GERMPLASM EVALUATION, CHARACTER ASSOCIATION, GENETIC DIVERGENCE, COMBINING ABILITY AND HETEROSIS FOR DIFFERENT QUANTITATIVE TRAITS IN MUNGBEAN [*Vigna radiata* (L.) Wilczek]

THESIS

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CERTIFICATE-I

This is to certify that the thesis entitled **"Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek"** submitted for the degree of **'Doctor of Philosophy'** in the subject of **Genetics and Plant Breeding** to the **Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.)** is a bonafied research work carried out by **Akriti Dutt, I.D. No. A-8852/15/17,** under my supervision and no part of this thesis has been submitted for any other degree.

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

Kumarganj, Ayodhya
March, 2021

(Vinod Singh)
Major Advisor and Chairman

CERTIFICATE-II

This is to certify that the thesis entitled **"Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek"** submitted by **Akriti Dutt, I.D. No. A-8852/15/17** to the Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya in partial fulfillment of the requirements for the degree of **"Doctor of Philosophy"** in subject of **Genetics & Plant Breeding** has been approved by the Student's Advisory Committee after an oral examination.

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INTRODUCTION

The mungbean (*Vigna radiata* (L.) Wilczek) is alternatively known as the green gram, mash or moong. Mungbean is mainly cultivated and grown in India, Bangladesh, Nepal, Pakistan, Sri Lanka, China, Korea,Taiwan, South Asia and South east Asia. It is used in the form of ingredient in both savory and sweet dishes. Mungbean belongs to the legume family. The Mungbean's progenitor (*Vigna radiata* subspecies sublobata) arised wild and it was first domesticated in Persia (Iran). About 4,500 years ago it was mainly found in eastern zone of Harappan civilization in Haryana and Punjab and date back about 4,000 years, it was found in South India mainly in the modern state of Karnataka. In India, mungbean is cultivated and grow in three different seasons, viz., *Kharif*, *Rabi* and *Zaid*. *Zaid* moong can be grown after harvesting of pea, gram, potato, mustard and linseed. Cultivation of *Zaid* Moong is important to increase soil fertility in those areas where paddy – wheat crop rotation is used. Mungbean has established itself as a high worth short stature grain legume crop having many desirable characteristics such as low input requirement, wider adaptability and ability to improve the soil fertility by the virtue of its capability to fix atmospheric nitrogen with the help of symbiotic bacteria found in root nodules. Moongbean and its seed husk can be soaked in water and utilized as cattle feed.

Vigna comprises about 80 species belonging to the genus, *Phaseolus,* sub genus Ceratotropis, a relatively homogenous, morphologically and taxonomically distinct group (Brink and Belay, 2006). *Vigna radiata* is an erect, bushy, annual shrub widely cultivated in

warm regions of India, Indonesia and United States for its edible nature of seeds and forage. It grows up to 60 cm in height. It branches freely, but not heavily foliaged. Leaves, stems and pods are slightly hairy. Leaves are trifoliate, *imparipinnate*, leaflets entire and membranous. Pale yellow flowers are borne in long pedicles in clusters of 12 –15 numbers which are usually at the apex of the plant. Fruits are thin cylindrical pods and the mature pods are variable in colour (yellowish-brown to black), five inches long and contain 10 to 15 seeds. The flowers are self pollinated. Mature seeds are globular and yellow, brown, mottled black or green in colour depending upon its variety. Germination is epigeal with the cotyledons and stem emerging from the seed bed.

The enormous potential of mungbean as a highly valuable crop stems from the fact that it is blessed with high amount of nutritive and digestible protein for serving a role in overcoming malnutrition, ability to improve soil fertility by symbiotic nitrogen fixation and capability to make tremendous contribution via intensive agriculture and integrated farming systems by virtue of being a short duration crop of multiple cropping seasons. Its early maturity enables it to mature on limited soil moisture. Mungbean can be cultivated in moisture stress condition and low fertility level. In spite of being such an important and valuable pulse crop, the production and productivity level of mungbean in India as well as Uttar Pradesh is quite low. In India, mungbean was grown in 28.28 million ha. with a production of 24.02 million tons and average productivity of 849 kg/ha (Anonymous, 2019).Uttar Pradesh is an important pulse growing state in the country with an area of 8.92 million ha and production of about 6.04 million tons resulting productivity of 677 kg/ha (Anonymous, 2018). Considering the prevalent malnutrition in the country and increasing

demand of pulses due to ever increasing population with decreasing resources like land and water, there is an urgent need to develop high yielding mungbean varieties suitable for various environments including abiotic and biotic stress conditions.

For a successful breeding programme, the most desirable pre-requisite is the availability of wider genetic variability in the germplasm collections for important characters of the plant species in samples. Therefore, it becomes imperative to evaluate the available germplasm and assess the existing genetic variability for agronomically important traits so that breeders may know which few of the numerous accessions available in the germplasm collections would be useful for serving the breeding objective. In absence of such information, it would be very difficult to launch a systematic breeding programme consuming optimum time and resources. Varietal development in mungbean has primarly aimed to exploitation of available genetic variability for establishment of homozygous lines possessing stability and higher yield. The release of such pureline varieties depends upon the management of genetic variability for developing efficient plant types having genes for higher performance for yield and its contributing traits.

The assessment of genetic divergence present in the germplasm collections is very important for success of hybridization programme leading to development of high yielding varieties of crop plants because optimum magnitude of parental diversity is required for generating superior hybrids for commercial exploitation as well as for isolating transgressive segregants in segregating generations.

The knowledge of responsible factors for high yields has been rendered difficult since yield is a complex character that manifests through

multiplicative interactions of other characters known as yield components (Grafius, 1959). Therefore, out of numerous plant traits the identification of important yield contributing characters are needed due to the reason that its impractical and impossible to work and concentrate on improving many characters at a time. The correlation and path coefficient analysis gives information about the inter-relationship between different characters for identification of important yield contributing characters.

For formulation and execution of intensive breeding programme, the Information about magnitude and nature of genes effects involved in the expression of character is mandatory. A sound understanding of inheritance of the desirable traits helps in formulation of appropriate breeding strategy for development of superior strains, the identification of genetically superior parent is an important prerequisite. A wrong choice of parents at this stage may undo a meticulously planned and well executed follow up programme. For formulation and execution of intensive breeding profgramme in any crop, some basic aspects are necessary to be known. In a particular situation, the decision for selection of breeding methodology and type of variety to be developed, the information revealed by combining ability analysis not only helps in discriminating the superior parents for utilization in hybridization programme and identification of crosses with higher genetic worth for further exploitation but also gives the information about the nature of gene action responsible for the characters. Among the several methods of combining ability analysis, line x tester analysis (Kempthorne, 1957) is relatively simple method for screening larger number of parents and crosses in comparison to other methods like diallel and partial diallel analysis.

Heterosis, a known valuable expression that results from genetic recombination, has been frequently used for the development and isolation of promising hybrids for further exploitation in both the cases of conventional as well as non-conventional/heterosis breeding programmes. In cross- fertilized as well as self- fertilized crops, the F_1 hybrids are known to show hybrid vigour but constructive exploitation of this phenomenon has been limited to few crops. In autogamous crops like urdbean, mungbean etc., the full exploitation of heterosis through development of hybrid varieties are not possible on the basis of high cost of hybrid seed production due to fertility restoration systems and lack of cytoplasmic male sterility or other avenues for cheap hybrid seed production. Even in the absence of full exploitation of heterosis through hybrid varieties, the assessment of nature and magnitude of heterosis for different characters serves in the identification of potential hybrid combinations for exploitation as breeding materials for isolating transgressive segregants used for evolving the high yielding pureline varieties. Although mungbean posseses high degree of heterosis but due to cleistogamous nature of flower and non-availability of proper sterility mechanisms, its commercial exploitation has found to be limited. For development of pure lines from the variable population, some of the major aspects pursued by the plant breeders working on this crop are mentioned.

Although, the information on above aspects in mungbean is available, the results of past studies are relevant to the plant materials and environments of those studies. The nature and magnitude of genetic parameters have been found to change drastically with changing plant materials and environments for same plant species. Therefore, further studies aimed at generating and comparing information on above aspects in

mungbean to facilitate development of high yielding pure line varieties in mungbean are warranted.

Keeping above facts in view, the present investigation entitled "Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek]" was under taken with the following objectives:

1. To evaluate mungbean germplasm lines for yield and yield components,
2. To study the character association among different quantitative characters,
3. To examine the genetic divergence existing in the germplasm collections,
4. To assess nature and magnitude of gene action for yield and other yield components,
5. To estimate general and specific combining ability variances and their effects,
6. To study nature and extent of heterosis over better- parent and standard variety for yield and its components, and
7. To sort out promising heterotic combinations for yield and its contributing traits.

Chapter-II

REVIEW OF LITERATURE

The development of improved cultivars has made a major contribution to the increased productivity and quality of plants. The prime objective of breeder is to bread varieties better than the best existing ones by improving those characteristics of a plant species that contribute to its economic value (yield). This requires availability of sufficient genetic variability in the breeding populations on which direct and indirect selection can be applied effectively. India has achieved self sufficiency in food production during the past decades and to keep pace with growing population, the country must now increase food production by at least 5.00 million tonnes every year to sustain the current level of self-sufficiency. Such constant increases in the food production can be achieved by increasing the production and productivity of different crops by developing and using improved high yielding varieties suited to various stress and non-stress environments and better production technologies of different way including mungbean.

In this regard, past studies form the basis for formulating new strategy. Hence, a brief review of literature available in mungbean in respect of various aspects of present investigation was collected and has been presented in this chapter under following sub heads:

1. Germplasm evaluation and genetic variability
2. Correlation and path coefficient analysis
3. Genetic divergence analysis
4. Combining ability and gene action
5. Heterosis

2.1. Germplasm evaluation and genetic variability:

The genetic variability existing in the germplasm collections serves as the raw material to the plant breeder on which selection is exercised to evolve superior genotypes. Thus, availability of sufficient genetic variability is the basic requirement for its efficient utilization in any crop improvement programme. The variation exploited in most breeding programmes is derived from naturally occurring variants and the wild relatives of main crop species as well as artificially developed strains and genetic stocks by human efforts. The reservoir of variability for different characters of a plant species resulting from available naturally or artificially synthesized variants or strains constitutes its germplasm. Thus, germplasm may include improved strains, primitive cultivars, wild relatives, obsolete cultivars, special genetic stocks, seeds, pollen and vegetative parts, etc.

Germplasm forms the most valuable natural resource in modern agriculture as it provides donors for important agronomic and economic traits for engineering superior genotypes in a crop improvement programme (Hawkes, 1981). Sometimes introduction of superior genotypes from the germplasm collections of other area may in certain cases accomplish the same purpose as development of superior varieties in breeding programmes.

Vavilov (1926) was the first to realize the essential need for a broad genetic base of germplasm for plant improvement. Vavilov (1951) advocated for genetic resource management and its enhancement through extensive explorations and systematic studies of the collection of land races from various parts of the world. He suggested the geographical

centres of genetic diversity of the cultivated plant species and their wild relatives.

Harlan (1956) also speculated the problem of germplasm conservation while discussing natural variability of plants and pointed out that centers of diversity are in constant process of genetic erosion as "partial or complete destruction of genetic resources in short span of time" which is greatly accelerated in areas of intensive agricultural production. Thus, in centres of plant origin, the primitive forms of cultivated plants and related wild species are fast disappearing (Hawkes, 1971; Harlan, 1972, 1975).

Rahim *et al.*(2010) estimated coefficient of variation, heritability and genetic advance for yield and its contributing characters in 26 mungbean genotypes. Significant variations among the genotypes were observed for all the characters. High heritability (broad sense) along with high genetic advance in per cent of mean was observed 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.

Jangra and yadav (2015) studied the nature and magnitude of genetic parameters for root infection to *Piriformospora indica*, nodulation, N and P uptake, seed yield and yield components in mungbean. PCV was higher than GCV for all the characters indicating influence of environmental factors on their expression. High heritability accompanied with high genetic advance was observed for 100-seed weight, seed yield, plant height, pods/plant, branches/plant and N and P content in seeds.

Katiyar *et al.* (2015) estimated genetic variability, heritability and genetic advance for seed yield per plant and its component traits. The

maximum variability was observed for pods per plant followed by seed yield per plant, clusters per plant, 100-seed weight and branches per plant. Heritability estimates were observed to be high for all the traits except branches per plant and seeds per pod. High expected genetic advance coupled with high heritability estimates were observed for seed yield per plant, days to flowering and plant height indicating least influenced by the environmental variation.

Kumar *et al.* (2015) evaluated fourty-five advance lines including four varieties of mungbean for assessment of genetic variability, heritability and genetic advance for seed yield per plant and its component traits. The maximum variability was observed for seed yield per plant followed by pods per plant, 100-seed weight, number of seeds per pod and branches per plant. Heritability estimates were observed to be high for all the traits. High expected genetic advance coupled with high heritability estimates were observed for seed yield per plant, pods per plant and plant height.

Titumeer *et al.* (2015) studied the genetic variability and genetic diversity among fifty mungbean genotypes. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed for number of primary branches and seed yield per plant but number of seeds per pod and days to 80% maturity showed low GCV. In all the cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in per cent of mean was observed for days to 50% flowering suggesting non-additive gene effects for the expression of the character and selection for such trait might not be rewarding. High heritability with high genetic advance in per cent of

mean was observed for number of primary branches per plant and thousand seed weight indicating that these traits were under additive genetic control and selection for genetic improvement for this trait would be effective.

Pinchhyo *et al.* (2016) conducted the experiment to test the 30 mungbean genotypes along with one check (Samrat) to study the genetic variability during *Kharif*, 2015 in Randomized Block Design with 3 replications. Significant differences were found 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 followed by primary branches per plant and seed index. Maximum heritability was recorded for biological yield, while maximum genetic advance as per cent of mean was recorded for seed yield.

Dahat *et al.* (2017) observed higher genotypic and phenotypic coefficient of variation for secondary branches per plant, primary branches per plant, pods per plant and grain yield per plant. Genetic advance was highest for plant height followed by days to maturity and pods per plant. High heritability coupled with moderate genetic advance was observed for plant height, days to maturity, pods per plant, protein content, days to 50 per cent flowering, secondary branches per plant and grain yield per plant.

Garg *et al.* (2017) assessed genetic variability, heritability and genetic advance and found considerable amount of genetic variability among all the genotypes for all the characters under study. GCV & PCV were highest for seed yield per plant, followed by harvest-index, biological yield and number of pods per plant. High genetic advance coupled with high heritability were observed for plant height, number of branches per plant, pod length, seeds per pod, 100-seed weight, number of pods per plant, biological yield, seed yield and harvest-index.

Keerthiga *et al.* (2017) assessed variability paramters for ten quantitative characters including seed yield per plant in mungbean utilizing thirty progenies of F4 population derived from two crosses *viz*., Meha x GJM-1006 (17 progenies) and Meha x GJM-1008 (13 progenies).F4 progenies of Meha x GJM-1006 had highest genotypic variance for days to maturity, pods per plant and seed yield per plant, while progenies of Meha x GJM-1008 depicted highest genotypic variance for days to 50% flowering, plant height, primary branches per plant, seeds per plant, clusters per plant, harvest-index and 100-seed weight. Most of the traits showed moderate to high heritability as well as genetic advance as per cent mean. High heritability values of more than 65 per cent were observed for plant height in the cross Meha x GJM-1006 and days to 50% flowering in Meha x GJM 1008. Higher genetic advance as per cent mean was observed for pods per plant and seed yield per plant, and low genetic advance as per cent mean for days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and 100-seed weight.

Shiv *et al.* (2017) studied the genetic variability, heritability and genetic advance in four F_3 populations for 11 quantitative traits including seed yield per plant. The material comprised of four F_3 generations derived from crosses *viz*., Meha x Pusa Vishal, Meha x GJM-1006, Meha x GM-4 and Meha x GJM-1008 comprising of 23, 20, 22 and 15 progenies, respectively. Low to moderate GCV and PCV values were observed for days to 50 % flowering, days to maturity, plant height, primary branches per plant, seeds per pod and 100-seed weight which 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. High heritability estimates coupled with high genetic advance were observed for pods per plant, clusters per plant, seed yield per plant, straw yield per plant and harvest-index coupled high genetic mean suggesting the importance of additive genetic variance for these traits.

Azam *et al.* (2018) evaluated 28 mungbean genotypes to study genetic variability for yield and yield related traits. The study revealed that all the traits showed highly significant differences 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). High broad sense heritability coupled with moderate genetic advance as per cent of mean was observed 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.

Dhole *et al.* (2018) employed induced mutation to create genetic variability in mungbean and assessed the amount of genetic variation present among 17 mutants developed through electron beam and gamma rays.Highest GCV was recorded for seed yield plant^{-1} followed by pods cluster^{-1} and clusters plant^{-1}. Considerable genetic variability was present in mutants which can be used in mungbean improvement.

Asari *et al.* (2019) evaluated forty-four mung bean genotypes to assess the genetic variability parameters for yield and yield contributing characters. The genotypes differed significantly for all twelve characters studied. High GCV and PCV were observed for primary branches per plant, pods per plant, seed yield per plant and clusters per plant. High heritability along with high genetic advance as per cent of mean was

observed for plant height, primary branches per plant, clusters per plant, pods per plant and seed yield indicating preponderance of additive gene action.

Sheeba *et al.* (2019) evaluated twenty-two mungbean cultures raised in three replications with check varieties Co (GG) 7 and VBN (GG) 3 and farmers were involved in selection process at Research Station. Among the cultures raised, sixteen cultures were selected based on yield and scores given by the farmers. The sixteen promising cultures identified were screened for Mungbean Yellow Mosaic Virus resistance in hot spot and thirteen cultures were categorized as resistant and moderately resistant. Mother trial was laid out with the above thirteen cultures along with check varieties. From mother trial, six cultures *viz*., TMGG 11007, TMGG 11018, TMGG 11034, TMGG 11035, TMGG 11038 and TMGG 11042 were identified for baby trials. From baby trials, three promising cultures *viz.,* TMGG 11034, TMGG 11007 and TMGG 11042 were identified based on farmers preference.

Hossain *et al.* (2020) opined that salt tolerance is a complex polygenic trait that is genotype specific and tolerance can depend upon a plants developmental stage. To evaluate reproductive stage specific salt tolerance as well as investigate the inherent variability of mungbean genotypes with respect to seed yield and yield-related traits, a pot culture experiment was conducted using 26 mungbean genotypes and exposure to salt stress (EC = 8.0 dS/m) was applied at the reproductive stage, just before the opening of the first flowers. Salt stress led to a significant decrease in seed yield per plant, with yields of the genotypes, BMX 11116, BMX 11176, BMX 11140, BMX 11111 and BMX 11163 being the least impacted by exposure to salt. Principal component analysis revealed that

the first two components explained 63.5% of the total variation among the mungbean genotypes. Cluster analysis grouped the 26 genotypes into five distinct clusters, where the tolerant genotypes were placed in cluster I. Based on their stress tolerance indices, BARI Mung-6, BMX 11176, BMX 11116, and BMX 11140 were categorized as tolerant genotypes, were selected for further study under direct field conditions and are recommended for the genetic improvement of salt stress tolerance in mungbean.

Kumar *et al.* (2020) studied genetic variability parameters for seed yield and its component traits in mungbean. Significant differences were observed among genotypes for all 11 characters studied. The high degree of genetic variability along with high heritability and high genetic advance as per cent of mean were recorded for seed yield per plant, number of pods per plant, harvest-index, biological yield per plant and plant height which indicated that these characters were under the control of additive gene action and therefore, form the basis of selection for mungbean improvement programme. Genotypes/ varieties exhibiting higher seed yield along with other desirable traits were Ganga-1, MUM-2, COGG-912, Keshwanand Mung-1, RMG-268, GM-4, SML-668, RMG-492, Samrat, MH 2-15, MH-421, ML-683, IPM 205-7, GAM-5, SML-832, RMG-344, IPM 99-125, IC-39409, Keshwanand Mung-2, Ganga-8, RMG-62, IPM 02-14 and IC-39288.

Majhi *et al.* (2020) conducted an experiment with the F_3 breeding lines derived from three crosses *viz*., DGGV-7 × V-02-709, DGGV-7 × V-02-802 and DGGV-2 × SML-1815 along with their parents used as checks. The progeny lines were evaluated for estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability

and genetic advance. The analysis of variance showed, the progeny lines derived from the cross DGGV-7 × V-02-709 recorded very high and significant variation for the characters like the number of branches per plant, pod length and seed yield per plant. The high 100-seed weight was observed in the cross derivative of DGGV-2 × SML-1815 with high heritability of 73.26 per cent and moderate genetic advance under mean (19.65%). The breeding lines of DGGV-7 × V-02-709 recorded mean seed yield 3.7 g with the range of 3.22 to 4.65 g and the PCV (17.35%), GCV (14.23%) were moderate with high heritability (72.12%) coupled with moderate genetic advance over mean (17.45%).

2.2. Correlation and path coefficient analysis:

The correlation coefficient provides information about inter-relationship among yield and its components. The information on character associations may be used in the prediction of correlated response to directional selection, construction of selection indices and identification of some characters which may have no value by themselves, but are useful as indicators of the more important ones under consideration (Johnson *et al.*, 1955).

Wright (1921) developed the concept of path coefficient as an attempt to analyse statistically the causes and effects in correlated variables and critically examine the real contribution of individual variables to the ultimate complex end product like yield. Li (1956) gave a detailed account of both basic and applied aspects of path coefficient analysis. Dewey and Lu (1959) applied this technique for the first time in plant breeding in crested wheat grass (*Agropyron cristatum*).

Rahim *et al.*(2010) observed that number of pods per plant, panicle length and number of seeds per pod are positively correlated with grain

yield. Based on path coefficient analysis, the number of pods per plant and number of seeds per pod were found to be the important characters for yield improvement in mungbean.

Jangra *et al.* (2015) conducted an experiment to study the nature and magnitude of genetic parameters for root infection to *Piriformospora indica*, nodulation, N and P uptake, seed yield and yield components.Seed yield exhibited positive correlation with pods/plant, branches/ plant, 100-seed weight, nodules/plant, nodules dry weight, N content in shoot and seeds, P content in seeds and *P. indica* infection in roots.

Katiyar *et al.* (2015) reported that seed yield per plant had significant and positive association with clusters per plant, pods per plant, 100-seed weight and seeds per pod.

Kumar *et al.* (2015) observed that seed yield per plant had significant and positive association with pods per plant, plant height, harvest-index and seeds per pod.

Pinchhyo *et al.* (2016) found that pod length, pods/plant and 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.

Suresh and Malathi (2016) recorded that the trait single plant yield had highly significant and positive association with number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100- seed weight and harvest-index. Path coefficient analysis indicated the role of number of seeds per pod, 100-seed weight and number of pods per plant for higher effect on single plant yield and so, suggesting that more emphasis should

be given on these parameters while executing the selection for genetic enhancement of seed yield in mungbean.

Garg *et al.* (2017) reported that combined results of correlation and path analysis revealed that pods per branch, pod length, biological yield and harvest-index were major component traits for the improvement of grain yield.

Ghimire *et al.* (2017) observed that yield had positive and significant correlation with primary branches, secondary branches, biological yield and grain weight. Biological yield, pod length, days to 50% flowering and number of grains per pod contributed maximum positive direct effect on yield indicating these four traits should be given emphasis while selecting high yielding mungbean cultivars for irrigated condition.

Kumar *et al.* (2018) observed that number of pods per plant, biological yield per plant, harvest-index, number of seeds per pod, 100-seed weight and pod length had significant positive correlation with seed yield and also directly contributed towards seed yield. In addition to these traits, plant height and days to 50 per cent flowering also had direct effect on seed yield in mungbean. Therefore, selection based on these component traits would result improvement in seed yield of mungbean.

Parihar *et al.* (2018) reported that days to 50 % flowering has positive significant correlation with days to maturity, plant height and pods per plant. Pods per plant had positive and significant correlation with plant height, secondary branches per plant and days to maturity. Plant height had significant positive correlation with days to maturity and secondary branches per plant. The path coefficient analysis revealed that days to 50%

flowering, primary branches per plant, secondary branches per plant, 100-seed weight and number of seeds per pod had positive direct effect on seed yield, while plant height, days to maturity and pods per plant had negative direct effects on seed yield. Late flowering with numerous primary and secondary branches with more seed weight and more number of seeds per pod directly lead to increase in seed yield. Less pods per plant with high seeds per pod is more desirable trait for high seed yield.

Asari *et al.* (2019) reported that clusters per plant and pods per plant showed positive and highly significant correlation with seed yield per plant. Among the characters studied, 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 in selection for high yielding mungbean cultivars.

Ahmad and Belwal (2020) reported that correlation analysis indicated that seed yield showed positive and significant correlation with number of pods per plant, pod diameter, pod length, 100-seed weight, number of clusters, number of leaves, seed diameter, plant height, seed length, pod wall thickness, number of branches and seed density. Path analysis revealed that number of pods per plant and 100-seed weight exerted a high magnitude of positive direct effect; pod length showed moderate possitive effect while number of clusters and seed density exerted positive but low magnitude of direct effect on seed yield. Selection strategy based on these characters having high direct effect coupled with positive correlation with seed yield will be rewarding in mungbean improvement programme.

Majhi *et al.* (2020) observed positive and significant correlation between plant height, number of clusters per plant, number of pods per plant, number of seeds per pod and seed yield per plant. Therefore, these characters should be given higher priority at the time of selection for improvement of yield in greengram.

2.3. Genetic divergence analysis:

Genetic divergence analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components of total divergence. A brief review of literature on genetic divergence studies in mungbean has been presented here under:

Rahim *et al.*(2010) reported that twenty-six genotypes were grouped into 3 clusters. Maximum number of genotypes (12) were grouped into cluster II. The maximum range of variability was observed for number of pods per plant (12.22 - 20.55) among all the characters in 3 clusters. Crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness.

Rahim *et al.* (2015) studied genetic diversity among fifty mungbean genotypes. There was a great deal of significant variation for all the characters among the genotypes.Total six clusters were formed for fifty genotypes. Considering group distance, cluster mean values and other agronomic performances, inter-genotypic crosses between G16 and G47; G16 and G13; G47 and G13: G21 and G19: G8 and G21, G21 and G35, G3 and G8, G3 and G35, G3 and G19, G8 and G19 might be suggested for future hybridization program.

Shyamalee *et al.* (2016) reported that the principal component analysis sorted the accessions into three principal components within

cluster similarities and inter-cluster variations. Over 70% of the total variance was explained by the resulted principal components. At rescaled cluster distance of five, 61 mungbean accessions were made into seven clusters. The first and second clusters contained similar number of genotypes (nine) and three recommended varieties 'MI-05', 'MI-06' and 'Ari' were grouped into cluster II. The cluster VII was the largest and most diverse consisting 18 mungbean genotypes with the variety 'Harsha'. This clustering pattern can be used for the selection of parental materials with diverse characteristics for the effective utilization and conservation of the genetic recourses and also be useful in variety development in future mungbean breeding programmes.

Sirohi *et al.* (2016) evaluated genetic divergence and clustering pattern of 40 genotypes of mungbean for selection of suitable parents that can be utilized in hybridization programme and to study the genetic parameters attributing to yield. The crosses of genotypes from cluster II, i.e., PLM-818, PLM-829, PLM-841, PLM-884 and PLM-891 with those of genotypes belonging to cluster V i.e., EC-206971, EC-206979, EC-206975, EC-206973, IC-08592-3, IC-10492, PLM-0003, PLM-0021, PLM-0032 and IC-10497 having highest inter-cluster distance might produce high level heterotic response of segregating populations with regard to yield.

Kesh *et al.* (2017) examined divergence for eleven seed quality traits for the identification of most diverse and promising genotypes. The genotypes differed significantly for all characters under study. D^2 analysis grouped 30 genotypes into 6 clusters. Cluster pattern revealed that cluster I and V were the largest ones with eight genotypes, followed by cluster III and VI with four genotypes each and cluster II and IV with three genotypes

each. The highest contribution towards the total genetic divergence was recorded for vigour index followed by electrical conductivity, shoot length, root length and seedling dry weight. Selection index (I) aimed at selection on several characters simultaneously indicated that genotypes, LGG-460, MH-805, Pusa-0672, IPM-06-5, TBM-11, EC-581523, KM-2241, GP-69, RMG-991 and MH-934 had performed better and were important for further breeding programme aimed at improvement of yield.

Sen *et al.* (2017) studied the nature and magnitude of genetic diversity among 30 mungbean genotypes for yield traits by using Mahalanobis's D^2 statistics. Thirty genotypes could be grouped in 6 clusters. Cluster VI showed maximum intra-cluster distance while the highest inter-cluster distance was observed between cluster III and VI. Cluster II recorded highest means for seeds per pod, 100-seed weight, seed yield per plant and shelling %. The per cent contribution towards genetic diversity was highest for shelling percentage (17.70%) followed by seed yield per plant (16.55%) and number of clusters per plant (14.71%). From the divergence analysis, it may be concluded that the genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization programme for developing high yielding mung bean varieties. Five genotypes viz., PDM-11, TARM-2, TM-98-50, PDM 54 and Basanti could be identified as most useful in the future breeding programme.

Dhole and Reddy (2018) reported that cluster analysis grouped 17 mutants into six clusters. Considerable genetic variability was present in mutants which can be used in mungbean improvement.

Mahalingam *et al.* (2018) evaluated four hundred and forty-five genotypes of greengram for eight quantitative traits *viz*. plant height,

number of branches/plant, number of clusters/plant, number of pods /cluster, number of pods/plant, pod length, 100- seed weight and seed yield /plant. The data was subjected to cluster analysis and the genotypes were grouped under three discrete clusters. This study concluded that an effective hybridization programme including the genotypes between the clusters I, II and III would produce wider segregation that might be used for development of improved greengram varieties.

Nadal *et al.* (2018) reported that 25 accessions were grouped into 16 genetically diverse clusters based on the Principal Component Analysis, which indicated the major contribution of seed width and 100-seed weight to the total variation existing in indigenous germplasm collected from all the governorates of Oman. With respect to seed color, six accessions numbering OMA 284, OMA 295, OMA 313, OMA 335, OMA 341 and OMA 345 were homogenous (pure) with their characteristic green color. The remaining 19 seed accessions were heterogeneous (mixture) with seeds of various colors such as green, brown and black. Critical analysis of seed colors of these samples indicated the presence of 4 groups of which the largest group had 12 seed accessions with green, black seed color followed by one group of three seed accessions with green, brown and black seed color and two groups of two accessions, each with green, black, brown, and green brown seeds, respectively.

Das *et al.* (2019) studied the nature and magnitude of genetic divergence among forty-five mutant lines of greengram variety, OBGG-52, developed by single and combination treatments with gamma rays, Ethyl Methane Sulphonate (EMS), N-methyl-N□-nitrosoguanidine (NG) and maleic hydrazide (MH) using multivariate analysis. These mutant

genotypes were grouped in to 12 clusters based on D^2 values using Tocher's method. A large proportion of mutant lines showed divergence from the parent variety and also among themselves. Sixteen genotypes were grouped with their parent in cluster I, while rest of 28 genotypes grouped in to other eleven divergent clusters. Cluster IV had maximum intra-cluster distance (3.95), while inter-cluster distance was highest (8.27) between cluster XI and cluster XII. Genotype of Cluster III was superior for yield per plant and seeds/pod whereas Cluster VIII was superior for 100-seed weight and pods per plant. Thus, hybridization of genotype belonging to cluster III with genotype in cluster VIII is suggested for development of superior genotypes.

Subramanian *et al.* (2020) studied genetic divergence of 100 mungbean genotypes using Mahalanobis D^2 analysis. Among the traits studied, the number of branches contributed maximum per centage towards the total genetic divergence. The genotypes were grouped into fifteen clusters, with cluster I having the maximum number of genotypes. Maximum intra-cluster distance was recorded in cluster I indicating higher diversity among genotypes of this cluster. Cluster V and XV recorded maximum inter-cluster distance indicating wider divergence between genotypes of these clusters. Likewise, clusters III and XII also recorded wider divergence. Hybridization between genotypes of cluster V (VGG 16-035, VGG 17- 004) and cluster XV (VGG 17-009), followed by genotypes of cluster III (VGG 18-012) and cluster XII (ADT 3) could yield better segregants. High mean performance for the number of clusters per plant, the number of pods per cluster, the total number of pods per plant and seed yield per plant was observed in cluster XIII (VGG 15-030). This genotype can be utilised for further crop improvement programmes in mungbean.

Win *et al.* (2020) conducted an experiment to assess the genetic diversity based on morphological and agronomic characters among 185 mungbean accessions by multivariate analyses such as cluster analysis and principal component analyses. The results exhibited that hierarchical cluster analysis grouped the germplasm into 7 clusters. The maximum number of accessions was observed in Cluster I with 60 accessions, followed by Cluster II and Cluster III with of 42 and 38 accessions, respectively. Cluster IV and VI comprised 18 accessions each whereas each of Cluster V and VII involved 5 accessions. Principal component analysis provided that the first three principal components accounted for 78.06 % of the total variability of agronomic characters. Among the study of agronomic characters, days to 50% flowering, days to maturity, plant height at flowering, plant height at maturity, number of pod bearing branches per plant and 100-seed weight were contributed with the first principal component (PC1) whereas the number of clusters per plant, pods per plant and yield per plant with PC2 and seeds per pod and pod length with PC3, respectively. According to the findings of this research, the significant presence of genetic diversity was recorded among the tested mungbean accessions and provides a good chance for the selection of parents for the improvement program.

2.4. Combining ability and gene action:

Sprague and Tatum (1942) gave the concept of general combining ability (gca) and specific combining ability (sca) based on gene interactions. They suggested that the general combining ability (gca) means the average performance of a line in hybrid combinations, while specific combining ability (sca) refers to those cases in which certain combinations do relatively better or worse than would be expected on the

basis of average performance of the lines involved. Good general combining parent results in higher frequency of heterotic hybrids than poor general combining parent. From the genetic point of view, general combining ability represents additive gene effects and specific combining ability results due to non-additive gene effects, depending on genes with dominance (intra-allelic interactions) and epistasis (inter-allelic interactions). In a hybrid breeding programme, plant breeder generally identifies parental lines with good general combining ability and crosses with high specific combining ability effects.

Griffing (1956) gave the generalized concepts and methodologies for combining ability analysis. He pointed out that gca involved both additive effects and additive × additive interaction effects which are fixable in nature. He outlined the procedure for determining the gca and sca effects and variances from diallel sets of varied composition.

Kempthorne (1957) suggested a procedure known as line × tester mating design, which is used to estimate genetic parameters and general and specific combining ability variances and effects from a set of homozygous lines.

Patel *et al.* (2013) conducted combining ability analysis by using 7 x 7 diallel mating design for seven quantitative characters in mungbean. Mean squares due to general and specific combining ability were highly significant for all the 7 characters studied. Non-additive type of gene effects were predominant for days to maturity, plant height, branches per plant, seed yield per plant and protein content, while additive gene effects were predominant for pods per plant and 100-seed weight. Parents, CO 4 and GBM 1 were the good general combiners for seed yield per plant and important yield components, while crosses, RM-10-503 x CO 4, RM-10-

509 x GBM 1, RM-10-501 x GBM 1 and CO 4 x GBM 1 exhibited the highest and significant sca effects for seed yield per plant and involved low x good parental interactions. These crosses can be used to obtain transgressive segregants for yield and yield contributing characters in future breeding programme.

Vaidya *et al.* (2015) reported that combining ability analysis revealed 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 in the expression of all the characters. Higher magnitude of general combining ability variances for most of the traits except for number of branches per plant, pod length, number of seeds per pod and harvest-index pointed out the preponderance of additive component of the genetic variance in the expression of most of the characters under study. The good general combiners for yield attributing traits were Co-4, GBM-1 and Meha and the best specific cross combinations having the high sca effects for yield and yield attributing traits were Co-4 x Meha, Co-4 x GBM-1, Rm-9-126 x Rm-9- 134, GBM-1 x Meha and Rm-9-133 x GBM-1. These cross combinations could be utilized for further breeding programmes for the development of *rabi* mungbean varieties with chilling tolerance ability or photo-thermo insensitivity, so as to exploit potential of *rabi* mungbean in heavy rainfall zone as rice fallow.

Purohit *et al.* (2016) used ten widely varied genotypes of mungbean crossed in a diallel fashion, excluding reciprocals to study general and specific combining ability (gca and sca) and gene action involved in the inheritance of characters. Analysis of variance for gca and sca were significant for all the traits. Predominance of non-additive gene action was

found for all the characters apart from harvest-index (%), where additive gene action was more evident. Parents, GM-4 and Pusa-0871 were found to be good general combiners for grain yield per plant and parent GM-4 was also good general combiner for most of traits, excluding number of branches per plant, pods per plant and protein content. Four promising hybrids out of 45 hybrids, *viz*., Sonamung-1 x Vamban-1 , Meha x IPM-02-19, Sonamung-1 x VGG-ru-1 and Pusa-0871 x VGG-ru-1 were revealed as the best hybrids for grain yield per plant.The hybrids, Meha x IPM-02-19, Meha x Vamban-1and GM-4 x Pusa-0871were the best specific combiners for increasing protein content.

Singh *et al.* (2016) investigated mungbean lines using diallel analysis. The parents *viz,* DMS-03-17-2 (for days to maturity, primary branches per plant, secondary branches per plant, seeds per pod, seed index, harvest-index and seed yield per plant); IPM-2K-14-9 (for plant height); Meha (for primary branches per plant, secondary branches per plant, average intermodal length, pod length, seeds per pod and seed yield per plant); DMS-01-34-2 (for secondary branches per plant and seed index) and SML 1151 (for seed index) were found to be best general combiners, whereas crosses, namely, IPM-2K-14-9/ DMS 03-17-2 (for plant height), SML 1151/ DMS 01-34-2 (seed index) and SML 1151/ Meha, IPM-2K-14-9/ Meha, IPM-2K-14-9/ DMS 03-17-2 and Meha/ DMS 01-34-2 (for seed yield/ plant) were top specific combiners and heterotic for respective traits. The pattern of heterotic grouping based on seed size and yield indicated that heterosis was not only dependent upon the genetic distance between clusters but diversity within group was also responsible for remarkable heterosis.

Surashe *et al*. (2017) conducted line × tester analysis to estimate the combining ability for yield and yield attributing traits in greengram.

Analysis of variance revealed significant differences among genotypes, crosses, lines, testers and line × 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 except for day to maturity. Parents; viz., IPM 2-3 and ML 1299 were considered as superior parents as they recorded high *per se* performance with positive and significant gca effects for seed yield per plant and other yield contributing traits. Cross combinations viz., BM 2003-2 x IPM 2-3, VAIBHAV x IPM 409-4, BM 4 x MH 2-15, BM 4 x PUSA 0612, VAIBHAV x ML 1299, AKM 4 x MH 2- 15, BM 2002-1 x ML 818 and AKM 4 x IPM 409-4 were found to be good specific combinations for seed yield per plant and other desirable traits. These cross combinations could be utilized for further amelioration of seed yield in greengram.

Verma *et al.* (2017) found that mean squares due to general combining ability (gca) and specific combining ability (sca) were significant for all the characters except mean squares 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 which pointed out the preponderance of non-additive gene effects in the expression of these characters. The predictability ratios were greater than the value of 0.5 for days to 50 % flowering, primary branches per plant, clusters per plant and seed yield per plant indicating the predominance of additive gene action for these characters.

Kumar *et al.* (2018) reported that combining ability analysis is frequently employed to identify the desirable parents for inclusion in hybridization programme. Highest yield in F_2 population was envisaged in the crosses, HUM-12 × PS-16 and HUM-12 × Bireswar. HUM-12 × PS-16 F_2 population was also found superior for plant height and as well as earliness. HUM-12 × Bireswar was found superior for a number of yield contributing characters like number of seeds per pod, pod width and pods per plant. Derivatives from these two hybrids may help to develop high yielding early maturing genotypes with significant improvement of many yield components through selection in progressive generations. HUM-12 × PS-16 and HUM-12 × Bireswar with high protein content could be involved for tailoring genotypes with high yield, protein content and early maturity. Likewise, *per* se performance of WBM-314 x Hum-12 followed by Hum-12 x Bireswar was found to be superior with respect to protein content and Hum-12 x PS-16 and Hum-12 x Basanti for earliness.

Latha *et al.*(2018) carried out combining ability analysis by using 36 F_1's derived out of half diallel using nine parents in greengram. Significant differences were observed for gca and sca among parents and hybrids for all the traits under study, respectively. Analysis of combining ability revealed that mean squares due to general and specific combining ability were highly significant for all the characters indicating importance of both additive as well as non-additive gene effects for all the characters. However, higher magnitude of specific combining ability variances for almost all the traits pointed out the preponderance of non additive component of the genetic variance in the expression of the characters.

Nath *et al.* (2018) employed diallel method in which eight genetically diverse lines of mungbean were crossed among themselves in

all possible combinations excluding reciprocals. The mean squares due to general combining ability (gca) and specific combining ability (sca) were significant for all the characters except mean squares 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 indicating preponderance of non-additive gene effects in the expression of these characters.

Zuge *et al.* (2018) crossed seven genotypes of mungbean in diallel fashion with fixed effect model (method II).The parents and crosses showed significant positive as well as negative general combining ability (gca) and specific combining ability (sca) effects for the traits. HUM-16 and IPM-410-3 with significant negative gca estimates for days to maturity were good general combiners and possessed favourable genetic architecture for early maturity. The general combining ability results indicated that the parent, LBG-460 was good general combiner for all the traits except seed yield per plant and harvest-index. The cross combination, BM-4 x Pusa Vishal had high sca effects for number of pods per plant, plant height and days to 50 % flowering, while the cross, HUM-16 x RMG-1028 showed significant gca effects for all the traits except for number of branches per plant. The study revealed that 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 and yield per plant, etc.

Mohan and Sheeba (2019) evaluated 40 hybrids and their 14 parents to estimate the combining ability effects and heterosis for yield and yield attributing traits in greengram using line x tester mating design. Combining ability analysis indicated the preponderance of non-additive gene action for all the traits studied. Considering the *per se* performance and gca effects, VBN 2 and ADT 3 (Lines) and IPM-02-03 and Pusa 0871 and EC 398897 (Testers) were adjudged as best parents and crosses involving these parents are expected to throw desirable segregants. Considering the *per se* performance, significant sca effects and desirable heterosis, the hybrids ADT 3 x IPM-02-03, ADT 3 x IPM-02-14, ADT 3 x PDM 139, ADT 3 x TM-11-34, IPM-409- 04 x EC 398897, SML 1074 x PUSA 0871, VBN 2 x EC 398897 and VBN 2 x PUSA 0871 were found to be superior for number of pod clusters per plant, number of pods per plant and single plant yield. These hybrids can be utilized to develop high yielding varieties with desirable traits.

Sujatha *et al.* (2019) carried out genetic analysis involving 12 parents and 20 crosses in mungbean which indicated that VC-1, TARM-18, TARM-1 and Vaibhav were the good general combiners based on the overall score across the traits in desirable direction. The cross combination, Chinamung x VC-1 exhibited significant sca effects for traits *viz*., seed yield per plant, seed yield per plot, number of pod bearing clusters per plant, number of pods per plant, hundred seed weight and harvest-index. Gene action study revealed that days to 50 flowering, days to maturity, number of pods per plant, hundred seed weight , total dry matter at harvest , harvest-index (%), seed yield per plant and seed yield per plot were governed predominantly by additive genetic variation.

Kakde *et al.* (2019) crossed six testers, BPMR 182, BPMR 132, BPMR 21, BPMR 126, BPMR 75 and BPMR 38 with four varieties as

lines BM 2002-1, BM 4, JL 781 and AKM 4 in line x tester fashion to estimate the combining ability for yield and yield attributing traits in mungbean. 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 gca estimates of lines and testers emphasized the importance of lines, BM 2002-1 and JL 781 and testers, BPMR 126 and BPMR 75 for their use as desirable parents for enhancing the yield potential through assembling the favorable genes for yield and yield components. The high yielding crosses *viz*., BM 2002-1 x BPMR 126, BM 2002-1 x BPMR 75, BM 4 x BPMR 75, JL 781 x BPMR 132, JL 781 x BPMR 126 and JL 781 x BPMR 75 were found to be the superior for seed yield and yield components and should be further tested across the different environments for their stability performance.

Rathod *et al.* (2020) conducted combining ability analysis for yield and yield components of mungbean by using an 8 x 8 diallel mating system both in F_1 and F_2 generations. 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. The parent, K 851 was a good general combiner for seed yield per plant, days to maturity, plant height, primary branches per plant, clusters per plant, pods per plant and seeds per pod in both generations, while Pant-M 4 was good general combiner for seed yield per plant, plant height, pods per cluster and pods per plant over generations. Parents, RMG 62 and Asha were the best combiners for early flowering.

GM 4 had good general combining ability for seed yield in F_1, but for pod length and 100-seed weight in F_1 and F_2. The crosses showing high sca effects for seed yield also had significant and positive effects for at least two important yield components.

2.5. Heterosis:

The term heterosis was first used by Shull in 1914. Heterosis may be defined as the superiority of an F_1 over both of its parents in terms of yield or some other character(s). Generally, heterosis is manifested as an increase in vigour, size, growth rate, yield or some other characteristics, but in some cases, the hybrid may be inferior to the weaker parent.

The exploitation of heterosis is considered as an outstanding application of the principles of the science of genetics in agriculture. Heterosis breeding had led to a breakthrough in yield increase in several crop plants. For the exploitation of heterosis, it is imperative to study the magnitude of heterosis. The expression of heterosis is greatly influenced by the magnitude of genetic differences among parents involved in the crosses. A brief review of literature pertaining to studies on heterosis for different characters in mungbean is presented in the following paragraphs:

Lavanya *et al.* (2015) used twenty-one hybrids of mungbean along with their seven parental lines crossed in diallel fashion excluding reciprocals to assess the extent of standard heterosis over standard check i.e., Samrat for yield and seven component characters. Out of 21 F_1 hybrids, two crosses, SML 382 x WGG 37 and PUSA 9871 x WGG 37 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, SML 382 X WGG 37 excelled for number of primary branches per plant. The crosses, SML 382 x WGG 37 and PUSA 9871 x WGG 37 exhibited high standard heterosis for seed yield per plant which could be an excellent source for developing high yielding mungbean genotypes.

Dhurai *et al.* (2016) reported that the highest mid-parent (71.02%) and better-parent (43.04 %) heterosis for seed yield was recorded by cross Kopergoan × HUM 12. The cross, ML 5 × HUM 12 recorded the highest standard heterosis (52.45%) and low inbreeding depression (-1.77%) for seed yield, followed by Kopergoan × HUM 12 (43.11%). The crosses showing heterosis for seed yield were not heterotic for all characters. HUM 16 × HUM 12, HUM 8 × ML-1720, Pusa Vishal × ML 1720 and HUM 16 × ML 1720 were identified as promising crosses for many desirable traits and they could be exploited for developing high yielding mungbean varieties.

Vaidya *et al.* (2016) evaluated twenty-one crosses resulting from 7 x 7 diallel excluding reciprocals to know the magnitude of heterosis over better- parent and standard variety for yield and its attributing characters in *rabi* mungbean. The highest heterosis to the extent of 37.23% over the check Co-4 and 82.20 % over the check GBM-1 was observed in cross combination Co-4 x Meha for seed yield per plant, which also exhibited high heterosis per centage for other yield components. The promising hybrids, *viz*. Co-4 x Meha, Co-4 x GBM-1, GBM-1 x Meha and Rm-9-129 x Co-4 were identified to have great potential to exploit the hybrid vigour or to isolate the desirable segregants for the development of *rabi* mungbean varieties with chilling tolerance ability or photo-thermo insensitivity, so as to exploit potential of *rabi* mungbean in heavy rainfall zone as rice fallows.

Nath *et al.* (2017) evaluated twenty-eight hybrids of greengram derived by crossing eight parental lines in 8 x 8 half diallel fashion excluding reciprocal crosses for assessing the extent of heterotic effects over mid- and better-parent for yield and nine component characters. Out of 28 F_1 hybrids, two crosses, BM-4 x PDM-139 and RMG-1035 x RMG-1045 showed superior *per se* performance with significant positive heterosis for seed yield and most of the yield contributing characters. IPM 99-125 X ML 131 exhibited high heterosis for 100-seed weight and harvest-index, whereas the cross, RMG 344 X RMG-1045 showed excellent heterosis for plant height and pods per cluster. Based on heterosis studies, the best direct yield contributing characters were pods per cluster, pods per plant, plant height, 100-seed weight and harvest-index.

Sandhiya *et al.* (2018) reported highest standard heterosis for number of clusters per plant. The highest mid-parent, better-parent and standard heterosis for number of clusters per plant were 182.66 per cent, 173.44 per cent and 196.61 per cent, respectively, for the hybrid EC 396120 x IPM 99125. The highest standard heterosis of 31.5 per cent for seed protein content was recorded for the hybrid between EC 396126 and COGG 930.The crosses, Pant M 103 x COGG 930, EC 396120 x IPM 99 125, AGG 10091 x CO 7, Pant M 103 x MH 565, AGG 10091 x IPM 99 125, EC 396120 x IPM 0214, Pant M 103 x CO 7 and EC 396120 x Pusa Vishal exhibited high and significant *per se* performance and standard heterosis for single plant yield. So these crosses were considered as superior crosses for further utilization in the breeding programme.

Latha *et al.* (2019) evaluated 36 hybrids along with 9 parents and three checks in randomized block design with three replications. The heterosis over mid-parent (MP), better-parent (BP) and standard check was

estimated for quantitative and quality traits. The highest positive and significant heterosis at all the three levels for seed yield per plant was exhibited by MGG 347 x KM 11-564. This cross combination also revealed highest *per se* performance for this trait. Another hybrid WGG 42 x RM 12-13 exhibited maximum positive and significant heterosis at all the three levels with high *per se* performance for seed yield per plant.

Hange *et al.* (2020) evaluated a line x tester set of 18 crosses along with the nine parents and one check (PKV Green Gold) in randomized block design with three replications during the *Kharif*, 2014 for days to 50 per cent flowering, days to maturity, grain yield per plant and seeds per pod. A considerable amount of heterosis was observed for all characters. The highest heterotic effect was observed in BM-2002-1 x AKM-0603 (145.93 %) for grain yield per plant. The hybrids showed significant positive heterosis over check PKV green gold for all the characters under study. The cross combination, BPMR-145 x AKM-10-07 for earliness and grain yield per plant is recommended for heterosis breeding for earliness and to boost low yield levels of green gram.

Chapter-III

MATERIALS AND METHODS

The edaphic and climatic conditions under which the present study was carried out along with the techniques applied and materials used therein have been described in this chapter.

3.1. Experimental site:

The present investigation was carried out at the Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya.

Geographically this place is located in between 26.47^0N latitude, 82.12^0E longitude and at an altitude of 113 meters above from mean sea level. This area falls in sub-tropical climatic zone. The climate of district Ayodhya is semi-arid with hot summer and cold winter. The details of weather conditions recorded during experiment period of *Zaid* and *Kharif*, 2019 were presented in Table 3.1.

3.2. Experimental details:

The present study consisted of two experiments as follows.

3.2.1. Germplasm evaluation experiment (Experiment-I):

Sixty mungbean germplasm lines along with four checks, namely, Pant Mung 4, HUM 16, IPM 99-125 and IPM 205-7 exhibiting wide spectrum of variation for different characters were evaluated to study genetic variability, character associations and genetic divergence in *Zaid* and *Kharif* seasons of 2019. The 60 genotypes and four checks were grown in augmented design in each season. The experimental plot was divided into six blocks. Each block had 14 single row plots of 4 m length. In *Zaid* season, the inter- row and intra- row spacings were kept 30 cm and 10 cm, respectively. In *Kharif* season, the inter-row and intra- row spacings were kept as 60 cm. and 10 cm, respectively. All the recommended agronomic practices for respective seasons were followed to raise a good crop.

Table 3.1: Details of weather conditions recorded during evaluation period of *Zaid-Kharif*, 2019 (19 March- 23 June and 18 July-18 October of 2019) for Experiment I and II.

Standard week	Temperature		Average relative humidity(%)	Total Rainfall (mm)	Wind Speed (km/hr)	Sunshine (hrs)
	Max.	Min.				
19-25 March	34.1	17.4	60.5	5.0	4.6	9
26-01April	34.6	18.9	62.5	2.0	2.6	8
02-08 April	36.7	21.3	57	00	4.3	9
09-15 April	34.7	19.2	67	00	3.3	8
16-22 April	40.5	23.3	53	00	4.8	10
23-29 April	40.0	24.5	55	00	5.1	10
30-6 May	42.4	24.9	45.5	00	6.3	9
07-13 May	39.6	24.3	46	00	8.3	9
14-20 May	41.4	25.8	44.5	00	4.8	9
21-27 May	40.0	24.9	46.5	00	5.4	10
28-03 June	40.4	26.5	52.5	00	6.9	9
04-10 June	41.1	27.9	49.5	00	6.0	8
11-17 June	36.2	25.6	61.5	00	7.5	6
18-24 June	38.1	27.9	60.5	24	6.1	7
16-22 July	31.7	25.6	83	101.4	3.0	4
23-29 July	33.6	27.0	79	16.6	4.9	7
30-05 August	33.9	26.6	78.5	18	5.6	6
06-12 August	32.6	26.8	78.5	4	5.8	6
13-19 August	30.9	24.8	86.5	84.6	5.0	2
20-26 August	34.2	26.8	80	00	3.1	6
27-02 Sept.	33.6	26.9	81.5	10	3.1	7
03-09 Sept.	32.6	26.6	86.5	104	3.9	4
10-16 Sept.	29.9	24.3	89.5	103	4.2	2
17-23 Sept.	27.2	22.9	91.5	179	2.6	1
24-30 Sept.	30.9	22.4	82.5	10	5.7	4
01-07 Oct.	32.6	20.9	74	00	1.6	8
08-14 Oct.	31.7	21.1	78	00	1.2	6
15-21 Oct.	29.0	17.4	76	00	.85	5

3.2.2. Combining ability experiment (Experiment-II):

A line x tester set of sixty hybrids (F_1s) was derived by crossing fifteen genotypes/varieties viz. MH 2-15, CoGG 912, PDM 139, LGG 450, ADT 3, TARM 1, TM 96-2 Pusa Vishal, IPM 2-3, HUM 12, VBN (GG) 2, TM 2000-2, LGG 460, Pusa 9072 and CoGG 8 as lines (females) with four testers (males), namely, Pant Mung 4, HUM 16, IPM 99-125 and IPM 205-7 during *Zaid* season of 2019 to study gene action, combining ability and heterosis for yield and yield contributing traits during *Kharif* season of 2019. The eighty genotypes comprising sixty crosses, nineteen parents and one check variety were evaluated in randomized complete block design with three replications during *Kharif* season of 2019. The eighty genotypes in a replication were grown in 4 m long single row plots following between rows and within rows spacing of 60 cm and 10 cm, respectively.

3.3. Observations recorded:

The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for thirteen characters. The mean values of observations recorded on five plants of each plot were used for analysis. The observations for different characters were recorded as follows:

3.3.1. Days to 50 percent flowering:

The days to 50 per cent flowering were recorded from the date of sowing to the date on which 50 per cent plants of each plot flowered.

3.3.2. Days to maturity:

Number of days form the date of sowing to the day on which 80 per cent of pods became buff to dark brown were taken as days to maturity.

3.3.3. Plant height (cm):

Plant height of five plants from ground level to the top of plant was measured in the centimeters at maturity.

3.3.4. Primary branches per plant:

The number of primary branches per plant were counted on five randomly selected plants from each plot at the time of maturity and average was done.

3.3.5. Clusters per plant:

The total number of clusters were counted in each of the randomly selected five plants of each plot and average was taken.

3.3.6. Pods per cluster:

It was calculated by dividing average pods per five plants from average clusters per five plants in a plot.

3.3.7. Pods per plant:

Number of pods per plant were counted on five randomly selected plants of each plot and average was taken.

3.3.8. Pod length (cm):

Five pods were selected randomly from each selected plant to measure the length and averaged.

3.3.9. Seeds per pod:

Five pods were selected randomly from each plant and the number of seeds in each pod was counted to work out average seeds per pod.

3.3.10. 100-seed weight (g):

The seeds of selected plants from each plot were mixed to draw a representative sample of 100-seeds, which was weighted in grams.

3.3.11. Biological yield per plant (g):

The whole plant weight including shoot and derived leaves of each selected plant was taken in grams.

3.3.12. Harvest-index (%):

It was computed as follows:

$$\text{Harvest-index (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \text{ x } 100$$

3.3.13. Seed yield per plant (g):

After threshing and cleaning, the seeds obtained from each selected plant were weighted in grams.

3.4. Statistical analysis :

The statistical and genetical analysis employed for analysis of various aspects of the two experiments of present study are explained as under:

3.4.1. Germplasm evaluation experiment (Experiment-I)

Mean data for each charecter of genotypes in each plot was used for statistical analysis.

3.4.1.1. Analysis of variance for augmented design:

Analysis of variance of augmented design was done by following **Federer (1956) .** The mean yield of checks and blocks were computed as under:

The first step in the analysis was to construct a two way table of check yields, total and means:

Checks	**Blocks**						**Total**	**Mean**
	1	**2**	**3**	**4**	**5**	**6**		
Pant Mung 4	$X_{1.1}$	$X_{1.2}$	$X_{1.3}$	$X_{1.4}$	$X_{1.5}$	$X_{1.6}$	C_1	$\bar{X}_1$
HUM 16	$X_{2.1}$	$X_{2.2}$	$X_{2.3}$	$X_{2.4}$	$X_{2.5}$	$X_{2.6}$	C_2	$\bar{X}_2$
IPM 99-125	$X_{3.1}$	$X_{3.2}$	$X_{3.3}$	$X_{3.4}$	$X_{3.5}$	$X_{3.6}$	C_3	$\bar{X}_3$
IPM 205-7	$X_{4.1}$	$X_{4.2}$	$X_{4.3}$	$X_{4.4}$	$X_{4.5}$	$X_{4.6}$	C_4	$\bar{X}_4$
Total	B_1	B_2	B_3	B_4	B_5	B_6	G	M

Where,

X_{ij} = Yield of the i^{th} check in the j^{th} block,

$B_j = \sum_i X_{ij}$ = Sum of all checks in j^{th} block,

$C_i = \sum_j X_{ij}$ = Sum of yield of i^{th} check over blocks,

$G = \sum_j B_j = \sum_i C_i$ = Grand total of all check yields,

$\overline{X_i}$ = Ci/b = Mean of the i^{th} check,

$M = \sum \overline{X_i} = G/b$ = Sum of all check means.

The block size of present experiment was constant (same number of entries in each block). Therefore, the following definitions and relationship hold;

c = Number of check varieties/block

v = Number of lines

b = Number of blocks

n = v/b = Number of lines/block

In the analysis of variance of check varieties the experimental error has (b-1) (c-1) degree of freedom.

An estimate of experimental error variance, which was used to compute standard errors and LSD's was obtained using following format for analysis of variance of the check yields.

Source of variation	**d.f.**	**S.S.**	**M.S.**
Blocks	b-1	SSB	MSB
Checks	c-1	SSC	MSC
Error	(b-1) (c-1)	SSE	MSE
Total	bc-1	SST	-

The ANOVA is simply a randomized block ANOVA on the check means. The entries in the ANOVA table were computed as follows:

$$SST = \sum_i \sum_j X^2_{ij} - G^2/bc$$

$$SSB = \left[\frac{1}{c}\right] \sum_j B^2_j - G^2/bc$$

$$SSC = \left[\frac{1}{b}\right] \sum_i C^2_i - G^2/bc$$

$$SSE = SST - SSB - SSC$$

$$MSE = SSE/ (b-1) (c-1)$$

Then compute block effect, r_j, for each block where,

$$r_j = \left(\frac{1}{C} \right) (B_j - M)$$

It is supposed that a check on the computation,

$$\sum r_j = 0$$

The yield adjusted for the effect of block in which the entries were grown can be calculated as follows:

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

$Y_i = Y_{ij} - r_j$ = adjusted yield of i^{th} genotype adjusted for block effect.

Variances for different pair wise comparison:

1. Difference between two check means = 2 MSE/b
2. Difference between adjusted yields of two genotypes in the same block = 2 MSE

3. Difference between adjusted yields of two genotypes in different blocks = 2 MSE (1+1/c)
4. Difference between adjusted yield of genotype and check mean = MSE (b+1) (c+1)/bc

Least significant difference values:

The least significant differences were computed using the above variances in the following way:

1. For two check means = $t\,\alpha\,\sqrt{2MSE/b}$
2. For two adjusted genotypes in same block = $t\,\alpha\,\sqrt{2MSE}$
3. For two adjusted genotypes in different blocks = $t\,\alpha\,\sqrt{2MSE\,(c+1)/c}$
4. For an adjusted yield of genotype against check mean = $t\,\alpha\,\sqrt{MSE\,(b+1)\,(c+1)/bc}$

For all L.S.D.'s the 't' value is two tail values at α percent level on (b-1) (c-1) degree of freedom.

3.4.1.2. Estimation of Correlation coefficients (r):

The simple correlation coefficients between different characters were estimated according to Searle (1961) as follows:

Correlation coefficient (r) between two characters x and y

$$r_{xy} = \frac{\text{Cov. xy}}{(\text{Var. x X Var. y})^{1/2}}$$

Where,

r_{xy} = Correlation coefficient between characters x and y

Cov. xy = Covariance between characters x and y

Var. x = Variance for x character

Var. y = Variance for y character

The significance of correlation coefficient was tested by comparing at an appropriate level of significance, the significant values of (r) at (n-2) d.f., where 'n' is the number of genotypes.

3.4.1.3. Path coefficient analysis:

Path coefficient analysis was done according to the formula given by Dewey and Lu (1959). The seed yield was assumed to be dependent variable (effect), which is influenced by all the twelve characters, the independent variables (causes) directly as well as indirectly through other characters. The variation in seed yield unexplained by the twelve causes was presumed to be contributed by a residual factor (x), which is uncorrelated with other factors. Path coefficients were estimated by following simultaneous equations indicating the basic relationship between correlation and path coefficient. The equations used are as follows.

$$r_{ij} = P_{iy} + \sum_{j=1}^{12} r_{ij} P_{iy} \text{ for } i = 1, 2, 3 \ldots\ldots 12$$

or

$$r_{iy} = \sum_{j=1}^{12} r_{ij} P_{iy} \text{ for } r_{ii} = 1$$

The above equations can be written in the form of matrix where;

$$[A]_{12x1} = [B]_{12x1} [C]_{12x1}$$

A is column vector of correlations r_{iy}

B is correlation matrix of r_{ij}, and

C is column vector of direct effects P_{iy}.

Residual factor was calculated as follows:

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

Where,

$$R^2 = \sum_j P_{iy}\, r_{iy}$$

The $r_{ij's}$ denote correlations between all possible combinations of independent characters i.e., **$r_{1.2}$ to $r_{11.12}$** and P_{1y} to P_{12y} denote direct effects of various characters x on character y.

r_{iy} = Correlation coefficient between i^{th} characters and dependent

P_{iy} = Direct effect of i^{th} character on y

3.4.1.4. Non-hierarchical Euclidean cluster analysis:

Genetic divergence among 60 genotypes and four checks planted in Augmented Design was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973).

According to Beale (1969), each observation is initially allocated to its closest cluster centre. The means of clusters are then calculated and are taken to new cluster centers. At the same time, sum of squared deviation of the observations from their respective cluster centre is computed. The observations are checked in turn to see if a shift to a different cluster centre results in a decrease in the total sum of squares. This assumes that $di^2 < dk^2$, where, di is the distance from centre of cluster i. However, more effective criterion involves reassigning the observation if the squared deviation from the centre of cluster i is less than that from centre of cluster k, even when the cluster centers are simultaneously repositioned that is when:

$$\frac{ni}{ni+1} d_i^2 < \frac{nk}{nk-1} dk^2$$

Where,

'ni' is the number of observations in cluster 'i'.

In delimiting clusters usually average deviance among a subset of 'm' points is considered, not the individual ½ m (m-1) deviances. If the i^{th} variable on j^{th} number is X_{ij} average deviance of a set of 'm' is as follows:

$$\frac{1}{m(m-1)}\sum_{i=1}^{p}\sum_{j=1}^{m}\sum_{k=1}^{m}(X_{ij}-X_{ik})^2$$

$$\frac{1}{m(m-1)}\sum_{i=1}^{p}\sum_{j=1}^{m}\sum_{k=1}^{m}[(X_{ij}-X_{i.})-(X_{ik}-X_{i.})]^2$$

Where,

$\overline{X}_{i.}$, is the mean of X_i over the 'm' members,

$$=\frac{1}{m(m-1)}\sum_{i=1}^{p}\left[\sum_{j}\sum_{k}(X_{ij}-X_{i.})^2+\sum_{j}\sum_{k}(X_{ik}-X_{i.})^2-2\sum_{i}\sum_{k}(X_{ij}-X_{i.})(X_{ik}-X_{j.})\right]$$

The cross product term vanishes and the other two are equal.

Thus, average deviance $=\frac{2}{m-1}\sum_{j=1}^{m}\sum_{i=1}^{p}(X_{ij}-X_i)^2$

Now, instead of calculating $\frac{1}{m}(m-1)$ deviances, 'm' deviances from the centre of gravity are calculated.

The assumption in this method are that this Euclidean distance 'D' separating 'n' points in a 'p'-dimensional space are proportional to the dissimilarities between the objects, and secondary that no object can belong simultaneously to two clusters.

Initially, a given number of vectors of cluster centers are located in the 'p' space. The positions of these centers are located in the 'p' space. The position of these centers can be chosen arbitrarily or randomly. However, a good choice of initial cluster centers reduces the amount of computation to a considerable extent.

To start with 'n' cases are allotted to a predetermined maximum number of clusters (C max.) according to the procedure suggested by Beale (1969).The residual sum of squares, RSS (C) for the solution involving 'C' clusters is calculated. Then the number of clusters 'C' is reduced by 1 (unless C = min.) and this procedure is repeated till 'C' min. is reached, i.e. further reduction is negligibly small. For each step RSS (C) is calculated. When RSS (C) values for max. $\geq$ C $\geq$ min. are available, these are used in a pseudo-F-ratio test of null hypothesis that the solution for the C_1 cluster provides no better fit than the solution for the C_2 clusters, with $C_1 > C_2$. This F-ratio is calculated as:

$$F = \frac{RSS\,(C_2) - RSS(C_1)}{RSS(C_1)} \Bigg/ \left(\frac{n - C_2}{n - C_1} - \frac{C_1}{C_2} - 2/P - 1 \right)$$

With P (C_2-C_1) and P (n-C_1) d.f. The null hypothesis is rejected if the calculated 'F' exceeds the table value of F.

For reducing the number of clusters by 1 till C minimum is reached, Beale has suggested certain procedures. Instead of using Beale's procedure for merging two clusters. Doshi *et al.* (1981) have adopted a simple procedure. When a solution is found for 'C' cluster. 'C' vectors of new clusters are calculated. From this set of new cluster centre vectors, last vector is dropped and (C-1) vectors are used of initial vectors of clusters centers for arriving at (C-1) clusters. For determining the appropriate number of clusters, F-test gives a rough guide in exploratory analysis.

3.4.2. Combining ability experiment (Experiment-II):

The experimental data collected on all the thirteen characters in respect of Experiment-II of the present study were compiled by taking the mean values over five randomly selected plants in each plot in each

replication. It was then subjected to various statistical and genetical analyses as follows.

3.4.2.1. Analysis of variance for Randomized Complete Block Design:

The analysis of variance for Randomized Complete Block Design was carried out following Panse and Sukhatme (1967) as follows:

Source of variation	d.f.	S.S.	M.S.	F-ratio
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Error	(r-1) (t-1)	SSE	MSE	-
Total	(rt-1)	TSS	-	-

Where,

r = Number of replications

t = Number of treatments

MSR = Mean squares due to replications

MST = Mean squares due to treatments

MSE = Mean squares due to error

d.f. = Degrees of freedom

The standard error and critical difference were calculated as follows:

$$\text{Standard error of mean (SEm)} = \sqrt{\text{MSE/r}}$$

$$\text{Standard error of mean (SEd)} = \sqrt{2\,\text{MSE/r}^2}$$

$$\text{Critical difference (CD)} = \sqrt{2\text{MSE/r}} * \text{t}$$ 't' value at 5% or 1% level of significance and error degree of freedom.

The analysis of variance was further extended to partition the variance due to treatments (genotypes) in to various components such as parents, crosses, parents *vs* crosses, females, males and females *vs* males as outlined below:

Source of variation	**d.f.**	**S.S.**	**M.S.**	**F-ratio**
Replications	(r-1)	SSR	MSR	MSR/MSE
Treatments	(t-1)	SST	MST	MST/MSE
Parents	(p-1)	SSP	MSP	MSP/MSE
Females	(f-1)	SSF	MSF	MSF/MSE
Males	(m-1)	SSM	MSM	MSM/MSE
Females vs Males	1	SSF vs SSM	MSF vs MSM	MSF vs MSM/MSE
Crosses	(F_1-1)	F_1SS	MSF_1	MSF_1/MSE
Parents vs Crosses	1	SSP vs F_1SS	MSP vs MSF_1	MSP vs MSF_1/MSE
Error	(r-1) (t-1)	SSE	MSE	-

Where,

r = number of replications

t = number of treatments

p = number of parents

f = number of females

m = number of males

F_1 = number of hybrids

S.S. = Sum of squares

M.S. = Mean sum of squares

d.f. = Degree of freedom

3.4.2.2. Coefficients of variation:

Phenotypic (PCV) and genotypic (GCV) coefficients of variation for different characters were estimated by formulae suggested by Burton and de Vane (1953) as follows:

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\text{Phenotypic variance}}}{\overline{X}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\overline{X}} \times 100$$

Where, $\overline{X}$ = Mean of the character.

3.4.2.3. Heritability in broad sense:

Heritability in broad sense (h^2b) was calculated as suggested by Hanson *et al.* (1956).

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

Where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

3.4.2.4. Genetic advance in per cent of mean:

The expected genetic advance (Ga) was estimated using formula suggested by Johnson *et al.* (1955).

$Ga = h^2b \times \sigma p \times K$

Where,

h^2b = Heritability in broad sense

σp = Phenotypic standard deviation

K = Standardized selection differential (2.06) a constant at 5% selection intensity.

Genetic advance as per cent of mean ($\overline{Ga}$) was worked out as:

$$\overline{Ga}\ (\%) = \frac{Ga}{\overline{X}} \times 100$$

Where,

Ga = Genetic advance

$\overline{X}$ = Mean of the character

3.4.2.5. Combining ability analysis:

The combining ability analysis was carried out following line × tester mating design outlined by Kempthorne (1957) and further elaborated by Arunachalam (1974). Line × tester analysis was used to estimate general combining ability (gca) and specific combining ability (sca) variances and their effects using the observations taken on F_1 generation of the line × tester sets of crosses. In this mating system, a random sample of 'l' lines is taken and each line is mated to each of the't' testers (Singh and Chaudhary, 1977).

The model underlying this analysis is as follows:

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

Where,

μ = General mean

g_i = gca effect of the i^{th} male (tester), i = 1,2,…m.

g_j = gca effect of j^{th} female (line), j = 1,2,…f.

s_{ij} = sca effect of the i^{th} tester and j^{th} line cross combination

e_{ijk} = Error associated with ijk^{th} observation, k = 1,2,…r.

The individual effects were estimated as follows:

(i) $$\mu = \frac{X...}{mfr}$$

Where,

X... = total of all hybrid combinations

(ii) $g_i = \frac{X_{i..}}{fr} - \frac{X...}{mfr}$

Where,

$X_{i}..$ = total of i^{th} male (tester) over all the females (lines) and replications.

(iii) $g_j = \frac{X._{j.}}{mr} - \frac{X...}{mfr}$

Where,

$X._{j}.$ = total of j^{th} female (line) over all the males (testers) and replications.

(iv) $s_{ij} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{fr} - \frac{X._{j.}}{mr} + \frac{X...}{mfr}$

Where,

$X_{ij.}$ = total of ij^{th} combination over all replications.

Standard errors for combining ability estimates were calculated as given below:

SE (gca for line) = $(Me/rm)^{1/2}$

SE (gca for tester) = $(Me/rf)^{1/2}$

SE (sca effect) = $(Me/r)^{1/2}$

SE (g_i-g_j) line = $(2Me/rm)^{1/2}$

SE (g_i-g_j) tester = $(2Me/rf)^{1/2}$

SE (S_{ij}-S_{kl}) = $(2Me/r)^{1/2}$

Where,

Me = Error MS

Critical differences (CD) were calculated as:

CD = SEd × t at 5% and 1% probability levels at error d.f.

The analysis of variance for combining ability was done as follows:

Source of variation	d.f.	S.S.	M.S.	Expected MS
Replications	(r-1)	-	-	-
Lines (females)	(l-1)	SS (l)	MS (l)	σ^2e + r (Cov. F.S.-2 Cov. H.S.) + rt Cov. H.S.
Testers (males)	(t-1)	SS (t)	MS (t)	σ^2e + r (Cov. F.S.-2 Cov. H.S.) + rl Cov. H.S.
Lines x Testers	(l-1)(t-1)	SS (l×t)	MS(l×t)	σ^2e + r (Cov. F.S.-2 Cov. H.S.)
Error	(rlt-1)	SS (e)	MS (e)	σ^2e

Where,

r = number of replications

l = number of lines

t = number of testers

σ^2e = variance due to error

Genetic components:

$$\text{Cov. Half sib (line)} = \frac{M_f - M_{fm}}{rm}$$

$$\text{Cov. Half sib (tester)} = \frac{M_m - M_{fm}}{rf}$$

$$\text{Cov. Half sib (average)} = \frac{1}{r(2fm - f - m)}\left[\frac{(f-1)M_f + (m-1)M_m}{f+m-2} - M_{fm}\right]$$

$$\text{Cov. F.S. (average)} = \frac{(M_f - M_e) + (M_m - M_e) + (M_{fm} - M_e)}{3r} +$$

$$\frac{6r\,\text{Cov. H.S. (average)} - r(f+m)\,\text{Cov. H.S. (average)}}{3r}$$

Where,

M_f = Mean squares due to lines (females)

M_m = Mean squares due to testers (males)

M_{fm} = Mean squares due to line × tester interactions

M_e = Mean squares due to error

r = number of replications

f = number of lines

m = number of testers

gca variance (σ^2gca) = Cov. H.S. (average) = $\left[\frac{1+F}{4}\right]$ σ^2A

Therefore,

Additive genetic variance (σ^2A) = 2 Cov. H.S. (average),

if F = 1 and

(σ^2A) = 4 Cov. H.S. (average), if F = 0

sca variance (σ^2sca) $= \frac{(M_{fm} - M_e)}{r}$

$\sigma^2 sca = \left[\frac{1+F}{2}\right]^2 \sigma^2 D$

Therefore,

Dominance variance (σ^2D) = σ^2 sca with F = 1, and

$\sigma^2D = 4\sigma^2sca$, if F = 0

Where,

F = Inbreeding coefficient

Average degree of dominance:

It was calculated using formula given by Kempthorne and Curnow (1961).

$$\text{Average degree of dominance} = \sqrt{(\sigma^2 sca)/(2\sigma^2 gca)} \text{ or } \sqrt{(\sigma^2 D)/(\sigma^2 A)}$$

Where, σ^2sca = Estimated variance due to sca.

σ^2gca = Estimated variance due to gca

Predictability ratio:

It was suggested by Baker (1978) and was calculated as follows:

$$\text{Predictability ratio} = \frac{2\sigma^2 gca}{2\sigma^2 gca + \sigma^2 sca}$$

Heritability in narrow sense:

Heritability in narrow sense (h^2n) was calculated as suggested by Kempthorne (1957).

$$h^2n\,(\%) = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s + \sigma^2 e} \times 100$$

Where,

$\sigma^2 g$ = variance due to gca

$\sigma^2 s$ = variance due to sca

$\sigma^2 e$ = variance due to error

Proportional contribution of lines, testers and their interactions:

$$\text{Contribution of lines (\%)} = \frac{\text{S.S.(lines)}}{\text{S.S.(crosses)}} \times 100$$

$$\text{Contribution of testers (\%)} = \frac{\text{S.S.(testers)}}{\text{S.S.(crosses)}} \times 100$$

$$\text{Contribution of lines} \times \text{testers} = \frac{\text{S.S.(lines x testers)}}{\text{S.S.(crosses)}} \times 100$$

3.4.2.6. Estimation of heterosis:

The heterosis was computed as per cent increase or decrease of the mean values of crosses (F_1's) over better-parent (Heterobeltiosis) and standard variety (Standard Heterosis).

$$1.\ \text{Heterosis over better-parent (Heterobeltiosis)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

$$2.\ \text{Heterosis over standard variety (Standard Heterosis)} = \frac{\overline{F_1} - \overline{SV}}{\overline{SV}} x100$$

Where,

F_1 = Mean of F_1

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

$\overline{SV}$ = Mean of standard variety or check variety

The test of significance was applied to determine the significance of heterosis by using the following formula:

$$'t'\ (\text{Heterobeltiosis}) = \frac{F_1 - \overline{BP}}{S.E.}$$

$$'t'\ (\text{Standard heterosis}) = \frac{F_1 - \overline{SV}}{S.E.}$$

$$S.E.\ \text{of heterosis over better-parent and standard variety} = \sqrt{2Me/r}$$

Where,

Me = Mean error variance

r = Number of replications.

Thus, C.D. = SE ×'t' value at error d.f. and 5% or 1% probability level. Critical difference was used to test the significance of difference in mean value of F_1 over better-parent and standard variety which signified significance of the respective heterosis.

Chapter-IV

EXPERIMENTAL FINDINGS

The results obtained in respect of various aspects of the two sets of experiments conducted in the present investigation have been described in this chapter under the following sections:

4.1 Germplasm evaluation experiment (Experiment-I)

4.1.1 Analysis of variance for experiment-1

4.1.2 Mean performance of genotypes

4.1.3 Correlation coefficients

4.1.4 Path coefficient analysis

4.1.5 Genetic divergence analysis

4.2 Combining ability experiment (Experiment-II)

4.2.1 Analysis of variance for experiment-II

4.2.2 Coefficient of variation, heritability and genetic advance

4.2.3 Correlation coefficients

4.2.4 Path coefficient analysis

4.2.5 Combining ability analysis

4.2.6 Heterosis over better-parent and standard variety

4.1.1. Analysis of Variance for Experiment-1:

The analysis of variance for augmented design used for evaluation of 60 germplasm lines with four checks in *Zaid* (Environment 1) and *Kharif* (Environment 2) was aimed out for thirteen characters under study seperately. The environment wise results are given below.

4.1.1.1. Environment 1:

The analysis of variance for augmented design was carried out for all the thirteen characters in *Zaid* season, 2019 (E1) and the results obtained are presented in Table 4.1 (a). The mean squares due to blocks were highly significant for days to 50% flowering, days to maturity, plant

Table 4.1 (a): Analysis of variance of augmented design for 13 characters of the mungbean germplasm in *Zaid* season (E1)

Characters	Sources of variation		
	Blocks	**Checks**	**Error**
	5	3	15
Days to 50% flowering	211.98**	90.81**	3.18
Days to maturity	759.96**	194.04**	5.37
Plant height	1386.54**	957.43**	34.33
Primary branches per plant	6.03**	0.46	0.33
Clusters per plant	7.36**	1.89*	0.40
Pods per cluster	9.20**	0.37	0.34
Pods per plant	564.01**	82.92*	20.21
Pod length	1.29	1.60	0.64
Seeds per pod	9.04**	6.89**	0.30
100-seed weight	1.14**	5.88**	0.04
Biological yield per plant	473.80**	35.00	15.61
Harvest-index	20.62**	12.25**	0.53
Seed yield per plant	47.53**	4.25	1.62

*, ** Significant at 5% and 1% probability level

height, primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, biological yield per plant, harvest-index and seed yield per plant. However, variation due to blocks was non-significant in case of pod length. The differences among the check varieties were highly significant for days to 50% flowering, days to maturity, plant height, clusters per plant, pods per plant, seeds per pod, 100-seed weight and harvest-index .

4.1.1.2. Environment 2:

The analysis of variance for augmented design was also carried out for all the thirteen characters in *Kharif* season, 2019 (E2) and the results obtained are presented in Table 4.1(b).The mean squares due to blocks were highly significant for days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, 100-seed weight, biological yield per plant, harvest-index and seed yield per plant. However, variation due to blocks was non-significant in case of only pod length. The differences among the check varieties were highly significant for days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per plant, seeds per pod, 100-seed weight, biological yield per plant, harvest-index and seed yield per plant.

4.1.2. Mean performance of genotypes:

The adjusted means of 60 genotypes of germplasm collections, check means , range and least significant differences for 13 characters in *Zaid* (E1) and *Kharif* (E2) seasons are presented in Table 4.2 (a) and Table 4.2 (b), respectively. The results are presented below:

4.1.2.1. Days to 50% flowering:

In *Zaid* season (E1), the days to 50% flowering ranged from 31.96 days recorded for PDM 139 to 72.71 days in case of 4RMG1028. Seven out of sixty entries were present in top non-significant group for early

Table 4.1(b): Analysis of variance of augmented design for 13 characters of the mungbean germplasm in *Kharif* season (E2)

Characters	Sources of variation		
	Blocks	**Checks**	**Error**
	5	3	15
Days to 50% flowering	28.66**	463.04**	2.24
Days to maturity	73.16**	1698.78**	2.45
Plant height	871.82**	128.80**	5.07
Primary branches per plant	3.13**	7.46**	0.19
Clusters per plant	4.35**	1.57**	0.24
Pods per cluster	5.56**	0.38	0.23
Pods per plant	380.78**	79.62**	9.70
Pod length	0.43	2.44*	0.69
Seeds per pod	11.83**	7.40**	0.15
100-seed weight	0.58**	3.39**	0.05
Biological yield per plant	570.23**	210.38**	7.75
Harvest-index	10.73**	12.24**	1.34
Seed yield per plant	58.95**	26.01**	0.78

*, ** Significant at 5% and 1% probability level

Table 4.2(a): Adjusted means of genotypes and checks, range and least significant differences for 13 characters in *Zaid* season (E1)

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
CoGG 912	41.96	77.46	53.31	4.13	4.77	5.12	24.17	7.57	6.62	2.90	16.59	28.26	4.55
MH 2-15	37.96	71.46	41.61	3.73	4.97	4.52	22.37	6.57	7.02	3.00	16.99	28.34	4.68
TM 96-2	48.96	79.46	24.21	3.33	3.77	5.52	20.77	7.57	8.82	3.80	24.29	30.77	7.43
ADT 3	42.96	71.46	31.21	2.73	5.37	6.32	34.77	7.57	8.42	2.20	23.39	29.19	6.73
SML 823	41.96	67.46	40.41	2.93	6.17	5.52	34.77	5.47	7.82	3.10	26.29	33.21	8.77
LGG 460	40.96	61.46	37.61	3.73	4.37	4.92	21.37	6.57	7.02	3.00	14.59	30.93	4.46
MH 421	42.96	64.46	41.51	3.33	5.17	5.92	31.17	6.47	6.62	3.20	23.39	28.89	6.65
P.Mung 2	37.96	64.46	37.31	3.33	5.37	6.12	33.37	6.47	6.02	3.10	20.09	30.89	6.16
Pusa 9531	40.96	62.46	34.61	4.13	4.97	5.32	26.77	6.67	6.42	3.60	19.09	32.45	6.20
TARM 1	51.96	85.46	35.81	3.13	4.77	4.52	21.37	5.87	5.62	2.90	11.59	28.59	3.18
DGGV 2	45.71	81.96	37.28	4.13	5.42	6.37	34.72	7.50	7.57	3.10	26.71	30.64	8.21
OUM 11-5	38.71	71.96	16.58	3.73	4.42	5.57	24.52	6.10	6.37	3.40	18.71	28.70	5.37
BM 4	42.71	69.96	25.58	3.53	6.82	5.37	36.52	6.20	7.97	2.80	26.71	30.60	8.20
IPM 2-3	38.71	78.96	16.98	4.13	5.02	5.57	28.12	4.80	5.57	3.30	18.71	30.23	5.15
DGGS 4	49.71	89.96	26.28	3.73	5.22	5.77	30.32	5.50	5.77	3.80	22.82	29.15	6.66
Phule Mung 2	35.71	70.96	37.38	3.13	5.02	3.37	16.12	6.10	8.57	4.20	19.62	31.46	6.19
HUM 12	38.71	69.96	18.08	5.33	4.82	4.77	23.12	6.00	6.77	4.90	24.62	32.05	7.92
DGGV 5	53.71	90.96	13.98	4.13	4.42	4.57	19.72	4.10	5.77	3.20	12.72	29.01	3.68
DGG 1	35.71	65.96	16.58	4.13	4.42	4.17	17.72	6.70	6.57	3.30	12.92	30.57	3.95
SML 1082	36.71	66.96	19.62	3.33	3.82	6.17	23.72	7.20	8.57	3.20	21.62	31.14	6.70

Contd…..

Table 4.2(a): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
KM 11-584	42.96	70.21	32.76	3.43	5.22	4.17	21.72	9.50	8.52	3.02	19.19	29.21	5.59
P.Mung 6	63.96	92.21	34.66	3.83	5.42	5.57	30.52	5.10	5.72	2.92	16.49	30.12	4.96
P.Mung 5	61.96	88.21	34.96	4.63	5.22	5.37	28.12	6.90	6.52	3.02	19.09	28.54	5.44
PDM 139	31.96	58.21	26.06	3.83	4.02	4.77	19.52	6.30	5.92	3.22	11.29	32.34	3.64
TM 2000-2	42.96	73.21	22.46	4.23	3.62	4.37	16.12	5.50	6.12	2.92	10.09	28.23	2.83
IPM 2-14	37.96	75.21	23.76	3.43	5.02	3.77	18.92	5.70	4.92	3.32	9.49	31.43	2.97
CO(GG) 8	48.96	74.21	27.26	2.83	3.62	4.57	16.72	5.00	5.72	3.02	9.39	30.19	2.82
KM 22-41	49.96	78.21	22.76	3.23	4.02	5.37	20.92	7.10	6.12	2.82	11.69	30.39	3.54
MGG 347	41.96	68.21	34.39	4.33	3.42	5.77	20.12	6.40	4.92	3.12	9.49	31.43	2.97
PKVAKM 4	50.96	87.21	27.56	3.43	4.22	5.17	21.92	5.10	5.72	3.22	13.49	29.23	3.93
P.Vishal	38.21	66.96	29.21	3.53	3.67	3.92	14.82	6.97	6.57	4.60	14.59	31.23	4.62
ML 613	51.21	84.96	30.21	2.73	5.47	4.72	25.82	5.47	5.97	3.10	17.29	29.16	5.17
IPM 410-3	39.21	70.96	26.11	2.73	5.67	4.12	23.02	5.97	5.57	3.30	14.09	32.95	4.65
ML 818	52.21	83.95	28.91	2.53	5.47	4.92	26.42	6.17	5.77	3.00	16.79	29.04	5.01
Pusa 9072	47.21	76.96	32.61	2.73	4.87	4.72	22.82	5.57	5.17	3.20	14.29	28.68	4.25
SML 668	42.21	65.96	26.81	4.13	5.47	4.52	24.42	7.37	6.77	3.10	16.59	32.96	5.47
VBN(GG) 2	44.21	76.96	34.41	3.53	4.67	4.92	23.22	5.77	5.17	3.10	14.59	27.56	4.21
CO 6	39.21	71.96	44.01	2.73	5.07	4.92	24.42	5.67	5.57	2.90	15.09	28.28	4.43
LGG 450	41.21	72.96	31.11	2.53	4.67	4.52	20.82	4.77	5.57	3.10	13.69	28.69	4.08
TMB 37	36.21	63.96	29.41	3.73	4.47	4.72	21.02	5.17	6.17	3.20	14.89	29.89	4.56
Kopergaon	68.71	100.96	32.08	2.48	2.82	2.87	8.37	5.32	3.27	3.20	1.97	27.94	0.63
4RMG1028	72.71	101.96	31.18	2.28	2.62	2.87	7.77	5.42	4.07	3.20	2.27	28.49	0.73

Contd…..

Table 4.2(a): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
MH 318	43.71	70.96	30.18	4.28	3.82	3.47	13.37	4.52	2.87	3.30	3.57	28.93	1.11
5-BWME	49.71	75.96	30.98	2.68	2.62	2.67	7.37	5.52	2.67	2.70	0.67	29.18	0.30
2-1 PM409	52.71	84.96	30.48	2.48	3.82	2.27	8.97	5.22	5.67	3.00	4.17	27.26	1.19
KM 18-117	55.71	93.96	27.68	2.28	2.62	2.27	6.37	5.42	2.67	2.90	0.47	29.60	0.25
KM 18-111	53.71	92.96	28.78	1.88	2.42	2.67	6.77	4.82	2.07	2.50	0.17	27.00	0.13
KM 18-115	54.71	95.96	31.18	2.68	3.42	2.27	7.97	4.32	2.67	2.80	1.07	27.21	0.37
KM 18-106	55.71	94.96	28.58	2.28	3.42	2.67	9.37	6.32	2.87	2.50	1.47	26.23	0.45
KM 18-99	51.71	88.96	32.48	2.28	3.02	2.47	7.77	5.32	2.87	2.70	0.97	28.46	0.37
KM 18-109	53.46	91.46	30.96	1.88	5.07	3.72	19.97	5.52	4.82	2.87	10.84	27.05	2.93
KM 18-121	56.46	95.46	27.66	2.28	5.27	4.12	22.57	4.52	4.02	2.57	9.74	26.60	2.59
KM 18-102	54.46	92.46	27.46	2.28	4.67	3.52	17.77	5.12	3.82	2.97	8.64	26.46	2.28
KM 18-114	53.46	90.46	32.26	2.48	4.87	3.72	19.17	5.92	4.22	2.77	10.04	24.23	2.48
KM 18-97	51.46	90.46	20.86	2.28	4.67	4.12	19.97	4.12	3.62	2.67	8.24	27.39	2.23
KM 18-105	56.46	93.46	21.76	1.28	5.07	3.72	19.57	3.92	3.82	2.97	9.44	2650	2.50
KM 18-116	54.46	92.46	23.86	2.48	5.27	3.52	19.77	4.12	3.62	3.07	9.34	26.59	2.48
KM 18-103	53.46	89.46	25.76	2.28	4.87	4.72	23.57	5.92	3.22	3.17	11.14	24.62	2.79
KM 18-122	52.46	92.46	32.86	1.68	5.87	3.72	23.17	5.12	3.82	2.87	10.64	26.54	2.83
KM 18-108	51.46	93.46	30.26	1.48	4.87	4.12	20.97	5.32	3.02	3.37	10.04	24.97	2.54
Check means													
P.Mung 4	42.67	72.67	33.37	3.33	5.70	4.83	27.70	6.42	6.13	3.18	18.15	29.80	5.41
HUM 16	39.00	62.83	31.95	3.80	5.40	4.67	25.13	7.33	5.20	5.25	21.13	32.65	6.89
IPM 99-125	41.33	67.67	50.70	3.83	4.63	4.73	21.87	6.63	7.20	3.15	15.22	32.45	4.93

Contd…..

Table 4.2(a): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
IPM 205-7	33.83	59.67	57.32	3.97	4.57	4.27	19.20	6.12	7.57	4.12	18.17	32.82	5.96
Range													
Lowest	31.96	58.21	13.98	1.28	2.42	2.27	6.37	3.92	2.07	2.20	0.17	24.23	0.13
Highest	72.71	101.96	53.31	5.33	6.82	6.37	36.52	9.50	8.57	4.90	26.71	33.21	8.77
LSD:	Check means												
5%	2.20	2.85	7.21	0.70	0.77	0.71	5.53	0.98	0.67	0.23	4.86	0.89	1.57
1%	1.03	1.33	3.38	0.33	0.36	0.34	2.59	0.46	0.32	0.11	2.28	0.41	0.74
LSD:	Same Block												
5%	5.38	6.98	17.66	1.72	1.89	1.75	13.55	2.41	1.65	0.56	11.91	2.19	3.84
1%	2.52	3.27	8.28	0.80	0.89	0.82	6.35	1.13	0.78	0.27	5.59	1.02	1.80
LSD:	Different blocks												
5%	6.02	7.81	19.74	1.92	2.12	1.96	15.15	2.69	1.84	0.63	13.31	2.44	4.29
1%	2.82	3.66	9.26	0.90	0.99	0.92	7.11	1.26	0.86	0.29	6.24	1.14	2.01
LSD:	(Adjusted means & check means)												
5%	4.59	5.96	15.08	1.46	1.62	1.50	11.57	2.06	1.41	0.48	10.17	1.87	3.28
1%	2.16	2.79	7.07	0.68	0.76	0.70	5.42	0.97	0.66	0.22	4.77	0.87	1.53

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Table 4.2 (b): Adjusted means of genotypes and checks, range and least significant differences for 13 characters in *Kharif* season (E2)

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
CoGG 912	34.46	63.92	59.53	4.98	6.12	5.11	31.28	10.13	8.28	3.60	30.83	30.42	9.60
MH 2-15	36.46	66.92	57.03	4.78	5.32	5.11	26.88	6.83	9.48	3.60	29.83	31.57	9.65
TM 96-2	54.46	93.92	28.53	2.98	4.52	5.51	24.08	6.33	8.48	3.70	26.43	29.37	7.92
ADT 3	37.46	64.92	45.53	3.98	5.72	7.51	43.08	7.93	9.68	2.90	36.03	32.76	12.12
SML 823	54.46	90.92	48.43	2.98	5.52	6.51	35.88	5.53	7.68	3.20	28.83	29.89	8.86
LGG 460	49.46	79.92	52.93	3.78	4.32	5.91	24.08	5.93	6.48	3.10	16.83	28.34	4.81
MH 421	37.46	62.92	53.93	3.78	6.12	5.11	31.68	6.13	7.48	3.80	30.43	29.67	9.23
P.Mung 2	36.46	64.92	50.93	4.38	5.72	5.51	31.08	7.53	8.48	3.70	29.83	32.93	10.10
Pusa 9531	46.46	66.92	41.53	3.98	4.32	4.51	18.88	6.33	7.28	3.80	18.83	29.08	5.55
TARM 1	51.46	80.92	42.43	3.38	3.72	7.11	25.28	5.13	6.28	3.50	19.23	28.84	5.62
DGGV 2	38.21	69.92	50.15	4.53	7.87	6.21	49.98	8.75	7.23	3.40	37.15	33.34	12.63
OUM 11-5	32.21	56.92	28.75	4.33	5.87	5.41	31.78	6.35	6.23	3.80	22.26	33.87	7.75
BM 4	36.21	67.92	36.95	4.13	7.27	5.01	36.58	7.55	7.03	3.10	24.06	32.67	8.04
IPM 2-3	32.21	60.92	27.25	4.73	6.07	5.61	34.58	6.15	6.03	3.70	23.06	32.55	7.94
DGGS 4	39.21	71.92	38.15	4.33	6.27	5.01	31.98	7.35	6.63	4.10	29.26	30.52	9.06
Phule Mung 2	47.21	74.92	40.95	2.53	5.07	4.41	21.98	7.85	7.03	3.90	20.16	30.37	6.22
HUM 12	46.21	78.92	30.65	3.13	4.87	4.61	22.58	6.55	6.03	4.99	26.66	27.13	7.25
DGGV 5	49.21	77.92	20.45	3.73	5.27	5.01	26.78	5.35	5.63	3.40	20.16	25.57	5.11
DGG 1	48.21	80.92	22.95	3.13	5.07	4.61	22.98	7.75	4.83	2.99	9.76	30.15	3.11
SML 1082	46.21	79.92	25.45	2.73	4.27	6.01	25.78	7.35	6.23	3.30	19.76	26.75	5.27

Contd…..

Table 4.2(b): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
KM 11-584	48.21	77.92	28.90	2.73	5.17	7.36	38.58	8.68	7.78	3.07	29.86	29.95	9.04
P.Mung 6	38.21	62.92	39.80	4.13	6.77	7.16	47.18	5.28	6.78	3.37	33.36	31.55	10.58
P.Mung 5	36.21	64.92	40.90	5.13	6.57	6.56	41.78	6.48	7.38	3.47	34.36	30.05	10.42
PDM 139	49.21	79.92	31.90	2.53	4.57	6.96	33.18	6.38	5.98	3.17	21.56	28.61	6.30
TM 2000-2	41.21	67.92	22.30	2.73	5.17	5.56	28.78	4.98	6.98	2.87	19.96	28.25	5.78
IPM 2-14	43.21	76.92	28.30	2.53	5.37	5.16	27.78	5.18	5.58	3.27	18.86	26.16	5.13
CO(GG) 8	42.21	69.92	25.30	1.13	4.37	5.96	26.58	4.88	5.38	3.17	16.86	26.46	4.65
KM 22-41	38.21	63.92	28.20	4.13	4.77	7.16	34.78	6.78	6.38	3.37	29.56	32.33	7.38
MGG 347	52.21	71.92	31.70	2.13	4.57	6.16	29.78	6.88	4.78	3.07	16.26	27.04	4.57
PKVAKM 4	33.21	59.92	32.30	4.73	5.37	6.96	36.38	4.88	6.58	3.37	25.56	30.77	7.94
P.Vishal	62.21	96.92	27.20	2.53	4.77	3.76	18.28	7.13	6.43	3.85	17.36	27.19	4.41
ML 613	34.21	61.92	27.20	3.93	5.77	5.36	31.08	5.53	6.63	3.35	22.46	31.99	6.78
IPM 410-3	51.21	89.92	17.20	1.73	5.77	3.76	22.08	3.93	6.03	3.25	16.96	26.98	4.27
ML 818	38.21	70.92	19.60	2.33	4.77	5.36	25.68	6.43	6.83	3.35	20.46	29.99	5.77
Pusa 9072	41.21	70.92	25.10	2.73	4.57	4.96	22.48	5.83	4.63	3.25	12.46	28.21	3.34
SML 668	49.21	80.92	26.00	1.93	4.17	4.76	14.08	6.03	4.43	3.05	11.46	25.94	2.70
VBN(GG) 2	36.21	69.92	25.20	3.33	4.37	5.56	25.08	5.93	5.63	3.35	16.06	31.31	4.65
CO 6	67.21	100.92	32.00	3.33	4.77	5.76	28.08	6.73	6.63	3.05	18.96	31.60	5.60
LGG 450	35.21	63.92	29.50	3.33	4.47	4.96	25.68	5.53	6.03	3.45	17.46	32.30	5.24
TMB 37	47.21	78.92	17.50	1.93	4.47	5.36	24.08	5.33	5.03	3.15	13.46	30.69	3.77
Kopergaon	36.71	64.17	26.03	2.98	3.67	5.36	23.23	6.48	5.43	3.30	13.03	30.90	4.08

Contd…..

Table 4.2(b): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
4RMG1028	34.71	62.17	20.23	3.38	3.87	4.56	20.23	6.08	6.63	3.49	14.13	31.99	4.57
MH 318	48.71	80.17	20.23	2.78	4.07	4.56	16.63	6.48	5.83	3.39	9.73	32.19	3.21
5-BWME	35.71	63.17	20.63	2.98	4.67	4.16	16.03	7.08	5.43	2.49	7.03	29.15	2.14
2-1 PM409	46.71	78.17	16.13	1.78	3.87	5.16	20.63	4.88	5.23	2.79	10.13	28.64	2.97
KM 18-117	41.71	69.17	21.23	2.58	4.07	3.76	18.03	5.58	4.83	3.19	8.93	29.69	2.73
KM 18-111	40.71	70.17	22.13	2.38	4.87	4.16	16.23	5.88	3.83	2.89	5.73	29.32	1.78
KM 18-115	42.71	59.17	19.53	2.78	4.07	4.56	18.03	5.08	4.43	2.79	7.73	27.38	2.20
KM 18-106	43.71	73.17	23.03	2.58	5.02	3.36	17.03	7.58	4.23	2.69	6.73	27.20	1.92
KM 18-99	41.71	71.17	21.23	2.58	5.42	4.36	17.63	7.08	4.43	2.59	7.13	26.98	2.01
KM 18-109	45.21	72.17	18.60	1.88	5.02	4.21	21.88	7.23	5.48	2.69	11.96	29.67	3.69
KM 18-121	48.21	76.17	22.30	2.08	5.42	4.61	25.08	5.63	4.68	2.39	9.86	29.83	3.09
KM 18-102	43.21	71.17	21.20	2.08	5.02	4.21	21.28	5.53	4.48	2.59	8.56	30.12	2.73
KM 18-114	44.21	74.17	20.30	2.08	5.62	4.81	27.68	6.83	4.88	2.39	11.76	28.66	3.52
KM 18-97	42.21	71.17	15.50	2.08	5.42	4.41	24.08	5.23	4.28	2.59	9.16	30.49	2.94
KM 18-105	46.21	76.17	15.50	1.28	5.82	3.81	22.68	5.03	4.88	2.59	9.06	32.99	3.12
KM 18-116	44.21	74.17	11.00	2.08	5.02	4.41	22.28	5.63	4.68	2.69	9.26	31.42	3.05
KM 18-103	47.21	76.17	20.60	2.08	5.62	4.81	27.08	6.83	3.88	2.79	9.56	32.06	3.20
KM 18-122	40.21	71.17	17.20	1.88	5.17	4.61	25.68	5.63	4.48	2.49	9.56	31.39	3.14
KM 18-108	42.21	70.17	18.40	1.28	5.17	4.61	26.08	6.63	3.88	2.99	9.46	33.22	3.27
Check means													
P.Mung 4	33.50	61.17	34.85	5.5	6.3	5.3	33.73	6.6	7.43	3.87	29.9	32.34	9.68

Contd…..

Table 4.2(a): Contd…..

Genotypes	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
HUM 16	43.50	82.33	43.87	3.13	5.67	4.8	27.23	7.8	4.73	4.8	20.93	29.50	6.18
IPM 99-125	55.00	98.67	33.50	3.13	5.1	5.13	26.33	6.33	6.23	2.97	16.05	29.28	4.97
IPM 205-7	43.83	94.50	38.48	3.93	5.4	4.8	26	6.98	5.9	3.75	19.35	29.72	5.76
Range													
Lowest	32.21	56.92	11.00	1.13	3.67	3.36	14.08	3.93	3.83	2.39	5.73	25.57	1.78
Highest	67.21	100.92	59.53	5.5	7.87	7.51	49.98	10.13	9.65	4.99	37.15	33.87	12.63
LSD:	Check means												
5%	1.84	1.92	2.77	0.54	0.59	0.59	3.83	1.02	0.47	0.27	3.43	1.42	1.08
1%	0.86	0.90	1.30	0.25	0.28	0.27	1.80	0.48	0.22	0.13	1.60	0.66	0.51
LSD:	Same Block												
5%	4.51	4.71	6.79	1.32	1.46	1.45	9.40	2.50	1.16	0.66	8.39	3.48	2.67
1%	2.12	2.21	3.18	0.62	0.69	0.68	4.40	1.17	0.54	0.31	3.94	1.64	1.25
LSD:	Different blocks												
5%	5.04	5.26	7.59	1.48	1.63	1.62	10.50	2.80	1.30	0.73	9.38	3.90	2.98
1%	2.36	2.47	3.56	0.69	0.76	0.76	4.92	1.31	0.61	0.34	4.40	1.83	1.39
LSD:	(Adjusted means & check means)												
5%	3.85	4.03	5.79	1.13	1.25	1.24	8.02	2.14	0.99	0.56	7.16	2.97	2.27
1%	1.80	1.88	2.72	0.53	0.59	0.58	3.76	1.00	0.46	0.26	3.36	1.39	1.07

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

flowering, and the genotypes having lowest flowering duration in order of merit were PDM 139, Phule Mung 2, DGG 1, SML 1082, MH 2-15, P. Mung 2 and IPM 2-14. The genotype, Kopergaon was statistically at par with the 4RMG1028, which took maximum days to 50% flowering.

In the *Kharif* season, the days to 50% flowering ranged from 32.21 days recorded for IPM 2-3 to 67.21 days in case of Co 6. Fourteen out of sixty entries were present in top non-significant group for early flowering and best five genotypes were OUM 11-5, PKVAKM 4, 4RMG1028, CoGG 912 and ML 613 being statistically equal with lowest flowering duration genotype IPM 2-3. The genotype P. Vishal was statistically at par with Co6, which took maximum days to 50% flowering.

4.1.2.2. Days to maturity:

In E1, the days to maturity ranged from 58.21 days recorded for PDM 139 to 101.93 days in case of 4RMG1028. Seven out of sixty entries were present in top non-significant group for days to maturity, which in order of lowest maturity durations were PDM 139, LGG 460, Pusa 9531, TMB 37, P. Mung 2 and MH 421. The genotypes, KM 18-106, KM 18-121, KM 18-115 and Kopergaon were statistically at par with the 4RMG1028, which took maximum days to maturity.

In E2, the days to maturity ranged from 56.92 days recorded for OUM 11-5 to 100.92 days in case of Co6. The line, OUM 11-5 was present alone in top non-significant group for early days to maturity. The genotype, P. Vishal was statistically at par with the Co6, which took maximum days to maturity.

4.1.2.3. Plant height:

In *Zaid* season, the highest and lowest values for plant height were observed in case of CoGG 912 (53.31cm) and DGGV 5 (13.98cm),

respectively. The tallest genotype, CoGG 912 was alone in top non-significant group for tall stature. Among the ten out of sixty genotypes, having stature statistically at par with the shortest line (DGGV 5), the shortest ones were DGG 1, OUM 11-5, HUM 12, SML 1082, IPM 2-14, TM 2000-2, IPM 2-3, KM 22-41, KM 18-97 and KM 18-105.

In *Kharif season*, the highest and lowest values for plant height were observed in case of CoGG 912 (59.53cm.) and KM 18-116 (11.00cm.), respectively. The tallest genotype, CoGG 912 along with LGG 460, MH 421 and MH 2-15 constituted in the top non-significant group for tall stature. Eight out of sixty genotypes, having stature statistically at par with the shortest line KM 18-116 were KM 18-105, KM 18-97, 2-1PM 409, IPM 410-3, KM 18-122, TMB 37 and KM 18-108.

4.1.2.4. Primary branches per plant:

In E1, the highest number of primary branches per plant (5.33) were exhibited by HUM 12, whereas KM 18-105 possessed least number of branches (1.28). Twenty-three out of sixty genotypes had primary branches per plant at par with (HUM 12), the line having maximum number of branches. The best 5 lines for primary branches per plant were HUM 12, P. Mung 5, MGG 347, MH 318 and TM 2000-2 . Thirty-seven lines were statistically at par with the genotype, KM 18-105, in producing low number of primary branches per plant.

In E2, the highest number of primary branches per plant (5.12) were exhibited by P. Mung 5, whereas CoGG 8 possessed least number of branches (1.13). Fifteen genotypes out of sixty had primary branches per plant statistically at par with (P. Mung 5), the line having maximum number of branches. The best 5 lines for primary branches per plant were ML 613, LGG 460, MH 421, Pusa 9531 and ADT 3 besides P.Mung 5.

Twenty-five lines were statistically at par with the genotype, CoGG 8, in producing low number of primary branches per plant.

4.1.2.5. Clusters per plant:

In *Zaid* season, the genotype, BM 4 (6.82) emerged with highest number of clusters per plant, while the lowest mean performance for this character was shown by KM 18-111 (2.42). Thirty-four genotypes possessed clusters per plant statistically equal to BM 4 and most promising among them, in addition to BM 4, were SML 823, KM 18-122, IPM 410-3, ML 613, ML 818 and P. Mung 6. Twenty-five germplasm lines out of sixty were statistically at par with the line producing lowest number of clusters per plant, KM 18-111.

In *Kharif* season, the genotype, DGGV 2 (7.87) emerged with highest number of clusters per plant, while the lowest mean performance for this character was shown by Kopergaon (3.67). Four genotypes possessed clusters per plant statistically equal to DGGV 2 which were DGGS 4, P. Mung 5, P. Mung 6 and BM 4. Thirty-seven out of sixty germplasm lines were statistically at par with the line producing lowest clusters per plant, Kopergaon.

4.1.2.6. Pods per cluster:

In environment 1, the highest number of pods per cluster was exhibited by DGGV 2 (6.37), while KM 18-117 and 2-1 PM 409 (2.27) produced lowest mean performance for this trait. The top non-significant group for higher pods per cluster was constituted by thirty-five entries, among which the most promising were ADT 3, SML 1082, P. Mung 2, MGG 347 and DGGS 4. Twenty-eight genotypes possessed pods per cluster at par with the two lines having lowest mean performance for this character, namely, 2-1PM 409 and KM 18-117.

In environment 2, the highest number of pods per cluster was exhibited by ADT 3 (7.51), while KM 18-106 (3.36) produced lowest mean performance for this character. The top non-significant group for higher pods per cluster was constituted by thirteen entries, among which the most promising were SML 823, LGG 460, TARM 1, DGGV 2 and KM 11-584. Twenty-five genotypes possessed pods per cluster at par with the line having lowest mean performance for this character, KM 18-106.

4.1.2.7. Pods per plant:

In E1, the highest number of pods per plant was exhibited by BM 4 (36.52) while KM 18-117 (6.37) produced lowest mean performance for this trait. The top non-significant group for greater pods per plant had thirty-one entries and best five among them were, ADT 3, SML 823, DGGV 2, P. Mung 2 and BM 4. The twenty-one lines showed pods per plant statistically equal to the poorest line KM 18-117.

In E2, the highest number of pods per plant was exhibited by DGGV 2 (49.98) while SML 668 (14.08) produced lowest mean performance for pods per plant. The top non-significant group for greater pods per plant had three entries, namely, ADT 3, P. Mung 6 and DGGV 2. The twenty-five lines showed pods per plant statistically equal to the poorest line, SML 668.

4.1.2.8. Pod length:

In *Zaid* season, maximum pod length was exhibited by KM 11-584 (9.50), while KM 18-105 (3.92) produced lowest mean performance for this character. The top non-significant group for greater pod length had nine entries , which were KM 11-584, CoGG 912, TM 96-2, ADT 3, SML 668, P. Vishal, KM 22-41, SML 1082 and DGGV 2. The fourty-eight lines showed pod length statistically equal to the poorest line, KM 18-105.

In *Kharif* season, the maximum pod length was exhibited by CoGG 912 (10.13), while IPM 410-3 (3.93) produced lowest mean performance for pod length. The top non-significant group for greater pod length had eleven entries and the top five among them were KM 18-106, ADT 3, P. Mung 2, DGGV 2 and CoGG 912. The fourty-one lines showed pod length statistically equal to the poorest line, IPM 410-3.

4.1.2.9. Seeds per pod:

In E1, the highest number of seeds per pod was exhibited by TM 96-2 (8.82), while KM 18-111 (2.07) produced lowest number of seeds per pod. The top non-significant group for greater number of seeds per pod had eleven entries, which were TM 96-2, Phule Mung 2 , BM 4, SML 1082, KM 11-584, DGGV 2, LGG 460, SML 823, MH 2-15, SML 668 and ADT 3. Fifteen lines showed seeds per pod statistically equal to the poorest line, KM 18-111 (2.07).

In E2, the highest number of seeds per pod was exhibited by ADT 3 (9.68), while KM 18-111 (3.83) produced lowest mean performance for this character. The top non-significant group for greater number of seeds per pod had only four entries, namely, ADT 3, P. Mung 2, TM 96-2 and MH 2-15. Eighteen lines showed seeds per pod statistically equal to the poorest line, KM 18-111 (3.83).

4.1.2.10. 100-seed weight:

In environment 1, the 100-seed weight varied from (4.90g) in case of HUM 12 to (2.20g) in case of ADT 3. The top non-significant group for higher 100-seed weight had only two entries, namely, P. Vishal and HUM 12. Eleven lines showed 100-seed weight statistically equal to the poorest line, ADT 3.

In environment 2, the 100-seed weight varied from (4.99g) in case of HUM 12 to (2.39g) in case of KM 18-114. The top non-significant

group for greater 100-seed weight had only two entries, namely, DGGS 4 and HUM 12. Twenty-three lines showed 100-seed weight statistically equal to the poorest line, KM 18-114.

4.1.2.11. Biological yield per plant:

In *Zaid* season, the highest and lowest mean performance for biological yield per plant was recorded for DGGV 2 (26.71) and KM 18-111 (0.17), respectively. BM 4, SML 823, HUM 12, TM 96-2 and ADT 3 were the genotypes which produced biological yield statistically at par with DGGV 2, the entry with highest biological yield. The lowest non-significant group for lesser biological yield compromised by twenty-nine genotypes.

In *Kharif* season, the highest and lowest mean performance for biological yield per plant was recorded for DGGV 2 (37.15) and KM 18-111 (5.73), respectively. ADT 3, P. Mung 5, P. Mung 6, CoGG 912 and MH 2-15 were the genotypes which produced biological yield statistically at par with DGGV 2, the entry with high biological yield. The lowest non-significant group for lesser biological yield was compromised by twenty-four genotypes.

4.1.2.12. Harvest-index :

In *Zaid* season, the highest and lowest mean performance for harvest-index was recorded for SML 823 (33.21) and KM 18-114 (24.23), respectively. SML 668, IPM 410-3, Pusa 9531, PDM 139 and HUM 12 were the genotypes which produced harvest-index statistically at par with SML 823, the entry with highest harvest-index . The lowest non-significant group for lesser harvest-index was compromised by nine genotypes and the poorest among them was KM 18-114.

In *Kharif* season, the highest and lowest mean performance for harvest-index was recorded for OUM 11.5 (33.87) and DGGV 5 (25.57),

respectively. DGGV 2, P. Mung 2, ADT 3, BM 4 and IPM 2-3 were the genotypes which produced harvest-index statistically at par with OUM 11-5, the entry with high harvest-index. The lowest non-significant group for lesser harvest-index comprised of nine genotypes.

4.1.2.13. Seed yield per plant:

In *Zaid* season, the highest and lowest mean performance for seed yield per plant was recorded for SML 823 (8.77g) and KM 18-111 (0.13g), respectively. DGGV 2, BM 4, HUM 12, TM 96-2 and ADT 3 were the genotypes which produced seed yield statistically at par with SML 823, the entry with highest seed yield. The lowest non-significant group for lesser seed yield compromised by thirty-three genotypes.

In environment 2, the highest and lowest mean performance for seed yield per plant was recorded for DGGV 2 (12.63g) and KM 18-111 (1.78g), respectively. ADT 3, P. Mung 6, P. Mung 5, P. Mung 2 and MH 2-15 were the genotypes which produced seed yield statistically at par with DGGV 2, the entry with highest seed yield. The lowest non-significant group for lesser seed yield comprised of by twenty-nine genotypes.

4.1.3. Correlation coefficients:

The estimates of correlation coefficients between the different characters of mungbean genotypes are presented in Table 4.3(a) & 4.3 (b).

4.1.3.1. In *Zaid* season (E1):

In *Zaid* season E1, seed yield per plant exhibited highly significant positive correlation with biological yield per plant (0.989), pods per plant(0.816), clusters per plant (0.735), harvest-index(0.516) and pods per cluster (0.482) but had highly significant and negative correlation with days to 50% flowering (-0.373) days to maturity (-0.323). Correlation of seed yield per plant with rest of the five characters were non-significant.

Harvest-index recorded highly significant and positive association with pods per plant (0.420), clusters per plant (0.388) and seeds per plant (0.344). Biological yield per plant possessed highly significant and positive correlations with pods per plant (0.786), clusters per plant (0.721) and pods per clusters (0.449) besides having highly significant and negative correlations with days to 50% flowering (-0.387) and days to maturity (-0.343). The 100-seed weight exhibited highly significant and negative correlations with pods per cluster (-0.571), pods per plant (-0.456), seeds per plant (-0.517) along with significant and negative correlation with pod length (0.300).

Pod length resulted highly significant and positive correlations with clusters per plant (0.437) and plant height (0.411) but possessed highly significant and negative association with days to 50% flowering (-0.365) and days to maturity (-0.340). Pods per plant exhibited highly significant and positive correlations with clusters per plant (0.781) and pods per clusters (0.765) and significant positive correlation with primary branches per plant (0.259) besides exhibiting significant and negative correlations with days to maturity (-0.298) and days to 50 % flowering (-0.290).

Pods per cluster showed highly significant and negative correlation with plant height (-0.363). Clusters per plant showed highly significant correlation of positive nature with primary branches per plant (0.331) and negative nature with days to 50% flowering (-0.602) and days to maturity (-0.488).

Primary branches per plant showed highly significant negative correlations with days to 50 % flowering (-0.751) and days to maturity (-0.615) while highly significant and positive association was observed between days to maturity and days to 50% flowering (0.884). Remaining estimates of correlation coefficients in this analysis were non-significant.

Table 4.3 (a): Estimates of simple correlation coefficients between different characters in mungbean germplasm in *Zaid* season (E1)

Traits	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-S.W	BY/P	HI	SY/P
D50%f	0.884**	-0.046	-0.751**	-0.602**	0.199	-0.290*	-0.365**	0.104	-0.059	-0.387**	-0.106	-0.373**
DM		0.122	-0.615**	-0.488**	0.065	-0.298*	-0.340**	0.030	0.031	-0.343**	-0.023	-0.323**
PH			0.047	0.091	-0.363**	-0.167	0.411**	0.143	-0.052	-0.138	-0.124	-0.153
PB/P				0.331*	0.032	0.259*	0.179	-0.197	-0.146	0.199	-0.013	0.201
C/P					0.206	0.781**	0.437**	0.028	-0.176	0.721**	0.388**	0.735**
P/C						0.765**	-0.243	0.075	-0.571**	0.449**	0.227	0.482**
P/P							0.137	0.081	-0.456**	0.786**	0.420**	0.816**
PL								-0.209	0.300*	0.224	0.045	0.207
S/P									-0.517**	0.189	0.344**	0.228
100-S.W										-0.007	-0.119	-0.060
BY/P											0.391**	0.989**
HI												0.516**

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, ** Significant at 5% and 1% probability level

Table 4.3(b): Estimates of simple correlation coefficients between different characters in mungbean germplasm in *Kharif season* (E2)

Traits	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100- SW	BY/P	HI	SY/P
D50%f	0.897**	-0.204	-0.930**	-0.775**	0.203	-0.483**	-0.284*	-0.376**	-0.222	-0.702**	-0.639**	-0.731**
DM		-0.147	-0.794**	-0.585**	0.030	-0.463**	-0.193	-0.423**	-0.118	-0.638**	-0.682**	-0.689**
PH			0.144	0.433**	-0.236	0.190	0.752**	-0.058	0.283*	0.330**	-0.111	0.262*
PB/P				0.718**	-0.182	0.454**	0.242	0.444**	0.085	0.644**	0.663**	0.690**
C/P					-0.120	0.713**	0.533**	0.194	0.243	0.777**	0.547**	0.787**
P/C						0.598**	-0.350**	0.181	-0.657**	0.208	0.340*	0.267*
P/P							0.184	0.316*	-0.256*	0.796**	0.676**	0.844**
PL								-0.200	0.462**	0.315*	-0.101	0.257*
S/P									-0.443**	0.518**	0.609**	0.572**
100-S.W										0.141	-0.368**	0.029
BY/P											0.573**	0.983**
HI												0.709**

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, ** Significant at 5% and 1% probability level

4.1.3.2. *Kharif* season (E2):

In *Kharif* season (E2), the seed yield per plant showed highly significant and positive correlation with biological yield per plant (0.983), pods per plant (0.844), clusters per plant (0.787), harvest-index (0.709), and primary branches per plant (0.690) and seeds per pod (0.572) besides having significant and positive correlation with pods per cluster (0.267), plant height (0.262) and pod length (0.257). The days to 50% flowering (-0.731) and days to maturity (-0.689) showed negative and highly significant correlation with seed yield per plant.

Harvest-index exhibited highly significant and positive correlation with pods per plant (0.676), primary branches per plant (0.663), seeds per pod (0.609), clusters per plant (0.547) and pods per cluster (0.340) but it recorded highly significant and negative correlations with days to maturity (-0.682) and days to 50% flowering (-0.639).

Biological yield per plant exhibited highly significant and positive association with pods per plant (0.796), clusters per plant (0.777), primary branches per plant (0.644), harvest-index (0.573), seeds per pod (0.518) and plant height (0.330) and significant positive correlation with pod length (0.315) while days to 50% flowering (-0.702) and days to maturity (-0.638) showed highly significant negative correlation.

The 100-seed weight showed highly significant and positive correlation with pod length (0.462) and significant and positive correlation with plant height (0.283). However, the 100-seed weight had negative correlations of highly significant degree with pods per cluster (-0.657), seeds per pod (-0.443) and harvest-index (-0.368) and significant degree with pods per plant (-0.256).

Seeds per pod possessed highly significant and positive correlation with primary branches per plant (0.444) and pods per plant (0.316) besides having highly significant and negative correlations with days to maturity (-0.423) and days to 50% flowering (0.376). Pod length showed highly significant and positive association with plant height (0.752) and clusters per plant (0.533) but it showed negative correlation of highly significant nature with pods per cluster (-0.350) and significant nature with days to 50% flowering.

Clusters per plant (0.713), pods per cluster (0.598) and primary branches per plant (0.454) resulted highly significant and positive correlation with pods per plant which showed highly significant and negative correlation with days to 50% flowering (-0.483) and days to maturity (-0.463).

Clusters per plant exhibited highly significant and positive correlation with primary branches per plant (0.718) and plant height (0.433) and highly significant negative correlation with days to 50% flowering (-0.930) and days to maturity (-0.794). Days to maturity and days to 50% flowering had highly significant and positive association with each other (0.897). The correlation for rest of the character pairs were non-significant.

4.1.4. Path Coefficient analysis:

The direct and indirect effects of different characters on seed yield per plant estimated in path coefficient analysis using simple correlations for *Zaid* and *Kharif* seasons are given in Table 4.4 (a) & 4.4 (b), respectively.

4.1.4.1. *Zaid* season (E1):

A perusal of Table 4.4 (a) reveals that the highest positive direct effects on seed yield per plant were exerted by biological yield per plant

(1.306) followed by harvest-index (0.239) and days to 50% flowering (0.104). The considerable negative direct effects were recorded on seed yield per plant by 100-seed weight (-0.416) followed by seeds per pod (-0.284), pods per cluster (-0.267), clusters per plant (-0.188) and pods per plant (-0.112). The direct effect of rest of the traits were too low to be considered of any consequence.

Pods per plant (1.026), clusters per plant (0.942), pods per cluster (0.586), pod length (0.293), primary branches per plant (0.260) and seeds per pod (0.246) exerted substantial positive indirect effects on seed yield per plant via biological yield per plant. In contrast, days to 50% flowering (-0.505) followed by days to maturity (-0.448) and plant height (-0.180)showed substantial negative direct effects on seed yield per plant via biological yield per plant. The indirect contribution of pods per plant (0.100) on seed yield per plant via harvest- index was also considerable in nature but indirect contribution of rest of the traits are too low to be considered here.

Pods per cluster (0.237) followed seeds per pod (0.215) and pods per plant (0.189) exerted considerable positive effects and pod length (-0.125) had considerable negative indirect efeects on seed yield per plant via 100-seed weight.

100-seed weight (0.147) exerted considerable positive effect on seed yield per plant via seeds per pod. The 100-seed weight (0.152) exerted considerable positive indirect effects on seed yield per plant via pods per cluster, but pods per plant (-0.204) and biological yield per plant (-0.120) exhibited substantial negative indirect effects on seed yield per plant via pods per cluster.

Days to 50% flowering (0.113) exhibited considerable positive direct effect on seed yield per plant via clusters per plant while biological

Table 4.4(a): Direct and indirect effects of different characters on seed yield per plant in mungbean germplasm in *Zaid* season (E1)

Traits	D 50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	GY/P
D 50%f	**0.104**	-0.043	0.001	0.022	0.113	-0.053	0.032	-0.014	-0.030	0.025	-0.505	-0.025	-0.373
DM	0.092	**-0.049**	-0.003	0.018	0.092	-0.017	0.033	-0.013	-0.008	-0.013	-0.448	-0.005	-0.323
PH	-0.005	-0.006	**-0.027**	-0.001	-0.017	0.097	0.019	0.016	-0.041	0.022	-0.180	-0.030	-0.153
PB/P	-0.078	0.030	-0.001	**-0.029**	-0.062	-0.009	-0.029	0.007	0.056	0.060	0.260	-0.003	0.201
C/P	-0.063	0.024	-0.002	-0.010	**-0.188**	-0.055	-0.087	0.017	-0.008	0.073	0.942	0.093	0.735**
P/C	0.021	-0.003	0.010	-0.001	-0.039	**-0.267**	-0.086	-0.009	-0.021	0.237	0.586	0.054	0.482
P/P	-0.030	0.015	0.004	-0.008	-0.147	-0.204	**-0.112**	0.005	-0.023	0.189	1.026	0.100	0.816**
PL	-0.038	0.017	-0.011	-0.005	-0.082	0.065	-0.015	**0.039**	0.059	-0.125	0.293	0.011	0.207
S/P	0.011	-0.001	-0.004	0.006	-0.005	-0.020	-0.009	-0.008	**-0.284**	0.215	0.246	0.082	0.228
100-SW	-0.006	-0.002	0.001	0.004	0.033	0.152	0.051	0.012	0.147	**-0.416**	-0.009	-0.028	-0.060
BY/P	-0.040	0.017	0.004	-0.006	-0.136	-0.120	-0.088	0.009	-0.054	0.003	**1.306**	0.093	0.989**
HI	-0.011	0.001	0.003	0.000	-0.073	-0.061	-0.047	0.002	-0.098	0.049	0.51	**0.239**	0.516

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Residual effect =0.0206, Bold values shows direct and normal values shows indirect effects

yield per plant (-0.136) and pods per plant (-0.147) exerted considerable positive and negative indirect effects on seed yield per plant via clusters per plant. The estimates of residual factors was negligible (0.0206) in this analysis.

4.1.4.2. *Kharif* season (E2):

A perusal of Table 4.4 (b) reveals that the highest positive direct effects on seed yield per plant were exerted by biological yield per plant (0.822) followed by pods per plant (0.226) and harvest-index (0.199). The considerable negative direct effects were recorded on seed yield per plant by clusters per plant (-0.132) and pods per cluster (-0.127).The direct effect of rest of the traits were too low to be considered of any consequence.

Pods per plant (0.654), clusters per plant (0.639), primary branches per plant (0.529), harvest-index (0.471), seeds per pod (0.426), plant height (0.271), pod length (0.259), pods per cluster (0.171) and 100-seed weight (0.116) exerted substantial positive indirect effects on seed yield via biological yield per plant. In contrast days to 50% flowering (-0.577) and days to maturity (-0.524) showed substantial negative direct effects on seed yield per plant via biological yield per plant. The indirect contribution of pods per plant (0.134), primary branches per plant (0.132), seeds per pod (0.121), biological yield per plant (0.114) and clusters per plant (0.109) on seed yield per plant via harvest-index were also high order positive in nature but indirect contribution of days to maturity (-0.136) and days to 50% flowering (-0.127) via harvest-index on seed yield per plant were high order negative effect. The indirect contributions of biological yield per plant (0.180), clusters per plant (0.161), harvest-index (0.153), pods per cluster (0.135) and primary branches per plant (0.103) exerted substantial

Table 4.4(b): Direct and indirect effects of different characters on seed yield per plant in mungbean germplasm in *Kharif* season (E2)

Traits	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
D50%f	**0.050**	-0.018	0.002	-0.024	0.103	-0.026	-0.109	-0.005	-0.001	0.001	-0.577	-0.127	-0.731**
DM	0.045	**-0.020**	0.002	-0.021	0.077	-0.004	-0.105	-0.004	-0.001	0.001	-0.524	-0.136	-0.689**
PH	-0.010	0.003	**-0.012**	0.004	-0.057	0.030	0.043	0.014	0.000	-0.001	0.271	-0.022	0.262
PB/P	-0.047	0.016	-0.002	**0.026**	-0.095	0.023	0.103	0.004	0.001	0.000	0.529	0.132	0.690**
C/P	-0.039	0.012	-0.005	0.019	**-0.132**	0.015	0.161	0.010	0.000	-0.001	0.639	0.109	0.787**
P/C	0.010	-0.001	0.003	-0.005	0.016	**-0.127**	0.135	-0.006	0.000	0.003	0.171	0.068	0.267
P/P	-0.024	0.009	-0.002	0.012	-0.094	-0.076	**0.226**	0.003	0.001	0.001	0.654	0.134	0.844**
PL	-0.014	0.004	-0.009	0.006	-0.071	0.044	0.041	**0.018**	0.000	-0.002	0.259	-0.020	0.257
S/P	-0.019	0.009	0.001	0.012	-0.026	-0.023	0.071	-0.004	**0.002**	0.002	0.426	0.121	0.572
100-SW	-0.011	0.002	-0.003	0.002	-0.032	0.083	-0.058	0.009	-0.001	**-0.005**	0.116	-0.073	0.029
BY/P	-0.035	0.013	-0.004	0.017	-0.103	-0.026	0.180	0.006	0.001	-0.001	**0.822**	0.114	0.983**
HI	-0.032	0.014	0.001	0.017	-0.072	-0.043	0.153	-0.002	0.001	0.002	0.471	**0.199**	0.709**

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Residual Effect = 0.0177, Bold values show direct and normal values show indirect effects.

positive indirect effects on seed yield via pods per plant. Days to 50% flowering (-0.109) and days to maturity (-0.105) had considerable negative indirect effect of seed yield per plant via pods per plant. Days to 50% flowering (0.103) and biological yield per plant (-0.103) exerted considerable positive and negative indirect effects on seed yield per plant via clusters per plant, respectively.The estimates of residual factor (0.0177) was negligible in this analysis.

4.1.5. Genetic divergence analysis:

The genetic divergence existing in sixty mungbean germplasm collections and four checks was studied by employing Non-hierarchical Euclidean cluster analysis for 13 quantitative characters. The sixty-four genotypes were grouped into 5 to 10 different cluster arrangements. The pseudo F-test revealed that ten cluster arrangements was the most appropriate for this material in both environments under study. Therefore, the sixty genotypes were accepted to be grouped into ten different non-overlapping clusters. The distribution of sixty mungbean lines in ten clusters in *Zaid* season (E1) and *Kharif* season (E2) is presented in Table 4.5 (a) and Table 4.5 (b), respectively.

In *Zaid* season (E1), the highest number of genotypes appeared in cluster VIII which contained 13 genotypes. Cluster II and IV possessed 8 genotypes each while cluster I and III were constituted by 7 genotypes each . Cluster VI and VII possessed 6 genotypes each while cluster IX and X contained 2 genotypes each having minimum entries in all ten clusters. Cluster V comprised of 5 genotypes.

In *Kharif* season (E2), the highest number of genotypes appeared in Cluster X which contained 12 genotypes.Cluster IV possessed 10 genotypes. Cluster III and VI were constituted by 9 and 8 genotypes,

Table 4.5 (a): Clustering pattern of 60 mungbean genotypes on the basis of Non-herarchical Euclidean cluster analysis for 13 characters in *Zaid* season (E1)

Cluster number	Number of genotypes	Genotypes
I	7	CoGG 912, LGG 460, SML 832, TM 96-2, HUM 12, TARM 1, P.Vishal
II	8	MH 421, KM 22-41, IPM 410-3, MGG 347, KM 18-116, MH 318, SML 1082, P.Mung 6
III	7	P.Mung 2, DGG 1, DGGV 2, OUM 11-5, DGGS 4, Pusa 9531, KM 11-584
IV	8	MH 2-15, Phule Mung 2, PKVAKM 4, KM 18-103, 5 BWME, BM 4, TM 2000-2, ADT 3
V	5	DGGV 5, ML 613, KM 18-117, PDM 139, KM 18-108
VI	6	P.Mung 5, Pusa 9072, ML 818, IPM 2-14, 4RMG1028, IPM 2-3
VII	6	KM 18-115, KM 18-99, KM 18-109, KM 18-97, KM 18-114, KM 18-102
VIII	13	CoGG 8, KM 18-121, TMB 37, 2-1 PM 409, Co 6, KM 18-106, KM 18-111, KM 18-122, SML 668, Kopergaon, VBN (GG) 2, KM 18-105, LGG 450
IX	2	P.Mung 4, HUM 16
X	2	IPM 99-125, IPM 205-7

Table 4.5(b): Clustering pattern of 60 mungbean genotypes on the basis of Non-herarchical Euclidean cluster analysis for 13 characters in *Kharif* season (E2)

Cluster number	Number of genotypes	Genotypes
I	**5**	MH 2-15, 5 BWME, Phule Mung 2, KM 18-103, PKVAKM 4
II	**7**	BM 4, PDM 139, TM 2000-2, DGGV 5, ML 613, KM 18-117, KM 18-108
III	**9**	TM 96-2, HUM 12, ADT 3, KM 18-114, MH 421, Pusa 9531, IPM 410-3, TARM 1, IPM 2-3
IV	**10**	IPM 2-14, KM 18-106, Co 6, KM 18-109, LGG 450, KM 18-121, Co(GG) 8, Kopergaon, KM 22-41, SML 668
V	**4**	2-1 PM 409, KM 18-122, P.Vishal, KM 18-111
VI	**8**	VBN(GG) 2, KM 18-99, KM 18.-102, P.Mung 4, HUM 16, KM 18-105, IPM 99-125, IPM 205-7
VII	**4**	TMB 37, 4RMG1028, KM 18-115, KM 18-97
VIII	**3**	LGG 460, OUM 11-5, SML 832
IX	**2**	P.Mung 2, DGG 1
X	**12**	DGGV 2, ML 818, P. Mung 5, Pusa 9072, KM 11-584, DGGS 4, KM 18-116, CoGG 912, SML 1082, P. Mung 6, MGG 347, MH 318

respectively. Cluster V and VII possessed 4 genotypes each. Cluster II and I were constituted by 7 and 5 genotypes, respectively. Cluster VIII had 3 genotypes while Cluster IX had 2 genotypes with minimum entries in all ten clusters.

4.1.5.1. Intra-cluster and Inter-cluster Distances:

The estimates of intra-cluster and inter-cluster distances for ten clusters in *Zaid* (E1) and *Kharif* (E2) are presented in Table 4.6 (a) and Table 4.6 (b), respectively.

In *Zaid* season, the highest intra-cluster distance was observed for cluster IV (11.58) followed by cluster X (11.12), cluster II (10.77) and cluster VIII (10.55). The lowest intra-cluster distance was recorded for cluster IX (0.94) followed by cluster VII (3.93) and cluster I (6.42). The highest inter-cluster distance was found between cluster III and IX (110.81) followed by cluster IV and IX (100.35) and cluster V and IX (88.78). Cluster IX also exhibited high order inter-cluster distances with cluster I (84.32) and cluster II (75.23). Cluster III (84.20) and cluster IV (65.95) had high order inter-cluster distances with cluster X. The lowest inter-cluster distance was recorded between cluster I and II (13.30) followed by cluster VII and VIII (13.63) and cluster VI and VII (14.42).

In the *Kharif* season, the highest intra-cluster distance was observed for cluster IX (16.12) followed by cluster III (12.77), cluster II (10.62) and cluster IV (10.41). The lowest intra-cluster distance was noted for cluster I (3.65), followed by cluster VII (5.83) and cluster X (6.18). The highest inter-cluster distance was found between cluster V and IX (91.88) which was followed by high inter-cluster distances of cluster IX with cluster III (83.52), cluster VI (82.04), cluster I (64.84) and cluster II (58.49). Cluster VIII also exhibited high order inter-cluster distances with cluster V

Table 4.6(a): Estimates of average intra and inter-cluster distances for the ten clusters in *Zaid* season (E1)

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**6.42**	13.30	14.88	19.67	14.77	19.55	25.46	21.13	84.32	55.04
II		**10.77**	16.12	20.84	21.16	18.58	19.17	17.99	75.23	50.77
III			**9.60**	26.38	30.32	26.48	35.16	36.07	110.81	84.20
IV				**11.58**	17.89	33.99	37.87	27.33	100.35	65.95
V					**7.55**	35.47	31.55	20.49	88.78	53.75
VI						**7.94**	14.42	22.19	49.05	40.41
VII							**3.93**	13.63	33.63	21.20
VIII								**10.55**	51.91	25.48
IX									**0.94**	23.74
X										**11.12**

Bold figures represents intra-cluster distances

Table 4.6(b): Estimates of average intra and inter-cluster distances for the ten clusters in *Kharif* season (E2)

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**3.65**	12.58	27.86	25.41	25.93	27.85	22.85	35.58	64.84	28.23
II		**10.62**	18.69	18.69	16.45	19.28	16.70	29.87	58.49	23.69
III			**12.77**	22.78	22.48	25.22	20.67	33.47	48.65	28.77
IV				**10.41**	13.54	12.13	20.53	55.39	83.52	40.30
V					**6.80**	18.93	30.93	59.28	91.88	48.55
VI						**7.37**	14.08	50.23	82.04	36.28
VII							**5.83**	25.23	45.77	12.94
VIII								**7.91**	18.74	13.88
IX									**16.12**	25.44
X										**6.18**

Bold figures represent intra-cluster distances.

(59.28), cluster IV (55.39) and cluster VI (50.23). The lowest inter-cluster distance was observed between cluster IV and VI (12.13) followed by cluster I and II (12.58) and cluster VII and X (12.94).

4.1.6. Clusters mean for different traits:

The cluster means for thirteen characters of different clusters in *Zaid* (E1) and *Kharif* (E2) season, 2019 have been presented in Table 4.7 (a) and Table 4.7 (b), respectively.

4.1.6.1. Days to 50% flowering:

In *Zaid* season (E1), the genotype of cluster IX took maximum days to 50% flowering ($\bar{x}$=70.00 days), followed by cluster VI ($\bar{x}$=55.50 days). The genotype with early flowering were concentrated in cluster v ($\bar{x}$=34.00 days), cluster VI ($\bar{x}$=38.88 days) and cluster VIII ($\bar{x}$=40.92 days).

In *Kharif* season (E2), the genotypes of cluster V took maximum days to 50% flowering ($\bar{x}$=56.75 days), followed by cluster III ($\bar{x}$=52.89 days) and cluster IV ($\bar{x}$=47.00 days) . The genotype with early flowering were concentrated in cluster X ($\bar{x}$=34.75 days), cluster VII ($\bar{x}$=35.00 days) and cluster VIII ($\bar{x}$=35.33 days).

4.1.6.2. Days to maturity:

In *Zaid* season (E1), the highest and lowest cluster mean for days to maturity were observed for cluster IX ($\bar{x}$=102.50 days) and cluster V ($\bar{x}$=60.40 days), respectively. Cluster IV ($\bar{x}$=63.13 days) was another cluster which contained mostly the shorter genotypes.

In *Kharif* season (E), the highest and lowest cluster mean for days to maturity were observed for cluster V ($\bar{x}$=98.00 days) and cluster VII ($\bar{x}$=62.50 days), respectively. Cluster X ($\bar{x}$=62.83 days) was another cluster which contained mostly the early maturing genotypes.

Table 4.7 (a): Cluster means for different characters of mungbean for ten clusters in *Zaid* season (E1)

Cluster No	Characters Mean (E1)												
	D50%f	**DM**	**PH**	**PB/P**	**C/P**	**P/C**	**P/P**	**PL**	**S/P**	**100-SW**	**BY/P**	**HI**	**SY/P**
I Cluster	41.57	69.57	57.20	4.37	5.31	5.06	26.69	6.36	6.80	3.24	19.17	30.62	5.86
II Cluster	41.38	71.75	29.38	3.60	5.13	5.28	26.68	6.61	6.90	3.35	20.24	30.08	6.10
III Cluster	42.71	70.14	46.94	3.54	6.17	6.00	36.63	6.63	7.00	3.13	26.01	30.53	7.96
IV Cluster	38.88	63.13	38.13	4.13	5.33	4.73	25.15	6.76	5.78	4.99	22.04	32.60	7.18
V Cluster	34.00	60.40	55.28	3.72	4.76	3.92	18.36	5.98	7.56	4.12	17.64	32.30	5.69
VI Cluster	55.50	87.33	34.13	3.90	5.17	5.23	26.93	5.02	5.60	3.27	16.92	29.24	4.95
VII Cluster	46.67	79.00	29.03	2.47	4.77	4.47	21.30	5.50	5.17	3.07	11.90	28.33	3.38
VIII Cluster	40.92	68.39	27.02	3.44	4.28	4.43	18.66	5.89	5.80	3.29	11.15	31.20	3.48
IX Cluster	70.00	102.50	23.25	2.30	2.50	2.80	6.90	5.65	4.20	3.10	3.25	27.37	0.89
X Cluster	46.00	74.50	22.20	3.40	3.00	3.00	9.20	5.30	3.30	2.90	3.25	28.21	0.92

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Table 4.7 (b): Cluster means for different characters of mungbean for ten clusters in *Kharif* season (E2)

Cluster No	Characters Mean (E2)												
	D50%f	**DM**	**PH**	**PB/P**	**C/P**	**P/C**	**P/P**	**PL**	**S/P**	**100-SW**	**BY/ P**	**HI**	**SY/ P**
I Cluster	43.20	82.00	44.16	3.24	5.64	4.88	27.56	7.90	4.72	4.78	21.06	29.47	6.22
II Cluster	44.86	85.14	39.07	3.63	5.23	4.74	24.86	7.03	6.49	3.87	21.33	29.45	6.26
III Cluster	52.89	89.44	37.51	3.09	4.93	6.42	31.60	6.20	6.82	3.20	22.54	30.65	6.91
IV Cluster	47.00	78.10	25.07	2.44	4.92	5.04	24.08	6.10	5.38	3.19	15.73	27.20	4.30
V Cluster	56.75	98.00	31.43	2.85	5.00	4.15	20.95	6.60	6.10	3.18	13.65	27.76	4.14
VI Cluster	39.88	69.38	21.21	2.68	4.28	4.93	21.23	6.20	5.85	3.20	13.33	30.12	4.01
VII Cluster	35.00	62.50	28.05	4.00	5.30	5.65	29.55	6.08	6.20	3.43	21.55	31.72	6.29
VIII Cluster	35.33	63.33	56.00	4.53	5.80	5.93	34.27	7.93	8.67	3.53	32.03	32.65	10.46
IX Cluster	37.50	66.50	49.00	4.20	7.00	7.30	50.10	8.00	8.70	3.05	39.05	33.71	13.17
X Cluster	34.75	62.83	36.76	4.80	6.55	5.52	36.23	6.40	7.22	3.71	29.97	32.12	9.63

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

4.1.6.3. Plant height:

In *Zaid* season (E1), the highest and lowest cluster mean for plant height were observed for cluster I ($\bar{x}$=57.20 cm) and cluster X ($\bar{x}$=22.20 cm), respectively. Cluster IX ($\bar{x}$=23.25 cm) was another cluster which contained mostly the shorter genotypes while cluster V ($\bar{x}$=55.28 cm) also had taller genotypes.

In *Kharif* season (E2), the highest and lowest cluster mean for plant height were observed for cluster VIII ($\bar{x}$=56.00 cm) and cluster VI ($\bar{x}$=21.21 cm), respectively. Cluster IV ($\bar{x}$=25.07 cm) was another cluster which contained mostly the shorter genotypes while cluster IX ($\bar{x}$=49.00 cm) also had taller entries.

4.1.6.4. Primary branches per plant:

In *Zaid* season (E1), considering the variation in number of primary branches per plant, cluster I ($\bar{x}$=4.37) showed highest mean value followed by cluster IV ($\bar{x}$=4.13) while cluster IX ($\bar{x}$=2.30), followed by cluster VII ($\bar{x}$=2.47) had lowest value for primary branches per plant. Remaining six clusters were characterized by moderate means for primary branches per plant.

In *Kharif* season (E2),cluster X ($\bar{x}$=4.80) showed highest mean value for primary branches per plant followed by cluster VIII ($\bar{x}$=4.53), cluster IX ($\bar{x}$=4.20) and cluster VII ($\bar{x}$=4.00). Cluster IV ($\bar{x}$=2.44), followed by cluster VI ($\bar{x}$=2.68) had lowest value for primary branches per plant. Remaining four clusters were characterized by moderate means for primary branches per plant.

4.1.6.5. Clusters per plant:

In *Zaid* season (E1), the genotypes with high number of clusters per plant were concentrated in cluster III ($\bar{x}$=6.17), followed by cluster IV ($\bar{x}$=5.33) and cluster I ($\bar{x}$=5.31). Cluster IX ($\bar{x}$=2.50), followed by cluster X ($\bar{x}$=3.00) appeared to possess entries having low clusters per plant while remaining five clusters represented moderate mean value for this trait.

In *Kharif* season (E2), the genotypes with high number of clusters per plant were concentrated in cluster IX ($\bar{x}$=7.00), followed by cluster X ($\bar{x}$=6.55). Cluster VI ($\bar{x}$=4.28), followed by cluster IV ($\bar{x}$=4.92) and cluster III ($\bar{x}$=4.93) appeared to possess genotypes having very low clusters per plant while remaining five clusters represented moderate mean value for this trait.

4.1.6.6. Pods per cluster:

In *Zaid* season (E1), the genotypes occurring in cluster III ($\bar{x}$=6.00) showed highest mean performance for pods per cluster followed by cluster II ($\bar{x}$=5.28) and cluster VI ($\bar{x}$=5.23). The entries of cluster IX ($\bar{x}$=2.80) followed by cluster X ($\bar{x}$=3.00) were responsible for lowest means for pods per cluster.

In *Kharif* season (E2), the genotypes occurring in cluster IX ($\bar{x}$=7.30) showed highest mean performance for pods per cluster followed by those of cluster III ($\bar{x}$=6.42). The entries of cluster V ($\bar{x}$=4.15) followed by cluster II ($\bar{x}$=4.74) were responsible for lowest means for pods per cluster.

4.1.6.7. Pods per plant:

In *Zaid* season (E1), the highest cluster mean for pods per plant was exhibited by cluster III ($\bar{x}$=36.63), followed by cluster VI ($\bar{x}$=26.93),

cluster I ($\bar{x}$=26.69) and cluster II ($\bar{x}$=26.68). The lowest and second lowest means were noted for cluster IX ($\bar{x}$=6.90) and cluster X ($\bar{x}$=9.20). Rest of the clusters were identified themselves with moderate number of pods per plant.

In *Kharif* season (E2), the highest cluster mean for pods per plant was exhibited by cluster IX ($\bar{x}$=50.10), followed by cluster X (=36.23) and cluster VIII ($\bar{x}$=34.27). The lowest and second lowest means were noted for cluster V ($\bar{x}$=20.95) and cluster VI ($\bar{x}$=21.23). Rest of the clusters were identified themselves with moderate number of pods per plant.

4.1.6.8. Pod length:

In *Zaid* season (E1), the highest and lowest mean for pod length were observed for cluster IV ($\bar{x}$=6.76 cm) and cluster VI ($\bar{x}$=5.02 cm), respectively. Cluster III ($\bar{x}$=6.63 cm) and cluster II ($\bar{x}$=6.61cm) also showed higher cluster means for this character. Rest of the clusters were identified themselves with average number of pod length.

In *Kharif* season (E2), the highest and lowest mean for pod length were observed for cluster IX ($\bar{x}$=8.00cm) and cluster VII ($\bar{x}$=6.08 cm), respectively. Cluster VIII ($\bar{x}$=7.93 cm) and cluster I ($\bar{x}$=7.90 cm) also possessed genotypes with longer pods. Rest of the clusters were identified themselves with average number of pod length.

4.1.6.9. Seeds per pod;

In *Zaid* season (E1), the entries occurring in cluster V ($\bar{x}$=7.56) followed by cluster III ($\bar{x}$=7.00)showed highest mean for seeds per pod while the genotypes of cluster X ($\bar{x}$=3.30) and cluster IX ($\bar{x}$=4.20) were responsible for lowest mean for seeds per pod.

In *Kharif* season (E2), the genotypes occurring in cluster IX ($\bar{x}$=8.70) followed by cluster VIII ($\bar{x}$=8.67) showed highest mean for seeds per pod while the genotypes of cluster I ($\bar{x}$=4.72) and cluster IV ($\bar{x}$=5.38) were responsible for lowest means for seeds per pod.

4.1.6.10. 100-Seed weight:

In *Zaid* season (E1), the 100-seed weight was highest in the entries of cluster IV ($\bar{x}$=4.99g), followed by cluster V ($\bar{x}$=4.12g) while the lowest and second lowest means were noted for cluster X ($\bar{x}$=2.90g) and cluster VII ($\bar{x}$=3.07g), respectively.

In *Kharif* season (E2), the 100-seed weight was highest in the genotypes of cluster I ($\bar{x}$=4.78g), followed by cluster II ($\bar{x}$=3.87g) and cluster X ($\bar{x}$=3.71g). The lowest and second lowest means were noted for cluster IX ($\bar{x}$=3.05g) and cluster V ($\bar{x}$=3.18g), respectively. Rest of the clusters were identified themselves with moderate number of 100-seed weight.

4.1.6.11. Biological yield per plant:

In *Zaid* season (E1), Cluster III ($\bar{x}$= 26.01g) was comprised of entries which produced highest mean for biological yield per plant. The lowest mean for biological yield per plant was observed for the cluster IX ($\bar{x}$=3.25g) and cluster X ($\bar{x}$=3.25g). Rest of the clusters showed moderate mean value for this character.

In *Kharif* season (E2), Cluster IX ($\bar{x}$= 39.05g) followed by cluster VIII ($\bar{x}$=32.03 g) and cluster X ($\bar{x}$=29.97 g) was comprised of entries which produced highest mean for biological yield per plant. The lowest mean for biological yield per plant were observed for the cluster VI

($\bar{x}$=13.33g) and cluster V ($\bar{x}$=13.65g), respectively. Rest of the clusters showed moderate mean value for this character.

4.1.6.12. Harvest-index:

In *Zaid* season (E1), the highest and lowest means for harvest-index were recorded for cluster IV ($\bar{x}$= 32.60%) and cluster IX ($\bar{x}$= 27.37%), respectively. The mean value for harvest-index of other eight clusters found moderate in nature. Cluster V ($\bar{x}$=32.30%) also possessed higher cluster mean for harvest-index.

In *Kharif* season (E2), the highest and lowest means for harvest-index were recorded for cluster IX ($\bar{x}$= 33.71) and cluster IV ($\bar{x}$= 27.20), respectively. The mean value for harvest-index of other eight clusters found moderate in nature.

4.1.6.13. Seed yield per plant:

In *Zaid* season (E1), the highest cluster mean for seed yield per plant was observed in case of cluster III ($\bar{x}$= 7.96g) which indicates that lines having very high seed yield were concentrated in this cluster. The genotypes with very low seed yield were found to be grouped in cluster IX ($\bar{x}$= 0.89g) and cluster X ($\bar{x}$= 0.92g). Remaining seven clusters had medium range of mean for seed yield per plant.

In *Kharif* season (E2), the highest cluster mean for seed yield per plant was observed in case of cluster IX ($\bar{x}$= 13.17g) which indicates that lines having very high seed yield were concentrated in this cluster. The genotypes with very low seed yield were found to be grouped in cluster VI ($\bar{x}$= 4.01g) and cluster V ($\bar{x}$= 4.14g). Remaining seven clusters had medium range of mean for seed yield per plant.

4.2. Combining ability experiment (Experiment-II)

4.2.1. Analysis of variance for experiment-II:

Analysis of variance was carried out with respect to thirteen characters to test the significance of differences between various treatments (genotypes) *viz.*, fifteen lines, four testers and sixty F_1s as depicted in Table 4.8. The mean squares due to treatments, parents and crosses were highly significant for the characters viz., days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per cluster, seeds per pod, 100- seed weight, biological yield per plant, harvest-index and seed yield per plant indicating presence of sufficient variability in the experimental material, while mean squares for pod length and pods per plant were found non–significant. The mean squares due to parents vs crosses were also found significant or highly significant for the characters viz., days to 50% flowering, days to maturity, plant height, clusters per plant, pods per cluster, seeds per pod, 100- seed weight and harvest-index , while primary branches per plant, pod length, pods per plant, biological yield per plant and seed yield per plant had non-significant mean squares.

4.2.2. Coefficients of variation, heritability and genetic advance:

The phenotypic (PCV) and genotypic (GCV) coefficients of variation for the thirteen characters under study have been presented in Table 4.9.

In general, the estimates of phenotypic correlation coefficients were higher than the corresponding genotypic coefficients of variation for all the traits. The high estimates (>20%) of phenotypic (PCV) and genotypic

Table 4.8: Analysis of variance for line x tester set of crosses and parents for 13 characters in mungbean in *Kharif* season

Source of variation	Df	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
Replications	2	18.40	54.49*	14.02*	0.28	2.77**	3.54**	451.54	4.21	1.12**	0.02	443.08**	2.15	45.60**
Treatments	78	208.97**	385.66**	272.01**	1.24**	1.53**	1.00**	144.76	1.83	5.42**	0.25**	202.72**	7.44**	19.06**
Parents	18	222.59**	444.12**	374.82**	2.65**	1.06**	1.02**	101.42	3.19	9.07**	0.75**	272.33**	10.69**	30.64**
Crosses	59	207.88**	366.18**	243.58**	0.84**	1.67**	0.91**	159.47	1.39	4.37**	0.10**	184.86**	6.16**	15.81**
P vs C	1	27.72*	483.04**	98.76**	0.03	1.72**	6.35**	56.82	3.45	1.41*	0.07*	3.22	24.21**	2.59
Error	156	6.72	11.97	3.54	0.15	0.21	0.24	15.35	0.20	0.23	0.01	15.32	3.08	1.24

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Table 4.9: Estimates of coefficient of variation, heritability in broad sense and genetic advance in per cent of mean for 13 traits in mungbean in *Kharif* season

Character	Coefficient of variation (%)		Heritability Broad sense	Genetic advance in (%) of mean
	Phenotipic	Genotipic		
D50F	19.69	18.78	90%	36.91
DM	15.02	14.35	91%	28.25
PH	26.39	25.88	96%	52.30
PB/P	22.13	18.89	72%	33.22
C/P	14.22	11.68	67%	19.78
P/C	11.35	8.07	50%	11.84
P/P	21.43	18.38	73%	32.48
PL	12.24	10.46	73%	18.43
S/P	21.36	20.02	87%	38.64
100-SW	8.71	8.07	85%	15.41
BY/P	33.12	29.62	79%	54.57
HI	7.05	4.01	32%	4.70
SY/P	32.82	29.78	82%	55.67

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

(GCV) coefficient of variation were recorded for biological yield per plant (PCV = 33.12%, GCV = 29.62%), seed yield per plant (PCV= 32.82%, GCV = 29.78%), plant height (PCV = 26.39%, GCV = 25.88%) and seeds per pod(PCV = 21.36%, GCV = 20.02%). Primary branches per plant (PCV = 22.13%, GCV = 18.89%) and pods per plant (PCV = 21.43%, GCV = 18.38%) had high PCV with moderate GCV. The moderate estimates (10-20%) of PCV and GCV were recorded for days to 50% flowering, days to maturity, clusters per plant and pod length while pods per cluster had moderate PCV with low GCV. The remaining characters , 100- seed weight and harvest-index exhibited low estimates (<10%) of PCV or GCV.

The estimates of heritability in broad sense (h^2b) and genetic advance in % of mean estimated for thirteen characters have been presented in Table 4.9. The estimates of broad sense heritability ranged from 32% (harvest-index) to 96% (plant height). The high heritability in broad sense (>75%) was recorded for days to 50% flowering, days to maturity, plant height, seeds per pod, 100-seed weight, seed yield per plant and biological yield per plant. Pods per plant, pod length, primary branches per plant, clusters per plant and pods per cluster showed moderate broad sense heritability (>50% to <75%) while low heritability (<50%) was found for harvest-index only.

The genetic advance in % of mean was very high (>50%) for seed yield per plant, biological yield per plant and plant height and the high (>20%) for the characters viz., days to 50% flowering, days to maturity, primary branches per plant, seeds per pod and pods per plant. Moderate (>10-20%) estimates of genetic advance in per cent of mean were observed for clusters per plant, pods per cluster, pod length and 100-seed weight, while harvest-index (4.70%) showed low genetic advance (<10%).

4.2.3. Correlation coefficients:

The estimates of phenotypic correlation coefficients estimated for thirteen characters on crosses and parents are presented in Table 4.10. The seed yield per plant exhibited highly significant and positive correlation with biological yield per plant (0.933), pods per plant (0.719), seeds per pod (0.616), clusters peer plant (0.600), pods per cluster (0.541), primary branches per plant (0.424), harvest-index (0.325), 100-seed weight (0.284) and plant height (0.238). The 100-seed weight showed positive correlation of highly significant level with biological yield per plant (0.262).

Biological yield per plant showed highly significant and positive association with pod length (0.710), clusters per plant (0.598), seeds per pod (0.545), pods per cluster (0.523) and primary branches per plant (0.353). Harvest-index showed highly significant positive correlation with primary branches per plant (0.300), plant height (0.273) and seeds per pod (0.252) but had negative association with days to maturity (-0.172) and days to 50% flowering (-0.156). Seeds per pod showed highly significant positive correlation with plant height (0.438), primary branches per plant (0.431) and pods per plant (0.231). Pod length was significantly and positively associated with plant height (0.234). Pods per plant showed highly significant positive correlation with clusters per plant (0.825) and pods per cluster (0.754). Pods per cluster showed highly significant positive correlation with clusters per plant (0.377). Primary branches per plant showed significant positive association with plant height (0.502) but had highly significant negative correlation with days to 50% flowering (-0.335) and days to maturity (-0.271). Days to maturity recorded highly significant and positive association with days to 50% flowering (0.864).

The estimates of genotypic correlation coefficients between thirteen characters given in Table 4.11 were generally similar in sign but higher in magnitude than the corresponding phenotypic correlation coefficients.

Table 4.10: Estimates of phenotypic correlation coefficients between 13 traits in mungbean in *Kharif* season

Traits	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100- SW	BY/P	HI	SY/P
D50%f	0.864**	-0.154	-0.335**	0.111	0.076	0.096	-0.010	-0.089	0.141	0.062	-0.156	0.004
DM		-0.083	-0.271*	0.077	0.090	0.070	0.104	-0.066	0.103	0.035	-0.172	-0.007
PH			0.502**	-0.018	0.013	-0.012	0.234**	0.438**	0.003	0.167	0.273*	0.238**
PB/P				0.085	0.099	0.129	0.118	0.431**	0.115	0.353**	0.300**	0.0424**
C/P					0.377**	0.825**	-0.028	0.051	0.101	0.598**	0.079	0.600**
P/C						0.754**	-0.053	0.041	0.020	0.523**	0.194	0.541**
P/P							-0.066	0.061	0.061	0.710**	0.173	0.719**
PL								0.231**	0.056	0.060	0.111	0.089
S/P									0.031	0.545**	0.252*	0.616**
100-SW										0.262*	0.126	0.284*
BY/P											0.174	0.933**
HI												0.325**

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, **.Significant at 5% and 1%probability level, respectively

Table 4.11: Estimates of genotypic correlation coefficients between 13 traits in mungbean in *Kharif* season

Traits	DM	PH	PB/P	C/P	P/C	P/P	P/L	S/P	100-SW	BY/P	HI	SY/P
D50%f	0.916	-0.172	-0.446	0.137	0.117	0.116	-0.002	-0.112	0.189	0.061	-0.255	-0.004
DM		-0.090	-0.368	0.115	0.116	0.096	0.147	-0.091	0.158	0.032	-0.262	-0.011
PH			0.626	-0.010	0.013	-0.015	0.304	0.482	-0.008	0.193	0.533	0.272
PB/P				0.120	0.095	0.132	0.113	0.590	0.283	0.474	0.615	0.571
C/P					0.762	0.947	-0.049	0.053	0.059	0.664	-0.003	0.671
P/C						0.938	-0.077	0.106	0.011	0.675	0.319	0.679
P/P							-0.076	0.099	0.035	0.738	0.209	0.726
PL								0.292	0.146	0.085	0.113	0.113
S/P									0.081	0.592	0.546	0.679
100-SW										0.350	0.139	0.362
BY/P											0.523	0.955
HI												0.575

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, **.Significant at 5% and 1% probability level, respectively

4.2.4. Path coefficient analysis:

The direct and indirect effects of twelve characters on seed yield per plant computed using phenotypic correlations are presented in Table 4.12.

The highest positive direct effect on seed yield per plant was exerted by pods per plant (0.457), followed by seeds per pod (0.408), biological yield per plant (0.324) and 100-seed weight (0.201). Seeds per pod showed substantial positive indirect effects on seed yield per plant via biological yield per plant (0.183). The remaining estimates of indirect effects in this analysis were too low to be considered important. The estimates of residual factor (0.1669) was quite low in this path analysis.

The direct and indirect effects of thirteen characters on seed yield per plant estimated by path coefficient analysis using genotypic correlations are given in Table 4.13.

The highest positive direct effect on seed yield per plant was exerted by pods per plant (6.705), followed by seeds per pod (0.632), 100-seed weight (0.339), biological yield per plant (0.236) and plant height (0.122). The substantial negative direct effects on seed yield per plant were extended by clusters per plant (-4.064), pods per cluster (-2.491), harvest-index (-0.348), pod length (-0.192) and days to 50% flowering (-0.108).

The100-seed weight exhibited high order of positive indirect effects on seed yield per plant via pods per plant (0.252). In contrast, high order of negative indirect effects were extended by clusters per plant (-4.064), pods per cluster (-2.491), harvest-index (-0.348), pod length (-0.192) and days to 50% flowering (-0.108). Seeds per pod exhibited high order of positive indirect effects on seed yield per plant via pods per plant (0.753) and biological yield per plant (0.142), but it had considerable negative indirect

Table 4.12: Estimates of direct and indirect effects of 13 traits on seed yield per plant in mungbean at phenotypic level in *Kharif* season

Traits	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
D50%f	**-0.023**	-0.008	0.004	-0.009	-0.001	0.000	0.044	0.000	-0.036	0.022	0.021	-0.010	0.004
DM	-0.020	**-0.009**	0.002	-0.007	0.000	0.000	0.033	0.000	-0.029	0.025	0.012	-0.011	-0.007
PH	0.004	0.001	**-0.028**	0.013	0.000	0.000	-0.005	-0.001	0.184	-0.002	0.054	0.016	0.238**
PB/P	0.008	0.003	-0.014	**0.025**	-0.001	-0.001	0.059	0.000	0.179	0.030	0.110	0.018	0.424**
C/P	-0.002	0.000	0.001	0.002	**-0.006**	-0.002	0.398	0.000	0.022	0.012	0.200	0.005	0.600**
P/C	-0.001	-0.001	-0.001	0.004	-0.003	**-0.004**	0.362	0.000	0.033	-0.004	0.182	0.013	0.541**
P/P	-0.002	-0.001	0.000	0.003	-0.006	-0.003	**0.457**	0.000	0.031	0.006	0.230	0.010	0.719**
PL	0.001	-0.001	-0.008	0.004	0.001	0.000	-0.020	**-0.002**	0.108	0.011	0.031	0.008	0.089
S/P	0.002	0.001	-0.013	0.011	0.000	0.000	0.035	-0.001	**0.408**	-0.005	0.183	0.015	0.616**
100-SW	-0.003	-0.001	0.000	0.004	0.000	0.000	0.013	0.000	-0.010	**0.201**	0.094	0.005	0.284**
BY/P	-0.002	0.000	-0.005	0.009	-0.004	-0.002	0.325	0.000	0.230	0.058	**0.324**	0.010	0.933**
HI	0.004	0.002	-0.008	0.008	-0.001	-0.001	0.080	0.000	0.108	0.018	0.056	**0.057**	0.325**

Residual effect= 0.1669, Direct effects on main diagonal (bold figures)

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Table 4.13: Estimates of direct and indirect effects of 13 traits on seed yield per plant in mungbean at genotypic level in *Kharif* season

Traits	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
D50%f	**-0.108**	-0.089	-0.021	-0.006	-0.415	-0.220	0.774	0.007	-0.072	0.042	0.015	0.089	-0.004
DM	-0.099	**-0.097**	-0.011	-0.005	-0.319	-0.194	0.641	-0.019	-0.058	0.046	0.008	0.097	-0.011
PH	0.018	0.009	**0.122**	0.009	0.139	-0.050	-0.087	-0.063	0.310	-0.003	0.047	-0.179	0.272**
PB/P	0.044	0.034	0.072	**0.014**	-0.482	-0.268	0.827	-0.035	0.333	0.083	0.101	-0.198	0.571**
C/P	-0.011	-0.008	-0.004	0.002	**-4.064**	-1.880	6.412	0.018	0.046	0.021	0.163	-0.019	0.671**
P/C	-0.010	-0.008	0.003	0.002	-3.068	**-2.491**	6.110	0.010	0.100	0.001	0.165	-0.128	0.679**
P/P	-0.012	-0.009	-0.002	0.002	-3.887	-2.270	**6.705**	0.012	0.071	0.013	0.174	-0.075	0.726
PL	0.004	-0.010	0.041	0.003	0.390	0.132	-0.432	**-0.192**	0.208	0.028	0.029	-0.039	0.113
S/P	0.012	0.009	0.060	0.008	-0.293	-0.393	0.753	-0.063	**0.632**	0.001	0.142	-0.188	0.679**
100-SW	-0.013	-0.013	-0.001	0.004	-0.256	-0.006	0.252	-0.016	0.001	**0.339**	0.079	-0.037	0.362**
BY/P	-0.007	-0.003	0.024	0.006	-2.802	-1.735	4.949	-0.024	0.380	0.113	**0.236**	-0.180	0.955**
HI	0.028	0.027	0.063	0.008	-0.221	-0.917	1.447	-0.022	0.342	0.036	0.122	**-0.348**	0.575**

Residual effect= 0.1612 , Direct effects on main diagonal (bold figures)

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

effects on seed yield per plant via pods per cluster (-0.393), clusters per plant (-0.293) and harvest-index (-0.188). The biological yield per plant recorded considerable indirect effects of positive nature on seed yield per plant via pods per plant (4.949), seeds per pod (0.380) and negative nature via clusters per plant (-2.802), pods per cluster (-1.735) and harvest-index (-0.180).

The estimates of residual factors (0.1612) obtained in this path analysis was much low.

4.2.5. Combining ability analysis:

4.2.5.1. Analysis of variance for line x tester set:

The analysis of variance for line x tester set comprising sixty crosses is presented in Table 4.14. The analysis of variance revealed that mean squares due to line x tester interactions were highly significant for all the twelve characters except harvest-index . The variance due to lines were highly significant for all the characters. The mean squares due to testers were highly significant for all the characters except clusters per plant, pods per cluster, pods per plant and seeds per pod.

4.2.5.2. Estimates of components of variance:

The estimates of general combining ability (gca) and specific combining ability (sca) variances, degree of dominance, additive and dominance variance and predictability ratio have been presented in the Table 4.14.

Estimates of sca variances were higher than the corresponding estimates of gca variances for the traits, viz., days to 50% flowering, plant height, primary branches per plant, clusters per plant, pods per cluster, pod length, pods per plant, seeds per pod and biological yield per plant, while days to maturity, harvest-index and seed yield per plant were having higher gca variance than sca variance. The value of degree of dominance were more than unity (>1) revealing over dominance for pods per cluster,

Table 4.14: Analysis of variance for combining ability and genetic components of variance for 13 traits in mungbean in *Kharif* season

Source of variation	d.f.	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
Lines	14	574.47**	822.35**	711.67**	2.08**	5.27**	2.16**	475.89**	2.57**	11.61**	0.247**	527.07**	15.97**	47.67**
Testers	3	528.58**	2407.21**	280.95*	1.60**	0.42	0.87	93.19	2.99**	4.44	0.29**	260.24*	9.08*	26.12*
Line X Testers	42	62.78**	68.33**	84.88**	0.37*	0.57**	0.50*	58.74**	0.88**	1.96**	0.04**	65.42**	2.68	4.46**
Error	118	8.12	11.97	4.15	0.17	0.23	0.25	16.27	0.193	0.24	0.01	14.49	2.81	1.21
Variance GCA		19.12	56.24	17.29	0.06	0.09	0.05	9.45	0.09	0.27	0.01	13.27	0.33	1.25
Variance SCA		18.68	18.78	27.11	0.07	0.12	0.09	14.46	0.23	0.57	0.01	16.69	0.13	1.07
Degree of Dominance		0.73	0.41	0.96	0.83	0.86	1.10	0.95	1.31	1.16	0.78	0.85	0.43	0.68
Additive variance		38.23	112.48	34.58	0.12	0.18	0.09	18.89	0.18	0.55	0.02	26.55	0.66	2.50
Dominance variance		18.68	18.78	27.11	0.07	0.12	0.09	14.46	0.23	0.57	0.01	16.69	0.13	1.07
Heritability in Narrow sense		62.10	82.65	50.50	45.57	45.73	29.87	44.73	31.13	39.53	52.85	51.37	43.51	60.47
Predictability Ratio		0.64	0.85	0.52	0.59	0.58	0.45	0.52	0.37	0.42	0.62	0.58	1.23	0.68

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, **. Significant at 5% and 1% probability level, respectively.

pod length and seeds per pod while less than one values of degree of dominance for rest of the traits indicated existence of dominance nature. The estimates of heritability in narrow sense (h^2n) have been classified by Robinson (1966) into three categories viz., high (>30%), medium (10-30%) and low (<10%) estimates of heritability in narrow sense was not found for any of the consulting traits. The characters having high narrow sense heritability were days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pod length, pods per plant, seeds per pod, 100-seed weight, biological yield per plant, harvest-index and seed yield per plant. Pods per cluster exhibited moderate narrow sense heritability.

The predictability ratio was less than one for all the character except harvest-index reveals prepondrance of additive gene action in the study.

4.2.5.3. Estimates of general combining ability effects:

The estimates of general combining ability (gca) effects in respect of 19 parents (15 lines and 4 testers) for the 13 characters have been set out in Table 4.15.

4.2.5.3.1. Days to 50% flowering:

The parents having negative and significant values of general combining ability effects were considered as good general combiners for this character as early flowering is desirable.The desirable negative and significant gca effects were exhibited by the lines, TM 2000-2 (-1.91), MH 2-15 (-2.99), VBN (GG) 2 (-4.16), IPM 2-3 (-4.57), CoGG 8 (-5.99), LGG 460 (-6.99) and ADT 3 (-7.16) while only tester, Pant Mung 4 (-4.73) recorded desirable negative and significant gcaeffect. The undesirable positive and significant gca effects, were recorded for lines, TARM 1 (5.09), TM 96-2 (5.34) and P. Vishal (20.59) along with testers, HUM 16 (1.32) and IPM 205-7 (3.34).

Table 4.15: Estimates of general combining ability (gca) effects of parents (lines and testers) for 13 traits in mungbean in *Kharif* season

Parents	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
Lines													
CoGG 912	-1.07	0.72	13.01**	1.00**	-0.54**	-0.27	-5.00**	-0.11	2.87**	0.14**	4.48**	0.41	1.97**
MH 2-15	-2.99**	-2.87**	15.54**	0.52**	-0.01	-0.4**	-2.84*	0.90**	0.55**	0.05	0.88	-0.32	-0.01
PDM 139	1.09	1.47	-5.23**	-0.52**	0.42**	0.184	3.64**	0.29*	-0.53**	-0.16**	0.28	-0.81	-0.32
LGG 450	1.09	1.47	-5.04**	-0.52**	0.51**	0.20	4.29**	0.38**	-0.28*	-0.10**	2.42*	-0.65	0.31
ADT 3	-7.16**	-8.70**	5.77**	0.29*	0.67**	0.33*	6.13**	0.73**	-0.883**	-0.25**	6.02**	1.11*	1.98**
TARM 1	5.09**	5.63**	4.06**	0.20	0.34*	0.47**	4.91**	-0.52**	-0.27	-0.03	1.87	1.32*	0.71*
TM 96-2	5.34**	8.72**	1.01	-0.21	0.52**	0.38**	5.61**	-0.59**	0.07	-0.02	5.55**	-0.13	1.36**
P.Vishal	20.59**	23.97**	-7.09**	-0.22	0.56**	0.25	5.06**	-0.18	0.23	0.30**	8.59**	-0.36	2.27**
IPM 2-3	-4.57**	-3.12**	-0.43	0.04	0.59**	0.60**	7.49**	0.15	0.30*	0.13**	7.29**	1.47**	2.55**
HUM 12	1.01	-0.20	0.78	-0.27*	-0.08	0.23	0.58	0.01	-0.23	0.17**	0.68	0.89	0.24
VBN (GG) 2	-4.16**	-2.45*	-4.33**	0.24	0.14	0.00	0.36	0.13	0.00	-0.12**	-4.27**	-0.05	-0.30
TM 2000-2	-1.91*	-4.28**	-9.75**	-0.20	0.04	-0.03	-0.12	-0.44**	-0.68**	0.01	-0.43	-2.22**	-0.93**
LGG 460	-6.99**	-5.70**	6.37**	0.25*	-1.24**	-0.60**	-10.79**	-0.57**	-1.27**	-0.12**	-11.98**	0.31	-3.78**
Pusa 9072	0.59	-4.62**	-6.06**	-0.27*	-1.46**	-0.58**	-12.12**	0.20	-0.50**	-0.02	-10.55**	1.22*	-3.23**
CoGG 8	-5.99**	-10.03**	-8.59**	-0.35**	-0.46**	-0.70**	-7.19**	-0.39**	-1.13**	0.01	-10.82**	-2.17**	-2.81**
SE (gi)	0.75	0.10	0.54	0.12	0.13	0.14	1.13	0.13	0.14	0.03	1.13	0.51	0.32
SE (gi-gj)	1.05	1.41	0.77	0.16	0.19	0.20	1.59	0.18	0.20	0.05	1.59	0.72	0.45
Testers													
P.Mung 4	-4.73**	-10.04**	-1.19**	0.10	0.11	0.16*	1.68**	-0.35**	0.41**	-0.01	3.49**	0.45	1.01**
HUM 16	1.32**	-0.33	2.86**	-0.03	-0.06	-0.08	-0.87	-0.05	-0.35**	0.08**	-1.84**	-0.20	-0.47**
IPM 99-125	0.07	3.51**	-2.80**	-0.25**	-0.10	-0.15*	-1.48*	0.16*	0.01	-0.11**	-1.29*	-0.53*	-0.69**
IPM 205-7	3.34**	6.87**	1.14**	0.18**	0.05	0.06	0.68	0.23**	-0.07	0.03	-0.36	0.28	0.16
SE (gi)	0.39	0.52	0.28	0.06	0.07	0.07	0.58	0.07	0.07	0.02	0.58	0.26	0.17
SE (gi-gj)	0.55	0.73	0.40	0.08	0.10	0.10	0.83	0.09	0.10	0.02	0.83	0.37	0.24

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

*, **. Significant at 5% and 1% probability level, respectively.

4.2.5.3.2. Days to maturity:

The negative and significant gca effects for days to maturity were exhibited by VBN(GG)2 (-2.45), MH 2-15 (-2.87), IPM 2-3 (-3.12), TM2000-2 (-4.28), Pusa 9072 (-4.62), LGG 460 (-5.70), ADT 3 (-8.70) and CoGG 8 (-10.03) while only tester, Pant Mung 4 (-10.04) recorded desirable negative and significant gca effect. The undesirable positive and significant gca effects were recorded for TARM 1 (5.63), TM 96-2 (8.72) and P. Vishal (23.97) along with testers, IPM 99-125 (3.51) and IPM 205-7 (6.87).

4.2.5.3.3. Plant height:

The negative and significant gca effects for plant height were exhibited by VBN(GG) 2 (-4.33), LGG 450 (-5.04), PDM 139 (-5.23), Pusa 9072 (-6.06), P. Vishal (-7.09), CoGG 8 (-8.59) and TM 2000-2 (-9.75)among the lines, and Pant Mung 4(-1.19) and IPM 99- 125 (-2.80) among the testers. The undesirable positive and significant gca effects were recorded by the lines TARM 1(4.06), ADT 3(5.77), LGG 460(6.37), CoGG 912(13.01)and MH 2-15(15.54) along with testers, IPM 205-7(1.14) and HUM 16(2.86).

4.2.5.3.4. Primary branches per plant:

Among the lines the desirable significant and positive gca effects for Primary branches per plant were exhibited by the lines, VBN(GG)2 (0.24), LGG 460 (0.25), ADT 3 (0.29) and MH 2-15 (0.52) and tester, IPM 205-7 (0.18). The lines, HUM 12 (-0.27), Pusa 9072 (-0.27), CoGG 8(-0.35), PDM 139 (-0.52), and LGG 450 (-0.52) and the tester, IPM 99-125 (-0.25) had significant and negative gca effects for primary branches per plant.

4.2.5.3.5. Clusters per plant:

Among the lines, the desirable significant and positive gca effects for clusters per plant were exhibited by TARM 1 (0.34), PDM 139 (0.42), LGG 450(0.51), TM 962 (0.52), P. VISHAL (0.56), IPM 2-3 (0.59) and ADT 3(0.67). The lines, CoGG 8 (-0.46), CoGG 912(-0.54), LGG 460 (-1.24) and Pusa 9072 (-1.46) showed negative and significant gca effects for this trait. The gca effects of all four testers were non-significant for this character .

4.2.5.3.6. Pods per cluster:

The positive and significant gca effects for pods per cluster were exhibited by the lines, ADT 3 (0.33), TM 96-2 (0.38), TARM 1 (0.47) and IPM 2-3 (0.60) and tester, Pant Mung 4 (0.16). The lines, MH 2-15 (-0.48), Pusa 9072 (-0.58), LGG 460 (-0.60) and CoGG 8 (-0.70) and the tester, IPM 99-125 (-0.15) had significant and negative gca effects for pods per cluster.

4.2.5.3.7. Pods per plant:

The positive and significant gca effects for pods per plant were exhibited by the lines, PDM 139 (3.64), LGG 450(4.29), TARM 1 (4.91), P. Vishal(5.06), TM 96-2 (5.61), ADT 3 (6.013) and IPM 2-3 (7.49) and the tester, P. Mung 4 (1.68). The lines, MH 2-15 (-2.84), CoGG 912 (-5.00), CoGG 8 (-7.19), LGG 460 (-10.79) and Pusa 9072 (-12.12) along with tester, IPM 99-125 (-1.48) showed negative and significant gca effects for this trait.

4.2.5.3.8. Pod length:

Among the lines, the desirable significant and positive gca effects for pod length were exhibited by the lines, PDM 139 (0.29), LGG 450

(0.38), ADT 3 (0.73) and MH 2-15 (0.90) and the testers, IPM 99-125 (0.16) and IPM 205-7 (0.23). The lines, CoGG 912 (-0.11), CoGG 8 (-0.39), TM 2000-2 (-0.44), TARM 1 (-0.52), LGG 460 (-0.57) and TM 96-2 (-0.59) along with tester, P. Mung 4 (-0.35) showed negative and significant gca effects for this trait.

4.2.5.3.9. Seeds per pod:

The desirable significant and positive gca effects for seeds per pod were exhibited by the lines, IPM 2-3 (0.30), MH 2-15 (0.55), ADT 3 (0.88) and CoGG 912 (2.87) , while positive and significant gca effect among testers was recorded by P. Mung 4 (0.41). The tester , HUM 16 (-0.35) and lines, LGG 450 (-0.28), Pusa 9072 (-0.50), PDM 139 (-0.53), TM 2000-2 (-0.68), CoGG 8 (-1.13) and LGG 460 (-1.27) had significant and negative gca effects for seeds per pod.

4.2.5.3.10. 100-seed weight:

The desirable significant and positive gca effects for 100-seed weight were exhibited by the lines, IPM 2-3 (0.13), CoGG 912 (0.14), HUM 12 (0.17) and P. Vishal (0.30) and by the tester, HUM 16 (0.08). The lines, LGG 450 (-0.10), LGG 460(-0.12), VBN(GG)2 (-0.12), PDM 139 (-0.16) and ADT 3 (-0.25) and the tester, IPM 99-125 (-0.11) showed negative and significant gca effects for seed weight.

4.2.5.3.11. Biological yield per plant:

Among the lines, the desirable significant and positive gca effects for biological yield per plant were exhibited by LGG 450 (2.42), CoGG 912 (4.48), TM 96-2 (5.55), ADT 3 (6.02), IPM 2-3 (7.29) and P. Vishal (8.59) and the tester, P. Mung 4 (3.49). The lines, VBN(GG) 2 (-4.27), Pusa 9072 (-10.55), CoGG 8 (-10.82), LGG 460 (-11.98) and testers, IPM

99-125 (-1.29) and HUM 16 (-1.84) showed negative and significant gca effects for biomass production.

4.2.5.3.12. Harvest-index:

The desirable significant and positive gca effects for harvest-index were exhibited by the lines, ADT 3 (1.11), Pusa 9072 (1.22), TARM 1 (1.32), IPM 2-3 (1.47). The lines, CoGG 8 (-2.17) and TM 2000-2 (-2.22) and tester, IPM 99-125 (-0.53) showed negative and significant gca effects for harvest-index.

4.2.5.3.13. Seed yield per plant:

Among the lines, the desirable significant and positive gca effects for seed yield per plant were exhibited by TARM 1 (0.71), TM 96-2 (1.36), CoGG 912 (1.97), ADT 3 (1.98), P. Vishal (2.27), IPM 2-3 (2.55) and the tester, P. Mung 4 (1.01). The lines, TM 2000-2 (-0.93), Pusa 9072 (3.23) and LGG 460 (3.78) and testers, HUM 16 (-0.47) and IPM 99-125 (-0.69) showed negative and significant gca for seed yield per plant.

4.2.5.4. Estimates of specific combining ability effects:

The specific combining ability effects of the sixty crosses have been presented in Table 4.16 and the results are explained below:

4.2.5.4.1. Days to 50% flowering:

Early flowering being desirable, the negative and significant estimates of sca effects were considered desirable. The negative and significant sca effects for days to 50% flowering were exhibited by twelve crosses. The twelve crosses having high negative sca effects for days to 50% flowering in order of merit were TM 2000-2 x IPM 205-7 (-8.67), TM 96-2 x HUM 16 (-7.23), CoGG 8 x IPM 205-7 (-5.59), HUM 12 x IPM 205-7 (-5.59), IPM 2-3 x HUM 16 (-4.98), IPM 2-3 x P. Mung 4 (-4.94),

Table 4.16: Estimates of specific combining ability (sca) effects of 60 crosses for 13 traits in mungbean in *Kharif* season

Cross	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
CoGG 912 x P. MUNG 4	-4.44**	-8.87**	-14.44**	0.88**	1.24**	0.94**	13.62**	-0.46	-2.44**	0.18**	6.57**	0.44	1.76**
CoGG 912 x HUM 16	-0.82	-1.58	6.34**	-0.18	-0.32	0.51	-0.77	-0.62*	1.52**	0.07	8.60**	0.92	2.13**
CoGG 912 x IPM 99-125	0.76	0.91	-0.16	-0.30	-0.68*	-0.89**	-8.33	1.11**	2.09**	-0.24**	-4.52*	-2.13*	-1.61*
CoGG 912 x IPM 205-7	4.49**	9.55**	8.26**	-0.40	-0.23	-0.56	-4.52*	-0.03	-1.16**	-0.02	-10.65**	0.77	-2.28**
MH 2-15 x P.MUNG 4	-0.86	-1.29	10.53**	1.16**	-0.23	-0.11	-1.41	0.97**	1.54**	-0.09	1.49	1.71	1.15
MH 2-15 x HUM 16	-2.90	1.00	4.08**	-0.23	-0.26	-0.67*	-5.33*	0.04	-0.50	0.26**	-2.85	-0.75	-1.23
MH 2-15 x IPM 99-125	0.34	0.16	4.87**	-0.22	0.58*	0.53	6.35**	-0.23	-0.53	-0.22**	1.44	-0.31	0.49
MH 2-15 x IPM 205-7	3.41*	0.13	-19.47**	-0.71**	-0.10	0.26	0.39	-0.77**	-0.51	0.04	-0.09	-0.64	-0.42
PDM 139 x P. MUNG 4	3.06*	3.38	1.14	-0.20	-0.06	0.09	0.18	0.75	-0.31	-0.01	-2.23	-0.06	-0.54
PDM 139 x HUM 16	0.35	4.00*	-2.75*	-0.20	-0.02	0.33	1.85	-0.96**	0.52	-0.09	2.73	0.47	0.80
PDM 139 x IPM 99-125	-2.74	-3.18	0.98	0.08	-0.18	-0.47	-3.93	0.37	-0.18	0.07	-2.75	-0.09	-0.65
PDM 139 x IPM 205-7	-0.67	-4.20*	0.64	0.32	0.27	0.06	1.91	-0.16	-0.03	0.03	2.25	-0.32	0.40
LGG 450 x P. MUNG 4	3.06	3.38	1.04	-0.20	-0.01	0.07	0.53	0.66	-0.29	-0.01	-1.91	-0.14	-0.40
LGG 450 x HUM 16	0.35	4.00*	-2.94**	-0.20	0.09	-0.09	0.07	-0.70**	-0.07	-0.15*	-1.51	0.64	-0.41
LGG 450 x IPM 99-125	-2.74	-3.18	0.79	0.08	-0.13	0.31	1.02	0.29	0.84**	-0.03	4.3	0.05	1.40*
LGG 450 x IPM 205-7	-0.67	-4.20*	1.11	0.32	0.05	-0.29	-1.61	-0.25	-0.48	0.19**	-0.89	-0.55	-0.59
ADT 3 x P. MUNG 4	0.64	4.54*	0.84	0.06	6.67	0.34	3.76	0.50	0.27	0.18**	4.89*	0.38	1.95**
ADT 3 x HUM 16	1.27	-0.17	-1.28	-0.20	6.40	-0.29	-0.90	0.44	-0.10	-0.24**	-3.21	0.50	-1.07
ADT 3 x IPM 99-125	-2.49	-3.01	-0.16	0.08	5.93	0.25	-0.68	-0.01	-0.86	0.09	-4.19	0.23	-1.11
ADT 3 x IPM 205-7	0.58	-1.37	0.60	0.05	6.33	-0.29	-2.18	-0.94**	0.69*	-0.02	2.51	-1.10	0.23
TARM 1 x P. MUNG 4	-3.61*	-5.79**	1.58	-0.19	5.47	-0.53	-7.49**	-0.41	-0.91**	-0.04	-10.62**	0.50	-3.02**
TARM 1 x HUM 16	-0.98	0.50	4.73**	0.22	6.07	-0.42	-1.88	0.33	0.58*	-0.02	1.34	-0.15	0.23
TARM 1 x IPM 99-125	1.59	1.66	-2.48*	-0.10	6.67	0.65*	9.33**	-0.38	-0.04	0.07	7.22**	-0.34	2.25**
TARM 1 x IPM 205-7	2.99*	3.63	-3.82**	0.07	5.80	0.31	0.04	0.45	0.37	-0.01	2.06	-0.01	0.54
TM 96-2 x P. MUNG 4	11.14**	8.13**	3.23**	-0.41	6.87	0.09	4.48	-0.34	-0.11	0.04	4.59*	-1.71	0.99
TM 96-2 x HUM 16	-7.23**	-3.25	-4.26**	0.09	6.20	-0.01	0.48	-0.01	-0.35	0.06	-1.11	0.95	-0.21
TM 96-2 x IPM 99-125	-1.99	-2.09	-3.06**	0.31	5.60	-0.20	-4.43	0.12	0.36	-0.02	-2.69	0.26	-0.49
TM 96-2 x IPM 205-7	-1.92	-2.78	4.09**	0.01	6.07	0.12	-0.53	0.22	0.11	-0.09	-0.79	0.49	-0.30
P. Vishal x P. MUNG 4	-4.11**	-5.12*	0.56	-0.04	6.13	-0.31	-3.31	-0.45	-0.14	0.03	-3.12	-0.52	-0.95
P. Vishal x HUM 16	-2.15	-1.50	-6.72**	-0.03	5.87	-0.07	-2.43	-0.21	-0.18	0.05	-1.25	-0.96	-0.82
P. Vishal x IPM 99-125	2.76	1.66	4.14**	0.18	6.13	0.06	0.32	0.55*	-0.14	-0.07	-1.74	0.59	-0.22
P. Vishal x IPM 205-7	3.49*	4.97*	2.03	-0.11	6.73	0.32	5.43*	0.11	0.47	-0.01	6.10**	0.89	1.99**

Contd…..

Table 4.16: Contd…..

Cross	D50%f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-SW	BY/P	HI	SY/P
IPM 2-3 x P.MUNG 4	-4.94**	-4.04*	-2.43*	-0.15	6.33	-0.40	-2.54	-0.45	0.59*	-0.13	-0.85	-0.27	-0.12
IPM 2-3 x HUM 16	-4.98**	-4.75*	-1.48	0.12	6.8	0.31	6.13**	0.15	0.08	-0.01	4.07	0.53	1.45*
IPM 2-3 x IPM 99-125	1.26	-1.59	1.88	0.07	5.67	-0.09	-4.05	-0.22	-0.74**	0.08	-6.50**	0.69	-1.80**
IPM 2-3 x IPM 205-7	8.66**	10.38**	2.04	-0.03	6.20	0.17	0.46	0.51	0.07	0.07	3.27	-0.95	0.46
HUM 12 x P. MUNG 4	0.48	2.38	1.53	-0.39	5.87	-0.23	-0.16	-0.17	0.86**	-0.041	2.30	0.12	0.99
HUM 12 x HUM 16	-0.57	-5.67**	0.41	0.02	5.27	0.08	-1.22	0.23	-0.58*	-0.02	-3.70	0.92	-1.11
HUM 12 x IPM 99-125	5.68**	3.82	-1.06	0.03	5.40	0.15	0.20	-0.28	0.26	-0.07	0.88	-0.22	0.35
HUM 12 x IPM 205-7	-5.59**	-0.53	-0.87	0.34	5.80	0.01	1.18	0.22	-0.53	0.13	0.52	-0.82	-0.24
VBN (GG)2 x P. MUNG 4	-2.69	-3.37	-1.17	-0.22	5.67	-0.26	-3.08	-0.13	0.89**	-0.05	2.24	1.73	0.14
VBN (GG)2 x HUM 16	1.60	1.92	1.02	0.12	5.87	-0.02	0.27	-0.20	0.05	0.04	-8.20**	-2.34	0.32
VBN (GG)2 x IPM 99-125	0.84	2.07	0.01	-0.20	5.67	-0.15	-1.05	0.17	-0.58*	0.16*	1.56	0.21	-0.51
VBN (GG)2 x IPM 205-7	0.24	-0.62	0.14	0.30	6.00	0.44	3.86	0.16	-0.36	-0.15*	4.40	0.40	0.06
TM 2000-2 x P. MUNG 4	2.06	4.13*	-4.22**	-0.25	5.47	-0.10	-2.80	-0.02	0.51	0.02	-0.59	-0.03	-0.06
TM 2000-2 x HUM 16	4.02**	2.75	1.57	0.28	5.87	0.41	3.88	0.01	-0.73*	-0.06	-0.26	-0.47	-0.31
TM 2000-2 x IPM 99-125	2.59	0.91	3.13**	0.23	6.07	-0.05	2.57	-0.39	-0.03	0.06	2.42	-0.19	0.82
TM 2000-2 x IPM 205-7	-8.67**	-7.78**	-0.48	-0.26	5.40	-0.26	-3.66	0.40	0.26	-0.02	-1.57	0.69	-0.45
LGG 460 x P. MUNG 4	-1.52	-3.12	3.67**	0.03	5.13	0.20	4.34	-0.06	-0.51	-0.15*	-0.97	-0.48	-0.25
LGG 460 x HUM 16	-1.57	-0.17	-0.31	0.10	4.07	0.11	-0.92	0.17	-0.22	0.01	0.15	-1.07	-0.21
LGG 460 x IPM 99-125	0.68	3.32	-4.62**	-0.02	4.47	-0.29	-0.23	0.27	0.22	0.13	0.97	0.73	0.63
LGG 460 x IPM 205-7	2.41	-0.03	1.27	-0.11	4.00	-0.03	-3.19	-0.37	0.51	0.02	-0.16	0.82	-0.18
Pusa 9072 x P. Mung 4	-3.44*	-1.54	-2.94**	-0.12	3.80	0.39	-1.93	-0.30	0.06	0.04	-2.07	-0.86	-0.61
Pusa 9072 x HUM16	9.52**	4.75*	-1.52	-0.25	4.33	-0.57*	-0.92	0.64*	0.22	0.06	1.05	0.01	0.22
Pusa 9072 x IPM 99-125	-2.91	1.24	0.44	0.23	4.20	0.30	2.17	-0.47	-0.34	-0.05	0.17	0.68	0.29
Pusa 9072 x IPM 205-7	-3.17*	-4.45*	4.03**	0.14	4.47	-0.11	0.68	0.13	0.07	-0.06	0.85	0.17	0.11
CoGG 8 x P.MUNG 4	5.14**	7.21**	1.09	0.03	4.73	-0.16	-4.19	-0.11	0.02	0.03	0.26	-0.81	-1.04
CoGG 8 x HUM 16	4.10**	-1.83	3.11**	0.37	5.00	0.41	1.68	0.70**	-0.22	0.05	4.15	0.82	0.23
CoGG 8 x IPM 99-125	-3.66*	-2.68	-4.66**	-0.48*	5.40	-0.12	0.77	-0.91**	-0.31	0.04	3.41	-0.17	0.15
CoGG 8 x IPM 205-7	-5.59**	-2.70	0.46	0.09	5.67	-0.13	1.74	0.32	0.51	-0.11	-7.82**	0.15	0.66
SE (Sij-Skl)	2.11	2.82	1.53	0.65	0.38	0.40	3.19	0.36	0.39	0.09	3.19	1.43	0.91

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).
*, **.Significant at 5% and 1% probability level, respectively.

CoGG 912 x P. Mung 4 (4.44), P.Vishal x P. Mung 4 (-4.11), CoGG 8 x IPM 205-7 (-3.66), TARM 1 x P. Mung 4 (-3.61), Pusa 9072 x P. Mumg (-3.44) and Pusa 9072 x IPM 205-7 (-3.17). The undesirable positive and significant sca effects were recorded for twelve crosses. viz., CoGG 8 x HUM 16, CoGG 8 x P. Mung 4, Pusa 9072 x HUM 16 , TM 2000-2 x HUM 16, HUM 12 x IPM 99-125, IPM 2-3 x IPM 205-7, P. Vishal x IPM 205-7, TM 96-2 x P. Mung 4, TARM1x IPM 205-7, PDM 139 x P. Mung 4, MH 2-15 x IPM 205-7 and CoGG 912 x IPM 205-7.

4.2.5.4.2. Days to maturity:

Ten crosses possessed negative and significant sca effects for days to maturity and these promising ten cross combinations for early maturity were CoGG 912 x P. Mung 4 (-8.87), TM 2000-2 x IPM 205-7 (-7.78), TARM 1 x P. Mung 4 (-5.79), HUM 12 x HUM 16 (-5.67), P. Vishal x P. Mung 4 (-5.12), IPM 2-3 x HUM 16 (-4.75), Pusa 9072 x IPM 205-7 (-4.45), PDM 139 x IPM 205-7 (-4.20), LGG 450 x IPM 205-7 (-4.20) and IPM 2-3 x P. Mung 4 (-4.04). The positive and significant sca effects were recorded for ten crosses, viz., CoGG 8 x P. Mung 4, Pusa 9072 x HUM 16, TM 2000-2 x P. Mung 4, IPM 2-3 x IPM 205-7, P. Vishal x IPM 205-7, TM 96-2 x P. Mung 4, ADT 3 x P. Mung 4, LGG 450 x HUM 16, PDM 139 x HUM 16 and CoGG 912 x IPM 205-7.

4.2.5.4.3. Plant height:

For plant height, fourteen crosses showed negative and significant sca effects, which were MH 2-15 x IPM 205-7 (-19.47), CoGG 912 x P. Mung 4 (-14.44), P. Vishal x HUM 16 (-6.72), CoGG 8 x IPM 99-125(-4.66), LGG 460 x IPM 99-125(-4.62), TM 96-2 x HUM 16 (-4.26), TM 2000-2 x P. Mung 4 (-4.22), TARM 1 x IPM 205-7 (-3.82), TM 96-2 x

IPM 99-125 (-3.06), Pusa 9072 x P. Mung 4 (-2.94), LGG 450 x HUM 16 (-2.94), PDM 139 x HUM 16 (-2.75), TARM 1 x IPM 99-125 (-2.48) and IPM 2-3 x P. Mung 4 (-2.43). The positive and significant sca effects were recorded for eight crosses, viz., CoGG 8 x HUM 16, Pusa 9072 x IPM 205-7, LGG 460 x P. Mung 4 , TM 2000-2 x IPM 99-125, P. Vishal x IPM 99-125, TM 96-2 x P. Mung 4, TM 96-2 x IPM 205-7 and TARM 1 x HUM 16.

4.2.5.4.4. Primary branches per plant:

For primary branches per plant , two crosses showed positive and significant sca effects , which were CoGG 912 x P. MUNG 4 (0.88) and MH 2-15 x P. Mung 4 (1.16). The negative and significant sca effects were also recorded for two crosses, namely, MH 2-15 x IPM 205-7 and CoGG 8 x IPM 99-125.

4.2.5.4.5. Clusters per plant:

Two crosses possessed positive and significant sca effects for clusters per plant and these promising crosses were CoGG 912 x P. Mung 4 (1.24) and MH 2-15 x IPM 99-125 (0.58) . The negative and significant sca effects were recorded only for CoGG 912 x IPM 99-125 (-0.68).

4.2.5.4.6. Pods per cluster:

For number of pods per cluster, two crosses showed positive and significant sca effects, which were TARM 1 x IPM 99-125 (0.65) and CoGG 912 X P. Mung 4 (0.94). The negative and significant sca effects were recorded for three crosses, namely, Pusa 9072 x HUM 16, MH 2-15 x HUM 16 and CoGG 912 x IPM 99-125.

4.2.5.4.7. Pods per plant:

Five crosses possessed positive and significant sca effects for pods per plant and these promising five cross combinations were CoGG 912 x P.

Mung 4 (13.62), TARM 1 x IPM 99-125 (9.33), MH 2-15 x IPM 99-125 (6.35), IPM 2-3 x HUM 16 (6.13) and P. Vishal x IPM 205-7 (5.43). The negative and significant sca effects were recorded for three crosses, namely, TARM 1 x P. Mung 4, MH 2-15 x HUM 16 and CoGG 912 x IPM 205-7.

4.2.5.4.8. Pod length:

Five crosses possessed positive and significant sca effects for pod length and these promising five cross combinations were CoGG 912 x IPM 99-125 (1.11), MH 2-15 x P. Mung 4 (0.97), CoGG 8 x HUM 16 (0.70), Pusa 9072 x HUM 16 (0.64) and P. Vishal x IPM 99-125 (0.55). The negative and significant sca effects were recorded for six crosses, namely, CoGG 912 x HUM 16, MH 2-15 x IPM 205-7, PDM 139 x HUM 16, LGG 450x HUM 16, ADT 3 x IPM 205-7 and CoGG 8 x IPM 99-125.

4.2.5.4.9. Seeds per pod:

Nine crosses recording positive and significant sca effects for seeds per pod were CoGG 912 x IPM 99-125 (2.09), MH 2-15 x P. Mung 4 (1.54), CoGG 912 x HUM 16 (1.52), VBN (GG) 2 x P. Mung 4 (0.89), HUM12 x P. Mung 4 (0.86), LGG 450 x IPM 99-125 (0.84), ADT 3 x IPM 205-7(0.69), IPM 2-3 x P.Mung 4 (0.59) and TARM1 x HUM 16 (0.58). The negative and significant sca effects were recorded for seven crosses which were CoGG 912 x P. Mung 4, CoGG 912 x IPM 205-7, TARM 1 x P. Mung 4, IPM 2-3 x IPM 99-125, HUM 12 x HUM 16, VBN(GG) 2 x IPM 99-125 and TM 2000-2 x HUM 16.

4.2.5.4.10. 100-seed weight:

The positive and significant sca effects for 100- seed weight were exhibited by five crosses which were MH 2-15 x HUM 16, (0.26), LGG 450 x IPM 205-7 (0.19), CoGG 912 x P. Mung 4 (0.18), ADT 3 x P.Mumg

4 (0.18) and VBN(GG)2 x IPM 99-125 (0.16). The negative and significant sca effects were shown by six crosses, namely, CoGG 912 x IPM 99-125, MH 2-15 x IPM 99-125, LGG 450 x HUM 16, ADT 3 x HUM 16, VBN(GG)2 x IPM 205-7 and LGG 460 x P. Mung 4.

4.2.5.4.11. Biological yield per plant:

The positive and significant sca effects for biological yield per plant were exhibited by six crosses which were CoGG 912 x HUM 16 (8.60), TARM 1 x IPM 99-125 (7.22), CoGG 912 x P. Mung 4 (6.57), P. Vishal x IPM 205-7 (6.10), ADT 3 x P. Mung 4 (4.89) and TM 96-2 x P. Mung 4 (4.59). The negative and significant sca effects were shown also by six crosses, namely, CoGG 912 x IPM 99-125, CoGG 912 x IPM 205-7, TARM 1 x P. Mung 4, IPM 2-3 x IPM 99-125, VBN(GG) 2 x HUM 16 and CoGG 8 x IPM 205-7.

4.2.5.4.12. Harvest-index:

The negative and significant sca effects were shown by only two crosses, namely, VBN(GG)2 x HUM 16 (-2.34) and CoGG 912 x IPM 99-125 (-2.13). Among all sixty crosses, none of the crosses were found with significant and positive effects for harvest-index.

4.2.5.4.13. Seed yield per plant:

The positive and significant sca effects for seed yield per plant were exhibited by seven crosses which were TARM 1 x IPM 99-125 (2.25), CoGG 912 x HUM 16 (2.13), P. Vishal x IPM 205-7 (1.99), ADT 3 x P. Mung 4 (1.95), CoGG 912 x P. Mung 4 (1.76), IPM 2-3 x HUM 16 (1.45) and LGG 450 x IPM 99-125 (1.40). The negative and significant sca effects were shown by four crosses, namely, TARM 1 x P. Mung 4, CoGG 912 x IPM 205-7, IPM 2-3 x IPM 99-125 and CoGG 912 x IPM 99-125.

4.2.5.5. Proportional contribution of lines, testers and line x tester interactions:

Proportional contribution of lines, testers and line x tester interactions for thirteen characters have been presented in Table 4.17. The maximum contribution of females (lines) was recorded for clusters per plant (74.58), followed by seed yield per plant (71.52), pods per plant (70.81), plant height (69.33), biological yield per plant (67.65), days to 50% flowering (65.57), seeds per pod (63), harvest-index (61.47), primary branches per plant (58.89), 100-seed weight (56.62), pods per cluster (56.10) anddays to maturity (53.29). The lowest contribution of lines was recorded for pod length (43.81).

Maximum contribution of males (testers) was recorded for days to maturity (33.43%), followed by100-seed weight (14.22%), days to 50% flowering (12.93), pod length (10.95%), primary branches per plant (9.71%), seed yield per plant (8.40%), harvest-index (7.49%), biological yield per plant (7.16%), plant height (5.86%), seeds per pod (5.17%), pods per cluster (4.85%) and pods per plant (2.97). The lowest contribution of males was recorded for clusters per plant (1.28%).

Proportional contribution of lines x testers was found maximum for the character pod length (45.23%), followed by pods per cluster (39.06%), seeds per pod (31.83%), primary branches per plant (31.40%), harvest-index (31.04%), 100-seed weight (29.16%), pods per plant (26.22%), biological yield per plant (25.19%), plant height (24.81%), clusters per plant (24.14%), days to 50% flowering (21.50%) and seed yield per plant (20.08%). The lowest contribution of lines x testers interactions was recorded for days to maturity (13.29%).

Table 4.17: Contribution of lines, testers and their interactions to the total variance for 13 traits in mungbean in *Kharif* season

Traits	Contribution (%)		
	Lines	**Testers**	**Lines x testers**
D50%f	65.57	12.93	21.50
DM	53.29	33.43	13.29
PH	69.33	5.86	24.81
PB/P	58.89	9.71	31.40
C/P	74.58	1.28	24.14
P/C	56.10	4.85	39.06
P/P	70.81	2.97	26.22
PL	43.81	10.95	45.23
S/P	63	5.17	31.83
100-SW	56.62	14.22	29.16
BY/P	67.65	7.16	25.19
HI	61.47	7.49	31.04
SY/P	71.52	8.40	20.08

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

4.2.6. Estimates of heterosis over better-parent and standard variety:

Heterosis was estimated as per cent increase or decrease of F_1 value over better-parent (BP) and standard variety, Pant Mung 5 (SV) for all the thirteen characters. The estimates of heterobeltiosis and standard heterosis for thirteen characters of sixty crosses are presented in Table 4.18. The character-wise results are described as follows:

4.2.6.1. Days to 50% flowering:

For days to 50% flowering, the heterosis over better-parent ranged from -38.32% (CoGG 8 x IPM 99-125) to 26.72% (Pusa 9072 x HUM 16). The heterosis over standard variety SV (Pant Mung 5) ranged from -19.09% (IPM 2-3 x P. Mung 4) to 94.55% (P. Vishal x IPM 205-7).

Twenty-seven hybrids showed negative and significant heterosis while six hybrids showed positive and significant heterosis over better-parent. On the other hand, thirty-seven hybrids showed positive and three hybrids showed negative and significant heterosis over SV.

The best five hybrids exhibiting significant heterosis in desirable direction for days to 50% flowering were CoGG 8 x IPM 99-125 (-38.32%), ADT 3 x IPM 99-125 (-38.32%), LGG 460 x IPM 99-125 (-32.34%), VBN(GG)2 x IPM 99-125 (-26.95%) and IPM 2-3 x IPM 99-125 (-26.95%) over BP and IPM 2-3 x P. Mung 4 (-19.09%), LGG 460 x P. Mung 4 (-16.36%), VBN(GG)2 x P. Mung 4 (-11.82%), ADT 3 x P. Mung 4 (-10.91%) and CoGG 912 x P. Mung 4 (-8.18%) over SV.

4.2.6.2. Days to maturity:

For days to maturity, the heterosis over better-parent (BP) ranged from -27.53% (CoGG 8 x IPM 99-125) to 18.28% (P. Vishal x IPM 205-7). The heterosis over standard variety (Pant Mung 5) ranged from -12.68 % (LGG 460 x P. Mung 4) to 67.32 % (P. Vishal x IPM 205-7).

Table 4.18: Estimates of heterobeltiosis and Standard heterosis for 13 traits in mungbean in *Kharif* season

Cross	D 50%f		DM		PH		PB/P	
	BP	SV	BP	SV	BP	SV	BP	SV
CoGG 912 x P. MUNG 4	-1.94	-8.18	-3.21	-11.71**	-38.20**	-13.18**	0	-5.81
CoGG 912 x HUM 16	-0.76	18.18**	-7.20*	13.17**	6.90*	50.17**	-13.70*	-26.74**
CoGG 912 x IPM 99-125	-21.56**	19.09**	-12.54**	22.44**	-15.19**	19.13**	-20.55**	-32.56**
CoGG 912 x IPM 205-7	16.03**	38.18**	4.36	40.00**	7.26*	50.68**	-13.70*	-26.74**
MH 2-15 x P.MUNG 4	-0.93	-3.64	-2.03	-5.85	6.89*	56.97**	-3.7	-9.3
MH 2-15 x HUM 16	-9.92*	7.27	-8.40*	11.71**	2.72	50.85**	-21.43**	-36.05**
MH 2-15 x IPM 99-125	-25.75**	12.73*	-17.07**	16.10**	-5.73*	38.44**	-25.71**	-39.53**
MH 2-15 x IPM 205-7	9.16	30.00**	-9.82**	20.98**	-41.17**	-13.61**	-27.14**	-40.70**
PDM 139 x P. MUNG 4	-8.45	18.18**	-7.56*	7.32	-7.84	-19.98**	-48.15**	-51.16**
PDM 139 x HUM 16	-1.41	27.27**	0.4	22.44**	-25.04**	-19.56**	-16.67	-53.49**
PDM 139 x IPM 99-125	-23.95**	15.45**	-16.03**	17.56**	-11.02*	-24.49**	-12.77	-52.33**
PDM 139 x IPM 205-7	0.7	30.00**	-9.82**	20.98**	-10.19*	-15.31**	-12.07	-40.70**
LGG 450 x P. MUNG 4	19.27**	18.18**	13.99**	7.32	-7.54	-19.73**	-48.15**	-51.16**
LGG 450 x HUM 16	6.87	27.27**	0.4	22.44**	-25.04**	-19.56**	-20.00*	-53.49**
LGG 450 x IPM 99-125	-23.95**	15.45**	-16.03**	17.56**	-11.02*	-24.49**	-18	-52.33**
LGG 450 x IPM 205-7	9.16	30.00**	-9.82**	20.98**	-8.39*	-13.61**	-12.07	-40.70**
ADT 3 x P. MUNG 4	-13.27*	-10.91	-0.52	-5.85	-9.47**	7.31	-28.40**	-32.56**
ADT 3 x HUM 16	-9.92*	7.27	-16.80**	1.46	-5.31	12.24**	-10.34	-39.53**
ADT 3 x IPM 99-125	-38.32**	-6.36	-26.48**	2.93	-15.06**	0.68	-8.62	-38.37**
ADT 3 x IPM 205-7	-6.87	10.91	-17.82**	10.24*	-4.95	12.67**	1.72	-31.40**
TARM 1 x P. MUNG 4	-23.75**	10.91	-15.98**	0	0	4.85	-34.57**	-38.37**
TARM 1 x HUM 16	-7.5	34.55**	1.2	23.41**	14.82**	23.21**	18.75	-33.72**
TARM 1 x IPM 99-125	-8.98*	38.18**	-6.62*	30.73**	-13.79**	-9.61*	4.26	-43.02**
TARM 1 x IPM 205-7	3.75	50.91**	3.27	38.54**	-7.46*	-2.98	0	-32.56**
TM 96-2 x P. MUNG 4	1.83	51.82**	-7.91*	24.88**	16.65**	1.28	-46.30**	-49.42**
TM 96-2 x HUM 16	-20.73**	18.18**	-9.71**	22.44**	-13.79**	-7.48	2.08	-43.02**
TM 96-2 x IPM 99-125-	-14.97**	29.09**	-7.32*	29.76**	-4.41	-18.88**	4.26	-43.02**
TM 96-2 x IPM 205-7	-7.32	38.18**	-1.44	33.66**	16.05**	9.44*	-12.07	-40.70**
P. Vishal x P. MUNG 4	-11.17**	51.82**	-9.66**	27.80**	-14.99**	-26.19**	-39.51**	-43.02**
P. Vishal x HUM 16	1.6	73.64**	4.14	47.32**	-38.91**	-34.44**	-2.08	-45.35**
P. Vishal x IPM 99-125	7.45*	83.64**	11.38**	57.56**	-7.11	-21.17**	0	-45.35**

Contd…..

Table 4.18: Contd…..

Cross	D 50%f		DM		PH		PB/P	
	BP	**SV**	**BP**	**SV**		**BP**	**SV**	**BP**
P. Vishal x IPM 205-7	13.83**	94.55**	18.28**	67.32**	-11.45**	-16.50**	-15.52	-43.02**
IPM 2-3 x P.MUNG 4	-11	-19.09**	-1.6	-10.24*	-4.21	-16.84**	-37.04**	-40.70**
IPM 2-3 x HUM 16	-18.32**	-2.73	-15.60**	2.93	-10.62**	-4.08	-22.06**	-38.37**
IPM 2-3 x IPM 99-125	-26.95**	10.91	-19.16**	13.17**	6.11	-9.95*	-27.94**	-43.02**
IPM 2-3 x IPM 205-7	17.56**	40.00**	1.09	35.61**	6.58	0.51	-20.59**	-37.21**
HUM 12 x P. MUNG 4	-12.23**	10.91	-10.92**	3.41	10.97*	-3.66	-46.91**	-50.00**
HUM 12 x HUM 16	-1.44	24.55**	-13.20**	5.85	-3.25	3.83	-9.62	-45.35**
HUM 12 x IPM 99-125	-8.98*	38.18**	-10.45**	25.37**	0.9	-14.37**	-15.38	-48.84**
HUM 12 x IPM 205-7	-7.91	16.36**	-7.64*	23.90**	1.98	-3.83	-5.17	-36.05**
VBN (GG)2 x P. MUNG 4	-6.73	-11.82*	-7.39	-8.29*	-11.95**	-23.55**	-34.57**	-38.37**
VBN (GG)2 x HUM 16	-2.29	16.36**	-6.80*	13.66**	-13.95**	-7.65	5.66	-34.88**
VBN (GG)2 x IPM 99-125	-26.95**	10.91	-14.63**	19.51**	-11.22*	-24.66**	-9.43	-44.19**
VBN (GG)2 x IPM 205-7	-0.76	18.18**	-10.18**	20.49**	-9.11*	-14.29**	6.9	-27.91**
TM 2000-2 x P. MUNG 4	-7.81	7.27	-3.3	0	-36.83**	-45.15**	-43.21**	-46.51**
TM 2000-2 x HUM 16	8.4	29.09**	-8.00*	12.20**	-25.52**	-20.07**	8.33	-39.53**
TM 2000-2 x IPM 99-125	-19.76**	21.82**	-17.77**	15.12**	-18.14**	-30.53**	2.13	-44.19**
TM 2000-2 x IPM 205-7	-16.03**	0	-20.00**	7.32	-25.43**	-29.68**	-18.97*	-45.35**
LGG 460 x P. MUNG 4	-14.02*	-16.36**	-7.73	-12.68**	-13.83**	16.07**	-29.63**	-33.72**
LGG 460 x HUM 16	-16.03**	0	-13.20**	5.85	-13.70**	16.24**	5.66	-34.88**
LGG 460 x IPM 99-125	-32.34**	2.73	-16.72**	16.59**	-32.58**	-9.18*	-3.77	-40.70**
LGG 460 x IPM 205-7	-2.29	16.36**	-13.09**	16.59**	-13.95**	15.90**	-3.45	-34.88**
Pusa 9072 x P. Mung 4	-16.15**	-0.91	-13.82**	-8.78*	-22.23**	-32.48**	-41.98**	-45.35**
Pusa 9072 x HUM16	26.72**	50.91**	-6	14.63**	-24.09**	-18.54**	-10.42	-50.00**
Pusa 9072 x IPM 99-125	-25.15**	13.64*	-17.77**	15.12**	-15.13**	-27.98**	0	-45.35**
Pusa 9072 x IPM 205-7	2.29	21.82**	-16.73**	11.71**	-3.25	-8.76*	-10.34	-39.53**
CoGG 8 x P.MUNG 4	-14.18**	4.55	-10.86**	-3.9	-17.83**	-28.66**	-40.74**	-44.19**
CoGG 8 x HUM 16	-2.29	18.18**	-20.40**	-2.93	-19.10**	-13.18**	6.25	-40.70**
CoGG 8 x IPM 99-125	-38.32**	-6.36	-27.53**	1.46	-38.08**	-47.45**	-25.53*	-59.30**
CoGG 8 x IPM 205-7	-20.15	-2.73	-20.73**	6.34	-19.75**	-24.32**	-13.79	-41.86**
"+ve" het	15	49	10	51	13	19	16	0
"-ve" het	45	11	50	9	47	41	44	60
Range	-38.32–26.72%	-19.09–94.55%	-27.53–18.28%	-12.68–67.32%	-38.91–16.65%	-47.45–56.97%	-48.15–18.75%	-59.30- 5.81%

Contd…..

Table 4.18: Contd…..

Cross	C/P		P/C		P/P		PL	
	BP	**SV**	**BP**	**SV**	**BP**	**SV**	**BP**	**SV**
CoGG 912 x P. MUNG 4	1.04	-3.96	0.94	9.18	17.83*	4.99	-29.39**	-14.75**
CoGG 912 x HUM 16	-19.32**	-29.70**	-8.49	-1.02	-25.30**	-33.43**	-27.86**	-12.90*
CoGG 912 x IPM 99-125	-22.62**	-35.64**	-29.25**	-23.47**	-46.11**	-51.98**	-5.73	13.82**
CoGG 912 x IPM 205-7	-11.9	-26.73**	-21.70**	-15.31*	-30.90**	-38.43**	-17.94**	-0.92
MH 2-15 x P.MUNG 4	-13.54*	-17.82**	-1.12	-10.2	-12.41	-24.21**	21.13**	18.89**
MH 2-15 x HUM 16	-9.09	-20.79**	-13.64*	-22.45**	-21.55*	-38.88**	-1.24	10.14*
MH 2-15 x IPM 99-125	4.55	-8.91	10.71	-5.1	15.38	-13.77	10.75*	9.22
MH 2-15 x IPM 205-7	-4.55	-16.83**	9.52	-6.12	3.85	-22.39**	-9.72*	2.76
PDM 139 x P. MUNG 4	-4.17	-8.91	13.48*	3.06	8.74	-5.9	3.1	7.37
PDM 139 x HUM 16	2.27	-10.89	14.77*	3.06	18.25	-7.87	-21.07**	-11.98*
PDM 139 x IPM 99-125	4.82	-13.86*	0	-10.2	5.34	-22.39**	4.87	9.22
PDM 139 x IPM 205-7	15.68*	-4.95	12.5	1.02	29.98**	-4.24	-9.72*	2.76
LGG 450 x P. MUNG 4	-2.08	-6.93	13.48*	3.06	11.36	-3.63	23.94**	7.37
LGG 450 x HUM 16	5.68	-7.92	7.95	-3.06	14.95	-10.44	-16.94**	-7.37
LGG 450 x IPM 99-125	7.23	-11.88*	26.58**	2.04	36.61**	-9.68	10.75	9.22
LGG 450 x IPM 205-7	13.25	-6.93	11.9	-4.08	35.01**	-10.74	-9.72*	2.76
ADT 3 x P. MUNG 4	-1.96	-0.99	9.18	9.18	6.58	7.87	3.91	10.14*
ADT 3 x HUM 16	-5.88	-4.95	-4.08	-4.08	-9.57	-8.47	1.65	13.36**
ADT 3 x IPM 99-125	-12.75*	-11.88*	3.06	3.06	-10.46	-9.38	3.91	10.14*
ADT 3 x IPM 205-7	-6.86	-5.94	-2.04	-2.04	-8.97	-7.87	-13.77**	-1.84
TARM 1 x P. MUNG 4	-14.58*	-18.81**	7.87	-2.04	-8.04	-20.42**	-5.95	-19.82**
TARM 1 x HUM 16	0	-9.9	5.62	-4.08	5.54	-13.46	-15.29**	-5.53
TARM 1 x IPM 99-125	9.89	-0.99	22.47**	11.22	34.87**	10.59	-11.21*	-12.44*
TARM 1 x IPM 205-7	-4.4	-13.86*	20.22**	9.18	15.13	-5.6	-12.15**	0
TM 96-2 x P. MUNG 4	7.29	1.98	2.97	6.12	10.84	8.32	-5.95	-19.82**
TM 96-2 x HUM 16	-3.13	-7.92	-1.98	1.02	-4.33	-6.51	-20.25**	-11.06*
TM 96-2 x IPM 99-125-	-12.50*	-16.83**	-5.94	-3.06	-17.18*	-19.06**	-5.14	-6.45
TM 96-2 x IPM 205-7	-5.21	-9.9	1.98	5.1	-3.1	-5.3	-15.79**	-4.15
P. Vishal x P. MUNG 4	-4.17	-8.91	7.87	-2.04	3.32	-10.59	-14.88**	-15.67**
P. Vishal x HUM 16	0	-12.87*	9.09	-2.04	9.9	-14.37	-17.77**	-8.29
P. Vishal x IPM 99-125	6.98	-8.91	24.36**	-1.02	38.75**	-9.53	6.05	5.07
P. Vishal x IPM 205-7	17.44**	0	23.81**	6.12	64.04**	6.96	-12.15**	0

Contd…..

Table 4.18: Contd…..

Cross	C/P		P/C		P/P		PL	
	BP	**SV**	**BP**	**SV**	**BP**	**SV**	**BP**	**SV**
IPM 2-3 x P.MUNG 4	-5.94	-5.94	9.89	2.04	4.24	-3.33	-4.93	-11.06*
IPM 2-3 x HUM 16	0.99	0.99	17.58**	9.18	19.25*	10.59	-9.09*	1.38
IPM 2-3 x IPM 99-125	-15.84**	-15.84**	9.89	2.04	-7.18	-13.92	0.47	-0.92
IPM 2-3 x IPM 205-7	-7.92	-7.92	17.58**	9.18	9.14	1.21	-3.24	10.14*
HUM 12 x P. MUNG 4	-8.33	-12.87*	5.43	-1.02	-0.17	-13.62	0.51	-9.22
HUM 12 x HUM 16	-10.23	-21.78**	6.52	0	0.39	-21.79**	-9.92*	0.46
HUM 12 x IPM 99-125	-2.41	-19.80**	6.52	0	7.3	-19.97**	-2.34	-3.69
HUM 12 x IPM 205-7	7.41	-13.86*	7.61	1.02	16.84	-12.86	-8.5	4.15
VBN (GG)2 x P. MUNG 4	-11.46	-15.84**	0	-5.1	-8.39	-20.73**	3.06	-6.91
VBN (GG)2 x HUM 16	0	-12.87*	0	-5.1	2.49	-18.91*	-13.64**	-3.69
VBN (GG)2 x IPM 99-125	0	-15.84**	-3.23	-8.16	-3.06	-23.30**	5.61	4.15
VBN (GG)2 x IPM 205-7	5.88	-10.89	9.68	4.08	17.21	-7.26	-7.69	5.07
TM 2000-2 x P. MUNG 4	-14.58*	-18.81**	6.74	-3.06	-8.92	-21.18**	1.62	-13.36**
TM 2000-2 x HUM 16	-7.37	-12.87*	12.5	1.02	11.05	-11.8	-18.18**	-8.76
TM 2000-2 x IPM 99-125	-4.21	-9.9	9.64	-7.14	5.52	-16.19*	-10.28*	-11.52*
TM 2000-2 x IPM 205-7	-14.74*	-19.80**	8.33	-7.14	-6.1	-25.42**	-11.74**	0.46
LGG 460 x P. MUNG 4	-21.43**	-23.76**	-2.15	-7.14	-23.15**	-29.20**	-1.08	-15.67**
LGG 460 x HUM 16	-37.76**	-39.60**	-7.53	-12.24*	-42.36**	-46.90**	-17.77**	-8.29
LGG 460 x IPM 99-125	-31.63**	-33.66**	-15.05*	-19.39**	-42.20**	-46.75**	-2.8	-4.15
LGG 460 X IPM 205-7	-38.78**	-40.59**	-7.53	-12.24*	-44.17**	-48.56**	-22.67**	-11.98*
Pusa 9072 x P. Mung 4	-40.63**	-43.56**	5.62	-4.08	-38.11**	-46.44**	-10.36*	-8.29
Pusa 9072 x HUM16	-26.14**	-35.64**	-13.64*	-22.45**	-35.73**	-49.92**	-2.48	8.76
Pusa 9072 x IPM 99-125	-24.10**	-37.62**	12.82	-10.2	-13.82	-44.33**	-5.86	-3.69
Pusa 9072 x IPM 205-7	-9.46	-33.66**	1.19	-13.27*	-9.35	-42.81**	-7.29	5.53
COGG 8 x P.MUNG 4	-26.04**	-29.70**	-16.00**	-14.29*	-33.89**	-40.39**	0	-13.82**
COGG 8 x HUM 16	-15.73*	-25.74**	-11	-9.18	-25.50**	-32.83**	-9.09*	1.38
COGG 8 x IPM 99-125	-8.99	-19.80**	-20.00**	-18.37**	-29.36**	-36.31**	-16.82**	-17.97**
COGG 8 x IPM 205-7	-4.49	-15.84**	-17.00**	-15.31*	-21.48**	-29.20**	-12.15**	0
"+ve" het	19	3	41	23	30	7	16	28
"-ve" het	41	57	19	37	30	53	44	32
Range	-40.63–17.44%	-43.56 – 1.98%	-29.25–26.58%	-23.47–11.22%	-46.11–64.04%	-51.98–10.59%	-29.39–23.94%	-19.82–18.89%

Contd…..

Table 4.18: Contd…..

Cross	S/P		100-SW		BY/P		HI		SY/P	
	BP	**SV**	**BP**	**SV**	**BP**	**SV**	**BP**	**SV**	**BP**	**SV**
CoGG 912 x P. MUNG 4	-37.29**	3.74	-3.39	5.56*	-18.57**	13.65	-0.43	0.64	-18.98**	14.35
CoGG 912 x HUM 16	-10.17**	48.60**	-23.13**	4.63	-25.12**	4.52	-0.96	0.11	-25.94**	4.53
CoGG 912 x IPM 99-125	-2.26	61.68**	-4.85	-9.26**	-50.03**	-30.26**	-11.64*	-10.69*	-50.65**	-30.34**
CoGG 912 x IPM 205-7	-30.51**	14.95**	-1.8	0.93	-60.34**	-44.65**	0.08	1.16	-49.54**	-28.79**
MH 2-15 x P.MUNG 4	7.09	27.10**	-12.71**	-4.63	-12.51	-10.33	0.47	2.36	-10.37	-8.47
MH 2-15 x HUM 16	-25.98**	-12.15*	-21.09**	7.41**	-19.67	-37.08**	-9.27*	-7.57	-27.28**	-42.46**
MH 2-15 x IPM 99-125	-22.05**	-7.48	-3.03	-11.11**	-2.48	-23.71**	-8.93*	-7.21	-10.59	-29.26**
MH 2-15 x IPM 205-7	-22.83**	-8.41	-2.7	0	-4.6	-25.37**	-7.44	-5.69	-11.22	-29.76**
PDM 139 x P. MUNG 4	-20.00**	-14.02*	-16.10**	-8.33**	-24.21**	-22.32*	-4.94	-4.81	-27.70**	-26.17**
PDM 139 x HUM 16	6.9	-13.08*	-32.65**	-8.33**	-2.12	-23.34**	-2.59	-5.21	-4.37	-27.34**
PDM 139 x IPM 99-125	1.15	-17.76**	-1.01	-9.26**	9.28	-36.99**	1.8	-8.07	11.31	-42.13**
PDM 139 x IPM 205-7	0	-16.82**	-9.01**	-6.48*	21.95	-20.57*	3.85	-6.21	36.14*	-25.35**
LGG 450 x P. MUNG 4	-16.52**	-10.28	-14.41**	-6.48*	-17.55*	-15.5	-5.52	-4.58	-21.02**	-19.35*
LGG 450 x HUM 16	-9.28	-17.76**	-32.65**	-8.33**	-9.54	-29.15**	-5.14	-4.19	-11.18	-32.52**
LGG 450 x IPM 99-125	10.31	0	-2.02	-10.19**	60.10**	-11.53	-8.05	-7.13	48.29**	-18.47*
LGG 450 x IPM 205-7	-11.34	-19.63**	-2.7	0	17.71	-23.34**	-7.39	-6.46	29.95*	-28.55**
ADT 3 x P. MUNG 4	0	14.02*	-13.56**	-5.56*	10.53	13.28	1.42	2.71	13.71	16.11*
ADT 3 x HUM 16	-13.93**	-1.87	-37.41**	-14.81**	-20.75*	-23.89**	-0.28	0.99	-21.04*	-23.55**
ADT 3 x IPM 99-125	-18.85**	-7.48	-3.03	-11.11**	-22.00*	-25.09**	-2.19	-0.94	-23.44**	-25.87**
ADT 3 x IPM 205-7	-0.82	13.08*	-12.61**	-10.19**	0	-3.97	-3.81	-2.59	-3.52	-6.59
TARM 1 x P. MUNG 4	-24.35**	-18.69**	-13.56**	-5.56*	-42.57**	-41.14**	3.61	3.76	-40.25**	-38.99**
TARM 1 x HUM 16	12.64	-8.41	-28.57**	-2.78	-1.41	-22.79*	2.34	-0.41	0.85	-23.38**
TARM 1 x IPM 99-125	8.05	-12.15*	3.03	-5.56*	53.73**	-4.98	5.15	-2.09	61.05**	-7.47
TARM 1 x IPM 205-7	11.24	-7.48	-6.31*	-3.7	27.90*	-16.7	9.1	1.59	47.90**	-15.02
TM 96-2 x P. MUNG 4	-9.57	-2.8	-11.02**	-2.78	8.46	11.16	-8.08	-7.95	0.03	2.15
TM 96-2 x HUM 16	-3.26	-16.82**	-26.53**	0	-2.56	-19.37*	1.2	-1.52	1.17	-21.43**
TM 96-2 x IPM 99-125-	14.13*	-1.87	0	-7.41**	-6.02	-22.23*	1.45	-4.79	-4.54	-25.87**
TM 96-2 x IPM 205-7	8.7	-6.54	-8.11**	-5.56*	3.46	-14.39	4.99	-1.47	7.27	-16.70*
P. Vishal x P. MUNG 4	-7.83	-0.93	-3.39	5.56*	-4.14	-1.75	-5	-4.87	-8.84	-6.91
P. Vishal x HUM 16	-12.15*	-12.15*	-20.41**	8.33**	13.19	-11.35	-5.83	-8.36	6.81	-18.85*
P. Vishal x IPM 99-125	-6.54	-6.54	-3.57	0	21.59	-11.16	3.56	-4.46	24.79*	-15.5
P. Vishal x IPM 205-7	0.93	0.93	1.79	5.56*	54.80**	13.1	7.4	-0.92	64.70**	11.53

Contd…..

Table 4.18: Contd…..

Cross	S/P		100-SW		BY/P		HI		SY/P	
	BP	**SV**	**BP**	**SV**	**BP**		**BP**	**SV**	**BP**	**SV**
IPM 2-3 x P.MUNG 4	2.61	10.28	-25.71**	-3.7	-22.69**	0.92	1.63	1.77	-19.18**	2.85
IPM 2-3 x HUM 16	0	-7.48	-25.17**	1.85	-23.55**	-0.2	3.42	2.25	-18.53**	3.68
IPM 2-3 x IPM 99-125	-7.07	-14.02*	-23.57**	-0.93	-44.81**	-27.95**	2.85	1.68	-42.61**	-26.96**
IPM 2-3 x IPM 205-7	4.04	-3.74	-20.71**	2.78	-22.12**	1.66	0.18	-0.96	-21.07**	0.44
HUM 12 x P. MUNG 4	-0.87	6.54	-8.47**	0	-10.89	-8.67	1.01	1.15	-9.59	-7.67
HUM 12 x HUM 16	3.85	-24.30**	-24.49**	2.78	-23.44*	-40.04**	4.44	1.63	-20.09	-39.28**
HUM 12 x IPM 99-125	22.22**	-7.48	5.05	-3.7	32.45*	-25.83**	8.67	-3.05	44.46**	-28.34**
HUM 12 x IPM 205-7	-3.37	-19.63**	2.7	5.56*	16.29	-24.26**	9.42	-2.38	34.91*	-26.02**
VBN (GG)2 x P. MUNG 4	2.61	10.28	-16.10**	-8.33**	-24.39**	-22.51*	3.15	3.29	-21.71**	-20.05*
VBN (GG)2 x HUM 16	17.50*	-12.15*	-29.25**	-3.7	-56.77**	-66.14**	-9.34*	-11.78*	-9.83	-31.49**
VBN (GG)2 x IPM 99-125	11.11	-15.89**	-0.97	-5.56*	-2.73	-37.64**	8.41	-4.7	5	-40.75**
VBN (GG)2 x IPM 205-7	3.37	-14.02*	-12.61**	-10.19**	11.76	-27.21**	12.04*	-1.51	27.25	-28.20**
TM 2000-2 x P. MUNG 4	-11.30*	-4.67	-11.02**	-2.78	-21.69*	-19.74*	-9.37*	-9.25*	-28.79**	-27.29**
TM 2000-2 x HUM 16	-19.10**	-32.71**	-28.57**	-2.78	-15.19	-33.58**	-10.30*	-12.72**	-24.30*	-42.49**
TM 2000-2 x IPM 99-125	-1.12	-17.76**	4.04	-4.63	20.32	-24.63**	-8.42	-12.89**	10.03	-34.55**
TM 2000-2 x IPM 205-7	2.25	-14.95**	-5.41*	-2.78	2.69	-33.12**	-2.75	-7.49	3.86	-38.22**
LGG 460 x P. MUNG 4	-32.17**	-27.10**	-18.64**	-11.11**	-53.92**	-52.77**	-2.74	-2.61	-55.05**	-54.10**
LGG 460 x HUM 16	-7.79	-33.64**	-29.93**	-4.63	-54.53**	-64.39**	-3.99	-6.58	-56.31**	-66.80**
LGG 460 x IPM 99-125	2.47	-22.43**	2.02	-6.48*	-33.59*	-60.61**	4.19	-1.89	-30.27*	-61.39**
LGG 460 x IPM 205-7	-3.37	-19.63**	-8.11**	-5.56*	-40.37**	-61.16**	7.24	0.98	-29.53*	-60.98**
Pusa 9072 x P. Mung 4	-14.78**	-8.41	-11.02**	-2.78	-53.02**	-51.85**	-1.05	-0.92	-53.41**	-52.43**
Pusa 9072 x HUM16	3.49	-16.82**	-26.53**	0	-46.29**	-57.93**	2.4	-0.24	-44.97**	-58.19**
Pusa 9072 x IPM 99-125	0	-19.63**	-4.81	-8.33**	-22.3	-58.86**	3.52	0.84	-10.12	-59.54**
Pusa 9072 x IPM 205-7	2.25	-14.95**	-7.21**	-4.63	-30.03*	-54.43**	4.52	1.82	-15.34	-53.57**
CoGG 8 x P.MUNG 4	-23.48**	-17.76**	-11.02**	-2.78	-47.43**	-46.13**	-11.71*	-11.59*	-53.50**	-52.51**
CoGG 8 x HUM 16	-5.19	-31.78**	-26.53**	0	-36.28**	-50.09**	-5.92	-8.45	-39.94**	-54.37**
CoGG 8 x IPM 99-125	-4.94	-28.04**	3.03	-5.56*	-6.79	-50.65**	3	-12.67**	-4.51	-57.01**
CoGG 8 x IPM 205-7	-1.12	-17.76**	-8.11**	-5.56*	-67.99**	-79.15**	7.8	-9.07*	0.27	-45.02**
"+ve" het	26	12	8	18	18	7	32	17	21	10
"-ve" het	34	48	52	42	42	53	28	43	39	50
Range	-37.29-22.22%	-33.64-61.68%	-37.41-5.05%	-14.81– 8.33	-67.99-60.10	-79.15-13.65%	-11.71-12.04%	-12.89- 3.76%	-56.31-64.70%	-66.80- 16.11%

Traits: D50% f = Days to 50% flowering, DM= Days to maturity, PH = Plant height (cm), PB/P = Primary branches per plant, C/P= Clusters per plant, P/C=Pods per cluster, PL= Pod length(cm), P/P= Pods per plant, S/P= Seeds per pod, 100-SW= 100-Seed weight (g), BY/P= Biological yield per plant (g), HI= Harvest-index (%), SY/P= Seed yield per plant (g).

Forty-one hybrids showed negative and significant heterosis while three hybrids showed positive and significant heterosis over better-parent. On the other hand, thirty-eight hybrids showed positive and significant heterosis and five hybrids showed negative and significant heterosis over SV.

The best five hybrids exhibiting significant heterosis in desirable direction for days to maturity were CoGG 8 x IPM 99-125 (-27.53%), ADT 3 x IPM 99-125 (-26.48%), CoGG 8 x IPM 205-7 (-20.73%), CoGG 8 x HUM 16 (-20.40%) and TM 2000-2 x IPM 205-7 (-20.00%) over BP and LGG 460 x P. Mung 4 (-12.68%), CoGG 912 x P. MUNG 4 (-11.71%), IPM 2-3 x P. Mung 4 (-10.24%), Pusa 9072 x P. Mung 4 (-8.78%) and VBN (GG) 2 x P. Mung 4 (-8.29%) over SV.

4.2.6.3. Plant height:

For plant height, the heterosis over better-parent (BP) ranged from -38.91% (P. Vishal x HUM 16) to 16.65% (TM 96-2 x P. Mung 4). The heterosis over standard variety (P. Mung 5) ranged from -47.45% (CoGG 8 x IPM 99-125) to 56.97% (MH 2-15x P. Mung 4).

Thirty-eight hybrids showed negative and significant heterosis while thirty-two hybrids showed positive and significant heterosis over better-parent. On the other hand, thirteen hybrids showed positive and significant heterosis thirty-five hybrids showed negative and significant heterosis over SV.

The best five hybrids exhibiting significant heterosis in negative direction for plant height were P. Vishal x HUM 16 (-38.91%), CoGG 912 x P. Mung 4 (-38.20%), CoGG 8 x IPM 99-125 (-38.08%), TM 2000-2 x P. Mung 4 (-36.83%) and LGG 460x IPM 99-125(-32.58%) over BP and CoGG 8 x IPM 99-125(-47.45%), TM 2000-2 x P. Mung 4 (-45.15%), P.

Vishal x HUM 16 (-34.44%), Pusa 9072 x P. Mung 4 (-32.48%) and TM 2000-2 x IPM 99-125 (-30.53%) over SV.

4.2.6.4. Primary branches per plant:

For primary branches per plant, the heterosis over better-parent (BP) ranged from -48.15% (PDM 139 x P. Mung 4) to 18.75% (TARM 1 x HUM 16). The heterosis over standard variety (P. Mung 5) ranged from -59.30% (CoGG 8 x IPM 99-125)to -5.81% (CoGG 912 x P. Mung 4).

Twenty-four hybrids showed negative and significant heterosis over better-parent. On the other hand, fifty-eight hybrids showed significant negative heterosis over SV.

None of the sixty hybrids exhibited significant and positive heterosis over better-parent as well as standard variety.

4.2.6.5. Clusters per plant:

For clusters per plant, the heterosis over better-parent(BP) ranged from -40.63% (Pusa 9072 x P. Mung 4) to 17.44% (P. Vishal x IPM 205-7). The heterosis over standard variety ranged from -43.56% (Pusa 9072 x P. Mung 4) to 1.98% (TM 96-2 x P. Mung 4).

Eighteen hybrids showed negative and significant heterosis while two hybrids showed positive and significant heterosis over better-parent. On the other hand, thirty-six hybrids showed significant negative heterosis over SV.

The best two hybrids exhibiting significant and possitive heterosis were P. Vishal x IPM 205-7 (17.44%) and PDM 139 x IPM 205-7 (15.68%) over BP while none of the hybrids had positive and significant heterosis over SV.

4.2.6.6. Pods per cluster:

For pods per cluster, the heterosis over better-parent (BP) ranged from -29.25% (CoGG 912 x IPM 99-125) to 26.58% (LGG 450 x IPM 99-125). The heterosis over standard variety ranged from -23.47% (CoGG 912 x IPM 99-125) to 11.22% (TARM 1 x IPM 99-125).

Eight hybrids showed negative and significant heterosis while ten hybrids showed positive and significant heterosis over better-parent. On the other hand, eleven hybrids showed significant negative heterosis over SV.

The best five hybrids exhibiting significant heterosis in positive direction for pods per cluster were LGG 450 x IPM 99-125 (26.58%), P. Vishal x IPM 99-125 (24.36%), P. Vishal x IPM 205-7 (23.81%), TARM 1x IPM 99-125 (22.47%) and TARM 1 x IPM 205-7 (20.22%) over BP.

4.2.6.7. Pod length:

For pod length, the heterosis over better-parent (BP) ranged from -29.39% (CoGG 912 x P. Mung 4) to 23.94% (LGG 450 x P. Mung 4). The heterosis over standard variety ranged from -19.82% (TM 96-2 x P. Mung 4) to 18.89% (MH 2-15 x P. Mung 4).

Twenty-nine hybrids showed negative and significant heterosis while three hybrids showed positive and significant heterosis over better-parent. On the other hand, seventeen hybrids showed significant negative heterosis and seven hybrids showed significant positive heterosis over SV.

The hybrids exhibiting significant heterosis in positive direction for pod length were LGG 450 x P.Mung 4 (23.94%), MH 2-15 x P. Mung 4 (21.13%) and MH 2-15 x IPM 99-125 (10.75) over BP and MH 2-15 x P.Mung 4 (18.89%), CoGG 912 x IPM 99-125 (13.82%), ADT 3 x HUM

16 (13.36%), ADT 3 x P. Mung 4 (10.14%), ADT 3 x IPM 99-125 (10.14%), MH 2-15 x HUM 16 (10.14%) and IPM 2-3 x IPM 205-7 (10.14%) over SV.

4.2.6.8. Pods per plant:

For pods per plant, the heterosis over better-parent (BP) ranged from -46.11% (CoGG 912 x IPM 99-125) to 64.04% (P. Vishal x IPM 205-70). The heterosis over standard variety ranged from -51.98% (CoGG 912 x IPM 99-125) to 10.59% (IPM 2-3 X HUM 16).

Fifteen hybrids showed negative and significant heterosis while nine hybrids showed positive and significant heterosis over better-parent. On the other hand, twent- nine hybrids showed significant negative heterosis over SV but none of the hybrids recorded positive and significant heterosis over SV for the character.

The best hybrids exhibiting significant heterosis in desirable direction for pods per plant were P. Vishal x IPM 205-7 (64.04%), P. Vishal x IPM 99-125 (38.75%), LGG 450 x IPM 99-125 (36.61%), LGG 450 x IPM 205-7 (35.01%), TARM 1 x IPM 99-125 (34.87%), PDM 139 x IPM 205-7 (29.98%), IPM 2-3 x HUM 16 (19.25%) and CoGG 912 x P. Mung 4 (17.83%) over BP.

4.2.6.9. Seeds per pod:

For seeds per pod, the heterosis over better-parent (BP) ranged from -37.29% (CoGG 912 x P. Mung 4) to 22.22% (HUM 12 x IPM 99-125). The heterosis over standard variety ranged from -33.64% (LGG 460 x HUM 16) to 61.68% (CoGG 912 x IPM 99-125).

Seventeen hybrids showed negative and significant heterosis while three hybrids showed positive and significant heterosis over better-parent.

On the other hand, five hybrids showed significant positive heterosis and thirty-one hybrids showed significant negative heterosis over SV.

The best hybrids exhibiting significant positive heterosis for seeds per pod were HUM 12 x IPM 99-125 (22.22%), VBN(GG)2 x HUM 16 (17.50%) and TM 96-2 x IPM 99-125 (14.13%) over BP and CoGG 912 x IPM 99-125 (61.68%), CoGG 912 x HUM 16 (48.60%), MH 2-15 x P. Mung 4 (27.10%), CoGG 912 x IPM 205-7 (14.95%) and ADT 3 x P. Mung 4 (14.02%) over SV.

4.2.6.10. 100-seed weight:

For 100-seed weight, the heterosis over better-parent (BP) ranged from -37.41% (ADT 3 x HUM 16) to 5.05% (HUM 12 x IPM 99-125). The heterosis over standard variety ranged from -14.81% (ADT 3 x HUM 16) to 8.33% (P. Vishal x HUM 16).

Thirty-eight hybrids showed negative and significant heterosis over better-parent. On the other hand, six hybrids showed significant positive heterosis and twenty-six hybrids showed significant negative heterosis over SV.

The best hybrids exhibiting significant heterosis in positive direction for 100-seed weight were P. Vishal x HUM 16 (8.33%), MH 2-15 x HUM 16 (7.41%), CoGG 912 x P. Mung 4 (5.56%), P. Vishal x P. Mung 4 (5.56%), P. Vishal x IPM 205-7 (5.56%) and HUM 12 x IPM 205-7 (5.56%) over SV and no desirable hybrid was found over BP.

4.2.6.11. Biological yield per plant:

For biological yield per plant, the heterosis over better-parent (BP) ranged from -67.99% (CoGG 8 x IPM 205-7) to 60.10% (LGG 450 x IPM

99-125). The heterosis over standard variety ranged from -79.15% (CoGG 8 x IPM 205-7) to 13.65% (CoGG 912 x P. Mung 4).

Twenty-six hybrids showed negative and significant heterosis while five hybrids showed positive and significant heterosis over better-parent. On the other hand, forty-one hybrids showed significant negative heterosis over SV.

The five hybrids exhibiting significant heterosis in positive direction for biological yield per plant over BP were LGG 450 x IPM 99-125 (60.10%), P. Vishal x IPM 205-7 (54.80%), TARM 1 x IPM 99-125 (53.73%), HUM 12 x IPM 99-125 (32.45%) and TARM 1 x IPM 205-7 (27.90%). None of the sixty hybrids possessed significant and positive heterobeltiosis.

4.2.6.12. Harvest-index:

For harvest-index , the heterosis over better-parent (BP) ranged from -11.71% (CoGG 8 x P. Mung 4) to 12.04% (VBN)GG2 x IPM 205-7. The heterosis over standard variety ranged from -12.89% (TM 2000-2 x IPM 99-125) to 3.76% (TARM 1x P. Mung 4).

Seven hybrids showed negative and significant heterosis while one hybrid showed positive and significant heterosis over better-parent. On the other hand, eight hybrids showed significant negative heterosis over SV.

The hybrid exhibiting significant heterosis in positive direction for harvest-index was VBN(GG)2 x IPM 205-7 (12.04%) over BP, while none of the sixty hybrids had positive and significant heterobeltiosis.

4.2.6.13. Seeds yield per plant:

For seeds yield per plant, the heterosis over better-parent (BP) ranged from -56.31% (LGG 460 x HUM 16) to 64.70% (P. Vishal x IPM

205-7). The heterosis over standard variety ranged from -66.80% (LGG 460 x HUM 16) to 16.11% (ADT 3 x P. Mung 4).

Twenty-five hybrids showed negative and significant heterosis while nine hybrids showed positive and significant heterosis over better-parent. On the other hand, forty-five hybrids showed significant negative and one hybrid showed significant positive heterosis over SV.

The best hybrids exhibiting significant heterosis in positive direction for seeds yield per plant were P. Vishal x IPM 205-7 (64.70%), TARM 1 x IPM 99-125 (61.05%), LGG 450 x IPM 99-125 (48.29%), TARM 1 x IPM 205-7 (47.90%) and HUM 12 x IPM 99-125 (44.46%) over BP and ADT 3 x P. Mung 4 (16.11%) over SV.

Chapter-V

DISCUSSION

Mungbean [*Vigna radiata* (L.) Wilczek] is a highly valuable pulse crop from agronomic as well as economic point of view because of having short duration, wide adaptability, low input requirements and ability to improve the soil alongwith protein rich seeds of high nutritive value. Though cultivated on large area in our country, this crop is characterized by low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions such as mixed culture and stress environments. Considering the various virtues endowed in mungbean, there is an urgent need for developing high yielding varieties suitable to different environments so that this crop may serve its full potential in combating the hunger and malnutrition prevalent in the rapidly increasing predominantly vegetarian population of our country.

The sound knowledge of various genetic aspects of a crop in the environments it is to be grown, is essential for laying the foundations of successful crop improvement programme. Among these aspects, the informations about inheritance of quantitative traits, identification of superior parents and crosses on the basis of combining ability, nature and magnitude of heterosis and direct and indirect selection parameters for important characters are required for devising a successful breeding programme aimed at development of superior strains or varieties through effective and efficient manipulation of available genetic variability . In view of limited utility of available literature pertaining to above aspects in mungbean in different seasons or environments, further studies are warranted in this respect. Therefore, present investigation was undertaken

to evaluate the germplasm collection, genetic diversity, gene effects, combining ability, heterosis and direct and indirect selection parameters for yield and yield contributing characters in mungbean in *Zaid* and *Kharif* seasons.

1. To evaluate mungbean germplasm lines for yield and yield components,
2. To study the character associations among different quantitative characters,
3. To examine the genetic divergence existing in the germplasm collections,
4. To asses nature and magnitude of gene action for yield and other yield components,
5. To estimate general and specific combining ability variances and their effects,
6. To study nature and extent of heterosis over better- parent and standard variety for yield and its components, and
7. To sort out promising heterotic combinations for yield and its contributing traits.

The present study was carried out during year 2019 at Student's Instructional Farm of A.N.D.U.A.&T., Kumarganj, Ayodhya. The present investigation comprised of two experiments, namely, the germplasm evaluation experiment (Experiment-I) and combining ability experiment (Experiment-II).

In the germplasm evaluation experiment (Experiment-I), 60 genotypes of mungbean germplasm collections, showing wide spectrum of variation for various characters, were evaluated along with four checks during *Zaid* and *Kharif* seasons of 2019. This experiment was conducted in

augmented design comprising 6 blocks of 14 plots each. The assessment of existing variability in the germplasm collections was done by computing means and least significant differences. The nature of association among different characters was studied by using simple correlations and path-coefficient analysis (Wright, 1921; Dewey and Lu, 1959). Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was employed to study the genetic divergence existing among the germplasm collections.

The combining ability experiment (Experiment-II) was based on evaluations of a line x tester set of 60 hybrids (F_{1s}) and their nineteen parents along with one check for thirteen characters in randomized block design with three replications during *Kharif*, 2019. The 60 F_{1s} were generated by crossing 15 lines with 4 testers during *Zaid*, 2019.The analysis of variance for randomized complete block design (Panse and Sukhatme, 1967), line x tester analysis for combining ability (Kempthorne, 1957), estimation of heterosis over better-parent and standard variety (Fonseca and Patterson, 1968), computation of heritability in broad sense (Hanson *et al*., 1963) and genetic advance in per cent of mean (Johnson *et al*., 1955), estimation of correlation coefficients (Searle, 1961) and path-coefficient analysis (Dewey and Lu, 1959) were carried out.

Salient findings from this investigation are discussed in light of relevant literature under following sections:

5.1 Germplasm Evaluation Experiment (Experiment-I)

5.1.1 Mean performance of genotypes

5.1.2 Correlation coefficients

5.1.3 Path coefficient analysis

5.1.4 Genetic divergence analysis

5.2 Combining Ability Experiment (Experiment-II)

5.2.1 Analysis of variance for Experiment-II

5.2.2 Coefficient of variation, heritability and genetic advance

5.2.3 Correlation Coefficients

5.2.4 Path coefficient analysis

5.2.5 Combining ability analysis

5.2.6 Heterosis over better-parent and standard variety

5.1.1. Mean performance of genotypes:

In order to evaluate the germplasm collections, the mean performance of 60 mungbean genotypes and four checks for 13 characters in *Zaid* (E1) and *Kharif* (E2) seasons are presented in Table 4.2 (a) and Table 4.2 (b), respectively. Very wide range of variation in mean performance of genotypes was observed for all the characters under study in both the seasons. The comparision of mean performance of 60 entries for 13 traits using least significant differences revealed existence of very high level of variability in the germplasm collections in both environments.

In *Zaid* season (Table 5.1 (a)), the highest seed yield per plant was produced by SML 823 (8.77g) followed by DGGV 2, BM 4, HUM 12, TM 96-2, and ADT 3. The above six lines were also statistically at par with each other to constitute in top non-significant group of high seed yield per plant. The high yielding genotype SML 823 was present in the top non-significant group for clusters per plant, pods per plant, seeds per pod, biological yield per plant and harvest-index besides having medium performance for rest of the characters. The second highest yielder DGGV 2 (8.21g) was also present in the top non-significant group for pods per cluster, pod length, pods per plant, seeds per pod and biological yield per plant. The third ranking genotype for seed yield per plant BM 4 (8.20g) was also found in top non-significant group for clusters per plant, pods per

plant, seeds per pod and biological yield per plant. HUM 12 (7.92g), fourth rank yielder was also part of top non-significant group for primary branches per plant, 100-seed weight, biological yield per plant and harvest-index. TM 96-2 (7.43g) was present in top non-significant group for pod length, seeds per pod and biological yield per plant besides being fifth ranked yielder. The sixth ranked genotype for seed yield per plant, ADT 3 was present in top non-significant group for pod length, pods per plant, seeds per pod and biological yield per plant.

The above six lines showing high mean performance in desirable direction for seed yield and some of its important yield components emerged as promising lines for exploitation in varietal development programmes for *Zaid* season in mungbean.

In case of *Kharif* season, (Table 5.1 (b)) the highest seed yield per plant was produced by DGGV 2 (12.63g) follwed by ADT 3 (12.12g), P. Mung 6 (10.58g), P. Mung 5 (10.42g), P. Mung 2 (10.20g) and MH 2-15 (9.65g). the above six lines constituted in top non-significant group for high seed yield per plant because of being statistically as par with the highest yielding genotype. The highest yielding genotypes DGGV 2 was found in top non-significant group for clusters per plant, pods per cluster, pod length, pods per plant, biological yield per plant and harvest-index. The second highest yielder ADT 3 appeared in top non-significant group for primary branches per plant, pods per cluster, pod length, pods per plant, seeds per pod, biological yield per plant and harvest-index. P. Mung 6, The third rankeed genotype for seed yield per plant was also part of top non-significant group of plant height, seeds per pod and biological yield per plant. The fourth ranked yielder, P. Mung 5 was present in the top non-significant group for pod length, seeds per pod and harvest-index. The

genotype ranked fifth for seed yield per plant P. Mung 2 was found in top non-significant group for clusters per plant, pods per plant and biological yield per plant. The genotype ranked sixth for seed yield per plant, MH 2-15 also emerged in the top non-significant group for primary branches per plant, clusters per plant and biological yield per plant. Thus, the above six lines showing high mean performance for seed yield and some other characters emerged as promising lines for used as donar parents in mungbean breeding programme for *Kharif* season.

In addition to the six high yielding lines each identified for *Zaid* and *Kharif* seasons, several other germplasm lines showed very high mean performance for one or more other characters in *Zaid* and / or *Kharif* seasons even if they had low or medium mean performance for seed yield per plant. These lines may also serve as valuable parents in a component breeding approach for improving the yield components leading to overall development of genotypes possessing high mean performance for seed yield and yield component.

In case of *Zaid* season, (Table 5.2 (a)) the lines showing very high mean performance in desirable direction were PDM 139, Phule Mung 2, Dgg 1, for days to 50% flowering; PDM 139, LGG 460, Pusa 9531 for days to maturity; DGGV 5, DGG 1, OUM 11-5 for plant height; HUM 12, P. Mung 5, MGG 347 for primary branches per plant and BM 4, SML 823, and KM 18-122 for clusters per plant. Similarly, DGGV 2, ADT 3, SML 1082 for pods per cluster; BM 4, ADT 3 and SML 823 for pods per plant; KM 11-584, CoGG 912 and TM 96-2 for pod length and TM 96-2, Phule Mung 2 and sMl 1082 were foumd to be desirable.

The most promising lines were HUM 12, P. Vishal for 100-seed weight; DGGV 2, BM 4 and SML 823 for biological yield per plant and SML 823, SML 668 and IMP 410-3 for harvest-index.

Table 5.1 (a):Summary of mean performance for other chaarecters of parents producing high seed yield per plant in *Zaid* season (E1)

Genotypes	SY/P	D50%f	DM	PH	PB/P	C/P	P/C	PL	P/P	S/P	100-SW	BY/P	HI
SML 823	8.77	0	0	0	0	+	0	0	+	+	0	+	+
DGGV 2	8.21	0	0	0	0	0	+	+	+	+	0	+	0
BM 4	8.20	0	0	0	0	+	0	0	+	+	0	+	0
HUM 12	7.92	0	0	+	+	0	0	0	0	0	+	+	+
TM 96-2	7.43	0	0	0	0	0	0	+	0	+	0	+	0
ADT 3	6.73	0	0	0	0	0	+	+	+	+	0	+	0

Present in top non-significant group

Table 5.1(b):Summary of mean performance for other chaarecters of parents producing high seed yield per plant in *Kharif* season (E2)

Genotypes	SY/P	D50%f	DM	PH	PB/P	C/P	P/C	PL	P/P	S/P	100-SW	BY/P	HI
DGGV 2	12.63	0	0	0	0	+	+	+	+	0	0	+	+
ADT 3	12.12	0	0	0	+	0	+	+	+	+	0	+	+
P. MUNG 6	10.58	0	0	+	0	0	0	0	0	+	0	+	0
P. MUNG 5	10.42	0	0	0	0	0	0	+	0	+	0	0	+
P. MUNG 2	10.10	0	0	0	0	+	0	0	+	0	0	+	0
MH 2-15	9.65	0	0	0	+	+	0	0	0	0	0	+	0

Present in top non-significant group

In case of *Kharif* season, (Table 5.2 (b)) the germplasm lines showing very high mean performance were IPM 2-3, OUM 11-5 and PKVAkM 4 for days to 50% flowering; OUM 11-5 for days to maturity, KM 18-116, KM 18-97 and KM 18-105 for plant height and P. Mung 5, SML 613, LGG 460 for primary branches per plant. The most promising lines were found to be DGGV 2, DGGS 4 and P. Mung 5 for clusters per plant; ADT 3, SML 823 and LGG 460 for pods per cluster; ADT 3, P.Mung 6 and DGGV 2 for pods per plant and CoGG 912 , KM 18-106 and ADT 3 for pod length; ADT 3, P.Mung 2 and tm 96-2 for seeds per pod; DGGS 4 and HUM 12 for 100-seed weight; ADT 3, P. Mung 5 and P. Mung 6 for biological yield per plant and DGGV 2, P.Mung 2 and ADT 3 were the lines identified for very high mean performance in desirable direction.

The germplasm lines showing very high mean performance for various yield component as identified and mentioned above for the respective seasons may be recommended for used as donar of those characters in a component breeding approach.

5.1.2. Correlation coefficients:

The seed yield or economic yield in almost all the crops, is referred to as super character which results from multiplicative interactions of several other characters that are termed as yield components. Thus, genetic architecture of seed yield in mungbean as well as other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another.

Correlation coefficients among seed yield and various other plant characters help us to understand the nature of associations or inter relationships among them which facilitates identification of characters

Table 5.2 (a): The most desirable genotypes identified for 13 characters in *Zaid* season (E1)

Characters	Genotypes
Days to 50% flowering	PDM 139, PhuleMung 2, DGG 1, SML 1082, MH 2-15, P>Mung 2, IPM 2-14
Days to maturity	PDM 139, LGG 460, Pusa 9531, TMB 37, P.Mung 2, MH 421
Plant height	DGGV 5, DGG 1, OUM 11-5, HUM 12, SML 1082, KM 18-97, IPM 2-14, TM 2000-2, IPM 2-3, KM 22-41, KM 18-105
Primary branches per plant	HUM 12, P>Mung 5, MGG 347, MH 318, TM 2000-2,
Clusters per plant	BM 4, SML 823, KM 18-122, IPM 410-3, ML 613, ML 818, P.Mung 6
Pods per cluster	DGGV 2, ADT 3, SML 1082, P.Mung 2, MGG 347, DGGS 4
Pods per Plant	BM 4, ADT 3, SML 823, DGGV 2, Phule Mung 2, MH 421
Pod length	KM 11-584, CoGG 912, TM 96-2, ADT 3, DGGV 2, SML 668, P.Vishal, KM 22-41, SML 1082
Seeds per pod	TM 96-2, PhuleMung 2, SML 1082, KM 11-584,ADT 3
100-seed weight	HUM 12, P.Vishal
Biological yield per plant	DGGV 2, BM 4, SML 823, HUM 12, TM 96-2, ADT 3
Harvest-index	SML 823, SML 668, IPM 410-3, Pusa 9531, PDM 139, HUM 12
Seed yield per plant	SML 823, DGGV 2, BM 4, HUM 12, TM 96-2, ADT 3

Entries of top non-significant group

Table 5.2 (b): The most desirable genotypes identified for 13 characters in *Kharif* season (E2)

Characters	Genotypes
Days to 50% flowering	IPM 2-3, OUM 11-5, PKVAKM 4, 4RMG1028, CoGG 912, ML 613
Days to maturity	OUM 11-5
Plant height	KM 18-116, KM 18-97, KM 18-105, 2-1PM 409, KM 18-122, TMB 37,IPM 410-3, KM 18-108
Primary branches per plant	P.Mung 5, ML 613, LGG 460, MH 421, Pusa 9531, ADT 3
Clusters per plant	DGGV 2, DGGS 4, P.Mung 5, P.Mung 6, BM 4
Pods per cluster	ADT 3, SML 823, LGG 460, TARM 1, DGGV 2, KM 11-584
Pods per Plant	ADT 3, P.Mung 6, DGGV 2
Pod length	CoGG 912, KM 18-106, ADT 3, P.Mung 2, DGGV 2
Seeds per pod	ADT 3, P.Mung 2, TM 96-2, MH 2-15
100-seed weight	DGGS 4, HUM 12
Biological yield per plant	ADT 3, P.Mung 5, P.Mung 6, CoGG 912, MH 2-15, DGGV 2
Harvest-index	DGGV 2, P.Mung 2, ADT 3, BM 4, IPM 2-3, OUM 11-5
Seed yield per plant	ADT 3, P.Mung 6, P.Mung 5, P.Mung 2, MH 2-15, DGGV 2

Entries of top non-significant group

influencing the manifestation of seed yield or economic yield. Proper identification of such yield attributing traits, known as yield components, plays an important role in devising the appropriate selection strategy for developing high yielding crop varieties.

In order to study the character associations existing in the germplasm collections evaluated in Experiment-I , the simple correlation coefficients were computed among thirteen characters in *Zaid* (E1) as well as *Kharif* (E2) seasons.

In the *Zaid* season (Table 4.3 (a)), seed yield per plant exhibited highly significant and positive correlation with biological yield per plant, pods per plant, clusters per plant, harvest-index and pods per cluster. Thus theses five traits emerged as most important factors in influencing seed yield in mungbean in *Zaid* season.The available literature has also identified the above characters as important associates of seed yield in mungbean (Katiyar *et al*. 2015; Suresh and Malathi., 2016; Garg *et al*., 2017; Kumar *et al*., 2018; Asari *et al*., 2019; Ahmad and Belwal, 2020).

Biological yield per plant showed strong positive association with pods per plant, clusters per plant and pods per cluster while harvest index was positively correlated with pods per plant, clusters per plant and seeds per pod. Similarly, pods per plant exhibited positive association with clusters per plant, pods per cluster and primary branches per plant while pod length was positively associated with clusters per plant and plant height. Pods per cluster was positively associated with primary branches per plant. The above results clearly show that characters exhibiting strong positive association with seed yield per plant, namely, biological yield per plant, pods per plant, clusters per plant, harvest-index and pods per cluster were mostly positively correlated with each other as well as some other

yield attributes like seeds per pod and primary branches per plant. The positive association among seed yield and important yield component augers well for development of high yield mungbean genotypes for *Zaid* season as selection practices would be highly effective due to correlated response in positively correlated characters. Such occurance of positive associations among yield and yield components has also been reported by earlier workers (Rahim *et al*., 2010; Suresh and Malathi.,2016; Ghimire *et al*., 2017; Parihar *et al*., 2018; Majhi *et al*., 2020).

In contrary to earlier reports, seed yield per plant along with biological yield per plant , pod length, pods per plant , clusters per plant and primary branches per plant showed strong negative associations with days to 50% flowering and days to maturity which appears beneficial as it indicates possibility of combining high mean performance for seed yield and important yield components with early flowering and maturity for breeding high yielding early maturing mungbean varieties for *Zaid* season.

In the *Kharif* season (Table 43 (b)), seed yield per plant recorded highly significant and positive association with biological yield per plant, pods per plant, clusters per plant, harvest-index, primary branches per plant and seeds per pod besides having significant positive correlation with pods per cluster, plant height and pod length. Thus, the above nine traits emerged as important associates of seed yield per plant in mungbean in *Kharif* season. These results are broadly in agreement with the results of earlier workers (Katiyar *et al*., 2015; Suresh and Malathi., 2016; Garg *et al*., 2017; Kumar *et al*., 2018; Asari *et al*., 2019; Ahmad and Belwal, 2020.)

In *Kharif* season, harvest-index had strong positive association with biological yield per plant , pods per plant, primary branches per plant,

seeds per pod, clusters per plant and pods per cluster while biological yield per plant was strongly associated with pods per plant, clusters per plant, primary branches per plant, seeds per pod and plant height besides having positive association with pod length. The 100-seed weight exhibited positive association with pod length and plant height while seeds per pod showed strong positive association with primary branches per plant and pods per plant. The strong positive association of pods per plant with clusters per plant, pods per cluster and primary branches per plant and clusters per plant with primary branches per plant and plant height were also noted. The above results unlined the fact that positive association between most of the yield components among themselves as well as seed yield per plant would be highly fruitful for ensuring faster advance through correlated response during selection. The favourable positive associations among yield and its components have also been reported in mungbean by Rahim *et al*.(2010); Suresh and Malathi.(2016); Parihar *et al*.(2018) and Majhi *et al*. (2020).

Seed yield per plant , biological yield per plant, harvest-index, seeds per pod, pods per plant, clusters per plant and primary branches per plant recorded strong negative association with days to 50% flowering and days to maturity. The existance of strong negative associations of seed yield per plant and majority of yield component characters with days to 50% flowering and maturity indicates the better possibility of developing high yielding and early maturing mungbean genotypes for *Kharif* season also.

5.1.3. Path coefficient analysis:

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on seed yield that provides more clear picture of character associations for

formulating efficient selection strategy. Path analysis differ from simple correlation in that it points out the causes and their relative importance, whereas the later measures simply the mutual association ignoring the causation.

Thus, path coefficient analysis enables us to assess the precise direct and indirect roles of different plant characters in influencing the manifestation of seed yield or economic yield so that a few important yield components can be identified for practicing efficient and successful simultaneous selection for developing better genotypes.

The path coefficient analysis using simple correlation coefficients between thirteen characters of sixty germplasm lines and four checks was carried out for *Zaid* and *Kharif* seasons as presented in Table 4.4(a) and Table 4.4(b), respectively.

In *Zaid* season (Table 4.4(a)), biological yield per plant followed by harvest-index and days to 50% flowering exerted highest positive direct effects on seed yield per plant to emerge as most important direct contributors of seed yield per plant in mungbean in *Zaid* season . Garg *et al*.(2017), Ghimire *et al*.(2017), Kumar *et al*.(2018); Parihar *et al*. (2018) and Asari *et al*.(2019) had also reported positive direct effect of biological yield per plant, harvest-index and days to 50% flowering on seed yield per plant. However, inspite of strong positive correlations with seed yield per plant as well as among themselves, pods per plant, clusters per plant and pods per cluster exhibited substantial negative direct effects on seed yield per plant in addition to 100 seed weight and seeds per plant. This indicated that their positive corre;lations with seed yield were conditioned by their high order positive indirect effect on seed yield via some other characters as mentioned below.

In *Zaid* season, pods per plant exerted very high order positive indirect effects via biological yield per plant and considerable positive indirect effects via 100 seed weight and harvest-index on seed yield per plant. However, pods per plant resulted in considerable negative indirect effects on seed yield per plant via clusters per plant and pods per cluster. Substantial positive indirect effects on seed yield per plant were also exerted by pods per cluster and seeds per pod via biological yield per plant and 100 seed weight while 100 seed weight recorded considerable positive indirect effects via pods per cluster and seeds per pod. Clusters per plant followed by harvest-index, pod length and primary branches per plant exerted high order positive indirect effects on seed yield per plant via biological yield per plant . Substantial negative indirect contributions on seed yield per plant were made by days to 50% flowering , days to maturity and plant height via biological yield per plant which made considerable negative indirect effects on seed yield via clusters per plant and pods per cluster. Days to 50% flowering resulted considerable positive indirect effect on seed yield per plant via cluster per plant.

Considering the results given above, pods per plant, pods per cluster, seeds per pod and 100-seed weight emerged as the most important indirect seed yield components in mungbean for *Zaid* season, by virtue of having substantial positive indirect effects via two or more characters, while clusters per plant, harvest-index, primary branches per plant and pod length appeared as indirect yield components of secondary importance sowing the substantial positive indirect effects via one character.

In the *Kharif* season (Table 4.4(b)), biological yield per plant followed by pods per plant and harvest-index exerted high order positive direct

effects on seed yield per plant to emerge as important direct contributors of seed yield in mungbean in *Kharif* season. Earlier workers have also identified these three characters as important contributers of seed yield in mungbean (Rahim *et al*., 2010; Garg *et al*., 2017; Kumar *et al*., 2018; Ahmad and Belwal, 2020.)

In contrast, clusters per plant and pods per cluster had considerable negative direct effects on grain yield per plant while direct effects of remaining seven traits were negligible.

Considering the indirect effects in the *Kharif* season, very high order positive indirect effects via biological yield per plant and substantial positive indirect effects via harvest-index were exerted by pods per plant, primary branches per plant, clusters per plant and seeds per pod on seed yield per plant. Primary branches per plant, clusters per plant, pods per cluster, biological yield per plant and harvest-index exhibited considerable positive indirect effects on seed yield per plant via pods per plant. Harvest-index, plant height, pod length, pods per cluster and 100-seed weight exerted substantial indirect effects on seed yield via biological yield per plant. Considerable positive indirect effects on seed yield were also exhibited by biological yield per plant via harvest-index and days to 50% flowering via clusters per plant.

On the basis of results explained above, pods per plant, primary branches per plant, clusters per plant, seeds per pod, harvest-index, pods per cluster and biological yield per plant can be identified as most important indirect seed yield attributes in mungbean for *Kharif* season owing to their high order positive indirect effects on seed yield via two or more characters.

The substantial negative indirect effects on seed yield per plant by days to 50% flowering and days to maturity via biological yield per plant, harvest-index and pods per plant indicated the possibility of combining high mean performance of yield components with early flowering and early maturity which appears beneficial.

5.1.4. Genetic divergence analysis:

The germplasm is the reservoir of genetic variability, which is often exploited to meet the changing needs for developing improved varities of a crop. The importance of genetic diversity for selecting parents for recombination breeding, in an autogamous crop such as mungbean to recover transgressive segregants has also been repeatedly emphasized.(Rahim *et al*., 2015; Shyamalee *et al*., 2016; Sen *et al*., 2017; Mahalingam *et al*., 2018; Das *et al*., 2019; Subramanian *et al*., 2020). Characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 statistics and Non-hierarchical Euclidean cluster analysis.

In the present study, the 64 genotypes of mungbean were grouped into ten distinct non-overlapping clusters using Non-hierarchical Euclidean cluster analysis in *Zaid* as well as *Kharif* seasons as presented in Table 4.5 (a) and Table 4.5 (b), respectively. This indicated substantial genetic diversity existed in the germplasm collection evaluated in the present study in context of *Zaid* as well as *Kharif* seasons. This is in agreement with earlier reports indicating substantial genetic diversity in mungbean materials (Rahim *et al*., 2015; Shyamalee *et al*., 2016; sen *et al*., 2017; Mahalingam *et al*., 2018; Das *et al*., 2019; Subramanian *et al*., 2020).

In *Zaid* season (E1), the highest number of genotypes appeared in cluster VIII which contained 13 genotypes. Cluster II and IV possessed 8 genotypes each while cluster I and III were constituted by 7 genotypes each . Cluster VI and VII possessed 6 genotypes each while cluster IX and X were represented by 2 genotypes each to emerge with minimum entries in all ten clusters. Cluster V had 5 genotypes.

In *Kharif* season (E2), the highest number of genotypes appeared in cluster X which contained 12 genotypes. Cluster V and VII possessed 4 genotypes each while cluster IV consisted of 10 genotypes. Cluster III and VI were constituted by 9 and 8 genotypes, respectively. Cluster II and I were represented by 7 and 5 genotypes, respectively. Cluster VIII has 3 genotypes while Cluster IX possessed 2 genotypes to record minimum number of entries among all ten clusters.

A Perusal of Table 4.5(a) and Table 4.5 (b) reveals that the major clusters in the aforesaid two divergence analysis, in general, contained genotypes of heterogeneous origin. Although the genotypes originated in same place or geographic region were also found to be grouped together, the instances of grouping of genotypes of different origin or geographic region were observed in case of all the clusters in both the seasons except in cluster X in *Zaid* season. This suggests lack of parellelism between genetic and geographic diversity. Therefore, the selection of parental materials for hybridization programme, simply based on geographic diversity may not be successful exercise. The choice of suitable diverse parents based genetic divergence analysis would be more rewarding than the choice on the basis of geographic diversity.

In *Zaid* season (Table 4.6 (a)), highest inter-cluster distance was observed between cluster III and IX followed by high inter-cluster

distances recorded for cluster IX with clusters IV, V, I and II while cluster X also had high order inter cluster distance with III and IV. Thus, crossing of the promising lines of cluster IX with promising genotypes of cluster III, IV, V, I and II is recommended for isolating transgressive segregates in advance generations for *Zaid* season. Similarly, crossing of suitable genotypes of cluster X with those of cluster III and IV may also be fruitful.

In case of *Kharif* season (Table 4.6 (b)), the cluster IX exhibited highest inter-cluster distance with cluster V which was followed by higher inter-cluster distance of cluster IX with clusters III, VI, I and II. Cluster VII also had high order inter-cluster distances with clusters V, IV and VI. Therefore, hybridization of genotypes of cluster IX showing desirable mean performance for yield and yield components with those of cluster V, III, VI, I and II is advocated for evolving superior genotypes in the segregating generations for *Kharif* season. The crossing of promising genotypes of cluster VIII with V, IV and VI may also be considered owing to comparatively higher inter-cluster distances recorded.

The intra-cluster group means for 13 characters of the clusters formed in divergence analysis of *Zaid* and *Kharif* seasons revealed considerable differences between the clusters in respect of cluster means of respective analysis (Table 4.7 (a) and Table 4.7 (b)). The crossing between genotypes belonging to clusters pairs seperated by larger inter-cluster distances and having high cluster means for one or other characters to be improved is likely to be more fruitful for deriving superior segregants leading to development of high yielding varieties of mungbean. Rahim *et al*. (2015), Sirohi *et al*.(2016), Sen *et al*. (2017), Mahalingam *et al*.(2018), Das *et al*. (2019) and Subramanian *et al*. (2020) have also proposed

Table 5.3: The most desirable genotypes identified for high mean performance for 13 characters in mungbean

Characters	Genotypes
Days to 50% flowering	IPM 2-3, P.Mung 4, CoGG 912, VBN(GG)2, LGG 460, LGG450, ADT 3, TM 2000-2, HUM 16, IPM 205-7, CoGG 8 and HUM 12
Days to maturity	P.Mung4, IPM 2-3, CoGG 912, LGG 450, ADT 3, LGG 460, MH 2-15, VBN(GG)2, TM 2000-2, Pusa 9072, CoGG 8, PDM 139, HUM 12
Plant height	TM 2000-2, CoGG 8, Pusa 9072, VBN(GG)2, P.Vishal, TM 96-2, PDM 139, IPM 2-3, LGG 450, HUM 12
Primary branches per plant	P.Mung 4, CoGG 912, MH 2-15, IPM 2-3, ADT 3, IPM 205-7, LGG 460, VBN(GG)2 and HUM 12
Clusters per plant	ADT 3, IPM 2-3, LGG 460, P.Mung4, TM 96-2, TM 2000-2 and TARM 1
Pods per cluster	CoGG 912, TM 96-2, CoGG 8, ADT 3, VBN(GG)2, LGG 460, HUM 12 and IPM 2-3
Pods per plant	ADT 3, TM 96-2, IPM 2-3, LGG 460, CoGG 8, CoGG 912 and P.Mung 4
Pod length	CoGG 912, IPM 205-7, HUM 16, ADT 3, PDM 139, Pusa 9072 and P.Vishal
Seeds per pod	CoGG 912, MH 2-15, ADT-3, P.Mung 4 and P.Vishal
100-seed weight	HUM 16, IPM 2-3, P.Mung 4, P.Vishal, IPM 205-7, Pusa 9072, VBN(GG)2 and CoGG 912
Biological yield per plant	CoGG 912, IPM 2-3, P.Mung 4, ADT 3, TM 96-2, HUM 16 and MH 2-15
Harvest-index	MH 2-15, ADT 3, CoGG 912, LGG 450, P.Mung4, IPM 2-3 and Pusa 9072
Seed yield per plant	CoGG 912, IPM 2-3, P.Mung 4, ADT 3, MH 2-15,TM 96-2 and HUM 16

hybridization between lines belonging to clusters seperated by large inter-cluster distances.

An examination of the estimates of intra- and inter-cluster distances obtained in two seasons revealed that the genotypes of same cluster had little genetic divergence from each other with respect to aggregate effect of 13 characters studied in Table 4.6 (a) and Table 4.6 (b). Therefore, the chances of obtaining good segregates by crossing the members of the same cluster are very low. It would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by larger inter-cluster distances.

5.2.1. Analysis of variance for experiment-II:

The analysis of variance revealed that mean squares due to treatments, parents and crosses were highly significant for the characters viz., days to 50% flowering, days to maturity, plant height, primary branches per plant, clusters per plant, pods per cluster, seeds per pod, 100-seed weight, biological yield per plant, harvest-index and seed yield per plant indicating presence of sufficient variability in the experimental material, while mean squares for pod length and pods per plant were found non – significant . The mean squares due to parents vs crosses were also found total significant for the characters viz., days to 50% flowering, days to maturity, plant height, clusters per plant, pods per cluster, seeds per pod, 100- seed weight and harvest-index, while primary branches per plant, pod length, pods per plant , biological yield per plant and seed yield per plant showed non-significant mean squares. This indicated presence of substantial variability in the materials and validated further statistical and genetical analysis.

5.2.2: Coefficients of variation, heritability and genetic advance:

The success of selection in improving plant characters depends mainly on presence of substantial genetic variability and nature of heritability and gene action. The genetic variability is the raw material of plant breeding programme on which selection acts to evolve superior genotypes. The phenotypic and genotypic coefficients of variation can be used for assessing and comparing the nature and magnitude of variability existing for different characters in the breeding materials. Heritability in the broad sense quantifies the proportion of heritable genetic variance to total phenotypic variance, while heritability in narrow sense represents the ratio of fixable additive genetic variance to total phenotypic variance. Estimates of heritability help in estimating expected progress through selection. The genetic advance in per cent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the character. The estimates of direct selection parameters, coefficients of variation, heritability and genetic advance in per cent of mean were computed for thirteen characters of 60 crosses and nineteen parents (Table 4.9).

The high estimates (<20) of phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded for biological yield per plant,seed yield per plant, plant height, primary branches per plant, pods per plant and seeds per pod which indicated substantial scope for improvement of these traits through selection. The moderate estimates (10-20%) of PCV and GCV were recorded for days to 50% flowering, days to maturity, clusters per plant, pod length and pods per cluster which suggested possibility of obtaining considerable selection advance owing to moderate varibility in there traits . The remaining characters , 100- seed weight and harvest-index

exhibited low estimates (<10%) of PCV or GCV. Low variability indicated that there is little scope of improvement in these traits.

The estimates of heritability in broad sense (h^2b) and genetic advance in % of mean estimated for thirteen characters have been presented in Table 4.8. The estimates of broad sense heritability ranged from 32% (harvest-index) to 96% (plant height). The high heritability in broad sense (>75%) recorded for days to 50% flowering, days to maturity, plant height, seeds per pod, 100-seed weight, seed yield per plant and biological yield per plant indicated existance of high transmissibility of above seven characters. Pods per plant, pod length, primary branches per plant, clusters per plant and pods per cluster showed moderate broad sense heritability (>50% to <75%) and transmissibility which suggested that selection may not be much effective in improving this trait owing to its low transmissibility in context of material evaluated while low heritability (<50%) was found for harvest-index only.

The genetic advance in % of mean was to be very high (>20%) for the characters viz., days to 50% flowering, days to maturity, plant height, primary branches per plant, seeds per pod, pods per plant, biological yield per plant and seed yield per plant. Moderate (>10-20%) estimates of genetic advance in per cent of mean were observed for clusters per plant, pods per cluster, pod length and 100- seed weight, while harvest-index(4.70%) showed low genetic advance (<10%) .

The occurance of high genotypic and phenotypic coefficients of variation and high heritability inbroad sense coupled with high genetic advance in per cent of mean for seed yield per plant, biological yield per plant, seeds per pod and plant height indicated that these four traits would be ideal traits for improvement through selection owing to their high variability and transmissibility in the present material.

The moderate to high GCV and or PCV values along with high heritability and genetic advance recorded for days to 50% flowering and days to maturity suggested that selection would also be efficient in improving these two characters. The moderate to high GCV and PCV estimates with moderate heritability coupled with moderate to high genetic advance observed for primary branches per plant, clusters per plant, pod length, and pods per plant indicated that this material will also be fruitful in obtaining reasonable response to selection due existance of moderate to high variability and transmissibility for there four characters. Pods per cluster showing low GCV with moderate PCV, h^2 and genetic advance and 100-seed weight exhibiting low GCV and PCV with high heritability and moderate genetic advance estimate appear unreliable indices for improvement through selection while very low estimates of all the four parameters recorded for harvest-index shows it as very poor trait for improvement through selection owing to existance of very low variability and transmissibility for this trait in the material evaluated.

The estimates of direct selection parameters observed for the above characters are broadly in agreement with earlier reports in mungbean (Rahim *et al*., 2010; Titumeer *et al*., 2015; Jangra and Yadav, 2015; Pinchhyo *et al*., 2016; Garg *et al*., 2017; Kumar *et al*., 2020).

5.2.3. Correlation coefficients:

Seed yield or economic yield, in almost all the crops, is the complex character which manifests from multiplicative interactions of several other characters that are termed as yield components. The genetic architecture of seed yield in mungbean as well as other crops is based on the balance of yield components directly or indirectly by interacting with one another.

Therefore, selection for yield per se alone would not matter much as such unless accompanied by the selection for various component characters responsible for conditioning it. Thus, identification of important components and information about their association with yield and with each other is very useful for developing efficient breeding strategy for evolving high yielding varieties/ hybrids. The correlation coefficient is the measure of degree of symmetrical association between two variables or characters which helps us in understanding the nature and magnitude of association among yield and yield components for identifying the important yield components.

In the experiment-II, phenotypic (Table 4.10) and genotypic (Table 4.11) correlation coefficients were computed among 13 characters of 60 crosses and their 19 parents. Seed yield per plant showed highly significant and positive phenotypic correlation and very high order positive genotypic correlations with biological yield per plant , pods per plant , seeds per pod , clusters per plant, pods per cluster , primary branches per plant , harvest-index , 100-seed weight and plant height Therefore, these nine characters showing significant positive association with seed yield per plant emerged as most important associates of seed yield per plant in mungbean. The reports of earlier workers have also identified these traits as important associates of seed yield in mungbean. (Katiyar *et al*., 2015; Kumar *et al*., 2015; Suresh and Malathi., 2016; Garg *et al*., 2017; Kumar *et al*., 2018).

Biological yield per plant exhibited strong positive associations at phenotypic as well as genotypic levels with pods per plant, clusters per plant, seeds per pod, pods per cluster and primary branches per plant along with positive association with 100-seed weight. Strong positive association with primary branches per plant and positive association with plant height

and seeds per pod were recorded by harvest-index at both levels. Seeds per pod had highly significant and positive associations at phenotypic level along with high order positive correlations at genotypic level with plant height and primary branches per plant. At both levels, pod length was positively associated with plant height and seeds per pod.

Pods per plant exhibited highly significant and positive correlation along with high or positive genotypic correlation with clusters per plant and pods per cluster which appears logical as there two traits are directly responsible for increasing the number of pods. Strong positive associations at both levels were found for pods per cluster with clusters per plant and primary branches per plant with plant height. The existence of mostly positive association among different character pairs is broadly in agreement of results of previous workers (Suresh and Malathi., 2016; Parihar *et al*., 2018; Ahmad and Belwal, 2020; Majhi *et al*., 2020)

In the present study, majority of significant estimates of phenotypic and high order genotypic correlations between yield and yield components were positive in nature. Out of 29 significant estimates among the total 78 phenotypic correlations obtained between different character pairs, 27 correlation coefficients were positive in nature, while, only two correlation coefficients were negative. Similar trend was observed in case of genotypic correlations also. Even the negative association of primary branches per plant with days to maturity and days to 50% flowering can be considered beneficial for combining greater number of primary branches with early maturity.This represents highly favourable situation for obtaining high response to selection in improving yield and yield components in mungbean. Thus, selection practiced for improving these traits individually or simultaneously would bring improvement in other due to correlated

response. This suggested that selection would be quite efficient in improving yield and yield components.

5.2.4. Path coefficient analysis:

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on seed yield. Path analysis provides clearer picture of character associations for formulating efficient selection strategy. Path coefficient analysis differs from simple correlation in that it points out the causes and their relative importance, whereas, the later measures, simply the mutual association ignoring the causation. The concept of path coefficient was developed by Wright (1921) and technique was first used for plant selection by Dewey and Lu (1959). Path analysis has emerged as a powerful and widely used technique for understanding the direct and indirect contributions of different characters to economic yield in crop plants so that the relative importance of various yield contributing characters can be assessed for devising suitable selection strategy for developing improved varieties.

In the present study, the path coefficient analysis was carried out using phenotypic and genotypic correlation coefficients between thirteen characters of sixty crosses and their 19 parents in *Kharif* season. The very high positive direct effects on seed yield per plant were exerted by pods per plant , followed by seeds per pod , biological yield per plant and 100-seed weight at phenotypic and genotypic levels (Tables 4.12 and 4.13). Thus, pods per plant, seeds per pod, biological yield per plant and 100-seed weight emerged as most important direct yield components on which emphasis should be given during simultaneous selection aimed at

improving seed yield in mungbean. These characters have also been identified as major direct contributors towards seed yield by Ghimire *et al*. (2017), Kumar *et al*. (2018), Parihar *et al*. (2018) and Ahmad and Belwal, (2020).

At phenotypic level, the direct effects of rest of the characters were too low to be considered of any consequence. However, the direct effects of clusters per plant, pods per cluster, harvest-index, pod length and days to 50% flowering were high order negative at genotypic level besides high order positive direct effect shown by plant height on seed yield per plant.

Pods per plant, clusters per plant, seeds per pod, pods per cluster and primary branches per plant exerted high order positive indirect effects on seed yield per plant at phenotypic as well as genotypic levels. Clusters per plant and pods per cluster also had high order positive indirect effects via pods per plant at both levels. Biological yield per plant, plant height, primary branches per plant, pod length and harvest-index recorded substantial positive indirect effects on seed yield per plant via two charecters at phenotypic as well as genotypic level. Biological yield per plant also showed high order positive indirect effects on seed yield per plant via pods per plant.The above results suggest that biological yield per plant, pods per cluster, clusters per plant and primary branches per plant should be considered as most important indirect yield components owing to their high order positive indirect effects on seed yield per plant at phenotypic and genotypic levels via two characters. Plant height, seeds per pod, pod length and harvest-index having substantial positive indirect effect on seed yield per plant at both levels via only one character may be taken as indirect yield components of secondry importance. Kumar *et al*.

(2015), Kumar *et al*. (2018), Garg *et al*. (2017) and Suresh and Malathi. (2016) have also identified above mentioned characters as important direct and indirect yield contributing characters. The indirect effects of remaining characters were too low to be considered important.

In contrary to the results of path analysis at phenotypic level providing small number of high order positive or negative direct and indirect effects, the genotypic path analysis showed fairly higher estimates of high order positive and negative nature. All the twelve characters exerted high order positive indirect effects on seed yield per plant via pods per plant with exception to negative effects of low order by plant height and high order by pod length. All the characters in question exhibited high order negative indirect effects on seed yield per plant at genotypic level via clusters per plant except high order positive indirect effects shown by pod length and plant height. Baring low order negative effects of plant height and 100-seed weight and high order positive effects of pod length, rest of the eight traits exerted high order negative indirect effects on seed yield per plant via pods per cluster at genotypic level. Similarly, primary branches per plant, seeds per pod, biological yield per plant, plant height and pods per cluster recorded considerable negative indirect effects on seed yield per plant via harvest-index at genotypic level. The above disscussion reveals much complex nature of character underlying character association than provided by path analysis at phenotypic level whereas the complex and contrasting nature of direct and indirect effects was unfurled by the path analysis at genotypic level. Thus, genotypic path effects provide deeper and clearer picture of reasons and mechanisms behind conditioning of yield in mungbean.

Majority of the estimates of direct and indirect effects were too low to be considered of any consequence. The existence of different characters combinations in mungbean genotypes might have led to different types of characters associations in different lines. Thus, presence of several contrasting types of character associations or inter-relationships might have resulted into cancellation of contrasting associations by each other ultimately leading to lowering of the net impact or effect.

5.2.5. Combining ability analysis:

The understanding of inheritance of various characters and identification of superior parents are important pre-requisites for launching an effective and efficient breeding programme (Dhillon, 1975). It is not always necessary that parents with high mean performance for yield and other traits would produce desirable F_1s and/or segregants. The selection of a few parents having high genetic potential as per breeding objectives is essential because analyzing and handling of very large number of crosses resulting from numerous parents available in germplasm collections of a crop would be an impractical and perhaps impossible task.

The concept of combining ability has assumed great importance in plant breeding as an effective means of selecting potential parents for hybridization and specific crosses for further exploitation. From the genetic view point, general combining ability (gca) measures additive gene effects and the specific combining ability (sca) measures non additive gene effects including dominance and epistasis. This information on the nature of the gene action present in the population would help to determine an appropriate breeding strategy. Among the various techniques of combining ability analysis, line × tester analysis (Kempthorne, 1957)

has been widely utilized for screening of germplasm to identify valuable donor parents and promising crosses in many crops including mungbean by Vaidya *et al*. (2015), Verma *et al*.(2017), Surashe *et al*.(2017), Hasan *et al*. (2019) and Kakde *et al*. (2019) . The present study, therefore, aims to study the combining ability of parents and crosses and gene action for seed yield per plant and its components by line x tester technique. The important findings of the analysis are discussed below:

5.2.5.1. Gene action and components of genetic variance:

The analysis of variance for combining ability for thirteen characters and estimates of components of genetic variance and other genetic parameters are given in Table 4.14. In the present study, the analysis of variance for combining ability revealed highly significant mean squares due to line x tester interactions for all the characters except harvest-index under study, indicating importance of specific combining ability and non-additive gene effects for all the characters under study except harvest-index. The above discussion suggests occurrence of non-additive gene effects for majority of characters. The mean squares due to testers were highly significant for all the characters except clusters per plant, pods per cluster, pods per plant and seeds per pod while mean squares for lines were significant for all the characters. The occurance of significant mean squares due to lines for all the characters and for testers for most of the characters suggested the importance of general combining ability and additive gene effects for all the characters under study.

The estimates of sca variance were higher than the corresponding estimates of gca variance for all the characters except days to 50% flowering, days to maturity, harvest-index and seed yield per plant . The

value of average degree of dominance were more than unity (>1) revealing over dominance for three characters, namely, pods per cluster, pod length and seeds per pod in the study. The predictability ratio was lesser than one for all the characters except harvest-index. The above results also suggested predominance of non-additive gene effects for all the characters. The importance of additive as well as non-additive gene effects with predominance of non-additive gene effects in inheritance of seed yield and most of the yield components of mungbean has also been reported earlier by Patel *et al*., (2013); Vaidya *et al*. (2015); Purohit *et al*. (2016), Verma *et al*. (2017), Latha *et al*.(2018), Mohan *et al*. (2019) and Kakde *et al*.(2019).

The predominance of non- additive gene effects representing non-fixable dominance and epistatic components of genetic variance indicated that maintenance of heterozygocity would be highly fruitful for improving the characters. Hence, the suitable breeding strategy for attaining high yield would be the full or partial exploitation of heterosis through development of hybrid cultivars for sodic soil. Since, the technology for development of hybrids rice varieties for commercial purposes is being widely and successfully used in different countries including India, it is recommended to explore possibility of isolating high yielding commercial hybrids utilizing the materials of the present investigation. The non-additive gene effects may also be exploited to some extent for improving the characters by resorting to breeding methods such as biparental mating followed by recurrent selection and population improvement methods as suggested by Jensen (1970) and Redden and Jensen(1974).

5.2.5.2. Heritability in narrow sense:

Estimates of heritability in narrow sense reflecting the importance of fixable (additive) gene effects are presented in Table 4.14. All the

characters were found to be highly heritable in nature having high estimates of narrow sense heritability (>30%). Moderate or Low estimates of narrow sense heritability were not found for any of the 13 characters in the present study. High estimates of narrow sense harritability representing existance of high transmissibility and fixable (additive) gene effects for all the 13 characters under study suggested that selection would be highly effective in improving these characters. High to moderate estimates of narrow sense heritability has also been reported by Asari *et al*.(2019), Majhi *et al*.(2020), Azam *et al*.(2018) and Keerthiga *et al*. (2017), for different characters in mungbean.

5.2.5.3. General combining ability:

For illustrating genetic worth of parents for hybridization programme, the general combining ability (gca) effects of 19 parents (15 lines + 4 testers) for thirteen characters are listed in Table 4.15, while the parents exhibiting significant gca effects for different characters are listed in Table 5.3.

The significant and positive gca effects for seed yield per plant were exhibited by the IPM 2-3, P.Vishal, ADT 3, CoGG 912, TM 96-2 and TARM 1 among the lines and Pant Mung 4 among the testers.

The best general combiner line for seed yield per plant, IPM 2-3 also emerged as good general combiner for biological yield per plant, harvest-index, pods per plant, pods per cluster, clusters per plant, 100-seed weight, seeds per pod, early flowering and early maturity besides being average general combiners for rest of the characters.

Table 5.4: Summary of general combining ability effects of parents for 13 characters in mungbean

Character	D50% f	DM	PH	PB/P	C/P	P/C	P/P	PL	S/P	100-S.W.	BY/P	HI	SY/P
Tester													
P.Mung4	+	+	+	0	0	+	+	-	+	0	+	0	+
HUM 16	-	0	-	0	0	0	0	0	-	+	-	0	-
IPM 99-125	0	-	+	-	0	-	-	+	0	-	-	-	-
IPM 205-7	-	-	-	+	0	0	0	+	0	0	0	0	0
Lines													
CoGG 912	0	0	-	+	-	0	-	0	+	+	+	0	+
MH 2-15	+	+	-	+	0	-	-	+	+	0	0	0	0
PDM 139	0	0	+	-	+	0	+	+	-	-	0	0	0
LGG 450	0	0	+	-	+	0	+	+	0	-	+	0	0
ADT 3	+	+	-	+	+	+	+	+	-	-	+	+	+
TARM 1	-	-	-	0	+	+	+	-	0	0	0	+	+
TM 96-2	-	-	0	0	+	+	+	-	0	0	+	0	+
P.Vishal	-	-	+	0	+	0	+	0	0	+	+	0	+
IPM 2-3	+	+	0	0	+	+	+	0	+	+	+	+	+
HUM 12	0	0	0	-	0	0	0	0	0	+	0	0	0
VBN(GG)2	+	+	+	+	0	0	0	0	0	-	-	0	0
TM 2000-2	+	+	+	0	0	0	0	-	-	0	0	-	-
LGG 460	+	+	-	+	-	-	-	-	-	-	-	0	-
Pusa 9072	0	+	+	-	-	-	-	0	-	0	-	+	-
CoGG 8	+	+	+	-	-	-	-	-	-	0	-	-	-

+ = Good combiner, - = Poor combiner, 0= Average combiner

The second ranked good general combiner line for seed yield per plant, P.Vishal was found to be good general combiner for biological yield per plant, 100-seed weight, pods per plant, clusters per plant and short stature but it was poor general combiner of early maturity and early flowering and average general combiner for remaining traits.

The third ranking line, ADT 3 possessed significant gca effects for harvest-index, biological yield per plant, pod length, pods per plant, pods per cluster and clusters per plant, primary branches per plant, tall stature, early flowering and early maturity but emerged as poor general combiner for seeds per pod and 100-seed weight.

The line, CoGG 912, fourth ranked good general combiner for seed yield per plant appeared as good general combiner for biological yield per plant, 100-seed weight, seeds per pod, primary branches per plant and tall stature besides being poor general combiner for pods per plant and clusters per plant.

The fifth ranking good general combiner line, TM 96-2 also showed significant gca effects in desirable direction for biological yield per plant, pods per plant, pods per cluster, clusters per plant besides showing significant gca effects in undesirable direction for pod length, days to 50% flowering and days to maturity.

The sixth ranked good general combiner line for seed yield per plant, TARM 1, was found to be good general combiner for harvest-index, pods per plant, pods per cluster, clusters per plant and plant height but it was poor general combiner for early days to 50% flowering, early maturity and pod length.

The only tester emerging as good general combiner for seed yield per plant, Pant Mung 4 emerged as good general combiner for biological

yield per plant, seeds per pod, pods per plant, pods per cluster, short stature, early days to 50% flowering and early maturity besides being poor general combiner for pod length.

The seven parents showing positive and significant gca effects for seed yield and other important traits as mentioned above may serve as valuable parents for hybridization programme or multiple crossing programme for obtaining high yielding pure line varieties and merit recommendation for exploitation in future hybridization programme.

Some other lines identified as good general combiners in desirable direction for characters other than seed yield per plant are also listed in Table 5.4. These parents may also be recommended for exploitation in hybridization programme as donor of component characters for which they emerged as good general combiners in spite of being average or poor general combiners for seed yield per plant.

It is evident from Table 5.4, that most of the parents (lines + testers) showing significant positive gca effects for seed yield per plant also exhibited positive and significant gca effects for some of the important yield components such as biological yield per plant, pods per plant, pods per cluster, clusters per plant, 100-seed weight and harvest-index. This indicated that the significant gca effects for seed yield in either direction resulted from similar gca effects of some other yield components suggesting that the combining ability for seed yield was influenced by the combining ability of its component traits. Therefore, simultaneous improvement in important yield components and other associated traits along with seed yield may be better approach for raising yield potential in mungbean. The above results are in conformity of the findings of Purohit *et al*.(2016), Verma *et al*.(2017), Surashe *et al*.(2017), Latha *et al*. (2018) and Zuge *et al*. (2018).

Table 5.5: The parents exhibiting significant and desirable general combining ability for different characters

Characters	Parents
Days to 50% flowering	MH 2-15, ADT 3, IPM 2-3, VBN(GG)2, TM 2000-2, LGG 460, CoGG 8, P.Mung 4
Days to maturity	MH 2-15, ADT 3, IPM 2-3, VBN(GG)2, TM 2000-2, LGG 460, Pusa 9072, CoGG 8, P.Mung 4
Plant height	PDM 139, LGG 450, P.Vishal, VBN(GG)2,TM 2000-2, Pusa 9072,CoGG 8, P.Mung 4, IPM 99-125
Primary branches per plant	CoGG 912, MH 2-15, ADT 3, VBN(GG)2,LGG 460, IPM 205-7
Clusters per plant	PDM 139, LGG 450, ADT 3, TARM 1, TM 96-2, P.Vishal, IPM 2-3
Pods per cluster	ADT 3, TARM 1, TM 96-2, IPM 2-3, P.Mung 4
Pods per plant	MH 2-15, PDM 139, LGG 450, ADT 3, IPM 99-125
Pod length	PDM 139, LGG 450, ADT 3, TARM 1, TM 96-2, P.Vishal, IPM 2-3, P.Mung4
Seeds per pod	CoGG 912, MH 2-15, IPM 2-3, P.Mung 4
100-seed weight	CoGG 912, P.Vishal, IPM 2-3, HUM 12, HUM 16
Biological yield per plant	CoGG 912, LGG 450, ADT 3, TM 96-2, P.Vishal, IPM 2-3, P.Mung4
Harvest-index	ADT 3, TARM 1, IPM 2-3, Pusa 9072
Seed yield per plant	CoGG 912, ADT 3, TARM 1, TM 96-2, P.Vishal, IPM 2-3, P.Mung 4

5.2.6.4. Specific combining ability effects:

The specific combining ability (sca) effects, which are supposed to be manifestation of non-additive components of genetic variance, are highly valuable for discrimination of crosses for their genetic worth as breeding materials. The estimates of sca effects of 60 crosses for 13 characters are given in Table 4.16. The most promising specific cross combinations for different characters along with their mean performance and gca effects of parents are listed in Table 5.5.

In present study, none of the crosses showed significant sca effects in desirable direction for all the characters. Several crosses exhibited significant and desirable sca effects for one or more characters but none of them emerged as good specific combination in desirable direction for more than nine characters.

Seven crosses, TARM 1 x IPM 99-125, CoGG 912 x HUM 16, Pusa Vishal x IPM 205-7, ADT 3 x Pant Mung 4, CoGG 912 x Pant Mung 4, IPM 2-3 x HUM 16 and LGG 450 x IPM 99-125 in order of merit showed significant and positive sca effects for seed yield per plant as well as some other yield components.

The cross TARM 1 x IPM 99-125 having highest positive and significant sca effect for seed yield per plant also recorded significant sca effects in desirable direction for biological yield per plant, pods per plant, pods per cluster and short stature.The second ranking cross for higher positive sca effects for seed yield per plant, CoGG 912 x HUM 16, exhibited significant positive sca effects for biological yield per plant, seeds per pod and tall stature but had undesirable negative and significant sca effects for pod length. The third ranking cross for seed yield per plant

Table 5.6: Most promising cross combinations for different characters along with their *per se* performance, sca effects and gca effects of parents.

Characters	Crosses with significant effects	*Per se* performance	Sca effects	gca effects of parents
Days to 50% flowering	IPM 2-3 X P.Mung 4	29.67	-4.939**	H X H
	LGG 460 X P.Mung 4	30.67	-1.522	HXH
	VBN(GG)2 X P.Mung 4	32.33	-2.689	HXH
	ADT 3X P.Mung 4	32.67	0.644	HXH
	CoGG 912 X P.Mung 4	33.67	-4.439**	AXH
Days to maturity	LGG 460 X P.Mung 4	59.67	-3.122	H X H
	CoGG 912 X P.Mung 4	60.33	-8.872**	A X H
	IPM 2-3 x P.Mung4	61.33	-4.039*	H X H
	Pusa 9072 X P.Mung 4	62.33	-1.539	H X H
	VBN(GG)2 X P.Mung 4	62.67	-3.372	H X H
Plant height	CoGG 8 x IPM 99-125	20.60	-4.664**	H X H
	TM 2000-2 X P.Mung 4	21.50	-4.215	H X H
	P.Vishal X HUM 16	25.70	-6.722**	H X L
	Pusa 9072 X P.Mung 4	26.47	-2.940**	H X H
	TM 2000-2 X IPM 99-125	27.23	3.127**	H X L
Primary branches per plant	CoGG 912 X P.Mung 4	5.40	0.881**	H X A
	MH 2-15 X P.Mung 4	5.20	1.164**	H X L
	CoGG 912 X IPM 205-7	4.20	-0.397	H X H
	VBN (GG) 2 x IPM 205-7	4.13	0.303	H X H
	ADT 3 X IPM 205-7	3.93	0.053	H X H
Clusters per plant	TM 96-2 X P.Mung 4	6.87	6.867	H X A
	IPM 2-3 X HUM 16	6.80	6.8	H X A
	P.Vishal X IPM 205-7	6.73	-6.733	H X A
	TARM 1 X IPM 99-125	6.67	-6.667	H X A
	CoGG 912 X P.Mung 4	6.47	-1.241**	L X A
Pods per cluster	TARM 1 X IPM 99-125	7.27	-0.648	H X L
	TARM 1 X IPM 205-7	7.13	-0.306	H X A
	TM 96-2 X P.Mung4	6.93	-0.087	H X H
	TM 96-2 X IPM 205-7	6.87	-0.122	H X A
	VBN(GG) 2 X IPM 205-7	6.80	0.439	A X A

Contd…..

Pods per plant	TARM 1 X IPM 99-125	48.73	9.333**	H X L
	TM 96-2 X P.Mung 4	47.73	4.475	H X H
	ADT 3 X P.Mung 4	47.53	3.758	H X H
	P.Vishal X IPM 205-7	47.13	5.425	H X H
	CoGG 912 X P.Mung 4	46.27	13.618	L X H
Pod length	MH 2-15 X P.Mung4	8.60	0.970**	H X L
	CoGG 912 X IPM 99-125	8.23	-1.107**	A X H
	ADT 3 X HUM 16	8.20	0.437	H X A
	MH 2-15 X HUM 16	7.97	0.037	H X A
	MH 2-15 X IPM 99-125	7.90	-0.234	H X H
Seeds per pod	CoGG 912 X IPM 99-125	11.53	2.089**	H X A
	CoGG 912 X HUM 16	10.60	1.516**	H X L
	MH 2-15 X P.Mung 4	9.07	1.539**	H X H
	CoGG 912 X IPM 205-7	8.20	1.160**	H X A
	ADT 3 X P.Mung4	8.13	0.272	L X H
100- seed weight	P.Vishal x HUM 16	3.90	0.046	H X H
	MH 2-15 X HUM 16	3.87	0.263**	A X H
	P.Vishal X P.Mung 4	3.80	0.026	H X A
	CoGG 912 X HUM 16	3.77	0.071	H X H
	HUM 12 X HUM 16	3.70	-0.021	H X H
Biological yield per plant	CoGG 912 X P.Mung 4	41.07	6.569**	H X H
	ADT 3 X P.Mung 4	40.93	4.894**	H X H
	P.Vishal X IPM 205-7	40.87	6.103**	H X A
	TM 96-2 X P.Mung 4	40.17	4.594*	H X H
	CoGG 912 X HUM 16	37.77	8.596**	H X L
Harvest-index	TARM 1 X P.Mung 4	32.50	0.502	H X A
	VBN(GG)2 X P.Mung 4	32.36	1.73	A X A
	ADT 3 X P.Mung 4	32.18	0.383	H X A
	MH 2-15 X P.Mung 4	32.07	1.706	A X A
	IPM 2-3 X HUM 16	32.03	0.531	H X A
Seed yield per plant	CoGG 912 X P.Mung 4	12.96	1.761**	H X H
	CoGG 912 X IPM 99-125	11.53	-1.605**	H X L
	CoGG 912 X HUM 16	10.60	2.125**	H X L
	MH 2-15 X P.Mung 4	9.07	1.149	A X H
	CoGG 912 X IPM 205-7	8.20	-2.280**	H X A

H= High, A= Average, L=Low

Pusa Vishal x IPM 205-7, was found to possess significant gca effects in desirable direction for biological yield per plant and pods per plant and in undesirable direction for days to 50% flowering and days to maturity. The fourth ranked cross ADT 3 x Pant Mung 4 resulted significant positive and desirable sca effects for seed yield per plant, biological yield per plant and 100-seed weight and undesirable sca effects for days to maturity.

The cross, CoGG 912 x Pant Mung 4, ranked fifth for higher positive and significant sca effects for seed yield per plant, exhibited significant sca effect in desirable direction for biological yield per plant, 100-seed weight, pods per plant, pods per cluster, clusters per plant, primary branches per plant, days to maturity and days to 50% flowering but had undesirable negative and significant sca effect of seeds per pod. This cross merits special attention for further exploitation in breeding programme because of having significant sca effects in desirable direction for nine characters that included seed yield per plant days to 50% flowering and days to maturity. The cross, IPM 2-3 x HUM 16 ranked sixth for higher positive and significant sca effects for seed yield per plant had significant sca effects in desirable direction for pods per plant, days to maturity and days to 50% flowering and also appears promising for combining higher seed yield with early flowering and maturity.

The seventh ranked cross exhibiting significant positive sca effects for seed yield per plant, LGG 450 x IPM 99-125, also had desirable positive and significant sca effects for seeds per pod.

The seven crosses having significant and positive sca effects for seed yield per plant also showed significant sca effects in desirable direction for some other characters, most commonly biological yield per

plant and pods per plant. This suggested that manifestation of sca effects for grain yield is related with higher sca effects for important yield components.

In general, the crosses showing significant and desirable sca effects were associated with better *per se* performance for respective traits. However, the crosses having high sca effects in desirable direction did not always have high mean performance for the character in question. Thus, the sca effect of the crosses may not be directly related to their *per se* performance. This may be attributed to the fact that per seperformance is a realized value, whereas, sca effect is an estimate of F_1 performance over parental one. Therefore, both *per se* performance along with sca effects should be considered for evaluating the superiority of a cross although the former may be more important if development of F_1 hybrids is the ultimate objective. The most promising five crosses having significant and desirable sca effects for different characters are listed along with their mean performance and gca effects of their parents in Table 5.5.

The critical examination of Table 5.5 would reveal that the crosses exhibiting high order significant and desirable sca effects for different characters involved parents having all types of combinations of gca effects such as high × high (H × H), high × average (H × A), high × low (H × L), average × average (A × A), average × low (A × L) and low × High (L × H) general combiner parents. The foregoing observation clearly indicated that there was no particular relationship between positive and significant sca effects of crosses with gca effects of their parents for the characters under study. Singh *et al*. (2016), Surashe *et al*. (2017), Latha *et al*. (2018), Kakde *et al*. (2019) and Rathod *et al*. (2020) have also reported similar findings.

High x high, high x average and average x average crosses give transgressive segregants and selection in early generations would be advantageous for development of pure lines as there is involvement of additive gene action, whereas, crosses having high x low, average x low and low x low general combining parents are suggested for heterosis breeding as their inheritance are controlled by non additive and epistatic gene action.

5.2.6. Heterosis:

The heterosis breeding has been extensively utilized in improving yield particularly in allogamous crops. The exploitation of heterosis in mungbean has been limited due to its autogamous nature. The presence of high heterosis for economically important characters is not only useful for developing hybrids through exploitation of heterosis, but also helps in obtaining transgressive segregants for development of superior homozygous lines in autogamous crops like mungbean. Several studies on heterosis in mungbean have revealed occurance of both significantly positive and negative heterosis for seed yield and other characters in mungbean (Lavanya *et al*., 2015; Dhurai *et al*., 2016; Vaidya *et al*., 2016; Nath *et al*., 2017; Latha *et al*., 2019; Hange *et al*., 2020).

In the present study, manifestation of heterosis in mungbean was examined by estimating heterosis over better parent (Heterobeltiosis) and check variety (standard heterosis) for 60 F_{1s} to assess their genetic potential as breeding material.

A wide range of variation in the estimates of heterobeltiosis and standard heterosis in positive and negative direction was observed for seed yield per plant (Table 4.18). In case of seed yield per plant, heterobeltiosis ranged from -56.31 to 64.70% and standard heterosis varied from -66.80 to

16.11% over standard variety, Pant Mung 5. Nine crosses showed positive and significant heterobeltiosis, which were P. Vishal x IPM 205-7 (64.70%),TARM 1 x IPM 99-125 (61.05%), LGG 450 x IPM 99-125 (48.29%),TARM 1 x IPM 205-7 (47.90%) and HUM 12 x IPM 99-125 (44.46%), PDM 139 x IPM 205-7 (36.14%), HUM 12 x IPM 205-7 (34.91%), LGG 450 x IPM 205-7 (29.95%) and P.Vishal x IPM 99-125 (24.79%). However, only one cross, ADT 3 x Pant Mung 4 exhibited positive and significant standard heterosis over Pant Mung 5 for seed yield per plant. The crosses mentioned above merit consideration for exploitation in breeding programme for isolating transgressive segregants for seed yield and yield components for developing superior mungbean varieties.

Among the nine crosses exhibiting positive and significant heterobeltiosis for seed yield per plant, the positive and significant heterobeltiosis was also recorded for pods per plant, biological yield per plant and pods per cluster by 6,5 and 5 crosses, respectively. This suggests that positive heterobeltiosis for some yield components like pods per plant, biological yield per plant and pods per cluster contributed towards manifestation of positive heterosis for seed yield per plant. Similarly, the crosses exhibiting negative and significant heterobeltiosis for seed yield per plant showed mostly negative and significant heterobeltiosis for such yield components. However, heterosis in seed yield per plant was not proportional to the heterosis in all the yield components and heterosis in some of the yield components registered heterosis in seed yield.

Besides yield, considerable heterosis over better-parent and standard varieties was also observed in negative as well as in positive direction for remaining characters (Table 4.11). However, the number of crosses

showing significant estimates of heterobeltiosis and standard heterosis and their range varied from one character to another. In the present study, comparatively much lesser number or proportion of the crosses registered positive and significant heterobeltiosis and standard heterosis for seed yield and its components than generally encountered in mungbean while crosses exhibiting negative and significant estimates of both types of heterosis were much higher as compared to earlier reports (Lavanya *et al*., 2015; Dhurai *et al*., 2016; Vaidya *et al*., 2016; Nath *et al*., 2017; Latha *et al*., 2019, Hange *et al*., 2020). This occurance of exceptionally greater number of negative and significant estimates of heterobeltiosis and standard heterosis in the present study may be attributed to unusual genotype x environment interactions resulting to adverse environmental conditions during later stages of crop season *Kharif* , 2019.

Chapter-VI

SUMMARY AND CONCLUSION

The present investigation entitled “Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek]” was under taken to : to evaluate mungbean germplasm lines for yield and yield components, (ii) to study the character associations among different quantitative characters, (iii) to examine the genetic divergence existing in the germplasm collections, (iv)to assess nature and magnitude of gene action for yield and other yield components, (v) to estimate general and specific combining ability variances and their effects, (vi) to study nature and extent of heterosis over better- parent and standard variety for yield and its components, (vii) to sort out promising heterotic combinations for yield and its contributing traits.

The present invstigation was comprised of two experiments, namely, the germplasm evaluation experiment (experiment-I) and combining ability experiment (experiment-II). Both experiments were conducted at Instructional Farm of Acharya Narendra Dev University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya during *Zaid* and *Kharif* seasons of 2019. Thirteen plant characters viz., days to 50% flowering, days to maturity, plant height (cm.), primary branches per plant, clusters per plant , pods per cluster, pod length (cm.), pods per plant, seeds per pod, 100- seed weight (g.), biological yield per plant (g.), harvest-index (%) and seed yield per plant (g.) were studied in the experiments.

In the germplasm evaluation experiment (experiment-I), sixty germplasm lines of mungbean and four checks were evaluated in augmented design in *Zaid* as well as *Kharif* seasons of 2019. The nature of

associations among different characters was studied by using simple correlations and path- coefficient analysis (Wright, 1921; Dewey and Lu, 1959). Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) was employed for studying the genetic divergence among the germplasm collections.

In the combining ability experiment (experiment-II), line x tester set of sixty F_{1s} and their 19 parents with one check (P.mung 4) were evaluated for thirteen characters in Randomized Block Design with three replications during *Kharif* season, 2019. The 60 F_{1s} were generated by crossing 15 lines and 4 testers during *Zaid*, 2019. The data on thirteen characters was subjected to analysis of variance for Randomized complete block design (Panse and Sukhatme, 1967), line x tester analysis for combining ability (Kempthorne, 1957), estimation of heterosis over better-parent and standard variety (Fonseca and Patterson, 1968), computation of heritability in broad sense (Hanson *et al.,* 1963) and genetic advance in per cent of mean (Johnson *et al.,* 1955), estimation of correlation coefficients (Searle, 1961) and path- coefficient analysis (Dewey and Lu, 1959).

The salient results of present study and conclusions drawn are summarized below:

1. In *Zaid* season, SML 823 produced (8.77g) hieghest seed yield per plant followed by DGGV 2, BM 4, HUM 12, TM 96-2 and ADT 3. Thus constituting the top non-significant group for higher seed yield per plant of six genotypes. These six lines also showed high mean performance for 3, 4 other characters by being in top non-significant group for those traits. Thus therefore these 6 lines may be considered for use in hybridization programme as parents aimed for development of high yielding varieties of mungbean in *Zaid* season.

2. In *Kharif* season, the highest seed yield per plant was produced by DGGV 2 (12.63 g) followed by ADT 3, P. Mung 6, P. Mung 5, P. Mung 2, MH 2-15, which were also statistically at par with DGGV 2 highest yielding line. The above six lines were also in the top non significant group for performance in desirable direction for 3 to 7 charecters. These genotypes also merit consideration for involving in crossing performance as parents for involving superior mungbean variety for *Kharif* season.
3. In addition to the genotypes identified above for high seed yield and some of its important components in respective (*Zaid* and *Kharif*) seasons some other lines showing very high mean performance for characters other than seed yield per plant were also identified which may be used as donors for other characters. A breeding programme based on component breeding approach even if they had medium or low mean performance for seed yield per plant.
4. Biological yield per plant, pods per plant, clusters per plant, harvest-index and pods per cluster exibited highly significant and possitive correlation with seed yield per plant in *Zaid* season, to appeaar as most important charecters in influencing seed yield in mungbean in *Zaid* season.
5. Seed yield per plant recorded highly significant and positive association with biological yield per plant, pods per plant, clusters per plant, harvest-index, primary branches per plant and seeds per pod besides having significant positive correlation with pods per cluster, plant height and pod length. Thus, these nine traits emerged as important associates of seed yield per plant in mungbean in *Kharif* season.

6. Biological yield per plant followed by harvest-index and days to 50% flowering exerted highest positive direct effects on seed yield per plant to become as most important direct contributors of seed yield per plant in mungbean in *Zaid* season .
7. Pods per plant, pods per cluster, seeds per pod and 100-seed weight emerged as the most important indirect seed yield components in mungbean for *Zaid* season, by virtue of having substantial positive indirect effects via two or more characters, while clusters per plant, harvest-index, primary branches per plant and pod length appeared as indirect yield components of secondary importance sowing the substantial positive indirect effects via one character.
8. Biological yield per plant followed by pods per plant and harvest-index exerted high order positive direct effects on seed yield per plant to emerge as important direct contributors of seed yield in mungbean in *Kharif* season.
9. Pods per plant, primary branches per plant, clusters per plant, seeds per pod, harvest-index, pods per cluster and biological yield per plant were identified as most important indirect seed yield attributes in mungbean for *Kharif* season owing to their high order positive indirect effects on seed yield via two or more characters.
10. In the present study, the 64 genotypes of mungbean were grouped into ten distinct non-overlapping clusters using Non-hierarchical Euclidean cluster analysis in *Zaid* as well as *Kharif* seasons, indicating presence of substantial genetic diversity in the germplasm collections evaluated in the present study in context of *Zaid* as well as *Kharif* seasons.

11. The major clusters in the aforesaid two divergence analyses, in general, contained genotypes of heterogeneous origin. Although the genotypes originated in same place or geographic region were also found to be grouped together, the instances of grouping of genotypes of different origin or geographic region were observed in case of all the clusters in both the seasons except in cluster X in *Zaid* season. This suggests lack of parellelism between genetic and geographic diversity. Therefore, the selection of parental materials for hybridization programme, should be based on genetic divergence analysis rather than geographic origin.
12. The highest inter-cluster distance was observed between cluster III and IX followed by high inter-cluster distances recorded for cluster IX with clusters IV, V, I and II while cluster X also had high order inter-cluster distance with III and IV. Thus, crossing of the promising lines of cluster IX with promising genotypes of cluster III, IV, V, I and II is recommended for isolating transgressive segregates in advance generations for *Zaid* season. Similarly, crossing of suitable genotypes of cluster X with those of cluster III and IV may also be fruitful.
13. In case of *Kharif* season, the cluster IX exhibited highest inter-cluster distance with cluster V which was followed by higher inter cluster distances of cluster IX with clusters III, VI, I and II. Cluster VII also had high order inter-cluster distances with clusters V, IV and VI. Therefore, hybridization of genotypes of cluster IX showing desirable mean performance for yield and yield components with those of cluster V, III, VI, I and II is advocated for evolving superior genotypes in the segregating generations for

Kharif season. The crossing of promising genotypes of cluster VIII with V, IV and VI may also be considered owing to comparatively higher inter-cluster distances recorded.

14. An examination of the estimates of intra- and inter-cluster distances obtained in two seasons revealed that the genotypes of same cluster had little genetic divergence from each other with respect to aggregate effect of 13 characters studied in the experiments. Therefore, the chances of obtaining good segregates by crossing the members of the same cluster are very low. It would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by larger inter-cluster distances.
15. The mean squares due to parents, crosses and parents vs crosses were found to be significant for most of the characters indicating thereby presence of substantial variability in the materials and validated further statistical and genetical analysis.
16. The occurance of high genotypic and phenotypic coefficients of variation and high heritability in broad sense coupled with high genetic advance in per cent of mean for seed yield per plant, biological yield per plant, seeds per pod and plant height indicated that these four traits would be ideal traits for improvement through selection owing to their high variability and transmissibility in the present material.
17. Seed yield per plant showed highly significant and positive phenotypic correlations and very high order positive genotypic correlations with biological yield per plant , pods per plant , seeds per pod , clusters per plant, pods per cluster , primary branches per plant , harvest-index , 100-seed weight and plant height. Therefore,

these nine characters showing significant positive association with seed yield per plant emerged as most important associates of seed yield per plant in mungbean.

18. Pods per plant, seeds per pod, biological yield per plant and 100-seed weight emerged as most important direct yield components on which emphasis should be given during simultaneous selection aimed at improving seed yield in mungbean.
19. Biological yield per plant, pods per cluster, clusters per plant and primary branches per plant should be considered as most important indirect yield components owing to their high order positive indirect effects on seed yield per plant at phenotypic and genotypic levels via two characters. Plant height, seeds per pod, pod length and harvest-index having substantial positive indirect effect on seed yield per plant at both levels via only one character may be taken as indirect yield components of secondry importance.
20. In the analysis of variance for combining ability of line x tester set, the mean square due to lines, testers and line x testers interactions were significant for most of the characters indicating importance of additive as well as non-additive gene effects in their inheritance. The estimates of sca variance were higher than the corresponding estimates of gca variance for all the characters except days to 50% flowering, days to maturity, harvest-index and seed yield per plant . The value of average degree of dominance were more than unity (>1) revealing over dominance for three characters, namely, pods per cluster, pod length and seeds per pod in the study. The predictability ratio was lesser than one for all the characters except harvest-index. The above results also suggested importance of

aditive as well as non-aditive gene effects with predominance of non-additive gene effects for all the characters.

21. The significant and positive general combining ability effects for seed yield per plant were exhibited by the IPM 2-3, P.Vishal , ADT 3, CoGG 912, TM 96-2 and TARM 1 among the lines and Pant Mung 4 among the testers. These parents merit consideration for exploitation in hybridization programme for developing high yielding mungbean genotypes.
22. Some other lines identified as good general combiners in desirable direction for characters other than seed yield per plant were identified which also be recommended for exploitation in hybridization programme as donor of component characters for which they emerged as good general combiners inspite of being average or poor general combiners for seed yield per plant.
23. Seven crosses, TARM 1 x IPM 99-125, CoGG 912 x HUM 16, Pusa Vishal x IPM 205-7, ADT 3 x Pant Mung 4, CoGG 912 x Pant Mung 4, IPM 2-3 x HUM 16 and LGG 450 x IPM 99-125 in order of merit showed significant and positive sca effects for seed yield per plant as well as some other yield components to emerge as crosses of potential genetic worth for further exploitation for isolating desirable segregates in segregating generation for developing high yielding mungbean varieties.
24. A wide range of variation in the estimates of heterobeltiosis and standard heterosis in positive and negative direction was observed for seed yield per plant. In case of seed yield per plant, heterobeltiosis ranged from -56.31 to 64.70% and standard heterosis varied from -66.80 to 16.11% over standard variety, Pant Mung 5.

25. Nine crosses showed positive and significant heterobeltiosis, which were P. Vishal x IPM 205-7 (64.70%), TARM 1 x IPM 99-125 (61.05%), LGG 450 x IPM 99-125 (48.29%), TARM 1 x IPM 205-7 (47.90%) and HUM 12 x IPM 99-125 (44.46%), PDM 139 x IPM 205-7 (36.14%), HUM 12 x IPM 205-7 (34.91%), LGG 450 x IPM 205-7 (29.95%) and P.Vishal x IPM 99-125 (24.79%). However, only one cross, ADT 3 x Pant Mung 4 exhibited positive and significant standard heterosis over Pant Mung 5 for seed yield per plant. The crosses mentioned above merit consideration for exploitation in breeding programme for isolating transgressive segregants for seed yield and yield component for developing superior mungbean varieties.

Chapter-VII

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APPENDIX-I

Name of all the sixty germplasm lines evaluated in the experiment

S.No.	Genotypes	S.No.	Genotypes
1.	CoGG 912	33.	VBN(GG) 2
2.	MH 2-15	34.	CO 6
3.	TM 96-2	35.	LGG 450
4.	ADT 3	36.	TMB 37
5.	SML 823	37.	Kopergaon
6.	LGG 460	38.	4RMG1028
7.	MH 421	39.	MH 318
8.	P. Mung 2	40.	5-BWME
9.	Pusa 9531	41.	2-1 PM409
10.	TARM 1	42.	KM 18-117
11.	DGGV 2	43.	KM 18-111
12.	OUM 11-5	44.	KM 18-115
13.	BM 4	45.	KM 18-106
14.	IPM 2-3	46.	KM 18-99
15.	DGGS 4	47.	KM 18-109
16.	Phule Mung	48.	KM 18-121
17.	HUM 12	49.	KM 18-102
18.	DGGV 5	50.	KM 18-114
19.	DGG 1	51.	KM 18-97
20.	SML 1082	52.	KM 18-105
21.	KM 11-584	53.	KM 18-116
22.	P. Mung 6	54.	KM 18-103
23.	P. Mung 5	55.	KM 18-122
24.	PDM 139	56.	KM 18-108
25.	TM 2000-2	57.	P.Mung4
26.	IPM 2-14	58.	HUM 16
27.	CO(GG) 8	59.	IPM 99-125
28.	KM 22-41	60.	IPM 205-7
29.	MGG 347	61.	ML 613
30.	PKVAKM 4	62.	IPM 410-3
31.	P. Vishal	63.	ML 818
32.	SML 668	64.	Pusa 9072

APPENDIX- II

Mean performance, general mean, range, coefficient of variation, critical difference and standard error for 13 characters of line x tester set of 60 F_{1s} and their 19 parents along with 1 check

Characters	D50%f	DM	PH	PB/ P	C/ P	P/ C	P/ P	Pl (cm.)	S/ P	100 S.W.	HI	BY/ P	GY/ P
CoGG 912 x P. MUNG 4	33.67	60.33	34.03	5.40	6.47	7.13	46.27	6.17	7.40	3.80	31.53	41.07	12.96
CoGG 912 x HUM 16	43.33	77.33	58.87	4.20	4.73	6.47	29.33	6.30	10.60	3.77	31.36	37.77	11.85
CoGG 912 x IPM 99-125	43.67	83.67	46.70	3.87	4.33	5.00	21.16	8.23	11.53	3.27	27.98	25.20	7.90
CoGG 912 x IPM 205-7	50.67	95.67	59.07	4.20	4.93	5.53	27.13	7.17	8.20	3.63	31.69	20.00	8.07
MH 2-15 x P.MUNG 4	35.33	64.33	61.53	5.20	5.53	5.87	33.40	8.60	9.07	3.43	32.07	32.40	10.38
MH 2-15 x HUM 16	39.33	76.33	59.13	3.67	5.33	5.07	26.93	7.97	6.27	3.87	28.96	22.73	6.52
MH 2-15 x IPM 99-125	41.33	79.33	54.27	3.47	6.13	6.20	38.00	7.90	6.60	3.20	29.07	27.57	8.02
MH 2-15 x IPM 205-7	47.67	82.67	33.87	3.40	5.60	6.13	34.20	7.43	6.53	3.60	29.54	26.97	7.96
PDM 139 x P. MUNG 4	43.33	73.33	31.37	2.80	6.13	6.73	41.47	7.77	6.13	3.30	29.82	28.07	8.37
PDM 139 x HUM 16	46.67	83.67	31.53	2.67	6.00	6.73	40.60	6.37	6.20	3.30	29.69	27.70	8.24
PDM 139 x IPM 99-125	42.33	80.33	29.60	2.73	5.80	5.87	34.20	7.90	5.87	3.27	28.80	22.77	6.56
PDM 139 x IPM 205-7	47.67	82.67	33.20	3.40	6.40	6.60	42.20	7.43	5.93	3.37	29.38	28.70	8.46
LGG 450 x P. MUNG 4	43.33	73.33	31.47	2.80	6.27	6.73	42.47	7.77	6.40	3.37	29.89	30.53	9.14
LGG 450 x HUM 16	46.67	83.67	31.53	2.67	6.20	6.33	39.47	6.70	5.87	3.30	30.01	25.60	7.65
LGG 450 x IPM 99-125	42.33	80.33	29.60	2.73	5.93	6.67	39.80	7.90	7.13	3.23	29.09	31.97	9.24
LGG 450 x IPM 205-7	47.67	82.67	33.87	3.40	6.27	6.27	39.33	7.43	5.73	3.60	29.30	27.70	8.10
ADT 3 x P. MUNG 4	32.67	64.33	42.07	3.87	6.67	7.13	47.53	7.97	8.13	3.40	32.18	40.93	13.16
ADT 3 x HUM 16	39.33	69.33	44.00	3.47	6.40	6.27	40.33	8.20	7.00	3.07	31.64	27.50	8.67
ADT 3 x IPM 99-125	34.33	70.33	39.47	3.53	5.93	6.73	39.93	7.97	6.60	3.20	31.03	27.07	8.40
ADT 3 x IPM 205-7	40.67	75.33	44.17	3.93	6.33	6.40	40.60	7.10	8.07	3.23	30.52	34.70	10.59
TARM 1 x P. MUNG 4	40.67	68.33	41.10	3.53	5.47	6.40	35.07	5.80	5.80	3.40	32.50	21.27	6.92
TARM 1 x HUM 16	49.33	84.33	48.30	3.80	6.07	6.27	38.13	6.83	6.53	3.50	31.20	27.90	8.69
TARM 1 x IPM 99-125	50.67	89.33	35.43	3.27	6.67	7.27	48.73	6.33	6.27	3.40	30.67	34.33	10.49
TARM 1 x IPM 205-7	55.33	94.67	38.03	3.87	5.80	7.13	41.60	7.23	6.60	3.47	31.82	30.10	9.63
TM 96-2 x P. MUNG 4	55.67	85.33	39.70	2.90	6.87	6.93	47.73	5.80	6.93	3.50	28.84	40.17	11.58
TM 96-2 x HUM 16	43.33	83.67	36.27	3.27	6.20	6.60	41.20	6.43	5.93	3.60	30.85	29.13	8.91

TM 96-2 x IPM 99-125	47.33	88.67	31.80	3.27	5.60	6.33	35.67	6.77	7.00	3.33	29.83	28.10	8.40
TM 96-2 x IPM 205-7	50.67	91.33	42.90	3.40	6.07	6.87	41.73	6.93	6.67	3.40	30.87	30.93	9.44
P. Vishal x P. MUNG 4	55.67	87.33	28.93	3.27	6.13	6.40	39.40	6.10	7.07	3.80	29.80	35.50	10.55
P. Vishal x HUM 16	63.67	100.67	25.70	3.13	5.87	6.40	37.73	6.63	6.27	3.90	28.71	32.03	9.20
P. Vishal x IPM 99-125	67.33	107.67	30.90	3.13	6.13	6.47	39.87	7.60	6.67	3.60	29.93	32.10	9.58
P. Vishal x IPM 205-7	71.33	114.33	32.73	3.27	6.73	6.93	47.13	7.23	7.20	3.80	31.04	40.87	12.64
IPM 2-3 x P.MUNG 4	29.67	61.33	32.60	3.40	6.33	6.67	42.60	6.43	7.87	3.47	31.88	36.47	11.66
IPM 2-3 x HUM 16	35.67	70.33	37.60	3.53	6.80	7.13	48.73	7.33	6.60	3.67	32.03	36.06	11.75
IPM 2-3 x IPM 99-125	40.67	77.33	35.30	3.27	5.67	6.67	37.93	7.17	6.13	3.57	31.85	26.03	8.28
IPM 2-3 x IPM 205-7	51.33	92.67	39.40	3.60	6.20	7.13	44.60	7.97	6.87	3.70	31.03	36.73	11.39
HUM 12 x P. MUNG 4	40.67	70.67	37.77	2.87	5.87	6.47	38.07	6.57	7.60	3.60	31.69	33.00	10.47
HUM 12 x HUM 16	45.67	72.33	40.70	3.13	5.27	6.53	34.47	7.27	5.40	3.70	31.84	21.67	6.88
HUM 12 x IPM 99-125	50.67	85.67	33.57	2.93	5.40	6.53	35.27	6.97	6.60	3.47	30.37	26.80	8.12
HUM 12 x IPM 205-7	42.67	84.67	37.70	3.67	5.80	6.60	38.40	7.53	5.73	3.80	30.58	27.37	8.39
VBN (GG)2 x P. MUNG 4	32.33	62.67	29.97	3.53	5.67	6.20	34.93	6.73	7.87	3.30	32.36	28.00	9.06
VBN (GG)2 x HUM 16	42.67	77.67	36.20	3.73	5.87	6.20	35.73	6.97	6.27	3.47	27.64	12.23	7.77
VBN (GG)2 x IPM 99-125	40.67	81.67	29.53	3.20	5.67	6.00	33.80	7.53	6.00	3.40	29.85	22.53	6.72
VBN (GG)2 x IPM 205-7	43.33	82.33	33.60	4.13	6.00	6.80	40.87	7.60	6.13	3.23	30.85	26.30	8.14
TM 2000-2 x P. MUNG 4	39.33	68.33	21.50	3.07	5.47	6.33	34.73	6.27	6.80	3.50	28.43	29.00	8.24
TM 2000-2 x HUM 16	47.33	76.67	31.33	3.47	5.87	6.60	38.87	6.60	4.80	3.50	27.34	24.00	6.52
TM 2000-2 x IPM 99-125	44.67	78.67	27.23	3.20	6.07	6.07	36.93	6.40	5.87	3.43	27.29	27.23	7.42
TM 2000-2 x IPM 205-7	36.67	73.33	27.57	3.13	5.40	6.07	32.87	7.27	6.07	3.50	28.98	24.17	7.00
LGG 460 x P. MUNG 4	30.67	59.67	45.50	3.80	5.13	6.07	31.20	6.10	5.20	3.20	30.51	17.07	5.20
LGG 460 x HUM 16	36.67	72.33	45.57	3.73	4.07	5.73	23.40	6.63	4.73	3.43	29.27	12.87	3.76
LGG 460 x IPM 99-125	37.67	79.67	35.60	3.40	4.47	5.27	23.47	6.93	5.53	3.37	30.73	14.23	4.38
LGG 460 x IPM 205-7	42.67	79.67	45.43	3.73	4.00	5.73	22.67	6.37	5.73	3.40	31.63	14.03	4.42
Pusa 9072 x P. Mung 4	36.33	62.33	26.47	3.13	3.80	6.27	23.60	6.63	6.53	3.50	31.04	17.40	5.39
Pusa 9072 x HUM16	55.33	78.33	31.93	2.87	4.33	5.07	22.07	7.87	5.93	3.60	31.25	15.20	4.74
Pusa 9072 x IPM 99-125	41.67	78.67	28.23	3.13	4.20	5.87	24.53	6.97	5.73	3.30	31.59	14.87	4.59
Pusa 9072 x IPM 205-7	44.67	76.33	35.77	3.47	4.47	5.67	25.20	7.63	6.07	3.43	31.90	16.47	5.26
CoGG 8 x P.MUNG 4	38.33	65.67	27.97	3.20	4.73	5.60	26.27	6.23	5.87	3.50	27.70	19.47	5.38
CoGG 8 x HUM 16	43.33	66.33	34.03	3.40	5.00	5.93	29.60	7.33	4.87	3.60	28.68	18.03	5.17

CoGG 8 x IPM 99-125	34.33	69.33	20.60	2.33	5.40	5.33	28.07	5.93	5.13	3.40	27.36	17.83	4.87
CoGG 8 x IPM 205-7	35.67	72.67	29.67	3.33	5.67	5.53	31.20	7.23	5.87	3.40	28.49	7.53	6.23
CoGG 912	34.33	62.33	55.07	4.87	5.60	7.07	39.27	8.73	11.80	3.43	31.66	50.43	16.00
MH 2-15	35.67	65.67	57.57	4.67	5.87	5.60	32.93	7.10	8.47	3.23	31.92	28.27	8.97
PDM 139	47.33	79.33	28.73	2.40	5.53	5.87	32.47	7.53	5.80	3.13	28.29	20.83	5.89
LGG 450	36.33	64.33	30.03	3.33	5.53	5.27	29.13	6.27	6.47	3.27	31.64	19.97	6.23
ADT 3	37.67	64.67	46.47	3.87	6.80	6.53	44.60	7.67	8.13	3.03	31.73	34.70	10.98
TARM 1	53.33	81.33	41.10	3.13	6.07	5.93	36.13	5.07	5.80	3.13	29.17	22.33	6.51
TM 96-2	54.67	92.67	28.57	2.93	6.40	6.73	43.07	5.07	6.13	3.33	29.40	29.90	8.80
P.Vishal	62.67	96.67	26.80	2.13	5.73	5.00	28.73	7.17	7.13	3.73	28.90	26.40	7.68
IPM 2-3	33.33	62.33	29.47	4.53	6.73	6.07	40.87	6.77	6.60	4.67	30.97	47.17	14.43
HUM 12	46.33	79.33	32.37	3.47	5.40	6.13	32.87	6.53	5.20	3.30	27.95	20.23	5.62
VBN (GG) 2	34.67	67.67	25.53	3.53	5.67	6.20	34.87	6.53	5.33	3.43	27.54	23.17	6.40
TM 2000-2	42.67	70.67	19.73	2.93	6.33	5.53	35.00	5.40	5.93	3.23	29.80	22.63	6.74
LGG 460	35.67	64.67	52.80	3.53	6.53	6.20	40.60	5.97	4.80	3.23	29.50	21.43	6.28
Pusa 9072	43.33	72.33	24.67	2.73	4.47	5.00	22.73	7.40	5.73	3.47	30.52	14.70	4.53
CoGG 8	44.67	73.67	22.57	1.73	5.93	6.67	39.73	6.23	3.87	3.30	26.33	19.13	5.06
P.Mung 4	33.33	60.33	34.03	5.40	6.40	5.93	38.13	6.17	7.67	3.93	31.37	37.03	11.58
HUM 16	43.67	83.33	42.07	3.20	5.87	5.87	34.33	8.07	5.13	4.90	30.48	28.30	8.61
IPM 99-125	55.67	95.67	33.27	3.13	5.53	5.20	28.47	7.13	5.40	3.30	26.56	19.13	5.10
IPM 205-7	43.67	91.67	36.97	3.87	4.93	5.60	27.80	8.23	5.93	3.70	26.43	23.53	6.22
P.Mung 5	36.67	68.33	39.20	5.73	6.73	6.53	44.07	7.23	7.13	3.60	31.33	36.13	11.34
Mean	**43.63**	**77.61**	**36.33**	**3.45**	**5.72**	**6.21**	**35.80**	7.01	6.53	3.48	30.07	26.72	8.21
C.V.	5.91	4.43	5.16	11.53	8.11	7.97	11.02	6.35	7.46	3.27	5.80	14.82	13.80
F ratio	31.27	32.47	76.62	9.05	7.23	4.08	9.35	9.15	22.61	19.24	2.44	12.99	14.98
F Prob.	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
S.E.	1.49	1.99	1.08	0.23	0.27	0.29	2.28	0.26	0.28	0.07	1.01	2.29	0.65
C.D. 5%	4.16	5.55	3.02	0.64	0.75	0.80	6.36	0.72	0.79	0.18	2.81	6.38	1.83
C.D. 1%	5.49	7.32	3.99	0.85	0.99	1.05	8.40	0.95	1.04	0.24	3.71	8.43	2.41
Range Lowest	29.67	59.67	19.73	1.73	3.80	5.00	21.16	5.07	3.87	3.03	26.33	7.53	3.76
Range Highest	71.33	114.33	61.53	5.73	6.87	7.27	48.73	8.73	11.80	4.90	32.50	50.43	16.00

DEPARTMENT OF GENETICS AND PLANT BREEDING
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Title: "Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek"

Major Advisor & Chairman
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ABSTRACT

The present investigation entitled "Germplasm evaluation, character association, genetic divergence, combining ability and heterosis for different quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek]" was comprised of two experiments, namely, the germplasm evaluation experiment (experiment-I) and combining ability experiment (experiment-II). Both experiments were conducted at Instructional Farm of Acharya Narendra Dev University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya during *Zaid* and *Kharif* seasons of 2019. Thirteen plant characters were studied in both experiments. In the germplasm evaluation experiment (experiment-I), sixty germplasm lines of mungbean and four checks were evaluated in augmented design in *Zaid* as well as *Kharif* seasons of 2019. The data was used for correlation and path coefficient analysis as well as non-hierarchical Euclidean cluster analysis. In the combining ability experiment (experiment-II), line x tester set of sixty F_{1s} and their 19 parents with one check (P. Mung 4) were evaluated for thirteen characters and data was subjected to analysis of variance, line x tester analysis, estimation of heterosis and direct and indirect selection parameters.

In germplasm evaluation experiment (experiment-I), SML 823 produced (8.77g) highest seed yield per plant followed by DGGV 2, BM 4, HUM 12, TM 96-2 and ADT 3 in *Zaid* season. In *Kharif* season, the highest seed yield per plant was produced by DGGV 2 (12.63 g) followed by ADT 3, P. Mung 6, P. Mung 5, P. Mung 2, MH 2-15. Biological yield per plant, pods per plant, clusters per plant, harvest-index and pods per cluster exhibited highly significant and positive correlation with seed yield per plant in *Zaid* season. Seed yield per plant recorded highly significant and positive association with biological yield per plant, pods per plant, clusters per plant, harvest-index, primary branches per plant and seeds per pod besides having significant positive correlation with pods per cluster, plant height and pod length. Biological yield per plant followed by harvest-index and days to 50% flowering exerted highest positive direct effects on seed yield per plant in *Zaid* season. Pods per plant, pods per cluster, seeds per pod and 100-seed weight emerged as the most important indirect seed yield components in mungbean for *Zaid* season. Biological yield per plant followed by pods per plant and harvest-index exerted high order positive direct effects on seed yield per plant in *Kharif* season. Pods per plant, primary branches per plant, clusters per plant, seeds per pod, harvest-index, pods per cluster and biological yield per plant were identified as most important indirect seed yield attributes in mungbean for *Kharif* season. In the present study, the 64 genotypes of mungbean were grouped into ten distinct non-overlapping clusters using Non-hierarchical Euclidean cluster analysis in *Zaid* as well as *Kharif* seasons, indicating presence of substantial genetic diversity in the germplasm collections evaluated in the present study in context of *Zaid* as well as *Kharif* seasons. The major clusters in the aforesaid two divergence analyses, in general, contained genotypes of heterogeneous origin. This suggests lack of parellelism between genetic and geographic diversity. Therefore, the selection of parental materials for hybridization programme, should be based on genetic divergence analysis rather than geographic origin. The highest inter-cluster distance was observed between cluster III and IX

followed by high inter-cluster distances recorded for cluster IX with clusters IV, V, I and II while cluster X also had high order inter-cluster distance with III and IV. In case of *Kharif* season, the cluster IX exhibited highest inter-cluster distance with cluster V which was followed by higher inter cluster distances of cluster IX with clusters III, VI, I and II. Cluster VII also had high order inter-cluster distances with clusters V, IV and VI.

In combining ability experiment (experiment-II), high genotypic and phenotypic coefficients of variation and high heritability in broad sense coupled with high genetic advance in per cent of mean were observed for seed yield per plant, biological yield per plant, seeds per pod and plant height. Seed yield per plant showed highly significant and positive phenotypic correlations and very high order positive genotypic correlations with biological yield per plant, pods per plant, seeds per pod, clusters per plant, pods per cluster, primary branches per plant, harvest-index, 100-seed weight and plant height. On the basis of path coefficient analysis, pods per plant, seeds per pod, biological yield per plant and 100-seed weight emerged as most important direct yield components while biological yield per plant, pods per cluster, clusters per plant and primary branches per plant should be considered as most important indirect yield components. In the analysis of variance for combining ability of line x tester set, the mean square due to lines, testers and line x testers interactions were significant for most of the characters indicating importance of additive as well as non-additive gene effects in their inheritance. The estimates of sca variance were higher than the corresponding estimates of gca variance for all the characters except days to 50% flowering, days to maturity, harvest-index and seed yield per plant. The value of average degree of dominance were more than unity (>1) revealing over dominance for three characters, namely, pods per cluster, pod length and seeds per pod in the study. The predictability ratio was lesser than one for all the characters except harvest-index. The above results also suggested importance of additive as well as non-additive gene effects with predominance of non-additive gene effects for all the characters. The significant and positive general combining ability effects for seed yield per plant were exhibited by the IPM 2-3, P. Vishal , ADT 3, CoGG 912, TM 96-2 and TARM 1 among the lines and Pant Mung 4 among the testers besides having significant and desirable gca effects for some other yield components also. These parents merit consideration for exploitation in hybridization programme for developing high yielding mungbean genotypes. Seven crosses, TARM 1 x IPM 99-125, CoGG 912 x HUM 16, Pusa Vishal x IPM 205-7, ADT 3 x Pant Mung 4, CoGG 912 x Pant Mung 4, IPM 2-3 x HUM 16 and LGG 450 x IPM 99-125 in order of merit showed significant and positive sca effects for seed yield per plant as well as some other yield components to emerge as crosses of potential genetic worth for further exploitation for isolating desirable segregates in segregating generations for developing high yielding mungbean varieties. A wide range of variation in the estimates of heterobeltiosis and standard heterosis in positive and negative direction was observed for seed yield per plant as well as other twelve characters studied. In case of seed yield per plant, heterobeltiosis ranged from -56.31 to 64.70% and standard heterosis varied from -66.80 to 16.11% over standard variety, Pant Mung 5. Nine crosses showed positive and significant heterobeltiosis, which were P. Vishal x IPM 205-7 (64.70%), TARM 1 x IPM 99-125 (61.05%), LGG 450 x IPM 99-125 (48.29%), TARM 1 x IPM 205-7 (47.90%) and HUM 12 x IPM 99-125 (44.46%), PDM 139 x IPM 205-7 (36.14%), HUM 12 x IPM 205-7 (34.91%), LGG 450 x IPM 205-7 (29.95%) and P.Vishal x IPM 99-125 (24.79%). However, only one cross, ADT 3 x Pant Mung 4 exhibited positive and significant standard heterosis over Pant Mung 5 for seed yield per plant. The crosses mentioned above merit consideration for exploitation in breeding programme for isolating transgressive segregants for seed yield and yield component for developing superior mungbean varieties.

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