improvement of crop plants.

Chhabra et al. (1990) reported the inheritance of seed colour on sap green seed coats brownish green, raw sienna, densely black spotted, black and greenish yellow seed coats color. In the F_2 , no more than 20 color classes were observed. Segregation in the F_3 and backcross generations indicated that at least 5 major genes were involved in seed coat color inheritance. Sap green appeared to be dominant over raw sienna. Segregation ratios further indicated the presence of non-allelic gene interactions (epistasis).

Metz et al. (1992) studied the inheritance of seedling color, in relation to the genetic control of flower color. They found that purple seedling color is likely to be controlled by a single gene and that the trait is dominant over green seedling color. White flowering prohibited the expression of the purple seedling color, and is therefore thought to be epistatic. This character can be used to estimate rate of out crossing in breeding programmes, as well as contribute to our knowledge of the biosynthesis of plant pigments and secondary metabolites such as tannins.

Khattak et al. (1999) observed the mode of inheritance of SC, GH and their joint segregation pattern in mungbean. The results showed monogenic inheritance for seed coat color. Black, black spotted and dull green seed coat colors were dominant over green, non-spotted (green) and shiny green color, respectively. The inheritance of twining plant growth habit was found to be dominant over non-twining growth habit. The joint segregation studies of mungbean seed coat color and plant growth habit in the F_2 and backcross generations revealed that these two traits are not linked. The absence of linkage between these two traits should make it possible to combine non-twining plant type and shiny green seed coat color in the F_2 and subsequent generations.

Khattak et al. (2000) reported from their findings that the mode of inheritance of hypocotyls colour and pubescence and were found dominancy of purple pigment over green hypocotyls and pubescence over non-pubescent. They suggested the monogenic inheritance for these traits. They also suggested that these traits are segregated independently.

Mukherjee and Pradhan (2002) studied the inheritance of anthocyanin pigmentation in hypocotyls. The hypocotyls of F_1 seedlings from crosses between plants with purple and purple-spotted hypocotyl were purple, indicating that the purple hypocotyl is monogenic and dominant over the purple-spotted hypocotyl. F_1 seedlings from crosses between plants with purple-spotted and green hypocotyls had purple-spotted hypocotyls, indicating that the purple-spotted hypocotyl is monogenetic and completely dominant over the green hypocotyl. The F_1 seedlings derived from crosses between plants with purple and green hypocotyls had purple hypocotyls, indicating that

the anthocyanin in hypocotyls of mungbean is controlled by two supplementary genes, designated as Shsh and Phph with recessive epistatic interaction.

Lambrides et al. (2004) conducted the genetic segregation experiments for understanding the inheritance of traits. They suggested that segregation distortion occurred after each generation of self-pollination from F_1 to F_7 , resulting in F_7 phenotypic frequencies of 151:56 instead of the expected 103.5:103.5. This study highlights the value of molecular markers for understanding the inheritance of a simply inherited trait influenced by segregation distortion.

Aliyu et al. (2007) observed the heritability and gene effects in cowpea and reported that very high heritability of pubescence traits. They also reported the involvement of one and two genes in governing the pubescence.

Mohammed et al. (2010) studied the inheritance of hairiness and found dominance of pubescence to non pubescent ones. They also noted that the dominant and epistatic gene action in governing pubescence traits in cowpea.

Ahmed and Belwal (2019) recorded data on various morphological and agronomic characters including hypocotyl pigmentation, days to 50 percent flowering, plant height, number of leaves, number of branches, number of clusters, number of pods per cluster, total number of pods per plant, pod length, pod diameter, pod wall thickness, seed length, seed diameter, 100-seed weight, seed density and seed yield. Analysis of variance revealed significant differences among all the genotypes for all the characters studied. Wide range of variation had been observed for all the characters except hypocotyl pigmentation.

Patel et al. (2019) reported that color of petal was yellow in two genotypes (EC 251810 and GM 06-08), while it was light yellow in 42 genotypes. Petiole color was observed green (seven genotypes), green with purple (14 genotypes) and purple (23 genotypes). Based on plant habit, genotypes were grouped as indeterminate (seven genotypes) and determinate (37 genotypes). Based on plant growth habit, genotypes were grouped as erect (seven genotypes), semi-erect (21 genotypes) and

spreading type (16 genotypes). Among 44 genotypes, plant height was short in one genotype (K 851), while it was long in 12 genotypes and medium in the remaining 31 genotypes. Pubescence was present in all the genotypes evaluated. Stem color was noted green in 17 genotypes and green with purple in 27 genotypes. Leaflet lobes were present in two genotypes (GJM 1103 and GM 06-08), whereas, it was absent in 42 genotypes. Leaf color was dark green in 29 genotypes and green in 15 genotypes. Based on leaf vein color, the genotypes were grouped as green (five genotypes) and purple (39 genotypes). Shape of leaf was ovate in 41 genotypes, whereas it was deltoid in three genotypes (GJM 1020, GJM 1022 and GM 1924). Leaf size was large in three genotypes (EC 496841, GJM 1026 and OUM 11-5), small in seven genotypes and medium in 34 genotypes. All the genotypes evaluated were having green premature pod color with pubescence on pods. Pod position was indeterminate in only one genotype (GM 1924), while it was observed above canopy in all the remaining 43 genotypes. Based on the pod color of mature pods, genotypes were grouped into two groups as black (18 genotypes) and brown (26 genotypes) color pods. Pod length of mature pods was long in three genotypes (GJM 1025, Kopergaon and TARM 18), short in 18 genotypes and medium in 23 genotypes. All the 44 mungbean genotypes evaluated were of green color seeds. Based on seed shape, genotypes were grouped into drum (42 genotypes) and oval shape (two genotypes GJM 1011 and IC 24789). Seed size was medium in 32 genotypes and large in 12 genotypes.

Sabatina et al. (2019) observed that 14 characters out of 24 characters of DUS descriptors differed significantly indicating a large and exploitable amount of genetic variability for the individual elite improved line profile development for identification and protection. The elite lines are similar for the important plant traits like semi erect and determinate growth habit but the development of erect types is the need of hour and indicates the incorporation of new germplasm for the improvement of this trait in the present material. The DUS descriptor data generated with unique profiles of the elite improved lines can be used for the registration with PPV & FRA and seed purity testing.

2.2 Genetic variability

Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt environmental changes. Hence, variability is the most key aspect of any research for a breeder, amount of which determines the extent of sources of selection. Various parameters of genetic variability are mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability and genetic advance as percentage of mean.

Rahim et al. (2010) noted that the coefficient of variation indicated significant differences among the genotypes for measured characters. The phenotypic variance (σ^2_p) and phenotypic coefficient of variation (CV_p) were slightly higher than the genotypic variance (σ^2_g) or genotypic coefficient of variation (CV_g) for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters.

Tabasum et al. (2010) noted that Primary and secondary branches, pods per cluster and pod length showed lesser variability while clusters per plant, 100 seed weight and harvest index exhibited intermediate range of variability. Sufficient genetic variability was observed for plant height, pods per plant, total plant weight and seed yield. Moderate to high heritability estimates were found for all traits.

Kumar et al. (2013) observed slightly higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) for all the characters, so it is evident that in expression of the characters mainly governed by the genotypes itself along with meager effect of environment.

Alom et al. (2014) observed significant variation among the studied 54 mungbean genotypes for all characters. Different genotypes were found superior for different characters. Among the genotypes, ACC-12810002 for plant height (71.80 cm), TPK-2558-97 for days to 50% flowering (48.67 days as minimum), BC-6960-88 and VO-1558 (B-G) for days to pod maturity

(89.00 days as minimum), VC-6149 (B-12) for pod length (17.30 cm), ACC-12810006 for pods plant⁻¹ (31.73), ACC-12890073 for seeds pod⁻¹ (17.60), VC-6960-88 for 100- seed weight (5.63 g) and GK-40 for seed yield (1846.00 kg ha⁻¹) were found to be the superior genotypes.

Degefa et al. (2014) observed that number of primary branches, pods per plant, seeds per plant and harvest index had high genotypic and phenotypic coefficients of variation at both locations. For all characters, phenotypic coefficient of variation was higher than genotypic coefficient of variation indicating that there was environmental influence on these traits.

Sarkar et al. (2014) observed slightly higher phenotypic coefficient of variation than the genotypic coefficient of variation for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters.

Tiwari et al. (2014) revealed highly significant differences for all the characters. The higher genotypic and phenotypic coefficient of variation were recorded for days to flowering, plant height (cm), days to maturity, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm) biological yield per plant (cm), and harvest index.

Khaimichho et al. (2015) studied that analysis of variance revealed highly significant varietal differences for all the characters studied hence there is enough scope for selection among the varieties.

Muralidhara et al. (2015) noted highest GCV and PCV for all the traits studied. Phenotypic coefficient of variation was slightly higher in magnitude than the genotypic coefficient of variation.

Anand et al. (2016) studied high genotypic coefficient of variation exhibited by plant height followed by number of pods per plant and seed yield per plant. The low genotypic coefficient of variation was given by days to 50% flowering.

Pinchhyo et al. (2016) reported significant differences among 30 genotypes for 12 quantitative characters in analysis of variance. Maximum genotypic coefficient and phenotypic coefficient of variation was recorded for seed yield per plant, primary branches per plant and seed index.

Pratibha et al. (2016) observed highly significant difference for all characters, under study among the genotypes, indicating the presence of sufficient amount of variability in the genotypes. Thus, there is ample scope for selection of different quantitative characters for crop improvement. The highest GCV and PCV were observed for primary branches per plant and biological yield per plant respectively

Jagdhane et al. (2017) noted that the genotypes differed significantly for all characters. Higher GCV and PCV was observed for cluster per plant followed by number of primary branches per plant, number of pods per plant, plant height, harvest index, seed yield per plant, seed per pod.

Khan et al. (2017) observed significant differences among mungbean genotypes for all the yield traits which showed that there is sufficient variability to have an effective selection.

Perera et al. (2017) reported that analysis of variance indicated highly significant ($p < 0.01$) differences for all the traits except for 1000 seed weight. The phenotypic and genotypic coefficient of variation was the highest for grain yield per plant, followed by pod length.

Shiv et al. (2017) observed low to moderate GCV and PCV values for days to 50 % flowering, days to maturity, plant height, primary branches per plant, seeds per pod and 100 seed weight indicated limited scope for improvement of these traits. While, GCV and PCV estimates were moderate to high for pods per plant, seed yield per plant, clusters per plant, straw yield per plant and harvest index suggesting that there is greater scope for improvement of these characters.

Abbas et al. (2018) reported high genotypic (GCV) and phenotypic (PCV) coefficients of yield variability for biological, harvest index and seed yield.

Azam et al. (2018) studied that all the traits showed highly significant difference among genotypes except seeds per pod. Pods per plant, plant height and 100 seed weight showed high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV).

Ghimire et al. (2018) studied that high genotypic coefficient of variation was exhibited by secondary branches and seed yield per plant. The low genotypic coefficient of variation was given by pod length, number of grains per pod and days to 50% flowering.

Kumar et al. (2019) noted highly significant differences among the genotypes for all the traits studied. Thirty six mungbean genotypes (collected from different parts of India) including four checks were analyzed for seed yield and its components by estimating genetic variability. Analysis of variance showed highly significant differences among the genotypes for all the traits under study. In general phenotypic coefficients of variation were observed to be greater than their corresponding genotypic coefficients of variation. Hence these traits could be used by breeders for the improvement of seed yield resulting in the unfolding of high yielding varieties of mungbean.

Mehandi et al. (2019) observed that the analysis of variance revealed statistically significant differences ($p < 0.05$) indicating the existence of genetic variability among the 48 genotypes for all the traits studied. The genotypic coefficient of variations was the highest for characters viz., harvest index, number of effective branches/plant. The heritability was observed highest for seed yield per plant, days to maturity and days to 50% flowering.

Soni et al. (2020) observed that GCV and PCV for pods per plant, number of cluster per plant, plant height and seed yield per plot showed very little differences indicating the greater role of genetic factors in the expression of these traits and ample scope for improvement.

Sabatina et al. (2021) noted significant differences for yield and yield traits indicating the existence of sufficient variability for their exploitation. The mean range of the traits was huge for most of the traits indicating use of simple selection while exploiting genetic variability of the material. The phenotypic coefficient of variation was higher than the genotypic coefficient variation indicating the influence of environment on the expression of the traits.

Singh et al. (2021) reported high phenotypic and genotypic coefficient of variation (>20%) for number of branches per plant, non-reducing sugar, grain yield per plant, harvest index and 100-seeds weight under late sown condition. The characters which exhibited moderate estimates (10-20%) of PCV and GCV were recorded for pod per plant, reducing sugar, seed per pods, TSS, plant height, pod length, biological yield per plant under late sown condition late sown condition.

2.3 Heritability and Genetic advance

Heritability is the proportion of phenotypic variation in a population that is attributable to genetic variation among individuals. Phenotypic variation among individuals may be due to genetic and/or environmental factors. Heritability analysis estimates the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. The estimate of heritability helps the plant breeder in selection of elite genotypes from diverse population and as a good index of the transmission of characters from parents to their offspring.

Genetic advance refers to the improvement in the genetic value of the selected plant over the base population and is the measure of genetic gain under selection. Heritability estimates along with genetic advance is normally more helpful in predicting the gain under selection from heritability estimates alone.

Rahim et al. (2010) observed high heritability (broad) along with high genetic advance in percent of mean for plant height, number of pods per plant, number of seeds per pod, 1000-grain weight and grain yield per plant indicating these characters would be best for phenotypic selection.

Tabasum et al. (2010) reported that high heritability was manifested by number of secondary branches, plant height, clusters per plant, pods per plant, pods per cluster, pod length, 100 seed weight seed yield and harvest index. Previously, high heritability for these traits has also been reported. These traits were expected to remain stable under varied environmental conditions, as environment is less influential on highly heritable traits and could easily be improved by applying selection pressure. In present study, lowest genetic

advance was observed (0.085) for primary branches followed by pod length (0.336) . High heritability and high genetic advance were indicating that these traits were controlled by additive genes and can easily be transferred to succeeding generations.

Kumar et al. (2013) observed that high heritability estimates coupled with high genetic advance was observed for 100 seed weight, indicating the preponderance of additive and fixable genetic variance; suggesting that this trait may be subjected to any selection scheme to develop the stable genotypes and selection pressure may be exercised in early generation. High heritability coupled with moderate genetic advance for number of pods per plant as well as high heritability coupled with low genetic advance indicating the presence of additive as well as non-additive gene action.

Alom et al. (2014) studied that including seed yield, all the characters, except seeds pod–1 exhibited high heritability accompanied by medium to high genetic advance as percent of mean. These characters also showed medium to high GCV and PCV. However seeds pod–1 showed moderate heritability and genetic advance as present of mean.

Degefa et al. (2014) observed that the combined results for heritability showed high estimates of heritability and genetic advance score for seeds per plant and seed yield indicating that these characters were under the control of additive genetic effects. High genetic advance expected as percent of mean coupled with high heritability was observed for number of primary branches at Hirna, number of seeds per plant at Rare and number of secondary branches, pods per plant and 100seed weight for combined analysis.

Sarkar et al. (2014) noted high heritability along with high genetic advance as percent of mean for the trait plant height, pods/plant and seed yield/plant indicating that these characters would be amenable for phenotypic selection.

Tiwari et al. (2014) observed high heritability for days to maturity, number of pods per cluster, harvest index, number of pods per plant, seed yield per plant, plant height, 100-seed weight, biological yield per plant,

number of seeds per pod and pod length and the moderate heritability was recorded for days to flowering. The estimates of high heritability coupled with high genetic advance were found for seed yield per plant, number of pods per plant, number of clusters per plant, biological yield per plant, number of pods per cluster and harvest index. The estimates of high heritability coupled with moderate genetic advance were recorded for 100-seed weight, plant height and pod length and low for days to maturity, number of seeds per pod and days to flowering

Khaimichho et al. (2015) observed high heritability accompanied by high genetic advance for seed yield plant-1 followed by 100 seed weight, number of branches plant -1 and number of pods plant -1 which indicated the importance of additive gene effects in controlling the expression of these characters. Simple breeding strategies may be adopted to obtain desirable changes and further improvement in these characters.

Muralidhara et al. (2015) studied that on the basis of genetic variability study all the growth and yield traits exhibited high heritability estimates (broad sense) coupled with high genetic advance, indicating the preponderance of additive gene action. Hence, direct selection may be exercised for improvement of these traits.

Anand et al. (2016) noted that high heritability was shown by seed yield per plant (97.17) followed and by plant height (83.24) and number of pods (80). These characters also showed high genetic advance and genotypic coefficient of variation. Moderate heritability was observed in days to 50% flowering number of clusters.

Pinchhyo et al. (2016) reported maximum heritability for biological yield, while maximum genetic advance (as percent of mean) was recorded for seed yield.

Pratibha et al. (2016) noted that higher heritability showed additive effects and more gain of selection in next generations when coupled with high genetic advance. High estimates of genetic advance as percent of mean were observed for plant height and biological yield per plant.

Jagdhane et al. (2017) observed high heritability coupled with high expected genetic advance in biological yield (99.00%; 7.59%) indicating the impact of additive gene expression.

Perera et al. (2017) noted high broad sense heritability (> 60 %) along with high genetic advance for total yield per plant, pod length, number of seeds per pod and plant height, indicating that these characteristics would be best for phenotypic selection.

Shiv et al. (2017) observed high heritability estimates coupled with high genetic advance for pods per plant, clusters per plant, seed yield per plant, straw yield per plant and harvest index coupled with high genetic advance as per cent mean suggested the importance of additive genetic variance for these traits. Hence, priority should be given to these traits in selection to obtain better gains.

Abbas et al. (2018) studied high heritability for all the traits except days to maturity and clusters per plant. Biological yield, harvest index and seed yield depicted high estimates of heritability coupled with greater genetic advance indicating the involvement of additive type of genes, and selection based on these traits may help to improve the germplasm.

Azamet al. (2018) noted high broad sense heritability coupled with moderate genetic advance as percent of mean for 100 seed weight, days to flower and pods per plant suggesting preponderance of additive gene action for these characters and selection of such traits might be effective for the improvement of grain yield.

Ghimire et al. (2018) studied that high genetic advance (as percent mean) were observed for seed yield per plant (50.82). Lowest heritability was exhibited by number primary branches per plant. Similarly, the genetic advance was highest for grain weight per plant and was lowest for grain per pod.

Kumar et al. (2019) noted high heritability coupled with high genetic advance as percent of mean by the characters like harvest index followed by seed yield per plant, number of pods per plant, number of clusters per plant,

biological yield per plant, number of primary branches, number of secondary branches, number of pods per cluster, plant height and 100 seed weight which depicts that these characters are governed by additive gene action and could go for selection program without progeny testing. High heritability estimates were recorded for the traits viz., 100-seed weight, followed by grain yield per plant, biological yield per plant, number of pods per plant, number of filled pods per plant, number of secondary branches per plant and plant height.

Mehandi et al. (2019) observed that high heritability and high genetic advance as percent of mean may be attributed due to additive gene action. Therefore, direct selection for characters viz., number of effective branches/plant, number of pods/cluster number of seeds/pod would be effective and therefore, considered to be of prime importance in formulating the selection programme.

Soni et al. (2020) observed that the estimates of heritability in broad sense were found higher in seeds per pod, Seed yield per plot and branches per plant. The genotypes showed wide and highly significant variation for all the traits. High heritability along with high genetic advance as percent of mean was observed for seed yield per plot, days to maturity, plant stand and plant height preponderance of additive gene action.

Singh et al. (2021) observed high estimates of heritability in broad sense for the all characters and days to maturity moderate in late sown condition. High heritability coupled with high estimate of genetic advance in per cent of mean was not found in late sown condition.

2.4 Correlation coefficient analysis

Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. It measures the mutual relationship between various plant characters and determines the component characters on which selection can be used for genetic improvement in yield

The concept of correlation was given by Fisher (1918) and Wright (1921), which helps in determining the nature and degree of relationship

between any two measurable characters. The available literature on correlation coefficient analysis is furnished hereunder.

Kumar et al. (2010) studied that the correlation coefficient between seed yield per plant and other quantitative attributing to yield showed that seed yield per plant was significantly and positively associated with pods per plant and harvest index at both genotypic and phenotypic levels. A negative non significant correlation was found between plant height and days to maturity at both genotypic and phenotypic levels. It indicates that an association of two characters is not only due to genes but also due to their influence of the environment.

Rahim et al. (2010) studied that grain yield was positively correlated with number of pods per plant, panicle length and number of seeds per pod. Positive correlation was found only between days to 50% flowering and days to 80% maturity. Days to 50% flowering are positively associated with plant height and number of seeds per pod and negatively correlated with 1000-grain weight. Days to 80% maturity showed strong positive correlation with pod length. Plant height had no significant correlation but it show positive correlation with number of pods per plant, pod length and number of seeds per pod and also negative correlation with 1000-grain weight and grain yield per plant..

Tabasum et al. (2010) observed that Primary and secondary branches per plant, pod length and 100-seed weight exhibited negative and non significant genotypic and phenotypic correlations with seed yield. Plant height showed positive non-significant and significant genotypic and phenotypic correlation. Pods per cluster correlated significantly negative with seed yield. Clusters per plant, pods per plant, total plant weight and harvest index showed positive significant genotypic and phenotypic correlations with seed yield.

Kumar et al. (2013) observed that plant height exhibited significant and positive correlation with number of bunches per plant, number of primary branches per plant and number of pods per plant, suggesting that plant height may be directly/indirectly responsible to enhance the magnitude of these afore said traits.

Alom et al. (2014) noted that in all cases significant genotypic correlation co-efficient were found to be higher than their corresponding phenotypic ones. The character 100-seed weight showed significant positive relationship with seed yield.

Degefa et al. (2014) reported that genotypic correlation was greater in magnitude than the corresponding phenotypic correlation. Generally, positive and significant association of pairs of characters at both phenotypic and genotypic level justified the possibility of correlated response to select while the negative correlations prohibit the simultaneous improvement of those traits.

Sarkar et al. (2014) studied from the correlation studies that the number of pods per plant, 1st picking and final picking of pods were highly positive and highly significant with seed yield/plant.

Muralidhara et al. (2015) observed that seed yield per plant between F_2 and F_3 population exhibited positive and significant association with plant height, primary branches per plant, clusters per plant, pods per plant, pods per cluster, pod yield per plant, threshing percentage. Pod length and seeds per pod in F_2 population alone exhibited positive and significant association with seed yield. Plant height between F_2 and F_3 population registered positive and significant association with branches per plant, clusters per plant, pods per plant, pods per cluster, pod yield per plant and threshing percentage. This may be responsible to enhance the yield of green gram. Primary branches per plant between F_2 and F_3 population showed positive and significant association with clusters per plant, pods per plant and pod yield per plant. Clusters per plant between F_2 and F_3 population showed positive and significant association with pods per plant, pod yield per plant and threshing percentage indicating that these characters may be responsible for enhancing the yield.

Anand et al. (2016) observed that genotypic correlations were greater than phenotypic correlations in all most the cases indicating that the environmental influences were not marked enough to alter the degree of association in all the characters. Seed yield per plant possessed highly

significant positive correlation with number of pods per plant and number of clusters per plant. Positive and significant correlation for number of pods per plant was observed with grain yield

Pinchhyo *et al.* (2016) observed that among all the characters studied, pod length, Pods/plant, seeds per pod, showed positive significant correlation and positive significant direct effect on seed yield per plant, suggesting due priority should be given to, pod length, Pods/plant, seeds per pod, for yield improvement.

Pratibha *et al.* (2016) reported that grain yield per plant had positive (Phenotypic) association with primary branches per plant, pods per plant, biological yield per plant and harvest index. Whereas grain yield per plant had negative correlation with days to 50% flowering, days to maturity, plant height, pod length, grains per pod and 100-grain weight.

Kritika and Yadav (2017) observed that seed yield was found to have positive significant correlation with plant height, number of branches plant-1, number of pods plant-1, number of seeds pod-1, 100-seed weight, biological yield and harvest index and negatively with days to flowering, days to maturity and reaction to MYMV.

Perera *et al.* (2017) noted a significant negative correlation between days to flowering and total yield per plant. Positive correlations were observed between plant height, pod length and 1000 seed weight with total yield per plant.

Abbas *et al.* (2018) revealed from their findings that seed yield showed positive and significant genotypic and phenotypic correlations with clusters per plant, pods per plant, biological yield and harvest index.

Azam *et al.* (2018) noted that seeds per pod, plant height and pods per plant showed positive significant phenotypic and genotypic correlation with yield.

Ghimire *et al.* (2018) observed positive correlation between seed and days to flowering, pod length, primary branches per plant, test weight, biological, seed yield per plant and number of pods per plant.

Asari et al. (2019) observed that the characters, clusters per plant and pods per plant showed positive and high significant correlation with seed yield per plant.

Sanhita et al. (2019) reported greater genotypic correlation than phenotypic correlation. Seed yield per plant was possessed that genotypic and phenotypic correlation exhibited significantly positive with number of pods plant-1 where number of seeds pod-1 showed significant positive correlation only in genotypic level at. The branches plant-1 and pod length were showed significant positive correlation in genotypic level at and in phenotypic level. In the genotypic and phenotypic correlation, higher significant positive interrelationship was observed between the number of seeds pod-1 with 100 seed weight, branches plant-1 with pods plant-1, pods plant-1 with harvest index.

Marawar et al. (2020) observed that yield per plant was positively and significantly correlated with plant stand at harvest, plant height, number of branches per plant, number of pod per plant, 100 seed weight, number of seed per pod.

Soni et al. (2020) noted that seed yield per plant showed highly significant and positive correlation with cluster per plant and plant height.

2.5 Path coefficient analysis

The concept of path coefficient analysis was originally developed by Wright (1921), but the technique was first used in plant breeding by Dewey and Lu in 1959. A path coefficient is simply standardized partial-regression coefficient and as such measures the direct influence of one variable upon another and permits the partitioning of the correlation coefficients into components of direct and indirect effects.

The correlation coefficient measures the sum total effects (direct and indirect) of all the characters to which it is correlated either positively or negatively and hence selection based on this value alone will be sometimes misleading unless the direct effect is very high and operates in the same direction. Hence, the study of direct and indirect effects through path analysis enables the breeders to judge the important component Characters during

selection. Correlation in combination with path analysis would give a better insight into the cause and effect relationship between different pairs of characters. A brief review on path analysis of yield and yield components reported in green gram is presented here under.

Hakim et al. (2008) observed that the direct effects of the number of pods per plant and plant height on seed yield as indicated by path coefficient were the highest, while other causal effects were small or negative.

Kumar et al. (2010) studied that harvest index, pods/plant, cluster per branch, seeds per pod, plant height, days to maturity, and pod length had highest positive direct effect on seed yield per plant, indicating that they are main contributors to yield. Plant height, primary branches per plant, seeds per pod, and days to maturity had direct positive effect at genotypic level and phenotypic level.

Rahim et al. (2010) noted that days to 50% flowering showed negative direct effect on grain yield and positive indirect effect via days to 80% maturity, numbers of pods per plant, pod length and 1000-grain weight. It is mainly due to negative indirect effect via plant height and number of seeds per pod and finally contributed to positive correlation with grain yield.

Tabasum et al. (2010) observed that positive direct effects were exerted through secondary branches, pods per plant, pod length, 100 seed weight, total plant weight and harvest index while primary branches, plant height, clusters per plant and pods per cluster had negative direct effects. The present findings could be useful for establishing selection criteria for high seed yield in the mungbean breeding.

Kumar et al. (2013) observed that number of secondary branches per plant, number of bunches per plant, number of pods per plant, number of grains per pod, pod length and 100 seed weight exhibited positive and significant correlation along with their positive and high direct effect on grain yield indicating that these characters may be considered as prime traits during the course of selection for enhancing the grain yield of green gram. The residual effect was obtained less than 0.5, suggesting that some of the

characters have not been included in the present investigation, which may be responsible to enhance the yield of green gram.

Alom et al. (2014) concluded from their findings that pods plant⁻¹ contributed maximum direct effects having positive on seed yield. Plant height, pod length and 100–seed weight had also positive direct effect on seed yield. Thus selection based on pods plant⁻¹, days to first flowering, plant height and 100–seed weight might be effective for improving seed yield in mungbean.

Degefa et al. (2014) reported that harvest index and biomass were the main determinants of yield per plot at both Hirna and Rare.

Sarkar et al. (2014) observed that based on path coefficient analysis, the 100 seeds weight, seeds/pods, number of pods per plant were the important characters for increasing yield in mungbean. The residual effect of 0.3489 suggested that it was in range of moderate which indicates that there are some more characters which contribute to the grain yield which need to be studied.

Muralidhara et al. (2015) from their findings revealed that number of pods per plant, pod yield per plant and threshing percentage had shown positive and significant correlation along with their high positive direct effect with seed yield, suggesting that these parameters may be considered as prime traits during the course of selection to have the higher potential of yield in green gram.

Anand et al. (2016) noted that the trait, number of clusters per plant had high positive direct effect on seed yield followed by number of pods per plant. These traits also recorded strong significant positive correlation with seed yield per plant. The residual effect is low (0.375) indicating appropriateness of characters chosen. The days to 50% flowering and plant height had negative direct and indirect effects for grain yield indicating that dwarf and early maturing produces higher yield. Number of clusters per plant and number of pods per plant are the most important yield contributing components as they recorded high direct and indirect effects towards seed yield in green gram.

Pinchhyo et al. (2016) studied among all the characters that pod length, Pods/plant, seeds per pod, showed positive significant correlation and positive significant direct effect on seed yield per plant, suggesting due priority should be given to, pod length, Pods/plant, seeds per pod, for yield improvement.

Pratibha et al. (2016) observed that path coefficient analysis revealed positive direct effect of plant height, pods per plant, biological yield and harvest index . These traits also recorded strong positive correlation with grain yield per plant .Similarly primary branches per plant had recorded high positive indirect effect on grain yield via number of pods per plants and highly negative indirect effect through harvest index and biological yield per plant. This indicates that the high yielding mungbean genotypes could be obtained by selecting plants having more pods per plant, and a direct selection through these characters should be effective.

Kritika and Yadav (2017) noted that Path coefficient analysis indicated that number of pods plant-1, number of seeds pod-1, biological yield plot-1 and harvest index had maximum direct contribution on seed yield hence these characters should be given due importance while formulating selection criteria for seed yield.

Abbas et al. (2018) observed that seed yield showed positive and significant genotypic and phenotypic correlations with clusters per plant, pods per plant, biological yield and harvest index. These traits also showed high positive direct effects on seed yield. Hence, indirect selection for these traits may facilitate for developing high yielding genotypes.

Azamet al. (2018) observed that the result of path analysis indicated that pods per plant had maximum direct effect on yield followed by plant height and 100 seed weight and they contribute 31% variation in yield.

Ghimireet al. (2018) observed that biological yield, pod length, days to 50% flowering and no. of grains per pod contributed maximum positive and direct effect on yield indicating these three traits should be given emphasis while selecting high yielding mungbean cultivar for irrigated condition.

Asariet *et al.* (2019) observed that days to 50% flowering had high positive direct effect on seed yield per plant while, test weight, clusters per plant, pods per plant and primary branches per plant had low positive direct effect on seed yield per plant. Therefore, more emphasis should be given on these characters while selection for high yielding mungbean cultivar.

Manivelan *et al.* (2019) observed that plant height, clusters per plant, number of branches per plant, number of pods per plant, number of seed per pod showed high direct positive effect in path analysis and positive significant association with grain yield. Hence selection may be effective based on these characters.

Sanhita *et al.* (2019) studied that, genotypic path analysis has been representing cause and effect relationships among quantitative traits and seed yield per plant. Since pods, plant-1 and pod length have been indicated high direct impacts could be considered for direct selection for high seed yield in contrast with the rest of the other traits which are valuable in indirect selection towards yield.

Marawar *et al.* (2020) studied the importance of yield contributing characters *viz.*, days to 50 percent flowering, number of branches per plant, number of pods per plant, which showed high positive direct effect as the major yield contributing traits, for enhancing the yield of green gram.

2.6 Heterosis

Heterosis is the increased vigour of F_1 generation of a cross in terms of size, duration or yield of economic product over the mean of the parents or better parent Hayes *et al* (1955). Shull (1914) first coined the term heterosis and Whaley (1952) extended the term for increased vigour of F_1 over the better parent which is now termed as 'heterobeltiosis'. The heterosis may be results from gene dispersion, directional dominance and non allelic interaction. It is computed as the deviation of F_1 from the mid-parent which is referred as relative heterosis, deviation of F_1 mean value from better parent value referred as heterobeltiosis and standard heterosis is the deviation of F_1 mean value from the standard variety. Significant heterosis over mid parent indicates partial dominance while, significant heterosis over better parent

indicates over-dominance. The standard heterosis over best check variety or hybrid is the real heterosis in which breeders are interested for development of high yielding hybrids. The magnitude of heterosis can be maximized if the parents are genetically diverse from each other. In green gram, the utility of heterosis per se may not be of much use but cross combinations showing excellent hybrid vigour can be used to isolate a higher frequency of productive derivatives in the advanced generations.

Xin et al. (2003) observed that the hybrid vigor was determined from both heterosis and heterobeltiosis for major agronomic characters, including yield and yield components. Considering overall characters, the superior F₁s were CM5 x K7, CM4 x K7, CM4 x KPS1 and CM3 x K7 while the most promising parental line for future hybrid production was K7. Although K7 per se had low seed yield per plant, its F₁s gave significant heterobeltiosis in most crosses.

Soehendi and Srinives (2005) observed that all crosses showed significant yield heterosis over the mid-parent and better-parent. Crosses showing heterosis for grain yield also showed heterosis for pod length, number of seeds per pod, and plant height. However, only plant height expressed heterobeltiosis. Superiority over the mid-parent for grain yield ranged from 52.2 to 95.7%, and that over the better parent ranged from 31.8 to 78.5%. The highest heterosis over the mid- and better parent was shown in the cross SM x LM.

Dethe and Patil (2008) reported that the highest heterosis to the extent of 26.1 % over mid parent and 22.8 % over better parent for seed yield per plant was observed in the cross BM 4 x TARM 18, which exhibited high heterosis (%) for either one or more yield components. The promising hybrids viz., BM 4 x TARM 18, Vaibhav x TARM 18, AKM 8802 x BM 4 and Kopargaon x TARM 18 were identified, which have immense potential to exploit the hybrid vigour or to isolate desirable segregants.

Zubair et al. (2010) observed high level of hybrid vigour for plant height, number of pods per plant and grain yield per plant. Considering overall performance, the superior F₁s were NM 51 x VC 3902, NM 51 x VC 4982, NM

20-21 x VC 1163, NM 51 x VC 3301 and VC 3301 x VC 1163 that revealed strong heterotic effects for number of pods per plant, number of grain per pod and grain yield per plant. These hybrids are, therefore, suggested to be utilized for developing high yielding mungbean cultivars.

Kumar and Prakash (2011) concluded his finding for this experiment that the hybrid VRMGG 1/VBN 1 can be rated as the best hybrid based on standard heterosis. It recorded positive and significant standard heterosis for most of the characters studied. Thus, the above cross can be exploited in subsequent breeding programmes and subsequent generations to isolate desirable segregants for developing mungbean varieties.

Shrivastava and Singh (2013) studied in their findings that the highest heterosis to the extent of 80.76% over standard variety and 72.39% over better parent for seed yield per plant was observed in the cross Narendra Mung-1 x PS-16 which exhibited high heterosis percentage for yield and yield components. The promising hybrids viz. Pusa Baisakhi x Pusa bold (vishal), Pusa Baisakhi x Pant M-3, Narendra Mung-1 x PS-16, Pusa Baisakhi x Pusa-105, Pusa Baisakhi x ML-613 were identified which have increased potential to exploit the hybrid vigour or to isolate the desirable segregants.

Khaimichho et al. (2015) reported that six parents out of fifteen showed positive significant relative heterosis of which, WBM-314 x Basanti being the highest along with positive heterobeltiosis. Cross combinations, Hum-12 x PS-16 and WBM-314 X PS-16 showed highest significant relative heterosis as well as heterobeltiosis followed by WBM-314 x Basanti, Hum-12 x Bireshwar and PS-16 x Bireshwar.

Kingsly et al. (2015) observed that two hybrids viz., CO 7 x VBN (Gg) 1 and K 1 x VBN (Gg) have recorded significant heterosis over the standard variety VBN (Gg) 1 for all the characters studied except days to maturity and plant height respectively. The hybrids VBN (Gg) 3 x VBN (Gg) 1 and CO 4 x VBN (Gg) 1 showed significant standard heterosis for eight traits. These crosses were heterotic for grain yield, also showed heterosis either for one or more characters. Thus the crosses CO 7 x VBN (Gg) 1 and K 1 x VBN (Gg) 1 for grain yield could be considered for exploiting hybrid vigour in mungbean.

Tantasawat et al. (2015) observed significant heterosis in most selected traits, except for the number of seeds per plant. When the heterosis of seed yield was evaluated in these hybrids, significant heterosis was found in 9 crosses, which were selected based on the number of pods per plant, number of clusters per plant, pod length, number of seeds per pod, total dry matter, and root length density. These crosses may be exploited for mungbean yield improvement.

Yadav et al. (2015) noted that of 21 F1 hybrids, two crosses SML382 x WGG37 and PUSA9871 x WGG37 exhibited highly significant positive standard heterosis for number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. The hybrid SML382 x WGG37 was excelled for number of primary branches per plant. The crosses SML382 x WGG37 and PUSA9871 x WGG37 exhibited high standard heterosis for seed yield per plant which could be an excellent source for developing high yielding mungbean genotypes.

Aung et al. (2016) noted that based on the estimate of standard heterosis, the cross Yezin-14 x MAS-1 showed the highest value of standard heterosis for number of clusters per plant, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant. Therefore, this cross could be exploited to produce high yielding variety.

Dhurai et al. (2016) recorded highest mid parent and better parent heterosis for seed yield by cross Kopergoan x HUM 12. The crosses ML 5 x HUM 12 observed the highest standard heterosis and low inbreeding depression for seed yield followed by Kopergoan x HUM 12. These crosses also showed significant standard heterosis for the component traits like days to 50% flowering, days to maturity, number of primary branches, number of seeds per plant and pods per plant. The crosses showing heterosis for seed yield was not heterotic for all characters.

Narasimhulu et al. (2016) observed that heterosis over mid parent, better parent and standard variety was significant for pods/plant and seed yield/plant. The cross exhibiting high heterosis also expressed high inbreeding

depression for pods/plant, pods/cluster and seed yield/ plant. Heterosis coupled with inbreeding depression revealed the predominance of non-additive gene action for most of the characters studied.

Salunke et al. (2016) reported significant and positive heterosis in 100 seed weight in both the crosses. None of character showed significant inbreeding depression in cross K 851 X AKM 6822 and in cross GM 4 X BPMR 145, forty percent plant population showed transgression for seed yield per plant, while in F_3 generation 50 % of plant population showed upper limit transgression segregants for seed yield per plant. However in cross K 851 X AKM 6822, F_2 generation showed the 80 % transgression segregants for seed yield per plant while in F_3 population maximum 90 % of transgressive segregants were observed for seed yield.

Bhavani et al. (2017) studied that the extent of heterosis varied from character to character. The highest standard heterosis for grain yield per plant was registered for the hybrid IPM-02-03 × G and GM-9926 × K-851. Low values of heterosis were observed for days to flowering, days to maturity and protein content, while moderate values of heterosis were recorded for the remaining characters.

Choudhary et al. (2017) observed in their findings that on the basis of mean performance for seed yield per plant that high relative heterosis, heterobeltiosis and economic heterosis performance for quantitative characters were recorded in RMG-275 x RMG-1052.

Purohit et al. (2017) observed low relative heterosis and heterobeltiosis values for the grain yield per plant and the high values of heterosis were observed for days to flowering, days to maturity and protein content, while moderate values of heterosis were recorded for the remaining characters, viz., plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and harvest index. Out of forty five crosses, ten crosses for relative heterosis, four crosses for heterobeltiosis and none of the crosses for standard heterosis registered significant and positive values for grain yield per plant.

Kumar and Sarkar (2018) observed relative heterosis as well as heterobeltiosis in high magnitude in F₂ population in cross PS-16 x TM-99-50 of for 50% maturity, days to 50% flowering and number of pods plant⁻¹. Among the F₂ population significant and maximum average heterosis and heterobeltiosis was observed in HUM-12 x Basanti for number of pods plant⁻¹. Relative heterosis as well as heterobeltiosis was observed in high magnitude for HUM-12 x Bireswar for protein content. Highest significant average heterosis and heterobeltiosis over mid parent was observed for pod length in HUM-12 x PS-16.

Sandhiya and Saravanan (2018) revealed the highest mid parent, better parent and standard parent heterosis for number of cluster per plant viz., 182.66 per cent, 173.44 per cent 196.61 per cent respectively, for the hybrid EC 396120 x IPM 99125. The highest standard heterosis of 31.5 percent for seed protein content was recorded for the hybrid between EC 396126 and CO GG 930. Based on *per se* performance and standard heterosis, hybrids were identified for heterosis breeding.

Chavan et al. (2019) noted that the significant heterosis for yield and yield component has been observed in number of pod per plant was recorded by F₁ cross BM 2002-1 x SML 668. While the crosses, BPMR 145 x SML 832 and BM 4 x BWUC 8-1-1 showed high percentage of heterosis for number of cluster per plant, number of pods per cluster and number of pods per plant. Useful heterosis in desirable direction was recorded in all characters except days to 50% flowering and days to maturity. The highest use full heterosis was observed in BPMR 145 x BWUC1-1-1 for number of cluster per plant. The best cross combination BPMR 145 x SML 832 was identified on the basis of mean performance heterosis and estimation of GCA and SCA effects. BPMR 145 x BWUC 10-1-1-2-1 was the best heterotic (201%) cross.

2.7 Combining ability

Combining ability refers to the capacity or ability of parents to transmit desirable performance to its hybrid progenies and is very useful in isolation desirable parents and their evaluation in hybrid development. Sprague and Tatum (1942) introduced the concepts of general combining ability (GCA) and

specific combining ability (SCA) through preliminary studies on maize. General combining ability is the average performance of a line in a set of hybrid combinations and is associated with genes which are additive in effect while SCA is attributed primarily to deviations from the additive scheme caused by dominance and epistasis Rojas and Sprague (1952). The knowledge on combining ability and type of gene action responsible for the regulation of expression of different traits would certainly help in planning appropriate breeding method for crop improvement in greengram comparatively to other important field crops, fewer attempts have been made to know the genetics of important traits. The review of literature on gene action governing the inheritance of different traits based on the combining ability analysis is briefly reviewed hereunder.

Khattak *et al.* (2001) noted significant additive gene action for nodes on main stem, average intermodal length, branches per plant, pods per cluster, pod length, and seeds per pod. The predominance of additive genetic variance was observed in all traits.

Marappa *et al.* (2008) observed that the variances due to specific combining ability (SCA) were found be higher than general combining ability (GCA) variances for days to flowering, plant height, number of clusters/plant, pods/plant, seeds/pod, 100 seed weight, dry weight/plant, harvest index and seed yield/plant, indicating predominance of non-additive gene action in the inheritance of these characters studied.

Sunil *et al.* (2010) noted the importance of additive and non-additive components of variation in the inheritance of seed yield/plant and 100 seed weight whereas additive gene action played a role in the expression of plant height and pods/plant. The estimates of *gca* effects indicated EC30072 as best general combiner for seed yield/plant and VRMGG Local, VBN-1 and PMB-27 for 100 seed weight with significant positive *gca* effects. In contrast, estimates of *sca* effects identified VRMGG Local × VBN-1, EC-30072×LGG-410, M-123×LGG-450 and VBN-1×PMB-27as best specific cross combinations for yield.

Punamand Roopa (2011) reported that the variances due to GCA and SCA were highly significant, indicating importance of additive and non additive gene action in the inheritance of six different characters such as, plant height, number of clusters/plant, pods/cluster, pods/plant, pod length and test weight. Genotypes SML 382, PUSA 9871, ML 287, NARP 1-1 and WGG 37 were identified as good general combiners. The crosses SML 382 × WGG 37, PUSA 9871 × WGG 37 and NARP 1-1 × SML 382 showed significant SCA effects for seed yield/plant and other yield contributing characters.

Sathya and Jayamani (2011) observed that magnitude of SCA variance was greater than GCA variance for all the characters except for seed fertility, indicating preponderance of non-additive gene action. The parents Co 6, Barimung 7 and Binamung 7 were identified as good general combines for yield and yield contributing characters. The crosses VBN(Gg)3 × SML1023 and VBN(Gg) 3 × EC 396117 were found to have superior mean performance and sca effects for number of seeds/pod, 100 seed weight, clusters/plant and single plant yield.

Bhagora et al. (2013) studied that the parents CO 4 and GBM 1 were the good general combiners for seed yield per plant and important yield components. The result of SCA effects showed that the crosses RM-10-503 × CO 4, RM-10-509 × GBM 1, RM-10-501 × GBM 1 and CO 4 × GBM 1, exhibiting the highest and significant SCA effect for seed yield per plant and involved low × good parental interactions, can be used to obtain transgressive segregants for yield and yield contributing characters in future breeding programme.

Sujatha and Kajjidoni (2013) investigated on genetic analysis of greengram genotypes involving 12 parents and 20 crosses obtained by Line × Tester mating system for 12 different characters. General combining effect of the parents indicated that TARM-1 was ranked top followed by VC-1, Vaibhav and TARM-18 as good general combiners based on the overall score across the traits in desirable direction. The cross Chinamung × VC-1 exhibited significant sca effects for traits viz., seed yield/plant, seed yield/plot, number of pod bearing clusters/plant, pods/plant, hundred seed weight and harvest index. Whereas gene action studies revealed that days to 50% flowering,

days to maturity, pods/plant, hundred seed weight, total dry matter at harvest, harvest index, seed yield/plant and seed yield/plot were governed predominantly by additive genetic variation. Since all these characters were also under significant influence of epistatic variation, it appears that additive $\times$ additive epistatic variation may be playing a decisive role in the inheritance of these characters.

Suresh et al. (2014) studied 32 hybrids along with their parents for combining ability analysis derived through Line $\times$ Tester mating design involving eight lines and four diverse testers in greengram. They observed preponderance of non additive gene action for most of the characters studied. Among the lines, VRM (Gg) 1 was the best general combiner for eight traits. The testers VGG04-028 had highly significant *gca* effects for nine traits. The crosses VBN (Gg) 2 $\times$ VGG04-028 and VRM (Gg) 1 $\times$ VGG04-005 were observed as good specific combiners for seed yield/plant.

Khaichhimo et al. (2015) observed that seed yield per plant exhibited highly significant variance for *gca* and significant variance for *sca* that indicated the influence of both additive and non-additive gene effects. Predominant role of additive component in expression of characters like number of branches per plant, pod width and seed yield per plant were also confirmed from predictability ratio of the concerned characters.

Katiyar and Kumar (2015) examined the combining ability of 30 hybrids between 10 lines and 3 testers evaluated with parents in mungbean revealed significant role of additive and non-additive gene actions, the former being predominant for number of branches per plant and 100-seed weight, and the later for plant height, number of pods/plant, number of seeds/plant and grain yield/plant. Good combining parents for different characters could be identified for use as a favorable source of gene (s) to effect improvement in specific traits. Seven cross combinations for plant height, six for number of branches, six for number of pods/plant, 4 for number of grains/pod and 12 each for 100-grain weight and 10 for grain yield per plant exhibited significant specific combining ability effect.

Vaidya et al. (2015) observed significant mean sum of squares due to general and specific combining ability for all the characters studied indicating importance of both additive as well as non-additive gene effects involved in the expression of all the characters. Higher magnitude of general combining ability variances for most of the traits except for no. of branches per plant, pod length, no. of seeds per pod and harvest index pointed out the preponderance of additive component of the genetic variance in the expression of the characters under study.

Purohit et al. (2016) noted that analysis of variance for gca and sca were shown significant for all the traits. Predominance of non-additive gene action for all the characters apart from harvest index (%), where additive gene action was more evident.

Nath et al. (2017) observed that the mean square due to general combining ability (gca) and specific combining ability (sca) were significant for all the characters except mean square due to (sca) for clusters per plant and seed yield per plant indicating importance of both additive as well as non-additive gene action. The estimates of variances due to specific combining ability were higher than general combining ability for all the traits except days to 50 % flowering, primary branches per plant, clusters per plant and seed yield per plant pointed out to be the preponderance of non-additive gene effects in the expression of these characters.

Samantaray et al. (2018) reported significant differences in gca and sca effects for the characters studied. OGG-12 was the best general combiner for pods/ plant and grain yield per plant where as OGG-57 was for seeds/ pod, OGG-12 and LGG-460 for 100-seed weight. Among the 15 crosses, six crosses showed significant positive and seven crosses had significant negative sca effects for seed yield/plant. Significant positive sca effects were observed in two crosses for pods/plant, four crosses for seeds/ pod and three crosses for 100-seed weight. Although some crosses were showing positive sca effect for yield and its components, the frequency of unfavorable cases were more.

Zuge et al. (2018) studied that all the parents and crosses showed significant positive as well as negative general combining ability (gca) and specific combining ability (sca) effects for the traits. The study revealed non additive gene action involved in controlling all the characters namely, days to 50 % flowering, days to maturity, plant height, number of branches per plant, pods per plant, pod length, seeds per pod, protein content, yield per plant etc. These crosses could help in further development of transgressive segregants with superior combinations of alleles for yield and yield contributing traits.

Kakde et al. (2019) observed that analysis of variance revealed significant differences among genotypes, crosses, lines, testers and line x tester interactions for most of the traits. Preponderance of non-additive gene effects was realized from higher values of specific combining ability compared to general combining ability and ratio of variances of sca to gca. The parents showed high gca can be used for the future hybridization programmes.

Viraj et al. (2020) noted that both gca and sca mean squares were significant for all the eleven characters in F_1 and F_2 generations, former being more pronounced for clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight and seed yield per plant in F_1 and for all the characters except days to maturity, seeds per pod and 100-seed weight in F_2 .

Kohakade et al. (2021) reported significant differences among genotypes, crosses for most of the traits. Preponderance of non-additive gene effects was realized from higher values of specific combining ability compared to general combining ability and ratio of variances of sca to gca. The parents showed high gca can be used for the future hybridization programs.

Marwiyah et al. (2021) noted that the expression of all studied traits indicated the low control of additive genes. Delaying selection to later segregating generations is suggested, and the reliable selection of transgressive recombinants is possible.

2.8 Generation mean analysis

The inheritance of quantitative economic traits is affected not only by polygenic nature but also by environmental effects. Hence, the choice of an

appropriate breeding method for improvement of quantitative characters depends largely on the nature of gene action. Many genetic models given by various workers have been employed to describe the action of genes controlling quantitative characters. Fisher (1918) was the first to attempt for the contribution of a gene model, which includes dominance at a single locus. He also indicated that there may be a deviation from simple additive effects between loci when more than one locus affects a given character.

Later, Fisher *et al.* (1932) used the gene model to describe gene action of any number of genes on a given character. Mather (1949) also developed gene models to study and assess the relative importance of additive and dominance gene effects assuming epistatic effects to be negligible. Anderson and Kempthorne (1954) in their gene model partitioned gene effects into additive, dominance and epistasis. Mather (1949) and Hayman and Mather (1957) proposed a gene model to assess the contribution of gene interaction to continuous variation. Hayman (1958) described the procedure for partition of generation means into six parameters viz., mean (m), additive (d), dominance (h), additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l) gene effects. The opposite sign of 'h' and 'l' indicate the presence of duplicate epistasis.

In any classical breeding program, breeders cannot undermine the role of epistasis otherwise the biased estimates of additive and dominance component of genetic variation leads to faulty breeding procedure Singh and Singh (1996). The estimation of epistasis assumes more significance in view of the fact that in its presence, variance components estimates are likely to be biased. The existence of large array of interactions in a polygenic system cause over estimation or under-estimation of heritability estimates (narrow sense) thereby causing additional bias in predicted gains. The generation mean analysis helps to understand the role of epistatic interactions in the expression of yield and its component characters, which is not possible with $L \times T$ analysis alone. The literature on the generation mean analysis studies to understand the gene effects is briefly reviewed.

Khattak *et al.* (2001) reported that epistasis was present significantly for number of pods per plant and number of seeds per pod when grown in the

spring/summer season (March to June). Partition of epistasis showed that additive x additive ('i' type) interaction was an important component of number of pods per plant, and number of seeds per pod was found to be of both types 'i' type, and additive x dominance, and dominance x dominance ('j' and 'l' type) interactions. This indicated that epistasis might be a non-trivial factor in the inheritance of pods per plant, and seeds per pod in mungbean. The expression of epistasis was influenced differentially by particular genotypes, indicating that a limited number of genotypes may not be sufficient to detect non-allelic interactions for a trait in mungbean.

Khattak *et al.* (2005) observed that the additive (d) and dominant (h) components of genetic variation were significant for all the traits in both the crosses, but dominant (h) component was non-significant for branches per plant and 1000 seed weight in cross ML-5 x NM 54, and for pod bearing nodes on main stem in cross 6601 x NM 92. The duplicate type of nonallelic interactions were found for pod cluster per plant and 1000 seed weight in cross 6601 x NM 92, and for 1000 seed weight in cross ML-5 x NM 54. The complementary type of non-allelic interaction for seed yield per plant was found in both crosses.

Rehman *et al.* (2005) noted that the data for both the generations was found partially adequate when subjected to adequacy tests. Estimation of genetic components of variation revealed significance of both additive and non-additive components in both generations. In F1 generation degree of dominance was less than 1, indicating preponderance of additive gene effects while in F2 it was more than 1 showing over dominance type of gene action. Graphical differences revealed presence of additive gene action in both the generations

Inderjit *et al.* (2006) studied the inheritance of genetic parameters through six generation mean analysis in four crosses of greengram and reported the importance of additive, dominance as well as epistatic effects in the genetic control of various characters studied. Among epistatic gene effects, additive × additive (i) type epistasis was significant in all the four crosses for days to 50% flowering, plant height, seeds/pod; three crosses for days to maturity, clusters/plant, pods/plant, seed yield/plant and

100seedweight. Additive $\times$ dominance (j) type of interaction was significant in three crosses for days to maturity, plant height and 100-seed weight. Dominance $\times$ dominance (i) gene interactions were significant in all the four crosses for pods/plant and 100 seed weight; three crosses for seed yield/plant, days to 50% flowering, days to maturity and plant height.

Singh et al. (2006) findings revealed that simple additive-dominance model was inadequate for all the crosses for almost all the characters studied except for branches per plant in the crosses ML 1271 $\times$ MUL 81 and VC 6370-30-65 $\times$ MUL 81. It indicated the importance of non-allelic interactions (Epistasis) in most of the cases.

Gawande and Patil (2007) studied the genetic analysis for yield and its components in five crosses of greengram through generation mean analysis using six parameter model. They observed predominance of additive effects for days to 50 per cent flowering in three crosses. However, in most of the crosses dominance gene action was observed for the expression of seed yield/plant, 100 seed weight, seeds/pod, clusters/plant, pods/plant, branches/plant and plant height.

Singh et al. (2007) analyzed nature of gene effects for yield and yield attributes in four crosses using six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) through generation mean analysis. Dominance and epistatic gene effects were observed for days to 50% flowering, days to maturity and plant height, branches/plant, pods/plant, seeds/pod, 100 seed weight and yield/plant. Duplicate type of epistasis was prevalent in most of the crosses. However, in certain crosses, additive and non-additive gene action was important for the expression of the traits like plant height, 100 seed weight and pods/plant.

Payasi et al. (2010) studied the nature of gene action for seed yield and yield attributing traits in four sets of crosses involving four parents through generation mean analysis and noticed digenic interactions between genes at different loci. However significant inbreeding depression indicated the prevalence of dominance genetic variance along with duplicate type of epistasis for seed yield and yield attributing traits in greengram.

Patel et al. (2012) conducted a study on five families in greengram and reported the importance of additive, dominance as well as epistatic effects in the genetic control of days to flowering. Even though all types of gene effects were significant for plant height, the magnitude of non-additive gene effect was much higher than additive component except in PDM 14 × GM 4 where the additive × additive (i) type of gene action was predominant. They concluded that additive × additive (i) and dominance × dominance (l) type of epistatic effect was significant for seed yield in most of the crosses.

Iqbal et al. (2014) observed that digenic epistatic interactions were engaged in both the crosses for all the traits studied except for days to ninety percent pods maturity, degree of indetermination of pod maturity from first flower to first pod maturity (DDd3) and seed yield in NM-2006 × AUM-9 cross, where additive and dominant gene effects were prominent.

Iqbal et al. (2015) observed that generation variance analysis demonstrated the engagement of additive and environmental components, with the preponderance of additive gene action. Narrow sense heritability estimates (>67%) also supported the same. In generation mean analysis both cross combinations manifested non allelic epistatic digenic interactions for the investigated traits except for plant height at first flower initiation and for seed yield per plant in one cross combination, where only additive and dominance components were important.

Pathak et al. (2015) noticed that the presence of epistasis was detected by joint scaling test and inadequacy of additive-dominance model was established except seeds/pod. Additive (*d*), dominance (*h*) gene effects along with one or more type of non-allelic interactions (*i, j, l*) contributed significantly towards the inheritance of all the quantitative characters in majority of the crosses. Duplicate type of epistasis and predominant dominance effects was also prevalent in most of the cases except in days to maturity in HUM 8 × ML 713 cross. Thus, postponement of selection in later generations may be suggested to obtain transgressive segregants for improvement of mungbean populations.

Khan et al. (2016) noticed that the complex genetic behaviour was seen for majority mention traits. Presence of epistatic effect were shown for plant height, root length, number of secondary roots, leaf area on main stem, leaf area on branches and number of seeds per pod in all crosses, except in cross 6601 x VC 1560D for root length, in cross NM92 x Local mung for number of secondary roots; in crosses L24 – 2 x Local mung and ML-5 x NM92 for number of seeds per pod epistasis was absent. The joint scaling test was found adequate for average petiole length of leaf.

Singh et al. (2016) reported that scaling and joint scaling tests revealed the presence of one or more kinds of epistatic effects for almost all the agro-morphological traits. The selection of elite lines from delayed generations and subsequent inter mating might be useful approach to recover/ develop the high yielding mungbean lines. There was also a possibility to recover the yellow and shiny seeded mungbean lines due to its monogenic inheritance of seed coat colour and lusture.

Yadav et al. (2017) reported that the individual scaling tests indicated the presence of epistatic interactions in all the traits under the both sowing environments. The analysis of joint scaling test indicated the additive-dominance model was inadequate in all the cases indicating the role of epistatic interactions to control the inheritance of the traits studied under both conditions. On the basis of six parameter models, both the main effects and their epistatic interactions involved in the inheritance of all the traits with the preponderance of non-additive gene effects.

Khajudparn et al. (2019) observed that most characters including TDM, number of pods per plant, seed weight per plant and root length density showed additive, dominance and epistatic gene effects, except for 100-seed weight, number of seeds per pod and pod length. One hundred-seed weight and number of seeds per pod possessed only additive gene effects, while pod length was controlled by both additive and dominance gene effects. The duplicate epistasis revealed the presence of a large number of non-additive gene actions controlling TDM, number of pods per plant, seed weight per plant and root length density that may hinder the improvement of these characters, and confirmed that selection of these characters in later generations would be more feasible.

Latha et al. (2019) observed involvement of both additive and non-additive gene actions with preponderance of non-additive gene actions for seed yield, its major yield components suggested that breeding can profitably be utilized for improving seed yield in greengram by exploiting dominance / non-additive gene action.

Chapter – III

MATERIAL AND METHODS

MATERIAL AND METHODS

The present investigation entitled “**Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]**” was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur (Madhya Pradesh) during summer 2020, Kharif 2020 and Summer 2021. The experimental area occupied was quite uniform in respect of topography and fertility. The details of materials used, experimental methods followed and statistical techniques adopted during the course of this investigation are presented below:

3.1 Climate and Weather

Jabalpur is situated between 23.90° North latitude and 79.58° East longitudes at the altitude of 411.87 m above mean sea level. The climate of the region is typically semi-humid and sub-tropical. Jabalpur is in the agro-climatic zone of Kymore Plateau and Satpura Hills and lies in rice-wheat crop zone of the state. The mean annual rainfall is nearly 1423 mm, which is received mostly between mid-Junes to mid-September. The mean maximum temperature during the hottest months of May-June varies from 45.5 °C to 46.4 °C while the average minimum temperature varies between 8.2° C to 8.7°C during December-January that are the coldest months of the year.

The weekly meteorological data during the course of the study *i.e.* year 2020 and 2021 are given in Table 3.1 and 3.2.

Table 3.1: Weekly meteorological data during the cropping season (2020)

Months	Weeks	Temperature		Sun Shine hrs.	Rainfall (mm)	RH		Evapo (mm)	Rainy days
		max.	min.			Mor	Eve		
February	5	24.2	8	7.3	0	88	41	3	0
	6	22.2	8	6.6	8.7	85	40	2	1
	7	26.8	8	9.8	0	90	32	3	0
	8	28.8	14	6.4	0	86	49	3	0
March	9	29.2	13	8.3	1.8	87	34	3	0
	10	28.5	13	7.4	0.8	84	45	3	0
	11	29.9	15	7.6	0.5	81	35	3	0
	12	31.6	17	7.2	36	69	40	3	1
	13	34.5	20	7.5	0.9	61	33	3	0
April	14	36.8	20	7.1	0	45	22	4	0
	15	38.9	22	9.4	0	37	21	5	0
	16	38.7	25	7.7	0	45	23	4	0
	17	37.9	23	7.8	0	51	28	4	0
May	18	39.3	24	10	0	50	26	5	0
	19	39.2	25	5.4	0	54	29	5	0
	20	40.1	24	8.8	2.3	60	25	6	0
	21	42.4	25	10.5	0	40	23	9	0
	22	39.2	25	8	1.5	59	42	8	0
July	27	32.2	25	2.6	205	88	75	5	5
	28	32.8	26	4.3	7.2	83	66	4	1
	29	33	25	5.2	38	84	71	4	4
	30	32.9	25	7.7	24	89	69	3	1
August	31	32.7	24	4.2	72	93	72	4	4
	32	29.5	25	1.9	202	94	82	3	5
	33	28.7	24	1.1	143	95	84	3	7
	34	30	24	3.2	84	91	77	4	5
	35	29.7	23	4	213	93	74	5	4
September	36	33.3	24	6.6	50	88	64	4	3
	37	34.2	24	5.7	4.6	87	65	3	1
	38	32.7	24	4.5	26	91	75	3	3
	39	30.9	23	4.5	68	92	66	4	2
	40	32.1	21	7.4	0	85	52	4	0
October	41	32.3	22.8	5.7	0	91	58	3.0	0
	42	33.0	21.2	8.2	0	89	49	3.6	0
	43	32.7	16.7	8.7	0	85	33	3.3	0
	44	30.8	12.7	8.3	0	80	25	3.1	0

Table 3.2: Weekly meteorological data during the cropping season (2021)

Months	Weeks	Temperature		Sun Shine hrs.	Rainfall (mm)	RH		Evapo (mm)	Rainy days
		max.	min.			Mor	Eve		
March	9	33	12	10	0	74	25	4	0
	10	35	13	9	0	74	20	5	0
	11	32	15	7	6	78	29	4	1
	12	34	17	5	0	67	27	5	0
April	13	37	17	9	0	57	13	7	0
	14	38	15	9	0	64	11	7	0
	15	38	19	8	1	61	22	6	0
	16	37	18	7	0	53	19	6	0
May	17	38	18	10	0	52	13	8	0
	18	39	23	8	3	47	24	6	1
	19	38	23	10	39	71	35	8	2
	20	36	24	7	36	78	46	5	2
	21	35	22	8	0	75	32	6	0

3.2 Experimental material

The experimental material used in the present study comprised of fourteen parental lines comprised of 10 lines and four testers, 40 F₁s, 40F₂s and 10 backcrosses. The seed material for this research was obtained from the project entitled “**Field Evaluation of Trombay Mutant Selections and Research Activities in Agriculture**” and **Mung and Urd Improvement Project**, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa vidyalaya, Jabalpur, IndiaMadhya Pradesh. Salient features and pedigree of the lines and testers, derivatives as F₁'s, F₂'s and backcrosses are furnished in Table 3.3, 3.4, 3.5 and 3.6.

Details of parental lines and cross combinations studied at F₁, F₂ and Backcross

Table3.3: Details of parents

S. No.	Lines	S. No.	Testers
1	TJM 196	1	PDM 139
2	TJM 136	2	Shikha
3	TJM 3	3	Kanika
4	TMB 37	4	Virat
5	Ganga 8		
6	LGG 60		
7	HUM I		
8	SL668		
9	Pusa Vishal		
10	PDM 11		

Table 3.4: Salient Features of Parental Lines of Greengram

S. No.	Name	Pedigree	Source
01.	TJM 196	-	BARC, Mumbai
01	TJM 136	-	BARC, Mumbai
03	TJM 3	Kopargoan X TARM 1B	BARC, Mumbai
04	TMB 37	Kopargoan X TARM 2B	BARC, Mumbai
05	Ganga 8	K 851 X Pusa 105	RAU, Sri Ganga Nagar
06	LGG 460	Lam M2 X ML 267	ANGRAU AP
07	HUM 1	BHUM 1 X Pant U 30	BHU, Varanasi
08	SL 668	-	PAU, Ludhiana
09	Pusa Vishal	Selection from NM 92	IARI, New Delhi
10	PDM 11	Selection from LM 595	IIPR, Kanpur
11	PDM 139	ML 20/19 X ML 5	IIPR, Kanpur
12	Shikha	IPM 03-1 X NM-1	IIPR, Kanpur
13	Kanika	PM 4/ EC398897	IIPR, Kanpur
14	Virat	IPM 2-1 X EC 398889	IIPR, Kanpur

Table 3.5: Cross combinations (F1's and F2's)

1	TJM 196 X PDM139	21	LGG 460 X PDM 139
2	TJM 196 X Shikha	22	LGG 460 X Shikha
3	TJM 196 X Kanika	23	LGG460 X Kanika
4	TJM 196 X Virat	24	LGG460 X Virat
5	TJM 136 X PDM139	25	HUM 1 X PDM139
6	TJM 136 X Shikha	26	HUM 1 X Shikha
7	TJM 136 X Kanika	27	HUM 1 X Kanika
8	TJM 136 X Virat	28	HUM 1 X Virat
9	TJM 3 X PDM139	29	SL668 X PDM139
10	TJM 3 X Shikha	30	SL668 X Shikha
11	TJM 3 X Kanika	31	SL668 X Kanika
12	TJM 3 X Virat	32	SL668 X Virat
13	TMB 37 X PDM139	33	Pusa Vishal X PDM139
14	TMB 37 X Shikha	34	Pusa Vishal X Shikha
15	TMB 37 X Kanika	35	Pusa Vishal X Kanika
16	TMB 37 X Virat	36	Pusa Vishal X Virat
17	Ganga 8 X PDM139	37	PDM 11 X PDM139
18	Ganga 8 X Shikha	38	PDM 11 X Shikha
19	Ganga 8 X Kanika	39	PDM 11 X Kanika
20	Ganga 8 X Virat	40	PDM 11 X Virat

Table 3.6: Details of Backcrosses

1	HUM 1 X Shikha X HUM 1	6	LGG 460 X Virat X Virat
2	HUM 1 X Shikha X Shikha	7	LGG 460 X Kanika X LGG 460
3	Ganga 8 X Shikha X Ganga 8	8	LGG 460 X Kanika X Kanika
4	Ganga 8 X Shikha X Shikha	9	TJM 196 X Kanika X TJM 196
5	LGG 460 X Virat X LGG 460	10	TJM 196 X Kanika X Kanika

3.3 Experimental details

Methods for generation of breeding material

3.3.1 Experiment I. (Summer 2020)

Hybridization

To generate breeding material, crossing was taken up on 5th March 2020 at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur (Madhya Pradesh). In crossing blocks, parents were sown at staggered intervals of 10 days to facilitate continuous availability of pollen grains. Each line was sown in 2 rows of 4 meter length with 1 meter row to row and 10 cm plant to plant distance. Each tester was sown in 8 rows of 4 meter row length, 30 cm row to row and 10 cm plant to plant distance. Hybridization was done by employing handemasculation where emasculation and pollination was done simultaneously at morning 6.30-10.00 a.m. and pollinated flower buds were tagged. The hybridization process was carried out until sufficient numbers of crossed pods were obtained. Ten lines viz., TJM 196, TJM 136, TJM 3, TMB 37, Ganga 8, LGG 460, HUM 1, SL 668, Pusa Vishal and PDM 11 were crossed with four testers viz., PDM 139, Shikha, Kanika and Virat in a Line × Tester mating design to generate F₁ seeds. A total of 40 cross combinations were made during summer, 2020.

3.3.2 Experiment II. (Kharif 2020)

Generation advancement of cross combinations made

This experiment was taken up under glasshouse and field condition. The F₁ seeds developed during summer 2020 were divided in to three parts for proper genetic studies.

(a) One set of all the 40 F₁s with 14 parents were sown in a Randomized Complete Block Design (RCBD) with three replications on 2nd July 2020 in two rows of 3 meter length following a spacing of 30 cm between the rows and 10 cm between the plants within a row to evaluate the yield and yield attributing traits and for obtaining the F₂ population. Out of 40 F₁s, five cross combinations viz., TJM 196 X Kanika, LGG 460 X Virat, LGG

460 X Kanika, Ganga 8 X Shikha and HUM 1 X Shikha were found promising for yield and yield attributing traits.

3.3.3 Characters studied and recording of data for Line x Tester analysis

Observations on 19 morphological traits, 12 quantitative traits and 4 quality traits were recorded. Quantitative traits were recorded on 5 randomly selected plants from each replication in each parent and F_1 except for days to 50% flowering and days to maturity. For days to 50% flowering and days to maturity data was recorded on plot basis. Data recorded on seed yield and its attributing characters is presented below.

3.3.4 Morphological traits

Observations were recorded according to Green gram DUS Descriptor developed by IIPR, Kanpur and approved by PPV & FRA, New Delhi.

1. Hypocotyl: Anthocyanin coloration: Anthocyanin coloration was observed when cotyledons were unfolded and it is classified into following two categories namely

- (a) Absent
- (b) Present

2. Time of flowering: Time of flowering is classified into following categories:

- (a) Early (<40 days)
- (b) Medium (40-50 days)
- (c) Late (>50 days)

3. Plant: Growth habit: The character was observed at the time of 50% flowering and classified on the basis of following categories:

- (a) Erect
- (b) Semi-erect
- (c) Spreading

4. **Plant: Habit:** Plant habit is categorized into following categories:
- (a) Determinate
 - (b) Indeterminate
5. **Stem: Color:** Stem color is divided into following 3 categories:
- (a) Green
 - (b) Green with purple splashes
 - (c) Purple
6. **Stem: Pubescence:** On the basis of stem pubescence this category is classified into:
- (a) Absent
 - (b) Present
7. **Leaflet: lobes (terminal):** It is classified into following categories
- (a) Absent
 - (b) Present
8. **Leaf: Shape:** On the basis of leaf shape, leaves are classified into following categories:
- (a) Deltoid
 - (b) Ovate
 - (c) Lanceolate
 - (d) Cuneate
9. **Leaf: Colour:** It is classified into following two categories:
- (a) Green
 - (b) Dark green
10. **Leaf: Vein colour:** Leaf vein colour is classified into following three groups:
- (a) Green
 - (b) Greenish Purple
 - (c) Purple

- 11. Flower: Colour of petal:** It is grouped into following two categories:
- (a) Yellow
 - (b) Light yellow
- 12. Pod: Pubescence:** On the basis of pubescence pods are grouped into::
- (a) Absent
 - (b) Present
- 13. Pod: Colour of premature pod:** On the basis of premature pod color this category is divided into following classes:
- a) Green
 - b) Green with pigmented suture
- 14. Pod: Colour:** Pods are grouped into following categories on the basis of colour:
- a) Brown
 - b) Black
- 15. Pod: Curvature of mature pod:** It is grouped into following classes:
- a) Straight
 - b) Curved
- 16. Seed: Colour:** On the basis of colour seeds are classified into following four groups:
- a) Yellow
 - b) Green
 - c) Mottled
 - d) Black
- 17. Seed: Shape:** Shape of grain is grouped into:
- a) Oval
 - b) Drum shaped

18. Seed: Lusture: Grains are classified into following classes on the basis of lusture:

- a) Shiny
- b) Dull

19. Seed: Size: (weight of 100 seeds): On the basis of 100 seed weight seeds are classified into:

- a) Small (<3 g)
- b) Medium (3 to 5 g)
- c) Large (> 5 g)

3.3.5 Quantitative Traits

1. Days to 50 percent flowering

Number of days taken from the date of sowing to the date on which 50 percent of the plants flowered in each entry in each replication.

2. Days to maturity

Number of days taken from the date of sowing to the date on which 80 percent of the pods matured on each plant was recorded and taken as the number of days to maturity.

3. Plant height (cm)

Plant height was measured from ground level to the tip of main raceme at maturity. The mean value of sample plants was recorded as plant height in centimeters.

4. Number of branches per plant

Number of branches was recorded for all sample plants in each entry in each replication. The mean value of sample plants was recorded as number of branches per plant.

5. Number of pods per plant

Number of well filled pods on each sample plant was counted and the mean value of the random sample plants was recorded as the number of pods/plant.

6. Number of pods per cluster

Number of well filled pods from all the clusters of each random plant was counted and averaged over per cluster.

7. Number of clusters per plant

Number of effective clusters on each sample plant was counted at the time of harvest and mean of all sample plant was recorded as the number of clusters per plant

8. Number of seeds per pod

The total number of seeds of five randomly selected pods from each plant were counted and averaged to obtain the number of seeds per pod.

9. Hundred seedweight (g)

Hundred well-developed seeds from each sample plant were counted and their weight was expressed in grams.

10. Biological yield per plant (g)

Each of the selected plant was harvested at maturity and weight was recorded in grams after complete sundry excluding roots.

11. Harvest index (%)

Harvest index was calculated by using the formula given below

$$\text{Harvest index(\%)} = \frac{\text{Grain yield/plant(g)}}{\text{Biological yield/plant(g)}} \times 100$$

12. Seed yield per plant (g)

Seed harvested from each sample plant was dried and weight was recorded in grams. The average of sample plants was expressed as seed yield per plant in grams.

3.3.6 Quality Traits

1. Protein (mg/g)

The protein content in sample was determined by using conventional micro - Kjeldahl digestion and distillation procedure as given in AOAC (1984).

1.1 Reagents:

1. Catalyst mixture- A mixture of 100g K₂SO₄, 20g of CuSO₄ and 2.5g of SiO₂.
2. Sodium hydroxide solution: 40% (w/v).
3. Boric acid solution: 2% (w/v).
4. Concentrated sulphuric acid AR (sp. gr. 1.81)
5. Mixed indicator: 2 parts of 0.2% (w/v) methyl red and 1 part of 0.2% (w/v) methyl blue in absolute alcohol
6. Standard Hydrochloric Acid (0.1N).

1.2 Procedure

The sample (0.2g) was weighed accurately and transferred to a Kjeldahl flask taking care to see that the material did not stick to the neck of the flask. The catalyst mixture of about 2 g and concentrated sulphuric acid (10ml) were added. Then the flask was heated in an inclined position in digestion chamber for about 4-6 hr. till the liquid became clear (green blue colour).

1.3 Distillation

The content in the flask were allowed to cool and the digested material was transferred quantitatively to a vacuum jacketed flask of micro Kjeldahl distillation apparatus and the ammonia liberated by the addition of 25ml of 40%NaOH on heating was absorbed in 25ml of boric acid containing 2-3 drops of mixed indicator in 100 ml conical flask. The distilled off ammonia was titrated against 0.1N sulphuric acid. The blank was also run in a similar way.

1.4 Calculation

$$N (\%) = \frac{N \text{ of } H_2SO_4 \times \text{Vol. of } 0.1N \text{ } H_2SO_4 \times 14}{\text{Weight of sample} \times 1000} \times 100$$

$$\text{Crude Protein } (\%) = N \% \times 6.25/5.83$$

2. Fat (%)

The fat content of the sample was determined by the procedure as described in AOAC (1984). The sample (5g) was weighed accurately, placed

in thimble and plugged with cotton. The extractor-containing thimble was placed over a pre-weighed extraction flask (A). Fat content was determined by extracting the sample with solvent petroleum ether (AR grade 60-80°C) for 8hr using Soxhlet's extraction procedure. After extraction the excess of solvent was distilled off and the residual solvent was removed by heating at 80°C in oven for 4-6 hr. the flask was weighted (B) and the fat content was determined as below:

2.1 Calculation

$$\text{Crude fat (\%)} = \frac{\text{Wt. of flask (B)} - \text{Wt. of flask (A)}}{\text{Weight of sample}} \times 100$$

3. Total Phenol Content (mg/g)

Total phenol content was determined according to the method given by Zhishen *et al.* (1999) using Folin- Ciocalteu's reagent.

3.1 Principle

Phenol in sample extract reacts with specific redox reagent (FC reagent) to form blue chromophers constituted by a phosphor-tungstic phosphor-molybdenum complex which is measured at 650nm.

3.2 Reagents

1. 80% Ethanol.
2. Folin-Ciocalteu Reagent.
3. Na₂CO₃, 20%.
4. Standard (100mg Catechol in 100ml Water).
5. Dilute 10 times for a working standard.

3.3 Procedure

Weigh exactly 0.5 to 1.0g of the sample and grind it with a pestle and mortar in 10-time volume of 80% ethanol. Centrifuge the homogenate at 10,000 rpm for 20 min. supernatant. Re-extract the residue with five times the volume of 80% ethanol, centrifuge and pool the supernatants.

1. Evaporate the supernatant to dryness.
2. Dissolve the residue in a known volume of distilled water (5mL).

3. Pipette out different aliquots (0.2 to 2mL) into test tubes.
4. Make up the volume in each tube to 3ml with water.
5. Add 0.5mL of Folin-Ciocalteu reagent.
6. After 3 min, add 2mL of 20% Na_2CO_3 solution to each tube.
7. Prepare Blank 1.5ml of distilled water was taken and treated same as sample.
8. Mix thoroughly. Place the tubes in a boiling water for exactly one min, cool and measure the absorbance at 650nm against a reagent blank.
9. Prepare a standard curve using different concentrations of catechol.

3.4 Calculation

From the standard curve find out the concentration of phenols in the test sample and express as mg phenols/100g material.

4. Total sugar (mg/g)

Total sugar was estimated by Shaffer – somogyi micro method as described by Ranganna (1991).

4.1 Reagents

- a. Copper sulphate solution: 100g ($\text{CuSO}_4 + 5\text{H}_2\text{O}$)
- b. 0.1N Potassium iodate solution: 3.567g of (KIO_3)
- c. Shaffer-Somogyi carbonate reagent: 25g anhydrous sodium carbonate (Na_2CO_3), Rochelle salt (potassium sodium tartrate), add with stirring 75ml of copper sulphate solution and 20g sodium bicarbonate. 250ml of 0.1N KIO_3 solution. Iodide – potassium oxalate solution: 2.5g potassium iodide (KI) and potassium oxalate ($\text{K}_2\text{C}_2\text{O}_4$)
- d. Thiosulphate standard solution
- e. 2 N Sulphuric acid solution

4.2 Preparation of sample

Weigh 2.5 – 5.0 g of sample, transfer to a 250ml beaker. Add about 50 ml of water, heat to boil, cool and transfer to a 250 ml volumetric flask. Add lead acetate solution, shake and let stand for 10 min. precipitate the excess of

lead using necessary amount of potassium oxalate solution (22% in water). Make up to volume with water and filter.

4.3 Procedure

Total sugar: To 25 ml of the filtrate in a 50 ml volumetric flask, add 5.0 ml of HCL (1+1). Allow to stand for 24 hr at room temperature. Neutralize exactly with sodium hydroxide and make up to volume with water. Take an aliquot and determine the total invert, sugar as in reducing sugar.

4.4 Calculation

$$\text{Total Sugar \%} = \frac{\text{mg of dextrose x vol. made up x 100}}{5 \times \text{wt of sample taken x 1000}}$$

(b) Second set of 40 F₁S, were planted on 15th September under glasshouse condition for the generation advancement and back crossing. Five promising F₁S (TJM 196 X Kanika, LGG 460 X Virat, LGG 460 X Kanika, Ganga 8 X Shikha and HUM 1 X Shikha) that were reported promising in field condition were backcrossed with their respective parents to obtain the backcross (B₁ and B₂) generations. Finally, six basic generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ were developed for each of the five crosses.

3.3.7 Experiment III. (Summer 2021)

Evaluation of six basic generations for generation mean analysis

The experimental material comprising of six populations viz., P₁, P₂, F₁, F₂, B₁ and B₂ of five cross combinations viz., TJM 196 X Kanika, LGG 460 X Virat, LGG 460 X Kanika, Ganga 8 X Shikha and HUM 1 X Shikha were grown at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur in Randomized Complete Block Design (RCBD) with three replications on 20th March 2021. Each replication had two rows each of parents and F₁'s, while F₂'s, B₁'s and B₂'s were grown in ten rows with the row length of 3 m, spaced 30 cm apart and with a plant spacing of 10 cm in each row.

3.3.8 Data recorded in experiment III

Data was recorded on 10 randomly selected plants from each replication in parents and F₁'s, 50 competitive plants in each backcross (B₁'s

and B₂'s) and 100 competitive plants in F₂ generation for 12 quantitative traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number clusters per plant, number of seeds per pod, 100 seed weight, biological yield per plant, harvest index and seed yield per plant as detailed under 3.3.5

3.4 Statistical analysis

The data in respect of various characters studied were subjected to the following statistical analysis:

3.4.1 Mean

The mean was calculated by conventional method as follows:

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

Where,

$\sum X_i$ = Sum of all observations

n = Number of observations

3.4.2 Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes.

3.4.3 Analysis of variance

The data on yield and quality traits were statistically analyzed on the basis of model described by Cochran and Cox (1950) for randomized complete block design. In order to test the significance of treatments Critical difference was computed (Fisher and Yates, 1963) (Table 3.3).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

- M = General mean
 b_i = True effect of i^{th} block
 t_j = True effect of j^{th} treatment
 e_{ij} = Random errors which are supposed be identically and independently distributed with normal distribution having mean zero and variance σ_e^2 .

Table 3.7: ANOVA for Randomized Complete Block Design

Source of variation	d.f.	Sum of squares	Mean squares	Expected mean squares
Replication	(r-1)	rss	M1	$\sigma_e^2 + g \sigma_r^2$
Genotypes	(g-1)	gss	M2	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1)(g-1)	ess	M3	σ_e^2
Total	(rg-1)			

1. Genotypic variance (σ_g^2) = $\frac{M_2 - M_3}{R}$
2. Phenotypic variance (σ_p^2) = $\frac{M_2 - M_3}{R} + M_3$
3. Environmental variance (σ_e^2) = M_3

Where,

- r = number of replications
 g = number of genotypes
 M_1 = mean square due to replication
 M_2 = mean square due to genotypes
 M_3 = mean square due to error

(a) Phenotypic coefficient of variation (PCV %)

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

$$P C V = (\sigma_p / \bar{X}) \times 100$$

Where

$$\sigma_p = \sqrt{\sigma_p^2}$$

(b) Genotypic Coefficient of Variation (GCV %)

$$GCV = (\sigma_g / \bar{X}) \times 100 \quad \text{where } \sigma_g = \sqrt{\sigma^2_g}$$

Where,

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

σ^2_g = Genotypic variance

σ_g = Genotypic standard deviation

σ^2_e = Environment variance

$\bar{X}$ = General Mean

The range of variation was categorized according to Sivasubramanian and Madhavamenon (1973) as detailed below:

Low = Less than 10%

Moderate = 10 – 20%

High = More than 20%

3.4.4 Heritability (Broad Sense %)

Heritability in broad sense (h^2) was estimated following the method described by Lush (1940) and expressed in percentage.

$$\text{Heritability in broad sense } (h^2) = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

h^2 (bs) = heritability in broad sense,

σ^2_g = Genotypic variance,

σ^2_p = Phenotypic variance

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson *et al.* (1955).

3.4.5 Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955).

$$GA = K \cdot \sigma_p \cdot h^2_{(bs)}$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having the value of 2.06 at 5 per cent level of selection intensity

$h^2_{(bs)}$ = Heritability of the character

σ_p = Phenotypic standard deviation

3.4.6 Genetic advance as percentage of mean

It was calculated by the following formula

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

GA was categorized as

> 20 Percent = High

10-20 Percent = Moderate

< 10 Percent = Low

3.4.7 Correlation coefficient analysis

Correlation coefficient among the characters in all possible combination was calculated with the help of procedure given by Miller *et al.* (1958). The variance and covariance components were used to compute the correlation coefficients, at genotypic and phenotypic level. Correlation coefficients were calculated for all the character combinations at genotypic and phenotypic levels, as per the formula given by Miller *et al.*, (1958).

$$r(X_i X_j) = \frac{\text{Cov.}(X_i X_j)}{\sqrt{\text{Var}(X_i) \text{Var}(X_j)}}$$

Where,

X_iX_j = Coefficient of correlation between characters X_i and X_j

$Cov (X_iX_j)$ = Covariance between characters X_i and X_j

$Var (X_i)$ = Variance of character X_i

$Var (X_j)$ = Variance of character X_j

3.4.8 Path coefficient analysis

Path coefficients are standardized partial regression coefficients and as such provide the means to direct influence of one character upon another character and also permit partitioning of correlation coefficient into direct and indirect effects *via* other character. For the path coefficient analysis the method originally proposed by Wright (1921), which was further modified by Dewey and Lu (1959). The cause and effect relationship is well defined in path coefficient analysis. It is possible to represent the whole system of variables in the form of a diagram known as path diagram. Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, in other words it is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects, *i.e.* it measures the direct and indirect contribution of various independent characters on a dependent character.

Designing new plant type, the knowledge of direct and indirect influence of yield contributing characters, path coefficient analysis was undertaken in parents and crosses. Wright (1921) proposed the original technique. Analysis was carried out by modified method devised by Dewey and Lu (1959). Following set of simultaneously equations were formed and solved for estimating direct and indirect effects. Genotypic path coefficients were calculated separately for yield and yield components. The dependent variable was seed yield per plant. The unexplained variation in the dependent variable was obtained as residual factor from the following equation.

$$r_1Y = P_1Y + r_{12} P_2Y + r_{13} P_3 Y + \dots + r_{1i} P_iY.$$

$$r_2Y = r_{21} P_1Y + P_2 Y + r_{23} P_3Y + \dots + r_{2i} p_iY.$$

$$r_kY = r_{k1} P_1Y + r_{k2} P_2Y + r_{k3}P_3Y + \dots + r_kP_kY.$$

Where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to i and dependent character Y

P_1Y to P_kY = Direct effect of characters 1 to i on character Y.

r_{12} to $r_{k-1,i}$ = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under-

$$\begin{matrix}
 \text{A} & & \text{C} & & \\
 \begin{bmatrix} r_1Y \\ r_2Y \\ \cdot \\ \cdot \\ r_kY \end{bmatrix} & \begin{matrix} r_{k1} & r_{k2} \end{matrix} & \begin{bmatrix} 1 & r_{12} & r_{13} \dots r_{1i} \\ r_{21} & 1 & r_{23} \dots r_{2i} \\ \cdot & & \\ \cdot & & \\ r_{k3} \dots 1 \end{bmatrix} & \begin{matrix} P_1Y \\ P_2Y \\ \cdot \\ \cdot \\ P_kY \end{matrix}
 \end{matrix}$$

Then,

$$B = [C]^{-1} A$$

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \dots C_{1i} \\ C_{21} & C_{22} & C_{23} \dots C_{2i} \\ \cdot & & \\ \cdot & & \\ C_{i1} & C_{i2} & C_{i3} \dots C_{ii} \end{bmatrix}$$

Then the direct effects were calculated as follows -

$$P_1Y = \sum_{i=1}^k C_{1i} r_{iy}$$

$$P_2Y = \sum_{i=1}^k C_{2i} r_{iy}$$

$$P_kY = \sum_{i=1}^k C_{ki} r_{iy}$$

Residual effect was obtained as per for formula given below –

$$R = \sqrt{1 - \sum d_i r_{ij}}$$

Where,

d_i = Direct effect of the i^{th} character

r_{ij} = Correlation coefficient of the i^{th} character with j^{th} character.

Path coefficient were to be rated based on the scales given below.
(Lenka and Mishra, 1973).

> 1.0 =Very high

0.30 – 0.99 =High

0.2 – 0.29 =Moderate

0.1 – 0.19 =Low

0.00 – 0.09 =Negligible

3.4.9 Estimation of Heterosis

The treatment mean value for each trait was used for the estimation of heterosis.

a) Relative heterosis (%): Relative heterosis was calculated and expressed as percent deviation of mean of F_1 from its mid parental value between two corresponding parents as per the formula given by Fonseca and Patterson (1968).

$$\text{Relative heterosis (\%)} = [(\overline{F_1} - \overline{MP}) / (\overline{MP})] \times 100$$

b) Heterobeltiosis (%): Heterobeltiosis was estimated as difference between the mean of the F_1 and that of the parent with greater expression for each of the character in each F_1 combination as per the formula of Liang *et al.* (1971) and Mather and Jinks (1971).

$$\text{Heterobeltiosis (\%)} = [(\overline{F_1} - \overline{BP}) / (\overline{BP})] \times 100$$

c) Standard heterosis (%): Standard heterosis was calculated as the percent deviation of mean of F_1 from standard parent (LGG-460) according to Virmani *et al.* (1982).

$$\text{Standard heterosis (\%)} = [(\overline{F_1} - \overline{SC}) / (\overline{SC})] \times 100$$

The significance of heterosis was tested by using 't' test as suggested by Snedecor and Cochran (1967) and Paschal and Wilcox (1975). To

compute the standard error (SE) of estimates of heterosis, mean squares due to error (M_e) was considered.

$$C.D = S.E \times t_{\alpha} (\text{error d.f})$$

$$SE_{\text{for Relative heterosis (RH)}} = (3M_e/2r)^{1/2}$$

$$SE_{\text{for Heterobeltiosis (HB)}} = (2M_e/r)^{1/2}$$

$$SE_{\text{for Standard heterosis (SH)}} = (2M_e/r)^{1/2}$$

Further, the 't' value is calculated to test the significance of heterosis as follows;

$$\text{'t' value for mid parent heterosis} = [(\overline{F1} - \overline{MP})]/SE(\overline{MP})$$

$$\text{'t' value for better parent heterosis} = [(\overline{F1} - \overline{BP})]/SE(\overline{BP})$$

$$\text{'t' value for standard heterosis} = [(\overline{F1} - \overline{SC})]/SE(\overline{SC})$$

The calculated 't' value was compared with table 't' value at error degrees of freedom,

Where,

M_e = Error MSS in general ANOVA table

r = Number of replications

$\overline{F1}$ = Mean of the hybrid

$\overline{MP}$ = Mid parental value: the arithmetic mean of two parents involved
In the respective cross combination.

$\overline{BP}$ = Better parental value: the mean of the superior parent in the
respective cross combination

$\overline{SC}$ = Standard parental value: the mean of PDM 139

3.4.10 Combining Ability Analysis

Combining ability analysis was carried out following Line $\times$ Tester design Kempthorne (1957). The mathematical model for combining ability analysis is given below:

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

Where,

Y_{ijk} = any measurable character of the cross ' $i \times j$ '

g_i = *gca* effect of the ' i^{th} ' female parent

g_j = *gca* effect of the ' j^{th} ' male parent

s_{ij} = *sca* effect of the ' $i \times j^{th}$ ' cross

r_k = ' k^{th} ' replication effect

e_{ijk} = environmental effect particular to ijk^{th} individual

μ = population mean effect

Table 3.8: ANOVA for Line $\times$ Tester Analysis

Source of variation	Degree of freedom	Sum of squares	Mean squares	Expectations
Replications (r)	(r-1)	Rss	rMS	-
Entries (en)	en-1	Enss	enMS	-
Parents (p)	p-1	Pss	pMS	-
Females (f)	f-1	Fss	fMS	-
Males (m)	m-1	Mss	mMS	-
f vs. m	1	Fmss	fmMS	-
Hybrids (c)	c-1	Css	cMS	-
Females in hybrids (fh)	f-1	fhSS	fhMS (M_1)	$\sigma_e^2 + r \text{ Cov (FS)} - 2 \text{ Cov (HS)} + mr \text{ Cov (HS)}$
Males in hybrids (mh)	m-1	mhSS	mhMS (M_t)	$\sigma_e^2 + r \text{ Cov (FS)} - 2 \text{ Cov (HS)} + fr \text{ Cov (HS)}$
fh $\times$ mh (L $\times$ T)	(f-1) (m-1)	fmhSS	fmhMS $M_{(l \times t)}$	$\sigma_e^2 + r \text{ Cov (FS)} - 2 \text{ Cov (HS)}$
P vs. C	1	pcSS	pcMS	-
Error (e)	(e-1) (r-1)	eSS	Ems (M_e)	σ_e^2
Total	(er-1)	TSS	-	-

(a) Estimation of combining ability effects

The individual effects are estimated as follows:

- (i) *gca effects of lines* (g_i) = $\frac{x_{i....}}{tr} - \frac{x_{....}}{ltr}$
- (ii) *gca effects of testers* (g_j) = $\frac{x_{.j....}}{tr} - \frac{x_{....}}{ltr}$
- (iii) *sca effects of crosses* (g_i) = $\frac{x_{ij....}}{r} - \frac{x_{i....}}{tr} \frac{x_{.j....}}{lr} + \frac{x_{....}}{ltr}$

where,

- $x_{i..}$ = Total of i^{th} line over 't' testers and 'r' replications
- $x_{.j.}$ = Total of j^{th} tester over 'l' lines and 'r' replications
- $x_{...}$ = Total of all cross combinations over all replications
- $x_{ij.}$ = Total of the hybrid between ' i^{th} ' line and ' j^{th} ' tester over 'r' replications.
- t = Number of testers
- l = Number of lines
- r = Number of replications

(b) Estimation of standard errors for combining ability effects

The standard errors pertaining to *gca* effects of lines and testers and *sca* effects of different cross combinations were calculated as shown below:

$$S.E.(g_i) \text{ lines} = \sqrt{\frac{M_e}{rt}}$$

$$S.E.(g_j) \text{ testers} = \sqrt{\frac{M_e}{rl}}$$

$$S.E. (S_{ij}) = \sqrt{\frac{M_e}{r}}$$

$$S.E. (g_i - g_j) \text{ lines} = \sqrt{\frac{2M_e}{rt}}$$

$$S.E. (g_i - g_j) \text{ testers} = \sqrt{\frac{2M_e}{rl}}$$

$$\text{Cov.H.S.}(\text{lines}) = M_l - M_{l \times t} / rt$$

$$\text{Cov. H.S. (testers)} = M_t - M_{l \times t} / r$$

$$\text{S.E. } (S_{ij} - S_{kl}) = \sqrt{\frac{2M_e}{r}}$$

$$\text{Cov. H.S. (average)} = \frac{1}{r(2l-t-l-t)} \left[\frac{(l-1)(M_1) + (t-1)(M_t)}{l+t-2} \right] - M_{l \times t}$$

$$\text{Cov. FS} = \frac{(M_l - M_e) + (M_t + M_e) + (M_{l \times t} - M_e)}{3r} + \frac{6r \text{Cov H.S.} - r(l+t) \text{Cov H.S.}}{3r}$$

$$\sigma^2_{gca} = \text{Cov. H. S.} \left[\frac{1+F}{4} \right] \sigma^2 A$$

$$\sigma^2_{gca} = M_{l \times t} - Me/r \text{ Or } \left[\frac{1+F}{4} \right] \sigma^2 D$$

$$\sigma^2_{gca} : \sigma^2_{sca} = \frac{\sigma^2_{gca}}{\sigma^2_{sca}}$$

$$\text{Additive variance} = \sigma^2_A = \frac{\sigma^2_{gca}}{\left[\frac{1+F}{4} \right]}$$

$$\text{Dominance variance} = \sigma^2_D = \frac{\sigma^2_{sca}}{\left[\frac{1+F}{2} \right]}$$

Where,

$$F (\text{Inbreeding coefficient}) = 1$$

3.4.11 Generation Mean Analysis

The means and variances of means for six basic generations were computed using individual plant data for five cross combinations viz., TJM 196 X Kanika, LGG 460 X Virat, LGG 460 X Kanika, Ganga 8 X Shikha and HUM 1 X Shikha. The variation among the plants within each replication was used for calculating the sampling variances (variances of mean).

The generation mean analysis was carried out following the methodology of Hayman (1958).

Individual scaling tests

The adequacy of simple additive-dominance model was verified by A, B, and C individual scaling tests of Mather (1949).

From six basic generation means, the scaling tests were calculated as follows.

$$\begin{aligned}
\text{Scale A} &= 2\overline{B_1} - \overline{P_1} - \overline{F_1} \\
\text{Scale B} &= 2\overline{B_2} - \overline{P_2} - \overline{F_2} \\
\text{Scale C} &= 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}
\end{aligned}$$

Where,

P_1, P_2, F_1, F_2, B_1 , and B_2 are means of different generations over the replications.

When the additive-dominance model is adequate, the values of A, B and C are expected to be zero within limits of sampling errors. The sampling variances of these scaling tests V_A, V_B and V_C were computed from the variances of generation mean as follows:

$$\begin{aligned}
V_A &= 4V_{(\overline{B_1})} + V_{(\overline{P_1})} + V_{(\overline{F_1})} \\
V_B &= 4V_{(\overline{B_2})} + V_{(\overline{P_2})} + V_{(\overline{F_1})} \\
V_C &= 16V_{(\overline{F_2})} + V_{(\overline{F_1})} + V_{(\overline{P_1})} + V_{(\overline{P_2})}
\end{aligned}$$

Where,

V_A, V_B and V_C are the variances of A, B and C;

$V_{P_1}, V_{P_2}, V_{F_1}, V_{F_2}, V_{B_1}$, and V_{B_2} are the variances of P_1, P_2, F_1, F_2, B_1 and B_2 generations respectively.

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

$$SE_{(A)} = \sqrt{V_A}$$

$$SE_{(B)} = \sqrt{V_B}$$

$$SE_{(C)} = \sqrt{V_C}$$

The 't' values are calculated by dividing the scale effects of A, B and C by their respective standard errors.

$$t \text{ cal for A-test} = \text{Scale A} / S.E_{(A)}$$

$$t \text{ cal for B-test} = \text{Scale B} / S.E_{(B)}$$

$$t \text{ cal for C-test} = \text{Scale C} / S.E_{(C)}$$

The calculated values of 't' are to be compared with 't' table values at 5 per cent and 1 per cent level of significance at their respective degrees of freedom. The significance of any scaling test indicates the presence of epistasis.

Digenic epistatic or six parameter model

Wherever the simple additive - dominance model was found inadequate, the digenic interaction model was applied to explain the genetic variation among the generation means.

A. Estimation of genetic effects

Hayman (1958) gave six-parameter model for estimation of various genetic components. The various genetic effects were obtained as per the formula given below.

$$m = \overline{F_2}$$

$$d = \overline{B_1} - \overline{B_2}$$

$$h = \overline{F_1} - 4\overline{F_2} - \left(\frac{1}{2}\right)\overline{P_1} - \left(\frac{1}{2}\right)\overline{P_2} + 2\overline{B_1} + 2\overline{B_2}$$

$$i = 2\overline{B_1} + 2\overline{B_2} - 4\overline{F_2}$$

$$j = 2\overline{B_1} - \overline{P_1} - 2\overline{B_2} - \overline{P_2}$$

$$l = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$$

B. Estimates of variances

$$V_m = V_{(\overline{F_2})}$$

$$V_d = V_{(\overline{B_1})} + V_{(\overline{B_2})}$$

$$V_h = V_{(\overline{F_1})} + 16V_{(\overline{F_2})} + \left(\frac{1}{4}\right)V_{(\overline{P_1})} + \left(\frac{1}{4}\right)V_{(\overline{P_2})} + 4V_{(\overline{B_1})} + 4V_{(\overline{B_2})}$$

$$V_i = 4V_{(\overline{B_1})} + 4V_{(\overline{B_2})} + 16V_{(\overline{F_2})}$$

$$V_j = 4V_{(\overline{B_1})} + 4V_{(\overline{P_1})} + 4V_{(\overline{B_2})} + V_{(\overline{P_2})}$$

$$V_l = V_{(\overline{P_1})} + V_{(\overline{P_2})} + 4V_{(\overline{F_1})} + 16V_{(\overline{F_2})} + 16V_{(\overline{B_1})} + 16V_{(\overline{B_2})}$$

C. Standard errors of estimates

Significant departure of the estimates of parameters *i.e.*, m, d, h, i, j and l from zero is tested by a 't' test as described by Hayman's (1958). The standard error of each of the gene effects was estimated as follows

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

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

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

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

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

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

The 't' values were worked out using following formulae

$$t_{(m)} = m / S.E_{(m)}$$

$$t_{(d)} = d / S.E_{(d)}$$

$$t_{(h)} = h / S.E_{(h)}$$

$$t_{(i)} = i / S.E_{(i)}$$

$$t_{(j)} = j / S.E_{(j)}$$

$$t_{(l)} = l / S.E_{(l)}$$



Plate 1: Overall view of experimental field layout



Plate 2: Hybridization technique in greengram

Chapter – IV

RESULTS

RESULTS

The present investigation entitled “Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]” was carried out at Seed Breeding Farm, Department of Plant Breeding & Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur.

To characterize the visual differences of the parental lines and cross combinations different morphological observations were recorded to adopt the DUS guidelines developed by IIPR, Kanpur and approved by PPV & FRA, New Delhi. To obtain a clear picture of variability in the parental lines and cross combinations, the genetic parameters of variability were studied. To know the degree of relationship between characters under study, correlation analysis was done. Also, path analysis was conducted to know the direct and indirect effects of various independent characters on dependent one. The Line $\times$ Tester mating design was utilized to assess the combining ability of parents and crosses for different quantitative characters as well as to study the extent of heterosis and nature of gene actions for yield and yield contributing characters. To estimate the different components of genetic variance and for testing the presence or absence of epistasis generation mean analysis was performed in five selected crosses. To understand quality traits, parental lines and cross combinations were analyzed for quality parameters adopted to screen the genotypes accordingly.

The experimental results of the present investigation have been presented under the following headings:

4.1 Characterization

4.2 Analysis of variance

4.3 Parameter of genetic variability

4.3.1 Range and mean performance for different characters

4.3.2 Genotypic and phenotypic coefficient of variation, Heritability (%) and Genetic advance as percentage of mean

4.4 Correlation coefficient analysis

- 4.5 Path coefficient analysis**
- 4.6 Heterosis**
- 4.7 Combining ability analysis**
- 4.8 Generation mean analysis**
- 4.9 Quality analysis**
- 4.1 Characterization**

For morphological characterization, different traits of 14 parents and 40 F1s were evaluated and results are presented in table 4.1 and 4.2 in this chapter. The frequency distribution of 19 morphological traits for parents and crosses are summarized in table 4.3 and 4.4.

1. Hypocotyl: Anthocyanin colouration

This trait was recorded at cotyledonary stage. In the present investigation, out of 14 parents, 13 showed anthocyanin colouration and only one was without pigmentation. Among the crosses, 36 showed presence for anthocyanin colouration and rest 4 were without pigmentation.

2. Time of flowering

Time of flowering was observed at days to 50% flowering stage of plant. Out of 14 parents, 4 were early and the rest 10 were medium in flowering duration. Late duration was not noted in any of the parents. Among the 40 crosses, 30 were early while, 10 were medium and none of them were late.

3. Plant growth habit

Plant growth habit was observed at 50% flowering. In the present investigation, 8 parents showed semi-erect type of growth habit and 6 of them were spreading while none were erect. Out of 40 crosses, 10 were semi-erect, 30 were spreading and erect type trait was not reported in any of the crosses evaluated for plant growth habit.

4. Plant habit

Mungbean descriptor described two types of plant habit: determinate and indeterminate. Two parents were determinate while 12 of them were indeterminate. All the crosses under study had indeterminate plant habit.

5. Stem colour

In the present study, green stem colour was noted in 6 parents while, rest of the 8 parents showed stem colour having green with purple splashes. Purple stem colour was not observed in any of the parents. In the crosses, green stem colour was reported in 10 while, 29 crosses had green with purple splashes. Only one cross had purple stem colour out of forty crosses.

6. Stem pubescence

Presence of stem pubescence was noted in all the fourteen parents as well as 40 crosses.

7. Leaflet lobes (terminal)

In the 14 parental lines, this trait was present in 9 while, it was absent in 5 parental lines. Among the crosses, leaflet lobes were absent in 36 and only 4 crosses possessed this trait.



Light yellow flower petal



yellow flower petal



Presence and absence of anthocyanin coloration



Black pod



Brown pod



Pod pubescence



Shiny green seeds

Plate 3: Morphological characterization in mungbean

8. Leaf shape

Ovate leaf shape was reported in 12 parents while 2 of them had deltoid. Further, none of the genotypes fell under the category of Cuneate and Lanceolate. All the 40 crosses were dominated with ovate leaf shape.

9. Leaf colour

As per mungbean DUS descriptor, two types of leaf colour; green and dark green were reported. In the present study, out of 14 parents 10 parents had green leaf colour and rest of the 4 showed dark green leaf colour. Among the 40 crosses, 29 were green and 11 had dark green leaf colour.

10. Leaf: Vein colour

In the parents, leaf vein colour was green in 1, greenish purple in 6 and purple in 7 parents. In the 40 cross combinations, 6 had green leaf vein colour. Twenty five crosses showed greenish purple leaf vein colour while, 9 of them possessed purple vein colour.

11. Flower: Colour of petal

Out of the 14 parental lines, Petal colour was yellow in 9 and light yellow in 5 of the parents. In the crosses, yellow petal colour was reported in 29 and light yellow was reported in 11 crosses.

12. Pod: Colour of pre mature pod

Among 14 parents, 13 had green pre mature pod colour while only one was green with pigmented suture. All the 40 crosses under study had green pre mature pod colour.

13. Pod: Pubescence

Pod pubescence was present in all the 14 parental lines as well 40 crosses.

14. Pod: Colour

The pod colour was brown in 9 and black in 5 parents. Among 40 crosses, pods were brown in 17 and black pod colour was present in 23 crosses.

15. Pod: Curvature of mature pod

Among 14 parents, 7 had straight while 7 were with curved pods.. Among 40 crosses, 13 had straight and 27 had curved pods.

16. Seed: Colour

Seed colour was green in 2 parental lines and mottled in 12 of the parents and it was green in 4 and mottled in 36 of the crosses.

17. Seed: Lusture

Lusture of the seed was reported as shiny in 4 and dull in 10 parents. Among the 40 crosses, shiny seeds were noted in 13 and dull seeds were reported in 27 crosses.

18. Seed: Shape

Among 14 parents, shape of the seed was oval in 9 and drum shaped seeds were reported in 5 parental lines. Among the 40 crosses, 20 had oval seed shape and rest of the 20 crosses had drum shaped seeds.

19. Seed: Size

The size of the seed was medium in 13 parental lines and large seed size was reported in only one. Among 40 crosses, 37 had medium seeds while 3 had large seeds. Small category of seeds was not noted in any of the crosses studied.

Table 4.1: Morphological characterization of 14 mungbean parental lines

S. No.	Characters	Stage of Observation	Parental lines													
			TJM196	TJM136	TJM3	TMB37	Ganga8	LGG460	HUM 1	SL668	Pusa Vishal	PDM11	PDM139	Shikha	Kanika	Virat
1	Hypocotyl: Anthocyanin colouration	Cotyledons unfolded	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Absent	Present	Present
2	Flowering time	50% plants with at least one open flower	Medium	Early	Medium	Medium	Medium	Medium	Medium	Early	Early	Medium	Early	Medium	Medium	Medium
3	Plant: Growth habit	50% flowering	Spreading	Semi-erect	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading	Spreading	Spreading	Semi-erect	Semi-erect	Semi-erect	Semi-erect	Spreading
4	Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Determinate	Indeterminate	Determinate	Indeterminate	Indeterminate	Indeterminate
5	Stem: color	50% flowering	Green	Green with purple splashes	Green	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green	Green	Green with purple splashes	Green with purple splashes
6	Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
7	Leaflet lobes (terminal)	50% flowering	Present	Present	Absent	Present	Present	Present	Absent	Absent	Absent	Absent	Present	Present	Present	Present
8	Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Deltoid	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Deltoid	Ovate	Ovate
9	Leaf: Color	50% flowering	Green	Dark green	Dark green	Dark green	Green	Green	Green	Dark green	Green	Green	Green	Green	Green	Green
10	Leaf: Vein color	50% flowering	Greenish purple	Purple	Green	Greenish purple	Purple	Purple	Purple	Greenish purple	Greenish purple	Greenish purple	Purple	Greenish purple	Purple	Purple
11	Flower: Petal Color (Standard)	50% flowering	Yellow	Yellow	Light Yellow	Light yellow	Yellow	Yellow	Light yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow	Yellow	Yellow
12	Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
13	Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green with pigmented suture	Green	Green	Green	Green	Green	Green
14	Pod: Color	Harvest maturity	Brown	Black	Brown	Black	Brown	Brown	Brown	Black	Brown	Black	Black	Brown	Brown	Brown
15	Curvature: Mature pod	Harvest maturity	Straight	Curved	Curved	Curved	Straight	Straight	Straight	Curved	Curved	Straight	Straight	Curved	Straight	Curved
16	Seed: color	Mature seeds	Mottled	Mottled	Mottled	Green	Mottled	Mottled	Green	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
17	Seed: Shape	Mature seeds	Oval	Oval	Drum shaped	Oval	Oval	Oval	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Oval	Oval
18	Seed: Lusture	Mature seeds	Dull	Dull	Dull	Shiny	Shiny	Dull	Shiny	Dull	Dull	Dull	Dull	Shiny	Dull	Dull
19	Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Large	Medium	Medium	Medium	Medium	Medium	Medium

Table 4.2: Morphological characterization of 40 mungbean crosses

S. No.	Characters	Stage of Observation	Crosses									
			TJM196 X PDM139	TJM196 X Shikha	TJM196 X Kanika	TJM196 X Virat	TJM136 X PDM139	TJM136 X Shikha	TJM136 X Kanika	TJM136 X Virat	TJM3 X PDM139	TJM3 X Shikha
1	Hypocotyl: Anthocyanin Colouration	Cotyledons unfolded	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
2	Flowering time	50% plants with at least one open flower	Early	Early	Medium	Medium	Early	Early	Medium	Early	Early	Early
3	Plant: Growth habit	50% flowering	Semi-erect	Spreading	Semi-erect	Spreading	Spreading	Spreading	Semi-erect	Semi-erect	Spreading	Spreading
4	Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
5	Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green
6	Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
7	Leaflet lobe (terminal)	50% flowering	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
8	Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
9	Leaf: Color	50% flowering	Green	Green	Green	Green	Green	Green	Green	Green	Dark green	Dark green
10	Leaf: Vein color	50% flowering	Purple	Greenish purple	Purple	Purple	Greenish purple	Purple	Purple	Greenish purple	Green	Greenish purple
11	Flower: Petal Color (Standard)	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Light yellow
12	Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
13	Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
14	Pod: Color	Harvest maturity	Black	Brown	Black	Black	Black	Black	Brown	Black	Black	Black
15	Curvature: Mature pod	Harvest maturity	Curved	Curved	Straight	Straight	Curved	Straight	Curved	Straight	Curved	Curved
16	Seed: color	Mature seeds	Mottled	Green	Green	Green	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
17	Seed: Shape	Mature seeds	Oval	Oval	Oval	Oval	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Drum shaped
18	Seed: Lusture	Mature seeds	Dull	Shiny	Shiny	Shiny	Dull	Dull	Dull	Dull	Dull	Dull
19	Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Large	Large	Medium	Medium	Medium	Medium

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S. No.	Characters	Stage of Observation	Crosses									
			TJM3 X Kanika	TJM3 X Virat	TMB37 X PDM139	TMB37 X Shikha	TMB37 X Kanika	TMB37 X Virat	Ganga8 X PDM139	Ganga8 X Shikha	Ganga8 X Kanika	Gang8 X Virat
1	Hypocotyl: Anthocyanin Colouration	Cotyledon unfolded	Present	Present	Present	Absent	Present	Present	Present	Absent	Present	Present
2	Flowering time	50% plants with at least one open flower	Early	Early	Early	Early	Early	Early	Early	Early	Medium	Early
3	Plant: Growth habit	50% flowering	Spreading	Spreading	Semi-erect	Spreading	Semi-erect	Spreading	Spreading	Spreading	Spreading	Semi-erect
4	Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
5	Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes
6	Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
7	Leaflet lobe (Terminal)	50% flowering	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
8	Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
9	Leaf: Color	50% flowering	Dark green	Dark green	Dark green	Dark green	Green	Green	Dark green	Dark green	Green	Dark green
10	Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Purple	Green	Greenish purple	Greenish purple	Purple	Greenish purple	Green	Greenish purple
11	Flower: Petal Color (Standard)	50% flowering	Light Yellow	Light Yellow	Yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow	Light yellow	Yellow
12	Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
13	Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
14	Pod: Color	Harvest maturity	Black	Brown	Black	Black	Black	Brown	Brown	Brown	Brown	Black
15	Curvature: Mature pod	Harvest maturity	Straight	Curved	Curved	Curved	Curved	Straight	Straight	Straight	Curved	Curved
16	Seed: color	Mature seeds	Mottled	Mottled	Mottled	Green	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
17	Seed: Shape	Mature seeds	Drum shaped	Drum shaped	Oval	Oval	Oval	Drum Shaped	Oval	Oval	Oval	Drum shaped
18	Seed: Lusture	Mature seeds	Dull	Dull	Shiny	Shiny	Dull	Shiny	Dull	Dull	Dull	Dull
19	Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

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S.N o.	Characters	Stage of Observation	Crosses									
			LGG460 X PDM139	LGG460 X Shikha	LGG460 X Kanika	LGG460 X Virat	HUM1 X PDM139	HUM1 X Shikha	HUM1 X Kanika	HUM1 X Virat	SL668 X PDM139	SL668 X Shikha
1	Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Present	Present	Absent	Present	Absent	Present	Present	Present	Present
2	Flowering time	50% plants with at least one open flower	Medium	Medium	Early	Early	Early	Early	Early	Early	Early	Early
3	Plant: Growth habit	50% flowering	Spreading	Spreading	Spreading	Spreading	Spreading	Spreading	Spreading	Semi-erect	Spreading	Spreading
4	Plant: Habit	50% flowering	Indeterminate	Indeterminat e	Indeterminat e	Indeterminat e	Indeterminate	Indeterminat e	Indeterminat e	Indeterminate	Indeterminat e	Indeterminat e
5	Stem: color	50% flowering	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Purple	Green with purple splashes
6	Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
7	Leaflet lobe (Terminal)	50% flowering	Present	Absent	Present	Absent	Absent	Absent	Absent	Absent	Present	Present
8	Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
9	Leaf: Color	50% flowering	Dark green	Dark green	Green	Green	Green	Green	Green	Green	Green	Green
10	Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Green	Greenish purple	Greenish purple	Greenish purple
11	Flower: Petal Color (Standard)	50% flowering	Yellow	Yellow	Yellow	Yellow	Light yellow	Light yellow	Light yellow	Yellow	Yellow	Yellow
12	Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
13	Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
14	Pod: Color	Harvest maturity	Brown	Brown	Brown	Brown	Black	Brown	Black	Black	Brown	Black
15	Curvature: Mature pod	Harvest maturity	Straight	Curved	Curved	Curved	Straight	Curved	Curved	Straight	Curved	Straight
16	Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
17	Seed: Shape	Mature seeds	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Oval	Drum shaped	Oval	Drum shaped	Drum shaped	Drum shaped
18	Seed: Lusture	Mature seeds	Dull	Dull	Dull	Dull	Shiny	Dull	Dull	Dull	Dull	Shiny
19	Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Large	Medium	Medium	Medium	Medium

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S. No.	Characters	Stage of Observation	Crosses									
			SL668 X Kanika	SL668 X Virat	Pusa Vishal X PDM139	Pusa Vishal X Shikha	Pusa Vishal X Kanika	Pusa Vishal X Virat	PDM11 X PDM139	PDM11 X Shikha	PDM11 X Kanika	PDM11 X Virat
1	Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
2	Flowering time	50% plants with at least one open flower	Medium	Early	Medium	Early	Medium	Early	Medium	Early	Early	Early
3	Plant: Growth habit	50% flowering	Spreading	Spreading	Spreading	Spreading	Spreading	Semi-erect	Spreading	Spreading	Semi-erect	Spreading
4	Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
5	Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green	Green
6	Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
7	Leaflet lobe (terminal)	50% flowering	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Absent
8	Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
9	Leaf: Color	50% flowering	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
10	Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Purple	Green	Greenish purple	Greenish purple	Purple	Green	Greenish purple	Greenish purple
11	Flower: Petal Color (Standard)	50% flowering	Yellow	Yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow	Yellow	Yellow	Yellow
12	Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
13	Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
14	Pod: Color	Harvest maturity	Black	Black	Brown	Brown	Black	Brown	Black	Black	Brown	Black
15	Curvature: Mature pod	Harvest maturity	Curved	Curved	Curved	Curved	Curved	Straight	Curved	Curved	Curved	Curved
16	Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
17	Seed: Shape	Mature seeds	Oval	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Oval	Oval	Oval
18	Seed: Lusture	Mature seeds	Shiny	Shiny	Shiny	Dull	Dull	Dull	Shiny	Shiny	Dull	Dull
19	Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

Table 4.3: Frequency distribution of morphological traits in 14 parental lines

S. No.	Characters	Classes	Number of entry	Percentage of entry (%)
1	Hypocotyl: Anthocyanin Colouration	Present	13	92.85
		Absent	1	7.14
2	Time of flowering	Early (<40 days)	4	28.57
		Medium (40-50 days)	10	71.42
		Late (More the 50 days)	00	00
3	Plant: Growth habit	Erect	00	00
		Semi-erect	8	57.14
		Spreading	6	42.85
4	Plant: Habit	Determinate	2	14.28
		Indeterminate	12	85.71
5	Stem: Colour	Green	6	42.85
		Green with purple splashes	8	57.14
		Purple	00	00
6	Stem: Pubescence	Absent	00	00
		Present	14	100
7	Leaflet: Lobes (terminal)	Absent	5	35.71
		Present	9	64.28
8	Leaf: Shape	Deltoid	2	14.28
		Ovate	12	85.71
		Lanceolate	00	00
		Cuneate	00	00
9	Leaf: Colour	Green	10	71.42
		Dark green	4	28.57
10	Leaf: Vein colour	Green	1	7.14
		Greenish purple	6	42.85
		Purple	7	50
11	Flower: Colour of Petal	Yellow	9	64.28
		Light yellow	5	35.71
12	Pod: Colour of pre mature pod	Green	13	92.85
		Green with pigmented suture	1	7.14
13	Pod: Pubescence	Absent	00	00
		Present	14	100
14	Pod: Colour	Brown	9	64.28
		Black	5	35.71
15	Pod: Curvature of mature pod	Straight	7	50
		Curved	7	50
16	Seed: Colour	Yellow	00	00
		Green	2	14.28
		Mottled	12	85.71
		Black	00	00
17	Seed: Lusture	Shiny	4	28.57
		Dull	10	71.42
18	Seed: Shape	Oval	9	64.28
		Drum shaped	5	35.71
19	Seed: Size	Small (<3g)	00	00
		Medium (3-5g)	13	92.85
		Large (> 5g)	1	7.69

Table 4.4: Frequency distribution of morphological traits in 40 Crosses

S. No.	Characters	Classes	Number of entry	Percentage of entry (%)
1	Hypocotyl: Anthocyanin Coloration	Present	36	90
		Absent	04	10
2	Time of flowering	Early (<40 days)	30	75
		Medium (40-50 days)	10	25
		Late (More the 50 days)	00	00
3	Plant: Growth habit	Erect	00	00
		Semi-erect	10	25
		Spreading	30	75
4	Plant: Habit	Determinate	00	00
		Indeterminate	40	100
5	Stem: Colour	Green	10	25
		Green with purple splashes	29	72.5
		Purple	01	2.5
6	Stem: Pubescence	Absent	00	00
		Present	40	100
7	Leaflet: Lobes (terminal)	Absent	36	90
		Present	04	10
8	Leaf: Shape	Deltoid	00	00
		Ovate	40	100
		Lanceolate	00	00
		Cuneate	00	00
9	Leaf: Colour	Green	29	72.5
		Dark green	11	27.5
10	Leaf: Vein colour	Green	06	15
		Greenish purple	25	62.5
		Purple	09	22.5
11	Flower: Colour of Petal	Yellow	29	72.5
		Light yellow	11	27.5
12	Pod: Colour of pre mature pod	Green	40	100
		Green with pigmented suture	00	00
13	Pod: Pubescence	Absent	00	00
		Present	40	100
14	Pod: Colour	Brown	17	42.5
		Black	23	57.5
15	Pod: Curvature of mature pod	Straight	13	32.5
		Curved	27	67.5
16	Seed: Colour	Yellow	00	00
		Green	4	10
		Mottled	36	90
		Black	00	00
17	Seed: Lusture	Shiny	13	32.5
		Dull	27	67.5
18	Seed: Shape	Oval	20	50
		Drum shaped	20	50
19	Seed: Size	Small (<3g)	00	00
		Medium (3-5g)	37	92.5
		Large (> 5g)	03	7.5

4.2 Analysis of Variance

Analysis of variance refers to the observable differences in individuals for a particular trait. To know the extent of variation of observed characters among the 14 parental lines and 40 crosses, analysis of variance was performed and presented in Table 4.5. The genotypes differed significantly for all the traits studied, indicating the existence of sufficient variability in the material.

Table 4.5: Analysis of variance for 12 quantitative characters (Parents and Crosses)

S. No.	Characters	Mean Sum of Squares		
		Replication (df=2)	Treatments (df=53)	Error (df=106)
1	Days to 50% flowering	3.08	24.98**	0.43
2	Day to maturity	3.38	20.29**	0.92
3	Plant height (cm)	3.99	109.48**	2.90
4	Number of branches/plant	0.87	2.02**	0.30
5	Number of pods/plant	4.55	422.98**	3.02
6	Number of pods/cluster	0.48	1.04**	0.19
7	Number of clusters/plant	3.63	25.30**	2.05
8	Number of seeds/pod	1.17	1.79**	0.96
9	100 seed weight (g)	0.29	1.40**	0.24
10	Biological yield/plant (g)	2.80	97.06**	2.15
11	Harvest Index (%)	26.12	212.43**	30.24
12	Seed yield/plant (g)	0.04	31.90**	1.02

**Significant at P= 0.00 level

4.3 Parameters of genetic variability

To predict genetic variability in a population, various parameters viz; range, mean, phenotypic and genotypic coefficient of variance, heritability and genetic advance for yield and attributing traits of parental lines and F₁s were estimated and presented in Table 4.6 and 4.7.

4.3.1 Mean and range

Mean and range performance for yield and its components traits of lines, testers and crosses are summarized in Table 4.6 and 4.7.

1. Days to 50% flowering

Among the lines, TJM 136 (32.33 days) flowered earlier whereas; PDM 11 (45.67 days) was late in days to 50% flowering. Five lines viz., TJM 196, TJM 136, TMB 37, SL 668 and Pusa Vishal were early in flowering compared to the mean flowering of the lines (41.53 days). Among testers, PDM 139 (39.67 days) flowered earliest while Kanika (44.33 days) flowered late. Three testers viz; PDM 139, Shikha and Virat were early in flowering compared to the mean flowering of the testers (41.33 days). Hence, the line TJM 136 and tester Virat were reported early in flowering.

Among crosses, TJM 136 X Virat was earliest in 50%flowering and PDM 11 X PDM 139 (42.67 days) was late as compared to the mean flowering of crosses (38.98 days) and it was surpassed by 26 crosses (Table 4.6 and 4.7).

2. Days to maturity

Among the lines, TJM 136 (55.33 days) was early in maturity whereas PDM 11 was found to be late (70.33 days). Six lines viz; TJM 3, Ganga 8, LGG 460, HUM 1, Pusa Vishal and PDM 11 were found early in maturity as compared to the mean maturity of lines (66.40 days). Similarly among testers, PDM 139 was found early in maturity (64.33 days) compared to Kanika which was late in maturity (69.33 days) and mean days to maturity of testers were 67.00 days which was exceeded by two testers i.e. Kanika and Virat.

The maturity duration of the crosses ranged from 56.67 days (TJM 137 X Virat) to 69.33 days (LGG 460 X Shikha) with a mean of 65.72 days which was surpassed by eighteen crosses (Table 4.6 and 4.7)

3. Plant height (cm)

Among lines, plant height ranged from 41.80 cm (TJM 196) to 58.43 cm (PDM 11) with a general mean height of 49.72 cm. Four lines viz; TJM 3, Ganga 8, Pusa Vishal and PDM 11 exceeded the general mean value. Among testers, plant height varied from 37.73 cm (PDM 139) to 60.47 cm (Kanika) with a mean height of 46.63 cm. Two testers viz; Shikha and Kanika exceeded the general mean of testers (Table 4.6 and 4.7).

Table 4.6: Mean performance of parents and crosses for seed yield and its attributing characters

S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of pods/plant	No. of pod/cluster	No. of clusters/plant	No. of seeds/pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
	Lines												
1	TJM 196	41.33	66.33	41.80	3.53	42.50	3.85	11.13	9.87	5.15	33.41	22.85	7.61
2	TJM 136	32.33	55.33	45.17	1.50	21.13	3.16	6.70	10.47	5.38	19.60	21.45	4.38
3	TJM 3	42.33	67.00	50.61	1.70	23.00	3.48	6.67	9.90	3.45	15.97	21.67	3.41
4	TMB 37	40.00	65.33	48.00	3.70	27.33	2.68	10.33	11.87	4.07	19.22	21.65	4.16
5	Ganga 8	45.33	69.67	52.77	2.70	27.27	3.74	7.30	10.10	3.38	25.12	26.35	6.55
6	LGG 460	44.67	69.00	48.67	1.63	30.68	3.01	10.18	9.10	4.62	21.61	26.98	5.81
7	HUM 1	43.00	66.67	47.01	1.20	23.87	3.13	7.63	10.07	5.27	13.96	34.76	5.02
8	SL668	39.67	66.00	49.27	2.03	24.40	2.88	8.63	9.83	6.22	22.41	19.39	4.26
9	Pusa Vishal	41.00	68.33	55.47	1.67	21.73	2.97	7.30	10.77	4.52	19.72	27.64	5.40
10	PDM 11	45.67	70.33	58.43	1.93	32.20	4.01	8.07	10.03	3.89	29.45	19.13	5.60
	Mean of lines	41.53	66.40	49.72	2.16	27.41	3.29	8.39	10.20	4.60	22.05	24.19	5.22
	Testers												
1	PDM 139	39.67	64.33	37.73	2.20	25.17	2.99	8.57	9.83	3.81	14.61	32.96	4.85
2	Shikha	40.67	66.67	47.37	2.10	40.17	3.78	10.63	10.00	4.26	21.94	23.85	5.26
3	Kanika	44.33	69.33	60.47	3.07	26.40	4.01	6.63	9.83	4.53	28.83	18.76	5.40
4	Virat	40.67	67.67	40.93	2.83	22.93	3.09	7.43	10.33	4.53	17.84	37.19	6.17
	Mean of Testers	41.33	67.00	46.63	2.55	28.67	3.47	8.32	9.98	4.28	20.81	28.19	5.42
	Crosses												
1	TJM 196 X PDM 139	39.33	64.67	43.40	3.77	52.00	3.77	14.07	9.87	4.75	20.15	39.33	7.95
2	TJM 196 X Shikha	38.67	64.67	41.97	3.30	40.73	3.52	11.70	9.53	3.93	26.44	43.26	11.37
3	TJM 196 X Kanika	40.67	64.67	49.70	2.47	40.20	3.86	10.67	10.33	4.82	25.59	43.97	11.14
4	TJM 196 X Virat	41.33	66.33	40.07	3.23	47.77	3.79	12.67	10.23	4.85	34.30	44.37	15.16

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S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of pods/plant	No. of pod/cluster	No. of clusters/plant	No. of seeds/pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
5	TJM 136 X PDM 139	35.67	62.33	37.21	2.03	34.70	3.71	9.47	10.33	5.58	25.85	29.85	7.73
6	TJM 136 X Shikha	39.33	64.67	39.20	2.50	39.70	3.83	10.37	10.17	5.38	26.90	38.47	10.35
7	TJM 136 X Kanika	40.00	65.33	50.67	2.80	45.50	4.07	11.20	11.95	4.21	13.42	31.72	4.32
8	TJM 136 X Virat	31.67	56.67	44.59	3.97	41.37	3.77	11.15	11.08	4.18	23.00	23.34	5.42
9	TJM 3 X PDM 139	40.00	65.33	43.00	1.90	34.53	3.80	9.23	9.43	5.23	18.38	41.36	7.60
10	TJM 3 X Shikha	42.00	66.33	46.97	2.43	57.97	3.98	14.83	10.07	4.49	26.20	46.07	12.07
11	TJM 3 X Kanika	39.33	64.67	39.50	2.17	55.97	3.48	16.13	10.30	4.07	25.44	35.38	9.01
12	TJM 3 X Virat	39.33	65.00	42.13	1.80	60.80	4.20	14.57	9.97	3.26	26.71	29.75	7.94
13	TMB 37 X PDM 139	38.33	62.67	38.53	2.77	32.30	2.74	11.97	9.80	3.96	22.52	38.30	8.63
14	TMB 37 X Shikha	35.33	65.67	40.86	4.03	42.80	2.89	15.00	11.93	3.78	29.94	33.85	10.10
15	TMB 37 X Kanika	35.00	65.67	48.80	3.63	50.23	4.36	11.60	10.33	4.08	26.46	36.61	9.61
16	TMB 37 X Virat	35.00	65.33	40.57	4.17	52.43	4.66	11.27	9.70	4.51	29.70	35.81	10.55
17	Ganga 8 X PDM 139	39.67	68.33	45.57	4.20	59.80	4.05	14.97	9.31	4.05	18.25	37.69	6.86
18	Ganga 8 x Shikha	39.67	64.33	46.27	2.80	44.03	3.18	13.90	10.83	4.37	33.18	43.39	14.38
19	Ganga 8 X Kanika	41.00	67.00	48.77	3.30	54.87	3.94	14.03	9.30	4.11	31.93	31.83	10.12
20	Ganga 8 X Virat	39.67	67.33	40.17	2.33	38.70	1.85	21.00	9.87	3.72	20.66	37.64	7.81
21	LGG 460 X PDM 139	41.00	67.67	56.10	1.80	24.97	2.25	11.27	10.03	3.35	19.62	21.23	4.20
22	LGG 460 X Shikha	41.33	69.33	45.87	2.07	27.63	2.60	10.63	9.80	4.13	16.59	25.58	4.20
23	LGG 460 X Kanika	38.67	65.67	40.10	3.33	69.53	3.89	17.97	9.50	4.63	35.08	35.29	12.38
24	LGG 460 X Virat	39.33	67.67	45.03	2.73	52.57	3.65	14.43	9.43	4.07	33.68	42.03	14.11
25	HUM 1 X PDM 139	38.00	68.33	43.00	1.93	38.67	3.80	10.20	10.07	4.01	21.50	28.44	5.99

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S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of pods/plant	No. of pod/cluster	No. of clusters/plant	No. of seeds/pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
26	HUM 1 X Shikha	40.33	66.67	39.70	4.77	54.63	4.32	12.70	10.83	6.59	29.43	49.13	14.48
27	HUM 1 X Kanika	36.00	66.00	50.37	1.97	42.20	3.44	12.43	9.17	3.66	25.37	38.73	9.82
28	HUM 1 X Virat	40.67	66.00	42.20	2.33	54.07	3.72	15.13	10.07	4.33	33.83	43.35	14.64
29	SL 668 X PDM 139	39.67	65.33	42.97	2.27	41.76	3.95	10.91	10.47	4.58	29.31	33.77	9.90
30	SL 668 X Shikha	38.67	65.00	44.53	2.40	37.50	3.21	11.77	10.30	4.39	24.33	40.72	9.83
31	SL 668 X Kanika	41.67	67.33	44.17	2.33	37.73	3.95	9.73	9.93	4.54	31.84	37.52	11.97
32	SL 668 X Virat	39.33	66.67	52.17	2.13	54.47	4.81	11.33	10.77	4.84	20.58	27.31	5.60
33	Pusa Vishal X PDM 139	41.33	66.33	61.33	2.03	32.33	3.28	9.87	10.00	3.27	17.94	23.78	4.21
34	Pusa Vishal X Shikha	39.00	65.00	48.03	1.77	50.17	3.84	13.07	10.30	4.16	24.33	48.06	11.69
35	Pusa Vishal x Kanika	42.00	68.33	51.40	1.63	44.53	3.27	13.93	9.57	4.03	25.71	46.69	12.01
36	Pusa Vishal X Virat	40.33	67.33	59.84	2.23	32.43	2.75	11.97	13.17	4.08	16.27	26.31	4.29
37	PDM 11 X PDM 139	42.67	68.33	45.80	3.33	40.69	3.13	13.13	9.04	3.53	20.55	38.33	8.38
38	PDM 11 X Shikha	34.33	64.67	41.23	1.50	54.96	4.28	12.97	9.33	3.96	24.14	42.63	10.28
39	PDM 11 X Kanika	36.67	65.67	55.10	2.53	39.47	3.74	10.57	9.08	4.69	22.13	34.01	7.60
40	PDM 11 X Virat	37.00	64.33	46.93	1.93	33.30	3.03	11.17	9.80	4.04	24.86	37.26	9.24
	Mean of crosses	38.98	65.72	45.60	2.67	44.75	3.61	12.62	10.12	4.30	25.05	36.55	9.32
	General mean	39.64	65.93	46.43	2.56	40.34	3.53	11.52	10.12	4.35	24.18	33.64	8.28
	CV (%)	1.66	1.45	3.67	21.42	4.31	12.17	12.43	9.67	11.24	6.07	16.35	12.23
	Standard error	0.38	0.55	0.98	0.32	1.00	0.25	0.83	0.57	0.28	0.85	3.18	0.58
	CD (5%)	1.06	1.55	2.76	0.89	2.81	0.70	2.32	1.59	0.79	2.38	8.90	1.64

Plant height in crosses ranged from 37.21 cm (TJM 136 X PDM 139) to 61.33 cm (Pusa Vishal X PDM 139). Seventeen crosses were found to exceed general mean height of crosses (45.60 cm).

4. Number of branches per plant

Among lines, number of branches per plant varied from 1.20 (HUM 1) to 3.70 (TMB 37) with an overall mean of 2.16. Three lines viz; TJM 196, TMB 37 and Ganga 8 recorded more number of branches per plant than the general mean. In testers, it ranged from 2.10 (Shikha) to 3.07 (Kanika). Two testers, Kanika and Virat recorded more number of branches than the total mean of testers (2.55) (Table 4.6 and 4.7).

Number of branches per plant in crosses ranged from 1.50 (PDM 11 X Shikha) to 4.77 (HUM 1X Shikha) with a general mean of 2.67. Branches per plant of 17 crosses exceeded the general mean. Among crosses, HUM 1 X Shikha (4.77) recorded more number of branches per plant followed by Ganga 8 X PDM 139 (4.20), TMB 37 X Virat (4.17), TMB 37 X Shikha (4.03), TJM 137 X Virat (3.97) and TJM 196 X PDM 139 (3.77) (Table 4.6 and 4.7)..

5. Number of pods per plant

Number of pods per plant varied from 21.13 (TJM 136) to 42.50 (TJM 196) among the lines. Three lines viz; TJM 196, LGG 460 and PDM 11 recorded more number of pods per plant as compared to general mean of lines (27.41). Among testers, number of pods per plant ranged from 22.93 (Virat) to 40.17 (Shikha). Only one tester i.e. Shikha, exceeded the general mean of the testers (28.67).

Among the crosses, number of pods per plant varied from 24.97 (LGG 460 X PDM 139) to 69.53 (LGG 460 X Kanika) with a general mean of 44.75 which was exceeded by seventeen crosses (Table 4.6 and 4.7). Highest number of pods were recorded by LGG 460 X Kanika (69.53) followed by TJM 3 X Virat (60.80), Gang 8 X PDM 139 (59.80), TJM 3 X Shikha (57.97) and TJM 3 X Shikha (55.97).

6. Number of pods per cluster

Mean of number of pods per cluster ranged from 2.68 (TMB 37) to 4.01 (PDM 11) with a general mean of 3.29. Four lines viz; TJM 196, TJM 3,

Ganga 8 and PDM 11 recorded more number of pods per cluster than the general mean of lines. The mean performance of testers for this trait ranged from 2.99 (PDM 139) to 4.01 (Kanika) with the overall general mean of 3.47. Two testers viz; Shikha and Kanika exhibited higher values than the general mean of testers.

In crosses, the trait ranged from 1.85 (Ganga 8 X Virat) to 4.81 (SL 668 X Virat). Twenty five crosses exhibited more number of pods per cluster than the mean of the crosses (3.61). Among crosses, SL 668 X Virat (4.81) recorded more number of pods per cluster followed by TMB 37 X Virat (4.66), TMB 37 X Kanika (4.36), HUM 1 X Shikha (4.32) and PDM 11 X Shikha (4.28) (Table 4.6 and 4.7).

7. Number of clusters per plant

Among the lines, number of clusters per plant ranged from 6.67 (TJM 3) to 11.13 (TJM 196). Four lines viz; TJM 196, TMB 37, LGG 460 and SL 668 recorded more number of clusters per plant than general mean of lines (8.39). Among the testers, this trait ranged from 6.63 (Kanika) to 10.63 (Shikha). Two testers (PDM 139 and Shikha) recorded more number of clusters per plant than general mean of clusters (8.32).

Mean performance of crosses ranged from 9.23 (TJM 3 X PDM 139) to 21.00 (Ganga 8 x Virat) with overall mean of crosses 12.62, which was surpassed by 18 crosses out of forty (Table 4.6 and 4.7). Among the crosses, Ganga 8 x Virat (21.00) recorded more number of clusters per plant followed by LGG 460 X Kanika (17.97), TJM 3 X Kanika (16.13), HUM 1 X Virat (15.13) and TMB 37 X Shikha (15.00).

8. Number of seeds per pod

The mean performance of lines for this trait ranged from 9.10 (LGG 460) to 11.87 (TMB 37). Three lines viz; TJM 136, TMB 37 and Pusa Vishal recorded more number of seeds per pod than the general mean of lines (10.20). In testers, number of seeds per pod ranged from 9.83 (PDM 139 and Kanika) to 10.33 (Virat) with overall mean performance of 9.98. Two testers viz; Shikha and Virat recorded higher values than the general mean of testers (Table 4.6 and 4.7).

In crosses, more number of seeds per pod was recorded by Pusa Vishal X Virat (13.17) whereas lowest number was registered by PDM 11 X PDM 139 (9.04). Sixteen crosses recorded more number of seeds per pod when compared to the general mean of crosses (10.12). Among crosses, highest number of seeds per pod was recorded by Pusa Vishal X Virat (13.17) followed by TJM 136 X Kanika (11.95), TMB 37 X Kanika (11.93), TJM 136 X Virat (11.08) and HUM 1 X Shikha (10.83).

9. Hundred seed weight (g)

Hundred (100) seed weight ranged from 3.38 g (Ganga 8) to 6.22 g (SL 668) among the lines included in this study and from 3.81g (PDM 139) to 4.53g (Kanika and Virat) among the testers. Among the lines, general mean (4.60 g) was exceeded by five lines viz; TJM 136, LGG 460, HUM 1 and SL 668. Testers represented an overall mean of 4.28 g and two testers viz; Kanika and Virat recorded higher values than the mean.

Mean performance of crosses ranged from 3.26 g (TJM 3 X Virat) to 6.59 g (HUM 1 X Shikha). Seventeen cross combinations registered higher test weight as compared to the overall mean performance of crosses (4.30 g). Highest value for 100 seed weight was recorded by HUM 1 X Shikha (6.95 g) followed by TJM 136 X PDM 139 (5.58 g), TJM 136 X Shikha (5.38 g), TJM 3 X Shikha (5.23 g) and TJM 196 X Virat (4.85) (Table 4.6 and 4.7).

10. Biological yield per plant (g)

Performance of lines for biological yield per plant ranged from 13.96 g (HUM 1) to 33.41 g (TJM 196) with the general mean of 22.05 g. Four lines viz; TJM 196, Ganga 8, SL 668 and PDM 11 recorded higher biological yield per plant than the general mean of lines. Mean performance of testers for this trait ranged from 14.61 g (PDM 139) to 28.83 g (Kanika) with the overall general mean of 20.81 g. Two testers Shikha and Kanika exhibited higher mean values than the general mean of testers (Table 4.6 and 4.7).

Among crosses, the trait ranged between 13.42 g (TJM 136 X Kanika) to 35.08 g (LGG 460 X Kanika). Twenty one crosses exhibited higher biological yield per plant than the mean of the crosses (25.05 g). The cross LGG 460 X Kanika (35.08 g) recorded maximum biological yield per plant

followed by TJM 196 X Virat (34.30 g), HUM 1 X VIRAT (33.83 g), LGG 460 X Virat (33.68 g) and Ganga 8 X Shikha (33.18 g) (Table 4.6 and 4.7)

11. Harvest index (%)

Highest harvest index was recorded in HUM 1 (34.76%) while PDM 11 (19.13%) had the lowest harvest index among the lines. Four lines viz; Ganga 8, LGG 460, HUM 1 and Pusa Vishal surpassed the mean value 24.19%. Among testers, Virat recorded the higher harvest index (37.19%) while; Kanika (18.76%) had the lowest harvest index. Two testers PDM 139 and Virat exceeded the mean value for harvest index (28.19%).

Among the crosses, HUM 1 X Shikha recorded the highest harvest index of 48.06% whereas lowest value of harvest index was observed in LGG 460 X PDM 139 (21.23%). Out of forty, 23 crosses exceeded the mean value for harvest index among crosses (36.55%). Highest value for harvest index was recorded in HUM 1 X Shikha (49.13%) followed by Pusa Vishal X Shikha (48.06%), Pusa Vishal X Kanika (46.69%), TJM 3 X Shikha (46.07%) and TJM 196 X Virat (44.37%) (Table 4.6 and 4.7).

12. Seed yield per plant (g)

The range of this trait varied from 3.41 g (TJM 3) to 7.61 g (TJM 196) among the lines. Five lines viz; TJM 196, Ganga 8, LGG 460, Pusa Vishal and PDM 11 recorded higher seed yield per plant than the general mean of the lines (5.22 g). Among testers, it ranged from 4.85 g (PDM 139) to 6.17 g (Virat). Virat registered higher seed yield per plant as compared to the general mean of the testers (5.42 g)

Among cross combinations, seed yield per plant ranged from 4.20 g (LGG 460 X PDM 139 and LGG 460 X Shikha) to 15.16 g (TJM 196 X Virat) and twenty one crosses were found to exceed the general mean value (9.32 g). The cross combinations viz; TJM 196 X Virat (15.16 g), HUM 1 X Virat (14.64 g), HUM 1 X Shikha (14.48 g), Ganga 8 X Shikha (14.38 g) and LGG 460 X Virat (14.11 g) showed superior mean seed yield per plant when compared to the respective parents involved in crosses (Table 4.6 and 4.7).

4.3.2 PCV, GCV, heritability and genetic advance

Phenotypic and genotypic coefficient of variation for yield and yield attributing traits are summarized in (Table 4.7). In general the phenotypic variance must be higher in magnitude than that of genotypic variance. The same trend was observed in the present investigation for all the traits.

1. Days to 50% flowering

Days to 50% flowering in parents registered relatively lower values of PCV (8.22%) and GCV (8.08%) however, the broad sense heritability estimate was high (96.4%) coupled with moderate genetic advance as percent of mean (16.33%).

In crosses, the PCV (6.34%) and GCV (6.14%) values were low for days to 50% flowering while, heritability and genetic advance as percent of mean were high (93.7%) and moderate (12.25%) respectively (Table 4.7).

2. Days to maturity

In parents, the PCV (5.68%) and GCV (5.43%) values were low for days to maturity while, heritability and genetic advance as percent of mean were high (91.2%) and moderate (10.67%) respectively.

In crosses, the PCV (3.41%) and GCV (3.13%) estimate were low for this character. High heritability (84.7%) estimates were recorded for this character with a low genetic advance as percent of mean (5.90%) (Table 4.7).

3. Plant height (cm)

In parents, the moderate values of PCV (13.66%) and GCV (13.05%) coupled with high broad sense heritability (91.3%) and high genetic advance expressed as percent of mean (25.69%) was observed for this trait.

In crosses, moderate values of PCV (12.89%) and GCV (12.40%) were observed while, broad sense heritability estimates were high (92.5%) with high genetic advance expressed as percent of mean (24.57%) (Table 4.7).

4. Number of branches per plant

In parents, high variation was observed in terms of PCV (37.97%) and GCV (32.04%) coupled with high broad sense heritability (71.2%) and genetic advance as percent of mean (55.69%) for this trait (Table 4.7).

Table 4.7: Range, mean, coefficient of variation, heritability (bs) and genetic advance (% of mean) for yield and yield attributing traits in parents and crosses

S. No.	Characters	Range		Mean		PCV (%)		GCV (%)		Heritability [h ² (b)] (%)		Genetic advance as % of mean	
		Parents	Crosses	Parents	Crosses	Parents	Crosses	Parents	Crosses	Parents	Crosses	Parents	Crosses
1	Days to 50% flowering	32.33-45.66	31.67-42.67	41.5	38.98	8.22	6.34	8.08	6.14	96.4	93.7	16.33	12.25
2	Days to maturity	55.33-70.33	56.67-69.33	66.6	65.72	5.68	3.41	5.43	3.13	91.2	84.7	10.67	5.90
3	Plant height (cm)	37.73-60.47	37.21-61.33	48.8	45.60	13.66	12.89	13.05	12.40	91.3	92.5	25.69	24.57
4	No. of branches/plant	1.20-3.70	1.50-4.77	2.27	2.67	37.97	35.92	32.04	28.19	71.2	63.5	55.69	46.27
5	No. of pods/plant	21.13-42.50	24.97-69.53	27.8	44.75	24.52	22.54	23.21	22.34	89.6	98.2	45.27	45.60
6	No. of pod/cluster	2.98-4.01	1.85-4.81	3.34	3.61	15.70	20.11	12.44	15.45	62.8	59.0	20.30	24.45
7	No. of clusters/plant	6.63-11.13	9.23-21.00	8.37	12.62	21.74	21.46	17.29	17.82	63.3	68.9	28.33	30.47
8	No. of seeds/pod	9.10-11.87	9.04-13.17	10.1	10.12	7.03	12.02	5.71	5.18	65.8	18.5	9.53	4.60
9	100 seed weight (g)	3.38-6.22	3.26-6.59	4.51	4.30	20.87	17.10	15.79	13.70	57.3	64.0	24.62	22.57
10	Biological yield/plant (g)	13.96-33.41	13.42-35.08	21.7	25.05	27.23	22.32	26.27	21.56	93.0	93.3	52.19	42.91
11	Harvest index (%)	18.76-37.19	21.23-49.13	25.3	36.55	32.17	22.36	17.81	17.91	30.6	64.1	20.31	29.54
12	Seed yield/plant (g)	3.41-7.61	4.20-15.16	5.28	9.32	25.02	34.64	17.69	32.79	50.0	89.6	25.77	63.94

In crosses, number of branches per plant registered higher values of PCV (35.92%) and GCV (28.19%). Estimates of broad sense heritability (63.5%) and genetic advance as percent of mean (46.27%) were high.

5. Number of pods per plant

High variation was recorded in parents for PCV (24.52%) and GCV (23.21%). Estimates of broad sense heritability (89.6%) and genetic advance expressed as percent of mean (45.27%) were relatively high for number of pods per plant.

Higher variation was observed in terms of PCV (22.54%) and GCV (22.34%) coupled with high heritability (98.2%) and genetic advance as percent of mean (45.60%) in crosses (Table 4.7).

6. Number of pods per cluster

PCV (15.70%) and GCV (12.44%) values were moderate in parents for number of pods per cluster while, heritability (62.8%) and genetic advance (20.30%) as percent of mean were high respectively.

The PCV (20.11%) and GCV (15.45%) estimate was moderate coupled with moderate broad sense heritability (59.00%) and high genetic advance as percent of mean (24.45%) in crosses (Table 4.7).

7. Number of clusters per plant

In parents, number of clusters per plant registered high values of PCV (21.74%) and low values of GCV (17.29%). However, broad sense heritability estimates was high (63.3%) coupled with high genetic advance as percent of mean (28.33%).

In crosses, estimates of PCV (21.46%) and GCV (17.82%) were found high and moderate. Heritability in broad sense was high (68.9%) with a high genetic advance as percent of mean (30.47%) (Table 4.7).

8. Number of seeds per pod

In parents, the PCV (7.03%) and GCV (5.71%) values were low coupled with high broad sense heritability (65.8%) and low genetic advance as percent of mean (9.53%) (Table 4.7).

Moderate PCV value (12.02%) and low GCV value (12.02%), low broad sense heritability (18.5%) coupled with low genetic advance expressed as percent of mean (4.60%) were observed in crosses.

9. 100 Seed weight (g)

High values of PCV (20.87%) and moderate values of GCV (15.79%) were registered in parents for 100 seed weight coupled with moderate broad sense heritability (57.3%) and high genetic advance as percent of mean (24.62%).

In crosses, moderate estimates of PCV (17.10%) and GCV (13.70%) coupled with high broad sense heritability (64.0%) and high genetic advance expressed as percent of mean (22.57%) were recorded (Table 4.7).

10. Biological yield per plant (g)

In parents, both PCV (27.23%) and GCV (26.27%) values were high coupled with high broad sense heritability (93.0%) and high genetic advance expressed as percent of mean (52.19%).

In case of crosses, higher variability (PCV 22.32% AND GCV 21.56%) was recorded. High heritability 93.3% coupled with high genetic advance as percent of mean (42.91%) was registered for this character (Table 4.7)

11. Harvest index (%)

High PCV (32.17%) and moderate GCV (17.81%) along with moderate broad sense heritability (30.6%) and high genetic advance as percent of mean (20.31%) were recorded in parents.

In crosses, high PCV (22.36%) and moderate GCV (17.91%) estimates were observed while high broad sense heritability (64.1%) coupled with high genetic advance as percent of mean (29.54%) were recorded for this character (Table 4.7).

12. Seed yield per plant (g)

Seed yield per plant registered high values of PCV (25.02%) and moderate values of GCV (17.69%) in parents. Moderate estimates of broad sense heritability (50.0%) and high value of genetic advance as percent of mean (25.77%) were observed for this trait (Table 4.7).

In case of crosses, high estimates of PCV (25.02%) and high GCV (32.79%) were observed. A high estimate of heritability (89.6%) was noticed along with high genetic advance as percent of mean (63.94%).

4.4 Correlation coefficient analysis

In the present investigation the phenotypic and genotypic correlation coefficients were worked out separately for parents and crosses to assess the direction and magnitude of association existing between seed yield and other component characters. This is presented in Table 4.8 to 4.11. The results revealed slightly higher estimates of genotypic correlation coefficients as compared to phenotypic correlation coefficients for almost all the traits studied. As significant phenotypic correlation will be useful criteria hence results of phenotypic correlation coefficients of parents and crosses are presented here under:

1. Days to 50% flowering

In the parental lines, days to 50% flowering had significant and positive correlation with days to maturity (0.834**) followed by plant height (0.347*), number of pods per plant (0.472**) and biological yield per plant (0.372*) whereas, significant and negative association of days to 50% flowering was observed with hundred seed weight (-0.318*) (Table 4.8). In the crosses, days to 50% flowering was associated positively and significantly with days to maturity (0.591**) and plant height (0.230*) (Table 4.10).

2. Days to maturity

Days to maturity showed significant and positive association with plant height (0.423**) and number of pods per pant (0.314*) in the parental lines (Table 4.8). There was no significant association of days to maturity with other traits except with days to flowering in the crosses (Table 4.10).

3. Plant height (cm)

In the parents, plant height showed significant and positive correlation with biological yield per plant (0.410**) and significant negative correlation of this trait was reported with harvest index (-0.379*) (Table 4.8). In crosses, significant and negative correlation of plant height was observed with number

of branches per plant (0.251**), number of pods per plant (-0.293**), number of clusters per plant (-0.251**), hundred seed weight (-0.301**), biological yield per plant (-0.429**), harvest index (-0.262**) and seed yield per plant (-0.395**) (Table 4.10).

4. Number of branches per plant

Among parents, number of branches per plant expressed significant and positive association with number of pods per plant (0.432**), number of clusters per plant (0.591**) and biological yield per plant (0.394**) (Table 4.8). In crosses, number of branches per plant registered significant and positive association with number of pods per plant (0.303**), number of pods per cluster (0.199*), hundred seed weight (0.217*), biological yield per plant (0.193*), harvest index (0.216*) and seed yield per plant (0.256**) (Table 4.10)

5. Number of pods per plants

Among parents, significant and positive association of this trait was expressed with number of clusters per plant (0.698**), biological yield per plant (0.550**) and seed yield per plant (0.407**) (Table 4.8). Among crosses the traits viz., number of pods per cluster (0.560**), number of clusters per plant (0.495**), biological yield per plant (0.436**), harvest index (0.309**) and seed yield per plant (0.435**) exhibited significant and positive association with number of pods per plant (Table 4.10).

6. Number of pods per cluster

In parents, number of pods per cluster displayed strong negative association with number of clusters per plant (-0.568**) (Table 4.8). In crosses, significant and positive associated of this trait was expressed with hundred seed weight (0.224*) followed by biological yield per plant (0.224*) and seed yield per plant (0.205*) respectively (Table 4.10). However, strong negative association of this trait was observed with number of clusters per plant (-0.407**).

Table 4.8: Phenotypic correlation coefficients for seed yield and its attributing characters in parents

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	1.000	0.834**	0.347*	0.190	0.472**	0.202	0.279	0.048	-0.318*	0.372*	-0.071	0.149
DM		1.000	0.423**	0.185	0.314*	0.208	0.162	0.030	-0.233	0.258	0.081	0.101
PH (cm)			1.000	-0.056	-0.113	0.253	-0.274	-0.160	-0.079	0.410**	-0.379*	-0.101
NBPP				1.000	0.432**	-0.281	0.591**	0.246	-0.291	0.394**	-0.162	0.239
NPPP					1.000	0.066	0.698**	0.137	-0.069	0.550**	-0.101	0.407**
NPPC						1.000	-0.568**	-0.298	-0.194	0.049	-0.221	-0.072
NCPP							1.000	0.284	-0.008	0.356*	0.049	0.255
NSPP								1.000	0.098	0.056	0.196	0.239
HSW (g)									1.000	-0.072	0.265	0.096
BYPP (g)										1.000	-0.482**	0.366*
HI (%)											1.000	0.337*

*, ** Significant at 5% & 1% level of significance respectively

DF: Days to 50% flowering, **DM:** Days to maturity, **PH:** Plant height (cm), **NBPP:** Number of branches per plant, **NPPP:** Number of pods per plant, **NPPC:** Number of pods per cluster, **NCPP:** Number of clusters per plant, **NSPP:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BYPP:** Biological yield (g), **HI:** Harvest index (%), **SYPP:** Seed yield per plant (g)

Table 4.9: Genotypic correlation coefficients for seed yield and its attributing characters in parents

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	1.000	0.927**	0.419**	0.224	0.538**	0.321*	0.357*	0.058	-0.455**	0.403**	-0.063	0.282
DM		1.000	0.462**	0.166	0.312*	0.386*	0.104	0.045	-0.524**	0.296	0.048	0.310*
PH (cm)			1.000	-0.144	-0.135	0.426**	-0.357*	-0.335*	-0.274	0.437**	-0.795**	-0.297
NBPP				1.000	0.448**	-0.042	0.588**	0.784**	-0.440**	0.553**	-0.286	0.583**
NPPP					1.000	0.149	0.810**	0.270	-0.092	0.621**	-0.268	0.733**
NPPC						1.000	-0.424**	-1.043**	-1.022**	0.100	-0.528**	-0.507**
NCPP							1.000	0.888**	0.346*	0.523**	-0.128	0.762**
NSPP								1.000	-0.442**	0.059	0.562**	0.755**
HSW (g)									1.000	-0.211	0.042	-0.093
BYPP (g)										1.000	-0.746**	0.754**
HI (%)											1.000	0.212

*, ** Significant at 5% & 1% level of significance respectively

DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NBPP:** Number of branches per plant, **NPPP:** Number of pods per plant, **NPPC:** Number of pods per cluster, **NCPP:** Number of clusters per plant, **NSPP:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BYPP:** Biological yield (g), **HI:** Harvest index (%), **SYPP:** Seed yield per plant (g)

Table 4.10: Phenotypic correlation coefficients for seed yield and its attributing characters in crosses

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	1.000	0.591**	0.230*	-0.170	-0.036	-0.064	0.000	-0.030	-0.098	0.051	0.062	0.088
DM		1.000	0.087	0.068	0.019	-0.056	0.046	0.017	-0.027	0.062	0.059	0.090
PH (cm)			1.000	-0.251**	-0.293**	-0.108	-0.251**	0.128	-0.301**	-0.429**	-0.262**	-0.395**
NBPP				1.000	0.303**	0.199*	0.125	0.006	0.217*	0.193*	0.216*	0.256**
NPPP					1.000	0.560**	0.495**	-0.081	0.117	0.436**	0.309**	0.435**
NPPC						1.000	-0.407**	-0.056	0.342**	0.224*	0.133	0.205*
NCPP							1.000	-0.032	-0.204*	0.236**	0.211*	0.262**
NSPP								1.000	0.029	-0.095	-0.228*	-0.189*
HSW (g)									1.000	0.178	0.247**	0.283**
BYPP (g)										1.000	0.269**	0.779**
HI (%)											1.000	0.799**

*, ** Significant at 5% & 1% level of significance respectively

DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NBPP:** Number of branches per plant, **NPPP:** Number of pods per plant, **NPPC:** Number of pods per cluster, **NCPP:** Number of clusters per plant, **NSPP:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BYPP:** Biological yield (g), **HI:** Harvest index (%), **SYPP:** Seed yield per plant (g)

Table 4.11: Genotypic correlation coefficients for seed yield and its attributing characters in crosses

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	1.000	0.716**	0.240**	-0.221*	-0.048	-0.159	0.050	-0.203*	-0.117	0.049	0.091	0.111
DM		1.000	0.083	0.086	0.018	-0.042	0.040	0.012	0.022	0.049	0.062	0.094
PH (cm)			1.000	-0.304**	-0.303**	-0.179	-0.288**	0.306**	-0.402**	-0.463**	-0.425**	-0.484**
NBPP				1.000	0.383**	0.293**	0.218*	0.287**	0.341**	0.252**	0.183*	0.238**
NPPP					1.000	0.707**	0.605**	-0.257**	0.152	0.459**	0.458**	0.505**
NPPC						1.000	-0.107	-0.130	0.514**	0.300**	0.262**	0.302**
NCPP							1.000	-0.185*	-0.274**	0.301**	0.378**	0.373**
NSPP								1.000	0.268**	-0.289**	-0.493**	-0.349**
HSW (g)									1.000	0.278**	0.361**	0.375**
BYPP (g)										1.000	0.462**	0.902**
HI (%)											1.000	0.790**

*, ** Significant at 5% & 1% level of significance respectively **DF**: Days to 50% flowering, **DM**: Days to maturity, **PH**: Plant height (cm), **NBPP**: Number of branches per plant, **NPPP**: Number of pods per plant, **NPPC**: Number of pods per cluster, **NCPP**: Number of clusters per plant, **NSPP**: Number of seeds per pod, **HSW**: Hundred seed weight (g), **BYPP**: Biological yield (g), **HI**: Harvest index (%), **SYPP**: Seed yield per plant (g)

7. Number of clusters per plant

Number of clusters per plant expressed significant and positive correlation with biological yield per plant in parents (Table 4.8). While in crosses significant and positive association of this trait was observed with biological yield per plant (0.236**), harvest index (0.211*) and seed yield per plant (0.205*) (Table 4.10). On the contrary, it had significant and negative association with hundred seed weight (-0.204*).

8. Number of seeds per pod

Number of seeds per pod does not revealed significant correlation with any of the traits in parents (Table 4.8). In crosses, this trait revealed significant and positive association with hundred seed weight (0.268**). Strong significant and negative association of number of seeds per pod was expressed with biological yield per plant (-0.289**), harvest index (-0.493**) and seed yield per plant (-0.349**) (Table 4.10).

9. Hundred seed weight (g)

This trait does not expressed any significant association with any of the traits in the parents (Table 4.8). Positive and significant association of hundred seed weight was observed with biological yield per plant (0.278**), harvest index (0.361**) and seed yield per plant (0.375*) in crosses (Table 4.10).

10. Biological yield per Plant (g)

In the parents, biological yield per plant showed significant and positive association with seed yield per plant (0.366*). However, strong negative and significant association of this trait was noted with harvest index (-0.482**) (Table 4.8). In crosses, this trait revealed highly significant and positive association with harvest index (0.462**) and seed yield per plant (0.902**) (Table 4.10).

11. Harvest index (%)

In parents as well as in crosses positive and significant association of harvest index was observed with seed yield per plant (0.337* and 0.798**) (Table 4.8 and 4.10).

4.5 Path coefficient analysis

In the present study, path coefficient analysis was carried out based on fourteen parents and 40 crosses for seed yield and its attributing characters and furnished in table 4.12 to 4.15. Phenotypic and genotypic path diagrams for parents are presented in fig. 4.1 and 4.2. While phenotypic and genotypic path diagrams for crosses are presented in fig. 4.3 and 4.4 respectively. The results are presented here under.

4.5.1 Direct effects of yield components on seed yield

In parents, number of pods per plant (3.857) exhibited higher positive direct effects on seed yield followed by number of branches per plant (1.618), harvest index (1.032), plant height (0.636), hundred seed weight (0.578), biological yield per plant (0.510) and days to maturity (0.113). Number of clusters per plant (-1.095), number of pods per cluster (-1.906) and days to 50% flowering (-0.328) exerted negative direct effects for this trait. Whereas the direct effect of number of seeds per pod (-0.031) was negative and negligible (Table 4.13).

In crosses, harvest index (0.733) had highest positive direct effect followed by biological yield per plant (0.725) and number of seeds per pod (0.396). The direct effect of number of pods per cluster (0.131) was low (Table 4.15). Conversely, hundred seed weight (-0.311), plant height (-0.165), displayed negative direct effects.

4.5.2 Indirect effects of yield components on seed yield

1. Days to 50% flowering

In parents, the direct effect of days to 50% flowering on seed yield was negative and high (-0.328) (Table 4.13). However, the positive association of days to 50% flowering with seed yield (0.282) was mainly attributed to its high indirect effects through number of pods per plant (2.073) followed by number of branches per plant (0.363), plant height (0.267), biological yield per plant (0.206) and days to maturity (0.105) (Table 4.13).

In crosses, this trait exhibited low negative direct effect on seed yield (0.123). All the indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in the crosses (Table 4.15).

Table 4.12: Phenotypic path matrix for seed yield and its attributing characters in parents

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	0.141	-0.212	-0.026	0.036	0.236	-0.047	-0.175	0.003	0.010	0.234	-0.050	0.149
DM	0.118	-0.254	-0.032	0.035	0.157	-0.048	-0.102	0.002	0.007	0.162	0.057	0.101
PH (cm)	0.049	-0.107	-0.076	-0.011	-0.056	-0.059	0.172	-0.009	0.002	0.258	-0.265	-0.101
NBPP	0.027	-0.047	0.004	0.188	0.216	0.065	-0.371	0.013	0.009	0.248	-0.113	0.239
NPPP	0.066	-0.080	0.009	0.081	0.499	-0.015	-0.438	0.007	0.002	0.346	-0.071	0.407**
NPPC	0.028	-0.053	-0.019	-0.053	0.033	-0.231	0.357	-0.016	0.006	0.031	-0.155	-0.072
NCPP	0.039	-0.041	0.021	0.111	0.349	0.131	-0.628	0.015	0.000	0.224	0.034	0.255
NSPP	0.007	-0.008	0.012	0.046	0.068	0.069	-0.179	0.054	-0.003	0.035	0.137	0.239
HSW (g)	-0.045	0.059	0.006	-0.055	-0.035	0.045	0.005	0.005	-0.031	-0.045	0.186	0.096
BYPP (g)	0.052	-0.066	-0.031	0.074	0.275	-0.011	-0.224	0.003	0.002	0.629	-0.338	0.366*
HI (%)	-0.010	-0.021	0.029	-0.030	-0.051	0.051	-0.031	0.011	-0.008	-0.303	0.700	0.337*

*, ** Significant at 5% & 1% level of significance respectively

Residual effect= (0.645), Diagonals: Direct effect, Off diagonals: Indirect effects; **DF**:Days to 50% flowering, **DM**:Days to maturity, **PH**: Plant height (cm), **NBPP**: Number of branches per plant, **NPPP**: Number of pods per plant, **NPPC**: Number of pods per cluster, **NCPP**: Number of clusters per plant, **NSPP**: Number of seeds per pod, **HSW**: Hundred seed weight (g), **BYPP**: Biological yield (g), **HI**: Harvest index (%), **SYPP**: Seed yield per plant (g)

Table 4.13: Genotypic path matrix for seed yield and its attributing characters in parents

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	-0.328	0.105	0.267	0.363	2.073	-0.612	-1.462	-0.002	-0.263	0.206	-0.065	0.282
DM	-0.304	0.113	0.294	0.269	1.203	-0.737	-0.425	-0.001	-0.303	0.151	0.050	0.310*
PH (cm)	-0.137	0.052	0.636	-0.233	-0.521	-0.813	1.463	0.010	-0.158	0.223	-0.820	-0.297
NBPP	-0.074	0.019	-0.092	1.618	1.729	0.081	-2.406	-0.024	-0.255	0.282	-0.296	0.583**
NPPP	-0.176	0.035	-0.086	0.725	3.857	-0.284	-3.317	-0.008	-0.053	0.317	-0.276	0.733**
NPPC	-0.105	0.044	0.271	-0.068	0.575	-1.906	1.735	0.032	-0.591	0.051	-0.545	-0.507**
NCPP	-0.117	0.012	-0.227	0.951	3.124	0.808	-4.095	-0.028	0.200	0.267	-0.132	0.762**
NSPP	-0.019	0.005	-0.213	1.269	1.040	1.988	-3.637	-0.031	-0.255	0.030	0.580	0.755**
HSW (g)	0.149	-0.059	-0.174	-0.712	-0.356	1.947	-1.415	0.014	0.578	-0.108	0.043	-0.093
BYPP (g)	-0.132	0.034	0.278	0.895	2.396	-0.191	-2.143	-0.002	-0.122	0.510	-0.769	0.754**
HI (%)	0.021	0.005	-0.506	-0.463	-1.032	1.006	0.523	-0.017	0.024	-0.380	1.032	0.212

*, ** Significant at 5% & 1% level of significance respectively

Residual effect=(0.893), Diagonals: Direct effect, Off diagonals: Indirect effects;**DF**:Days to 50% flowering, **DM**:Days to maturity, **PH**: Plant height (cm), **NBPP**: Number of branches per plant, **NPPP**: Number of pods per plant, **NPPC**: Number of pods per cluster, **NCPP**: Number of clusters per plant, **NSPP**: Number of seeds per pod, **HSW**: Hundred seed weight (g), **BYPP**: Biological yield (g), **HI**: Harvest index (%), **SYPP**: Seed yield per plant (g)

Table 4.14: Phenotypic path matrix for seed yield and its attributing characters in crosses

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	0.007	0.002	0.010	-0.002	0.000	0.003	0.000	0.000	-0.003	0.032	0.040	0.088
DM	0.004	0.004	0.004	0.001	0.000	0.002	-0.001	0.000	-0.001	0.039	0.038	0.090
PH (cm)	0.002	0.000	0.044	-0.003	-0.001	0.005	0.007	0.001	-0.010	-0.271	-0.168	-0.395**
NBPP	-0.001	0.000	-0.011	0.010	0.002	-0.008	-0.003	0.000	0.007	0.122	0.138	0.256**
NPPP	0.000	0.000	-0.013	0.003	0.005	-0.024	-0.013	-0.001	0.004	0.276	0.198	0.435**
NPPC	0.000	0.000	-0.005	0.002	0.003	-0.042	0.011	-0.001	0.011	0.141	0.085	0.205*
NCPP	0.000	0.000	-0.011	0.001	0.002	0.017	-0.026	0.000	-0.007	0.149	0.136	0.262**
NSPP	0.000	0.000	0.006	0.000	0.000	0.002	0.001	0.009	0.001	-0.060	-0.146	-0.189*
HSW (g)	-0.001	0.000	-0.013	0.002	0.001	-0.014	0.005	0.000	0.032	0.113	0.158	0.283**
BYPP (g)	0.000	0.000	-0.019	0.002	0.002	-0.009	-0.006	-0.001	0.006	0.632	0.172	0.779**
HI (%)	0.000	0.000	-0.012	0.002	0.002	-0.006	-0.006	-0.002	0.008	0.170	0.641	0.799**

*, ** Significant at 5% & 1% level of significance respectively

Residual effect= (0.121), Diagonals: Direct effect, Off diagonals: Indirect effects; **DF**: Days to 50% flowering, **DM**: Days to maturity, **PH**: Plant height (cm), **NBPP**: Number of branches per plant, **NPPP**: Number of pods per plant, **NPPC**: Number of pods per cluster, **NCPP**: Number of clusters per plant, **NSPP**: Number of seeds per pod, **HSW**: Hundred seed weight (g), **BYPP**: Biological yield (g), **HI**: Harvest index (%), **SYPP**: Seed yield per plant (g)

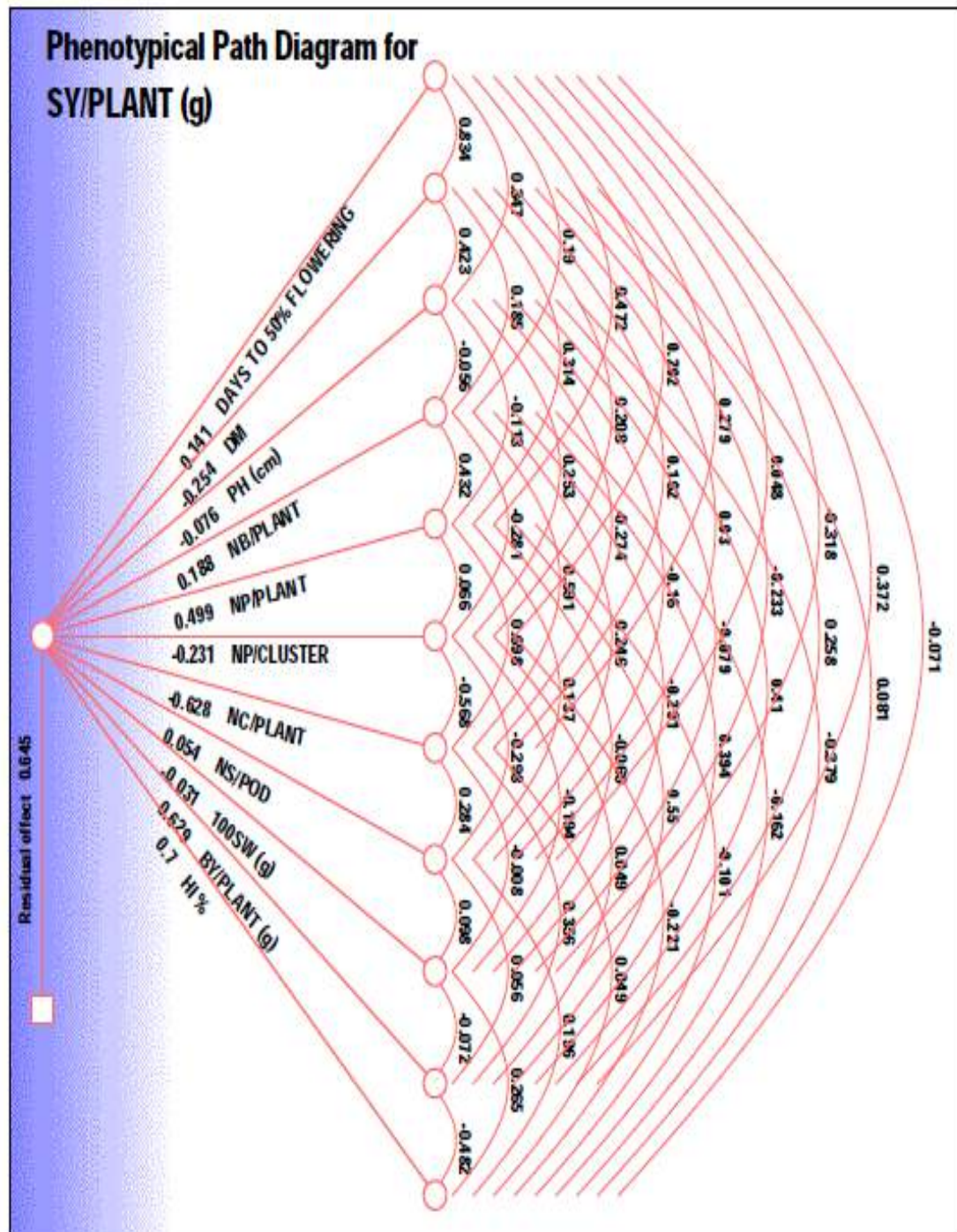
Table 4.15: Genotypic path matrix for seed yield and its attributing characters in crosses

Traits	DF	DM	PH (cm)	NBPP	NPPP	NPPC	NCPP	NSPP	HSW (g)	BYPP (g)	HI (%)	SYPP (g)
DF	0.123	-0.028	-0.040	0.023	0.002	-0.021	-0.007	-0.080	0.036	0.036	0.067	0.111
DM	0.088	-0.039	-0.014	-0.009	-0.001	-0.006	-0.005	0.005	-0.007	0.035	0.046	0.094
PH (cm)	0.030	-0.003	-0.165	0.031	0.010	-0.023	0.038	0.121	0.125	-0.336	-0.311	-0.484**
NBPP	-0.027	-0.003	0.050	-0.103	-0.012	0.038	-0.029	0.113	-0.106	0.182	0.134	0.238**
NPPP	-0.006	-0.001	0.050	-0.039	-0.032	0.093	-0.079	-0.102	-0.047	0.333	0.336	0.505**
NPPC	-0.020	0.002	0.029	-0.030	-0.022	0.131	0.014	-0.051	-0.160	0.217	0.192	0.302**
NCPP	0.006	-0.002	0.047	-0.022	-0.019	-0.014	-0.131	-0.073	0.085	0.218	0.277	0.373**
NSPP	-0.025	-0.001	-0.050	-0.029	0.008	-0.017	0.024	0.396	-0.083	-0.210	-0.361	-0.349**
HSW (g)	-0.014	-0.001	0.066	-0.035	-0.005	0.067	0.036	0.106	-0.311	0.202	0.264	0.375**
BYPP (g)	0.006	-0.002	0.076	-0.026	-0.015	0.039	-0.039	-0.115	-0.087	0.725	0.339	0.902**
HI (%)	0.011	-0.003	0.070	-0.019	-0.015	0.034	-0.049	-0.195	-0.112	0.335	0.733	0.790**

*, ** Significant at 5% & 1% level of significance respectively

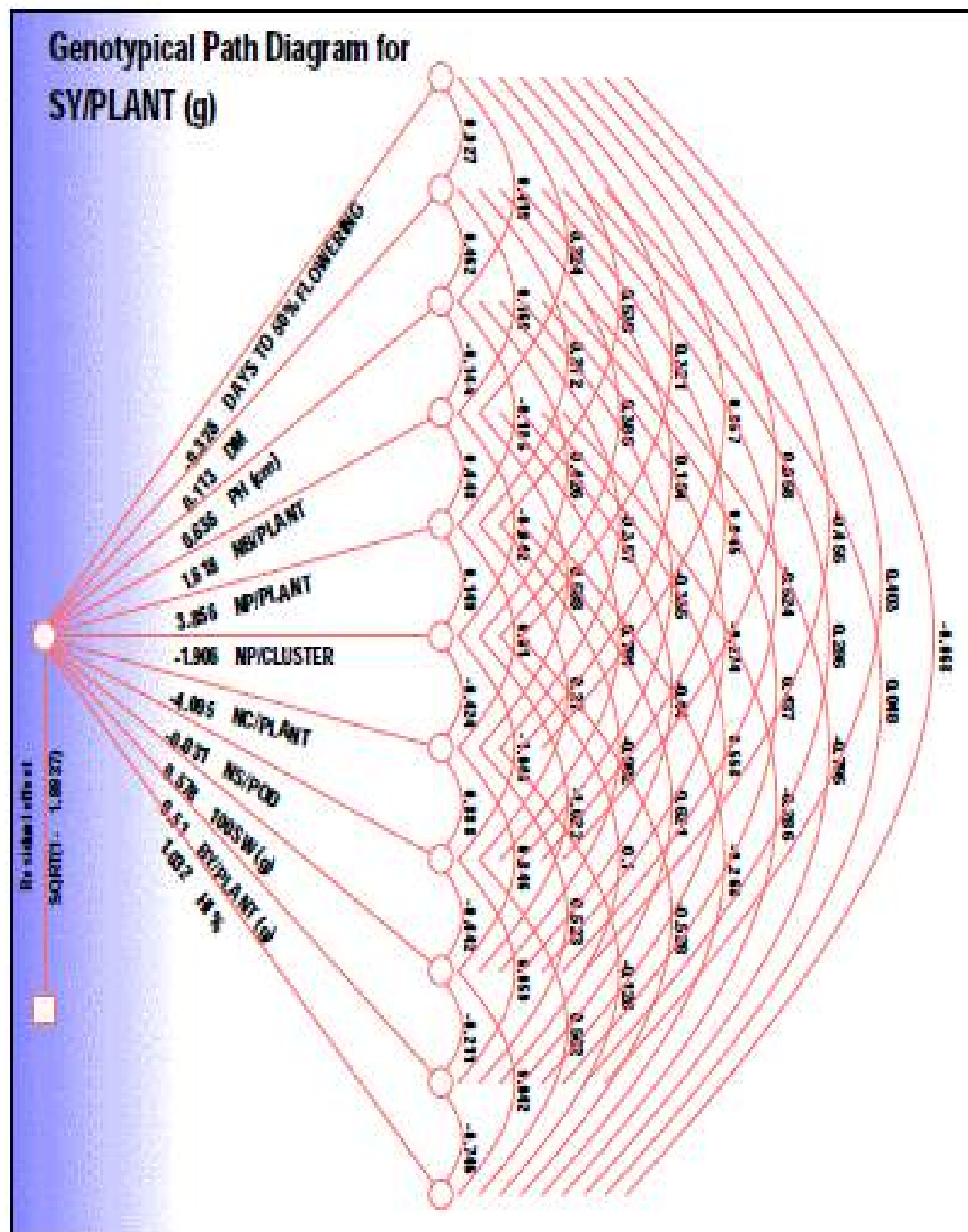
Residual effect= (0.018), Diagonals: Direct effect, Off diagonals: Indirect effects; **DF**:Days to 50% flowering, **DM**:Days to maturity, **PH**: Plant height (cm), **NBPP**: Number of branches per plant, **NPPP**: Number of pods per plant, **NPPC**: Number of pods per cluster, **NCPP**: Number of clusters per plant, **NSPP**: Number of seeds per pod, **HSW**: Hundred seed weight (g), **BYPP**: Biological yield (g), **HI**: Harvest index (%), **SYPP**:Seedyield per plant (g)

Fig 4.1: Phenotypic path diagram of seed yield and yield components in parents



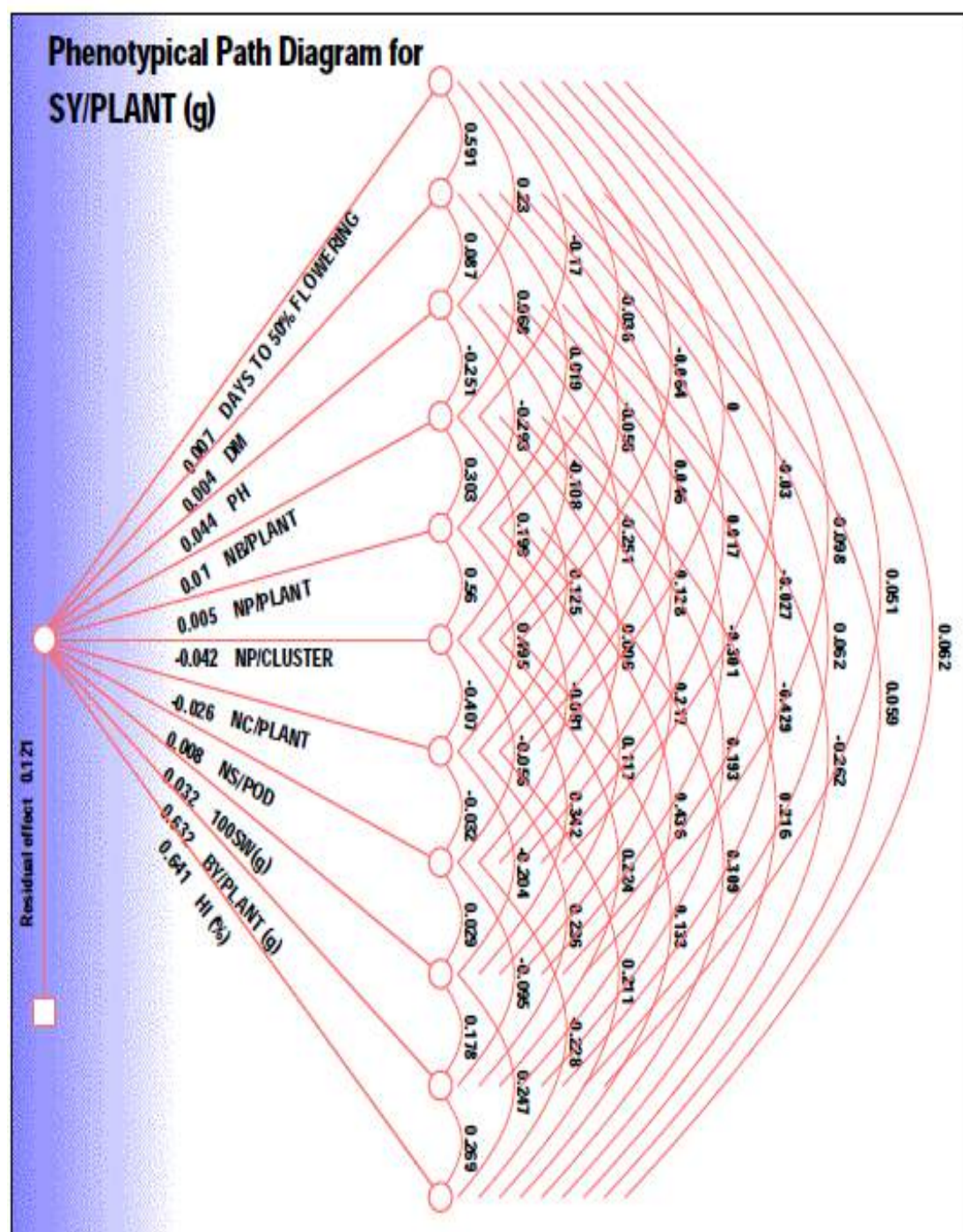
DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NB/P:** Number of branches per plant, **NP/P:** Number of pods per plant, **NP/C:** Number of pods per cluster, **NC/P:** Number of clusters per plant, **NS/P:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BY/P:** Biological yield (g), **HI:** Harvest index (%), **SY/P:** Seed yield per plant (g)

Fig 4.2: Genotypic path diagram of seed yield and yield components in parents



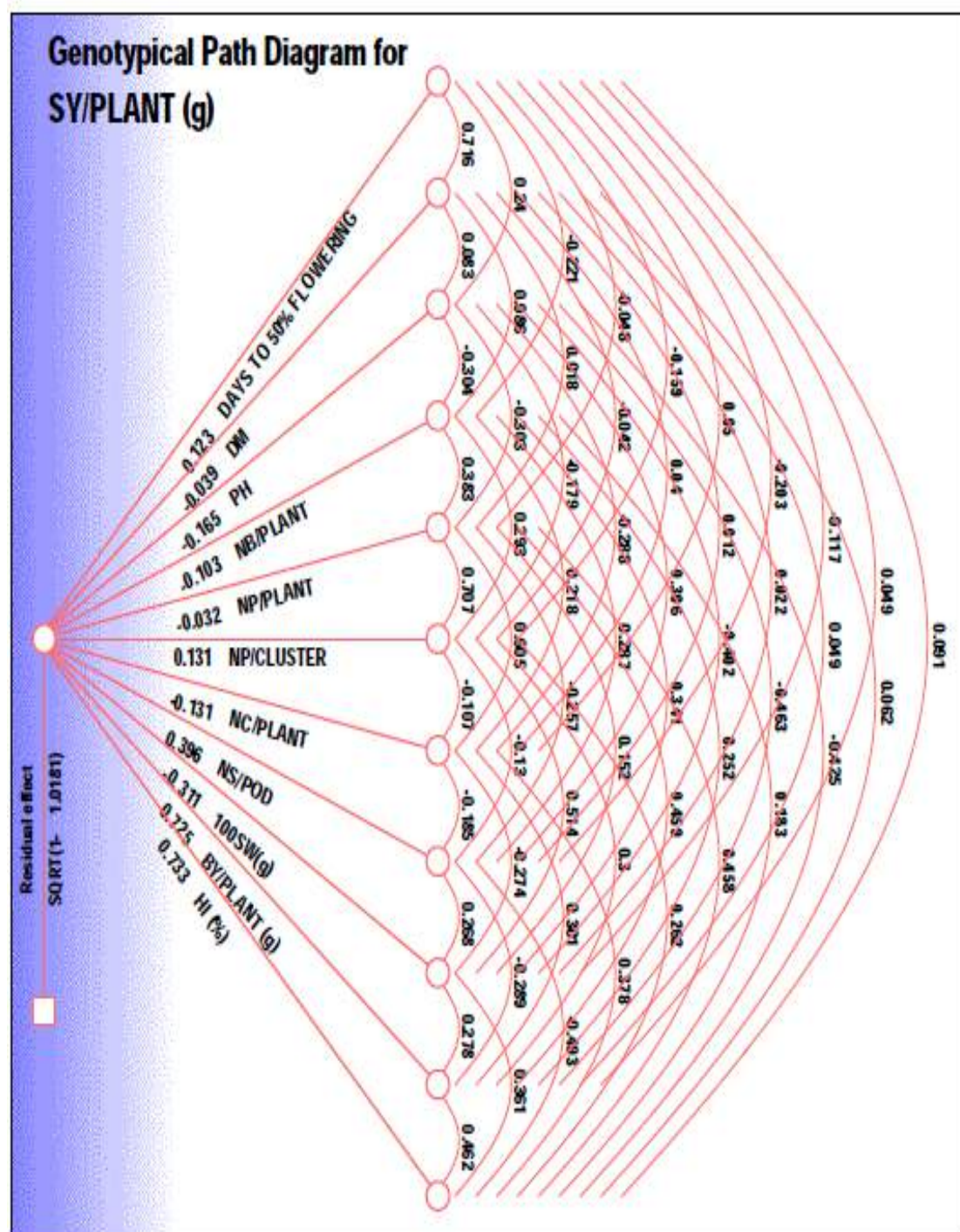
DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NB/P:** Number of branches per plant, **NP/P:** Number of pods per plant, **NP/C:** Number of pods per cluster, **NC/P:** Number of clusters per plant, **NS/P:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BY/P:** Biological yield (g), **HI:** Harvest index (%), **SY/P:** Seed yield per plant (g)

Fig 4.3: Phenotypic path diagram of seed yield and yield components in crosses



DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NB/P:** Number of branches per plant, **NP/P:** Number of pods per plant, **NP/C:** Number of pods per cluster, **NC/P:** Number of clusters per plant, **NS/P:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BY/P:** Biological yield (g), **HI:** Harvest index (%), **SY/P:** Seed yield per plant (g)

Fig 4.4: Genotypic path diagram of seed yield and yield components in crosses



DF:Days to 50% flowering, **DM:**Days to maturity, **PH:** Plant height (cm), **NB/P:** Number of branches per plant, **NP/P:** Number of pods per plant, **NP/C:** Number of pods per cluster, **NC/P:** Number of clusters per plant, **NS/P:** Number of seeds per pod, **HSW:** Hundred seed weight (g), **BY/P:** Biological yield (g), **HI:** Harvest index (%), **SY/P:** Seed yield per plant (g)

2. Days to maturity

Days to maturity exhibited relatively low and positive direct effect on seed yield (0.113). However, positive and high association of this trait with seed yield (0.310) was due to positive and indirect contribution *via* number of pods per plant (1.203), plant height (0.294), number of branches per plant (0.269) and biological yield per plant (0.151). However, this trait exhibited negative indirect effects through number of pods per cluster (-0.737), number of clusters per plant (-0.425) and hundred seed weight (-0.303) (Table 4.13). Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in the parents

In crosses, days to maturity exhibited negative and negligible direct effect on seed yield per plant (-0.0039). Indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in the crosses.

3. Plant Height (cm)

In parent's plant height registered high and positive direct effect (0.636) on seed yield (Table 4.13). However, it exhibited moderate and negative indirect effect on seed yield (-0.297) and positive indirect contribution *via* number of clusters per plant (1.463) and biological yield per plant (0.223). Whereas, negative indirect effects were exerted through harvest index (-0.820), number of pods per cluster (-0.813), number of pods per plant (-0.521), number of branches per plant (-0.233), hundred seed weight (-0.158) and days to 50% flowering (-0.137).

In crosses, plant height exhibited low and negative direct effect on seed yield (-0.165). While, it exhibited high and negative indirect effect on seed yield (-0.484) positive indirect effects of this trait were exhibited *via* hundred seed weight (0.125) and number of seeds per pod (0.121) (Table 4.15). Plant height exhibited negative indirect effect on seed yield through biological yield per plant (-0.336) and harvest index (-0.311) other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses

4. Number of branches per plant

In parents, number of branches per plant had very high and positive direct effect (1.618). The indirect positive effect of this trait on seed yield (0.583) was exhibited via positive effects of number of pods per plant (1.729) and biological yield per plant (0.282), (Table 4.13). Number of branches per plant exhibited negative effects on seed yield through number of clusters per plant (-2.406), harvest index (-0.296) and hundred seed weight (-0.255).

In crosses, number of branches per plant showed low negative direct effect on seed yield (-0.103). Its positive indirect effects via biological yield per plant (0.182), harvest index (0.134) and number of seeds per pod (0.113) resulted in positive correlation with seed yield (0.238). Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses (Table 4.15).

5. Number of pods per plant

In parents, number of pods per plant exerted very high positive direct effect on seed yield (3.857). It exhibited high and positive indirect effect on seed yield (0.733) through positive and indirect effects *via* number of branches per plant (0.725) and biological yield per plant (0.317) while, negative indirect effects of number of pods per plant on seed yield was showed by number of clusters per plant (-3.317), harvest index (-0.276), number of pods per cluster (-0.284) and days to 50% flowering (-0.176) (Table 4.13).

In crosses, direct effect of number pods per plant on seed yield was negative and negligible (-0.032). Its high and positive indirect effect on seed yield (0.505) was exerted via positive indirect effects of harvest index (0.336) and biological yield per plant (0.333) (Table 4.15). Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses

6. Number of pods per cluster

In parents, number of pods per cluster showed negative and very high and direct effect on seed yield (-1.906). Negative and indirect effect of this trait on seed yield (-0.507) was exhibited via positive and indirect effects of

number of clusters per plant (1.735), number of pods per plant (0.575) and plant height (0.271) (Table 4.13). However negative indirect effects of this trait on seed yield was contributed through hundred seed weight (-0.591), harvest index (-0.545) and days to 50% flowering (-0.105) Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses.

Number of pods per cluster had low positive direct effect on seed yield (0.131). Its high and positive indirect effect on seed yield (0.302) was exhibited through indirect and positive effects of biological yield per plant (0.217) and harvest index (0.192). Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses (Table 4.15).

7. Number of clusters per plant

In parents, number of clusters per plant exerted very high and negative direct effect on seed yield (-4.095) (Table 4.13). Positive and indirect effect of this trait on seed yield (0.762) was contributed through number of pods per plant (3.124), number of branches per plant (0.951), number of pods per plant (0.808) and biological yield per plant. Whereas, indirect and negative effects of this trait on seed yield was exerted via plant height (-0.227), harvest index (-0.132) and days to 50% flowering (-0.117).

In crosses, this trait exhibited low and negative direct effect on seed yield (-0.131). However, its indirect and positive effect on seed yield (0.373) was exhibited through positive and indirect effects through harvest index (0.277) and biological yield per plant (0.218) Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses (Table 4.15).

8. Number of Seeds per pod

Number of seeds per pod registered negative negligible direct effect on seed yield (-0.031), but it showed positive indirect effect on seed yield (0.755) through positive indirect effects contributed by number of pods per cluster (1.988), number of pods per plant (1.040), number of branches per plant (1.269) and harvest index (0.580). Whereas, number of clusters per

plant (-3.637), plant height (-0.213) and hundred seed weight (-0.255) exhibited negative indirect effects of number of seeds per pod on seed yield in parents (Table 4.13).

In crosses, high and positive direct effect of number of seeds per pod was observed on seed yield (0.396). It exerted negative indirect effect on seed yield (-0.349) via negative exhibited by harvest index (-0.361) and biological yield per plant (-0.210) other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both the parents and crosses (Table 4.15).

9. Hundred Seed Weight

In parents the direct effect of 100 seed weight on seed yield was high and positive (0.578). Its indirect effect for seed yield was negative and negligible (-0.093). Number of pods per cluster (1.947), days to 50% flowering (0.149), harvest index (0.043) and number of seeds per pod contributed towards positive indirect effect of this trait on seed yield (Table 4.13). Whereas, number of clusters per pod (-1.415), number of branches per plant (-0.712), number of pods per plant (-0.356) and plant height (-0.174), biological yield per plant (-0.108) exhibited negative indirect effects of hundred seed weight on seed yield.

In crosses, it exerted high negative direct effect on seed yield (-0.311) its indirect effect on seed yield was high and positive (0.375) which was contributed via positive indirect effects of harvest index (0.264), biological yield per plant (0.202) and number of seeds per pod (0.106) Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses (Table 4.15).

10. Biological yield per plant (g)

Direct effect of this trait was high and positive on seed yield (0.510) in parents (Table 4.13). This trait also exerted indirect high and positive effect on seed yield (0.754) via indirect positive effects contributed by number of pods per plant (2.396), number of branches per plant (0.895) and plant height (0.278) while, indirect negative effects of this trait on seed yield was exhibited through number of clusters per plant (-2.143), harvest index (-0.769), number

of pods per cluster (-0.191), days to 50% flowering (-0.132) and hundred seed weight (-0.122).

In crosses, direct effect of this trait was high and positive (0.725). Biological yield per plant exhibited high positive indirect effect on seed yield (0.902) contributed via indirect positive effects through harvest index (0.339) (Table 4.15). Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses

11. Harvest index (%)

In parents, harvest index exerted very high and positive direct effect (1.032) on seed yield (Table 4.13). Its indirect positive effect on seed yield (0.212) was exhibited through indirect positive effects via number of pods per cluster (1.006) and number of clusters per pod (0.523). Indirect negative effects of this trait on seed yield was contributed through number of pods per plant (-1.032), plant height (-0.506), number of branches per plant (-0.463) and biological yield per plant (-0.380).

In crosses, direct effect of harvest index on seed yield was high and positive (0.733). This trait also exhibited high and positive indirect effect on seed yield (0.790) via indirect positive effects of biological yield/plant (0.335). Whereas, number of seeds per pod (-0.195) and hundred seed weight (-0.112) exhibited negative indirect effects of this trait on seed yield other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses (Table 4.15).

4.6 Heterosis for yield and yield attributing traits

In the present study the estimates of heterosis in 40 crosses over mid parent (relative heterosis), better parent (heterobeltiosis) and over standard variety (standard heterosis) is presented in Table 4.16 to 4.19.

1. Days to 50% flowering

Among the 40 crosses, for this trait, significant negative heterosis over mid parent in the desirable direction was observed in 28 crosses. It ranged from -20.46 per cent (PDM 11 X Shikha) to 7.76 per cent (TJM 136 X Shikha). With respect to heterobeltiosis, the trait varied from -24.82 per cent (PDM 11

X Shikha) to 0.81 per cent (Pusa Vishal X PDM 139) for days to 50% flowering. Out of 40 crosses 35 crosses showed significant negative heterosis in desirable direction.

Standard heterosis over the standard variety (PDM 139) varied from -20.17 per cent (TJM 136 X Virat) to 7.56 per cent (PDM 11 X PDM 139). Eleven crosses out of 40 crosses viz., TJM 136 X PDM 139, TJM 136 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, HUM 1 X PDM 139, HUM 1 X Kanika, PDM 11 X Shikha, PDM 11 X Kanika and PDM 11 X Virat exhibited significant negative heterosis (Table 4.16).

2. Days to Maturity

Heterosis over mid parent ranged from -7.86 per cent (TJM 136 X Virat) to 6.01 per cent (TJM 136 X Shikha). Fifteen crosses out of 40 crosses showed significant desirable negative heterosis over mid parent whereas 5 crosses showed significant positive heterosis for earliness. Heterobeltiosis for days to maturity ranged from -16.26 per cent (TJM 136 X Virat) to 2.50 per cent (HUM 1 X PDM 139). Twenty seven out of 40 crosses, recorded significant negative heterosis over better parent in desirable direction. The standard heterosis over standard variety PDM 139 for this trait varied from -11.92 per cent (TJM 136 X Virat) to 7.77 per cent (LGG 460 X Shikha). Three Crosses viz., TJM 136 X PDM 139, TMB 37 X PDM 139 and TJM 136 X Virat registered significant negative heterosis (Table 4.16)

3. Plant height (cm)

Among the 40 crosses, the relative heterosis for plant height ranged from -28.88 (TJM 3 X Kanika) to 31.62 per cent (Pusa Vishal X PDM 139). Five crosses viz., TJM 196 X PDM 139, LGG 460 X PDM 139, SL 668 X Virat, Pusa Vishal X PDM 139 and Pusa Vishal X Virat expressed significant positive heterosis over mid parent. Heterobeltiosis for plant height ranged from -34.67 per cent (TJM 3 X Kanika) to 15.27 per cent (LGG 460 X PDM 139). Four crosses out of 40 (LGG 460 X PDM 139, SL 668 X Virat, Pusa Vishal X PDM 139 and Pusa Vishal X Virat) resulted heterobeltiosis in positive direction and remaining 33 crosses recorded significant heterobeltiosis in negative direction. A range of -1.39 (TJM 136 X PDM 139) to 62.54 per cent

(Pusa Vishal X PDM 139) of standard heterosis over the best cultivar PDM 139 was recorded for plant height. Among 40 crosses, 32 crosses showed significant standard heterosis in positive direction, whereas none of the cross showed standard heterosis in negative direction (Table 4.16).

Table 4.16: Estimation of Relative Heterosis (RH), Heterobeltiosis (HB) and Standard Heterosis (SH) for days to 50 % flowering, days to maturity and plant height

S. No.	Crosses	Days to 50% flowering			Days to maturity			Plant height (cm)		
		RH	HB	SH	RH	HB	SH	RH	HB	SH
1	TJM 196 X PDM 139	-2.88 *	-4.84 **	-1	-1	-2.51 *	0.52	9.14 **	3.83	15.02 **
2	TJM 196 X Shikha	-5.69 **	-6.45 **	-3	-2.76 **	-3.00 *	0.52	-5.87 *	-11.40 **	11.22 **
3	TJM 196 X Kanika	-5.06 **	-8.27 **	2.5	-4.67 **	-6.73 **	0.52	-3	-17.81 **	31.71 **
4	TJM 196 X Virat	0.81	0	4.20 **	-1	-1.97	3.11 *	-3	-4.15	6.18
5	TJM 136 X PDM 139	-0.93	-10.08 **	-10.08 **	4.18 **	-3.11 *	-3.11 *	-10.23 **	-17.62 **	-1.39
6	TJM 136 X Shikha	7.76 **	-3.28 *	-1	6.01 **	-3.00 *	0.52	-15.27 **	-17.24 **	3.89
7	TJM 136 X Kanika	4.35 **	-9.77 **	0.8	4.81 **	-5.77 **	1.55	-4	-16.21 **	34.28 **
8	TJM 136 X Virat	-13.24 **	-22.13 **	-20.17 **	-7.86 **	-16.26 **	-11.92 **	3.6	-1.28	18.16 **
9	TJM 3 X PDM 139	-2.44 *	-5.51 **	0.8	-1	-2.49 *	1.55	-3	-15.03 **	13.96 **
10	TJM 3 X Shikha	1.2	-0.79	5.88 **	-1	-1	3.11 *	-4	-7.18 *	24.49 **
11	TJM 3 X Kanika	-9.23 **	-11.28 **	-1	-5.13 **	-6.73 **	0.52	-28.88 **	-34.67 **	4.68
12	TJM 3 X Virat	-5.22 **	-7.09 **	-1	-3.47 **	-3.94 **	1.04	-7.95 **	-16.74 **	11.66 **
13	TMB 37 X PDM 139	-3.77 **	-4.17 **	-3.36 *	-3.34 **	-4.08 **	-2.59 *	-10.11 **	-19.72 **	2.12
14	TMB 37 X Shikha	-12.40 **	-13.11 **	-10.92 **	-1	-1.5	2.07	-14.31 **	-14.87 **	8.29 *
15	TMB 37 X Kanika	-17.00 **	-21.05 **	-11.76 **	-2.48 *	-5.29 **	2.07	-10.02 **	-19.29 **	29.33 **
16	TMB 37 X Virat	-13.22 **	-13.93 **	-11.76 **	-2	-3.45 **	1.55	-8.77 **	-15.49 **	7.51 *
17	Ganga 8 X PDM 139	-6.67 **	-12.50 **	0	2	-1.91	6.22 **	0.7	-13.64 **	20.76 **
18	Ganga 8 x Shikha	-7.75 **	-12.50 **	0	-5.62 **	-7.66 **	0	-7.59 **	-12.32 **	22.61 **
19	Ganga 8 X Kanika	-8.55 **	-9.56 **	3.36 *	-3.60 **	-3.83 **	4.15 **	-13.87 **	-19.35 **	29.24 **
20	Ganga 8 X Virat	-7.75 **	-12.50 **	0	-2	-3.35 **	4.66 **	-14.27 **	-23.88 **	6.45

Cont.....

S. No.	Crosses		Days to 50% flowering			Days to maturity			Plant height (cm)		
			RH	HB	SH	RH	HB	SH	RH	HB	SH
21	LGG 460 X PDM 139		-2.77 *	-8.21 **	3.36 *	1.5	-1.93	5.18 **	29.86 **	15.27 **	48.67 **
22	LGG 460 X Shikha		-3.13 **	-7.46 **	4.20 **	2.21 *	0.48	7.77 **	-4	-5.75 *	21.55 **
23	LGG 460 X Kanika		-13.11 **	-13.43 **	-3	-5.06 **	-5.29 **	2.07	-26.51 **	-33.68 **	6.27
24	LGG 460 X Virat		-7.81 **	-11.94 **	-1	-1	-1.93	5.18 **	0.5	-7.47 *	19.35 **
25	HUM 1 X PDM 139		-8.06 **	-11.63 **	-4.20 **	4.33 **	2.50 *	6.22 **	1.5	-8.52 **	13.96 **
26	HUM 1 X Shikha		-3.59 **	-6.20 **	1.7	0	0	3.63 **	-15.87 **	-16.19 **	5.21
27	HUM 1 X Kanika		-17.56 **	-18.80 **	-9.24 **	-2.94 **	-4.81 **	2.59 *	-6.27 **	-16.70 **	33.48 **
28	HUM 1 X Virat		-2.79 *	-5.43 **	2.5	-2	-2.46 *	2.59 *	-4	-10.23 **	11.84 **
29	SL 668 X PDM 139		0	0	0	0.3	-1.01	1.55	-1	-12.79 **	13.87 **
30	SL 668 X Shikha		-3.73 **	-4.92 **	-3	-2	-2.50 *	1.04	-7.83 **	-9.61 **	18.02 **
31	SL 668 X Kanika		-0.79	-6.02 **	5.04 **	-0	-2.88 *	4.66 **	-19.50 **	-26.96 **	17.05 **
32	SL 668 X Virat		-2.07	-3.28 *	-1	-0	-1.48	3.63 **	15.67 **	5.89 *	38.25 **
33	Pusa Vishal X PDM 139		2.48 *	0.81	4.20 **	0	-2.93 *	3.11 *	31.62 **	10.58 **	62.54 **
34	Pusa Vishal X Shikha		-4.49 **	-4.88 **	-2	-3.70 **	-4.88 **	1.04	-6.58 **	-13.40 **	27.30 **
35	Pusa Vishal x Kanika		-1.56	-5.26 **	5.88 **	-1	-1.44	6.22 **	-11.33 **	-14.99 **	36.22 **
36	Pusa Vishal X Virat		-1.22	-1.63	1.7	-1	-1.46	4.66 **	24.15 **	7.88 **	58.59 **
37	PDM 11 X PDM 139		0	-6.57 **	7.56 **	1.5	-2.84 *	6.22 **	-5	-21.62 **	21.38 **
38	PDM 11 X Shikha		-20.46 **	-24.82 **	-13.45 **	-5.60 **	-8.06 **	0.52	-22.05 **	-29.44 **	9.28 *
39	PDM 11 X Kanika		-18.52 **	-19.71 **	-7.56 **	-5.97 **	-6.64 **	2.07	-7.32 **	-8.88 **	46.02 **
40	PDM 11 X Virat		-14.29 **	-18.98 **	-6.72 **	-6.76 **	-8.53 **	0	-5.54 *	-19.68 **	24.38 **
	S.E (Heterosis)		0.47	0.54	0.5	0.7	0.78	0.78	1.2	1.39	1.39
	Range	Lowest	-20.46	-24.82	-20.17	-7.86	-16.26	-11.92	-28.88	-34.67	-1.39
		Highest	7.76	0.81	7.56	6.01	2.50	7.77	31.62	15.27	62.54

*, ** Significant at 5% 1% level of significance

4. Number of branches per plant

Relative heterosis among 40 crosses for number of branches per plant varied from -30.99 (Pusa Vishal X Kanika) to 188.89 per cent (HUM 1 X Shikha). Out of 40 crosses, 8 crosses viz., TJM 196 X PDM 139, TJM 136 X Virat, TMB 37 X Shikha, TMB 37 X Virat, Ganga 8 X PDM 139, LGG 460 X Kanika, HUM 1 X Shikha and PDM 11 X PDM 139 expressed significant positive heterosis whereas, only one cross (TJM 196 X Kanika) displayed significant negative heterosis over mid parent. Heterobeltiosis for number of branches per plant ranged from -46.74 (Pusa Vishal X Kanika) to 126.98 per cent (HUM 1 X Shikha). Four crosses viz., HUM 1 X Shikha, Ganga 8 X PDM 139, PDM 11 X PDM 139 and TJM 136 X Virat in positive direction and seven crosses in negative direction registered negative heterosis over better parent. Standard heterosis over the standard variety PDM 139 for number of branches per plant ranged from -31.82 (PDM 11 X Shikha) to 116.67 per cent (HUM 1 X Shikha). Twelve crosses showed significant positive heterosis while none of them showed significant negative heterosis over standard variety (Table 4.17).

5. Number of pods per plant

Relative heterosis varied from -21.99 (LGG 460 X Shikha) to 164.7 per cent (TJM 3 X Virat). 37 crosses over mid parent displayed significant and positive heterosis for this trait. Heterosis over the better parent ranged from -31.20 (LGG 460 X Shikha) to 164.35 per cent (TJM 3 X Virat). 32 crosses registered positive and significant heterobeltiosis for number of pods per plant.

Standard heterosis ranged from -0.79 (LGG 460 X PDM 139) to 176.29 per cent (LGG 460 X Kanika). Out of 40 crosses significant positive standard heterosis was displayed by 38 crosses while none of them showed significant negative standard heterosis (Table 4.17).

Table 4.17: Estimation of Relative Heterosis (RH), Heterobeltiosis (HB) and Standard Heterosis (SH) for number of branches/plant, number of pods/plant and Number of pods/cluster

S. No.	Crosses	No. of branches/plant			No. of pods/plant			No. of pods/cluster		
		RH	HB	SH	RH	HB	SH	RH	HB	SH
1	TJM 196 X PDM 139	31.40 *	6.6	71.21 **	53.69 **	22.35 **	106.62 **	10.14	-2.16	25.98 *
2	TJM 196 X Shikha	17.16	-6.6	50.00 *	-1.45	-4.16	61.85 **	-7.77	-8.57	17.73
3	TJM 196 X Kanika	-25.25 *	-30.19 *	12.12	16.69 **	-5.41	59.74 **	-1.7	-3.66	29.21 *
4	TJM 196 X Virat	1.57	-8.49	46.97 *	46.00 **	12.39 **	89.80 **	9.18	-1.65	26.64 *
5	TJM 136 X PDM 139	9.91	-7.58	-7.58	49.89 **	37.88 **	37.88 **	20.54 *	17.3	23.97 *
6	TJM 136 X Shikha	38.89	19.05	13.64	29.53 **	-1.16	57.75 **	10.32	1.23	28.09 *
7	TJM 136 X Kanika	22.63	-8.7	27.27	91.44 **	72.35 **	80.79 **	13.53	1.5	36.12 **
8	TJM 136 X Virat	83.08 **	40.00 *	80.30 **	87.75 **	80.38 **	64.37 **	20.70 *	19.3	26.09 *
9	TJM 3 X PDM 139	-2.56	-13.64	-13.64	43.36 **	37.19 **	37.19 **	17.63	9.4	27.20 *
10	TJM 3 X Shikha	28.07	15.87	10.61	83.56 **	44.33 **	130.36 **	9.73	5.29	33.22 **
11	TJM 3 X Kanika	-9.09	-29.35 *	-1.52	126.59 **	111.99 **	122.38 **	-7.12	-13.3	16.28
12	TJM 3 X Virat	-20.59	-36.47 *	-18.18	164.73 **	164.35 **	141.59 **	28.09 **	20.90 *	40.58 **
13	TMB 37 X PDM 139	-6.21	-25.23 *	25.76	23.05 **	18.17 **	28.34 **	-3.29	-8.36	-8.36
14	TMB 37 X Shikha	39.08 **	9.01	83.33 **	26.81 **	6.56	70.07 **	-10.63	-23.70 *	-3.46
15	TMB 37 X Kanika	7.39	-1.8	65.15 **	86.97 **	83.78 **	99.60 **	30.51 **	8.81	45.93 **
16	TMB 37 X Virat	27.55 *	12.61	89.39 **	108.62 **	91.83 **	108.34 **	61.83 **	51.08 **	55.96 **
17	Ganga 8 X PDM 139	71.43 **	55.56 **	90.91 **	128.10 **	119.32 **	137.62 **	20.32 *	8.3	35.34 **
18	Ganga 8 x Shikha	16.67	3.7	27.27	30.60 **	9.63 **	74.97 **	-15.51	-16.04	6.24
19	Ganga 8 X Kanika	14.45	7.61	50.00 *	104.47 **	101.22 **	118.01 **	1.81	-1.66	31.88 **
20	Ganga 8 X Virat	-15.66	-17.65	6.06	54.18 **	41.93 **	53.77 **	-45.77 **	-50.49 **	-38.13 **

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S. No.	Crosses		No. of branches/plant			No. of pods/plant			No. of pods/cluster		
			RH	HB	SH	RH	HB	SH	RH	HB	SH
21	LGG 460 X PDM 139		-6.09	-18.18	-18.18	-10.58 *	-18.61 **	-0.79	-25.04 *	-25.33 *	-24.75 *
22	LGG 460 X Shikha		10.71	-1.59	-6.06	-21.99 **	-31.20 **	9.8	-23.59 *	-31.37 **	-13.2
23	LGG 460 X Kanika		41.84 *	8.7	51.52 *	143.65 **	126.67 **	176.29 **	10.87	-2.91	30.21 *
24	LGG 460 X Virat		22.39	-3.53	24.24	96.11 **	71.36 **	108.87 **	19.67	18.25	22.07
25	HUM 1 X PDM 139		13.73	-12.12	-12.12	57.72 **	53.64 **	53.64 **	24.01 *	21.17	26.98 *
26	HUM 1 X Shikha		188.89 **	126.98 **	116.67 **	70.64 **	36.02 **	117.09 **	24.82 **	14.1	44.37 **
27	HUM 1 X Kanika		-7.81	-35.87 *	-10.61	67.90 **	59.85 **	67.68 **	-3.69	-14.21	15.05
28	HUM 1 X Virat		15.7	-17.65	6.06	131.05 **	126.54 **	114.83 **	19.61 *	18.72	24.41 *
29	SL 668 X PDM 139		7.09	3.03	3.03	68.49 **	65.92 **	65.92 **	34.55 **	32.00 **	32.00 **
30	SL 668 X Shikha		16.13	14.29	9.09	16.16 **	-6.64	49.01 **	-3.6	-15.15	7.36
31	SL 668 X Kanika		-8.5	-23.91	6.06	48.56 **	42.93 **	49.93 **	14.71	-1.5	32.11 **
32	SL 668 X Virat		-12.33	-24.71	-3.03	130.14 **	123.22 **	116.42 **	61.32 **	55.83 **	60.87 **
33	Pusa Vishal X PDM 139		5.17	-7.58	-7.58	37.88 **	28.48 **	28.48 **	10.12	9.81	9.81
34	Pusa Vishal X Shikha		-6.19	-15.87	-19.7	62.09 **	24.90 **	99.34 **	13.67	1.5	28.43 *
35	Pusa Vishal x Kanika		-30.99	-46.74 **	-25.76	85.04 **	68.69 **	76.95 **	-6.44	-18.54 *	9.25
36	Pusa Vishal X Virat		-0.74	-21.18	1.52	45.22 **	41.42 **	28.87 **	-9.35	-11.02	-8.14
37	PDM 11 X PDM 139		61.29 **	51.52 *	51.52 *	41.86 **	26.37 **	61.68 **	-10.48	-21.86 *	4.79
38	PDM 11 X Shikha		-25.62	-28.57	-31.82	51.88 **	36.82 **	118.37 **	9.84	6.73	43.14 **
39	PDM 11 X Kanika		1.33	-17.39	15.15	34.70 **	22.57 **	56.82 **	-6.65	-6.65	25.20 *
40	PDM 11 X Virat		-18.88	-31.76 *	-12.12	20.80 **	3.42	32.32 **	-14.7	-24.52 **	1.23
	S.E (Heterosis)		0.39	0.45	0.45	1.23	1.42	1.42	0.30	0.35	0.35
	Range	Lowest	-30.99	-46.74	-31.82	-21.99	-31.20	-0.79	-45.77	-50.49	-38.13
		Highest	188.89	126.98	116.67	164.73	164.35	176.29	61.83	55.83	60.87

*, ** Significant at 5% 1% level of significance

6. Number of pods per plant

Relative heterosis varied from -21.99 (LGG 460 X Shikha) to 164.7 per cent (TJM 3 X Virat). 37 crosses over mid parent displayed significant and positive heterosis for this trait. Heterosis over the better parent ranged from -31.20 (LGG 460 X Shikha) to 164.35 per cent (TJM 3 X Virat). 32 crosses registered positive and significant heterobeltiosis for number of pods per plant.

Standard heterosis ranged from -0.79 (LGG 460 X PDM 139) to 176.29 per cent (LGG 460 X Kanika). Out of 40 crosses significant positive standard heterosis was displayed by 38 crosses while none of them showed significant negative standard heterosis (Table 4.17).

7. Number of pods per cluster

The magnitude of heterosis exhibited by crosses over their corresponding mid parental values for pods per cluster ranged from -45.77 per cent (Ganga 8 X Virat) to 61.83 per cent (TMB 37 X Virat). Twelve crosses viz., TJM 136 X PDM 139, TJM 136 X Virat, TJM 3 X Virat, TMB 37 X Virat, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, HUM 1 X Shikha, HUM 1 X Virat, SL 668 X PDM 139 and SL 668 X Virat out of 40 crosses exhibited significant and positive heterosis over mid parent. The magnitude of heterobeltiosis ranged from -50.49 (Ganga 8 X Virat) to 55.83 per cent (SL 668 X Virat). The significant and positive heterobeltiosis was recorded by four crosses viz., TJM 3 X Virat, TMB 37 X Kanika, SL 668 X PDM 139 and SL 668 X Virat. Standard heterosis over the standard variety ranged from -38.13 (Ganga 8 X Virat) to 60.87 per cent (SL 668 X Virat). 24 crosses exhibited significant and positive standard heterosis for this trait (Table 4.17).

8. Number of clusters per plant

Relative heterosis for this trait ranged from 2.18 per cent (LGG 460 X Shikha) to 185.07 per cent (Ganga 8 X Virat). 32 crosses exhibited significant positive relative heterosis and none of the crosses showed significantly negative relative heterosis. Similarly heterobeltiosis ranged from -4.19 (TJM 196 X Kanika) to 182.51 Per cent (Ganga 8 X Virat) and 23 crosses expressed significant and positive heterobeltiosis while none of them exhibited significant and negative heterobeltiosis.

Table 4.18: Estimation of Relative Heterosis (RH), Heterobeltiosis (HB) and Standard Heterosis (SH) for number of clusters/plant, number of seeds/pod and 100 seed weight

S. No.	Crosses	No. of clusters/plant			No. of seeds/pod			100 seed wt.(g)		
		RH	HB	SH	RH	HB	SH	RH	HB	SH
1	TJM 196 X PDM 139	42.81 **	26.35 *	64.20 **	0.17	0	0.34	6.02	-7.76	24.65 *
2	TJM 196 X Shikha	7.5	5.09	36.58 **	-4.03	-4.67	-3.05	-16.47 *	-23.74 **	3.06
3	TJM 196 X Kanika	20.08	-4.19	24.51	4.91	4.73	5.08	-0.55	-6.53	26.31 *
4	TJM 196 X Virat	36.45 **	13.77	47.86 **	1.32	-0.97	4.07	0.14	-5.95	27.10 *
5	TJM 136 X PDM 139	24.02	10.51	10.51	1.81	-1.27	5.08	21.51 **	3.84	46.42 **
6	TJM 136 X Shikha	19.62	-2.51	21.01	-0.65	-2.87	3.39	11.63	0	41.00 **
7	TJM 136 X Kanika	68.00 **	67.16 **	30.74 *	17.73 *	14.17	21.53 **	-14.97 *	-21.64 **	10.49
8	TJM 136 X Virat	57.78 **	50.00 **	30.16 *	6.54	5.86	12.68	-15.52 *	-22.19 **	9.7
9	TJM 3 X PDM 139	21.23	7.78	7.78	-4.39	-4.71	-4.07	44.17 **	37.24 **	37.24 **
10	TJM 3 X Shikha	71.48 **	39.50 **	73.15 **	1.17	0.67	2.37	16.49	5.4	17.66
11	TJM 3 X Kanika	142.61 **	142.00 **	88.33 **	4.39	4.04	4.75	1.92	-10.29	6.64
12	TJM 3 X Virat	106.62 **	95.96 **	70.04 **	-1.48	-3.55	1.36	-18.31 *	-28.06 **	-14.6
13	TMB 37 X PDM 139	26.63 *	15.81	39.69 **	-9.68	-17.42 *	-0.34	0.51	-2.7	3.93
14	TMB 37 X Shikha	43.08 **	41.07 **	75.10 **	9.15	0.56	21.36 *	-9.24	-11.2	-0.87
15	TMB 37 X Kanika	36.74 **	12.26	35.41 *	-4.76	-12.92	5.08	-5.11	-9.93	7.08
16	TMB 37 X Virat	26.83 *	9.03	31.52 *	-12.61 *	-18.26 **	-1.36	4.81	-0.44	18.18
17	Ganga 8 X PDM 139	88.66 **	74.71 **	74.71 **	-6.62	-7.85	-5.36	12.56	6.12	6.12
18	Ganga 8 x Shikha	55.02 **	30.72 **	62.26 **	7.79	7.26	10.17	14.41	2.58	14.51
19	Ganga 8 X Kanika	101.44 **	92.24 **	63.81 **	-6.69	-7.92	-5.42	3.83	-9.41	7.69
20	Ganga 8 X Virat	185.07 **	182.51 **	145.14 **	-3.43	-4.52	0.34	-5.78	-17.75 *	-2.36

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S. No.	Crosses		No. of clusters/plant			No. of seeds/pod			100 seed wt.(g)		
			RH	HB	SH	RH	HB	SH	RH	HB	SH
21	LGG 460 X PDM 139		20.2	10.67	31.52 *	5.99	2.03	2.03	-20.63 *	-27.56 **	-12.2
22	LGG 460 X Shikha		2.18	0	24.12	2.62	-2	-0.34	-6.87	-10.53	8.39
23	LGG 460 X Kanika		113.72 **	76.49 **	109.73 **	0.35	-3.39	-3.39	1.24	0.29	21.50 *
24	LGG 460 X Virat		63.89 **	41.78 **	68.48 **	-2.92	-8.71	-4.07	-11.01	-11.9	6.73
25	HUM 1 X PDM 139		25.93 *	19.07	19.07	1.17	0	2.37	-11.6	-23.80 **	5.24
26	HUM 1 X Shikha		39.05 **	19.44	48.25 **	7.97	7.62	10.17	38.33 **	25.06 **	72.73 **
27	HUM 1 X Kanika		74.30 **	62.88 **	45.14 **	-7.87	-8.94	-6.78	-25.37 **	-30.57 **	-4.11
28	HUM 1 X Virat		100.88 **	98.25 **	76.65 **	-1.31	-2.58	2.37	-11.64	-17.85 *	13.46
29	SL 668 X PDM 139		26.82 *	26.33	27.32 *	6.44	6.44	6.44	-8.8	-26.46 **	20.02
30	SL 668 X Shikha		22.15 *	10.66	37.35 **	3.87	3	4.75	-16.28 *	-29.51 **	15.03
31	SL 668 X Kanika		27.51 *	12.74	13.62	1.02	1.02	1.02	-15.53 *	-27.00 **	19.14
32	SL 668 X Virat		41.08 **	31.27 *	32.30 *	6.78	4.19	9.49	-10.02	-22.28 **	26.84 *
33	Pusa Vishal X PDM 139		24.37	15.18	15.18	-2.91	-7.12	1.69	-21.47 *	-27.63 **	-14.2
34	Pusa Vishal X Shikha		45.72 **	22.88 *	52.53 **	-0.8	-4.33	4.75	-5.32	-8.11	9
35	Pusa Vishal x Kanika		100.00 **	90.87 **	62.65 **	-7.12	-11.15	-2.71	-10.93	-11.03	5.77
36	Pusa Vishal X Virat		62.44 **	60.99 **	39.69 **	24.80 **	22.29 **	33.90 **	-9.83	-9.87	6.99
37	PDM 11 X PDM 139		57.92 **	53.31 **	53.31 **	-9.03	-9.93	-8.1	-8.39	-9.33	-7.43
38	PDM 11 X Shikha		38.68 **	21.94 *	51.36 **	-6.82	-6.98	-5.08	-2.9	-7.05	3.76
39	PDM 11 X Kanika		43.76 **	30.99 *	23.35	-8.56	-9.47	-7.63	11.39	3.53	23.08 *
40	PDM 11 X Virat		44.09 **	38.43 **	30.35 *	-3.76	-5.16	-0.34	-4.04	-10.75	5.94
	S.E (Heterosis)		1.01	1.17	1.17	0.69	0.80	0.80	0.35	0.40	0.40
	Range	Lowest	2.18	-4.19	7.78	-12.6	-18.26	-8.1	-25.37	-30.57	-14.6
		Highest	185.07	182.51	145.14	24.80	22.29	33.90	44.17	37.24	72.73

*, ** Significant at 5% 1% level of significance

Estimates of percent standard heterosis exhibited by the 40 crosses over the standard variety PDM 139 ranged from 7.78 (TJM 3 X PDM 139) to 145.14 per cent (Ganga 8 X Virat). Thirty one crosses recorded positive and significant heterosis over standard parent (Table 4.18).

9. Number of seeds per pod

The relative heterosis among 40 crosses for number of seeds per pod varied from -12.61 (TMB 37 X Virat) to 24.80 per cent (Pusa Vishal X Virat). Two crosses viz., TJM 136 X Kanika and Pusa Vishal X Virat expressed significant positive and one cross TMB 37 X Virat showed significant negative heterosis over mid parent. Heterobeltiosis for number of seeds per pod ranged from -18.26 (TMB 37 X Virat) to 22.29 per cent (Pusa Vishal X Virat). One cross Pusa Vishal X Virat in positive direction performed significant heterosis over better parent.

Standard heterosis over standard variety PDM 139 ranged from -8.1 per cent (PDM 11 X PDM 139) to 33.90 per cent (Pusa Vishal X Virat). Three crosses viz., TJM 136 X Kanika, TMB 37 X Shikha and Pusa Vishal X Virat showed significant positive heterosis over standard variety (Table 4.18).

10. Hundred seed weight (g)

Among 40 crosses, only three crosses viz., TJM 136 X PDM 139, TJM 3 X PDM 139 and HUM 1 X Shikha exhibited significant and positive heterosis and it ranged from -25.37 (HUM 1 X Kanika) to 44.17 per cent (TJM 3 X PDM 139). Two crosses viz., TJM X PDM 139 and HUM 1 X Shikha recorded positive and significant heterobeltiosis while 14 crosses exhibited significant negative heterobeltiosis in negative direction and it ranged from -30.57 (HUM 1 X Kanika) to 37.24 per cent (TJM 3 X PDM 139).

Standard heterosis ranged from -14.6 per cent (TJM 3 X Virat) to 72.73 per cent (HUM 1 X Shikha). Ten crosses recorded positive and significant heterosis over standard parent while none of the crosses could excel the better parent (Table 4.18).

Table 4.19: Estimation of Relative Heterosis (RH), Heterobeltiosis (HB) and Standard Heterosis (SH) for biological yield/plant, harvest index and seed yield/plant

S. No.	Crosses	Biological yield/plant (g)			Harvest index (%)			Seed yield/plant(g)		
		RH	HB	SH	RH	HB	SH	RH	HB	SH
1	TJM 196 X PDM 139	-16.09 **	-39.69 **	37.89 **	40.92 **	19.32	19.32	27.49 *	4.38	63.74 **
2	TJM 196 X Shikha	-4.47	-20.87 **	80.93 **	85.26 **	81.37 **	31.26 *	76.65 **	49.39 **	134.34 **
3	TJM 196 X Kanika	-17.76 **	-23.40 **	75.14 **	111.36 **	92.42 **	33.41 *	71.17 **	46.32 **	129.53 **
4	TJM 196 X Virat	33.82 **	2.64	134.69 **	47.79 **	19.31	34.61 *	119.98 **	99.12 **	212.36 **
5	TJM 136 X PDM 139	51.14 **	31.93 **	76.92 **	9.73	-9.43	-9.43	67.30 **	59.20 **	59.20 **
6	TJM 136 X Shikha	29.51 **	22.59 **	84.08 **	69.85 **	61.29 **	16.73	114.51 **	96.58 **	113.19 **
7	TJM 136 X Kanika	-44.59 **	-53.46 **	-8.19	57.77 **	47.86 *	-3.77	-11.65	-19.99	-10.9
8	TJM 136 X Virat	22.88 **	17.38 **	57.41 **	-20.4	-37.24 **	-29.20 *	2.78	-12.1	11.74
9	TJM 3 X PDM 139	20.22 **	15.11 *	25.80 **	51.41 **	25.48	25.48	83.86 **	56.52 **	56.52 **
10	TJM 3 X Shikha	38.19 **	19.38 **	79.27 **	102.40 **	93.14 **	39.78 **	178.32 **	129.32 **	148.70 **
11	TJM 3 X Kanika	13.59 **	-11.75 **	74.11 **	75.03 **	63.27 **	7.34	104.46 **	66.75 **	85.65 **
12	TJM 3 X Virat	58.00 **	49.71 **	82.80 **	1.08	-20.01	-9.75	65.76 **	28.69 *	63.60 **
13	TMB 37 X PDM 139	33.12 **	17.17 **	54.08 **	40.27 **	16.21	16.21	91.56 **	77.82 **	77.82 **
14	TMB 37 X Shikha	45.50 **	36.46 **	104.90 **	48.78 **	41.92 *	2.71	114.44 **	91.89 **	108.10 **
15	TMB 37 X Kanika	10.13 *	-8.23	81.04 **	81.19 **	69.07 **	11.07	101.05 **	77.85 **	98.01 **
16	TMB 37 X Virat	60.30 **	54.57 **	103.26 **	21.71	-3.71	8.64	104.39 **	71.04 **	117.45 **
17	Ganga 8 X PDM 139	-8.15	-27.35 **	24.86 **	27.11 *	14.36	14.36	20.35	4.79	41.35 *
18	Ganga 8 x Shikha	41.01 **	32.10 **	127.05 **	72.84 **	64.66 **	31.63 *	143.47 **	119.60 **	196.22 **
19	Ganga 8 X Kanika	18.36 **	10.74 *	118.48 **	41.13 *	20.8	-3.43	69.32 **	54.53 **	108.45 **
20	Ganga 8 X Virat	-3.82	-17.74 **	41.38 **	18.49	1.23	14.21	22.88 *	19.35	60.99 **

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S. No.	Crosses		Biological yield/plant (g)			Harvest index (%)			Seed yield/plant(g)		
			RH	HB	SH	RH	HB	SH	RH	HB	SH
21	LGG 460 X PDM 139		8.34	-9.21	34.28 **	-29.17 *	-35.60 *	-35.60 *	-21.14	-27.61	-13.4
22	LGG 460 X Shikha		-23.84 **	-24.41 **	13.5	0.66	-5.18	-22.38	-24.18	-27.73	-13.5
23	LGG 460 X Kanika		39.09 **	21.68 **	140.05 **	54.32 **	30.8	7.07	120.93 **	113.26 **	155.15 **
24	LGG 460 X Virat		70.74 **	55.85 **	130.50 **	31.00 *	13.02	27.52 *	135.68 **	128.74 **	190.80 **
25	HUM 1 X PDM 139		50.47 **	47.13 **	47.13 **	-16	-18.18	-13.7	21.3	19.24	23.42
26	HUM 1 X Shikha		63.94 **	34.13 **	101.41 **	67.63 **	41.33 **	49.06 **	181.53 **	175.11 **	198.35 **
27	HUM 1 X Kanika		18.57 **	-12.00 **	73.61 **	44.73 **	11.41	17.51	88.30 **	81.68 **	102.27 **
28	HUM 1 X Virat		112.72 **	89.59 **	131.50 **	20.51	16.58	31.53 *	161.64 **	137.33 **	201.72 **
29	SL 668 X PDM 139		58.34 **	30.79 **	100.59 **	29	2.45	2.45	117.42 **	104.05 **	104.05 **
30	SL 668 X Shikha		9.70 *	8.55	66.49 **	88.30 **	70.70 **	23.53	106.44 **	86.70 **	102.47 **
31	SL 668 X Kanika		24.26 **	10.43 *	117.86 **	96.70 **	93.47 **	13.83	147.90 **	121.59 **	146.70 **
32	SL 668 X Virat		2.26	-8.16	40.85 **	-3.48	-26.57 *	-17.15	7.35	-9.29	15.32
33	Pusa Vishal X PDM 139		4.49	-9.04	22.76 **	-21.5	-27.84 *	-27.84 *	-17.91	-22.09	-13.3
34	Pusa Vishal X Shikha		16.78 **	10.88 *	66.49 **	86.68 **	73.89 **	45.82 **	119.19 **	116.35 **	140.87 **
35	Pusa Vishal x Kanika		5.89	-10.83 *	75.91 **	101.25**	68.91 **	41.65 **	122.21 **	122.21 **	147.39 **
36	Pusa Vishal X Virat		-13.40 *	-17.53 **	11.31	-18.8	-29.25 *	-20.18	-25.92 *	-30.52 *	-11.7
37	PDM 11 X PDM 139		-6.73	-30.22 **	40.60 **	47.18 **	16.29	16.29	60.40 **	49.70 **	72.73 **
38	PDM 11 X Shikha		-6.06	-18.03 **	65.17 **	98.37 **	78.72 **	29.34 *	89.26 **	83.57 **	111.81 **
39	PDM 11 X Kanika		-24.04 **	-24.84 **	51.46 **	79.55 **	77.81 **	3.19	38.08 **	35.65 *	56.52 **
40	PDM 11 X Virat		5.12	-15.59 **	70.10 **	32.32 *	0.19	13.04	56.95 **	49.70 **	90.32 **
	S.E (Heterosis)		1.04	1.20	1.20	3.89	4.49	4.49	0.72	0.83	0.83
	Range	Lowest	-44.59	-53.46	-8.19	-29.17	-37.24	-35.60	-25.92	-30.52	-13.5
		Highest	112.72	89.59	140.05	111.36	93.47	49.06	181.53	175.11	212.36

*, ** Significant at 5% 1% level of significance

11. Biological yield per plant (g)

The magnitude of heterosis exhibited by cross combinations over their corresponding mid parental values for biological yield/plant ranged from -44.59 (TJM 136 X Kanika) to 112.72 per cent (HUM 1 X Virat). Twenty six out of 40 crosses exhibited positive heterosis while six crosses recorded significant negative heterosis over mid parent. The magnitude of heterobeltiosis ranged from -53.46 (TJM 136 X Kanika) to 89.59 per cent (HUM 1 X Virat). Significant positive heterobeltiosis was recorded by 19 crosses while other 15 crosses showed significant negative heterosis over better parent. The range of standard heterosis varied from -8.19 (TJM 136 X Kanika) to 140.05 per cent (LGG 460 X Kanika). 37 crosses exhibited significant positive standard heterosis while none of the crosses expressed significant negative heterosis for this trait (Table 4.19).

12. Harvest index (%)

Relative heterosis varied from -29.17 (LGG 460 X PDM 139) to 111.36 per cent (TJM 196 X Kanika) and 27 out of 40 crosses exhibited significant and positive heterosis with regard to the mid parental value. The magnitude of heterobeltiosis ranged from -37.24 (TJM 136 X Virat) to 93.47 per cent (SL 668 X Kanika). Sixteen crosses registered significant and positive heterobeltiosis while five crosses exhibited significant and negative heterosis for this trait. The range of standard heterosis over the standard variety varied from -30.60 per cent (LGG 460 X PDM 139) to 49.06 per cent (HUM 1 X Shikha). Eleven crosses exhibited significant positive standard heterosis for this trait (Table 4.19)

13. Seed yield per plant (g)

The magnitude of relative heterosis among 40 crosses for seed yield per plant varied from -25.92 (Pusa Vishal X Virat) to 181.53 per cent (HUM 1 X Shikha). 32 crosses over mid parent displayed significant positive heterosis for this trait. Heterosis over the better parent ranged from -30.52 (Pusa Vishal X Virat) to 175.11 per cent (HUM 1 X Shikha). 29 crosses registered positive significant heterobeltiosis for seed yield/plant while one cross Pusa Vishal X Virat showed negative significant heterosis over better parent (Table 4.19).

4.7 Combining ability analysis

In the present study, the combining ability analysis was carried out based on mean value of five plants for fourteen parents and forty crosses derived from 10 lines x 4 testers programme to obtain information on *gca* effects of parents and *sca* effects of crosses which would help in selection of better parents, cross combinations and breeding method to be employed for the improvement of the yield and yield attributing traits.

4.7.1 Analysis of variance for combining ability

Analysis of variance for the combining ability using Line X Tester mating design for twelve characters was given in Table 4.20. It revealed that treatments registered highly significant differences for all the characters. The parents differed significantly for all the characters except for number of seeds per pod. Mean sum of squares due to parents vs. crosses were significantly different for all the characters except number of seeds per pod. The effect of crosses was partitioned into lines, testers and their interactions. The mean sums of squares due to lines were significant for all the characters except for number of seeds per pod. The mean sums of squares due to testers were also significant for eight characters except for number of branches per plant, number of seeds per pod, hundred seed weight and seed yield per plant. The mean sum of squares due to Line X Tester interaction effects were significant for five characters while it was non-significant for remaining characters *viz.*, days to 50 % flowering, days to maturity, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight and seed yield per plant.

4.7.2 Estimates of combining ability variances

In the present study, the magnitude of SCA variance was higher than GCA variance for all the quantitative characters (Table 4.21). The ratio of variance due to general combining ability ranged from 0.002 to 0.639. As judged by the ratio of additive and dominance variance among all twelve characters, the ratio of GCA/SCA was less than one for all the biometrical characters except plant height.

Table 4.20 Analysis of variance of combining ability (line x tester) for

Source of variation	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	No. of pods/ cluster	No. of clusters/ plant	No. of seeds/ pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
Replications	2	3.08**	3.38*	3.99	0.87	4.55	0.5	3.64	1.17	0.29	2.8	26.12	0.04
Treatments	53	24.98**	20.29**	109.48**	2.02**	422.98**	1.04**	25.30**	1.78**	1.40**	97.06**	212.43**	31.90**
Parents	13	34.09**	40.38**	125.79**	1.80**	129.47**	0.62**	7.50**	1.66	1.90**	99.83**	107.10**	3.49**
Crosses	39	17.60**	13.53**	98.50**	2.02**	301.65**	1.15**	17.46**	2.03**	1.24**	89.63**	152.52**	29.12**
Lines	9	44.98**	53.61**	71.37**	2.24**	124.68**	0.61**	7.81**	1.59	2.53**	105.13**	68.96*	4.70**
Testers	3	12.67**	13.11**	303.60**	0.67	182.51**	0.77**	9.04**	0.17	0.34	112.80**	211.49**	0.91
Line x Testers	1	0.34	3.09	81.99**	1.30*	13.51*	0.3	0.05	0.34	0.84	13.18*	137.22*	0.35
Parents vs Crosses	1	194.63**	22.73**	326.43**	4.84**	8970.30**	2.23**	562.35**	0.01	1.26*	351.16**	3918.43**	509.16**
Error	106	0.43	0.92	2.91	0.30	3.02	0.2	2.05	0.96	0.24	2.15	30.24	1.02

different quantitative characters

*, ** Significant at 5% and 1% Level of Probability

Table 4.21 Estimation of genetic components for seed yield and its attributing characters

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of pods/ plant	No. of pods/ cluster	No. of clusters/ plant	No. of seeds/ pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/ plant (g)
gca variance	1.824	1.5	9.857	0.195	13.352	0.063	1.658	0.17	0.07	4.577	11.252	1.684
sca variance	17.444	13.1	95.721	2.172	413.93	1.787	17.44	2.230	1.65	114.26	198.273	34.28
GCA/SCA	0.105	0.115	0.103	0.090	0.032	0.035	0.095	0.075	0.045	0.040	0.057	0.049
σ^2A	3.327	2.262	97.160	0.038	178.276	0.004	2.749	0.028	0.005	20.949	126.608	2.836
σ^2D	17.444	13.1	95.721	2.172	413.93	1.787	17.44	2.230	1.65	114.26	198.273	34.28
Ratio (σ^2A/σ^2D)	0.191	0.173	1.015	0.018	0.431	0.002	0.158	0.013	0.003	0.183	0.639	0.083

4.7.3 GCA and SCA Performance of Genotypes and Crosses

The estimates of *gca* effects in respect of parents and estimates of *sca* effects of 40 crosses in F_1 generation for 12 quantitative characters were furnished in Table 4.22 and 4.23.

1. Days to 50% flowering

The magnitude of *gca* effects varied from -3.05 (TMB 37) to 1.69 (Pusa Vishal) in lines and from -0.60 (Virat) to 0.59 (PDM 139) in testers (Table 4.22). Among lines TMB 37 (-3.05) and TJM 136 (-2.30) and among testers Virat (-0.60) registered negative and significant *gca* effects, which were desirable for earliness and may be considered as desirable parents in crop improvement programmes for the development of short duration genotypes.

Sca effects varied from -4.39 (TJM 136 X Virat) to 4.40 (PDM 11 X PDM 139). Among crosses, TJM 136 X Virat (-4.39) registered negative and significant *sca* effects while, the cross PDM 11 X PDM 139 (4.40) exhibited positive and significant *sca* effects (Table 4.23). The cross TJM 136 X Virat was best specific combiner for earliness with high significant negative *sca* effects (-4.39).

2. Days to maturity

Among lines, low *gca* effect of -3.46 was observed in (TJM 136) and high *gca* effect of 1.86 was observed in (LGG 460). Whereas among testers *gca* effects for this trait varied from -0.45 (Virat) to 0.31 (Kanika). The line TJM 136 (-3.46) and the tester Kanika (-0.45) showed significant negative *gca* effects indicating their use as general combiner in getting early maturing types (Table 4.22)

The *sca* effect of this trait varied from -5.13 (TJM 136 X Virat) to 2.76 (TJM 136 X Kanika). Five crosses viz., TJM 136 X Virat (-5.13), TMB 37 X PDM 139 (-2.38), GANGA 8 X Shikha (-2.33), LGG 460 X Kanika (-2.23) and Pusa Vishal X Shikha (-1.66) showed significant and negative *sca* effects indicating the possibility to get early maturing segregants while, TJM 196 X Virat (1.70), TJM 136 X Shikha (2.50), TJM 136 X Kanika (2.76), Ganga 8 X PDM 139 (1.36), LGG 460 X Shikha (1.83), HUM 1 X PDM 139 (1.36), Pusa

Vishal X Kanika (1.26) and PDM 11 X PDM 139 (2.36) registered significant and positive *sca* effects indicating late maturity (Table 4.23)

3. Plant height (cm)

Among lines highest significant positive *gca* effect for plant height was recorded by Pusa Vishal (9.55) followed by PDM 11 (1.67) and LGG 460 (1.18), while highly negative *gca* effect was observed in TMB 37 (-3.40) followed by TJM 3 (-2.69), TJM 136 (-2.67), TJM 196 (-1.81) and HUM 1 (-1.77). Among testers, Kanika showed highly significant positive *gca* effect (2.26), while highly significant negative *gca* effect was observed in Shikha (-2.13). It was evident that Pusa Vishal, PDM 11, LGG 460 and Kanika are the good parents for plant height as they exhibited highly significant positive *gca* effects for this trait (Table 4.22).

The *sca* effects of crosses for plant height varied from -8.93 (LGG 460 X Kanika) to 9.22 (LGG 460 X PDM 139). Among 40 crosses, the highly significant positive *sca* effect was recorded for LGG 460 X PDM 139 (9.22) followed by SL 668 X Virat (6.43), TJM 3 X Shikha (6.20), Pusa Vishal X PDM 139 (6.08) PDM 11 X Kanika (5.57), TJM 136 X Kanika (5.48), Pusa Vishal X Virat (4.91), TMB 37 X Kanika (4.34), UM 1 X Kanika (4.28), TJM 196 X Kanika (3.65) and GANGA 8 X Shikha (3.20) (Table 4.23). Highly significant negative *sca* effect was recorded for LGG 460 X Kanika (-8.93) followed by Pusa Vishal X Kanika (-6.01), TJM 136 X PDM 139 (-5.80), TJM 3 X Kanika (-5.66), Pusa Vishal X Shikha (-4.98), Ganga 8 X Virat (-4.79), PDM 11 X Shikha (-3.90), TMB 37 X PDM 139 (-3.75), TJM 196 X Virat (-3.49) and SL 668 X PDM 139 (-3.08).

4. Number of branches per plant

Among lines, the highest significant positive *gca* effect for number of branches per plant was recorded for TMB 37 (0.98) followed by TJM 196 (0.52) and GANGA 8 (0.49) while highest significant negative *gca* effect was observed for Pusa Vishal (-0.74) followed by TJM 3 (-0.59), SL 668 (-0.38) and PDM 11 (-0.34). Among testers, *gca* effect varied from -0.06 (PDM 139) to 0.09 (Shikha) while none of the testers showed significant *gca* effects (Table 4.22).

Table 4.22: Estimates of general combining ability (gca) effects of parents for seed yield/plant and its attributing characters

S. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of pods/plant	No. of pod/cluster	No. of clusters/plant	No. of seeds/pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/plant (g)
	Lines												
1	TJM 196	1.02 **	-0.63 *	-1.81**	0.52**	0.42	0.12	-0.34	-0.13	0.28*	1.56**	6.17**	2.08**
2	TJM 136	-2.30 **	-3.46**	-2.67**	0.15	-4.43**	0.23	-2.07**	0.75**	0.53**	-2.75**	-5.70**	-2.36**
3	TJM 3	1.19 **	-0.38	-2.69**	-0.59**	7.56**	0.25*	1.06*	-0.18	-0.04	-0.86*	1.58	-0.16
4	TMB 37	-3.05 **	-0.88 **	-3.40**	0.98**	-0.30	0.05	-0.16	0.31	-0.22	2.10**	-0.41	0.40
5	Ganga 8	1.02**	1.03 **	-0.40	0.49**	4.60**	-0.35**	3.35**	-0.29*	-0.2	0.95*	1.08	0.46
6	LGG 460	1.10**	1.86**	1.18*	-0.18	-1.07*	-0.51**	0.95*	-0.43	-0.25	1.19**	-5.52**	-0.59*
7	HUM 1	-0.225	1.03**	-1.77**	0.08	2.64**	0.21	-0.00	-0.09	0.34*	2.48**	3.36*	1.90**
8	SL668	0.85**	0.36	0.36	-0.38*	-1.88**	0.37**	-1.68**	0.24	0.28	1.46**	-1.72	0.00
9	Pusa Vishal	1.69**	1.03**	9.55**	-0.74**	-4.88**	-0.32*	-0.41	0.63*	-0.41**	-3.99**	-0.34	-1.27**
10	PDM 11	-1.30**	0.03	1.67**	-0.341*	-2.64**	-0.06	-0.66	-0.81**	-0.3	-2.13**	1.50	-0.44
	SE(gi)	0.18	0.27	0.49	0.15	0.50	0.12	0.41	0.28	0.14	0.42	1.58	0.29
	Testers												
1	PDM 139	0.59**	0.21	0.09	-0.06	-5.57**	-0.16*	-1.11**	-0.29	-0.07	-3.64**	-3.34**	-2.17**
2	Shikha	0.10	-0.08	-2.13**	0.09	0.26	-0.04	0.06	0.18	0.21*	1.09**	4.56**	1.55**
3	Kanika	0.12	0.31	2.26**	-0.04	3.27**	0.19*	0.20	-0.17	-0.02	1.24**	0.62	0.47*
4	Virat	-0.60**	-0.45*	-0.22	0.02	2.04**	0.01	0.84**	0.28	-0.11	1.30**	-1.83	0.15
	SE(gj)	0.12	0.17	0.31	0.10	0.31	0.07	0.26	0.17	0.08	0.26	1.00	0.18

*, ** Significant at 5% & 1% level of Significance respectively

Table 4.23: Estimates of specific combining ability (sca) effects of crosses for seed yield per plant and its attributing characters

S. No.	Cross combinations	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches /plant	No. of pods/pl ant	No. of pods/cl uster	No. of cluster/ plant	No. of seeds/ pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/pla nt (g)
1	TJM 196 X PDM 139	-1.25**	-0.6	-0.47	0.63*	12.40**	0.19	2.90**	0.16	0.24	-2.82**	-0.06	-1.28*
2	TJM 196 X Shikha	-1.22**	-0.3	0.31	0.01	-4.70**	-0.16	-0.64	-0.64	-0.86**	-1.27	-4.03	-1.58**
3	TJM 196 X Kanika	0.54	-0.73	3.65**	-0.67*	-8.24**	-0.06	-1.81*	0.52	0.25	-2.27**	0.62	-0.73
4	TJM 196 X Virat	1.94**	1.70**	-3.49**	0.02	0.55	0.03	-0.45	-0.04	0.37	6.37**	3.47	3.60**
5	TJM 136 X PDM 139	-1.59**	-0.1	-5.80**	0.63*	-0.04	0.02	0.03	-0.25	0.81**	7.20**	2.35	2.95**
6	TJM 136 X Shikha	2.77**	2.50**	-1.58	0.01	-0.88	0.03	-0.24	-0.9	0.32	3.51**	3.06	1.84**
7	TJM 136 X Kanika	3.20**	2.76**	5.48**	-0.67*	1.91	0.03	0.45	1.24*	-0.60*	-10.12**	0.25	-3.10**
8	TJM 136 X Virat	-4.39**	-5.13**	1.89	0.02	-0.99	-0.08	-0.24	-0.08	-0.53	-0.59	-5.67	-1.68**
9	TJM 3 X PDM 139	-0.75*	-0.21	0.00	-0.11	-12.21**	0.09	-3.34**	-0.21	1.04**	-2.15*	6.56*	0.62
10	TJM 3 X Shikha	1.94**	1.08	6.20**	0.26	5.39**	0.16	1.07	-0.06	0.01	0.91	3.36	1.36*
11	TJM 3 X Kanika	-0.95*	-0.98	-5.66**	0.14	0.37	-0.58*	2.23**	0.53	-0.17	0.01	-3.37	-0.6
12	TJM 3 X Virat	-0.22	0.11	-0.54	-0.29	6.44**	0.32	0.03	-0.25	-0.88**	1.22	-6.55*	-1.36*
13	TMB 37 X PDM 139	1.82**	-2.38**	-3.75**	-0.82*	-6.56**	-0.76**	0.62	-0.35	-0.04	-0.99	5.5	1.08
14	TMB 37 X Shikha	-0.47	0.91	0.80	0.293	-1.90	-0.73**	2.47**	1.30*	-0.51	1.69*	-6.85*	-1.17*
15	TMB 37 X Kanika	-1.04**	0.51	4.34**	0.032	2.51*	0.50*	-1.06	0.07	0.02	-1.94*	-0.15	-0.6
16	TMB 37 X Virat	-0.30	0.95	-1.39	0.49	5.95**	0.98**	-2.03*	-1.02	0.54	1.24	1.50	0.67
17	Ganga 8 X PDM 139	-0.92*	1.36*	0.27	1.10**	16.02**	0.95**	0.1	-0.23	0.05	-4.11**	3.40	-0.8
18	Ganga 8 x Shikha	-0.22	-2.33**	3.20**	-0.44	-5.58**	-0.03	-2.14*	0.82	0.09	6.08**	1.18	3.03**
19	Ganga 8 X Kanika	0.87*	-0.06	1.31	0.19	2.24*	0.49*	-2.14*	-0.34	0.06	4.68**	-6.42*	-0.1
20	Ganga 8 X Virat	0.27	1.03	-4.79**	-0.84*	-12.69**	-1.41**	4.18**	-0.24	-0.22	-6.65**	1.84	-2.13**

Cont.....

S. No.	Cross combinations	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches /plant	No. of pods/pl ant	No. of pods/cl uster	No. of cluster/ plant	No. of seeds/ pod	100 seed weight (g)	Biological yield/plant (g)	Harvest index (%)	Seed yield/pla nt (g)
21	LGG 460 X PDM 139	0.32	-0.1	9.22**	-0.62	-13.13**	-0.68**	-1.19	0.63	-0.62*	-2.97**	-6.46*	-2.34**
22	LGG 460 X Shikha	1.35**	1.83**	1.22	-0.50	-16.30**	-0.45	-3.01**	-0.07	-0.12	-10.75**	-10.01**	-6.07**
23	LGG 460 X Kanika	-1.54**	-2.23**	-8.93**	0.89**	22.58**	0.60*	4.18**	-0.01	0.60*	7.59**	3.63	3.18**
24	LGG 460 X Virat	-0.14	0.53	-1.51	0.22	6.85**	0.53*	0.01	-0.54	0.14	6.13**	12.83**	5.23**
25	HUM 1 X PDM 139	-1.34**	1.36*	-0.91	-0.75*	-3.14**	0.14	-1.3	0.32	-0.56	-2.38**	-8.12*	-3.06**
26	HUM 1 X Shikha	1.69**	0.00	-1.98*	1.92**	6.97**	0.54*	0.01	0.61	1.73**	0.8	4.65	1.69**
27	HUM 1 X Kanika	-2.87**	-1.06	4.28**	-0.73*	-8.46**	-0.57*	-0.38	-0.68	-0.96**	-3.40**	-1.80	-1.89**
28	HUM 1 X Virat	2.52**	-0.30	-1.39	-0.43	4.63**	-0.11	1.67*	-0.25	-0.20	4.99**	5.27	3.25**
29	SL 668 X PDM 139	-0.75*	-1.00	-3.08**	0.04	4.46**	0.12	1.08	0.39	0.06	6.44**	2.28	2.75**
30	SL 668 X Shikha	-1.05**	-1.00	0.70	0.02	-5.62**	-0.72**	0.76	-0.25	-0.41	-3.28**	1.32	-1.04
31	SL 668 X Kanika	1.70**	0.93	-4.05**	0.09	-8.40**	-0.22	-1.40	-0.25	-0.02	4.07**	2.07	2.17**
32	SL 668 X Virat	0.10	1.03	6.43**	-0.17	9.56**	0.81**	-0.44	0.11	0.36	-7.23**	-5.68	-3.88**
33	Pusa Vishal X PDM 139	0.07	-0.63	6.08**	0.17	-1.95	0.16	-1.22	-0.46	-0.54	0.525	-9.08**	-1.66**
34	Pusa Vishal X Shikha	-1.55**	-1.66**	-4.98**	-0.24	10.03**	0.60*	0.78	-0.64	0.06	2.17*	7.28*	2.09**
35	Pusa Vishal x Kanika	1.20**	1.26*	-6.01**	-0.23	1.39	-0.21	1.52	-1.01	0.16	3.40**	9.85**	3.48**
36	Pusa Vishal X Virat	0.27	1.03	4.91**	0.29	-9.47**	-0.55*	-1.08	2.12**	0.31	-6.10**	-8.06*	-3.91**
37	PDM 11 X PDM 139	4.40**	2.36**	-1.56	1.07**	4.16**	-0.25	2.29**	0.01	-0.45	1.27	3.61	1.68**
38	PDM 11 X Shikha	-3.22**	-1.00	-3.90**	-0.91**	12.59**	0.77**	0.93	-0.16	-0.3	0.12	0.01	-0.1
39	PDM 11 X Kanika	-1.12**	-0.40	5.57**	0.25	-5.91**	0.00	-1.59	-0.05	0.65*	-2.02*	-4.66	-1.75**
40	PDM 11 X Virat	-0.05	-0.96	-0.10	-0.41	-10.84**	-0.53*	-1.63	0.2	0.10	0.63	1.03	0.20
	SE (Sij)	0.38	0.55	0.98	0.32	1.00	0.25	0.83	0.57	0.28	0.84	3.18	0.6

*, ** Significant at 5% & 1% level of Significance respectively

Table 4.24: Best general combiners identified based on per se performance and gca effects

S. No.	Characters	Best parents based on		
		Per se performance	gca effects	Per se performance and gca effects
1	Days to 50% flowering	TJM 136	TMB 37, TJM 136, PDM 11, Virat	TJM 136
2	Day to maturity	TJM 136	TJM 136, TMB 37, TJM 196, Virat	TJM 136
3	Plant height (cm)	Ganga 8, Kanika	Pusa Vishal, LGG 460, PDM 11, Kanika	Kanika
4	Number of branches/plant	TMB 37, TJM 196	TJM 196, TMB 37, Ganga 8	TJM 196, TMB 37
5	Number of pods/plant	TJM 196	TJM 3, HUM 1, Kanika, Virat	-
6	Number of pods/cluster	PDM 11, Shikha	SL 668, TJM 3, Kanika	-
7	Number of clusters/plant	TJM 196	Ganga 8, TJM 3, LGG 460, Virat	-
8	Number of seeds/pod	TMB 37	TJM 136, Pusa Vishal	-
9	100 seed weight (g)	SL 668	TJM 196, TJM 36, HUM 1, Shikha	-
10	Biological yield/plant (g)	TJM 196	TJM 196, TMB 37, Ganga 8, LGG 460, HUM 1, SL 668, Shikha, Kanika, Virat	TJM 196
11	Harvest Index (%)	Virat	TJM 196, HUM 1, Shikha	-
12	Seed yield/plant (g)	TJM 196	TJM 196, HUM 1, Shikha, Kanika	TJM 196

Thus, TMB 37, TJM 196 and Pusa Vishal among the lines were considered to be desirable genotypes as these genotypes exhibited significantly high gca effects for number of branches per plant. Whereas all

the testers showed non-significant *gca* effects hence none of them were considered as desirable genotypes for number of branches per plant.

The *sca* effects for number of branches/plant varied from -0.91 (PDM 11 X Shikha) to 1.92 (HUM 1 X Shikha). Six out of 40 crosses viz., HUM 1 X Shikha (1.92), Ganga 8 X PDM 139 (1.10), PDM 11 X PDM 139 (1.07), LGG 460 X Kanika (0.89), TJM 196 X PDM 139 and TJM 136 X PDM 139 (0.63) showed highly significant positive *sca* effects while, significant negative *sca* effects were registered in seven crosses (Table 4.23).

5. Number of pods per plant

Among the lines, highly significant *gca* effects in positive direction for number of pods per plant was recorded by TJM 3 (7.56) followed by Ganga 8 (4.60) and HUM 1 (2.64) while, highly significant *gca* effect in negative direction was exhibited by Pusa Vishal (-4.88), followed by TJM 136 (-4.43), PDM 11 (-2.64), SL 668 (-1.88) and LGG 460 (-1.07). Similarly, among the testers, Kanika (3.27) showed highly significant *gca* effect in positive direction followed by Virat (2.04) while, PDM 139 (-5.57) exhibited highly significant and negative *gca* effect for this trait (Table 4.22)

The parents TJM 3, Ganga 8, HUM 1, Kanika and Virat were considered as desirable parents as these exhibited significantly high *gca* effects for this trait. Hence these parents could be effectively used in further breeding programmes aimed at increasing number of pods per plant in greengram.

Low *sca* effects for this trait was recorded in LGG 460 X Shikha (-16.30) whereas high *sca* effects (22.59) was registered in LGG 460 X Kanika. 16 crosses out of 40 viz., LGG 460 X Kanika (22.59), Ganga 8 X PDM 139 (16.02), PDM 11 X Shikha (12.59), TJM 196 X PDM 139 (2.40), Pusa Vishal X Shikha (10.03), SL 668 X Virat (9.56), HUM 1 X Shikha (6.97), LGG 460 X Virat (6.85), TJM 3 X Virat (6.44), TMB 37 X Virat (5.95), TJM 3 X Shikha (5.39), HUM 1 X Virat (4.63), SL 668 X PDM 139 (4.46), PDM 11 X PDM 139 (4.16), TMB 37 X Kanika (2.51) and Ganga 8 X Kanika (2.2) registered significant *sca* effects in positive direction whereas 13 crosses registered significant *sca* effect in negative direction (Table 4.23).

6. Number of pods per cluster

The magnitude of *gca* effects of lines for number of pods per cluster was low in LGG 460 (-0.51) and high in SL 668 (0.37). Highest positive significant *gca* effect was observed for SL 668 (0.37) and TJM 3 (0.25) among lines whereas, among the testers PDM 139 (-0.16) registered low *gca* effect and Kanika (0.19) recorded high *gca* effect. All the other testers showed non-significant *gca* effects (Table 4.22).

The lines SL 668 and TJM 3 and the tester Kanika were found to be good general combiners for the improvement of number of pods per cluster as these genotypes exhibited significant *gca* effects in positive direction.

The *sca* effects for this trait ranged from -1.41 (Ganga 8 X Virat) to 0.98 (TMB 37 X Virat). Among 40 crosses 10 crosses viz., TMB 37 X Virat (0.98), Ganga 8 X PDM 139 (0.95), SL 668 X Virat (0.81), PDM 11 X Shikha (0.77), Pusa Vishal X Shikha and LGG 460 X Kanika (0.60), HUM 1 X Shikha (0.54), LGG 460 X Virat (0.53), TMB 37 X Kanika (0.50) and Ganga 8 X Kanika (0.49) recorded significant *sca* effects in positive direction. Whereas, 9 crosses registered as significant *sca* effects in negative direction (Table 4.23).

7. Number of clusters per plant

Gca effect varied from -2.07 (TJM 136) to 3.35 (Ganga 8) among the lines and from -1.11 (PDM 139) to 0.84 (Virat) among testers. Among the lines Ganga 8 (3.35), had highly significant *gca* effect in positive direction followed by TJM 3 (1.06) and LGG 460 (0.95). On the contrary, significant *gca* effect in negative direction was recorded in TJM 136 (-2.07) and SL 668 (-1.68). Among testers *gca* effect were highly significant and positive in Virat (0.84) and highly significant and negative in PDM 139 (-1.11).

Among lines, Ganga 8, TJM 3 and LGG 460 and in testers Virat were found to be good general combiners. Hence, these parents could be effectively used in further breeding programmes aimed at increasing the number of clusters per plant (Table 4.22).

The *sca* effects of crosses for number of clusters per plant were found to be low in TJM 3 X PDM 139 (-3.34) and high in Ganga 8 X Virat (4.18). Seven crosses viz., Ganga 8 X Virat (4.18), LGG 460 X Kanika (4.18), TJM

196 X PDM 139 (2.90), TMB 37 X Shikha (2.47), PDM 11 X PDM 139 (2.29), TJM 3 X Kanika (2.23) and HUM 1 X Virat (1.67) recorded significant *sca* effects in positive direction whereas six crosses viz., TJM X PDM 139 (-3.34), LGG 460 X Shikha (-3.01), Ganga 8 X Shikha and Ganga 8 X Kanika (-2.14), TMB 37 X Virat (-2.03) and TJM 196 X Kanika (-1.81) registered significant negative *sca* effects (Table 4.23).

8. Number of seeds per pod

Gca effects for number of seeds per pod varied from PDM 11 (-0.81) to TJM 136 (0.75). None of the lines showed significant positive or significant negative *gca* effects for this trait except TJM 136 which was significantly positive and PDM 11 which was significantly negative. Among testers, this trait varied from PDM 139 (0.29) to Virat (0.28) while none of the testers displayed significant *gca* effect for number of seeds per pod (Table 4.22).

The line TJM 136 could be utilized for the improvement of this trait, as this exhibited significant and positive *gca* effects for number of seeds per pod.

Sca effects for number of seeds per pod varied from -1.02 (TMB 37 X Virat) to 2.12 (Pusa Vishal X Virat). 3 crosses viz., Pusa Vishal X Virat (2.12), TMB 37 X Shikha (1.30) and TJM 136 X Kanika (1.24) recorded positive significant *sca* effects for this trait whereas none of the crosses showed significant *sca* effects for number of seeds per pod (Table 4.23).

9. Hundred seed weight (g)

Low *gca* effect of -0.41 in Pusa Vishal and high *gca* effect of 0.53 in TJM 136 was observed among the lines. Among the lines highly significant positive *gca* effect was recorded in TJM 136 (0.53) followed by HUM 1 (0.34) and TJM 196 (0.28) whereas, highly significant negative *gca* effect was recorded in Pusa Vishal (-0.41). The trait ranged from -0.11 (Virat) to 0.21 (Shikha) among testers. None of the testers showed significant negative *gca* effects whereas positive significant *gca* effect was recorded for Shikha (Table 4.22).

Thus the lines TJM 136, HUM 1, TJM 196 and tester Shikha with positive significant *gca* effect can be effectively used in breeding programme to achieve larger seed size.

Estimates of *sca* effects of crosses for 100 seed weight ranged from -0.96 (HUM 1 X Kanika) to HUM 1 X Shikha (1.73). Highly significant positive *sca* effect for this trait was recorded for HUM 1 X Shikha (1.73) followed by TJM 136 X PDM 139 (0.81), PDM 11 X Kanika (0.65) and LGG 460 X Kanika (0.60). Whereas highly significant negative *sca* effect was recorded for HUM 1 X Kanika (-0.96) followed by TJM 3 X Virat (-0.88), TJM 196 X Shikha (-0.86), LGG 460 X PDM 139 (-0.62) and TJM 136 X Kanika (-0.60) (Table 4.23).

10. Biological yield per pant

Among the lines HUM 1 showed highly significant positive *gca* effect (2.48) followed by TMB 37 (2.10), TJM 196 (1.56), SL 668 (1.46), LGG 460 (1.19) and Ganga 8 (0.95) while Pusa Vishal (-3.99), TJM 136 (-2.75), PDM 11 (-2.13) and TJM 3 (-0.86) expressed significant negative *gca* effects. Among the testers, Virat (1.30) recorded highly significant positive *gca* effect followed by Kanika (1.24) and Shikha (1.09) while PDM 139 (-3.64) displayed highly significant negative *gca* effects (Table 4.22).

The lines HUM 1, TMB 37, TJM 196, SL 668, LGG 460 and Ganga 8 and testers Virat, Kanika and Shikha found to be good combiners. Hence these parents could be effectively used in further breeding programmes aimed at increasing biological yield per plant.

Sca effects for biological yield per plant varied from LGG 460 X Shikha (-10.75) TO LGG 460 X Kanika (7.59). Out of 40 crosses 11 crosses viz., LGG 460 X Kanika (7.59) followed by TJM 136 X PDM 139 (7.20), SL 668 X PDM 139 (6.44), TJM 196 X Virat (6.37), LGG 460 X Virat (6.13), Ganga 8 X Shikha (6.08), HUM 1 X Virat (4.99), Ganga 8 X Kanika (4.68), TJM 136 X Shikha (3.51), Pusa Vishal X Kanika (3.40) and Pusa Vishal X Shikha (2.17) registered significant *sca* effects in positive direction, while 15 crosses exhibited significant negative *sca* effects in negative direction (Table 4.23).

11. Harvest index %

The magnitude of *gca* effects varied from -5.70 (TJM 136) to 6.17 (TJM 196) in lines and from -3.34 (PDM 139) to 4.56 (Shikha) in testers. Among lines, TJM 196 (6.17) and HUM 1 (3.36) and among testers Shikha (4.56) registered significant and positive *gca* effects (Table 4.22). Hence, these

parents could be effectively used in further breeding programmes for obtaining better harvest index.

High *sca* effect of 12.83 was recorded in LGG 460 X Virat whereas, low *sca* effect of -10.01 was recorded in LGG 460 X Shikha. Out of 40 crosses 4 crosses viz., LGG 460 X Virat (12.83), Pusa Vishal X Kanika (9.85), Pusa Vishal X Shikha (7.28) and TJM 3 X PDM 139 (6.56) exhibited significant *sca* effects in positive direction while 8 crosses registered significant *sca* effects in negative direction (Table 4.23).

12. Seed yield per plant

Among lines, high and significant *gca* effects in positive direction were recorded in TJM 196 (2.08) and HUM 1 (1.90) whereas TJM 136 (-2.36), Pusa Vishal (-1.27) and LGG 460 (-0.59) displayed significant negative *gca* effect. Among the testers, Shikha (1.55) accounted for the highest significant *gca* effect in positive direction followed by Kanika (0.47) while PDM 139 (-2.17) recorded significant negative *gca* effect (Table 4.22).

The lines, TJM 196 and HUM 1 and the testers Shikha and Kanika showed significant and positive *gca* effects for this trait. Hence, these parents could be effectively used in further breeding programme aimed at increasing seed yield in greengram.

Estimates of *sca* effects of crosses for seed yield/plant ranged from - 6.07 (LGG 460 X Shikha) to 5.23 (LGG 460 X Virat). 14 crosses recorded significant *sca* effect in positive direction, while 15 crosses exhibited significant *sca* effects in negative direction (Table 4.23).

Table 4.25: Promising cross combinations identified for recombination breeding

S. No.	Characters	Significant gca effects		Possible cross combinations	Sca effects of crosses	Promising crosses for recombination breeding
		Lines	Testers			
1	Days to 50% flowering	TJM 136, TTMB 37, PDM 11	Virat	TJM 136 X Virat, TMB 37 X Virat, PDM 11 X Virat	-4.399**, -0.30, -0.05	TMB 37 X Virat, PDM 11 X Virat
2	Day to maturity	TJM 136, TTMB 37, TJM 196	Virat	TJM 136 X Virat, TMB 37 X Virat, TJM 196 X Virat	.5.13*, 0.95, 1.70**	TMB 37 X Virat
3	Plant height (cm)	Pusa Vishal, PDM 11, LGG 460	Kanika	Pusa Vishal X Kanika, PDM 11 X Kanika, LGG 460 X Kanika	-6.01**, 5.57**, -8.93**	-
4	Number of branches/plant	TJM 196, TMB 37, Ganga 8	-	-	-	-
5	Number of pods/plant	TJM 3, Ganga 8, HUM 1	Kanika, Virat	TJM3 X Kanika, TJM 3 X Virat, Ganga 8 X Kanika, Ganga 8 X Virat, HUM1 X Kanika, HUM1 X Virat	0.37, 6.44**, 2.24*, -12.69**, -8.46**, 4.63**	TJM 3 X Kanika
6	Number of pods/cluster	TJM 3, SL 668	Kanika	TJM 3 X Kanika, SL 668 X Kanika	-0.58*, -0.22	SL 668 X Kanika
7	Number of clusters/plant	Ganga 8, LGG 460, TJM 3	Kanika	Ganga 8 X Kanika, LGG 460 X Kanika, TJM 3 X Kanika	-2.14*, 4.18**, 2.23**	
8	Number of seeds/pod	TJM 136, Pusa Vishal	-	-	-	-
9	100 seed weight (g)	TJM 196, TJM 136, HUM 1	Shikha	TJM 196 X Shikha, TJM 136 X Shikha, HUM1 X Shikha	-0.86**, 0.32, 1.73**	TJM 136 X Shikha
10	Biological yield/plant (g)	TJM 196, TMB 37, Ganga 8, LGG 460, HUM 1, SL 668	Shikha, Kanika, Virat	TJM 196 X Shikha, TJM 196X Kanika, TJM 196 X Virat, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X Shikha, Ganga X Kanika, Ganga 8 X Virat, LGG 460 X Shikha, LGG 460 X Kanika, LGG X Virat, HUM1 X Shikha, HUM1 X Kanika, HUM1 X Virat, SL 668 X Shikha, SL 668 X Kanika, SL 668 X Virat	-1.27, -2.27**, 6.37**, 1.69*, -1.94*, 1.24, 6.08**, 4.68**, -6.65**, -10.75**, 7.59**, 6.13**, 0.8, -3.40**, 4.99**, -3.28**, 4.07**, -7.23**	TJM 196 X Shikha, TMB 37 X Virat, HUM 1 X Shikha
11	Harvest Index (%)	TJM 196, HUM 1	Shikha	TJM 196 X Shikha, HUM 1 X Shikha	-4.03, 4.65	TJM 196 X Shikha, HUM 1 X Shikha
12	Seed yield/plant (g)	TJM 196, HUM 1	Shikha, Kanika	TJM 196 X Shikha, TJM 196 X Kanika, HUM 1 X Shikha, HUM1 X Kanika	-1.58**, -0.73, 1.69**, -1.89**	TJM 196 X Kanika

Table 4.26: Best heterotic cross combinations identified for yield and yield components based on *per se* performance, significant sca effects and standard heterosis

S. No.	Characters	Best heterotic crosses based on		Standard heterosis	Per se performance, sca effects and standard heterosis
		Per se performance	Sca effects		
1	Days to 50% flowering	TJM 136 X Virat, TJM 136 X PDM 139, TMB 37 X Kanika, TMB 37 X Virat	TJM 136 X Virat, TJM 136 X PDM 139, TJM 196 X PDM 139, TJM 196 X Shikha, TMB 37 X Kanika, Ganga 8 X PDM 139, TJM 3 X PDM 139	TJM 136 X PDM 139, TJM 136 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, HUM 1 X PDM 139, HUM 1 X Kanika, PDM 11 X Shikha, PDM 11 X Kanika, PDM 11 X Virat	TJM 136 X Virat, TJM 136 X PDM 139, TMB 73 X Kanika
2	Day to maturity	TJM 136 X Virat, TJM 136 X PDM 139, TMB 37 X PDM 139	TJM 136 X Virat, TMB 37 X PDM 139, Ganga 8 X Shikha	TJM 136 X PDM 139, TJM 136 X Virat, TMB 37 X PDM 139	TJM 136 X Virat, TMB 37 X PDM 139
3	Plant height (cm)	Pusa Vishal X PDM 139, Pusa Vishal X Virat, LGG 460 X PDM 139	LGG 460 X PDM 139, TJM 3 X Shikha, TJM 136 X Kanika, TJM 196 X Kanika, TMB 37 X Kanika, Ganga 8 X Shikha	TJM 196 X PDM 139, TJM 196 X Shikha, TJM 196 X Kanika, TJM 136 X Kanika, TJM 136 X Virat, TJM 3 X PDM 139, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, Ganga X Kanika, LGG 460 X PDM 139, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X PDM 139, HUM 1 X Kanika, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Shikha, SL 668 X Kanika, SL 668 X Virat, Pusa Vishal X PDM 139, Pusa Vishal X Shikha, Pusa Vishal X Kanika, Pusa Vishal X Virat, PDM 11 X PDM 139, PDM 11 X Shikha, PDM 11 X Kanika, PDM 11 X Virat	Pusa Vishal X PDM 139, Pusa Vishal X Virat, LGG 460 X PDM 139
4	Number of branches/plant	HUM 1 X Shikha, TMB 37 X Virat, TMB 37 X Shikha, Ganga X PDM 139, TJM 136 X Virat	Ganga 8 X PDM 139, TJM 136 X PDM 139	TJM 196 X PDM 139, TJM 196 X Shikha, TJM 196 X Virat, TJM 136 X Virat, TMB 37 X Shikha, TMB 37 X Virat, TMB 37 X Kanika, Ganga 8 X Kanika, LGG 460 X Kanika, HUM 1 X Shikha, PDM 11 X PDM 139	HUM 1 X Shikha
5	Number of pods/plant	LGG 460 X Kanika, TJM 3 X Virat, Ganga 8 X PDM 139, TJM 3 X Shikha	Ganga 8 X PDM 139, TJM 196 X PDM 139, TJM 3 X Virat, TMB 37 X Virat, TJM 3 X Shikha, TMB 37 X Kanika, Ganga 8 X Kanika	TJM 196 X PDM 139, TJM 196 X Shikha, TJM 196 X Kanika, TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 136 X Kanika, TJM 136 X Virat, TJM 3 X PDM 139, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, Ganga 8 X Kanika, Ganga 8 X Virat, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X PDM 139, HUM 1 X Shikha, HUM 1 X Kanika, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Shikha, SL 668 X Kanika, SL 668 X Virat, Pusa Vishal X PDM 139, Pusa Vishal X Shikha, Pusa Vishal X Kanika, Pusa Vishal X Virat, PDM 11 X PDM 139, PDM 11 X Shikha, PDM 11 X Kanika, PDM 11 X Virat	LGG 460 X Kanika, TJM 3 X Virat, Ganga 8 X PDM 139, TJM 3 X Shikha

Cont.....

S. No.	Characters	Best heterotic crosses based on		Standard heterosis	Per se performance, sca effects and standard heterosis
		Per se performance	Sca effects		
6	Number of pods/cluster	SL 668 X Virat, TMB 37 X Virat, TMB 37 X Kanika, HUM 1 X Shikha, PDM 11 X Shikha	TMB B37 X Virat, Ganga 8 X PDM 139, TMB 37 X Kanika, Ganga 8 X Kanika	TJM 196 X PDM 139, TJM 196 X Kanika, TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 136 X Kanika, TJM 136 X Virat, TJM 3 X PDM 139, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Kanika, Ganga 8 X Virat, LGG 460 X Kanika, HUM 1 XPDM 139, HUM 1 X Shikha, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Kanika, SL 668 X Virat, Pusa Vishal X Shikha, PDM 11 X Shikha, PDM 11 X Kanika	TMB 37 X Virat, TMB 37 X Kanika
7	Number of clusters/plant	Ganga 8 X Virat, LGG 460 X Kanika, TJM 3 X Kanika, TMB 37 X Kanika	Ganga 8 X Virat, TJM 196 X PDM 139, TMB 37 X Shikha, TJM 3X Kanika, LGG 460 X Kanika, HUM 1 X Virat, PDM 11 X Shikha	TJM 196 X PDM 139, TJM196 X Shikha, TJM 196 X Virat, TJM 136 X Kanika, TJM 136 X Virat, TJMM 3 X Shikha, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, Ganga 8 X Kanika, Ganga 8 X Virat, LGG 460 X PDM 139, LGG 460 X Shikha., LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X Shikha, HUM 1 X Kanika, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Shikha, SL 668 X Virat, Pusa Vishal X Shikha, Pusa Vishal X Kanika, Pusa Vishal X Virat, PDM 11 X PDM 139, PDM 11 X Shikha, PDM 11 X Virat	Ganga 8 x Virat, LGG 460 X Kanika, TJM 3 X Kanika, TMB 37 X Shikha
8	Number of seeds/pod	Pusa Vishal X Virat, TJM 136 X Kanika, TMB 37 X Shikha, TJM 136 X Virat, HUM 1 X Shikha, Ganga 8 X Shikha	TJM 136 X Kanika, TM 37 X Shikha, Pusa Vishal X Virat	TJM 136 X Kanika, TMB 37 X Shikha, Pusa Vishal X Virat	Pusa Vishal X Virat, TJM 136 X Kanika, TMB 37 X Shikha
9	100 seed weight (g)	HUM 1 X Shikha, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 3X PDM 139	TJM 136 X PDM 139, TJM 3 X PDM 139, LGG 460 X Kanika, HUM 1 X Shikha, PDM 11 X Kanika	TJM 196 X PDM 139, TJM 196 X Kanika, TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 3 X PDM 139, LGG 460 X Kanika, HUM 1 X Shikha, PDM 11 X Kanika, SL 668 X Virat	HUM 1 X Shikha, TJM 136 X PDM 139, TJM 3 X PDM 139

Cont.....

S. No.	Characters	Best heterotic crosses based on		Standard heterosis	Per se performance, sca effects and standard heterosis
		Per se performance	Sca effects		
10	Biological yield/plant (g)	LGG 460 X Kanika, TJM 196 X Virat, HUM 1 X Virat, LGG 460 X Virat, Ganga 8 X Shikha	TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TMB 37 X Shikha, Ganga 8 X kanika, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Kanika, Pusa Vishal X Shikha, Pusa Vishal X Kanika	TJM 196 X PDM 139, TJM196 X Shikha, TJM 196 X kanika, TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 136 X Virat, TJM 3 X PDM 139. TJMM 3 X Shikha, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, Ganga 8 X Kanika, Ganga 8 X Virat, LGG 460X PDM 139, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X PDM 139, HUM 1 X Shikha, HUM 1 X Kanika, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Shikha, SL 668 X Kanika, SL 668 X Virat, Pusa Vishal X PDM 139, Pusa Vishal X Shikha, Pusa Vishal X Kanika, PDM 11 X PDM 139, PDM 11 X Shikha, PDM 11 X Kanika, PDM 11 X Virat	LGG 460 X Kanika, TJM 196 X Virat, HUM 1 X Virat, LGG 460 X Virat
11	Harvest Index (%)	HUM 1 X Shikha, Pusa Vishal X Shikha, Pusa Vishal X Kanika, TJM 3 X Shikha	TJM 3 X PDM 139, LGG 460 X Virat, Pusa Vishal X Shikha, Pusa Vishal X Kanika	TJM 196 X Shikha, TJM 196 X Kanika, TJM 196 X Virat, TJM 136 X Virat, TJM 3 X Shikha, Ganga 8 X Shikha, LGG 460 X Virat, HUM 1 X Shikha, HUM 1 X Virat, Pusa Vishal X Shikha, Pusa Vishal X Kanika, PDM 11 X Shikha, PDM 11 X Kanika	Pusa Vishal X Shikha, Pusa Vishal X Kanika
12	Seed yield/plant (g)	TJM 196 X Virat, HUM 1 X Virat, HUM 1X Shikha, Ganga 8 X Shikha, LGG 460 X Virat	TJM 196 X VIRAT, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 3 X Shikha, Ganga 8 X Shikha, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X Shikha, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Kanika, Pusa Vishal X Shikha, Pusa Vishal X Kanika, PDM 11 X PDM 139	TJM 196 X PDM 139, TJM196 X Shikha, TJM 196 X kanika, TJM 196 X Virat, TJM 136 X PDM 139, TJM 136 X Shikha, TJM 3 X PDM 139. TJMM 3 X Shikha, TJM 3 X Shikha, TJM 3 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, Ganga 8 X Kanika, Ganga 8 X Virat, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X Shikha, LGG 460X PDM 139, LGG 460 X Shikha, HUM 1 X Kanika, HUM 1 X Virat, SL 668 X PDM 139, SL 668 X Shikha, Pusa Vishal X PDM 139, Pusa Vishal X Shikha, Pusa Vishal X Kanika, PDM 11 X PDM 139, PDM 11 X Shikha, PDM 11 X Kanika, PDM 11 X Virat	TJM 196 X Virat, HUM 1 X Virat, HUM 1 X Shikha, Ganga X Shikha, LGG 460 X Virat

4.8 Generation Mean Analysis

The mean performance of six generations with respect to yield associated traits along with standard errors and the estimates of individual scaling tests (A, B and C) and genetic effects viz., additive (d), dominance (h), additive x additive (i), additive x dominance (j), and dominance x dominance (l) were collated in table 4.27 to 4.50 and presented the same on character wise.

1. Days to 50% flowering

The crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika flowered early as compared with early flowering parent. All the segregating generations of the crosses flowered early as compared with early flowering parent except Ganga 8 X Shikha which had mean value intermediate to its corresponding parents (Table 4.27).

In backcross population, the mean produced was much lower than their recurrent parent, except in TJM 196 X Kanika (B_1), HUM 1 X Shikha (B_2), Ganga 8 X Shikha (B_2) and LGG 460 X Virat (B_2) population had higher means than their corresponding recurrent parent.

Significance of one or more scaling tests indicated the presence of epistatic effects in all the crosses (Table 4.28). Estimates of mean (m) effects were positive and significant for all the crosses. Estimates of additive (d) effects were positive and significant in three crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat while negative and significant in TJM 196 X Kanika. All the crosses exhibited highly positive and significant dominance (h) as well as additive x additive (i) interaction effects with higher magnitude except in HUM 1 X Shikha and Ganga 8 X Shikha which had non significant effects. Additive x dominance (j) gene effects were found significant and negative in the crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha, and LGG 460 X Kanika while significant and positive in TJM 196 X Kanika. Dominance x dominance (l) interaction effects were negative and significant in LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika while non significant in HUM 1 X Shikha and Ganga 8 X Shikha. The direction of dominance (h) and dominance x dominance (l) components were dissimilar for all crosses except for HUM 1 X Shikha.

Table 4.27: Estimates of generation mean analysis and standard errors for days to 50% flowering

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	43.00 ± 0.00	40.67±0.33	40.33±0.33	40.33±0.33	40.00±0.58	41.67±0.33
2	Ganga 8 X Shikha	45.33±0.33	40.67 ± 0.33	39.67 ± 0.67	41.00 ± 0.58	41.00 ± 0.58	42.33 ± 0.33
3	LGG 460 X Virat	44.67 ± 0.33	40.67 ± 0.33	39.33 ± 0.33	38.33 ± 0.33	42.00 ± 0.00	41.00 ± 0.58
4	LGG 460 X Kanika	44.67 ± 0.33	44.33 ± 0.67	38.67 ± 0.33	33.33 ± 0.33	40.00 ± 0.58	41.33 ± 0.33
5	TJM 196 X Kanika	41.33 ± 0.33	44.33 ± 0.67	40.67 ± 0.33	38.67 ± 0.33	42.00 ± 0.58	41.67 ± 0.33

Table 4.28: Scaling tests and estimates of gene effects for days to 50% flowering in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	- 3.33**±1.20	2.33**± 0.82	-3.00 *± 1.53	39.83** ± 1.89	1.167**± 0.17	1.5 ± 4.85	2.00 ± 1.89	-2.8**± 0.69	1.00 ± 3.07	C
2	Ganga 8 X Shikha	-3.00** ± 1.37	4.33** ± 1.00	-1.33 ± 2.71	40.33** ± 2.68	2.33** ± 0.24	3.33 ± 6.19	2.67 ± 2.67	-3.67** ± 0.71	-4.00 ± 3.80	D
3	LGG 460 X Virat	-3.33**± 1.29	2.00 ± 1.25	-10.67**± 1.56	30.00** ± 1.78	2.00** ± 0.24	24.00** ± 4.44	12.67**± 1.76	-1.00± 0.62	-14.67**± 2.79	D
4	LGG 460 X Kanika	-3.33** ± 1.25	-0.33 ± 1.00	-33.00** ± 1.67	15.17** ± 1.92	0.167 ± 0.37	49.17** ± 4.95	29.33** ± 1.89	-1.5* ± 0.76	- 25.67**±3.15	D
5	TJM 196 X Kanika	2.00 ± 1.25	-1.67 ± 1.00	-12.33**± 1.67	30.17** ± 1.92	-1.5** ± 0.37	23.5** ± 4.95	12.67**± 1.89	1.83* ± 0.76	-13.00**± 3.14	D

*, ** Significant at 5% and 1% level of significance

2. Days to maturity

Mean number of days to maturity of the crosses viz., Ganga 8X Shikha, LGG 460 X Kanika and TJM 196 X Kanika were found early as compared with early maturing parent, while in case of Hum 1 X Shikha the mean days to maturity was identical to the mean of both parents, whereas in the cross LGG 60 X Virat the mean days to maturity was same as early maturing parent (Table 4.29). In F_2 population of the crosses LGG 460 X Virat and LGG 460 X Kanika had mean values lower than their corresponding parents, while it was higher than their corresponding parents in the case of HUM 1 X Shikha, whereas intermediate to both of the parents in case of TJM 196 X Kanika and mean days to maturity was identical to early maturing parent for Ganga 8 X Shikha.

Backcross population of these crosses viz., TJM 196 X Kanika (B_1), HUM 1 X Shikha (B_2), Ganga 8 X Shikha (B_2) and LGG 460 X Virat (B_2) had mean values higher as compared with their recurrent parent, while in HUM 1 Shikha (B_1), Ganga 8 X Shikha (B_1), LGG 460 X Virat (B_1), LGG 460 X Kanika (B_1), LGG 460 X Kanika (B_2) and TJM 196 X Kanika (B_2) mean values were lower than their recurrent parents.

Among the five crosses studied the A, B and C scales were non-significant in the case of HUM 1 X Shikha which indicated the adequacy of additive – dominance model for this cross, while the remaining four crosses viz., Ganga 8 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika had predominantly positive mean (m) effects. Additive (d) gene effect was positive and significant in Ganga 8 X Shikha and it was significant and negative in TJM 196 X Kanika. Dominance (h) effects and additive x additive (i) interaction effects were positive and significant in LGG 460 X Virat and LGG 460 X Kanika while it was non-significant for rest of the crosses. Additive x dominance (j) interaction effect was positive and significant in Ganga 8 X Shikha and non-significant for rest of the crosses whereas dominance x dominance (l) interaction effect was positive and significant in LGG 460 X Virat and negatively significant in LGG 460 X Kanika. The sign of (h) and (l) component were in opposite direction for all crosses except for LGG 460 X Virat (Table 4.30).

Table 4.29: Estimates of generation mean analysis and standard errors for days to maturity

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	66.67 ± 0.33	66.67 ± 0.33	66.67 ± 0.33	67.33 ± 0.33	66.33 ± 0.33	67.00 ± 0.58
2	Ganga 8 X Shikha	69.67 ± 1.20	66.67 ± 0.33	64.33 ± 0.33	66.67 ± 0.33	65.33 ± 0.88	69.00 ± 0.58
3	LGG 460 X Virat	69.00 ± 1.00	67.67 ± 0.33	67.67 ± 0.33	64.67 ± 0.33	68.33 ± 0.67	69.00 ± 0.00
4	LGG 460 X Kanika	69.00 ± 1.00	69.33 ± 0.33	65.67 ± 0.33	62.33 ± 0.33	65.67 ± 0.67	67.00 ± 0.58
5	TJM 196 X Kanika	66.33 ± 0.67	69.33 ± 0.33	64.67 ± 0.33	66.67 ± 0.33	67.67 ± 0.33	67.00 ± 1.00

Table 4.30: Scaling tests and estimates of gene effects for days to maturity in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-0.67 ± 0.82	0.67 ± 1.25	2.67 ± 1.56	69.33** ± 1.90	-5.33 ± 0.53	-5.33 ± 4.87	-2.67 ± 1.89	-0.67 ± 0.71	2.67 ± 3.09	D
2	Ganga 8 X Shikha	-3.33 ± 2.16	7.00**±1.25	1.67 ± 1.94	66.17** ± 2.57	1.50* ± 0.62	3.83 ± 7.12	2.00 ± 2.49	5.16** ± 1.22	-5.67 ± 4.64	D
3	LGG 460 X Virat	0.00 ± 1.70	2.67** ± 0.22	-13.33** ± 1.83	52.33** ± 1.96	0.67 ± 0.53	34.00** ± 5.07	16.00**± 1.89	-1.33 ± 0.85	18.67**± 3.23	C
4	LGG 460 X Kanika	-3.33 ± 1.70*	-1.00 ± 1.25	-20.33** ± 1.83	53.17** ± 2.27	-0.17 ± 0.53	24.17** ± 6.14	16.00** ± 2.21	-1.67 ± 1.03	-11.67** ± 3.97	D
5	TJM 196 X Kanika	4.33** ± 1.00	0.67± 1.25	1.67 ± 1.67	65.17** ± 2.52	-1.50** ± 0.37	6.50 ± 6.96	2.67 ± 2.50	2.17 ± 1.11	-7.00 ± 4.53	D

*, ** Significant at 5% and 1% level of significance

3. Plant height

F₁ generations viz., HUM 1 Shikha, Ganga 8 X Shikha and LGG 460 X Kanika recorded lower mean plant height than their parental value while crosses viz., LGG 460 X Virat and TJM 196 X Kanika exhibited mean plant height intermediate to both of the parents. In F₂ population lower mean values were observed in HUM 1 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika whereas higher mean plant height was recorded in Ganga 8 X Shikha when compared with their parental values.

Backcross population viz., HUM 1 X Shikha (B₁), HUM 1 X Shikha (B₂), Ganga 8 X Shikha (B₁), LGG 460 X Kanika (B₂) and TJM 196 X Kanika (B₁ and B₂) recorded lower mean values than their recurrent parent, while, in Ganga 8 X Shikha (B₂), LGG 460 X Virat (B₁ and B₂) and LGG 460 X Kanika (B₁) higher mean values were found when compared with their recurrent parent (Table 4.31).

Inadequacy of simple additive – dominance model to explain the genetic control of this trait was suggested by significance of one or more scaling tests in all the crosses studied. Mean (m) effect was positive and significant for all the crosses. The additive (d) gene effects were significant and positive for Ganga 8 X Shikha and LGG 460 X Virat whereas cross combinations viz., LGG 460 X Kanika and TJM 196 X Kanika had significant and negative (d) effects. The dominance (h) gene effects were significant and positive in HUM 1 X Shikha and Ganga 8 X Shikha while significant and negative in LGG 460 X Virat and LGG 460 X Kanika (Table 4.32).

Among the interaction components, additive x additive (i) effects were negative and significant in HUM 1 X Shikha and Ganga 8 X Shikha whereas positive and significant in LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika. The additive x dominance (j) interaction effect was positive and significant in TJM 196 X Kanika and negatively significant in Ganga 8 X Shikha and LGG 460 X Virat whereas, non significant in HUM 1 X Shikha and LGG 460 X Kanika. Dominance x dominance (l) interaction effects were significant and positive in HUM 1 X Shikha, Ganga 8 X Shikha and TJM 196 X Kanika while significant and negative in LGG 460 X Virat and LGG 460 X Kanika. The signs of (h) and (l) components were dissimilar for all crosses.

Table 4.31: Estimates of generation mean analysis and standard errors for plant height (cm)

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	47.00 ± 0.90	47.37 ± 1.42	39.70 ± 0.93	40.00 ± 0.25	39.57 ± 0.19	37.92 ± 0.67
2	Ganga 8 X Shikha	52.77 ± 1.33	47.37 ± 1.42	46.27 ± 0.93	52.87 ± 0.18	43.30 ± 1.10	48.67 ± 0.18
3	LGG 460 X Virat	48.67 ± 1.35	40.93 ± 1.27	45.03 ± 0.93	46.10 ± 0.60	48.77 ± 0.73	47.47 ± 0.08
4	LGG 460 X Kanika	48.67 ± 1.35	60.47 ± 1.52	40.21 ± 1.42	41.53 ± 0.07	48.70 ± 0.95	53.33 ± 1.04
5	TJM 196 X Kanika	41.80 ± 1.33	60.47 ± 1.52	49.70 ± 0.93	36.20 ± 0.80	39.63 ± 0.37	39.77 ± 0.78

Table 4.32: Scaling tests and estimates of gene effects for plant height (cm) in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-7.57** ± 1.34	-11.23**± 2.16	-13.77** ± 2.70	52.22** ± 1.91	-0.18 ± 0.84	-36.36** ± 5.34	-5.03**± 1.71	1.83 ± 1.08	23.84**± 3.87	D
2	Ganga 8 X Shikha	-12.43** ± 2.7	3.71* ± 1.74	18.80** ± 2.78	77.59** ± 2.53	2.70**± 0.98	-67.56** ± 7.50	-27.52** ± 2.34	-8.07** ± 1.48	36.24**± 5.26	D
3	LGG 460 X Virat	3.83 ± 2.19	8.97** ± 1.58	4.73 ± 3.56	36.73** ± 2.97	3.87**± 0.93	29.17** ± 7.17	8.07** ± 2.83	-2.57**± 1.18	-20.87**± 4.62	D
4	LGG 460 X Kanika	8.63** ± 2.73	6.10* ± 2.94	-23.20** ± 3.50	16.63** ± 3.00	-5.90** ± 1.02	76.13** ± 9.09	37.93**± 2.82	1.27 ± 1.73	-52.67**± 6.62	D
5	TJM 196 X Kanika	-12.23** ± 1.78	-30.63**± 2.38	-56.86** ± 4.22	37.13** ± 3.78	-9.33** ± 1.01	-16.30* ± 8.83	14.00**± 3.64	9.20**± 1.33	28.87** ± 5.46	D

*, ** Significant at 5% and 1% level of significance

4. Number of branches per plant

In F_1 population, crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Kanika exhibited higher mean value for number of branches per plant than their better parents, while mean recorded by LGG 460 X Virat was intermediate between its corresponding parents. TJM 196 X Kanika recorded lower mean value than its corresponding parents. F_2 population of the crosses viz., HUM 1 X Shikha and LGG 460 X Virat showed higher mean values when compared with their better parents whereas, crosses Ganga 8 X Shikha and TJM 196 X Kanika showed lower mean values than their corresponding parents. The mean value was intermediate between corresponding parents in the case of LGG 460 X Kanika. Mean of all the backcrosses were generally higher than their recurrent parents except for Ganga 8 X Shikha (B_1 and B_2) (Table 4.33).

Significance of one or more scaling tests suggested the presence of non-allelic interactions. Mean (m) effect was positive and significant in crosses viz., Ganga 8 X Shikha and negative and significant for HUM 1 X Shikha. Additive (d) gene effects were significant and negative in HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika while non-significant for rest of the two crosses. Dominance (h) gene effects were significant and positive in all the crosses except in Ganga 8 X Shikha which showed significant and negative (h) effect.

Among the interaction effects positive and significant additive x additive (i) effects were recorded in crosses HUM 1 X Shikha, LGG 460 X Kanika and TJM 196 X Kanika and positive and significant effects were observed in Ganga 8 X Shikha and LGG 460 X Virat. Additive x dominance (j) interaction effect was significant and negative in all crosses except LGG 460 X Kanika. Dominance x dominance (l) interaction effect was positive and significant in Ganga 8 X Shikha whereas it was negative and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika and non-significant in LGG 460 X Kanika. The direction for dominance (h) and dominance x dominance (l) gene effects were dissimilar for all crosses (Table 4.34).

Table 4.33: Estimates of generation mean analysis and standard errors for number of branches/plant

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	1.20 ± 0.11	2.10 ± 0.36	4.77 ± 0.89	2.40 ± 0.35	2.53 ± 0.33	5.32 ± 0.34
2	Ganga 8 X Shikha	2.70 ± 0.10	2.10 ± 0.36	2.80 ± 0.60	1.40 ± 0.12	1.27 ± 0.07	1.73 ± 0.07
3	LGG 460 X Virat	1.63 ± 0.09	2.83 ± 0.23	2.73 ± 0.04	3.40 ± 1.20	3.47 ± 0.37	6.07 ± 0.47
4	LGG 460 X Kanika	1.63 ± 0.09	3.07 ± 0.33	3.33 ± 0.41	2.20 ± 0.42	3.60 ± 0.31	3.13 ± 0.73
5	TJM 196 X Kanika	3.53 ± 0.13	3.07 ± 0.33	2.47 ± 0.18	2.93 ± 0.18	3.37 ± 0.03	3.60 ± 0.12

Table 4.34 Scaling tests and estimates of gene effects for number of branches/plant

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-0.90 ± 1.11	3.77** ± 1.17	-3.32 ± 2.28	-4.45** ± 1.69	-0.45* ± 0.19	18.18** ± 4.10	6.10** ± 1.68	-2.33** ± 0.51	-8.97** ± 2.97	D
2	Ganga 8 X Shikha	-2.97** ± 0.62	-1.43* ± 0.71	-4.80** ± 1.34	2.00** ± 0.53	0.30 ± 0.19	-3.20* ± 1.36	0.40 ± 0.49	-0.77** ± 0.21	4.00** ± 1.39	D
3	LGG 460 X Virat	2.56** ± 0.75	6.57** ± 0.96	3.67 ± 4.80	-3.23 ± 4.95	-0.60** ± 0.12	20.57* ± 10.25	5.47 ± 4.95	-2.00** ± 0.61	-14.60** ± 5.37	D
4	LGG 460 X Kanika	2.23** ± 0.74	-0.13 ± 1.56	-2.57 ± 1.88	-2.32 ± 2.30	-0.72** ± 0.17	12.42* ± 5.85	4.67* ± 2.30	1.18 ± 0.81	-6.77 ± 3.69	D
5	TJM 196 X Kanika	0.73** ± 0.23	1.67** ± 0.44	0.20 ± 0.87	1.10 ± 0.77	0.23 ± 0.18	5.97** ± 1.68	2.20** ± 0.75	-0.47* ± 0.22	-4.60** ± 0.99	D

*, ** Significant at 5% and 1% level of significant

5. Number of pods per plant

Mean number of pods per plant varied widely among generations. F_1 generations of all the crosses produced mean values of higher magnitude than their corresponding better parent except for TJM 196 X Kanika where it was slightly less than its better parent. All the F_2 progenies produced mean values of lower magnitude than their corresponding better parent except in LGG 460 X Virat where it was higher. Means of all the backcrosses exceeded their corresponding parental means, while in TJM 196 X Kanika (B_1) and Ganga 8 X Shikha (B_2) were slightly less than the recurrent parent (Table 4.35).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. Mean (m) effects were negative and significant in all the crosses while positive and significant in LGG 460 X Virat. The additive (d) gene effects were positive and significant in all the crosses except for HUM 1 X Shikha and Ganga 8 X Shikha that showed significant and negative additive gene effects. Dominance (h) gene effects and additive x additive (i) interactions effects were significant and positive in all the crosses. Additive x dominance (j) interaction effects were negative and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika while it was significant and positive in Ganga 8 X Shikha and non-significant in LGG 460 X Kanika. Dominance x dominance (l) interaction effects for significant and negative in all the crosses. The signs of (h) and (l) components were opposite for all the crosses (Table 4.36).

Table 4.35: Estimates of generation mean analysis and standard errors for number of pods/plant

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	23.87 ± 1.81	40.17 ± 0.15	54.63 ± 0.92	34.10 ± 0.21	34.13 ± 0.58	85.98 ± 0.63
2	Ganga 8 X Shikha	27.27 ± 1.10	40.17 ± 0.15	44.03 ± 0.83	21.10 ± 0.75	38.73 ± 0.96	34.97 ± 0.77
3	LGG 460 X Virat	30.68 ± 0.96	22.93 ± 0.37	52.57 ± 0.09	52.07 ± 0.57	51.67 ± 0.73	62.50 ± 1.01
4	LGG 460 X Kanika	30.68 ± 0.96	26.40 ± 0.58	69.53 ± 0.52	29.80 ± 0.50	54.53 ± 0.57	52.30 ± 0.99
5	TJM 196 X Kanika	42.50 ± 0.32	26.40 ± 0.58	40.20 ± 0.81	40.30 ± 0.26	33.70 ± 1.01	71.43 ± 0.47

Table 4.36: Scaling tests and estimates of gene effects for number of pods/plant in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-10.23**± 2.34	77.17** ± 1.57	-36.90** ± 2.72	-71.82** ± 2.12	-8.15** ± 0.91	297.22**± 6.14	103.83**± 1.91	-43.70**± 1.25	-170.77** 4.38	D
2	Ganga 8 X Shikha	6.17** ± 2.36	-14.27** ± 1.75	-71.10** ± 3.61	-29.28** ± 3.92	-6.45** ± 0.55	128.22**± 9.69	63.00** ± 3.88	10.22**± 1.35	-54.90**± 6.90	D
3	LGG 460 X Virat	20.09** ± 1.76	49.50** ± 2.07	49.52** ± 2.51	6.74* ± 3.42	3.87** ± 0.52	135.49**± 8.92	20.07** ± 3.39	-14.71** ± 1.36	-89.66**± 5.60	D
4	LGG 460 X Kanika	8.86** ± 1.58	8.67** ± 2.12	-76.94** ± 2.53	-65.93** ± 3.09	2.14** ± 0.56	247.45**± 8.12	94.47** ± 3.04	0.10 ± 1.27	-111.99**± 5.21	D
5	TJM 196 X Kanika	-15.30** ± 2.21	76.27** ± 1.37	11.90** ± 2.04	-14.62** ± 2.50	8.05** ± 0.33	164.85** ± 7.15	49.07** ± 2.48	-45.78** ± 1.17	-110.03** ± 4.92	D

*, ** Significant at 5% and 1% level of significance

6. Number of pods per cluster

F₁ generations of crosses viz., Ganga 8 X Shikha, LGG 460 X Kanika and TJM 196 X Kanika produced lower mean values than their corresponding better parent while HUM 1 X Shikha and LGG 460 X Virat showed higher mean values for number of pods per cluster than their corresponding better parent. F₂ population recorded lower mean value than corresponding better parent for all of them except in Ganga 8 X Shikha. Backcross populations exhibited higher mean values than their corresponding recurrent parent in all the crosses except in Ganga 8 X Shikha (B₁ and B₂), TJM 196 X Kanika (B₁) and LGG 460 X Kanika (LGG 460 X Kanika (B₂)) (Table 4.37).

Among the five crosses studied the A, B and C scales were non-significant in the case of TJM 196 X Kanika which indicated the adequacy of additive – dominance model for this cross. Mean (m) effects were significant and positive in Ganga 8 X Shikha and TJM 196 X Kanika while it was significant and negative in LGG 460 X Virat and non-significant in HUM 1 X Shikha and LGG 460 X Kanika. Additive (d) gene effects were significant and negative in HUM 1 X Shikha and LGG 460 X Kanika whereas it was non-significant in rest of the crosses. Dominance (h) gene effects were positive and significant in HUM 1 X Shikha and LGG 460 X Virat while non-significant in rest of the 3 crosses.

Among the epistatic interaction effects additive x additive (i) gene effects were significant and positive in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat while, non significant for rest of the two crosses. Additive x dominance (j) gene effects were negative and significant in HUM 1 X Shikha and TJM 196 X Kanika and non-significant in rest of the three crosses. Dominance x dominance (l) interaction effects were significant and negative in HUM 1 X Shikha and LGG 460 X Virat. Signs of (h) and (l) components were opposite in all 5 crosses (Table 4.38).

Table 4.37: Estimates of generation mean analysis and standard errors for number of pods/cluster

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	3.13 ± 0.15	3.78 ± 0.10	4.32 ± 0.16	3.47 ± 0.22	3.45 ± 0.08	5.12 ± 0.24
2	Ganga 8 X Shikha	3.74 ± 0.12	3.78 ± 0.10	3.18 ± 0.13	2.88 ± 0.09	3.56 ± 0.27	3.25 ± 0.17
3	LGG 460 X Virat	3.01 ± 0.11	3.09 ± 0.09	3.65 ± 0.10	2.72 ± 0.05	3.86 ± 0.14	3.95 ± 0.08
4	LGG 460 X Kanika	3.01 ± 0.11	4.01 ± 0.28	3.89 ± 0.21	4.22 ± 0.25	7.47 ± 3.72	3.21 ± 0.18
5	TJM 196 X Kanika	3.85 ± 0.24	4.01 ± 0.28	3.86 ± 0.41	3.32 ± 0.23	3.27 ± 0.19	4.03 ± 0.20

Table 4.38: Scaling tests and estimates of gene effects for number of pods/cluster in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-0.56* ± 0.27	2.14** ± 0.51	-1.68 ± 0.97	0.19 ± 1.03	-0.33** ± 0.09	8.98** ± 2.35	3.27 ** ± 1.03	-1.35** ± 0.26	-4.85** ± 1.39	D
2	Ganga 8 X Shikha	0.21 ± 0.56	-0.47 ± 0.37	-2.37** ± 0.46	1.65* ± 0.73	-0.02 ± 0.08	3.37 ± 2.03	2.11** ± 0.72	0.34 ± 0.32	-1.85 ± 1.34	D
3	LGG 460 X Virat	1.05** ± 0.33	1.16** ± 0.21	-2.51** ± 0.32	-1.66** ± 0.40	-0.04 ± 0.07	12.23** ± 1.10	4.71** ± 0.39	-0.05 ± 0.18	-6.92** ± 0.47	D
4	LGG 460 X Kanika	8.04 ± 7.45	-1.49** ± 0.50	2.07 ± 1.11	0.97 ± 7.52	-0.50** ± 0.15	15.89 ± 22.46	4.48 ± 7.52	4.77 ± 1.28	-11.03 ± 14.96	D
5	TJM 196 X Kanika	-1.17 ± 0.61	0.19 ± 0.64	-2.31 ± 1.27	2.60* ± 1.08	-0.08 ± 0.18	1.61 ± 2.56	1.33 ± 1.06	-0.68*± 0.33	-0.35 ± 1.69	D

*, ** Significant at 5% and 1% level of significance

7. Number of clusters per plant

Mean values for number of clusters per plant in F_1 generation was higher than the better parent in all the crosses except in TJM 196 X Kanika which produced intermediate mean value between corresponding parents. Mean value in F_2 generation was lower than better parent in case of HUM 1 X Shikha whereas, it was higher than mean value of better parent in LGG 460 X Virat, and TJM 196 X Kanika while, intermediate mean value between corresponding parents was produced in Ganga 8 X Shikha and LGG 460 X Kanika. Means of all Backcrosses were higher than corresponding recurrent parents except in TJM 196 X Kanika (B_1) (Table 4.39).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. Mean (m) effects were significant and negative in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Kanika while, it was significant and positive for LGG 460 X Virat and non significant for TJM 196 X Kanika. Additive (d) gene effects were significant and positive in LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika while, significant and negative in HUM 1 X Shikha and Ganga 8 X Shikha. Dominance (h) gene effects and additive x additive (i) interaction effects were significant and positive in all crosses except LGG 460 X Virat which exhibited negative significant (h) effect. Additive x dominance (j) gene effects were negative and significant in all crosses except Ganga 8 X Shikha which was positive and significant. Dominance x dominance (l) gene effects were negative and significant in HUM 1 X Shikha, Ganga 8 X Shikha and TJ 196 X Kanika while non-significant for rest of the two crosses. The signs of (h) and (l) components were dissimilar for all crosses (Table 4.40).

8. Number of seeds per pod

F_1 generation produced intermediate mean values between its corresponding parents for number of seeds/pod whereas HUM 1 X Shikha and TJM 196 X Kanika showed higher mean values than corresponding better parent while Ganga 8 X Shikha recorded same mean value as that of its better parent. F_2 population recorded lower mean than better parent in HUM 1

Table 4.39: Estimates of generation mean analysis and standard errors for number of clusters/plant

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	7.63 ± 0.62	10.63 ± 0.30	12.70 ± 0.51	9.93 ± 0.73	9.90 ± 0.15	16.87 ± 0.79
2	Ganga 8 X Shikha	7.30 ± 0.26	10.36 ± 0.30	13.90 ± 0.60	7.33 ± 0.07	11.00 ± 0.80	10.80 ± 0.31
3	LGG 460 X Virat	10.18 ± 0.10	7.43 ± 0.12	14.43 ± 0.41	19.13 ± 0.42	13.43 ± 0.37	15.87 ± 0.55
4	LGG 460 X Kanika	10.18 ± 0.10	6.63 ± 0.35	17.97 ± 0.94	7.10 ± 0.32	10.87 ± 3.59	16.40 ± 0.85
5	TJM 196 X Kanika	11.13 ± 0.74	6.63 ± 0.35	10.67 ± 1.24	12.23 ± 0.72	10.34 ± 0.50	17.80 ± 0.81

Table 4.40: Scaling tests and estimates of gene effects for number of clusters/plant in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	- 0.53±0.86	10.40**± 1.68	-3.93 ± 3.18	-4.67± 3.36	-1.50**± 0.34	41.03** ± 7.68	13.80** ± 3.34	-5.47** ± 0.87	-23.67**± 4.52	D
2	Ganga 8 X Shikha	0.80 ± 1.73	-2.93**± 0.91	-16.40**± 1.30	-5.30**± 1.75	-1.67**± 0.20	31.33** ± 5.24	14.27** ± 1.73	1.87* ± 0.88	-12.13**± 3.66	D
3	LGG 460 X Virat	2.25** ± 0.85	9.87** ± 1.17	30.05** ± 1.87	26.74**± 2.13	1.37**± 0.08	-18.12**± 5.19	-17.93 ± 2.13	-3.81** ± 0.66	5.81 ± 3.23	D
4	LGG 460 X Kanika	6.41 ± 7.23	8.20** ± 1.97	-24.35**± 2.30	-17.73*± 7.49	1.77**± 0.18	63.61** ± 22.29	26.13** ± 7.48	-7.31** ± 3.69	-27.92 ± 14.92	D
5	TJM 196 X Kanika	-1.11 ± 1.76	18.30** ± 2.07	9.83* ± 3.88	1.53 ± 3.47	2.25**± 0.41	33.68** ± 8.28	7.35* ± 3.44	-9.71** ± 1.04	-24.54**± 5.44	D

*, ** Significant at 5% and 1% level of significance

X Shikha, Ganga 8 X Shikha and TJM 196 X Kanika while higher mean than better parent was recorded in LGG 460 X Kanika and intermediate value of mean between its corresponding parents was observed in LGG 460 X Virat. Mean recorded by all backcrosses was higher than corresponding recurrent parent expect in Ganga 8 X Shikha (B_1 and B_2), LGG 460 X Virat (B_2) and LGG 460 X Virat (B_2) (Table 4.41).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. Mean (m) effect was positive and significant in all crosses except HUM 1 X Shikha. The additive (d) gene effect was significant and negative in LGG 460 X Virat while non-significant in rest of the crosses. Dominance (h) gene effects were positive and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika and non-significant values were recorded in rest of the two crosses.

Among interaction effects additive x additive (i) gene effects were positive and significant in HUM 1 X Shikha, TJM 196 X Kanika whereas non-significant in rest of the three crosses. The additive x dominance (j) gene effect was positive and significant in LGG 460 X Virat and non significant in rest of the four crosses. Dominance x dominance (l) gene effect was negative and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika and (l) effect was non-significant in rest of the crosses. The signs of (h) and (l) components were opposite for all crosses (Table 4.42).

9. Hundred seed weight (g)

Means of F_1 progenies was higher than better parental means in HUM 1 X Shikha, Ganga 8 X Shikha, and LGG 460 X Kanika, lower mean than better parent in LGG 460 X Virat while intermediate to both the corresponding parents in TJM 196 X Kanika. All F_2 progenies showed lower mean than better parent except in Ganga 8 X Shikha. Mean of backcrosses was less than corresponding recurrent parent except in Ganga 8 X Shikha (B_1), LGG 460 X Virat (B_1), LGG 460 X Virat (B_2) and TJM 196 X Kanika (B_2) (Table 4.43).

Table 4.41: Estimates of generation mean analysis and standard errors for number of seeds/pod

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	10.07 ± 0.13	10.00 ± 0.35	10.83 ± 0.43	9.03 ± 0.59	10.97 ± 0.39	11.01 ± 0.70
2	Ganga 8 X Shikha	10.07 ± 0.13	9.83 ± 0.20	10.07 ± 0.07	9.60 ± 0.12	8.93 ± 0.77	9.20 ± 0.00
3	LGG 460 X Virat	9.10 ± 0.15	10.33 ± 0.24	9.43 ± 0.19	9.70 ± 0.44	10.80 ± 0.31	10.13 ± 0.18
4	LGG 460 X Kanika	9.10 ± 0.15	9.83 ± 0.42	9.50 ± 0.17	10.20 ± 0.35	10.63 ± 0.30	11.43 ± 1.13
5	TJM 196 X Kanika	9.87 ± 0.18	9.83 ± 0.42	10.33 ± 0.47	9.60 ± 0.31	10.20 ± 0.31	11.46 ± 0.54

Table 4.42: Scaling tests and estimates of gene effects for number of seeds/pod in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	1.03 ± 0.91	1.19 ± 1.51	-5.60* ± 2.54	2.21 ± 2.86	0.03 ± 0.19	18.68** ± 6.78	7.83**±2.85	-0.08 ± 0.82	-10.05* ± 4.09	D
2	Ganga 8 X Shikha	-2.27 ± 1.54	-1.50** ± 0.21	-1.63** ± 0.54	12.08** ± 1.61	0.012 ± 0.12	-7.92 ± 4.72	-2.13 ± 1.61	-0.38 ± 0.78	5.90 ± 3.12	D
3	LGG 460 X Virat	3.07** ± 0.66	0.50 ± 0.47	0.50 ± 1.81	6.65** ±1.89	-0.62** ± 0.14	9.42* ± 4.11	3.07 ± 1.88	1.28** ± 0.38	-6.63** ± 2.29	D
4	LGG 460 X Kanika	2.67** ± 0.64	3.53 ± 2.31	2.87 ± 1.50	6.13* ± 2.73	-0.37 ± 0.22	12.90 ± 7.59	3.33 ± 2.72	-0.43 ± 1.19	-9.53 ± 4.92	D
5	TJM 196 X Kanika	0.20 ± 0.79	2.75* ± 1.25	-1.97 ± 1.60	4.93** ± 1.75	0.02 ± 0.22	13.28** ± 4.52	4.92** ± 1.74	-1.28 ± 0.66	-7.87** ± 2.95	D

*, ** Significant at 5% and 1% level of significance

Table 4.43: Estimates of generation mean analysis and standard errors for 100 seed weight (g)

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	5.27 ± 0.12	4.04 ± 0.58	6.59 ± 0.25	3.51 ± 0.18	2.68 ± 0.31	3.40 ± 0.28
2	Ganga 8 X Shikha	3.38 ± 0.88	4.04 ± 0.58	4.37 ± 0.19	4.14 ± 0.26	3.84 ± 0.15	3.19 ± 0.15
3	LGG 460 X Virat	4.62 ± 0.07	4.53 ± 0.27	4.07 ± 0.06	4.17 ± 0.05	4.92 ± 0.20	5.26 ± 0.22
4	LGG 460 X Kanika	4.62 ± 0.07	4.53 ± 0.36	4.63 ± 0.43	3.31 ± 0.17	3.30 ± 0.32	4.19 ± 0.19
5	TJM 196 X Kanika	5.15±0.33	4.53 ± 0.36	4.82 ± 0.39	4.37 ± 0.30	4.78 ± 0.40	5.10 ± 0.29

Table 4.44: Scaling tests and estimates of gene effects for 100seed weight (g) in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-6.50** ± 0.68	-3.82** ± 0.84	-8.45** ± 1.07	6.52** ± 1.15	0.61* ± 0.30	-12.12**± 3.05	-1.87 ± 1.11	-134** ± 0.51	12.19** ± 1.99	D
2	Ganga 8 X Shikha	-0.06 ± 0.95	-2.03** ± 0.68	0.42 ± 1.54	6.23** ± 1.26	-0.33 ± 0.53	-6.48 ± 2.95	-2.52* ± 1.14	0.99 ± 0.57	46.62** ± 1.77	D
3	LGG 460 X Virat	1.14*** ± 0.42	1.93** ± 0.53	-0.62 ± 0.37	0.88 ± 0.66	0.04 ± 0.14	9.96** ± 1.92	3.69** ± 0.64	-0.39 ± 0.33	-6.77** ± 1.27	D
4	LGG 460 X Kanika	-2.65** ± 0.78	-0.78 ± 0.68	-5.18 ± 1.16	2.82** ± 1.03	0.04 ± 0.18	0.13 ± 0.15	1.75 ± 1.01	-0.93* ± 0.42	1.67 ± 1.90	C
5	TJM 196 X Kanika	-0.41 ± 0.95	0.86 ± 0.79	-.1.83 ± 1.50	2.57 ± 1.57	0.31 ± 0.24	4.97 ± 3.91	2.27 ± 1.55	-0.63 ± 0.55	-2.72 ± 2.49	D

*, ** Significant at 5% and 1% level of significance

Among the five crosses studied the A, B and C scales were non-significant in the case of TJM 196 X Kanika which indicated the adequacy of additive – dominance model for this cross. Mean (m) effects were positive and significant in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Kanika whereas non significant for rest of the crosses. Additive (d) gene effect was positive and significant for hundred seed weight in HUM 1 X Shikha while non-significant in rest of the crosses. The dominance (h) gene effect was significant and positive in LGG 460 X Virat whereas it was significant and negative in HUM 1 X Shikha and non-significant in rest of the crosses. Among interaction effects additive x additive (i) gene effect was negative and significant in Ganga 8 X Shikha while positive and significant in LGG 460 X Virat. Additive x dominance (j) gene effects were negative and significant in HUM 1 X Shikha and LGG 460X Kanika. The dominance x dominance (l) gene effects were positive and significant in HUM 1 X Shikha and Ganga 8 X Shikha whereas significant and negative in LGG 460 X Virat. The signs of (h) and (l) components were opposite for HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat while it was same for LGG 460 X Kanika (Table 4.44).

10. Biological yield per plant (g)

Biological yield per plant in F_1 generations expressed higher magnitude of mean values as compared to their respective better parents except in TJM 196 X Kanika. Mean expressed by F_2 population was intermediate to their corresponding parents in case of HUM 1 X Shikha and TJM 196 X Kanika while mean was higher than parental mean in case of LGG 460 X Virat and mean value was less than respective better parent in crosses Ganga 8 X Shikha and LGG 460 X Kanika. Mean values of backcrosses were higher than respective recurrent parents in most of the cases except in Ganga 8 X Shikha (B_1) and TJM 196 X Kanika (B_1) (Table 4.45).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. The mean (m) effects and additive (d) gene effects were significant and positive in all the crosses and negative and significant in HUM 1 X Shikha and LGG 460 X Kanika. The crosses viz., HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika recorded positive and

Table 4.45: Estimates of generation mean analysis and standard errors for biological yield/plant (g)

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	13.96 ± 0.82	21.94 ± 1.19	29.43 ± 0.83	16.47 ± 0.31	20.72 ± 0.64	39.15 ± 0.53
2	Ganga 8 X Shikha	25.11 ± 0.89	21.94 ± 1.19	33.18 ± 1.14	19.44 ± 1.04	20.93 ± 0.35	22.73 ± 0.88
3	LGG 460 X Virat	21.61 ± 1.21	17.84 ± 0.38	33.68 ± 1.18	26.86 ± 0.89	25.80 ± 0.95	32.44 ± 0.87
4	LGG 460 X Kanika	21.61 ± 1.21	28.83 ± 0.86	35.08 ± 0.86	16.73 ± 0.81	28.86 ± 0.53	31.75 ± 0.54
5	TJM 196 X Kanika	33.41 ± 0.90	28.83 ± 0.86	25.59 ± 1.52	31.60 ± 0.82	17.58 ± 0.57	39.21 ± 0.90

Table 4.46: Scaling tests and estimates of gene effects for days to biological yield/plant (g) in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-1.96 ± 1.73	26.92**± 1.80	-28.88**± 2.52	-35.89**± 2.19	-3.99** ± 0.72	144.14**± 6.03	53.85**± 2.07	-14.44** ± 1.10	-78.81**± 4.17	D
2	Ganga 8 X Shikha	-16.43** ± 1.61	-9.67** ± 2.42	-35.66**± 4.96	13.97** ± 4.62	1.59* ± 0.74	2.67±10.37	9.56* ± 4.56	-3.38** ± 1.21	16.54** ± 6.26	C
3	LGG 460 X Virat	-3.70 ± 2.54	13.36**± 2.14	0.62 ± 4.46	10.69* ± 4.44	1.89** ± 0.64	41.69** ± 10.75	9.04* ± 4.40	-8.53** ± 1.44	-18.69** ± 6.82	D
4	LGG 460 X Kanika	1.02 ± 1.83	-0.40 ± 1.62	-53.68**± 3.98	-29.08** ± 3.67	-3.61** ± 0.74	119.08**± 8.29	54.30**± 3.59	0.71 ± 1.06	-54.92**± 4.99	D
5	TJM 196 X Kanika	-23.85** ± 2.10	23.66**± 2.51	12.98** ± 4.63	43.96** ± 3.95	2.29** ± 0.62	-31.07**± 9.45	-12.84**± 3.90	-23.92**± 1.23	12.70* ± 6.30	D

*, ** Significant at 5% and 1% level of significance

significant dominance (h) effects whereas TJM 196 X Kanika showed significant and positive (h) effect. The additive x additive (i) gene effects were positive and significant in all crosses and negatively significant in cross TJM 196 X Kanika. Additive x dominance (j) epistatic interactions were negative and significant in all the crosses except LGG 460 X Kanika. Dominance x dominance (l) gene effects were negative significant in HUM 1 X

Shikha, LGG 460 X Virat and LGG 460 X Kanika. It was positively significant in Ganga 8 X Shikha and TJM 196 X Kanika. The signs of (h) and (l) components were opposite for all crosses except for Ganga 8 X Shikha (Table 4.46).

11. Harvest index (%)

Mean values for harvest index in F_1 generations as well as in F_2 populations were higher than their respective better parent in all cases except in LGG 460 X Virat (F_2), LGG 460 X Kanika (F_2) and Ganga 8 X Shikha (F_2). In backcross populations, the mean appeared to be higher than their corresponding recurrent parents in all the crosses, except HUM 1 X Shikha (B_1) and TJM 196 X Kanika (B_1) where, the mean was lower than recurrent parent (Table 4.47).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses (Table 4.48). Mean (m) effects were positive and significant in HUM 1 X Shikha and TJM 196 X Kanika while it was negative and significant in Ganga 8 X Shikha and LGG 460 X Kanika whereas non-significant in LGG 460 X Virat. Additive (d) gene effect was positive and significant in LGG 460 X Kanika, negative and significant in LGG 460 X Virat while, it was non-significant in rest of the crosses. Dominance (h) gene effects were positive and significant in all crosses except HUM 1 X Shikha where it was negative and significant and TJM 196 X Kanika which showed non-significant (h) effect. Additive x additive (i) interaction effects were positive and significant in all crosses except in HUM 1 X Shikha and TJM 196 X Kanika which exhibited non-significant (i) gene interaction effects. The additive x dominance (j) gene effects were significant and negative in all the crosses except in Ganga 8 X Shikha and LGG 460 X Virat where it was non-

Table 4.47: Estimates of generation mean analysis and standard errors for harvest index (%)

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	34.76 ± 7.36	23.85± 2.16	49.13 ± 2.29	43.90 ± 0.90	27.15 ± 1.97	-39.07 ± 1.34
2	Ganga 8 X Shikha	26.35 ± 4.24	23.85 ± 2.16	43.39 ± 0.78	18.27 ± 1.42	31.04 ± 1.48	32.34 ± 1.79
3	LGG 460 X Virat	26.98 ± 1.06	37.19 ± 3.99	42.03 ± 1.98	33.94 ± 3.02	43.56 ± 3.60	45.16 ± 0.60
4	LGG 460 X Kanika	26.98 ± 1.06	18.76 ± 0.45	35.29 ± 0.55	25.73 ± 1.47	42.99 ± 0.82	49.64 ± 0.87
5	TJM 196 X Kanika	22.85 ± 2.14	18.76 ± 0.45	43.97 ± 4.09	43.22 ± 2.38	18.69 ± 0.32	50.49 ± 2.03

Table 4.48: Scaling tests and estimates of gene effects for harvest index (%) in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-29.60**± 8.66	5.16± 4.14	18.73 ± 9.63	72.48** ± 7.10	5.46 ± 3.84	-90.96** ± 19.85	-43.17** ±5.97	-17.38**± 4.52	67.61** ± 13.55	D
2	Ganga 8 X Shikha	-7.65 ± 5.66	-2.57 ± 4.25	-63.88**± 7.58	-28.57** ± 8.02	1.25 ± 2.38	115.40**± 20.45	53.67**± 7.66	-2.54± 3.50	-43.45** ± 12.75	D
3	LGG 460 X Virat	18.11* ± 7.54	11.09* ± 4.61	-12.47 ± 13.35	-9.59 ± 14.25	-5.10*± 2.06	122.50**± 33.21	41.67**± 14.10	3.51± 4.19	-70.88** ± 19.77	D
4	LGG 460 X Kanika	23.71** ± 2.04	45.23**± 1.88	-13.38* ± 6.11	-59.45** ± 6.39	4.11**± 0.58	245.10** ±13.92	82.34**± 6.36	-10.76**± 1.33	-151.26** ± 7.76	D
5	TJM 196 X Kanika	-29.45** ± 4.66	38.26** ± 5.79	43.34** ± 12.77	55.34** ± 10.45	2.05 ± 1.09	-37.10 ±23.33	-34.53** ± 10.39	-33.86** ±2.33	25.73 ±15.19	D

*,** Significant at 5% and 1% level of significance

significant. Dominance x dominance (l) gene effects was negative in all the crosses except in HUM 1 X Shikha which was positive and significant and TJM 1196 X Kanika which was non-significant. The signs of (h) and (l) components were opposite for all crosses

12. Seed yield per plant (g)

Mean seed yield/plant for all F_1 and F_2 progenies were higher than their respective better parents except in Ganga 8 X Shikha (F_2) and LGG 460 X Kanika (F_2) where mean value was lower than their respective better parents. All the backcross populations recorded slightly higher mean value than their respective recurrent parents, except Ganga 8 X Shikha (B_1) and TJM 196 X Kanika (B_1) (Table 4.49).

Significance of one or more scaling tests suggested the presence of non-allelic interactions in all the crosses. Among the main effects, the mean (m) effects and additive (d) gene effects were significant and negative in all the crosses except TJM 196 X Kanika which was positive and significant. Dominance (h) gene effects were significant and positive in all crosses except in TJM 196 X Kanika which was non-significant. Among interaction effects, additive x additive (i) gene effects were positive and significant in all crosses except TJM 196 X Kanika which was negative and significant. Additive x dominance (j) gene effects were significant and negative in all the crosses. Dominance x dominance (l) gene effects were negative and significant in all the crosses except Ganga 8 X Shikha and TJM 196 X Kanika which were non-significant. The signs of (h) and (l) were opposite for all the crosses except for TJM 196 X Kanika (Table 4.50).

Table 4.49: Estimates of generation mean analysis and standard errors for seed yield/plant (g)

S. No.	Crosses	Generations					
		P1	P2	F1	F2	B1	B2
1	HUM 1 X Shikha	5.02 ± 0.33	5.26 ± 0.69	14.48 ± 0.94	7.23 ± 0.05	5.61 ± 0.31	15.30 ± 0.59
2	Ganga 8 X Shikha	6.55 ± 0.67	5.26 ± 0.69	14.38 ± 0.24	3.58 ± 0.44	6.49 ± 0.28	7.32 ± 0.24
3	LGG 460 X Virat	5.81 ± 0.13	6.17 ± 0.34	14.11 ± 0.27	9.07 ± 0.55	11.17 ± 0.60	14.65 ± 0.20
4	LGG 460 X Kanika	5.81 ± 0.13	5.40 ± 0.14	12.38 ± 0.41	4.29 ± 0.22	12.40 ± 0.03	15.77 ± 0.54
5	TJM 196 X Kanika	7.61 ± 0.60	5.40 ± 0.41	11.14 ± 0.57	13.63 ± 0.50	3.28 ± 0.09	19.76 ± 0.34

Table 4.50: Scaling tests and estimates of gene effects for seed yield/plant (g) in selected crosses

S. No.	Crosses	Parameters of scaling tests			Gene effects						Types of Epistasis
					Parameters m, d, h & digenic interaction parameters						
		A	B	C	(m)	(d)	(h)	(i)	(j)	(l)	
1	HUM 1 X Shikha	-8.29**± 1.17	10.86**± 1.65	-10.34**± 2.03	-7.76** ± 1.40	-0.12 ± 0.38	37.72** ± 4.28	12.91**± 1.35	-9.57** ±0.77	-15.47** ±3.35	D
2	Ganga 8 X Shikha	-7.95**± 0.91	-4.99** ± 0.87	-26.26**± 2.06	-7.41** ± 1.96	0.64 ± 0.48	22.16** ± 40.40	13.31**± 1.90	-1.48* ±0.61	-0.37± 2.53	D
3	LGG 460 X Virat	2.43* ± 1.23	8.10** ± 0.58	-3.92 ± 2.30	-9.36** ± 2.54	-0.18 ± 0.18	50.24** ± 5.83	15.35**± 2.54	-3.29** ±0.65	-26.77** ±3.40	D
4	LGG 460 X Kanika	6.60** ± 0.44	13.75**± 1.17	-18.80**± 1.23	-33.55**± 1.41	0.20* ± 0.10	105.45**± 3.74	39.16**± 1.40	-3.58** ±0.55	-59.52** ±2.49	D
5	TJM 196 X Kanika	-12.18** ± 0.85	22.98** ± 0.89	19.21** ± 2.38	14.93** ± 2.14	1.11** ± 0.31	-1.42 ± 4.64	-8.12** ± 2.12	-17.58** ±0.46	-2.37 ± 2.76	C

*,** Significant at 5% and 1% level of significance

4.9 Quality analysis

In the present investigation protein, sugar, phenol and fat content were analyzed for 14 parents and 40 crosses of mungbean (Table 4.51 and 4.52) and results are presented here under:

4.9.1 Protein content (mg/g)

In parents, protein content ranged from 18.39 mg/g (Shikha) to 24.10 mg/g (Pusa Vishal) with overall mean of 20.70 mg/g. Out of 14 parents, the general mean (20.70 mg/g) was exceeded by 7 parents. Highest protein content was reported in Pusa Vishal (24.10 mg/g) followed by LGG 460 (22.33 mg/g) and TJM 196 (22.31 mg/g).

In crosses, highest protein content was noted in SL 668 X Virat (26.29 mg/g) whereas lowest protein content was recorded in LGG 460 X Kanika (20.14 mg/g). The overall mean (24.06 mg/g) was surpassed by 23 crosses. Among crosses, highest protein content was recorded in SL 668 X Virat (26.29 mg/g), HUM 1 X PDM 139 (26.26 mg/g) and LGG 460 X Virat (26.25 mg/g).

4.9.2 Sugar content (mg/g)

Sugar content in parents ranged from 5.38 mg/g (HUM 1) to 7.59 mg/g (Ganga 8) with overall mean of 6.89 mg/g. The general mean (6.89 mg/g) was surpassed by 7 parents out of 14. Highest sugar content was reported for Ganga 8 (7.59 mg/g) followed by SL 668 (7.53 mg/g) and TJM 3 (7.42 mg/g).

In crosses, sugar content ranged from 6.38 mg/g (TJM 196 X PDM 139) to 8.21 mg/g (TJM 136 X PDM 139). Out of 40 crosses the overall mean (7.39 mg/g) was exceeded by 20 crosses. Highest sugar content was found in TJM 136 X PDM 139 (8.21 mg/g), Ganga 8 X PDM 139 (7.98 mg/g), TJM 196 X Virat and PDM 11 X Virat (7.96 mg/g).

4.9.3 Phenol content (mg/g)

Phenol content ranged from 140.84 mg/g (TMB 37) to 954.11 mg/g (Pusa Vishal) in parents. The general mean (566.68 mg/g) was surpassed by 8 parents.

Table 4.51: Estimation of quality traits in parents

S. No.	Parents	Protein (mg/g)	Sugar (mg/g)	Phenol (mg/g)	Fat (%)
1	TJM 196	22.31	6.46	609.17	1.05
2	TJM 136	21.44	6.86	764.24	1.03
3	TJM 3	20.14	7.42	196.20	1.28
4	TMB 37	18.83	7.16	140.84	1.46
5	GANGA 8	19.24	7.59	675.62	0.65
6	LGG 460	22.33	6.38	441.44	1.03
7	HUM I	20.17	5.38	787.96	0.75
8	SL668	21.04	7.53	430.37	0.84
9	PUSA VISHAL	24.10	6.93	954.11	1.26
10	PDM 11	20.13	7.25	805.36	0.71
11	PDM 139	21.05	6.87	539.56	1.42
12	SHIKHA	18.39	7.13	639.31	0.91
13	KANIKA	19.25	6.85	587.05	1.36
14	VIRAT	21.44	6.64	362.34	1.32
Mean		20.70	6.89	566.68	1.10
Range	Lowest	18.39	5.38	140.84	0.65
	Highest	24.10	7.59	954.11	1.46

Table 4.52: Estimation of quality traits in crosses

S. No.	F1	Protein (mg/g)	Sugar (mg/g)	Phenol (mg/g)	Fat (%)
1	TJM196XPDM139	24.94	6.38	563.74	1.21
2	TJM196XSHIKHA	22.75	7.04	561.71	1.01
3	TJM196XKANJIKA	24.08	7.89	582.27	1.24
4	TJM196XVIRAT	24.95	7.96	591.75	1.16
5	TJM136XPDM139	24.52	8.21	564.72	1.24
6	TJM136XSHIKHA	23.64	7.45	563.44	0.96
7	TJM136XKANJIKA	25.41	6.92	565.68	1.16
8	TJM136XVIRAT	21.86	7.74	580.27	1.16
9	TJM3XPDM139	20.55	6.84	571.50	1.34
10	TJM3XSHIKHA	22.33	7.05	580.42	1.11
11	TJM3XKANJIKA	24.51	6.99	591.78	1.30
12	TJM3XVIRAT	25.39	7.24	585.61	1.11
13	TMB37XPDM139	24.95	7.85	566.29	1.36
14	TMB37XSHIKHA	24.93	7.04	566.82	1.22
15	TMB37XKANJIKA	23.18	7.82	562.63	1.41
16	TMB37XVIRAT	22.75	7.73	560.13	1.35
17	GANGA8XPDM139	25.82	7.98	583.64	1.02
18	GANGA8XSHIKHA	24.52	7.18	577.51	0.76
19	GANGA8XKANJIKA	23.63	7.22	587.07	1.01
20	GANGA8XVIRAT	23.02	7.77	585.03	0.97
21	LGG460XPDM139	24.95	7.05	572.54	1.33
22	LGG460XSHIKHA	25.40	6.95	577.73	1.06
23	LGG460XKANJIKA	20.14	7.85	569.51	1.35
24	LGG460XVIRAT	26.25	7.14	561.71	1.33
25	HUM1XPDM139	26.26	6.82	598.07	1.07
26	HUM1XSHIKHA	25.37	7.45	596.55	0.84
27	HUM1XKANJIKA	24.07	7.64	599.06	1.03
28	HUM1XVIRAT	25.84	7.42	582.29	0.81
29	SL668XPDM139	24.07	7.76	564.87	1.11
30	SL668XSHIKHA	22.32	6.93	553.82	0.88
31	SL668XKANJIKA	25.36	6.95	591.74	1.16
32	SL668XVIRAT	26.29	7.47	599.69	1.05
33	PUSA VISHALXPDM139	23.21	7.58	593.54	1.34
34	PUSA VISHALXSHIKHA	25.83	7.55	593.33	1.05
35	PUSA VISHALXKANJIKA	24.21	6.71	602.85	1.30
36	PUSA VISHALXVIRAT	23.18	7.23	599.09	1.27
37	PDM11XPDM139	21.43	7.12	589.97	1.07
38	PDM11XSHIKHA	23.65	7.09	591.75	0.85
39	PDM11XKANJIKA	23.73	7.74	590.71	1.03
40	PDM11XVIRAT	22.76	7.96	591.73	1.02
Mean		24.06	7.39	580.33	1.13
Range	Lowest	20.14	6.38	553.80	0.76
	Highest	26.29	8.21	602.85	1.41

Highest phenol content was recorded for Pusa Vishal (954.11 mg/g) followed by PDM 11 (805.36 mg/g) and HUM 1 (787.96 mg/g).

In crosses, highest phenol content was recorded for Pusa Vishal X Kanika (602.85 mg/g) whereas lowest phenol content was observed for SL 668 X Shikha (553.82 mg/g). General mean (580.33 mg/g) was exceeded by 20 crosses out of 40. Pusa Vishal X Kanika (602.85 mg/g) recorded for highest phenol content followed by SL 668 X Virat (599.69 mg/g) and Pusa Vishal X Virat (599.09 mg/g).

4.9.4 Fat content (%)

Among parents, fat content ranged from 0.65 % (Ganga 8) to 1.46% (TMB 37). General mean (1.10%) was exceeded by 6 parents out of 14. Highest fat content was recorded in TMB 37 (1.46%) followed by PDM 139 (1.42%) and Kanika (1.36%).

In crosses, fat content ranged from 0.76% (Ganga 8 X Shikha) to 1.41% (TMB 37 X Kanika). Out of 40 crosses 18 crosses exceeded the overall mean (1.13%). Highest fat content was observed in TMB 37 X Kanika (1.41%), TMB 37 X PDM 139 (1.36%) and LGG 460 X Kanika (1.35%).



Digestion process during Protein content estimation in mungbean



Sugar Content Estimation in Mungbean



Spectrophotometer

Plate 4: Estimation of quality traits in greengram

Chapter -V

DISCUSSION

DISCUSSION

Pulse crops are an excellent source of dietary protein and important for the human diet. Pulse crops play an important role in crop rotation due to their ability to fix biological nitrogen and thus enhance the soil fertility. Greengram [*Vigna radiata*(L.) Wilczek] holds an important position among the pulse family because of its adaptation to the multiple environments, short duration maturity, low need for agricultural inputs, high ability to increase soil fertility due to availability of rhizobium bacterium in the root zones. Greengram is favoured for consumption due to the easy digestibility and less flatulence problem owing to lower content of raffinose, stachyose and verbalose Poehlman (1991).

Yield is not a simple trait rather; it is a complex one, an aggregate of traits that is highly influenced by the environment. The yield of greengram worldwide is very low and limited success has been achieved so far in augmenting its yield. The low yield is due to the narrow genetic base and also very few study of the genetic inheritance. For the fulfillment of the present demand, systematic studies for genetic analysis regarding high yielding traits are urgently required for the development high yielding varieties of greengram. Though there are many other research areas for the improvement of greengram but breeding for high yielding and resistance to Mungbean Yellow Mosaic Virus (MYMV) are the most important aspects for the improvement of greengram.

In present day, pulse breeders are focusing mainly on breeding for high yielding varieties, which is largely depends on the choice of parents for hybridization and the choice of crosses to be advanced from among the several crosses affected by using them. The choice of parental material and breeding methodology becomes convoluted for improvement or development of new mungbean cultivars. Combining ability analysis provides guide line for the assessment of relative breeding potential of the parents and help in choice of parents Gnanasekaran *et al.* (2006) which may be hybridized either to exploit hybrid vigour by accumulating unfixable gene effects or to evolve cultivars by accumulating fixable gene effects Nadarajan and Gunasekaran

(2005). The Line $\times$ Tester mating design as suggested by Kempthorne (1957) is an appropriate method to identify superior parents and hybrids. However, the information obtained in this process on the nature of gene action may be biased estimates of additive and dominance components due to interaction effects. Generation mean analysis provides accurate genetic patterns of the individual crop for the systematic study of the important genes contributing in yield improvement. Selection procedure is more difficult in quantitative traits, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and association studies among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits.

Keeping that in view the present investigation entitled “**Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]**” was carried out at Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur India during summer 2020, Kharif 2020 and summer 2021.with the following heads:

5.1 Characterization

5.2 Analysis of variance

5.3 Parameter of genetic variability

5.3.1 Range and mean performance for different characters

5.3.2 Genotypic and phenotypic coefficient of variation, Heritability (%) and Genetic advance as percentage of mean

5.4 Correlation coefficient analysis

5.5 Path coefficient analysis

5.6 Heterosis

5.7 Combining ability

5.8 Generation mean analysis

5.9 Quality analysis

5.1 Morphological characterization

Based on standard scores on morphological descriptors, 14 parental lines, 40 crosses were categorized in various groups. Morphological characterization helps in effective utilization of germplasm in the crop improvement programmes. Characterization is essential for identification of genotypes with desirable traits. Individually and in combination, mungbean parents and crosses exhibited a wide range of variation on morphological traits.

Hypocotyl anthocyanin pigmentation has great importance in hybrid breeding programme to detect the pure crosses due to its monogenic dominant inheritance pattern Khattak et al. (2000), Mukherjee and Pradhan (2002). This trait can be used as a morphological marker for screening of breeding material at seedling stage. In present investigation, out of 14 parents, 13 showed anthocyanin colouration and only one was without pigmentation. Among crosses, 36 showed presence for anthocyanin colouration and 4 were without pigmentation.

Based on flower characteristics, such as time of flowering and petal colour, parents and crosses could be grouped into different categories (Table 4.1 & 4.3). Out of 14 parents, 4 were early, whereas rests of the 10 parents were medium in their flowering duration while late duration was not noted in any of the parents. Among 40 crosses, 30 were early while 10 were medium in their flowering time and none of them were late. Petal colour was yellow in 9 and light yellow in 5 of the parents while it was yellow in 29 and light yellow in 11 crosses. Similar findings and groupings of genotypes based on flower morphological characters were made by Jain et al. (2002), Singh et al. (2014) and Kaur et al. (2017) in mungbean.

Use of plant diagnostic characteristics to identify a variety has been classical taxonomic approach for both varietal purity and varietal identification. On the basis of the plant, morphological characteristics such as plant growth habit and plant habit, parents and crosses were grouped into different categories (Table 4.1 and 4.3). In the present study, 8 parents showed semi-erect type of growth habit and 6 of them were spreading while none of them

were erect. Out of 40 crosses, 10 were semi-erect and 30 were spreading. Erect plants were not reported in any of the crosses. Mungbean descriptor described two types of plant habit: determinate and indeterminate. 2 parents were determinate while 12 of them were indeterminate. All the crosses under study had indeterminate plant habit.

All the 14 parents and 40 crosses of mungbean evaluated did not show any variation for stem pubescence (Table 4.1 and 4.3). Pubescence was present in all the parents and crosses. Based on stem colour, parents and crosses were grouped into different categories i.e. green, green with purple splashes and purple. In the present study, green stem colour was noted in 6 parents while rest of the 8 parents showed green with purple splashes type of stem colour. Purple stem colour was not observed in any of the parents. In crosses, 10 were with green stem colour, 29 had green with purple splashes while, only one cross had purple stem colour. Therefore, the evaluated 14 parents and 40 crosses of mungbean had good diversity in stem colour. Similar characterization and grouping based on stem morphological characters were made by Jain *et al.* (2002), Singh *et al.* (2014) and Kaur *et al.* (2017) in mungbean, Chakarabarthi and Agarwal (1989) in black gram.

The leaflet lobes, leaf colour, leaf vein colour and leaf shape plays an important role in the yielding ability of plants, as the leaves are the food synthesis site of the plants. In the present study, the characteristics related with leaves have been recorded and based on these characteristics, the parents and crosses were categorized into different groups. Among 14 parents leaflet lobe was present in 9 parents while it was absent in 5. Among the crosses studied, this trait was absent in 36 of the crosses while 4 possessed this trait. In the present study, 10 parents were having green and 4 had dark green leaf colour. Among the 40 crosses, 29 were having green while 11 had dark green leaf colour. Leaf vein colour was green in 1, greenish purple in 6 and purple in 7 parents respectively while it was green in 6, greenish purple in 25 and purple in 9 crosses respectively. Ovate leaf shape was found in 12 parents while 2 of them had deltoid leaf shape. Further, none of the genotypes fell under the category of Cuneate and Lanceolate. All the 40 crosses had ovate leaf shape. Similar characterization and grouping based on

leaf morphological characters were made by Kaur *et al.* (2017) in mungbean, Chakarabarthi and Agarwal (1989) in black gram.

The pod morphological characteristics influence the yielding ability of the plant. The variation was observed for various characteristics of pod such as mature pod colour and curvature of mature pod. All the 14 parents and 40 crosses evaluated did not show any variation for pod pubescence. Among 14 parents, 13 had green pre mature pod colour while only one was with green with pigmented suture. All the 40 crosses under study had green pre mature pod colour. Among 14 parents 7 had straight while 7 were with curved pods. Among 40 crosses, 13 had straight whereas 27 had curved pods. Similar observations and grouping based on pod morphological characters were made by Singh *et al.* (2014) and Kaur *et al.* (2017) in mungbean.

The price of premium genotypes of green gram or consumer acceptance of a variety is decided by its seed characteristics like colour, lusture, shape and size. Based on seed morphology, parents and crosses were grouped into different categories according to seed colour, seed shape, seed lusture and seed size (Table 4.1 and 4.3). Seed colour was green in 2 and mottled in 12 of the parents and it was green in 4 and mottled in 36 of the crosses. Lusture of the seed was shiny in 4 and dull in 10 parents. Among the 40 crosses studied, shiny and dull seeds were reported in 13 and 27 crosses. Among 14 parents, the shape of the seed was oval in 9 and drum shaped in 5 of the parents respectively. Among the 40 crosses, 20 had oval seed shape while rest of the 20 crosses had drum shaped seeds. The size of the seed was medium in 13 and large in 1 parent respectively while small category of seed was not present in any of the parents. Among 40 crosses, 37 had medium seeds while, 3 had large seeds. Similar observations and grouping based on seed morphological characters were made by Venkateswarlu *et al.* (2001) and Khajudparn and Tantasawat (2011).

5.2 Analysis of variance

The mean sum of squares due to parents and crosses were highly significant for all the traits under study viz. days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per

plant, number of pod per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, biological yield per plant, harvest index and seed yield per plant (Table 4.5). This indicates that substantial variability has been created and genetic base is broadened for most of the important traits among different parents and crosses. The exploitation of the present variability may lead to development of potential and suitable genotypes in future. Similar results have been reported by Alom *et al.* (2014) for days to 50% flowering, days to maturity, number of pods per plant, number of seeds per pod, hundred seed weight and seed yield per plant, Tiwari *et al.* (2014) for days to flowering, plant height, days to maturity, number of cluster per plant, number of pods per cluster, number of pods per plant, biological yield per plant and harvest index.

5.3 Parameters of genetic variability

5.3.1 Phenotypic and genotypic coefficient of variation, heritability [h² (b)] and genetic advance as percent of mean

Estimation of variability in the breeding population is a pre-requisite for breeding programme aimed at improving yield, quality and other important characters under consideration. Unless a major portion of variation is heritable, attempts to improve characters by selection would be futile. Hence, the information on heritability along with genetic advance will be helpful in formulating the selection criteria.

To obtain a clear picture about the variability in all the parents and crosses, the variability was further splitted into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). In the present investigation, the genetic parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad sense and genetic advance as percent of mean were estimated for yield and yield attributing traits involving 14 parents and 40 cross combinations. The values of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation for all the characters.

Low PCV and GCV coupled with high broad sense heritability and moderate genetic advance as percent of mean was observed both in parents and crosses for days to 50% flowering and in the parents for days to maturity. Whereas, low PCV and GCV values coupled with high heritability and low genetic advance expressed as per cent of mean were observed among crosses for days to maturity and among parents for number of seeds per pod whereas, moderate PCV and GCV along with high broad sense heritability and genetic advance was registered for both parents and crosses for the trait plant height, among parents for number of pods per cluster and for crosses in 100 seed weight. High PCV and GCV with high heritability and genetic advance was recorded for number of branches per plant, number of pods per plant and biological yield per plant in both the parents and crosses and high PCV and GCV with high heritability and genetic advance was reported for seed yield per plant among the crosses. In crosses, the trait number of pods per cluster exhibited moderate PCV and GCV coupled with moderate broad sense heritability and high genetic advance as percent of mean. High PCV and low GCV with high heritability and genetic advance was found in parents for the trait number of clusters per plant and in crosses for harvest index. Crosses exhibited high PCV and moderate GCV with high heritability and genetic advance as percent of mean for number of clusters per plant whereas, for number of seeds per pod moderate values of PCV and low values of GCV along with low heritability and genetic advance was observed. In parents for the traits viz., 100 seed weight, harvest index and seed yield per plant, high PCV and moderate GCV coupled with moderate heritability and high genetic advance was observed (Table 4.7).

Low estimates of GCV and PCV observed in both parents as well in 40 crosses. The finding reveals the existence of narrow range of variability and thus less scope for improvement of the character through simple selection. This is in conformity with the findings of Reddy *et al.* (2003) and Priyanka *et al.* (2011). High heritability in parents and crosses coupled with low genetic advance as percent of mean suggests the operation of non additive gene action in the inheritance of the character. Similar results were reported by Loganathan *et al.* (2001) and Mallikarjuna *et al.* (2006) in greengram.

Whereas study of high heritability coupled with low genetic advance as per cent of mean indicates the importance of non-additive gene effects for concerned traits. Similar results were also reported by Reddy *et al.* (2003) and Mallikarjuna *et al.* (2006).

Low to moderate estimates of GCV and PCV coupled with moderate to high heritability and genetic advance as per cent of mean indicates the importance of both additive and non additive gene action in the inheritance of the characters. Similar results were also reported by Loganathan *et al.* (2001), Mallikarjuna *et al.* (2006) and Wani *et al.* (2007).

Higher GCV and PCV both in parents and crosses indicate the existence of high variability of particular character amenable for selection in early generation. This is in the agreement with the findings of Raje and Rao (2000), Sirohi and Lokendra kumar (2006), Marappa (2008), Tabasum *et al.* (2010) and Narasimhulu *et al.* (2014) in greengram. High heritability along with the high genetic advance as per cent of mean observed in parents and crosses indicates the selection will effective because of additive gene action in the concerned trait. These results are in conformity with the findings of Borah and Hazarika (1995), Raje and Rao (2000), Khajudparn and Tantasawat (2011), Srivastava and Singh (2012), Hozayn *et al.* (2013), Jyotsana and Anuradha (2013), Mehendi *et al.* (2013), Paramesh *et al.* (2014) and Mohan *et al.* (2014).

Moderate to high estimates of variability for the trait among the parents and crosses indicated the existence of wide variability and thus selection can be exercised in early generations. This is in accordance with the results of Mishra and Sahu (1985), Borah and Hazarika (1995), Khairnar *et al.* (2003), Rahim *et al.* (2010) and Vinay *et al.* (2010). Whereas high heritability and moderate to high genetic advance as per cent of mean revealed the role of additive gene action in the genetic control of particular trait and low environmental influence. Hence simple selection could be effective in the improvement of the trait. Similar results were also reported by Khairnar *et al.* (2003), Rao *et al.* (2005), Mehendi *et al.* (2013) and Mohan *et al.* (2014).

Very low variability both in parents and crosses indicated a limited scope of selection for the concerned character. This finding is in conformity with the results of Veerabhadhira and Jehangir (1995). Moderate to low heritability coupled with low genetic advance as per cent of mean indicated that the character is controlled by non-additive gene action. This is supported by the findings of Begum *et al.* (2013) and Zaid *et al.* (2012) in greengram.

5.4 Correlation coefficient analysis

Most of the characters are associated with each other but the extent of correlation values varies with different pairs of character. A positive correlation between the desired characters is favorable to the breeder as it helps in selection. However, a negative correlation hinders the recovery of the recombinants in both characters. In such a situation, strong selection applied to a character also brings about change in other character. In present investigation, the results obtained revealed that genotypic correlation was higher than the corresponding phenotypic values both for parents as well as crosses (Table 4.8 and 4.10), indicating that there is strong inherent association between characters, however the expression was suppressed due to effect of the environment, which modified the phenotypic expression and phenotypic coefficient values. This is in confirmation with the findings of Sreedevi and Sekhar (2004), Ramesh *et al.* (2005), Verma and Garg (2007), Khanpara *et al.* (2012) and Narasimhulu *et al.* (2014).

In parents, seed yield per plant registered significant and positive phenotypic association with number of pods per plant (0.407**) followed by biological yield per plant (0.366*) and harvest index (0.337*). Rest of the characters exhibited non-significant but positive association with seed yield per plant except plant height and number of pods per cluster. In crosses, highest positive and significant phenotypic association with seed yield was expressed by biological yield per plant and harvest index (0.779*) followed by number of pods per plant (0.435**), hundred seed weight (0.283**), number of clusters per plant (0.262**), number of branches per plant (0.256*) and number of pods per cluster (0.205*). On the contrary, strong significant and negative association was observed with plant height (-0.395**) and number of seeds per pod (-0.189*). These findings are in confirmation with the findings

of Ramesh *et al.* (2005), Pandiyan *et al.* (2006), Biradar *et al.* (2007), Wani *et al.* (2007), Hakim *et al.* (2008), Gul *et al.* (2008), Peerajade *et al.* (2009), Vinay *et al.* (2010), Tabasum *et al.* (2010), Khajudparn and Tantasawat (2011), Srivastava and Singh (2012), Khanpara *et al.* (2012), Zaid *et al.* (2012), Ahmad *et al.* (2013), Baisakh *et al.* (2013), Jyothsna and Anuradha (2013), Begum *et al.* (2013), Itefa *et al.* (2014), Lalinia and Khameneh (2014), Narasimhulu *et al.* (2014) for pods per plant and Anbumalarmathi *et al.* (2005), Iranna and Kajjidoni (2005), Ramesh *et al.* (2005), Pandiyan *et al.* (2006), Mallikarjuna *et al.* (2006), Biradar *et al.* (2007), Kaveri *et al.* (2007), Saxena *et al.* (2007), Tabasum *et al.* (2010), Khajudparn and Tantasawat (2011), Khanpara *et al.* (2012), Ahmad *et al.* (2013), Baisakh *et al.* (2013) for cluster per plant.

Significant and positive associations of seed yield with pods per clusters were in conformity with the reports of Iranna and Kajjidoni (2005), Kaveri *et al.* (2007), Wani *et al.* (2007), Peerajade *et al.* (2009), Srivastava and Singh (2012), Khanpara *et al.* (2012), Srikanth *et al.* (2013), Narasimhulu *et al.* (2014); Dhuppe *et al.* (2005), Saxena *et al.* (2007), Shwetha (2011), Srivastava and Singh (2012), Ahmad *et al.* (2013), Jyothsna and Anuradha (2013) and Itefa *et al.* (2014). For number of branches per plant was in the agreement with conformity of the findings of Bhattacharya and Vijaylaxmi (2005), Saxena *et al.* (2007), Verma and Garg (2007), Singh *et al.* (2009), Tabasum *et al.* (2010), Khajudparn, Tantasawat (2011), Itefa *et al.* (2014) and Narasimhulu *et al.* (2014). For biological yield per plant, the present findings were in conformity with the findings of Pratibha *et al.* (2016). Thus the seed yield in greengram can be increased by selecting genotypes with more number of pods per plant, number pods per cluster, number of clusters per plant, number of branches per plant, biological yield per plant and harvest index.

In parents, days to 50% flowering had significant and positive correlation with days to maturity (0.834**) followed by plant height (0.347*), number of pods per plant (0.472**) and biological yield per plant (0.372*) whereas, significant and negative association of days to 50% flowering was observed with hundred seed weight (-0.318*). In crosses, days to 50%

flowering was associated positively and significantly with days to maturity (0.591**) and plant height (0.230*). The result revealed that if days to flowering increases, then days to maturity and plant height also increased. Azam *et al.* (2018) also reported similar findings.

Days to maturity showed significant and positive association with plant height (0.423**) and number of pods per plant (0.314*) in parents while, there was no significant association of days to maturity with other traits except with days to flowering in crosses. Hence it can be concluded that the late maturing tall plants may bear more clusters and produce higher biomass and grain yield. Similar findings were reported by Abbas *et al.* (2018).

In parents, plant height showed significant and positive correlation with biological yield per plant (0.410**) and significant negative correlation of this trait was observed with harvest index (-0.379*). In crosses, significant and negative correlation of plant height was observed with number of branches per plant (0.251**), number of pods per plant (-0.293**), number of clusters per plant (-0.251**), hundred seed weight (-0.301**), biological yield per plant (-0.429**) and harvest index (-0.262**). The negative and significant correlation of plant height with harvest index indicated that tall plants are generally low yielder and this finding is supported by finding of Narasimhulu *et al.* (2014) and Abbas *et al.* (2018).

In parents, number of branches per plant expressed significant and positive association with number of pods per plant (0.432**), number of clusters per plant (0.591**) and biological yield per plant (0.394**). Whereas in crosses, number of branches per plant registered significant and positive association with number of pods per plant (0.303**), number of pods per cluster (0.199*), hundred seed weight (0.217*), biological yield per plant (0.193*) and harvest index (0.216*). Reddy *et al.* (2019) reported similar findings for number of pods per plant and number of clusters per plant.

Significant and positive association of number of pods per plant was expressed with number of clusters per plant (0.698**), biological yield per plant (0.550**) in parents. While in crosses, the traits viz., number of pods per cluster (0.560**), number of clusters per plant (0.495**), biological yield per

plant (0.436**) and harvest index (0.309**) exhibited significant and positive association with number of pods per plant. Significant and positive correlation of number of pods per plant with harvest index is supported by findings of Sarkar *et al.* (2014).

In parents, number of pods per cluster displayed strong negative association with number of clusters per plant (-0.568**). In crosses, significant and positive association of this trait was expressed with hundred seed weight (0.224*) and biological yield per plant (0.224*). However, strong negative association of this trait was observed with number of clusters per plant (-0.407**).

Number of clusters per plant expressed significant and positive correlation with biological yield per plant (0.356*) in parents. While in crosses, significant and positive association of this trait was observed with biological yield per plant (0.236**) and harvest index (0.211*). On contrary, it had significant and negative association with hundred seed weight (-0.204*). Thus plants having more clusters would bear more pods resulting increase in yield. Similar results were reported by Sarwar *et al.* (2002) and Sadiq *et al.* (2005). Negative and significant association of this trait with 100 seed weight was reported by Narasimhulu *et al.* (2014).

Number of seeds does not revealed significant correlation with any of the traits in the parents. In crosses, this trait revealed significant and positive association with hundred seed weight (0.268**) whereas, strong significant and negative association of number of seeds per pod was expressed with biological yield per plant (-0.289**) and harvest index (-0.493**).

Hundred seed weight does not expressed any significant association with any of the traits in parents. Positive and significant association of hundred seed weight was observed with biological yield per plant (0.278**) and harvest index (0.361**) in crosses. Which is in accordance with the observations of Pandey *et al.* (2007), Haritha and Reddysekhar (2002), Gul *et al.* (2008) and Narasimhulu *et al.* (2014) who showed that 100 seed weight had significant and positive association with harvest index.

In parents, biological yield per plant showed strong negative and significant association with harvest index (-0.482**). However, in crosses this trait revealed highly significant and positive association with harvest index (0.462**).

5.5 Path coefficient analysis

Correlation studies permit only a measure of relationship between pair of traits. The actual contribution of an attribute and influence through other characters could be arrived only by way of partitioning the correlation coefficient into direct and indirect effects by path coefficient analysis. This will be very much helpful in rationalizing the basis of selection more meaningfully in a breeding programme.

In the present study, path coefficient analysis was carried out based on fourteen parents and 40 crosses for seed yield and its attributing characters. The genotypic direct and indirect effects were found slightly higher in magnitude as compared to phenotypic direct and indirect effects (Table 4.13 and 4.15). The discussion is presented here under.

5.5.1 Direct effects of yield attributing traits on seed yield in parents and crosses

In parents, number of pods exerted highest direct effect on seed yield followed by number of branches per plant, harvest index, plant height, hundred seed weight, biological yield per plant and days to maturity. Conversely, highest negative direct effects on seed yield was exhibited by number of clusters per plant followed by days to 50% flowering.

In crosses, harvest index exhibited higher positive direct effect on seed yield followed by biological yield per plant, number of seeds per pod, number of pods per cluster and days to 50% flowering. Conversely hundred seed weight, plant height, number of clusters per plant and number of branches per plant exerted negative direct effects on seed yield. Other negative indirect effects were negligible. The findings of earlier researcher's viz., Saifullah and Mahmood (2002), Mallikarjuna *et al.* (2006), Pandey *et al.* (2007), Itefa *et al.* (2014) and Narasimhulu (2014) were in the line with present findings for harvest index. Positive direct effects of number of pods per plant, number of

branches per plant, number of seeds per pod and hundred seed weight on seed yield were reported by Sanhita *et al.* (2019). Positive direct effect of plant height on seed yield was reported by Manivelan *et al.* (2019) whereas positive direct effect of days to 50% flowering as well as negative direct effects of days to maturity, plant height, hundred seed weight and number of seeds per pod was reported earlier by Marawar *et al.* (2020).

The critical analysis of the results of path analysis for seed yield revealed that direct effect of biological yield per plant and harvest index were high and positive in both parents and crosses, indicating that they are the major contributing characters for seed yield in greengram. Direct effects of number of pods per plant and number of clusters per plant were negative in both parents and crosses. Similar trends were evident from the studies of Haritha and Reddydekhar (2002), Mallikarjuna *et al.* (2006), Pandey *et al.* (2007), Itafa *et al.* (2014) and Narasimhulu *et al.* (2014). In parents, number of pods per plant exhibited highest direct effect on seed yield per plant hence, number of pods per plant also appeared as important direct yield components at genotypic level. Number of pods per plant was identified as important yield component by Pandey *et al.* (2007), Khajudparn and Tantasawat (2011), Ahmed *et al.* (2013), Jyothsna and Anuradha (2013), Srikanth *et al.* (2013), Lalinia and Khameneh (2014).

5.5.2 Indirect effects of yield attributing traits on seed yield in parents and crosses

Majority of indirect effects of various independent traits *via* other traits were negligible of either signs. There were only few characters having higher, moderate and low positive or negative indirect effects.

In parents, days to 50% flowering exerted moderately positive indirect effect on seed yield per plant through indirect positive effects of number of pods per plant followed by number of branches per plant, plant height, biological yield per plant and days to maturity. While negative indirect effects were exhibited through number of clusters per plant, number of clusters per pod and hundred seed weight. Remaining indirect effects of this trait *via* other traits were negative and relatively low and negligible. In crosses, indirect

effects of days to 50% flowering on seed yield per plant via other traits was extremely low and negligible. Positive indirect effect of days to 50% flowering on seed yield per plant was observed via positive indirect effects of number of pods per plant and plant height whereas, negative indirect effect of this trait on seed yield per plant via hundred seed weight was in conformity with the result of Alom *et al.* (2014).

In parents, days to maturity exhibited high and positive indirect effect on seed yield per plant via indirect and positive effects of number of pods per plant, plant height, number of branches per plant and biological yield per plant whereas, negative indirect effects were exerted via number of pods per cluster, number of clusters per plant and hundred seed weight. In crosses, indirect effects of days to maturity on seed yield via other traits were extremely low and negligible. The result of positive indirect effect of days to maturity via number of pods per plant and biological yield per plant was in conformity with the findings of Abbas *et al.* (2018).

In parents, moderate and negative indirect effect of plant height was exhibited on seed yield per plant through positive indirect effects via number of clusters per plant and biological yield per plant. Harvest index, number of pods per cluster, number of pods per plant, number of branches per plant, hundred seed weight and days to 50% flowering contributed towards negative indirect effects of plant height on seed yield per plant. In crosses, high negative indirect effect of this trait on seed yield per plant was showed by positive indirect effects of hundred seed weight and number of seeds per pod whereas, biological yield per plant and harvest index exhibited negative indirect effects on seed yield per plant. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses. Similar results for positive indirect effects on seed yield per plant via number of pods per plant, number of branches per plant, hundred seed weight, number of seeds per pod and days to 50% flowering was reported by Sarkar *et al.* (2014). Whereas, positive indirect effect via number of pods per plant and biological yield per plant was earlier reported by Abbas *et al.* (2018). Indirect negative effects of plant height on seed yield per plant via number of branches per plant, number of pods per plant, hundred

seed weight and number of seeds per pod were in conformity with the findings of Marawar *et al.* (2020).

In parents, number of branches per plant exerted positive and high indirect effect on seed yield per plant via positive and indirect of other traits viz., number of pods per plant and biological yield per plant while, negative indirect effects were contributed via number of clusters per plant, harvest index and hundred seed weight. In crosses, this trait registered moderately positive indirect effect on seed through indirect positive effects of biological yield per plant, harvest index and number of seeds per pod whereas, hundred seed weight exhibited negative indirect effect on seed yield per plant. Other indirect effects of this trait via other traits either positive or negative were relatively low and negligible in both parents and crosses. Manivelan *et al.* (2019) reported same results as the present findings for the positive indirect effect via number of seeds per pod and number of pods per plant

Number of pods per plant exerted high and positive indirect effect on seed yield per plant through indirect positive effects via number of branches per plant and biological yield per plant. Whereas, indirect and negative effects were exhibited via number of clusters per plant, harvest index, number of pods per cluster and days to 50% flowering in parents. In crosses, positive and high indirect effect of this trait was registered by indirect positive effects of harvest index and biological yield per plant. Whereas number of seeds per pod exerted negative indirect effect on seed yield per plant. Other indirect effects of this trait via other traits either positive or negative were relatively low and negligible in both parents and crosses.

In parents, number of pods per cluster had negative and indirect effect on seed yield per plant through positive and indirect effects via number of clusters per plant, number of pods per plant and plant height while negative and indirect effects were registered through hundred seed weight, harvest index and days to 50% flowering. In crosses, number of pods per cluster registered high and positive indirect effect on seed yield per plant through indirect and positive effects exerted by biological yield per plant and harvest index while, hundred seed weight showed negative indirect effect on seed

yield per plant. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses.

Number of clusters per plant in parents registered high and positive indirect effect on seed yield per plant via indirect and positive effects exhibited by number of pods per plant, number of branches per plant, number of pods per cluster, biological yield per plant and hundred seed weight. Plant height, harvest index and days to 50% flowering exhibited negative indirect effects on seed yield per plant. In crosses, this trait registered high and positive indirect effect on seed yield per plant via indirect and positive effects of harvest index and biological yield per plant. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses. The result of positive indirect effect via number of pods per plant and biological yield per plant is in conformity with the findings of Abbas *et al.* (2018).

Number of seeds per pod exhibited high and positive indirect effect on seed yield per plant via indirect positive effects of number of pods per cluster, number of branches per plant, number of pods per plant and harvest index. Whereas number of clusters per plant, plant height and hundred seed weight registered negative indirect effects on seed yield per plant in parents. In crosses, highly negative indirect effect of this trait on seed yield was observed through indirect negative effects contributed via harvest index and biological yield per plant. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses. Manivelan *et al.* (2019) also reported positive indirect effect of this trait with number of branches per plant and seed yield per plant.

In parents, hundred seed weight registered negative and negligible effect on seed yield per plant. Number of pods per cluster and days to % flowering exhibited indirect positive effect on seed yield whereas negative indirect effects were exerted via number of clusters per plant, number of branches per plant, number of pods per plant and plant height. In crosses, this trait exhibited high positive indirect effect on seed yield per plant via positive and indirect effects contributed by harvest index, biological yield per plant and number of seeds per pod. Other indirect effects of this trait *via* other traits

either positive or negative were relatively low and negligible in both parents and crosses. Positive indirect effect of 100 seed weight on seed yield per plant via number of seeds per pod was reported by Manivelan *et al.* (2019), positive indirect effect via number of seeds per pod was reported by Azam *et al.* (2018) and positive indirect effect via biological yield per plant was from Abbas *et al.* (2018).

Biological yield per plant recorded highly positive indirect effect on seed yield per plant *via* indirect and positive effects exhibited via number of pods per plant, number of branches per plant and plant height. While number of clusters per plant, harvest index, number of pods per cluster, days to 50 % flowering and hundred seed weight exerted indirect negative effects on seed yield. In crosses, highly positive indirect effect of this trait on seed yield per plant was exhibited through indirect positive effect via harvest index and negative indirect effect via number of seeds per pod. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses. Positive indirect effect on seed yield per plant through number of pods per plant was earlier reported by Abbas *et al.* (2018) and Kritika *et al.* (2017) whereas positive indirect effect via number of branches per plant was reported by Kritika *et al.* (2017).

In parents, harvest index registered moderately positive indirect effect on seed yield per plant through positive and indirect effects exhibited via number of pods per cluster and number of clusters per plant while, indirect negative effects were contributed via number of pods per plant, plant height, number of branches per plant and biological yield per plant. In crosses, high and positive indirect effect of this trait on seed yield per plant was observed which was contributed via indirect positive effect of biological yield per plant. Number of seeds per pod and hundred seed weight exerted indirect negative effects on seed yield per plant. Other indirect effects of this trait *via* other traits either positive or negative were relatively low and negligible in both parents and crosses.

5.6 Heterosis for yield and yield attributing traits

The *per se* performance alone may not be useful to predict the best cross combination. The studies on extent of heterosis are useful to support the results on the basis of *per se* performance particularly undertaken in comparison with the checks for their practical utility at field level. The heterosis plays an important role for increasing the productivity of crop without much increase in the cost of production. Therefore, it is of great importance to plant breeders. The aim of the present study was to identify superior cross combinations which will exhibit good amount of heterosis for seed yield per plant and its component traits.

1. Days to 50% flowering

Earliness in flowering is highly desirable character in Mungbean therefore the cross combination exhibited negative heterosis are considered as superior. The parents requiring less number of days to flower are considered as the better parents in respective cross. The highest significant negative mid parent, better parent and standard heterosis was recorded by crosses viz., TJM 136 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Kanika, TMB 37 X Virat and HUM 1 X PDM 139 (Table 4.16). Similar results were also reported by Halkunde (1992) and Patil (1992), Jahagirdar (2001), Singh and Chauhan (2011).

2. Days to maturity

For days to maturity among 40 crosses, the crosses TJM 136 X Virat and TMB 37 X PDM 139 exhibited the highest significant negative standard heterosis, mid and better parent heterosis (Table 4.16). This is an indicative of the possibility of isolating early maturing individuals in the succeeding generations. These results were in consonance with the findings of Naidu and Satyanarayana (1993), Jahagirdar (2001), Singh and Chauhan (2011) and Kuldeep *et al.* (2006).

3. Plant height (cm)

For plant height (cm) the highest significant positive heterosis over mid parent, better parent and standard heterosis was recorded in crosses viz., LGG 460 X PDM 139, SL 668 X Virat, Pusa Vishal X PDM 139 and Pusa

Vishal X Virat respectively (Table 4.16). These results were in agreement with the finding of Halkunde (1992), Patil (1992) and Jahagirdar (2001).

4. Number of branches per plant

The crosses HUM 1 X Shikha, Ganga 8 X PDM 139, PDM 11 X PDM 139 and TJM 136 X Virat registered the highest positive significant heterosis over mid parent, better parent and standard variety PDM 139 (Table 4.17). Hence, these crosses can be considered as good heterotic crosses for number of branches per plant, which may resulted in higher productivity. Similar results of higher magnitude of heterosis and heterobeltiosis for number of branches per plant was also reported by Khattaka *et al.* (2002), Singh and Chauhan (2011) and Sunil and Prakash (2011).

5. Number of pods per plant

For standard heterosis, heterobeltiosis and relative heterosis, the crosses viz., TJM 3 X Virat, LGG 460 X Kanika, HUM 1 X Virat, SL 668 X Virat, Ganga 8X PDM 139, TMB 37 X Virat, TJM 3 X Kanika and Ganga 8 X Kanika were found superior. Findings indicated that these crosses can be well utilized in the genetic enhancement number of pods per plant (Table 4.17). These findings are in agreement with the reports of Jahagirdar (2001), Zubair *et al.* (2010), Singh and Chauhan (2011) and Sunil and prakash (2011). They all reported that heterosis for seed yield per plant was due to heterosis in number of pods per plant.

6. Number of pods per cluster

For standard heterosis, heterobeltiosis and relative heterosis, the crosses viz., TJM 3 X Virat, SL 668 X PDM 139 and SL 668 X Virat recorded highest significant positive heterosis (Table 4.17). These crosses which were found to be heterotic for the number of pods per cluster may be utilized to increase the seed yield. This is in conformity with the results of Jahagirdar (2001), Khattaka *et al.* (2002) and Singh and Chauhan (2011) in greengram.

7. Number of clusters per plant

The crosses viz., Ganga 8 X virat, TJM 3 X PDM 139, LGG 460 X Kanika, TJM 3 X Virat and HUM 1 X Virat registered positive and significant average

heterosis, heterobeltiosis and standard heterosis over the best cultivar (Table 4.18). Similarly high better parent heterosis was recorded earlier by Cheralu *et al.* (2002), Singh and Chauhan (2011), Sathya and Jayamani (2011) and Sunil and Prakash (2011).

8. Number of seeds per pod

the cross combination Pusa Vishal X Virat registered positive and significant average heterosis, heterobeltiosis and standard heterosis over the best cultivar (Table 4.18). Hence this cross can be considered as best heterotic cross to increase seed yield in greengram which is in conformation with the findings of Sekhar *et al.* (1994).

9. Hundred seed weight (g)

The crosses viz., TJM 3 X PDM 139 and HUM 1 X Shikha exhibited positive and significant average heterosis, heterobeltiosis and standard heterosis over the best cultivar PDM 139 (Table 4.18). Hence these two crosses can be considered as best heterotic crosses for hundred seed weight and for increasing seed yield in greengram.

10. Biological yield per plant (g)

For standard heterosis, heterobeltiosis and relative heterosis, the crosses viz., HUM 1 X Virat, LGG 460 X Virat, LGG 460 X Kanika, HUM 1 X Shikha, TMB 37 X Virat, TJM 3 X Virat, SL 668 X PDM 139, TJM 136 X PDM 139 HUM 1 X PDM 139 and TMB 37 X Shikha occupied top ten positions respectively (Table 4.19). These crosses were found to be more heterotic for biological yield per plant.

11. Harvest index (%)

The cross combinations viz., TJM 196 X Shikha, TJM 196 X Kanika, TJM 3 X Shikha, Ganga 8 X Shikha, Pusa Vishal X Shikha, Pusa Vishal X Kanika and PDM 11 X Shikha recorded positive and significant relative heterosis, heterobeltiosis and standard heterosis (Table 4.19). These crosses can be advanced to further generations to isolate desirable segregants with higher harvest index to result in high economic yield, conforming the results of Vikas and Singh (1998) and Khattaka *et al.* (2002).

12. Seed yield per plant (g)

Out of 40 crosses, 10 crosses viz., HUM 1 X Shikha, TJM 3 X Shikha, HUM 1 X Virat, SL 668 X Kanika, Ganga 8 X Shikha, LGG 460 X Virat, LGG 460 X Kanika, TJM 196 X Virat, Pusa Vishal X Shikha and SL 668 X PDM 139 were registered as top 10 for exhibiting significant positive relative heterosis, heterobeltiosis as well as standard heterosis for this trait (Table 4.19). This finding indicating that these crosses may throw superior segregants for seed yield per plant in the succeeding generations. High heterosis over better parent for seed yield was also reported earlier by Jahagirdar (2001), Bhagora et al. (2013), Srivastava and Singh (2013) in greengram.

5.6.1 Recombination breeding

Recombination breeding makes use of a fixable additive gene action. The criteria for the selection of crosses for recombination breeding to obtain outstanding recombinants in segregating generations are based on the fact that the parents should have significant *gca* effect and corresponding crosses with non significant *sca* effects for the character whose improvement is sought. The segregation of such crosses is likely to throw desirable recombinants possessing favorable additive genes from both the parents Khorgade *et al.* (1989). Based on the aforesaid consideration, the 40 cross combinations were evaluated for recombination breeding for each of the twelve biometrical traits studied; the lines and testers with significant GCA effects, possible cross combinations and the promising crosses for recombination breeding are presented in (Table 4.25). The cross TMB 37 X Virat for days to 50 % flowering, days to maturity, biological yield per plant and PDM X Virat for days to % flowering; TJM 3 X Kanika for number of pods per plant, could be expected to produce superior recombinants.

For number of pods per cluster SL 668 X Kanika was identified for recombination breeding, while for hundred seed weight, the cross TJM 136 X Shikha was considered for recombination breeding; for biological yield per plant and harvest index the crosses TJM 196 X Shikha and HUM 1 X Shikha

were expected to produce superior recombinants. The cross TJM 196 X Kanika was identified as superior recombinant for seed yield per plant.

High *sca* effects show predominance of non-additive gene effects mainly dominance gene effects Nadarajan and Gunasekaran (2005). Cross combinations which exhibited high *sca* and derived from parents having high *gca* effects can also be used for recombination breeding. However, the selection of superior genotypes for cultivar development must be delayed to later generations to allow for the fixation of maximum homozygosity Nadarajan and Gunasekaran (2005).

5.6.2 Heterosis breeding

In general, the extent of heterosis has often been estimated over mid-parent or better parent with the objective of studying the nature of gene action involved in the parental combinations. However, the heterosis recorded over mid or better parent has little applied utility if parents involved have relatively poor *per se* performance. For commercial exploitation, the magnitude of heterosis should be at least 20-30 per cent higher in yield than best cultivated variety. Swaminathan *et al.* (1972) stressed the need for computing standard heterosis for commercial exploitation of hybrid vigour. Hence, for the evaluation of crosses, standard heterosis over the best cultivar PDM 139 was estimated for different characters in greengram and discussed for their performance here under.

Among the crosses, TJM 136 X PDM 139 recorded significant standard heterosis for number of pods per plant, number of pods per cluster, hundred seed weight, biological yield per plant, seed yield per plant with earliness in 50% flowering and maturity. The cross combination TJM 136 X Virat for plant height, number of branches per plant, number of pods per plant, number of pods per cluster, biological yield per plant, harvest index with earliness in 50% flowering and maturity both. The cross TJM 136 X Kanika for plant height, number of pods per cluster, number of clusters per plant and number of seeds per pod while, the cross TJM 136 X Virat for plant height, number of branches per plant, number of pods per plant, number of pods per cluster and harvest index. TMB 37 X PDM 139 for days to flowering, days to maturity, number of

pods per plant, number of clusters per plant, biological yield per plant and seed yield per plant; TMB 37 X Shikha for days to flowering, plant height, number of branches per plant, number of pods per plant, number of clusters per plant, number of seeds per pod, biological yield per plant and seed yield per plant; TMB 37 X Kanika for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant and seed yield per plant; TMB 37 X Virat for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant and seed yield per plant.; HUM 1 X PDM 139 for days to 50% flowering, plant height, number of pods per plant, number of pods per cluster and biological yield per plant; HUM 1 X Kanika for days to 50% flowering, plant height, number of pods per plant, biological yield per plant and seed yield per plant.

Similarly, the cross combinations viz., PDM 11 X Shikha for days to 50% flowering, plant height, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant, harvest index and seed yield per plant while PDM 11 X Kanika for days to flowering, plant height, number of pods per plant, number of pods per cluster, number of seeds per pod, hundred seed weight, biological yield per plant, harvest index and seed yield per plant; PDM 11 X Virat for days to flowering, plant height, number of pods per plant, number of clusters per plant, biological yield per plant and seed yield per plant; TJM 196 X PDM 139 for plant height, number of branches per plant, number of pods per cluster, number of clusters per plant, hundred seed weight, biological yield per plant and seed yield per plant; TJM 196 X Shikha for plant height, number of branches per plant, number of clusters per plant, biological yield per plant, harvest index and seed yield per plant; TJM 196 X Kanika for plant height, number of pods per cluster, number of seeds per pod, hundred seed weight, biological yield per plant, harvest index and seed yield per plant; TJM 3 X PDM 139 for plant height, number of pods per plant, number of pods per cluster, hundred seed weight, biological yield per plant and harvest index; TJM 3 X Shikha for plant height, number of pods per cluster, number of clusters per plant, biological yield per plant,

harvest index and seed yield per plant; TJM 3 X Virat for plant height, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant and seed yield per plant and the cross combination Ganga 8 X PDM 139 for plant height, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant and seed yield per plant. Similar results were also observed by Aher *et al.* (2000) for seed yield; Joseph and Santhoshkumar (2000) for plant height, number of branches per plant, pods per plant, test weight and seed yield; Loganathan *et al.* (2001) for number of seeds per pod; Sunil and Prakash (2011) for number of branches per plant, pods per plant, test weight and seed yield per plant and Srivastava and Singh (2013) for seed yield per plant.

5.6.3 *per se* performance, sca effects and heterosis percent

Hybrid vigor can be very well exploited through *per se* performance, sca effects and magnitude of heterosis. Selection based on any one of the criteria may be often misleading. The cross with high heterosis may also be observed with low mean performance and the cross with high mean value always may not record high sca effects. Therefore, all the three criteria have to be considered together for selection of superior crosses. Thus, in the present investigation, among 40 crosses analyzed (Table 4.26), the crosses TJM 136 X Virat, TJM 136 X PDM 139 and TMB 37 X Kanika exhibited a superior mean, sca effects and standard heterosis for days to 50% flowering and it was followed by crosses TJM 136 X Virat and TMB 37 X PDM 139 for days to maturity. Whereas the crosses Pusa Vishal X PDM 139, Pusa Vishal X Virat and LGG 460 X PDM 139 for plant height. it was followed by the cross HUM 1 X Shikha for the trait number of branches per plant. The desired combination of *per se* performance, sca effects and standard heterosis were exhibited by the crosses LGG 460 X Kanika, TMB 37 X Virat, Ganga 8 x PDM 139 and TJM 3 X Shikha for number of pods per plant; cross combinations TMB 37 X Virat and TMB 37 X Kanika for number of pods per cluster; Ganga 8 X Virat, LGG 460 X Kanika, TJM 3 X Kanika and TMB 37 X Shikha for number of clusters per plant; Pusa Vishal X Virat, TJM 136 X Kanika and TMB 37 X Shikha for number of seeds per pod; whereas crosses HUM 1 X Shikha, TJM 136 X PDM 139 and TJM 3 X PDM 139 for the trait hundred seed weight

followed by the crosses LGG 460 X Kanika, TJM 196 X Virat, HUM 1 X Virat and LGG 460 X Virat for biological yield per plant; Pusa Vishal X Shikha and Pusa Vishal X Kanika for harvest index and crosses TJM 196 X Virat, HUM 1 X Virat, HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat for seed yield per plant.

5.7 Combining ability analysis

A suitable breeding methodology and the identification of superior parents are the most important pre-requisites for the development of high yielding genotypes. Combining ability analysis provides guidelines for the assessment of relative breeding potential of parental material through characterization of the nature and magnitude of gene action involved in the expression of quantitative traits, which can be used in pursuing a systematic breeding programme. General combining ability is the average performance of the genotype in combination with all the other genotypes in a set of crosses and it is attributed to additive and additive $\times$ additive gene action and is fixable in nature, whereas the specific combining ability is the average performance of specific cross combination expressed as deviation from the population mean and it is primarily due to non-additive gene effects that includes dominance, epistasis and other interaction effects which are non-fixable, but often brings about in phenotypes that are not attainable under normal additive gene action Sprague and Tatum (1942). Thus, in the present study, the combining ability analysis was carried out for 14 parents and 40 crosses derived from 10 lines $\times$ 4 testers programme to obtain information on *gca* effects of parents and *sca* effects of crosses which would help in selection of better parents, cross combinations and breeding method to be employed for the improvement of the yield and related traits.

5.7.1 Analysis of variance for combining ability

Analysis of variance for the combining ability using Line X Tester mating design for twelve characters was given in (Table 4.20). It revealed that treatments registered highly significant differences for all the characters. The parents differed significantly for all the characters except for number of seeds per pod indicating the existence of sufficient variability in the material studied.

Mean sum of squares due to parents vs. crosses were significantly different for all the characters except number of seeds per pod, revealing good scope for manifestation of heterosis in all the characters studied. The effect of crosses was partitioned into lines, testers and their interactions. The mean sum of squares due to lines were significant for all the characters except for number of seeds per pod, suggesting larger contribution of lines towards general combining ability variance components for most of the traits. The mean sum of squares due to testers were also significant for eight characters except for number of branches per plant, number of seeds per pod, hundred seed weight and seed yield per plant, indicating significant contribution of testers towards component of gca variance. The mean sum of squares due to Line X Tester interaction effects were significant for five characters indicating significant contribution of crosses for specific combining ability variance components while it was non-significant for remaining characters viz., days to 50 % flowering, days to maturity, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight and seed yield per plant. These results indicate the presence of considerable variability among hybrids rather than lines and testers. Similar results were reported by Saxena and Sharma (1989), Khairnar *et al.* (2003) and Rao *et al.* (2006).

5.7.2 Estimates of combining ability variances

In the present study, the magnitude of SCA variance was higher than GCA variance for all the quantitative characters (Table 4.21) indicating the preponderance of non-additive gene action in the expression of these traits. The ratio of variance due to general combining ability ranged from 0.002 to 0.639. As judged by the ratio of additive and dominance variance among all twelve characters, the ratio of GCA per SCA was less than one for all the biometrical characters except plant height which indicated that all the eleven characters were governed by non additive gene action and only one character was governed by additive gene action. The present findings were in congruent with the reports of Kumar *et al.* (2010); Srivastava and Singh (2013) and Anbu Selvam (2012) in mungbean.

From the estimates of additive and dominance variance, it was observed that dominance variance was predominant for all the characters

except for plant height, indicating the major role of non-additive gene action and was highest for number of pods per plant followed by harvest index, biological yield per plant and plant height.

Anbumalarmathi *et al.* (2004) reported similar results for days to 50 per cent flowering, plant height, number of branches per plant, clusters per plant, pods per cluster, pods per plant, seeds per pod and single plant yield in greengram. Marappa (2008) observed the non-additive gene action for days to flowering, plant height, number of clusters per plant, pods per plant, seeds per pod, dry weight per plant, harvest index and seed yield per plant. Similar results were also reported by Joseph and Santhosh Kumar (2000) for number of branches per plant, pods per cluster, pods per plant, seeds per pod and single plant yield; Patil *et al.* (2011) for days to 50 per cent flowering, days to maturity, number of branches per plant, clusters per plant and single plant yield; Rohman *et al.* (2003) for single plant yield; Ajmal *et al.* (2007) for number of pods per plant, seeds per pod and single plant yield. From the above discussion, it is clearly evident that almost all the traits were controlled by non-additive gene action. To exploit the non-additive gene action of these traits, heterosis breeding or hybridization followed by selection in later generations is recommended for the improvement of these traits in greengram.

However, present results were contradictory to the reports of Saxena and Sharma (1989), Reddy *et al.* (1992) and Ramamoorthi *et al.* (1997) who reported additive gene action for the most of the characters studied.

5.7.3 General combining ability

The *gca* effects reflect performance of parental lines in combination with all other lines, so parents with highest *gca* effects should have greater impact on the trait improvement. Dhillon (1975) suggested that combining ability provides useful information on the choice of parents in terms of expected performance of the hybrids and progenies. Singh and Hari Singh (1985) and Tiwari *et al.* (1993) had also suggested that parents with high *gca* effects could produce transgressive segregants in F_2 or later generations.

The close examination of the general combining ability effects of the parents indicated that none of the parents were found to be good combiner for all traits Samantaray *et al.* (2018). Among the lines, TJM 196 ranked as top by exhibiting significant *gca* effects for six traits viz., days to maturity, number of branches per plant, hundred seed weight, biological yield per plant, harvest index and seed yield per plant. This was followed by HUM 1 as a good combiner for five traits viz., number of pods per plant, hundred seed weight, biological yield per plant, harvest index and seed yield per plant. The TMB 37 was also a good general combiner for date to 50% flowering, date to maturity, number of branches per plant and biological yield per plant followed by TJM 136 for days to 50% flowering, days to maturity, number of seeds per pod and hundred seed weight while, LGG 460 for plant height, number of clusters per plant and biological yield per plant. Ganga 8 was for number of branches per plant, number of clusters per plant and biological yield per plant. TJM 3 for number of pods per plant, number of pods per cluster and number of clusters per plant; SL 668 for number of pods per cluster and biological yield per plant; Pusa Vishal for plant height and number of seeds per pods and PDM 11 for days to 50% flowering and plant height.

Among testers, Kanika was the best general combiner for most of the traits viz., plant height, number of pods per plant, number of pods per cluster biological yield per plant and seed yield per plant followed by Virat for days to flowering, days to maturity, number of pods per plant, number of clusters per plant and biological yield per plant. Shikha for hundred seed weight, biological yield per plant, harvest index and seed yield per plant (Table 4.22). Similar results were reported by Jahagirdar (2001), Aher *et al.*, (1999), Singh (2005), Barad *et al.*, (2008), and Surashe *et al.*, (2017).

5.7.4 *Per se* performance and general combining ability (*gca*) effects

Combination of *per se* performance and *gca* effects would result in the selection of potential parents with good reservoir of superior genes (Singh and Harisingh 1985).

In the present investigation, TJM 196 was the best parent based on both *per se* and *gca* effects for number of branches per plant, biological yield

per plant and seed yield per plant followed by TJM 136 which had desirable performance for days to flowering and days to maturity. TMB 37 had desirable performance for number of branches per plant and Kanika was the best parent for plant height (Table 4.24). Thus it was evident that crosses involving TJM 196, TJM 136, TMB 37 and Kanika as parents would result in the identification of superior segregants with favorable genes for yield and attributing characters.

5.7.5 Specific combining ability

In the present investigation, the cross TMB 37 X Kanika recorded significant sca effects for days to flowering, plant height, number of pods per plant, number of pods per cluster and number of clusters per plant, while the cross TJM 136 X PDM 139 showed significant sca effect for days to flowering, number of branches per plant, hundred seed weight, biological yield per plant and seed yield per plant. Whereas the cross LGG 460 X Kanika for number of clusters per plant, hundred seed weight, biological yield per plant and seed yield per plant followed by the crosses TJM 196 X PDM 139 for days to flowering, number of pods per plant and number of clusters per pod. Ganga 8 X PDM 139 for number of branches per plant, number of pods per plant and number of pods per cluster, while the cross Ganga 8 X Shikha for days to maturity, plant height and seed yield per plant. TJM 3 X Shikha for plant height, number of pods per plant and seed yield per plant. Whereas the cross TMB 37 X Shikha for number of clusters per plant, number of seeds per pod and biological yield per plant. The cross HUM 1 X Virat for number of clusters per plant, biological yield per plant and seed yield per plant followed by the crosses Pusa Vishal X Shikha and Pusa Vishal X Kanika for biological yield per plant, harvest index and seed yield per plant (Table 4.23). The crosses which were identified as superior crosses can be effectively utilized in hybrid breeding programme. Similar results for specific combining ability were reported by, Manjare *et al.* (1976), Ahuja (1980), (2012), Barad *et al.* (2008), and Patil *et al.* (2011),

It is evident from the cross combinations, which expressed high sca effects for seed yield per plant have invariable positive sca effects for one or more yield related traits also. Grafius (1959) has already suggested that there

may not be separate genes for yield per se and yield being end product of multiple gene interactions among various yield components.

5.8 Generation mean analysis

With a view to study the nature and mode of gene action of yield and its components, generation mean analysis was carried out utilizing mean data of six basic generations viz., P_1 , P_2 , F_1 , F_2 , B_1 and B_2 of five selected crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika. The significance of A and B scales indicates the presence of all the three types of non-allelic interactions viz., additive $\times$ additive (i), additive $\times$ dominance (j) and dominance $\times$ dominance (l). The significance of C scale suggests dominance $\times$ dominance (l) type of interaction. The significance of D scale reveals additive $\times$ additive (i) type of gene interaction and significance of both C and D scales indicates additive $\times$ additive and dominance $\times$ dominance type of gene interactions. The significance of any one of the scaling tests indicates inadequacy of simple additive - dominance model.

The mean performance of six generations with respect to yield associated traits along with standard errors and the estimates of individual scaling tests (A, B and C) and genetic effects viz., mean (m), additive (d), dominance (h), additive $\times$ additive (i), additive $\times$ dominance (j), and dominance $\times$ dominance (l) were collated in table 4.27 to 4.50 and discussion for the same is presented on character wise here under:

1. Days to 50% flowering

Significance of one or more scaling tests indicated that the simple additive- dominance model was inadequate for this trait in all the crosses. Mean (m) effects were significant and positive in all crosses. Estimates of additive (d) gene effects were negative and significant for one cross TJM 196 X Kanika while positive and significant in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat. Dominance (h) gene effects and additive $\times$ additive (i) interaction effects were significant and positive in all crosses except HUM 1 X Shikha and Ganga 8 X Shikha. Additive $\times$ additive (j) gene effects were significant and negative in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460

X Kanika while positive and significant in TJM 196 X Kanika. Dominance x dominance (l) gene effects was negative and significant for LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika. The estimates of (h) and (l) components were dissimilar in direction for all crosses indicating the presence of duplicate type of epistasis in the genetic control of this trait except in HUM 1 X Shikha indicating complementary type of epistasis. In majority of the crosses dominance gene effects were higher in magnitude than additive gene effects. Godhani *et al.* (1978) and Murthy (2000) reported additive gene action while Hegde *et al.* (1994) reported non-additive gene action for days to 50% flowering. Duplicate type of epistasis was present in all the crosses except in HUM 1 X Shikha, where complementary epistasis was predominant. Presence of non-allelic interactions (duplicate and complementary) indicates the transgressive segregants can be expected which leads to improved performance in F_{2S} and backcrosses. Rao *et al.* (1984) and Murthy (2000) also reported duplicate epistasis for days to 50% flowering. Positive signs of (i) in crosses LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika revealed that selection could be practiced in early segregating generations. Presence of duplicate epistasis and significant additive, dominance and non-allelic interactions was in agreement with the report of Seenaiiah (1995) and Patel *et al.* (2012) which indicated that it is worthwhile to inter mate the selects in segregating generations, which would result into the accumulation of favorable genes. Hence, bi parental mating or few cycles of recurrent selection followed by pedigree method of selection may be followed for bringing improvement in this trait.

2. Days to maturity

Among the five crosses studied the A, B and C scales were non-significant in the case of HUM 1 X Shikha which indicated the adequacy of additive-dominance model for this cross. The mean (m) effects were significant and positive in all crosses. Additive (d) gene effects were positive and significant for Ganga 8 X Shikha while significant and negative for TJM 196 X Kanika. Significant and positive dominance (h) gene effects were reported by LGG 460 X Virat and LGG 460 X Kanika while significant and positive additive x additive (i) interaction effects were observed for LGG 460 X

Virat and LGG 460 X Kanika. Significant (i) and non-significant (d) in crosses LGG 460 X Virat and LGG 460 X Kanika indicated the dispersion of genes in parents. Additive x dominance (j) gene effect was significant and positive in Ganga 8 X Shikha. Dominance x dominance (l) gene effect was significant and positive for LGG 460 X Virat whereas significant and negative for LGG 460 X Kanika. Positive and significant effects of (j) and (l) in Ganga 8 X Shikha and LGG 460 X Virat indicated that genes with positive effects were more often dominant and predominance of dominance x dominance interactions, respectively. The crosses HUM 1 X Shikha, Ganga 8 X Shikha, LGG 460 X Kanika and TJM 196 X Virat showed opposite signs of (h) and (l) components indicated presence of duplicate type of epistasis in the inheritance of days to maturity. Rao *et al.* (1984), Hegde *et al.* (1994), Murthy (2000) and Inderjit *et al.* (2006) also reported duplicate epistasis for this trait. Duplicate epistasis can be exploited by adopting recurrent selection for specific combining ability in order to exploit dominance and epistatic gene effects.

3. Plant height (cm)

Inadequacy of simple additive – dominance model to explain the genetic control of this trait was suggested by significance of one or more scaling tests in all the crosses studied. Among main effects mean (m) effect was significant and positive for all crosses. Additive (d) gene effect was significant and positive in Ganga 8 X Shikha and LGG 460 X Virat whereas, in cross combinations of LGG 460 X Kanika and TJM 196 X Kanika, negative and significant additive gene effects were observed. Dominance (h) gene effects were significant and positive in LGG 460 X Virat and LGG 460 X Kanika whereas it was significant and negative in HUM 1 X Shikha and Ganga 8 X Shikha. In general, magnitude of dominance was higher compared to additive effects. Godhani *et al.* (1978), Hegde *et al.* (1994), Ram (1997) and Gawande and Patil (2007) reported importance of dominance effect for this trait. Malik and Singh (1983), Ajit and Singh (1996) and Singh *et al.* (2007) observed that plant height was under the control of both additive and dominance gene effects.

Among interaction effects additive x additive (i) gene effects were negative in HUM 1 X Shikha and Ganga 8 X Shikha which suggests that selection may be deferred to later generations when desirable recombinants

become available. Similar results were also obtained by Inderjit *et al.* (2006) and Patel *et al.* (2012). whereas for LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika significant positive effects of (i) were observed. Additive x dominance (j) epistatic effects were significant and positive for TJM 196 X Kanika while crosses viz., Ganga 8 X Shikha and LGG 460 X Virat recorded a significant and negative additive dominance gene effect which indicates that genes with positive effects were more often recessive. Dominance x dominance (l) gene effects were positive and significant for HUM 1 X Shikha, Ganga 8 X Shikha and TJM 196 X Kanika whereas, significant and negative (l) gene effect were recorded for LGG 460 X Virat and LGG 460 X kanika. Hegde *et al.* (1994), Murthy (2000), Seenaiiah (1995), Inderjit *et al.* (2006) and Patel *et al.* (2012) also reported dominance x dominance effects for this trait. The estimates of (h) and (l) components were with opposite direction for all the crosses indicating presence of duplicate nature of epistasis in the inheritance of the trait. Hence, selection can be delayed until later generations when the dominance effects would have diminished.

4. Number of branches per plant

Significance of one or more scaling tests suggested the presence of non-allelic interactions. For number of branches per plant HUM 1 X Shikha recorded significant and mean (effect) while Ganga 8 X Shikha showed significant and positive mean effect. Additive (d) gene effects were significant and negative for HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika. Dominance (h) gene effect was significant and negative in Ganga 8 X Shikha whereas significant and positive dominance gene effects were observed for HUM 1 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika which indicates the complex nature of inheritance for branches per plant in these crosses which exhibited significant and positive dominance gene effects. Gawande and Patil (2007) and Singh *et al.* (2007) also reported the importance of dominance effect for this trait.

Among the interaction effects, positive and significant additive x additive (i) effects were recorded for HUM 1 X Shikha, LGG 460 X Kanika and TJM 196 X Kanika while other crosses recorded non-significant additive x additive gene effects. Additive x dominance (j) gene effects were significant and negative for HUM 1 X Shikha, Ganga 8 X Shikha, LGG 460 X Virat and TJM 196 X Kanika. Dominance x dominance (l) epistatic effects were positive

and significant in cross Ganga 8 X Shikha whereas crosses viz., HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika showed significant and negative dominance x dominance gene effects. Significant and positive dominance (h) gene effects observed in HUM 1 X Shikha, LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika indicated the presence of increaser alleles. The direction of dominance (h) and dominance x dominance (l) gene effects were opposite in all the crosses indicating the duplicate nature of epistasis in the genetic control of this trait. This is in conformity with the results of Singh *et al.* (2007). Presence of additive, dominance and non-allelic interaction effects suggests that intermating the selects in segregating generations to exploit both additive and non-additive components of genetic variability would be desirable to bring improvement in branches per plant.

5. Number of pods per plant

A, B and C scales indicated that the simple additive – dominance model was inadequate in all the crosses except TJM 196 X Kanika for number of branches per plant which indicated the adequacy of additive – dominance model for this cross. Mean (m) effects were significant and negative for all crosses except LGG 460 X Virat which showed significant and positive mean effect. Dominance (h) gene effects were significant and positive in all crosses and were found to be predominant with higher magnitude. Predominance of dominance effects for number of pods was also reported by Godhani *et al.* (1978), Hegde *et al.* (1994), Singh *et al.* (1994), Ram (1997), Murthy (2000), Gawande and Patil (2007) and Singh *et al.* (2007).

The additive x additive (i) effects were positive and significant in all crosses. Additive x dominance (j) gene effects were negative and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika whereas Ganga 8 X Shikha showed significant and positive additive x dominance gene effect. All the crosses recorded significant and negative dominance x dominance (l) gene effects. The dominance (h) and dominance x dominance (l) gene effects were found to be with dissimilar direction for all the crosses. Similar results were reported by Malik and Singh (1983), Hegde *et al.* (1994), Aher and Dahat (1999) and Singh *et al.* (2007). Predominant non-additive gene effects may retard the selection process in the earlier generations. Therefore, superior lines may be derived upon advancing the generations letting new combinations of alleles to arise.

6. Number of pods per cluster

Inadequacy of simple additive – dominance model to explain the genetic control of this trait was suggested by significance of one or more scaling tests indicating the presence of non-allelic interactions in the genetic control of number of pods per cluster. The mean (m) effects were positive and significant in Ganga 8 X Shikha and TJM 196 X Kanika whereas LGG 460 X Virat showed significant and negative mean effect. Additive (d) mean effects were significant and negative in HUM 1 X Shikha and LGG 460 X Kanika whereas other crosses showed non-significant additive mean effects. Significant and positive dominance (h) effects were recorded for HUM 1 X Shikha and LGG 460 X Virat while other crosses exhibited non-significant dominance (h) gene effects. Among the epistatic interaction effects, additive x additive (i) gene effects were significant and positive in HUM 1 X Shikha, Ganga 8 X Shikha and LGG 460 X Virat while other crosses recorded non-significant (i) gene effects. Additive x dominance (j) gene effects were significant and negative in HUM 1 X Shikha and TJM196 X Kanika. Dominance x dominance (l) gene effects was significant and negative in HUM 1 X Shikha and LGG 460 X Virat. The estimates of (h) and (l) components were with opposite signs in all the crosses studied indicating the duplicate type of epistasis in the inheritance of pods per cluster. Predominant role of non-additive gene action coupled with duplicate epistasis for this trait mostly restricts the scope for further improvement through direct selection. However, there is a scope to accumulate favorable genes by inter mating of transgressive segregants and to select still better performing homozygous progenies

7. Number of clusters per plant

Inadequacy of simple additive – dominance model to explain the genetic control of this trait was suggested by significance of one or more scaling tests indicating the presence of non-allelic interactions in the genetic control of number of clusters per plant. Among main effects, the mean (m) effects were significant and negative in Ganga 8 X Shikha and LGG 460 X Kanika while it was non-significant in remaining crosses. Additive (d) gene effects were significant and positive for LGG 460 X Virat, LGG 460 X Kanika and TJM 196 X Kanika whereas HUM 1 X Shikha and Ganga 8 X Shikha

exhibited negative additive gene effects. All the crosses showed significant and positive dominance (h) gene effects and additive x additive (i) interaction effects except LGG 460 X Virat where negative dominance gene effect and additive x additive interaction effects were observed. Similar results were reported by Hegde *et al.* (1994), Kute and Deshmukh (2002) and Gawade and Patil (2007). Additive x dominance (j) gene effects were negative and significant for all the four crosses and it was positive and significant for Ganga 8 X Shikha. Dominance x dominance (l) gene effect was negative and significant in HUM 1 X Shikha, Ganga 8 X Shikha and TJM 196 X Kanika whereas (l) gene effect was non-significant for rest of the two crosses. The estimates of (h) and (l) components were with opposite signs in all the crosses studied indicating the duplicate type of epistasis in the inheritance of number of clusters per plant.

8. Number of seeds per pod

Among the five crosses studied the A, B and C scales were significant in all of them indicating the inadequacy of simple additive – dominance model for all the crosses. Mean (m) effects were significant and positive for all the crosses except HUM 1 X Shikha which was non-significant. Additive (d) gene effect was significant and negative in LGG 460 X Virat whereas it was non-significant for rest of the crosses. Dominance (h) gene effects were positive and significant in HUM 1 X Shikha, LGG 460 X Virat and TJM 196 X Kanika while remaining crosses showed non-significant dominance gene effects. Dominance gene effects were found predominant over additive gene effects. Hegde *et al.* (1994), Singh *et al.* (1994), Ram (1997), Gawande and Patil (2007) and Singh *et al.* (2007) also reported similar results.

Among interaction effects additive x additive (i) interaction effects were significant for HUM 1 X Shikha and TJM 196 X Kanika whereas non-significant for rest of the crosses suggesting that selection may be deferred to later generations when desirable recombinants become available. Godhani *et al.* (1978), Ajit and Singh (1996) and Murthy (2000) also reported predominance of additive x additive effect for this trait. Additive x dominance (j) gene effect was positive and significant in Ganga 8 X Shikha whereas non-significant for rest of the crosses. Dominance x dominance (l) gene effects were negative and significant in HUM 1 X Shikha, Ganga 8 X Shikha and TJM

196 X Kanika whereas remaining crosses exhibited non-significant (l) gene effects. Operation of duplicate type of gene interaction was evidenced from the opposite signs of (h) and (l) estimates.

9. Hundred seed weight (g)

Among the five crosses studied the A, B and C scales were non-significant in the case of TJM 196 X Kanika which indicated the adequacy of additive – dominance model for this cross. While remaining four crosses exhibited significance of one or more scaling tests suggesting the presence of non-allelic interactions. Mean (m) effects were significant and positive in all the crosses except for LGG 460 X Virat and TJM 196 X Kanika. Hum 1 X Shikha exhibited significant and positive additive (d) gene effect whereas other crosses showed non-significant additive gene effects for this trait. Significance of additive (d) component for this trait was also reported by Singh *et al.* (1994), Aher and Dahat (1999), Kute and Deshmukh (2002) and Singh *et al.* (2007). Dominance (h) gene effect was significant and positive for LGG 460 X Virat whereas, it was significant and negative for HUM 1 X Shikha while remaining crosses showed non-significant dominance gene effects. Among interaction effects, additive x additive (i) gene effect was significant and positive in LGG 460 X Virat while significant and negative gene effect was recorded for Ganga 8 X Shikha and rest of the crosses showed non-significant additive x additive gene effects. Additive x dominance (j) gene effects were significant and negative for HUM 1 X Shikha and LGG 460 X Kanika whereas rest of the crosses exhibited non-significant (j) gene effects. Dominance x dominance (l) gene effects were significant and positive for HUM 1 X Shikha and Ganga 8 X Shikha whereas, significant and negative gene effect was recorded for LGG 460 X Virat. The direction of gene effects viz., dominance (h) and dominance x dominance (i) were opposite for all the crosses except LGG 460 X Kanika indicating the presence of duplicate type of epistasis Malik and Singh (1983) whereas in the cross LGG 460 X Kanika the complementary type of epistasis was recorded Rao *et al.* (1984) for the inheritance of this character. The predominant role of dominance and epistasis was also observed by Malik and Singh (1983), Seenaiiah (1995) and Ajit and Singh (1996).

10. Biological yield per plant (g)

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. The mean (m) effects were significant and negative for HUM 1 X Shikha and LGG 460 X Kanika whereas remaining crosses exhibited significant and positive mean effects. Additive (d) gene effects were significant and positive for all the crosses except for the cross combination LGG 460 X Kanika which showed significant and negative gene effect for this trait. Dominance (h) gene effects were positive and significant for HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika whereas it was significant and negative for TJM 196 X Kanika. Among interaction effects, all the crosses showed significant and positive additive x additive (i) gene effects except LGG 460 X Kanika which was significant and negative. Additive x dominance (j) gene effects were significant and negative for all the crosses studied except LGG 460 X Kanika which showed non-significant gene effect. Dominance x dominance (l) gene effects were negative and significant in HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika whereas crosses viz., Ganga 8 X Shikha and TJM 196 X Kanika showed significant and positive (l) gene effects. Positive and significant effects of (l) in Ganga 8 X Shikha and TJM 196 X Kanika indicated the predominance of dominance x dominance interaction. The operation of duplicate type of epistasis was evident by the estimates of (h) and (l) components with opposite signs in all the crosses except Ganga 8 X Shikha in which complementary type of epistasis was observed. Both additive and non-additive gene effects were also found for this trait by Khattak *et al.* (2001) in greengram with predominance of additive effects.

11. Harvest index (%)

Significance of one or more scaling tests suggested the presence of non-allelic interactions in the crosses. Mean (m) effects were positive and significant for HUM 1 X Shikha and TJM 196 X Kanika while Ganga 8 X Shikha and LGG 460 X Kanika showed significant and negative gene effects for this trait. Significant and positive Additive (d) gene effect was recorded for LGG 460 X Kanika while significant and negative gene effect was recorded for LGG 460 X Virat whereas remaining crosses exhibited non-significant gene

effects. Dominance (h) gene effects were positive and significant in Ganga 8 X Shikha, LGG 460 X Virat and LGG 460 X Kanika while significant and negative gene effect was recorded for HUM 1 X Shikha. Additive x additive (i) gene effects were observed in Ganga 8 X Shikha, LGG 460 X Virat and LGG 460 X Kanika while other crosses showed non-significant gene effects. Additive x dominance (j) gene effects were found to be negative and significant for HUM 1 X Shikha, LGG 460 X Kanika and TJM 196 X Kanika whereas remaining of the crosses showed non-significant gene effects for this trait. Dominance x dominance (l) gene effect was positive and significant for HUM 1 X Shikha while Ganga 8 X Shikha, LGG 460 X Virat and LGG 460 X Kanika. Operation of duplicate type of gene interaction was evidenced from the opposite signs of (h) and (l) estimates.

12. Seed yield per plant (g)

Significance of one or more scaling tests suggested the presence of non-allelic interactions in all the crosses. Among the main effects, the mean (m) effects were significant and negative for all the crosses and main effect was significant and positive for TJM 196 X Kanika. Crosses viz., HUM 1 X Shikha, Ganga 8 X Shikha, LGG 460 X Virat and LGG 460 X Kanika showed significant and negative additive (d) gene effects whereas significant and positive mean effect was recorded for TJM 196 X Kanika. Dominance (h) gene effects were significant and positive in all the crosses except TJM 196 X Kanika which showed non-significant gene effect. In general dominance effects were higher in magnitude in all crosses Godhani *et al.* (1978), Hegde *et al.* (1994), Inderjit *et al.* (2006) and Gawande and Patil (2007). Among interaction effects, all the crosses showed positive and significant additive x additive (i) gene effects except TJM 196 X Kanika for which significant and negative gene effect was observed. Similar results were reported by Singh *et al.* (1994), Murthy (2000) and Kute and Deshmukh (2002). Additive x dominance (j) epistatic gene effects were found to be significant and negative in all the crosses. Dominance x dominance (l) gene effects were significant and negative in HUM 1 X Shikha, LGG 460 X Virat and LGG 460 X Kanika whereas remaining crosses showed non-significant gene effects. Presence of both duplicate and complementary epistasis indicates that improvement of

yield mainly depends on the cross selected for improvement. Bi parental mating in early generations followed by selection in advance generations would be more effective than direct selection in early segregating generations. Malik and Singh (1983), Rao *et al.* (1984), Aher and Dahat (1999), and Khattak *et al.* (2004) also reported the importance of both duplicate and complementary epistasis for this character.

5.9 Quality analysis

Protein is one of the key quality factors. Protein of *Vigna radiata* is known as complete protein due to the presence of many types of essential amino acids. Amino acids are required by man and other animals for their normal growth and health. Phenolics, as secondary metabolites, play a key role in plant growth and reproduction (Song *et al.* 2010). Phenolic compounds serve as defense mechanism against herbivores. Recent research indicates that mungbean consumption produces a small increase in blood glycemic index in humans making it attractive option for diabetic patients. Consumption of mungbean sprouts also lower cholesterol level in the blood and provides protection against diabetes. It is also useful in weight control due to its low calories content. Keeping in view the importance of legumes, the present investigation was carried out for the estimation of protein, sugar, phenol and fat content in 14 parents and 40 crosses of mungbean (Table 4.51 and 4.52) to highlight the nutritional importance by analyzing *Vigna radiata* for its above mentioned chemical constituents and discussions are presented here under:

In parents, protein content ranged from 18.39 mg/g (Shikha) to 24.10 mg/g (Pusa Vishal) with overall mean of 20.70 mg/g. Highest protein content was found in Pusa Vishal (24.10 mg/g) followed by LGG 460 (22.33 mg/g) and TJM 196 (22.31 mg/g). In crosses, highest protein content was observed in SL 668 X Virat (26.29 mg/g) whereas lowest protein content was recorded in LGG 460 X Kanika (20.14 mg/g) with the overall mean of 24.06 mg/g. Among crosses, highest protein content was recorded in SL 668 X Virat (26.29 mg/g), HUM 1 X PDM 139 (26.26 mg/g) and LGG 460 X Virat (26.25 mg/g). The above mentioned results are in line with the results reported by Ullah *et al.* (2014), Dahiya *et al.* (2015), Varma *et al.* (2018) and Wang *et al.* (2021)

Sugar content in parents ranged from 5.38 mg/g (HUM 1) to 7.59 mg/g (Ganga 8) with overall mean of 6.89 mg/g. Highest sugar content was observed for Ganga 8 (7.59 mg/g) followed by SL 668 (7.53 mg/g) and TJM 3 (7.42 mg/g). In crosses, sugar content ranged from 6.38 mg/g (TJM 196 X PDM 139) to 8.21 mg/g (TJM 136 X PDM 139). General mean observed for crosses was 7.39 mg/g. highest sugar content was found in TJM 136 X PDM 139 (8.21 mg/g), Ganga 8 X PDM 139 (7.98 mg/g), TJM 196 X Virat and PDM 11 X Virat (7.96 mg/g). The range for sugar content mentioned above resembles with the findings of Rosaiah *et al.* (1995).

Phenol content ranged from 140.84 mg/g (TMB 37) to 954.11 mg/g (Pusa Vishal) in parents. The general mean was 566.68 mg/g. Highest phenol content was recorded for Pusa Vishal (954.11 mg/g) followed by PDM 11 (805.36 mg/g) and HUM 1 (787.96 mg/g). In crosses, highest phenol content was recorded for Pusa Vishal X Kanika (602.85 mg/g) whereas lowest phenol content was observed for SL 668 X Shikha (553.82 mg/g). In crosses mean for this trait was 580.33 mg/g. Pusa Vishal X Kanika (602.85 mg/g) recorded for highest phenol content followed by SL 668 X Virat (599.69 mg/g) and Pusa Vishal X Virat (599.09 mg/g). Varma *et al.* (2018) found same results as mentioned above

Among parents, fat content ranged from 0.65 % (Ganga 8) to 1.46% (TMB 37) with the observed General mean of 1.10%. Highest fat content was recorded in TMB 37 (1.46%) followed by PDM 139 (1.42%) and Kanika (1.36%). In crosses, fat content ranged from 0.76% (Ganga 8 X Shikha) to 1.41% (TMB 37 X Kanika) with the mean of 1.13%. Highest fat content was observed in TMB 37 X Kanika (1.41%), TMB 37 X PDM 139 (1.36%) and LGG 460 X Kanika (1.35%). The above mentioned results are in line with the results reported by Ullah *et al.* (2014), Dahiya *et al.* (2015), Varma *et al.* (2018), and Wang *et al.* (2021).

Chapter -VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FURTHER WORK

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

The present investigation entitled “**Generation Mean Analysis for Yield and Quality Components in Greengram [*Vigna radiata* (L.) Wilczek]**” was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (Madhya Pradesh) during summer 2020, kharif 2020 and summer 2021.

Ten lines viz., TJM 196, TJM 136, TJM 3, TMB 37, Ganga 8, LGG 460, HUM 1, SL 668, Pusa Vishal and PDM 11 were crossed with four testers PDM 139, Shikha, Kanika and Virat in Line X Tester mating design to generate a total of 40 crosses during summer, 2020. All the 40 F₁s along with 14 parents were raised during kharif, 2020 in field condition for their evaluation and allowed to self pollination to produce F₂ population. After two months the material for generation mean studies was generated for this five out of 40 F₁s cross combinations viz., TJM 196 X Kanika, LGG 460 X Virat, LGG 460 X Kanika, Ganga 8 X Shikha and Hum 1 X Shikha selected on the basis of yield and yield contributing traits. Finally the evaluation of experimental material comprising of six basic generations of selected five crosses was carried out for generation mean analysis during summer 2021.

6.1 Summary

In present investigation, out of 14 parents, 13 showed anthocyanin colouration and only one was without pigmentation. Among crosses, 36 showed presence for anthocyanin colouration and 4 were without pigmentation. Based on flower characteristics, such as time of flowering and petal colour, parents and crosses could be grouped into different categories. Out of 14 parents, 4 were early, whereas rests of the 10 parents were medium in their flowering duration while late duration was not noted in any of the parents. Among 40 crosses, 30 were early while 10 were medium in their flowering time and none of them were late. Petal colour was yellow in 9 and light yellow in 5 of the parents while it was yellow in 29 and light yellow in 11

crosses. On the basis of the plant, morphological characteristics such as plant growth habit and plant habit, parents and crosses were grouped in different categories. In the present study, 8 parents showed semi-erect type of growth habit and 6 of them were spreading while none were erect. Out of 40 crosses, 10 were semi-erect and 30 were spreading and erect plants could not be observed in any of the crosses. 2 parents were determinate while 12 of them were indeterminate. All the crosses under study had indeterminate plant habit.

All the 14 parents and 40 crosses of mungbean evaluated did not show any variation for stem pubescence. Pubescence was present in all the parents and crosses. Based on stem colour parents and crosses were grouped into different categories as green, green with purple splashes and purple. In the present study, green stem colour was noted in 6 parents while rest of 8 of the parents showed stem colour having green with purple splashes and purple stem colour was not observed in any of the parents. In crosses, 10 were with green stem colour, 29 had green with purple splashes while only one cross had purple stem colour. Therefore, the evaluated 14 parents and 40 crosses of mungbean can be differentiated on the basis of stem colour only.

In the present study, the characteristics related with leaves have been recorded and based on these characteristics, the parents and crosses were categorized into different groups. Leaflet lobe present in 9 parents while it was absent in 5. Among the crosses studied, this trait was absent in 36 of the crosses while 4 possessed this trait. In the present study, 10 parents were having green and 4 had dark green leaf colour. Among the 40 crosses, 29 were having green while 11 had dark green leaf colour. Leaf vein colour was green in 1, greenish purple in 6 and purple in 7 parents respectively while it green in 6, greenish purple in 25 and purple in 9 crosses respectively. Ovate leaf shape was found in 12 parents while 2 of them had deltoid. Further, none of the genotypes fell under the category of Cuneate and Lanceolate. All the 40 crosses had ovate leaf shape.

The variation was observed for various characteristics of pod such as mature pod colour and curvature of mature pod. All the 14 parents and 40 crosses evaluated did not show any variation for pod pubescence. Among 14

parents, 13 had green pre mature pod colour while only one was with green with pigmented suture. All the 40 crosses under study had green pre mature pod colour. Among 14 parents 7 had straight while 7 were with curved pods. Among 40 crosses, 13 had straight whereas 27 had curved pods.

Based on seed morphology, parents and crosses were grouped into seed colour, seed shape, seed lusture and seed size. Seed colour was green in 2 and mottled in 12 of the parents and it was green 4 and mottled in 36 of the crosses. Lusture of the seed was dull in shiny in 4 and dull in 10 parents. Among the 40 crosses, shiny seeds in 13 and dull seeds in 27 crosses was observed. Among 14 parents, the shape of the seed was oval in 9 and drum shaped in 5 of the parents respectively. Among the 40 crosses, 20 had oval seed shape while rest of the 20 crosses had drum shaped seeds. The size of the seed was medium in 13 and large in 1 parent respectively while small category of seed was not present in any of the parents. Among 40 crosses, 37 had medium seeds while 3 had large seeds while small category of seeds could not recovered in any of the crosses.

Analysis of variance revealed significant differences among the genotypes for various traits studied indicating the presence of ample scope for effective selection. An overall view of mean performance of parents revealed that no single genotype was superior in respect of all the traits studied. However, among the lines, TJM 196 emerged as the best parent for five traits viz., number of branches per plant, number of pods per plant, number of clusters per plant, biological yield per plant and seed yield per plant, TJM 136 recorded significant per se values for days to 50% flowering and days to maturity. Ganga 8 recorded significant per se performance for plant height, TMB 37 recorded significant per se performance for number of branches per plant and number of seeds per pod. *Per se* value was significant for number of pods per cluster in PDM 11 and for number of pods per plant in SL 668. Among testers, Kanika recorded significant per se performance for plant height whereas, Shikha for number of pods per cluster and Virat for harvest index.

Higher estimates of variability, heritability and genetic advance as per cent of mean was observed for number of branches per plant, number of pods

per plant and biological yield per plant among parents and for the traits viz., number of branches per plant, number of pods per plant, biological yield per plant and seed yield per plant among the crosses suggesting the presence of sufficient amount of variability, operation of additive gene action, least influence of environment and thus these traits are more amenable for direct selection. It would be rewarding to lay emphasis on the selection of these traits for rapid improvement of seed yield in greengram. Moderate to high heritability and low genetic advance was observed for number of seeds per pod in parents and for days to maturity in crosses suggesting the importance of non-additive gene action in the inheritance of above mentioned traits. Hence, improvement in these traits can be done by exploitation of non-additive genetic variance through hybridization and selection. High heritability associated with moderate genetic advance as per cent of mean was observed in parents for days to flowering and days to maturity and among crosses for days to maturity suggesting the importance of both additive and non-additive gene actions in the inheritance of these traits.

Character association studies revealed that selection based on number of pods per plant, biological yield per plant and harvest index in both parents and crosses would be beneficial. In addition, exercising selection based on hundred seed weight, number of clusters per plant, number of branches per plant and number of pods per cluster may also be considered for improvement in seed yield as they had exhibited significant and positive correlation with seed yield per plant in crosses. Non-significant positive associations with seed yield per plant with hundred seed weight, number of clusters per plant and number of branches per plant became significant and positive in crosses. Similarly, non-significant and negative association of seed yield per plant with number of pods per cluster in parents became positive and significant in crosses which might be due to the formation of recombinants. Hence, simultaneous selection for these traits may result into considerable improvement in seed yield per plant.

Path analysis for seed yield revealed that direct effect of number of pods per plant followed by number of branches per plant, harvest index plant height, hundred seed weight and biological yield per plant were high and

positive in parents. Among crosses, harvest index exhibited higher positive direct effect on seed yield followed by biological yield/plant and number of seeds/pod. Number of branches per plant, number of pods per plant, plant height, number of pods per cluster, number of clusters per plant, harvest index, hundred seed weight and number of seeds per pod exhibited substantial positive indirect effects via other traits. Occurrence of negative as well as positive indirect effects of yield attributing traits on seed yield via one or other traits simultaneously presents a complex situation wherein a compromise has to be made for different yield attributes in determining the ideotype for high seed yield in greengram.

The magnitude of heterosis among the crosses for 12 traits indicated that all the traits distinctly differed for the upper limits in both positive and negative direction. The magnitude of standard heterosis was high for days to 50% maturity, plant height, number of pods per plant, number of seeds per pod, hundred seed weight, biological yield per plant and seed yield per plant. The observation of heterotic trends revealed that out of 40 crosses, 20 crosses viz., TJM 136 X Virat, TJM 3 X PDM 139, TJM 3 X Shikha, TJM 3 X Kanika, TJM 3 X Virat, TMB 37 X PDM 139, TMB 37 X Shikha, TMB 37 X Virat, LGG 460 X Kanika, LGG 460 X Virat, HUM 1 X PDM 139, HUM 1 X Shikha HUM 1 X Virat, Ganga 8 X PDM 139, Ganga 8 X Shikha, SL 668 X PDM 139, SL 668 X Virat, Pusa Vishal X Shikha, Pusa Vishal X Virat and PDM 11 X Shikha registered significant and high heterosis for seed yield contributing traits viz., days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, biological yield per plant and harvest index. It clearly indicated that high degree of heterosis for seed yield per plant was mainly through heterosis for individual yield components, which might be due to multiplicative effects of partial dominance of component traits.

Combining ability analysis revealed the presence of considerable variability for majority of the traits among the lines compared to testers and substantial variability for most of the traits among crosses. Comparison of relative magnitudes of the estimates of *gca* and *sca* variances revealed the

preponderance of non-additive gene action for all the traits except for plant height suggesting good scope for heterotic breeding followed by selection at later generations. Based on *gca* effects, the genotypes viz, TJM 196, HUM 1, TMB 37, TJM 136, Kanika and Virat were found to be the best general combiners for most of the traits. Based on *sca* effects the cross combinations viz., TMB 37 X Virat, PDM 11 X Virat, TJM 3 X Kanika, SL 668 X Kanika, TJM 136 X Shikha, TJM 196 X Shikha, TJM 196 X Kanika and HUM 1 X Shikha were adjudged as the best hybrids for yield attributes.

Results of A, B and C scaling tests revealed that simple additive-dominance model was inadequate for all the crosses and almost all the traits studied except for days to maturity in HUM 1 X Shikha; number of pods per plant as well as hundred seed weight in TJM 196 X Kanika, where in all the four scales were found to be non-significant. It suggests the importance of epistatic effects besides the major components viz., (m), (d) and (h) for important yield and quality attributes of the material studied in the investigation. Partitioning of variance indicated that mean values (m) were significant in all five crosses for days to 50% flowering, days to maturity, plant height, number of pods per plant, biological yield per plant and seed yield per plant, in four crosses for number of seeds per pod and harvest index. For number of pods per cluster, number of clusters per plant and hundred seed weight mean effects were significant in three crosses. Mean effect was significant for number of branches per plant in two crosses.

Additive (d) gene effects were significant in all five crosses for number of pods per plant, number of clusters per plant and seed yield per plant and in four crosses for days to flowering and plant height. Three crosses showed significant additive gene effects for number of branches per plant whereas, two crosses for days to maturity, number of pods per cluster, biological yield per plant and harvest index. For number of seeds per pod and hundred seed weight additive component was significant in one cross suggesting the importance of additive gene effects in the expression of these traits and good response to simple selection.

Dominance (h) component was significant in all five crosses for number of branches per plant, number of pods per plant and number of clusters per

plant. For plant height, biological yield per plant, harvest index and seed yield per plant dominance component was significant in four crosses. Three crosses showed significant dominance gene effects for days to 50% flowering and number of seeds per pod. Dominance gene effects were found to be significant in two crosses for days to maturity, number of pods per cluster and hundred seed weight indicating the importance of dominance gene effects in expression of these traits. In general the magnitude of dominance was higher as compared to additive effects.

Additive x additive (i) type of epistasis was significantly predominant in all the five crosses for plant height, number of pods per plant, number of clusters per plant, biological yield per plant and seed yield per plant; in three crosses for days to 50% flowering, number of branches per plant, number of pods per cluster and harvest index. For days to maturity number of seeds per pod and hundred seed weight additive x additive component was significant in two crosses.

Additive x dominance (j) gene effects were significant for number of clusters per plant and seed yield per plant in five crosses; for days to 50% flowering, number of branches per plant, number of pods per plant and biological yield per plant in four crosses; for plant height and harvest index in three crosses; for number of pods per cluster and hundred seed weight in two crosses and for days to maturity and number of seeds per pod in one cross.

Dominance x dominance (l) gene effects were significant in all the five crosses for plant height, number of pods per plant and biological yield per plant; four crosses for number of branches per plant and harvest index. For days to 50% flowering, number of clusters per plant, number of seeds per pod, hundred seed weight and seed yield per plant dominance x dominance type of epistasis was found to be significant in three crosses and for days to maturity and number of pods per cluster in two crosses. These findings indicated that additive, dominance and epistatic interaction effects are contributed significantly in the inheritance of the traits in greengram.

Results of dominance (h) gene effects and dominance x dominance (l) type of interaction effects revealed the operation of duplicate type of epistasis

in HUM 1 X Shikha for days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, harvest index and seed yield per plant; in Ganga 8 X Shikha for days to 50% flowering, days to maturity, plant height, number of branches per plant, number o pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, harvest index and seed yield per plant; in LGG 460 X Virat for days to 50% flowering, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, biological yield per plant, harvest index and seed yield per plant; in LGG 460 X Kanika for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, biological yield per plant, harvest index and seed yield per plant; in TJM 196 X Kanika for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod, hundred seed weight, biological yield per plant and harvest index.

In parents, highest protein content was found in Pusa Vishal (24.10 mg/g) followed by LGG 460 (22.33 mg/g) and TJM 196 (22.31 mg/g). Among crosses, highest protein content was recorded in SL 668 X Virat (26.29 mg/g), HUM 1 X PDM 139 (26.26 mg/g) and LGG 460 X Virat (26.25 mg/g)

In parents highest sugar content was observed in Ganga 8 (7.59 mg/g) followed by SL 668 (7.53 mg/g) and TJM 3 (7.42 mg/g). In crosses, highest sugar content was found in TJM 136 X PDM 139 (8.21 mg/g), Ganga 8 X PDM 139 (7.98 mg/g), TJM 196 X Virat and PDM 11 X Virat (7.96 mg/g).

Highest phenol content was recorded in Pusa Vishal (954.11 mg/g) followed by PDM 11 (805.36 mg/g) and HUM 1 (787.96 mg/g) in parents while in crosses, highest phenol content was recorded in Pusa Vishal X Kanika (602.85 mg/g) followed by SL 668 X Virat (599.69 mg/g) and Pusa Vishal X Virat (599.09 mg/g).

Among parents, highest fat content was recorded in TMB 37 (1.46%) followed by PDM 139 (1.42%) and Kanika (1.36%). In crosses, highest fat content was observed in TMB 37 X Kanika (1.41%), TMB 37 X PDM 139 (1.36%) and LGG 460 X Kanika (1.35%).

6.2 Conclusion

1. Maximum morphological variability was recorded in leaf vein colour, colour of petal, leaf colour, leaflet lobe, pod colour, pod curvature, seed lusture and anthocyanin colouration. The distribution frequency of the traits like seed size (7.69%) followed by colour of pre-mature pods (7.14%), leaf vein colour (7.14%) and anthocyanin colouration (7.14%) was very low in parents while among crosses, maximum variability was noted in leaf vein colour, leaf colour, colour of petal, pod colour, pod curvature, seed lusture, seed shape, leaflet lobes and hypocotyl colouration. Low frequency was observed in leaf vein colour (15%) followed by seed colour (10%), leaflet lobes (10%), anthocyanin colouration (10%), seed colour (10%), seed size (7.5%) and stem colour (2.5%). Frequency distributions in above mentioned traits both in parents as well as crosses were very low and these traits were unique. Above mentioned morphological traits may be utilized in breeding programme for the development of diverse morphology based genotypes/varieties so that on the basis of these unique identities varieties may be identified very easily as per linked morphological traits.
2. In the present investigation, considerable amount of genetic variability was present among the parental lines and crosses for all the traits under study which revealed that exploitable level of variability existed in the population.
3. Among the parental lines and crosses, high estimates of variability, heritability and genetic advance as percent of mean were recorded for number of branches per plant, number of pods per plant and biological yield per plant. High estimates of PCV, GCV and heritability for the trait seed yield per plant was reported only among the crosses. It suggested the presence of sufficient amount of variability, operation of additive

gene action, least influence of environment and thus these traits are more amenable for direct selection. It would be rewarding to lay emphasis on the selection of these traits for rapid improvement of seed yield in greengram.

4. Character association studies revealed that selection based on number of pods per plant, biological yield per plant and harvest index in both parents and crosses would be beneficial in the genetic improvement of mungbean. In addition, exercising selection based on hundred seed weight, number of clusters per plant, number of branches per plant and number of pods per cluster may also be considered for improvement in seed yield as they had exhibited significant and positive correlation with seed yield per plant in crosses.
5. Path analysis for seed yield revealed that direct effects of number of pods per plant followed by number of branches per plant, harvest index, plant height, hundred seed weight and biological yield per plant were high and positive in parents. Among crosses, harvest index exhibited higher positive direct effect on seed yield followed by biological yield/plant and number of seeds/pod. Hence, these traits having high positive direct effects on seed yield per plant must be used as selection criteria for the crop improvement programme in mungbean.
6. Based on *gca* effects, the genotypes viz, TJM 196, HUM 1, TMB 37, TJM 136, Kanika and Virat were found to be the best general combiners for most of the traits. On the basis of *sca* effects, the cross combinations viz., TMB 37 X Virat, PDM 11 X Virat, TJM 3 X Kanika, SL 668 X Kanika, TJM 136 X Shikha, TJM 196 X Shikha, TJM 196 X Kanika and HUM 1 X Shikha were adjudged as the best hybrids for yield attributes. Parents having high and significant *gca* effects were found superior for most of the traits and they may be utilized in breeding programme for crop improvement. Promising cross combinations can be utilized effectively for cultivar development.

7. TJM 136 X Virat, TJM 136X PDM 139, TMB 37 X Kanika, Pusa Vishal X PDM 139, HUM 1 X Shikha, LGG 460 X Kanika, TMB 37 X Shikha and Pusa Vishal X Kanika were identified as best heterotic crosses based on *per se* performance, sca effects and standard heterosis.
8. It was evident from the results of generation mean analysis that the components of seed yield could be improved by exploiting both additive and non-additive types of gene effects in the present set of biological material through inter-mating of superior segregants at early generations followed by bi parental mating and recurrent selection especially reciprocal recurrent selection. The transgressive segregants produced as a result of this technology will lead to the identification of desirable high yielding recombinants in the segregating population.
9. In parents, highest protein content was reported in Pusa Vishal followed by LGG 460 and TJM 196. Among crosses, highest protein content was recorded in SL 668 X Virat, HUM 1 X PDM 139 and LGG 460 X Virat. It is concluded that parental lines with high protein content can be utilized as parental line in the hybridization programme for the enhancement of high protein content in the crosses subsequently in the varietal development programme.
10. In the parents highest sugar content was recorded in Ganga 8 followed by SL 668 and TJM 3. In crosses, highest sugar content was found in TJM 136 X PDM 139, Ganga 8 X PDM 139, TJM 196 X Virat and PDM 11 X Virat. Ganga 8 was reported as promising parental line for total sugar content and it can be a good donor for this trait.
11. Highest phenol content was recorded in Pusa Vishal followed by PDM 11 and HUM 1 in parents while in crosses, highest phenol content was recorded in Pusa Vishal X Kanika followed by SL 668 X Virat and Pusa Vishal X Virat. Parental line Pusa Vishal was reported as a good source of phenol content so that it will be utilized as a parent in the mungbean hybridization programme for the increase phenol content.
12. Among parents, highest fat content was recorded in TMB 37 followed by PDM 139 and Kanika. In crosses, highest fat content was observed in TMB 37 X Kanika TMB 37 X PDM 139 and LGG 460 X Kanika. Parental line TMB 37 was reported as good source of fat content.

6.3 Suggestions for future work

As per the information generated in the present investigation, some of the important findings for future work are proposed below:

1. Good general combiner's viz., TJM 196, HUM 1, TMB 37, TJM 136, Kanika and Virat may be further used in hybridization programme for the future breeding material development. these parental lines may be utilized for the accurate study of combining ability in mungbean.
2. Cross combinations which showed good performance for qualitative and quantitative traits, can be advanced to develop mapping populations (RILs and NILs) for the localization of quantitative trait loci.
3. Number of branches per plant, number of pods per plant, number of pods per cluster, number of clusters per plant, biological yield per plant and harvest index can be used for the constructing of selection indices for selecting desirable segregants with enhanced seed yield.
4. Desirable segregants identified in the study can be handled through reciprocal recurrent selection or bi-parental mating in early segregating generations in a judicious approach to harness both additive and non-additive gene action to develop high yielding greengram genotypes.
5. In the mungbean, many of the genes regarding yield and resistance are controlled by different genetic components present in the genomic DNA arrangements so, systematic study on generation mean analysis with inclusion of genome based molecular study will facilitate very good option for the improvement of genetic background of mungbean. It is suggested to widen the genetic components by adopting interspecific crossing to isolate the best recombinants dominated with yield, resistance and quality parameters.

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TJM 196



TJM 19*6 X Kanika



Kanika



LGG 460



LGG 460 X Virat



Virat



LGG 460



LGG 460 X Kanika



Kanika



Ganga 8



Ganga 8 X Shikha



Shikha



HUM 1



HUM 1 X Shikha



Shikha

Plate 5: Five superior crosses of present study in greengram

APPENDICES

APPENDICES

Appendix – I :Morphological characterization of 40 F₂ generations of mungbean

Characters	Stage of Observation	F ₂									
		TJM196 X PDM139	TJM196 X Shikha	TJM196 X Kanika	TJM196 X Virat	TJM136 X PDM139	TJM136 X Shikha	TJM136 X Kanika	TJM136 X Virat	TJM3 X PDM139	TJM3 X Shikha
Hypocotyl: Anthocyanin Colouration	Cotyledons unfolded	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Flowering time	50% plants with at least one open flower	Early	Early	Medium	Medium	Early	Early	Medium	Early	Early	Early
Plant: Growth habit	50% flowering	Semi-erect	Spreading	Semi-erect	Semi-erect	Semi-erect	Semi-erect	Spreading	Semi-erect	Semi-erect	Semi-erect
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (terminal)	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Green	Green	Green	Green	Green	Dark green	Green	Green	Dark green	Dark green
Leaf: Vein color	50% flowering	Purple	Purple	Purple	Purple	Greenish purple	Greenish purple	Purple	Greenish purple	Greenish purple	Greenish purple
Flower: Petal Color	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Black	Brown	Brown	Brown	Brown	Curved	Brown	Black	Black	Brown
Curvature: Mature pod	Harvest maturity	Straight	Straight	Straight	Curved	Curved	Brown	Curved	Curved	Straight	Straight
Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
Seed: Shape	Mature seeds	Oval	Oval	Oval	Oval	Drum shaped	Oval	Oval	Oval	Oval	Drum shaped
Seed: Lusture	Mature seeds	Dull	Dull	Dull	Dull	Dull	Dull	Dull	Dull	Dull	Dull
Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Large	Medium	Medium	Small

Cont.....

Characters	Stage of Observation	F2									
		TJM3 X Kanika	TJM3 X Virat	TMB37 X PDM139	TMB37 X Shikha	TMB37 X Kanika	TMB37 X Virat	Ganga8 X PDM139	Ganga8 X Shikha	Gang8 X Kanika	Gang8 X Virat
Hypocotyl: Anthocyanin Colouration	Cotyledons Unfolded	Present	Present	Present	Absent	Present	Present	Present	Absent	Present	Present
Flowering time	50% plants with at least one open flower	Early	Early	Early	Early	Early	Early	Early	Early	Medium	Early
Plant: Growth habit	50% flowering	Semi-erect	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading	Spreading	Semi-erect	Spreading	Semi-erect
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green	Green	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green with purple splashes
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (terminal)	50% flowering	Present	Present	Absent	Absent	Absent	Absent	Absent	Absent	Present	Absent
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Deltoid	Ovate	Deltoid	Ovate	Ovate
Leaf: Color	50% flowering	Dark green	Dark green	Green	Dark green	Dark green	Green	Dark green	Dark green	Dark green	Dark green
Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Purple	Greenish purple	Greenish purple	Greenish purple	Purple	Greenish purple	Greenish purple	Greenish purple
Flower: Petal Color	50% flowering	Yellow	Light yellow	Light yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow	Light yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Brown	Black	Black	Black	Black	Brown	Black	Brown	Black	Brown
Curvature: Mature pod	Harvest maturity	Curved	Curved	Straight	Straight	Straight	Straight	Straight	Straight	Straight	Straight
Seed: color	Mature seeds	Mottled	Green	Mottled	Green	Mottled	Mottled	Drum	Mottled	Mottled	Mottled
Seed: Shape	Mature seeds	Oval	Drum shaped	Oval	Oval	Oval	Oval	Green	Oval	Oval	Oval
Seed: Lusture	Mature seeds	Dull	Dull	Dull	Shiny	Dull	Dull	Shiny	Dull	Dull	Shiny
Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

Cont.....

Characters	Stage of Observation	F2									
		LGG460 X PDM139	LGG460 X Shikha	LGG460 X Kanika	LGG460 X Virat	HUM1 X PDM139	HUM1 X Shikha	HUM1 X Kanika	HUM1 X Virat	SL668 X PDM139	SL668 X Shikha
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Absent	Present	Absent	Absent	Present	Present	Absent	Present	Present	Present
Flowering time	50% plants with at least one open flower	Medium	Medium	Early	Early	Early	Early	Early	Early	Early	Early
Plant: Growth habit	50% flowering	Spreading	Spreading	Spreading	Spreading	Spreading	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green	Green	Green with purple splashes	Purple
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (terminal)	50% flowering	Present	Absent	Present	Absent	Absent	Absent	Absent	Absent	Absent	Present
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Dark green	Dark green	Green	Green	Green	Green	Dark green	Green	Dark green	Dark green
Leaf: Vein color	50% flowering	Green	Purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Purple
Flower: Petal Color	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Light yellow	Yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green with pigmented suture	Green with pigmented suture
Pod: Color	Harvest maturity	Brown	Brown	Brown	Brown	Black	Brown	Brown	Black	Black	Brown
Curvature: Mature pod	Harvest maturity	Straight	Curved	Straight	Straight	Straight	Curved	Straight	Straight	Curved	Curved
Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Green	Mottled	Mottled	Mottled	Mottled
Seed: Shape	Mature seeds	Drum shaped	Oval	Oval	Oval	Oval	Oval	Oval	Oval	Oval	Oval
Seed: Lusture	Mature seeds	Dull	Dull	Shiny	Dull	Dull	Shiny	Dull	Dull	Dull	Dull
Seed: Size	Mature seeds	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Large	Medium	Medium

Cont.....

Characters	Stage of Observation	F2									
		SL668 X Kanika	SL668 X Virat	Pusa Vishal X PDM139	Pusa Vishal X Shikha	Pusa Vishal X Kanika	Pusa Vishal X Virat	PDM11 X PDM139	PDM11 X Shikha	PDM11 X Kanika	PDM11 X Virat
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Present	Present	Present	Present	Absent	Present	Absent	Present	Present
Flowering time	50% plants with at least one open flower	Medium	Early	Medium	Early	Medium	Early	Medium	Early	Early	Early
Plant: Growth habit	50% flowering	Spreading	Spreading	Semi-erect	Semi-erect	Spreading	Spreading	Semi-erect	Semi-erect	Semi-erect	Semi-erect
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green	Purple	Green with purple splashes	Green with purple splashes	Green	Green	Green	Green
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (terminal)	50% flowering	Absent	Absent	Present	Present	Present	Present	Absent	Present	Absent	Absent
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Green	Green	Green	Dark green	Green	Green	Green	Green	Green	Green
Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Green	Greenish purple
Flower: Petal Color	50% flowering	Yellow	Yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow	Yellow	Light yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green with pigmented suture	Green with pigmented suture	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Brown	Black	Brown	Black	Brown	Brown	Brown	Brown	Brown	Brown
Curvature: Mature pod	Harvest maturity	Curved	Straight	Curved	Curved	Curved	Straight	Straight	Straight	Straight	Straight
Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled
Seed: Shape	Mature seeds	Oval	Oval	Oval	Oval	Drum shaped	Oval	Oval	Oval	Oval	Oval
Seed: Lusture Seed: Size	Mature seeds Mature seeds	Dull Medium	Dull Medium	Dull Medium	Shiny Medium	Dull Medium	Dull Medium	Shiny Medium	Dull Medium	Dull Medium	Dull Medium

Cont.....

Characters	Stage of Observation	B1&B2								
		TJM136XVIRAT X TJM136	TJM136XVIRAT X Virat	TJM136XShikha X TJM136	TJM136XShikha X Shikha	TJM136XPDM139 X TJM136	TJM136XPDM139 X PDM139	TMB37XPDM139 X TMB37	TMB37XPDM139 X PDM139	TMB37XShikha X TMB37
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Present	Present	Present	Present	Present	Present	Present	Absent
Flowering time	50% plants with at least one open flower	Early	Early	Early	Early	Early	Medium	Medium	Early	Early
Plant: Growth habit	50% flowering	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (Terminal)	50% flowering	Present	Present	Present	Absent	Present	Absent	Absent	Absent	Absent
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Dark green	Green	Dark green	Dark green	Green	Dark green	Green	Green	Green
Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Purple	Greenish purple	Greenish purple	Greenish purple	Purple	Greenish purple	Green
Flower: Petal Color	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Light yellow	Yellow	Light yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Brown	Black	Black	Black	Brown	Brown	Black	Black	Black
Curvature: Mature pod	Harvest maturity	Curved	Curved	Curved	Curved	Curved	Straight	Curved	Curved	Curved
Seed: color	Mature seeds	Mottled	Mottled	Mottled	Mottled	Mottled	Mottled	Green	Mottled	Green
Seed: Shape	Mature seeds	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Oval
Seed: Lusture	Mature seeds	Dull	Dull	Dull	Dull	Dull	Dull	Dull	Dull	Shiny
Seed: Size	Fully developed green pods	Large	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

Appendix –II: Morphological characterization of B₁ and B₂ generations of mungbean

Characters	Stage of Observation	TMB37XShikha X Shikha	TMB37XVirat X TMB37	TMB37XVirat X Virat	TMB37XKanika X TMB37	TMB37XKanika X Kanika	Ganga8XPDM138 X Ganga8	Ganga8XPDM139 X PDM139	Ganga8XVirat X Ganga8	Ganga8XVirat X Virat
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Absent	Present	Present	Present	Present	Present	Present	Absent	Absent
Flowering time	50% plants with at least one open flower	Early	Early	Early	Early	Medium	Medium	Medium	Medium	Early
Plant: Growth habit	50% flowering	Semi-erect	Semi-erect	Spreading	Spreading	Semi-erect	Semi-erect	Semi-erect	Spreading	Spreading
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (Terminal)	50% flowering	Absent	Absent	Absent	Present	Present	Absent	Absent	Absent	Absent
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Deltoid	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Dark green	Green	Green	Green	Dark green	Dark green	Green	Green	Green
Leaf: Vein color	50% flowering	Greenish purple	Purple	Purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple
Flower: Petal Color	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Light yellow	Light yellow	Yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Black	Brown	Brown	Black	Brown	Black	Black	Black	Black
Curvature: Mature pod	Harvest maturity	Straight	Straight	Curved	Curved	Curved	Straight	Straight	Curved	Straight
Seed: color	Mature seeds	Green	Mottled	Mottled	Green	Green	Mottled	Mottled	Green	Green
Seed: Shape	Mature seeds	Oval	Drum shaped	Drum shaped	Oval	Oval	Drum shaped	Drum shaped	Oval	Oval
Seed: Lusture	Mature seeds	Shiny	Dull	Dull	Shiny	Shiny	Dull	Dull	Shiny	Shiny
Seed: Size	Fully developed green pods	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

Cont.....

Characters	Stage of Observation	B1&B2								
		Ganga8XShikha X Ganga8	Ganga8Xshikha X Shikha	LGG460XShikha X LGG460	LGG460XShikha X Shikha	LGG460XKanika X LGG460	LGG460XKanika X Kanika	LGG460XVirat X LGG460	LGG460XVirat X Virat	HUM1XPDM139 X HUM1
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Present	Absent	Absent	Absent	Absent	Absent	Present	Present
Flowering time	50% plants with at least one open flower	Medium	Medium	Early	Early	Early	Medium	Medium	Medium	Medium
Plant: Growth habit	50% flowering	Spreading	Semi-erect	Spreading	Spreading	Spreading	Spreading	Spreading	Spreading	Spreading
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (Terminal)	50% flowering	Absent	Absent	Absent	Absent	Absent	Absent	Present	Absent	Absent
Leaf: Shape (terminal)	50% flowering	Deltoid	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Dark green	Green	Dark green	Dark green	Green	Green	Green	Green	Green
Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Greenish purple	Purple	Purple	Greenish purple
Flower: Petal Color	50% flowering	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Brown	Brown	Brown	Brown	Black	Brown	Black	Black	Brown
Curvature: Mature pod	Harvest maturity	Straight	Curved	Curved	Curved	Curved	Straight	Straight	Straight	Curved
Seed: color	Mature seeds	Mottled	Green	Mottled	Mottled	Green	Mottled	Green	Mottled	Mottled
Seed: Shape	Mature seeds	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Oval	Drum shaped	Drum shaped	Oval
Seed: Lusture	Mature seeds	Dull	Dull	Dull	Dull	Shiny	Dull	Shiny	Shiny	Shiny
Seed: Size	Fully developed green pods	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium	Medium

Cont.....

Characters	Stage of Observation	B1&B2								
		HUM1XPDM139 X PDM139	HUM1XShikha X HUM1	HUM1Xshikha X Shikha	SL668XVirat X SL668	SL668XVirat X Virat	Pusa VishalXVirat X Pusa Vishal	Pusa VishalXVirat X Virat	TJM196XKanika X TJM196	TJM196XKanika X Kanika
Hypocotyl: Anthocyanin Coloration	Cotyledons unfolded	Present	Absent	Absent	Present	Present	Present	Absent	Present	Absent
Flowering time	50% plants with at least one open flower	Early	Early	Medium	Early	Early	Medium	Medium	Medium	Medium
Plant: Growth habit	50% flowering	Spreading	Spreading	Spreading	Spreading	Spreading	Semi-erect	Spreading	Semi-erect	Spreading
Plant: Habit	50% flowering	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Stem: color	50% flowering	Green	Green with purple splashes	Green	Green with purple splashes	Green with purple splashes	Green with purple splashes	Green with purple splashes	Greenish purple	Green
Stem: Pubescence	50% flowering	Present	Present	Present	Present	Present	Present	Present	Present	Present
Leaflet lobe (Terminal)	50% flowering	Absent	Absent	Absent	Absent	Absent	Present	Absent	Present	Absent
Leaf: Shape (terminal)	50% flowering	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate	Ovate
Leaf: Color	50% flowering	Green	Green	Green	Green	Green	Green	Green	Green	Green
Leaf: Vein color	50% flowering	Greenish purple	Greenish purple	Green	Greenish purple	Greenish purple	Purple	Greenish purple	Greenish purple	Purple
Flower: Petal Color	50% flowering	Light yellow	Light yellow	Light yellow	Yellow	Yellow	Light yellow	Light yellow	Light yellow	Yellow
Pod: Pubescence	Fully developed green pods	Present	Present	Present	Present	Present	Present	Present	Present	Present
Pod: Pre mature pod color	Fully developed green pods	Green	Green	Green	Green	Green	Green	Green	Green	Green
Pod: Color	Harvest maturity	Brown	Brown	Brown	Black	Black	Brown	Brown	Brown	Brown
Curvature: Mature pod	Harvest maturity	Straight	Straight	Straight	Straight	Straight	Straight	Straight	Straight	Straight
Seed: color	Mature seeds	Green	Mottled	Mottled	Oval	Oval	Mottled	Mottled	Mottled	Mottled
Seed: Shape	Mature seeds	Oval	Drum shaped	Drum shaped	Drum shaped	Drum shaped	Oval	Oval	Oval	Oval
Seed: Lusture	Mature seeds	Shiny	Shiny	Dull	Shiny	Shiny	Dull	Dull	Shiny	Shiny
Seed: Size	Fully developed green pods	Medium	Small	Medium	Medium	Medium	Small	Medium	Medium	Medium

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Study of Morphological Breeding Traits in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes as per DUS Guidelines

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ABSTRACT: An experiment was conducted to study 14 mungbean genotypes for 19 morphological traits as per DUS guidelines at Jawaharlal Nehru Krishi Vigyan Vidyapeeth, Jabalpur (M.P.) India, during Kharif 2020 as well as in summer 2021. All the genotypes were grown in randomized block design in a replication of three in the seasons mentioned above. Morphological traits were recorded as per crop DUS guideline approved by PPV & FR, New Delhi. Maximum morphological variability was recorded in leaf vein colour, colour of petal, leaf colour, leaflet lobe, pod colour, pod curvature, seed lustre and anthocyanin colouration. The distribution frequency of the traits like seed size (7.69%) followed by colour of pre-mature pods (7.14%), leaf vein colour (7.14%) and anthocyanin colouration (7.14%) was very low. Genotype SL 668 was reported as diverse mungbean variety dominated with green with pigmented suture in pre-mature pod colour and also dominated with large seed size. The trait anthocyanin colouration was absent in variety Shikha (IPM 410-83) while in TJM 3, leaf vein colour was green. These identified diverse morphological breeding traits are present in very few of the genotypes included in this investigation. The identified diverse breeding traits may be employed in hybridization programme in developing diverse morphology based genotype/variety so, that the genotypes with unique morphological identity will easily be identified in between the group of varieties. Maintenance of the varietal purity has been one of the major challenges in the research area and it is very important to check whether the genotypes or treatments or population under study are satisfying the requirements of morphological characterization protocols which includes distinctness, uniformity and stability. These unique identities will be helpful as an important morphological trait to distinguish one variety from the other in seed production programme. By the diverse identity of the varieties, genetic purity maintenance will be very easy and may stay in seed production chain for a very long time.

Keywords: Greengram, Morphological characterization, variability, Distinctness, Uniformity and Stability (DUS), breeding trait.

INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek] being a self-pollinated, short duration leguminous crop that comes under family Fabaceae, subgenus *Ceratropis* and genus *Vigna* with 2n=22 number of chromosomes. Its genome size is 579 Mb/1C (Salatun *et al.*, 2021). This crop is of Indian origin and has two wild species and only one cultivated species. It is well suited to dry areas, mainly under irrigated conditions. This crop gives good response when subjected to numerous cropping systems contributing in protein an important element of human diet. During 2019-20, the total coverage under mungbean has been about 40.20 million ha with the production of 1.42 million tons (Anonymous, 2019-20). The protein available in this crop is palatable, simple to cook and absent in flatulence factors contrary to other legumes. Mungbean seeds contain protein (22.88 to 24.65%), carbohydrates

(62.6%), crude fibre (4.30 to 4.80%) and lipid (1.53 to 2.63%). Apart from this, this particular crop adds a good range of micronutrients to the Indian vegan diet (Ramasubramanian *et al.*, 2013). Like other pulses, the protein of greengram has abundant lysine, which is an essential amino acid that is absent in cereals (Salatun *et al.*, 1998).

PPV & FRA, 2001 was enacted by the India Government to ensure the protection of plant varieties which provides legal protection to the newly developed varieties, breeder's, researcher's, and farmer's right to bring motivation in the developmental growth of seed industry and provide the new varieties with economic importance which are used for breeding programme. PPV & FRA implements DUS testing that was initiated in 2007 with twelve crops. The criteria of novelty, distinctness, uniformity and stability is essential for the registration of new variety. A DUS test is generally taken up for two successive planting seasons either in

field or glasshouse condition. Evaluation period primarily comprises characterization of various morphological traits of the concerned crop on the basis of the internationally agreed protocols (Rademacher, 2015).

Morphological characterization is considered as an important phenomenon for classification, visual identification and differentiation of the germplasm. Characterization is considerably beneficial to plant breeder in utilizing these germplasm in area of research programmes. Morphological markers are simple, inexpensive rapid to score and are highly heritable traits which are employed for the study of morphological characterization (Kumar et al., 2020). Germplasm characterization aids in grouping specific traits to obtain idea about traits that distinguish one genotype from the other (Lee et al., 2004). Piyada et al., (2010) also emphasized on morphological characterization to check for variability and differentiate the crop germplasm. Some of the agro-morphological traits may be used as morphological breeding traits in crop improvement programme. These diverse traits will be utilized in mungbean breeding programme for improving the seed physical quality. It also helps in assessment of genetic variability and diversity present in available mungbean germplasm. (Singh et al., 2014).

MATERIALS AND METHODS

The experimental material comprised 14 diverse lines of mungbean received from the project entitled "Field Evaluation of Transgenic Mutant Selection and Research Activities in Agriculture" and also from the pulse improvement programme, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharbal Nehrui Krishi Vidyalaya, Jabalpur, Madhya Pradesh, India. The experiment was conducted in a randomized block design with three replications during Kharif 2020 and summer 2021. All the lines were planted in four rows in four meter length adopting 30 cm row to row distance and 10 cm plant to plant distance respectively. The observations were recorded at specific stages of crop growth period as per DUS descriptor. The anthocyanin pigmentation was noted at cotyledonary stage. Time of flowering was observed when 50 percent plants were with at least one open flower. Plant growth habit, plant habit, stem colour, stem pubescence, leaflet lobes (terminal), leaf colour, leaf vein colour and flower colour of petal (standard) were observed at 50 percent flowering stage. The colour of pre mature pod, pod pubescence was observed at the stage of fully developed green pods. The characters pod colour and curvature of mature pod was observed at the stage of maturity. The characters like seed colour, seed lustre, and seed shape and seed size were observed at matured seed stage.

RESULTS AND DISCUSSIONS

Hypostyl Anthocyanin Colouration. This trait was observed at cotyledonary stage. Out of 14 parents, 13

showed anthocyanin colouration and only one was without pigmentation (Table 1). The intensity of cotyledon colour is affected with both storage condition and time. So this trait can be utilized only for varietal protection before entering into active seed multiplication chain.

Plant Characters. The characters like growth habit and plant habit were observed at days to 50 percent flowering. Among 14 genotypes, six were grouped into spreading and eight into semi-erect type of plant growth habit. Further two of the genotypes Pusa Vishal and PDM 139 showed determinate plant habit where roots were indeterminate in nature (Table 1). This result was supported by Jain et al., (2002); Singh et al., (2014); Kaur et al., (2017) in mungbean.

Stem Characters. 6 genotypes showed green stem colour and eight genotypes showed green with purple glaucous type of stem colour revealing variation in the lines. All the genotypes showed pubescence (Table 1) indicating similarity in all of the genotypes for this trait (Jain et al., 2002); (Katiyar et al., 2006); (Singh et al., 2014); (Kaur et al., 2017) in mungbean.

Leaf Characters. All these characters showed variability in the studied genotypes and these were classified into different categories (Table 1). 9 genotypes showed the presence of leaflet lobes and the remaining 5 were deprived of leaflet lobes. Leaf shape was deltoid in TMB17 and Shikha and ovate in 12 genotypes. 4 genotypes had dark green leaf color while 10 had green leaf colour. Leaf vein colour was greenish purple in six genotypes, purple in seven genotypes and green in one genotype i.e. TMB (Kaur et al., 2017 in mungbean); Chakrabarty and Agarwal (1989) in blackgram.

Flower Characters. Flower colour is an authentic morphological marker for differentiating the green gram genotypes. 9 genotypes showed yellow flower colour and 5 genotypes showed light yellow colour. Out of 14 parents, 4 were early, whereas roots of the 10 parents were medium in their flowering duration while late duration was not noted in any of the parents (Table 1).

Flowering time ranged from 32 days (TMB16) to 45 days (PDM11). The short duration genotypes have the ability to mitigate the unfavourable effects of terminal heat stress and unpredictable rains at harvesting time. Similar findings and groupings of genotypes based on flower morphological characters were made by Jain et al., (2002); Singh et al., (2014); Kaur et al., (2017) in mungbean.

Pod Characters. Greengram pod characteristics are highly useful in the identification of genotypes. These are important yield attributing traits and affect the yielding ability of plants. Considerable variation was observed in characters mentioned above and were classified into different group. All these characters showed variation and were categorized into distinct groups except for the traits pod pubescence and colour of pre-mature pod.

The trait, colour of pre-mature pod was green in 13 genotypes and green with pigmented suture reported in only one genotype (SL668). Pod pubescence was present in all the genotypes indicating these traits are of abundant in the studied material and may not use for identification of lines in the present material. Pod colour is quite useful morphological marker and may be used in quality seed production programmes at maturity stage to monitor the maturity of other varieties. 9 genotypes showed brown pod colour and five genotypes showed black pod colour. Curvature of mature pod was straight in 7 genotypes and curved in rest of seven genotypes. Thus, these pod characteristics can be exploited for identification and characterization but are found to be variable due to more number of genes and environmental influence on the expression. Sami *et al.*, (2014) observed straight pods without curvature in their study and this morphology may be helpful to identify the inbred lines during quality seed production programme. Based in pod morphological characters, similar observations

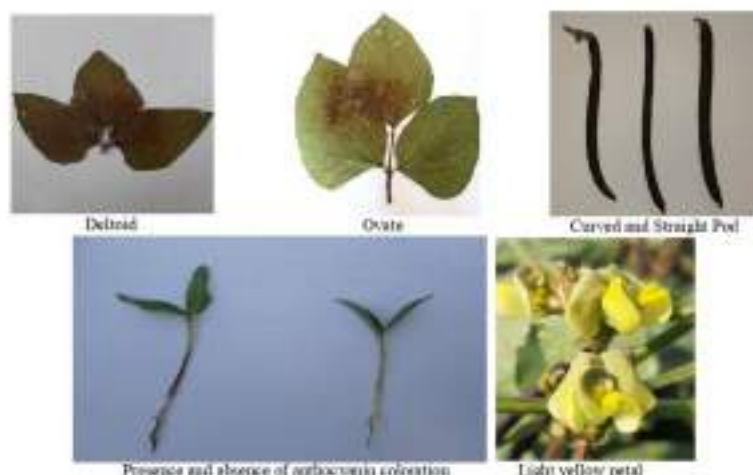
were made by Singh *et al.*, (2014) and Kaur *et al.*, (2017) in mungbean and Gurmukh *et al.*, (2009), Rayak and Bhatnagar (2015) in chickpea.

Seed characters. The price of premium genotypes of pogram or consumer acceptance of a variety is decided by the seed characteristics like colour, lustre, shape and size (Pratap *et al.*, 2013). Seed morphological characters like colour, lustre, shape and size were observed at mature seed stage of plant in the present experiment (Table 1).

All these characters were assigned into distinct groups. Seed colour was mottled in twelve genotypes, green in 2 genotypes (TMB37 and HUM1) respectively. Seed lustre was shiny in 4 and dull in 10 genotypes. Seed shape was oval in 9 genotypes and drum shaped in 5 genotypes. Except SL668 which fell under the large seed category, all the genotypes has seeds of median size (Table 1). (Vankateswarlu *et al.*, 2001) and (Khadgopur and Tamaswar 2011) also discussed the usefulness of seed characters in the characterization of lines in groundnut.

Table 2: Frequency distribution of morphological traits of fourteen mungbean genotypes.

Character	Class	Number of entry	Percentage of entry (%)
Hypothesis: Anthracnose Colonization	Present	15	92.85
	Absent	1	7.14
Time of flowering	Early (<40 days)	4	25.00
	Median (40-50 days)	10	61.42
	Late (>50 days)	80	50.00
	None	80	50.00
Plant: Growth habit	Spreading	8	50.00
	Upright	8	50.00
Plant: Habit	Prostrate	2	12.50
	Erect	12	75.00
Stem: Colour	Green	8	50.00
	Green with purple splotches	8	50.00
Stem: Pubescence	Present	80	50.00
	Absent	80	50.00
Leaflet: Lobes (terminal)	Present	14	100
	Absent	1	7.14
Leaflet: Shape	Prostrate	9	56.25
	Erect	7	43.75
Leaf: Shape	Oval	12	75.00
	Longitudinal	80	50.00
Leaf: Colour	Green	10	61.42
	Dark green	4	25.00
Leaf: Vein colour	Green	1	7.14
	Brownish purple	8	50.00
Flower: Colour of Petal	Yellow	7	43.75
	Light yellow	1	7.14
Pod: Colour of pre mature pod	Green	15	92.85
	Green with pigmented suture	1	7.14
Pod: Pubescence	Present	80	50.00
	Absent	14	100
Pod: Colour	Brown	9	56.25
	Black	7	43.75
Pod: Curvature of mature pod	Straight	7	43.75
	Curved	7	43.75
Seed: Colour	Yellow	80	50.00
	Green	1	7.14
Seed: Lustre	Shiny	12	75.00
	Dull	80	50.00
Seed: Shape	Oval	9	56.25
	Drum shaped	7	43.75
Seed: Size	Small (<1g)	80	50.00
	Medium (1-2g)	1	7.14
	Large (>2g)	1	7.14



In the present investigation, anthocyanin coloration, plant habit, stem pubescence, pre mature pod colour and leaflet lobes were same in all the lines and were not useful for discrimination but rest of the traits had lots of variability which can be exploited for the elite lines identification and utilization as reported by (Patel *et al.*, 2019) and facilitate the easy registration with these distinct characters present in the genotypes with PPV/SFRA.

CONCLUSION

The study highlighted the importance of introducing new material in the breeding programmes to broaden the genetic base of the crop. Thus, characterization of elite improved lines holds an important significance in the identification of lines and their registration with PPV/SFRA and maintenance of line having the information of genetic base. Lines found with unique traits and present only in few of the genotypes will be of great importance for the development of morphologically diverse breeding populations. These lines with unique morphological identity will be considered as a variational marker in the seed production chain to maintain the genetic purity of the variety. These traits may also be useful when varieties may mix and purities can easily be isolated very easily by normal selection method.

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Characterization in F₁ generation of mungbean [*Vigna radiata* (L.) Wilczek] for morphological traits

Tasphiya Elahi, RS Shukla, Sanjay Kumar Singh and Pratik Kumar

Abstract

A total of nineteen morphological traits were studied on forty mungbean crosses during Summer-2021. All the crosses were grown in randomized complete block design with three replications. All the morphological traits were recorded as per crop DUS guideline. The maximum variability was noted in leaf vein colour, leaf colour, colour of petal, pod colour, pod curvature, seed lustre, seed shape, leaflet lobes and hypocotyl colouration. Low frequency was observed in leaf vein colour (1.5%) followed by seed colour (10%), leaflet lobes (10%), anthocyanin colouration (10%), seed colour (10%), seed size (7.5%) and stem colour (2.5%). Frequency distribution in these traits is very low and these traits are unique. On the basis of these traits germplasm can be identified very easily.

Keywords: Crosses, morphological, characterization, evaluated, trait

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is an important legume crop. The mungbean is also known as green gram, golden gram and moong. Mungbean belonging to the sub-genus *ceratotropis* is diploid species with 2n=2x=22 chromosomes with a genome size of 579 Mb/1C. Mungbean is of Indian origin. *Vigna radiata* var. *sublobata* Verde, is the closest wild relative of the cultivated mungbean. Its capacity to restore soil fertility through nitrogen fixation makes it a valuable crop in various cropping systems, particularly in wheat-rice. Due to rich in quality protein, minerals and vitamins they are inseparable ingredients in the diets of a vast majority of Indian population. A seed of mungbean is highly nutritious containing 24-28% protein, 1.0-1.5% fat, 3.5-4.5% fibre and 4.5-5.5% ash on dry weight basis and provide 334-344 kcal energy. Mungbean protein is considered to be easily digestible. Heterosis has important implications for both in F₁ and obtaining transgressive segregants in F₂ generation. Genetic information regarding heterosis provides a clue for selecting the most suitable parents for hybridization. The presence of heterosis in food legumes has been demonstrated by (Singh *et al.*, 1975, Shinde and Deshpande 1989) [15, 16]. Little information about morphological characterization is available in F₁.

Maintenance of genetic purity of genotypes is of primary importance for preventing varietal deterioration during successive regeneration cycles and for ensuring varietal performance at an expected level. The aspects of Distinctness, Uniformity and Stability (DUS) are fundamental for characterization of genotypes. In countries having plant breeders right (PBR) in operation, a new variety is registered only, if it is distinct from other varieties, uniform in its characteristics and genetically stable. Keeping this in view, the present study entitled "Morphological characterization of mungbean [*Vigna radiata* (L.) Wilczek] crosses (F₁s) based on DUS guidelines" was carried out (Patel *et al.*, 2019) [18].

Materials and Methods

The present study on Morphological characterization of 14 mungbean crosses was taken up at seed breeding farm, Department of Plant Breeding and Genetics. Selected 14 genotypes (10 lines and 4 testers) were crossed in Line x Tester fashion under BARC project and 40 crosses (F₁s) were obtained. These 40 crosses were evaluated in the field using randomized block design with three replications. Data were recorded for different morphological characters following standard procedures and the F₁s were grouped.

Results and Discussion

Anthocyanin: Hypocotyl colouration

Hypocotyl anthocyanin pigmentation has great importance in cross based breeding programme to detect the pure crosses due to its monogenic dominance inheritance pattern (Khutak *et al.*, 2000; Mukherjee and Pradhan 2002) [8-9]. This trait can be used as a morphological marker for screening of breeding material at seedling stage. In present investigation, 90% crosses exhibited anthocyanin colouration while 10% did not viz. TMB37XShikha, Ganga8XShikha, LGG460XVirat and HUMIXShikha (Table 2).

Flower characteristics

Based on flower characteristics such as time of flowering and petal colour, crosses could be grouped into different categories (Table 1). Time of flowering varied with the crosses ranging from 25% (medium) to 75% (early) whereas petal colour ranged from yellow (72.5%) to light yellow (27.5%) (Table 2). Similar findings and groupings of genotypes based on flower morphological characters were made by Jain *et al.*, (2002) [1], Singh *et al.*, (2014) [12] and Kaur *et al.*, (2017) [17] in mungbean; Chandrasekhar *et al.*, (2008) [14] and Das *et al.*, (2014) [11] in french bean; Yadav and Srivastava (2002) [10], Gnyandev (2009) [15] and Joshi and Yasin (2014) [6] in chickpea.

Plant morphological characteristics

Use of plant diagnostic characteristics to identify a variety has been classical taxonomy approach for both varietal purity and varietal identification. On the basis of the plant morphological characteristics such as plant growth habit and plant habit, crosses were grouped in different categories (Table 1). Crosses for the plant growth habit ranged from 75% (spreading) to 25% (semi-erect) whereas the plant habit of all the crosses was indeterminate in nature (Table 2). Similar characterization in grouping based on plant morphological characters were made by Jain *et al.*, (2002) [1], Singh *et al.*, (2014) [12] and Kaur *et al.*, (2017) [17] in mungbean.

Stem morphological characteristics

All the 40 mungbean crosses evaluated did not show any variation for stem pubescence (Table 1). Pubescence was present in all the crosses evaluated. Based on stem colour the crosses were grouped into different categories as green, green with purple splashes and purple. Among 40 crosses, stem colour was green in 25% of crosses whereas it was observed

green with purple splashes in 72.5% of crosses and with purple in 2.5% crosses only (Table 2). Therefore, the evaluated 40 crosses of mungbean can be differentiated on the basis of stem colour only. Similar characterization and grouping based on stem morphological characters were made by Jain *et al.*, (2002) [1], Singh *et al.*, (2014) [12] and Kaur *et al.*, (2017) [17] in mungbean; Chakraborthy and Agarwal (1989) [11] in blackgram.

Leaf morphological characteristics

The leaflet lobes, leaf colour, leaf vein colour and leaf shape plays an important role in the yielding ability of plants, as the leaves are the food synthesis site of the plants. In the present study, the characteristics related with leaves have been recorded and based on these characteristics, the crosses were categorized in two different groups (Table 1). The frequency of leaflet lobes, leaf colour, leaf vein colour and leaf shape ranged from 90% (absent) to 10% (present), 72.5% (green) to 27.5% (dark green), 62.5% (greenish purple) to 22.5% (purple) and 15% (green) and 100% ovate showing negligible variation respectively (Table 2). Similar characterization and grouping based on leaf morphological characters were made by Kaur *et al.*, (2017) [17] in mungbean; Chakraborthy and Agarwal (1989) [11] in blackgram.

Pod morphological characters

The pod morphological characteristics, influence the yielding ability of the plant. The genotypic variation was observed for various characteristics of pod such as mature pod colour and curvature of mature pod. All the 40 crosses evaluated did not show any variation for pod pubescence and pre-mature pod colour. Based on mature pod colour crosses were grouped in two different groups as black (57.5%) and brown (42.5%) and curvature of pod ranged from 67.5% (curved) to 32.5% (straight). Similar observations and grouping based on pod morphological characters were made by Singh *et al.*, (2014) [12] and Kaur *et al.*, (2017) [17] in mungbean.

Seed morphological characters

Based on seed morphology crosses were grouped into seed colour, seed shape and seed size (Table 1). Seed colour ranged from 90% (mottled) to 10% (green). Seed lustre range from 67.5% (dull) to 32.5% (shiny). Seed shape ranged from 50% (oval) to 50% (drum shaped). Seed size ranged from 92.5% (medium) to 7.5% (large).

[illegible]

Table 2: Frequency distribution of morphological traits (40 Crosses)

Character	Classes	Number of entry	Percentage of entry (%)
Hypocotyl Andocytosis Coloration	Present	36	90
	Absent	04	10
Time of flowering	Early (<40 days)	36	75
	Medium (40-50 days)	10	25
	Late (More than 50 days)	00	00
		00	00
Plant Growth habit	Erect	00	00
	Semi-erect	10	25
	Spreading	30	75
Plant Habit	Determinate	00	00
	Indeterminate	40	100
Stem Colour	Green	10	25
	Green with purple splashes	30	75
Stem Pubescence	Purple	01	2.5
	Absent	00	00
Leaflet: Lobe (terminal)	Present	40	100
	Absent	10	25
Leaflet: Shape	Present	04	10
	Deloid	00	00
	Ovate	40	100
Leaf: Colour	Lanceolate	00	00
	Cuneate	00	00
	Ovate	20	50
Leaf: Vein colour	Dark green	11	27.5
	Green	00	00
	Greenish purple	29	72.5
Flower: Colour of Petal	Purple	00	00
	Yellow	30	75
	Light yellow	10	25
Pod: Colour of pre mature pod	Green	40	100
	Green with pigmented stripes	00	00
Pod: Pubescence	Absent	00	00
	Present	40	100
Pod: Colour	Brown	17	42.5
	Black	23	57.5
	Straight	13	32.5
Pod: Curvature of mature pod	Curved	27	67.5
	Yellow	00	00
	Green	4	10
Seed: Colour	Mottled	16	40
	Black	00	00
	Shiny	13	32.5
Seed: Surface	Dull	27	67.5
	Oval	20	50
Seed: Shape	Round shaped	20	50
	Small (<1g)	00	00
Seed: Size	Medium (1-5g)	17	42.5
	Large (>5g)	03	7.5

**Suggestion**

Hybridization is the one of the breeding methodology to accumulate important genes for the development of new

diverse genotypes. Characterization of F_1 progeny is also important to identify the genetics of breeding traits so that systematic breeding strategy may be followed for the

development of new morphologically variant genotypes/varieties. On the basis of this result, identification of such plant types which have heterozygous condition and appearance of their morphological traits at this stage can be easily carried out. This study will be fruitful for the identification of pure ones in their heterozygous condition.

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S. No.	Name of Exam	University/ Board	Percentage/ OGPA	Division	Year of Passing	Subject (s) (Major)
1	10 th	CBSE	63.00	First	2009	All subject
2	12 th	CBSE	70.04	First	2011	PCB
3	B.Sc.(Ag.)	JNKVV, Jabalpur	7.63	First	2016	Agriculture
4	M.Sc. (Ag.)	JNKVV, Jabalpur	7.50	First	2018	Genetics and Plant Breeding
5	Ph.D(Ag.)	JNKVV, Jabalpur	7.83	first	2021	Genetics and Plant Breeding

For the partial fulfilment of the requirements for the Degree of Doctor of Philosophy in Agriculture (Genetics and Plant Breeding), she was allotted the research problem on “**Generation Mean Analysis for Yield and Quality Components in Greengram [*Vignaradiata* (L.) Wilczek]**” which was successfully conducted by her and being submitted in the form of the thesis.