

**Generation Mean Study for Yield Components and
Inheritance Pattern of Mungbean Yellow Mosaic
Virus (MYMV) in *Vigna***

By

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Inheritance Pattern of Mungbean Yellow Mosaic
Virus (MYMV) in *Vigna***

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Certificate

This is to certify that the work recorded in this thesis entitled “**Generation Mean Study for Yield Components and Inheritance Pattern of Mungbean Yellow Mosaic Virus (MYMV) in *Vigna***” submitted in partial fulfilment of the requirements for the award of the degree of **DOCTOR OF PHILOSOPHY IN PLANT BREEDING** of the faculty of Post-graduate studies, Rajendra Agricultural University, Bihar, Pusa is a genuine record of *bona fide* research work carried out by **SIMA SINHA** under my guidance and supervision.

The results of the investigation reported in this thesis have not so far been submitted for any other degree or diploma. The assistance and help received during the course of investigation and sources of literature have been duly acknowledged.

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This is to certify that the thesis entitled “**Generation Mean Study for Yield Components and Inheritance Pattern of Mungbean Yellow Mosaic Virus (MYMV) in *Vigna***” submitted by **SIMA SINHA** in partial fulfilment of the requirements for the award of the degree of **DOCTOR OF PHILOSOPHY IN PLANT BREEDING** of the faculty of Post-Graduate Studies, Rajendra Agricultural University, Pusa, Bihar was examined and approved on _____.

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ABSTRACT

The present investigation was conducted at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar during 2009 - 2011. The experimental material comprising the sixty one genotypes including standard varieties (SML 668) involving three of each resistant as well as one of each susceptible variety of mung and urd beans to develop the six intra and four inter specific crosses comprising the P₁, P₂, F₁, F₂, BC₁ and BC₂ population were grown in RBD design with three replications in two sets of experiment including and excluding parent. Observations were recorded for thirteen quantitative traits including the yield.

Significant differences among the genotypes for all the character in both sets of experiment were observed.

On the basis of mean performance fourteen genotypes were found significantly superior than check SML 668 for phenol content, among them Uttara x LGG 450 was having the highest phenol content (2.03 mg/g of fresh leaf). For grain yield only one treatment HUM 16 x LGG 450 exhibited significant superior over the check variety SML 668.

For all the characters PCV was slightly higher than GCV. High heritability coupled with high GA was observed for all the traits except pod per cluster, days to 50 per cent flowering and days to maturity.

Grain yield exhibited positive and significant correlation with 100 seed weight and grains per pod alongwith their positive and high direct effects in both sets of the experiment.

Based on the joint scaling test few intraspecific combinations showed the presence of epistasis; whereas in most of the interspecific crosses epistasis was observed. As per the three parameters model additive and/or dominant components seems to play an important role in the inheritance of most of the yield attributing traits in intra and interspecific crosses. As evident from the six parameter model, preponderance of significant reducing (-ve) additive gene effects in intraspecific crosses, whereas additive and dominance components were equally important in interspecific crosses for the expression of most of the yield attributing traits.

Among epistatic interactions additive x additive gene effects for days to 50 per cent flowering and dominant x dominant gene effect for 100 seed weight in four intraspecific crosses, whereas in interspecific crosses all three types of epistatic interactions were observed for the expression of most of the yield attributing traits.

In most of the intra as well as inter specific crosses duplicate type of epistasis was observed.

For most of the yield attributing traits desirable heterosis was observed in intraspecific crosses TMB 37 x LGG 450 and Sekhar x Barabanki, whereas in interspecific cross PU 31 x LGG 450 were found promising.

In *Vigna* the MYMV resistance is found digenic recessive in nature.

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INTRODUCTION

Pulses are known as grain legumes valued for their protein rich grain which is two to three times more than cereal. Mungbean is one of the cheapest source of plant protein, which contains about 22-27 per cent protein. It is also good source of mineral such as calcium and sodium. Dried mungbean seed are high in vitamin A and B, while the sprouted mungbean are rich in vitamin B and C. Ascorbic acid is synthesized in sprouted seeds of mungbean with increment in riboflavin and thiamine. These quality of pulses are sufficient to overcome the protein deficiency. Food legumes are versatile human foods as they contain many of the nutrient required for a healthy human body. They are valued as cheaper source of protein and energy as compared to animal protein.

Globally, grain legumes are the second most important group of crops. Among pulses *Vigna radiata* L. (mungbean) and *Vigna mungo* (Urd bean) are included in dry beans, which occupy an area of 25.88 million ha and produces 18.13 million tonnes with an average yield of 701 kg/ha at global level (FAO, 2005).

India a major pulse producing country, accounts roughly for 25 percent of total world production (Indian Statistics at a glance, 2008). However, in 2008-09 pulse production was 14.5 mt in 22.09 million ha land (Directorate of Economics and Statistics Department of Agriculture and Cooperation 2010) with 659 kg/ha yield. Among pulses, mungbean and urd bean jointly have only 2.21 mt production, which is nearly 15 per cent of pulse production.

The major pulse producing states are Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Orissa, Bihar, Punjab, Gujarat, which accounts for 68 per cent of total India. Drybeans, which occupy 6.51 million ha with 2.39 million tonnes of production having average yield of 317 kg/ha for mungbean and 419 kg/ha for urd bean, while in Bihar Mungbean occupy 176.83 thousand ha and produces 95.52 thousand tonnes with a 540 kg/ha productivity; whereas, urd bean occupies only 24.51 thousand hectare with 9.59 thousand production having 709 kg/ha yield. (Directorate of Statistics and Evaluation, Bihar 2007-08)

At the time of independence, National availability of pulse was 70 g per capita per day. But, now availability has declined to 37g (Indian Statistics at a Glance, 2009), while only 20 g per capita per day at state level. According to world health organization (WHO), 80g per capita per day is required for balanced nutrition of an individual.

Presence of limited variability is one of the main factors responsible for the poor progress made in breeding programme of pulse crop for enhancing the production and productivity in present day cultivar (Jain, 1975). Genotypic and phenotypic interrelationship of seed yield in green gram with its component character is very useful to the breeder in development of an appropriate breeding strategy.

However, seed yield is a complex character and influenced by a number of component traits. Hence, selection of genotype with desirable characters could be greatly enhanced, if significant correlation between yield and its component character are established as well as path co-efficient analysis suggested by Dewey and Lu (1959) is very useful in understanding the cause and effect relationship between the dependable variable like seed yield and independent yield components.

Scaling test at the most, indicates types of the epistatic interaction effects in the crosses; whereas, joint scaling test estimates the main gene effects and also indicates the epistatic interaction. However, generation mean analysis provides estimates of main gene effects and interactions effects, which are of more value to understand the performance of the parents in crosses and potential of the crosses to be used either for heterosis exploitation or pedigree selection.

Genetics of yield and its components in intervarietal crosses of mungbean has been studied by Tiwari *et al.*, 1993, Sandhu *et al.*, 1994 and Rosaiah *et al.*, 1994. The additive gene effect was observed by Senaiah *et al.*, (1993) and Rosaiah *et al.*, (1994). However, non additive gene effect were observed by Hazara *et al.* 1993 and found that equally important for the inheritance of most of the yield traits. In inter specific crosses involving mungbean and urdbean might be useful in

efficient handling of the segregating population to identify desirable recombinants in advanced generation.

The magnitude of heterosis provides a basis for determining genetic diversity and also serve as a guide to the choice of desirable parents as well as exploitation of hybrid vigour will depend on the direction and magnitude of heterosis. Although the advantage of hybrid vigour cannot be exploited commercially in highly self pollinated crops like mungbean and urdbean.

The low productivity of dry beans are due to high incidence of biotic and abiotic stresses, where yield loss ranged from 20-40 per cent and reached up to 100 per cent under epidemic condition. Among the biotic stresses Mung Yellow Mosaic Virus (MYMV) is a major problem causes the heavy yield loss in northern states of India. The virus is transmitted through whitefly (*Bencisia tabaci*). Therefore, breeding for MYMV resistance has prime importance in black gram and mungbean varietal improvement programme.

MYMV is the most serious and widely distributed in India. Nariani (1960) for the first time reported yellow mosaic of mungbean in India. He considered that the disease is caused by a Virus.

Nene (1968) made exhaustive study on this disease of mungbean and named it Mungbean yellow mosaic Virus. Later on the same disease has been reported as yellow mosaic virus by other workers (Ahmad and Harwood, 1973; Virmani *et al.* 1976).

Mungbean yellow mosaic virus causes considerable losses to mungbean and urdbean crops (Nene, 1970, Chand and Verma, 1983; Ghafoor *et al.* 2000, Khatak *et al.* 2000 b) in India, Pakistan, Bangladesh and Srilanka.

For developing high yielding MYMV resistant varieties of dry beans, it is desirable to understand the inheritance of resistance. Saleem *et al.* (1998) and Khatlak *et al.* (1999) reported that resistance to yellow mosaic virus is governed by a single recessive gene, whereas Reddy and Singh (1993) and Dahia *et al.* (1997) reported that resistance is governed by two recessive gene.

Plant contains a large number of aromatic compound with hydroxyl groups which are collectively referred to as phenolics or phenols. They are derivatives of phenol molecule. They occur in all parts of plant and believed to be resistant to disease and pests in plants caused by presence of this compound.

Phenolic compounds have correlated with the resistance of plants to infections agents (Link, 1933; Walker and Link 1935; Sokolava *et al.*, 1971; Mansfield and Deverall, 1971). The resistant cultivar had more total phenols as compare to those in susceptible cultivars. (Singh, and Bedi, 1976).

Thus keeping in view the above facts present investigation entitled “**Generation Mean Study for Yield Components and Inheritance Pattern of Mungbean Yellow Mosaic Virus (MYMV) in *Vigna***” was undertaken with the following objectives :

1. To study the character association between the traits, direct and indirect effects of causally connected traits with grain yield.
2. Estimate the gene effects of certain yield traits through generation mean analysis.
3. To workout the extent of heterosis in Intra and inter specific crosses.
4. To study the genetic of resistance of mungbean yellow mosaic virus in intra as well as inter specific crosses of *Vigna*.

□□□□□

REVIEW OF LITERATURE

1. Genetic variability

Sharma (1999) found high heritability and high genetic advance for days to flowering, pods/plant, seeds/plant, 100-seed weight and seed yield.

Islam *et al.* (1999) reported that high values for heritability and genetic advance were estimated for plant height, number of pods per plant, seeds per pod, 1000-seed weight and yield per plant.

Singh, A.B. (2001) found significant variation in yield attributing characters such as number of primary and secondary/plant, height of plant, number of seeds/pod, 1000-seed weight and yield by the application of phenolic compound.

Reddy *et al.* (2002) studied on effect of phenolic compounds on growth and yield of mungbean. Found that Triaccontanol, a phenolic compound is one of the chemicals in use for modifications of various growth and development process of plants.

Kumar *et al.* (2005) observed the phenotypic and genotypic coefficients of variation were high for biological yield, number of pods per plant, harvest index, seed yield per plant.

Pandey *et al.* (2007) observed the genetic parameters exhibited high to moderate values for genotypic coefficient of variation, broad-sense heritability and genetic advance for plant height, pod number, cluster number and harvest index. The highest heritability has been observed for cluster number per branch (85%) followed by plant height (79%) and pod number per cluster (78%), while the lowest was for biological yield per plant (35.5%).

Prakash *et al.* (2007) estimated high genotypic and phenotypic variances were recorded for seed yield/plot, plant height, pods/cluster, clusters/plant and pod length. High estimates of heritability along with high genetic advance and GCV

values were observed for the seed yield, plant height and pods/plant. Days to 50% flowering, pod length, cluster/plant and seed/pod exhibited low estimates of genetic advance.

Sadiq and Abbas (2007) observed highly significant differences for all the characters. High heritability values (81-89%) were observed for days to flower, days to mature, plant height and 100 seed weight. Harvest index had 62.6% heritability along with maximum value of genetic advance (41.13%). Harvest index showed positive and significant association with seed yield. Days to flower and plant height showed positive and significant relationship with biological yield. The magnitude of direct effect of harvest index was maximum and 100 seed weight had the highest indirect effect via harvest index.

Peerajade and Ravi Kumar (2009) studied the phenotypic and genotypic variances, coefficient of variance, heritability and genetic advances for yield and yield attributing components. Number of pods per plant, pod length and number of pods per cluster were found to be contributing maximum positive and direct effect on yield.

Dhananjay *et al.* (2009) observed high GCV and PCV for pods per cluster, seeds per pod, days to 50% flowering and pods per plant indicating considerable variation in these traits. High heritability coupled with high genetic advance was observed for seeds per pod and pods per plant indicating preponderance of additive gene action and greater scope for improvement in these traits through selection.

Rahim *et al.* (2010) observed significant variations among the genotypes for all the characters. High heritability (broad) along with high genetic advance in percent 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.

2. Correlation and path analysis

Malik *et al.* (1987) reported that yield was positively and significantly correlated with plant height, primary branches/plant, pods/plant, clusters/plant and biological yield. Path analysis revealed that days to pod initiation, plant height and

biological yield had the highest direct positive effects on seed yield/plant. The direct effects of days to flower initiation, days to maturity, clusters/plant, pod length and seeds/pod on seed yield were high and negative.

Pundir *et al.* (1992) reported that seed yield was positively correlated with branches/plant, clusters/plant, pods/plant, pod length, seeds/pod and 100-seed weight. Plant height and fruiting height were negatively correlated with seed yield. Pod length was significantly correlated with seeds/pod and 100-seed weight. Pods/plant and 100-seed weight had marked, positive direct and indirect effects on seed yield and should be given priority in selecting for high yielding strains

Mishra and Yadav (1992) observed that harvest index, plant height, number of branches and biological yield per plant had a direct positive influence on seed yield.

Sharma and Gupta (1994) studied on cross of urdbean and mungbean for seed yield was correlated with biological yield/plant, harvest index, clusters/plant, pods/plant, plant height and 100-seed weight. Path analysis showed that biological yield/plant had the greatest positive direct effect on seed yield, followed by harvest index, pods/plant, seed sulfur content, days to maturity, days to flowering, clusters/plant, 100-seed weight and pod length. Seeds/pod, seed phosphorus content, seed crushing hardness, plant height and protein content had negative direct effects on seed yield/plant.

Sharma (1995) reported highly significant and positive correlations were observed for number of seeds/plant and 100-seed weight with seed yield.

Hegde *et al.* (1996) studied F₂ population of their inter varietal crosses on correlation coefficients among yield and related characters. Grain yield was found to have a significant positive correlation with clusters/plant, pods/plant, pod/cluster, pod length and seed/pod in all these crosses and negative with maturity variables indicating the possibility of evolving early maturity high yielding genotypes.

Sharma (1999) observed on seed yield was significantly correlated with branches/plant, seeds/plant, pods/plant, pod clusters/plant, seeds/plant and 100-seed weight. Phenotypic and genotypic path analysis revealed that seeds/plant had the highest positive direct effect on grain yield followed by 100-seed weight, plant height and pods/plant.

Sabaghapur et al. (1998- 1999) studied on mungbeans (*Vigna radiata*) for seed yield/plant had highly significant and positive correlation with seeds/plant and pods/plant. Path coefficient analysis revealed that seeds/plant and 100-seed weight had the largest positive direct effect on mungbean yield.

Islam et al. (1999) Studied on yield per plant was significantly and positively correlated with plant height, number of primary branches per plant, number of pods per plant, pod length, number of seeds per pod and 1000-seed weight. Pod length exerted the highest positive direct effect on yield.

Joseph and Kumar (1999) studied on character association and cause effect analysis in F₂ population of green gram. The correlation co-efficient of plant height and yield varied between 0.640-0.920 for the hybrid. Inter relationship of plant height with branch number as well as pod number were positive and significant. It has positive association with pod number and negative with seeds per pod and test weight. Direct effect of pod number was very high and had low indirect effects. Seeds per pod and test weight had low direct and indirect effects respectively.

Rajan et al. (2000). Worked out correlation and path co-efficient analysis on parent and P₁ population. Seed yield had significant positive genotypic correlation with number of secondary roots at maturity, plant height, cluster per plant, pods per plant, seed per pod and hundred grain weight and harvest index. Path analysis recorded that pods per plant had the highest positive direct effect on grain yield. Plant height showed high indirect effect through number of pods, seeds per pod and hundred grain weight on grain-yield. Genetic improvement of grain yield is possible by selecting characters having high positive correlation and positive direct effect.

Srivastava *et al.* (2003) studied character association for three segregating population with parent. The characters, cluster/plant, Pods/plant, seed/plant and harvest index in general have significant positive association with yield in both population. Plant height, pod length and 100-seed weight were also positively associated seed yield in all the segregating population.

Nazir *et al.* (2005) observed the direct and indirect effects of different genetic parameters in different mung bean lines/cultivars. According to the results, high heritability coupled with moderate to high genetic advance was observed for plant height (97.00 and 23.40), seed yield (86.00 and 32.41), harvest index (86.00 and 36.78) and 100-seed weight (74.00 and 17.01).

Kumar *et al.* (2005) observed on the maximum positive and significant phenotypic correlation coefficient (0.825) was observed between the number of pods per plant and seed yield per plant, followed by seed yield per plant with harvest index (0.822), days to 50% flowering and plant height (0.752). Path coefficient analysis showed that number of pods per plant (0.561), harvest index (0.425), 1000 seed weight (0.216), had positive and direct effect towards seed yield, whereas at phenotypic level biological yield (0.195) number of seeds per pod (0.087), days to 50% flowering (0.011) had relatively low direct effect. .

Nazir *et al.* (2005) showed positive and significant genotypic correlation with seed yield. Clusters per plant (0.71), pods per plant (0.69), pod length (0.45), 100-seed weight (0.48) and seeds per pod (0.77) also had significant phenotypic correlation with seed yield. Plant height (0.12), clusters per plant (0.47), pods per plant (0.64), pod length (0.33) and harvest index (0.52) showed positive direct effects on seed yield.

Obaidullah *et al.* (2006) studied on Correlation and path coefficient analyses of green gram. All characters, except days to maturity, plant height and number of branches, had positive direct effects on grain yield. Number of clusters (4.329) showed the highest effect on grain yield, followed by days to 50% flowering and number of pods with the direct pat of 3.755 and 3.445, respectively. The maximum negative effect (-3.444) was observed for number of branches per plant which also had negative genotypic correlation with grain yield.

Shantipriya and Reddy (2006) observed the strong positive correlation of seed yield with pods per plant, clusters per plant, pods per cluster and seeds per pod had high positive direct effects on grain yield in F₃ progenies. However, the indirect effects of most of the characters through pods per plant, pods per cluster and seeds per pod were high and positive.

Saxena and Singh (2007) reported that seed yield per plant had positive association with cluster per plant, pods per plant, biological yield per plant, and primary branches per plant. Path-coefficient analysis indicated that biological yield and harvest index would be suitable for higher seed yield in mungbean.

Pandey *et al.* (2007) studied character association revealed significant and positive correlation of harvest index, pod number, 100-seed weight and pod length with seed yield. Path coefficient analysis revealed a high positive direct effect of harvest index and biological yield on seed yield with considerable positive effect of maturity duration and plant height.

Prakash, *et al.* (2007) seed yield, showed significant positive correlation with pods/cluster and pod length whereas, characters like days to 50% flowering and days to maturity revealed significant negative correlation with grain yield. Path analysis indicated a greater contribution of pods/cluster, pod length and seed/pod toward grain yield.

Sadiq and Abbas (2007) reported harvest index had positive and significant association with seed yield. Days to flower and plant height showed positive and significant relationship with biological yield. The magnitude of direct effect of harvest index was maximum and 100 seed weight had the highest indirect effect via harvest index.

Verma and Garg (2007) studied genotypic correlations were higher than their phenotypic correlations.. The path analysis revealed that seed yield per plant was influenced directly by biological yield and harvest index. It was indirectly influenced by days to 50 percent flowering and plant height via biological yield and harvest index. It is concluded that the characters biological yield and harvest index are main components of seed yield.

Srivastava *et al.* (2008) studied on character association and path coefficient analysis of various traits with seed yield in F₂ generation of mungbean. Experimental materials consisted F₂ seeds of 16 crosses and 16 parents of mungbean. The number of clusters per plant, number of pods per plant, pod length and plant height exhibited significant and positive association with seed yield per plant. Number of pods per plant was found to be the most important character determining seed yield as it associated positively with all characters, except days to 50% flowering and days to maturity. It had significant and positive association with number of clusters per plant. All characters under the study had positive direct effect on seed yield at the phenotypic level, except days to 50% flowering and number of seeds per pod, while the number of pods per plant exerted highest direct effect on seed yield per plant.

Priya and Reddy (2008) reported the strong positive correlation of seed yield with pods per plant, clusters per plant, pods per cluster and plant height and among themselves. However, path coefficient analysis showed that the characters pods per plant, pods per cluster and seeds per pod had high positive direct effects on grain yield in F₃ progenies. Moreover, the indirect effects of most of the characters through pods per plant, pods per cluster and seeds per pod were high and positive.

Arshad *et al.* (2009) studied on plant height among the characters exhibited positive and significant association with yield per plant at both genotypic and phenotypic levels. In addition, positive and significant correlation of plant height with days to flowering and secondary branches per plant was also observed. Primary branches per plant and days to flowering also revealed significant and positive association. Only negative and significant association was noted between secondary branches and pod length. Association among other traits was either positive or negative but non-significant. Maximum direct positive effects were observed for plant height (1.114) and days to flowering (0.424) on yield per plant. Among the characters having high positive indirect effect, pod length showed the higher value (1.161) with yield per plant through secondary branches per plant.

Singh *et al.* (2009) studied on seed yield showed positive and significant association with number of pods/cluster, number of pods/plant, number of seeds/pod, 100 seed weight, biological yield and harvest index. biological yield and harvest index as important parameters and positive direct effect on yield.

Peerajade and Ravi Kumar *et al.* (2009) conducted correlation coefficient and path coefficient analysis were conducted for yield and yield attributing components. Number of pods per plant, pod length and number of pods per cluster contributed maximum positive and direct effect on yield.

Singh *et al.* (2009) reported that primary branches/plant, clusters/plant, pods/cluster and pods/plant were found to be positively associated at genotypic, phenotypic and environmental level barring non-significant correlation between primary branches/plant at environmental level. Positive association at phenotypic and genotypic level was also recorded between pods/cluster and seeds/pod and between pods per plant and harvest index. Path analysis using phenotypic and genotypic correlations identified biological yield per plant, clusters per plant and seeds per pods as most important direct and indirect yield components.

Rahim *et al.* (2010) observed the 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 are the important characters.

Marrappa *et al.* (2010) observed that yield is significant and positively correlated all the characters except seeds per pod both at genotypic level. Path analysis of highly correlated characters exhibited that pod yield per plant had maximum direct effect on seed yield at both phenotypic and genotypic levels. The traits such as days to 50% flowering, primary branches per plant, clusters per plant, pods per plant, pod length and test weight recorded maximum positive indirect effect via pod yield per plant.

3. Generation Mean Analysis

Pal *et al.* (1991) observed F₂ and backcross segregation ratios from crosses involving susceptible and resistant varieties indicated that resistance to bean yellow mosaic potyvirus was controlled by 2 recessive genes in crosses within *V. radita* and also in interspecific crosses between *V. radiata* and both *V. mungo* and *V. sublobata*. Resistance was monogenic recessive in crosses within *V. mungo*.

Ram (1997) studied the gene effects for yield and six yield trait in green gram crosses via generation mean analysis. Additive gene effects were important in most crosses for the majority of traits. Dominance gene action was involved in the expression of yield, pods/plant, plant height, pod length and clusters/plant in some crosses. Among the digenic interactions additive x additive and dominance x dominance effects played an important role in the expression of plant height, branches/plant, clusters/plant, pods/plant and grain yield/plant in some crosses

Kute and Deshmukh (2002) studied Genetic analysis of mungbean through generation mean analysis using five parameters model. The studies indicated predominance of additive effects for days to flowering, pods/cluster, pods/plant and 100-seed weight in most of the crosses. The dominance effect was also noticed in most of the crosses for clusters/plant, pods/plant and seed yield/plant. Among the epistatic effects, significant additive x additive (i) for clusters/plant and seed yield/plant, whereas significant dominance x dominance (l) interaction was observed for days to flowering, pods/cluster and pods/plant in one cross. As all the three types of gene effects are involved, the recurrent selection and diallel selective mating will be effected for the genetic improvement in mungbean.

Khattak *et al.* (2004) observed the nature of gene action for number of days to flowering, plant height at different growth stages, synchrony in pod maturity, and indeterminate plant growth habit was evaluated in Peshawar, Pakistan, during kharif 2003 through generation mean analysis. The mean data of 6 populations (both parents, F₁, BC₁, BC₂ and F₂) were subjected to joint scaling test. In the presence of epistasis, 6-parameter model was used to detect all types of gene effects. The analysis indicated that most of the traits appeared to be complex

in the expression of gene effects in both crosses. Both additive and dominant gene effects were important in both crosses for all traits except number of days to first flower and first pod maturity in which the dominant gene effects was not significant.

Khattak *et al.* (2004) reported genetic variation for yield and some important yield components was evaluated in Peshawar, Pakistan, through generation mean analysis. In the presence of epistasis, 6-parameter model was used to detect all types of gene actions. Both crosses showed complex genetic behaviour for all the traits evaluated, except number of branches per plant and pod cluster per plant. The additive and dominant components of genetic variation were significant for all traits .but the dominant component was not significant for number of branches per plant, 1000-seed weight in cross, and pod-bearing nodes on the main stem. The duplicate type of non-allelic interactions was recorded for pod cluster per plant and 1000-seed weight .The complementary type of non-allelic interaction for seed yield per plant was found. The intercrossing of F2 plants are recommended to produce superior recombinants for traits having complex genetic behaviour and selection in the latter generations of segregating populations for developing high-yielding mungbean genotype.

Ammavasai *et al.* (2005) reported the nature of gene effects for yield and yield related traits in mungbean involving six parents through generation mean analysis. The analysis indicated that most of the characters appeared to be complex in the expression of gene effects in different crosses. Additive and dominance gene effects were important in most of the crosses for majority of the traits. Among the digenic interactions, additive x additive and dominance x dominance played an important role in the expression of all the traits. The additive x dominance gene effects played important role in case of days to maturity, days to 50% flowering, leaf length, seeds per pod and seed yield per plant in all the three crosses.

Gawande and Patil (2005) observed the dominance was predominant in the inheritance of days to 50% flowering, plant height, primary branches per plant and pods per plant in all crosses. Dominance gene action was important for days to maturity, pod clusters per plant and 100-seed weight . Seed yield was controlled

by dominance gene action and by additive gene action. Both crosses are considered promising for exploitation through biparental mating and selection.

Singh *et al.* (2006) reported that genetic analysis of yield and other quantitative traits in mung bean through generation mean analysis. Simple additive-dominance model was found inadequate in all the crosses for most of the traits, indicating importance of non-allelic interactions. Both additive and dominance gene effects were significant in most of the cases but the magnitude of dominance component was more in general and negative, hence, decreasing the expression of the traits. Epistasis was also important in most of the traits in different crosses. Thus, to exploit all the 3 types of gene actions present in most of the cases, recurrent selection has been suggested. Epistasis was mostly of duplicate type which will reduce variation in F₂ and subsequent generations and hinder the pace of progress through selection.

Singh *et al.* (2006) studied the inheritance of genetic parameters in mung bean from 6 generations by using generation mean analysis. Observations were recorded on different yield attributing traits, namely days to 50% flowering, days to maturity, plant height, branches per plant, clusters per plant, pods per plant, seeds per pod, grain yield per plant and 100-grain weight on single plant basis. The data were first subjected to A, B and C scaling tests to detect presence of epistasis and then the epistatic model given by Hayman was used for estimation of gene effects. The results indicated that additive, dominance and epistatic gene effects contributed significantly to the inheritance of the various traits studied.

Khan *et al.* (2007) reported that assessment of gene effect for some secondary yield characters and detection of epistasis in mungbean crosses. The significant epistatic effect was detected in cross for number of pods bearing branches and stem and root dry weight. Similar non-allelic gene interaction was for days to first pod initiation, first pod maturity, 90% pod maturity and stem and root dry weight. In cross the significant epistatic effect was found for node bearing first pod, number of leaves initiated at the time of first peduncle initiation, days to first pod maturity, days to 90% pod maturity, stem dry weight, root dry weight and number of pods bearing branches.. The duplicate type of non-allelic interaction were found for number of leaves initiated all crosses, for node bearing

first pod in cross. The complementary type of non-allelic gene interaction was found for days to first pod initiation and first pod maturity in cross.

Payasi *et al.* (2010) studied the means of P1, P2, F1, F2 and F3 generations in each cross, estimates of various gene effects were obtained by partitioning method of weighted least square analysis of three parameter model fitted to the five generation means of each cross for twelve characters. The results of generation mean analysis indicated varying nature of genes under different genetic backgrounds. Significant inbreeding depression also gave an indication of prevalence of dominance genetic variance along with duplicate type of epistasis for most of the characters under study. Intermitting or recurrent selection would be followed for genetic enhancement of grain yield in mungbean

4. Heterosis and Inbreeding depression(ID)

Ghafoor *et al.* (1990) found the highest heterotic effects for pods per plant, harvest index and grain yield per plant. Therefore, these crosses could be exploited for future mungbean improvement.

Patil *et al.* (1992) evaluated highest value of heterosis (over the better parent) for pods/plant (139.6%) followed by seed yield/plant (76.0%) and pod weight/plant (64.1%). The crosses BM86 x MH1, Kopergaon x BM4 and BM4 x TAP7 had high heterosis over better parents and the control cultivar BM4.

Singh and Pathak (1992) studied on heterosis over the better parent from a study of 11 characters in 90 F1 hybrids in kharif.

Sharma and Yadav (1993) showed Pusa Baisakhi x Kopergaon has positive heterosis for plant height (7.76%), pods/plant (22.92%), seeds/plant (7.78%) and seed yield/plant (10.43%). P16 x Kopergaon showed positive heterosis for seed yield/plant (8.25%). Pusa Baisakhi x P16 exhibited negative values for 100-seed weight (-10.33%). P16 x Kopergaon showed similar trends for days to 50% flowering (-11.82%) and maturity (-13.01%). Inbreeding depression ranged from -13.69 to 15.3% for days to flowering, from -10.96 to 18.85% for maturity, from -10.6 to 5.89% for plant height, from -27.18 to 4.89% for pods/plant, from -33.33 to 2.22% for seed/plant, from -22.65 to 7.8% for seed

yield/plant, from -44.06 to 3.53% for 100-seed weight and from -6.81 to 8% for biological yield/plant.

Naidu and Satyanarayanan (1993) estimated heterosis for seed yield varied from 1.77 to 32.95% and from -8.49 to 25.81% over mid parent and better parent values, respectively. All the crosses showing heterosis for seed yield also showed heterosis for shoot dry matter. This cross also showed heterosis for branches/plant, pods/plant, pod length, seed weight, shoot dry matter and shoot nitrogen.

Naidu and Satyanarayanan (1993) evaluated average heterosis over mid and better parents was positive for seed yield/plant, pods/plant, branches/plant and clusters/plant, and negative for days to 50% flowering and days to maturity. Additive genetic variance was important for days to 50% flowering, days to maturity, pods/plant and seed protein content. Non-additive gene action was mainly responsible for plant height, seed weight, shoot dry matter and seed yield. Both additive and non-additive gene actions were important for branches/plant, clusters/plant, pod length, seeds/pod and shoot nitrogen. The average relative heterosis and heterobeltiosis were high for seed yield (18.83 and 7.92), shoot dry weight (17.25 and 4.27) and pods/plant (10.04 and 1.09) but they were low for the other characters studied.

Sekhar *et al.* (1994) studied heterosis over mid-parent and better parent for yield and yield components. ML267 x K851 was the best combination for grain yield per plant, pods per plant and pods per cluster. In most cases, significant positive heterosis for grain yield was associated with heterosis for pods per cluster, pods per plant, clusters per plant and seeds per pod. PDM54, K851, LGG407 and ML267 were the best general combiners for a combination of traits.

Hegde *et al.* (1996) evaluated significant heterosis over mid parent and better parent values was present for most of the components. In general, crosses showing high heterosis also exhibited high inbreeding depression for most components with some exceptions.

Patil *et al.* (1996) evaluated genotypes of *Vigna radiata* and the F1 and F2 generation of their ten crosses for nine characters. High heterosis for seed yield was coupled with high heterosis for primary branches/plant, clusters/plant, pods/plant and seeds/pod. Highest heterosis and inbreeding depression for seed yield was observed in KDM1 x Russian Mung.

Aher and Dahat (1999) found heterosis values of 76.7 and 38.42% over the mid parent and better parent, respectively, were observed for seed yield per plant. Heterosis for yield was generally accompanied by heterosis for yield components. Three hybrids were identified as promising for many desirable traits and they may be of much use in exploiting hybrid vigour and isolating desirable segregants from further generation in mung bean.

Sharma (2000) exhibited maximum heterosis for seed yield/plant, followed by seeds/pod and pod clusters/plant. Highest value of heterosis over better parent (92.8%) was recorded for seed yield/plant in the hybrid TPU-4 x NP-21.

Aher *et al.* (2000) found pronounced hybrid vigour for yield and most of the 12 yield components. Heterosis to the extent of 63.45 and 61.69% over the mid-parent and better parent respectively was recorded for grain yield per plant. Heterosis for yield was generally accompanied by heterosis for yield components

Aher *et al.* (2000) evaluated maximum better parent heterosis for grain yield/plant was observed to be 42.23% and that of standard variety found to be 53.65%. The crosses showing heterosis for grain yield were not heterotic for all the characters. Tata mung local x KDM-1, AKM-9504 x PIP-2-54-4, AKM 8802 x Tata mung local, Tata mung local x TARM-18 and Kopargaon x KDM-1 hybrids were identified as promising for many desirable traits and they may be useful in exploiting hybrid vigour in mung bean.

Gawande *et al.* (2001) studied twenty-one crosses from 7x7 diallel excluding reciprocals were studied to determine the magnitude of heterosis over midparent, better parent and a standard cultivar PM 2 for yield and its components in mung bean in Rahuri, Maharashtra, India. PIP 3-85-2 x TARM 18 had the highest heterosis for grain yield/plant compared to midparent, better parent and PM2. Heterosis for crop yield was generally accompanied by heterosis for yield

contributing characters. The crosses, AKM 9242 x AKM 8802, PIP 3-85-2 x TARM 18, AKM 9242 x PM 9339, PIP 2-54-2 x AKM 9242 and PIP 3 85-2 x AKM 8802 were identified as promising for many desirable characters and they have immense value and can be exploited for hybrid vigour in mung bean.

Jahagirdar (2001) studied on average mid and better parent heterosis were maximum for seed yield per plant, pods per plant, branches per plant and clusters per plant. The average heterosis for days to 50% flowering and maturity over mid and better parent was negative.

Singh *et al.* (2003) observed significant heterosis for seed yield in 30 cross combinations over the best control (UG-218). Heterosis for yield was generally accompanied by heterosis for yield components. Of the 48 cross combinations, 26 and 45 crosses revealed significantly negative heterosis over the best control for days to 50% flowering and maturity.

Reddy *et al.* (2003) evaluated heterosis values of 110.77 and 77.54% over the mid parent and better parent, respectively, were recorded for grain yield per plant. Heterosis for yield was generally accompanied by heterosis for yield components. Eight hybrids were identified as promising for many desirable traits and they may be of much use in exploiting hybrid vigour in mungbean.

Soehendi and Srinivas (2005) showed all crosses have significant yield heterosis over the mid-parent and better-parent. Crosses showing heterosis for grain yield and also heterosis for pod length, number of seeds per pod, and plant height. However, only plant height expressed heterobeltiosis. Superiority over the mid-parent for grain yield ranged from 52.2 to 95.7%, and that over the better parent ranged from 31.8 to 78.5%.

Khan *et al.* (2005) studied the presence and magnitude of heterosis over mid and better parents in mung bean for yield and yield components. Data on pod clusters per plant, pods per cluster, pods per plant, seeds per pod, 1000-seed weight and seed yield per plant were recorded. The extent of heterosis varied bi-directionally according to crosses and characters, with the highest pods per plant, seeds per pod and pod clusters per plant in hybrid NM-92 x VC-6368. For seed yield per plant, NM-92 x VC-6369 recorded the maximum heterotic effect. The

hybrids involving parents NM-92, VC-6368 and VC-6369 gave superior yield and yield components compared to others.

Kuldeep *et al.* (2006) estimated heterosis over BP and MP and inbreeding. All the crosses showed positive heterosis over BP and MP for days to 50% flowering, days to maturity and plant height.

Sanjay *et al.* (2007) studied on the range of heterosis was maximum and nearly equal for pods per plant and seed yield per plant. High range was also observed in branches per plant while other characters showed limited range. The magnitude of heterosis was positive for days to 50% flowering and maturity in most of the hybrids, which indicated that there is lack of tendency of earliness in the hybrids. High heterosis for seed yield per plant was mostly accompanied by high heterosis in pods per plant in most of the crosses. Medium heterosis was expressed for branches per plant in all the crosses. The magnitude and direction of heterosis for pod length, seeds per pod, 100-seed weight and protein content were low and negative, indicating lack of genetic variability among the parents for these characters.

Sirohi *et al.* (2008) studied on the analysis of relative heterosis (over mid parent) and heterobeltiosis (over better parent) was based on pooled data obtained for quantitative characters: plant height, number of primary branches per plant, days to 50% flowering, number of clusters per plant, number of pods per plant, 100-seed weight, seed yield per plant, biological yield and harvest index..

Elangaimannan *et al.* (2008) reported heterosis and inbreeding depression (ID) for yield and yield components of urd bean (black gram). The mean seed yields of all the hybrids were higher than the yields of their respective parents. Significant positive heterobeltiosis was observed for number of clusters per plant, number of pods per plant and seed yield per plant in all crosses; test weight in 3 crosses; number of branches per plant in 2 crosses; and pod length and number of seeds per pod in one cross.

Rout *et al.* (2010) estimated the magnitude of heterosis over mid and better parent for yield and yield components. Significant positive heterotic effect over mid parent and better parent was observed for grain yield/plant in hybrids OGG-12/LGG-460, LGG-460/Pant-M-4 and LGG-460/OGG-57. The heterosis for grain yield was found to be associated with heterosis for clusters/plant and pods/plant. The cross OGG-12/LGG-460 was the top heterotic cross which manifested 79.19 and 72.33% of higher yield over better parent and mid parent, respectively, whereas LGG-460 x Pant M-4 was the best performing hybrid which recorded the highest single plant yield of 6.85 g.

5. Genetics of Resistance to MYMV

Kosuage, T. (1969) studied on changes in phenolic compounds and sugar in relation to white rust of Indian Mustard found that phenols and sugars are responsible for disease resistance in different crops. (Farkas and Kirlyay, 1962, Singh and Chohan, 1973; Kannoian, Vidhyasekaran and Kundaswamy, 1977; and Chand and Verma, 1980).

Singh and Bedi (1975) studied on phenolic and sugar constituents of gram cultivars resistant and susceptible to *operculella padwickii*. Found that resistant cultivar had more total phenols, flavonols and tannins as compared to those in the susceptible cultivar. As a result of infection, total phenols, flavonols and tannins, increased in both the cultivars but increase in the phenolics was more in resistant cultivar.

Sharma *et al.* (1983) estimated higher level of phenole in resistant inbred CM-104 than the susceptible inbred CM-600. After inoculation the resistant plants showed a tendency to accumulate higher amounts of phenols than the amounts of phenols than the susceptible plants.

Chiemsombat (1991, 1992) mung bean yellow mosaic bigeminivirus was first detected in Thailand in 1977 when it caused very severe damage to *Vigna radiata* crops, but the disease has not been reported since 1987. It is important to determine the factors responsible for outbreaks of MYMV and its vector (*Bemisia tabaci*) in Thailand and to develop effective control measures, which should include breeding for resistance.

Malik (1991-1992) the status of *Vigna radiata* and its production in Pakistan, general constraints to production, the importance of mung bean yellow mosaic disease, seasonal occurrence of mung bean yellow mosaic bigeminivirus and its vector, economic losses due to the disease, inheritance of resistance to virus and vector, screening for resistance, and the performance of resistant materials developed under experimentation are reviewed.

Sohal *et al.* (1993) Biochemical changes in leaves of mung bean yellow mosaic bigeminivirus (MYMV) resistant (ML267) and susceptible (ML5) varieties indicated that MYMV infection results in malfunctioning of polyphenol metabolism by increasing total sugars, free amino acids and total phenols in both varieties, whereas orthodihydroxy phenols and flavonols increased only in the resistant variety upon MYMV infection. Polyphenol oxidase activity increased in the resistant variety, whereas it decreased in the susceptible one on infection. Phenylalanine ammonia-lyase (PAL), tyrosine ammonia-lyase [PAL] and peroxidase activity decreased with MYMV infection in both varieties.

Anand *et al.* (1998) studied on Inheritance of resistance to mung bean yellow mosaic bigeminivirus (MYMV) Reaction of parents, F1, F2 and backcrosses suggested that 2 recessive genes are involved in imparting resistance against MYMV in *V. mungo* .

Saleem *et al.* (1998) evaluated crosses between the local and exotic lines of mungbean for resistance in Faisalabad, Pakistan. The F2 populations segregated into 3 susceptible and 1 resistant lines .

Khattak *et al.* (1999) studied on mode of inheritance of mungbean yellow mosaic virus (MYMV) for F1, F2, F3 and backcrosses of a highly resistant mung bean line. Observations on the F2, F3 and backcross generations indicated that a single recessive gene was involved in imparting resistance against the disease. No maternal effect was observed in inheritance of mung bean.

Khattak *et al.* (2000) showed significant differences in MYMV disease infection, yield and yield components. These progenies exhibited an 18.5 to 40.5% decrease in plant height, an 11.7 to 64.0% reduction in the number of pods per plant, a 5.8 to 82.2% reduction in seeds per pod, a 7.4 to 35.0% decrease in

pod length, a 10.6 to 53.3% reduction in 1000 seed weight and a 32.2 to 78.6% decrease in grain yield per plant. The MYMV incidence showed a significant correlation (0.526) with the decrease in 1000 seed weight. The decrease in yield and other yield components showed was not significantly correlated with MYMV incidence.

Khattak *et al.* (2000) was Studied genetic basis of mungbean yellow mosaic virus (MYMV) in F₁ F₂, suggesting that susceptibility and resistance were controlled by a single genetic factor. It is suggested that susceptibility was dominant over resistance.

Sirohi *et al.* (2002) studied on Inheritance of resistance to mungbean yellow mosaic virus (MYMV) of blackgram, namely, DPU 88-5, DPU 88-1 and UG 400 and a susceptible line Barabanki. The parents, F₁, F₂ and back cross progenies were grown along with the susceptible lines Barabanki and Kullu 4 as spreader rows after every fourth row. Susceptibility to MYMV was dominant over resistance in the F₁ generation of all the crosses. Observations on disease incidence of F₂ and backcross generations indicated that two recessive genes imparted resistance against MYMV in each of the three blackgram lines.

Mishra (2003) evaluated the inheritance of yellow mosaic virus (MYMV) resistance in mung bean was evaluated in F₁, F₂ and F₃ progenies of different genotypes. The results indicated that a single recessive gene confers MYMV resistance in mungbean, and that the expression of the gene responsible for MYMV resistance is affected by the action of modifying genes.

Ammavasi *et al.* (2004) studied the inheritance of resistance to mungbean yellow mosaic virus in green gram and resulting P₁, P₂, F₁, BC₁, BC₂ and F₂ generations The expected susceptible : resistant ratio of 15:1 for the 3 crosses indicated the presence of duplicate type of gene action. All plants in the BC₁ generation were susceptible : resistant ratio of 3:1 was observed in the 3 crosses. All 3 crosses showed the presence of recessive genes governing resistant.

Gupta *et al.* (2005) evaluated the inheritance of resistance to mungbean yellow mosaic virus (MYMV) in the F₁, F₂ and F₃ populations of intervarietal crosses of black gram was also sown all around in the field to increase the MYMV

incidence. Disease severity on F2 plants segregated 3:1 (resistant : susceptible; R:S) as expected for a single dominant resistant gene in all R/S crosses. The results of F3 analysis confirmed the presence of a dominant gene for resistance to MYMV.

Singh and Singh (2006) studied the inheritance of resistance to Mung bean yellow mosaic virus (MYMV) Susceptibility to MYMV was dominant over resistance in the F1 generation of all the crosses. Observations on disease incidence of F2 and F3 generations indicated that two recessive genes imparted resistance against MYMV in each of the crosses.

Khan *et al.* (2007) the mode of inheritance of resistance to Mung bean yellow mosaic virus (MYMV) in mung bean genotypes the MYMV resistance was inherited through a major recessive gene. No maternal effect was found for the inheritance of MYMV resistance in mung bean.

Ahmed, *et al.* (2009) found that total phenol levels increased during the early stage of infection but later declined. Phenols may serve as defence compound against pathogen. (Kosuge, 1969).

□□□□□

MATERIALS AND METHODS

The present investigation was undertaken during the spring season of 2009 to summer 2011 at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar is situated at the side of Budhi Gandak river of North Bihar in the humid subtropical zone. It is situated at 25°50' N latitude and 85°75' E longitude with an altitude of 51 meters above mean sea level.

Weather condition during the crop season

The data on weather condition for summer 2011 with respect to maximum and minimum temperature, rainfall and relative humidity were obtained from Agrometrological department of Rajendra Agricultural University, Pusa, Samastipur. Weather data of crop years (summer, 2011) in table – 1.

Experimental Material

The experimental material consisted of three resistant mungbean donor viz., HUM-16, TMB-37 and Samrat with susceptible donor LGG 450. Three of resistant donor of urd bean like pant U-31, Uttara and Sekhar with a susceptible donor Barabanki local. Their source and Pedigree is listed in Table 2.

Procedures

1st year

All six genotypes of mung and urd bean were grown in a crossing block in spring 2009.

Set I- In this, three genotype of mungbean planted in a crossing block with susceptible parent as LGG 450. Two rows of both resistant donor of mungbean and susceptible variety LGG450 was planted twice at interval of fifteen days.

HUM 16 x LGG 450

TMB-37 x LGG 450

Samrat x LGG 450

Table 1 : Meterological data during cropping season of summer 2011

Week No.	Temperature (°C)		Relative humidity (%)		Rainfall (mm)
	Max.	Min.	Max.	Min.	
11	32.5	14.2	85	35	0.0
12	33.8	17.2	84	38	0.0
13	32.6	18.2	83	40	1.5
14	33.7	17.7	82	39	18.0
15	36.2	20.0	78	38	0.0
16	36.2	21.7	83	32	12.0
17	25.2	21.3	73	38	14.0
18	32.8	23.4	80	54	0.0
19	34.8	23.4	80	50	9.5
20	34.6	23.9	85	57	40.8
21	33.5	24.4	85	60	19.4
22	35.1	24.3	81	52	81.4
23	35.6	25.5	78	50	12.0
24	34.8	26.1	87	60	33.6
25	33.9	26.7	83	61	46.1
26	31.0	25.8	88	78	265.8

Source : Deptt. of Agrometerology, R.A.U., Pusa, Bihar.

Table 2 : List of genotypes, pedigree, year of release, and MYMV disease reaction

Genotypes	Pedigree	Year of release	Disease reaction (MYMV)
HUM 16	Pusa bold -1 x HUM-8	2006	R
TMB 37	TARM 2	2005	MR
Samrat	ML-20/19 x ML 5	2001	R
Pant U-31	UPU 97-10 x DPU 88-31	2005	R
Uttara	NP 19 x T 19	1999	R
Shekhar	T 9/7378/2	2001	R
LGG 450	Mutant of Pant M ₂	1995	S
Barabanki local	Land races	-	S
SML 668	Selection from NM 94 lines	2002	MR

R = Resistant, MR = Moderately resistant, S = Susceptible, T – Tolerant

Set II - Urd bean resistant donors in PU-31 Uttara and Sekhar were planted like set 1 for crossing with susceptible parent Barabanki local and made three crosses.

Set III- It was interspecific crosses of mungbean x urdbean. Two resistant donor of mungbean were crossed with susceptible urdbean parent Barabanki local.

Samrat x Barabanki local

TMB-37 x Barabanki local

In another set also two resistant donor of urd bean were crossed with susceptible mungbean parent LGG 450

Pant U 31 x LGG 450

Uttara x LGG 450

IInd Year

Experiment conducted during 2010 Kharif.

Half of the hybrid seed of three intra specific crosses of each mung and urd bean as well as interspecific crosses alongwith parents were raised to obtain F₂ seeds BC₁ and BC₂ seeds. 6 F₁ hybrid of intra specific and four inter specific hybrid F₁ were selfed to obtain F₂ seed as well as backcrossed to both the parent to obtain BC₁ and BC₂.

IIIrd Year

Experiment conducted during 2011 March- May.

The F₁, F₂, BC₁ and BC₂ Population derived from three intra specific crosses of each mung and urdbean as well as four inter specific F₁s progenies F₂, BC₁, BC₂ along with their parents were grown in RBD (Randomized Block Design) with three replications having the plot size of 2.4 m² with row to row spacing at 30 cm and Plant to plant 10 cm, while F₂ populations of each cross was grown in 4.8 m² plots having the 10 rows with 4 m length. SML 668 was used as a check.

One row of LGG 450 was planted as infector row for MYMV after every two rows of the test entries to intensity MYMV inoculum in natural condition. In order to maintain a good natural population of white flies and no pesticide was sprayed.

Observations

Ten randomly plants were selected, from P₁, P₂, F₁, BC₁, BC₂ and forty plants from F₂ for each cross to recorded the observations on following traits.

1. Days to 50 per cent flowering

For days to 50 per cent flowering, the whole plot was taken into consideration. This was counted as the number of days taken from the date of sowing to the 50per cent flowering of a genotype in a particular plot.

2. Plant height (cm)

Height were recorded in cm from the base (ground level) to the tip of the stem at maturity.

3. Number of primary branches

The branches arising directly from the main stem were recorded.

4. Number of cluster per plant

Number of clusters were counted from selected plants.

5. Number of pod per cluster

Number of pod per cluster were estimated by dividing the total number of pod per plant by total number of clusters pod per plant.

6. Number of pod per plant

All the pods bearing seed on each selected plant was counted.

7. Days to maturity

Number of days from the date of sowing to maturity (when pods become light brown to dark brownish) were recorded.

8. Pod length (cm)

Pod length was measured in cm.

9. Number of grains per pod

Number of grains of selected pods were counted.

10. 100-seed weight (g)

100-seed from each plant were taken and weight recorded in gram.

11. Harvest Index (HI)

Harvest index calculated by following formula (Donald, 1962)

$$\text{Harvest index} = \frac{\text{Economic yield}}{\text{Biological yield}}$$

12. Phenol content (mg)

Phenol was estimated from 1 g of fresh leaf. It was estimated in mg/g of fresh weight.

13. Grain yield per plot (kg)

Plants of each plot were harvested separately and weight of grain was recorded in kg.

14. Score of Mungbean Yellow Mosaic Virus

Scoring of MYMV was done on the basis of 1-9 scale as per the method suggested by *Shukla (1977)* and *Shukla et al. (1978)* in mungbean and *Singh (1980)* in urd bean. The F₂ plants were classified into resistant comprising the scale (1-3) and susceptible (5-9) scales.

Scale	Per cent of infection	Disease reaction
1.	No infection (complete free)	Resistant
3.	Up to 10per cent (trace of necrotic mottle)	Moderately resistant
5.	10.1per cent-20per cent (Moderate necrotic mottle)	Moderately Susceptible
7.	20.1per cent-40per cent (Restricted yellow mottle)	Susceptible
9.	Above 40per cent (Complete yellow mottle)	Highly susceptible

Estimation of phenol content in leaf

Total phenol estimation was carried out with Folin-Ciocalteu Reagent (FCR). The method opted and protocol given by Bray and Thorpe (1954). Phenol reacts with an oxidising agent phosphomolybdate in Folin- Ciocaltur reagent under alkaline condition. Formation of blue coloured complex, the molybednum blue which is measured at 650 nm wave length in photolorometric instrument.

Chemicals

1. 80per cent Ethanol
2. Folin-ciocalteu reagent (FCR)
3. 20per cent Na_2CO_3
4. Standard (100 mg cathecol in 100 ml of water) Diluted 10 times for a marking standard.

Procedure

1. Weighted exactly 1.0 g of fresh leaf sample and grind it in a pestle and mortar in 10 time volume of 80per cent ethanol.
2. Centrifuged the homogenate for 20 minutes, and saved the supernatants. Re-extract the residue with five times the volume of 80per cent ethanol, centrifuged and pooled the supernatants.
3. Evaporated the supernatant to dryness.
4. Dissolved the residue in a known volume of distilled water (5 ml)
5. Pipette out different aliquots (0.1 to 1ml) into test tubes.
6. Prepared up the volume in each tube to 3 ml with water.
7. Added 0.5 ml of Folin ciocalteu reagent.
8. After 3 minutes, added 2 ml of 20per cent Na_2CO_3 solution to each tube.
9. Mixed thoroughly and placed the tubes in a boiling water for exactly one minute, cooled and measured the absorbance at 650 nm against a reagent blank.
10. Prepared standard curve using different concentration of catechol.

Calculation

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

To study the inheritance of MYMV

Number of infested plants was counted in F_1 's, F_2 's, BC_1 and BC_2 of intra and inter specific crosses along with their parents.

Statistical Analysis

The data recorded on five randomly selected plants were compiled by taking the mean of each treatment for individual replication. The data were then subjected to the following biometrical analysis.

1. Range and Mean
2. Analysis of variance (ANOVA) for the designs of experimentation.
3. Heritability
4. Genetic Advance and per cent of mean
5. Correlation coefficients
6. Path analysis
7. Generation mean analysis
8. Heterosis and Inbreeding depression

Range : Difference between the lowest and highest values of the observations.

Mean : Mean values for each genotype over replications were calculated

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

\bar{X} = General mean

X_i = Observations

N = Total No. of observations

Analysis of variance

The analysis of variance for each character was carried out by using the following model.

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Performance of i^{th} entry in j^{th} replication

μ = overall mean effect

t_i = i^{th} treatment effect ($i=1,2,3,\dots, V$)

b_j = j^{th} replication effect ($j=1,2,3,\dots,r$)

e_{ij} = random error component

It was carried out by the procedure as given by Panse and Sukhatme (1967) following Linear Model of Ostle (1975).

$$\text{Correction factor (CF)} = \frac{(\text{Grand total})^2}{\text{Number of observations}}$$

Analysis of variance and expectations of mean squares

Source of variance	Df	MS	EMS	F-ratio
Replication	(r-1)	M_{sr}	$\sigma_e^2 + \sigma_r^2$	M_{sr}/M_{se}
Treatment	(t-1)	M_{st}	$\sigma_e^2 + r\sigma_t^2$	M_{st}/M_{se}
Error	(r-1)(t-1)	M_{se}	σ_e^2	

Where,

r = number of replications

t = number of treatments

M_{sr} , M_{st} and M_{se} stands for mean squares due to replications, treatment and error respectively.

σ_e^2 = Environmental variance

σ_t^2 = Variance due to treatment, and

σ_r^2 = Variance due to replication

The F-test applied in order to find out the significant differences among the treatment means.

Phenotypic and Genotypic variances

The phenotypic variance was calculated by the formula as given below :

$$\sigma^2_{ph} = \sigma^2_g + \sigma^2_e \text{ [When Cov. Gxe=0]}$$

The genotypic variance was calculated by the formula as given below :

$$\sigma^2_g = \frac{M_t - M_e}{r}$$

Where,

σ^2_{ph} = Phenotypic variance

σ^2_g = Genotypic variance

σ^2_e = Environmental variance

T_t = Treatment mean sum of square

M_e = Error mean sum of squares

r = Number of replication

Coefficient of variability

Variability present in the grain yield and yield contributing characters was estimated according to the method advocated by Burton (1952).

Phenotypic Coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance

\bar{X} = General mean of the character

Genotypic Coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where,

σ^2_g = Genotypic variance

\bar{X} = General mean of the character

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_{St} - M_{Se}}{\text{Number of replication (r)}}$$

Error variance (σ^2_e) = M_{Se}

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Estimation of selection parameters

Heritability

Heritability in broad sense h^2 was estimated by the proportion of genotypic variance to the phenotypic variance expressed in per centage as defined by Lush (1949) and and Johnsen *et al.*(1955).

$$h^2 \text{ (bs)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (bs) = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Genetic advance (GA)

The expected genetic advance was calculated by the formula suggested by Lush (1940) and Johnson *et al.* (1955).

$$\text{G.A.} = K. \sigma_p. h^2$$

Where,

K = Selection different which is 2.06 at 5per cent selection intensity in large sample from normally distributed population.

σ_p = Phenotypic standard deviation, and

h_2 = Heritability in broad sense.

Genetic advance as percentage of mean was calculated by following formula :

$$\text{G.A. (as per cent of mean)} = \frac{\text{G.A.}}{\bar{X}} \times 100$$

Where,

$$\begin{aligned} \bar{X} &= \text{Mean of the character and} \\ \text{GA} &= \text{Genetic advance} \end{aligned}$$

Correlation coefficient

Correlation coefficients give the measure of the degree of association between two or more than two variables. Correlation coefficient were calculated to find out the relationship of the independent variables with yield and inter-relationship between themselves. Phenotypic and genotypic correlation coefficients were calculated from the variance and covariance component as suggested by Aljibouri *et al.* (1958) and Panse and Sukhatme (1967).

Phenotypic correlation coefficient

$$r_{x_i, x_j} (P) = \frac{\text{Cov. } X_i, X_j (P)}{\sqrt{\sigma_{p_i}^2 \cdot \sigma_{p_j}^2}}$$

Where,

$$\begin{aligned} r_{x_i, x_j} (P) &= \text{Phenotypic correlation between } x_i \text{ and } x_j \\ \text{Cov. } X_i, X_j (P) &= \text{Phenotypic covariance between character } x_i \text{ and } x_j \\ \sigma_{p_i}^2 &= \text{Phenotypic variance of character } x_i, \text{ and} \\ \sigma_{p_j}^2 &= \text{Phenotypic variance of character } x_j \text{ and} \end{aligned}$$

Genotypic correlation coefficient

$$r_{x_i, x_j} (g) = \frac{\text{Cov. } X_i, X_j (g)}{\sqrt{\sigma_{g_i}^2 \cdot \sigma_{g_j}^2}}$$

Where,

$r_{x_i, x_j}(g)$ = Genotypic correlation between x_i and x_j

$Cov.X_i, x_j(g)$ = Genotypic covariance between character x_i and x_j

σ^2_{pi} = Genotypic variance of character x_i , and

σ^2_{pj} = Genotypic variance of character x_j and

Phenotypic correlation coefficient was tested for significance by comparing the 'r' value given in Fisher and Yates (1963) table at (rv-2) degrees of freedom at 5 and 1 per cent level of significance.

Path Co-efficient analysis

The Correlation co-efficient of yield with various quantitative and qualitative characters were portioned into measures of direct effect with the help of both co-efficient analysis as suggested by Dewey and Lu (1959). The following simultaneous equation were formed and solved for estimating the various direct and indirect effects.

i. Estimation of direct effect

$$P_{1y} + r_{1.2} P_{2y} + r_{1.3} P_{3y} + \dots + r_{1n} P_{ny} = r_{1y}$$

$$P_{2y} + r_{2.1} P_{1y} + r_{2.3} P_{3y} + \dots + r_{2n} P_{ny} = r_{2y}$$

$$r_{n.1} + P_{1Y_2} + r_{n.2} P_{n.3} P_{3y} + \dots + P_{ny} = r_{nn}$$

Where,

r_{1y} to r_{ny} = Co efficient of correlation between independent characters 1 to n and dependent character, yield (y)

n = Total number of pairs of observations.

P_{1y} to P_{ny} = The direct effect of independent characters 1 to n on the dependent character.

Estimation of indirect effect

The indirect effects for a particular characters through the other character J was obtained by multiplication of direct path and corresponding correlation coefficient between character 'i' and 'j' respectively.

$$\text{Indirect effect} = r_{ij} \times P_{ij}$$

Where,

i and j = 1, 2, n (total no of character) (i ≠ j)

iii. Residual effect

The contribution of residual factor was estimated as

$$\text{Residual factors (X), } P_{xy} = \sqrt{1-R^2}$$

Where,

$$R^2 = \sum_{i=1}^n P_{iy}^2 + 2 \sum_{i \neq j = 1}^n P_{iy} P_{jy} r_{ij}$$

n = Number of independent characters

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

p_{jy} = Direct effect of j^{th} character on yield (y)

r_{ij} = Correlation co-efficient between i^{th} and j^{th} characters.

Joint Scaling Test

Mather (1949) defined scaling tests where we calculated some relationship such as $A = 2B_1 - P_1 - F_1 = 0$, on the assumption of additive type of model. In these tests only a few combinations of families are used once at a time. For example, in scaling test 'A', we use B_1 , P_1 and F_1 families but not other families at the same time.

Cavalli (1952) devised a method, known as joint scaling test, to include any combination of such families at the same time.

Important feature of this test are :

- i. It can combine any combination of families at the same time.
- ii. At least 4 generations are required.

- iii. It also estimates the parameters of the model viz. m , $[d]$ and $[h]$.
- iv. It test the goodness of fit, of the model, if more than 3 families are available. To estimates 3 parameters (m), (d) and (h), minimum 3 families are required, and in such case no degrees of freedom is left for testing the goodness of fit of the model. Degree of freedom equal to number of generation minus number of parameter estimated.

Procedure of Joint Scaling Test

Cavalli (1952) joint scaling tests is based on the using weighted least square method (Nelder, 1960; Hayman, 1960). Weights are reciprocals of variance of means. Both parents and F_1 population being homogenous, the estimates of variance of means must be equal to σ^2_e in each case. If this is not so, then to notify this effect weighted analysis developed by Nelder (1960) and Hayman (1960) were applied. If the assumption of equality of standard error is fulfilled, there is no need to use the weight as multiplier. Hence in the character where above assumption was fulfilled non-weighted analysis was done and in other characters weighted analysis was done. The following steps are involved in joint scaling given below :

(a) Mean variance for different generation

Mean variance for different viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 was calculated in same manner as described for five parameter model.

(b) Weight for different generations

The weights $[1/V(x)]$ for different generation viz. P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 are estimated as follows :

$$\begin{aligned}
 P_1 &= 1/V(P_1) \\
 P_2 &= 1/V(P_2) \\
 F_1 &= 1/V(F_1) \\
 F_2 &= 1/V(F_2) \\
 BC_1 &= 1/V(BC_1) \\
 BC_2 &= 1/V(BC_2)
 \end{aligned}$$

Where,

$V(P_1)$, $V(P_2)$, $V(F_1)$, $V(F_2)$, $V(BC_1)$ and $V(BC_2)$ are the mean variance of sample mean of respective generation.

(c) Coefficient of parameters (m, d and h) for different generations

Coefficient of these three parameters m, [d] and [h] are the same as given by Mather (1949) in components of variation for each generation.

For instance

$$\bar{P}_1 = m + [d]$$

$$\bar{P}_2 = m - [d]$$

$$\bar{F}_1 = m + [h]$$

$$\bar{F}_2 = m + \frac{1}{2} [h]$$

$$\bar{BC}_1 = m + \frac{1}{2} [d] + \frac{1}{2} [h] \text{ and } \bar{BC}_2 = m - \frac{1}{2} [d] + \frac{1}{2} [h]$$

Where,

\bar{P}_1 , \bar{P}_2 , \bar{F}_1 , \bar{F}_2 , \bar{BC}_1 and \bar{BC}_2 were the mean of higher parent, lower parent, respectively.

Generations and coefficient of parameters (m, d and h) given below :

Sl. No.	Generation	Coefficient of parameters		
		m	[d]	[h]
1.	P_1	1	-1	0
2.	P_2	1	1	0
3.	F_1	1	0	1
4.	F_2	1	0	$\frac{1}{2}$
5.	BC_1	1	$-\frac{1}{2}$	$\frac{1}{2}$
6.	BC_2	1	$\frac{1}{2}$	$\frac{1}{2}$

Further estimation of m, d and h, three equations are required as given below :

(i) Equation first with respect to [m]

Multiply each family equations by the coefficient of 'm' and its weight.

Say for,

$$P_1 = 1 \times 1 \times \text{weight (m)} + 1 \times (-1) \times \text{weight (d)} + 1 \times 0 \times \text{weight (h)}$$

Where,

1 = family equation

* = coefficient of parameters m, d and h, weight = weights of m, d and h.

These coefficient are arranged in respective column of m, d and h, Extra column of mean * added, obtained by taking of sum of over all six families.

Where,

mean* = mean x weight x coefficient

Similarly, we obtained equations for all other families. Finally take sum overall the five families.

(ii) Equation Second and Third

Equation second and third respect to (d) and (h) respectively were obtained in similar fashion as above equation.

Now the 3 equations were arranged as follows :

$$m + d + h = \text{mean}^* \text{ (I)}$$

$$m + d + h = \text{mean}^* \text{ (II)}$$

$$m + d + h = \text{mean}^* \text{ (III)}$$

Where,

I, II and III equations m, d and h were showed with coefficient of value for respective equations, mean* showed the sum of over all the five families.

From above 3 equations, we can estimate the parameters with help of matrix in following ways.

$$\begin{bmatrix} M & D & H \\ M & D & H \\ m & D & h \end{bmatrix} \begin{bmatrix} \text{in} \\ d \\ h \end{bmatrix} = \begin{bmatrix} \text{mean}^* \\ \text{mean}^* \\ \text{mean}^* \end{bmatrix}$$

Say A.B. = C

Hence B = A⁻¹, C

Accordingly,

$$\begin{bmatrix} M \\ D \\ H \end{bmatrix} = \begin{bmatrix} M & D & h \\ M & D & h \\ M & D & h \end{bmatrix} \begin{bmatrix} \text{mean}^* \\ \text{mean}^* \\ \text{mean}^* \end{bmatrix}$$

Where,

‘+’ significant diagonal element of inverse matrix.

(d) Test of Significance

Standard error of each of these estimates were obtained as under root of the diagonal element of the inverse matrix as given below :

$$SE (m) = (m^+)^{1/2}$$

$$SE (d) = (d^+)^{1/2}$$

$$SE (h) = (h^+)^{1/2}$$

The significance of these parameters are tested against their standard error as :

$t = \text{Estimate of parameter} / \text{standard error of the parameter}$, This ‘t’ value tested against 1.96 and 2.57 at 5per cent and 1per cent respectively.

Testing of Goodness of Fit

Following two steps were utilized for testing the goodness of fit of model.

- (a) Compute the expected means of these five families (P_1, P_2, F_1, F_2, BC_1 and BC_2) using estimates of (m), (d) and (h) in a following manner.

$$\bar{P}_1 = m + d$$

$$\bar{F}_2 = m + \frac{1}{2} h$$

$$\bar{P}_2 = m - d$$

$$\bar{BC}_1 = m + \frac{1}{4} h$$

$$\bar{F}_1 = m + h$$

$$\bar{BC}_2 =$$

- (b) Calculate the square of the deviation of the observed mean from the expected mean for each family and find out χ^2 value.

$$\chi^2 = (O-E)^2 \times \text{weights}$$

Where,

χ^2 = Chi-square value,

O = observed mean

E = expected mean

Weight = weights of respective families

Generation Mean Analysis

For each family the plot mean values in each generation were averaged over replications to obtain generation means. These generation means formed the basis of calculation of various genetic parameters. The mean, variance, variance of mean and standard errors of each of the six generation were estimated using the following formula :

$$\text{Mean} = \frac{\sum X_i}{n}$$

$$\text{Variance} = \frac{1}{n-1} \left[\sum X_i^2 - \frac{(\sum X_i)^2}{n} \right]$$

$$\text{Variance of sample mean} = \frac{\text{Variance}}{n}$$

$$\text{Standard error (S.E.)} = \sqrt{\frac{\text{Variance}}{n}}$$

Where,

X_i = i^{th} observations of a population and

n = number of observations/replications

Components of Generation Means

@ Six parameter Model

Hayman (1958) and Jinks and Jones (1958) gave six parameter model for estimation of various genetic components. According to Hayman (1958).

m	=	Mean = \bar{F}_2
d	=	additive effect = $\bar{B}_1 - \bar{B}_2$
h	=	Dominance effect = $\bar{F}_1 - 4\bar{F}_2 - \frac{1}{2}\bar{P}_1 - \bar{P}_2 + 2\bar{B}_1 + 2\bar{B}_2$
i	=	Additive x Additive
	=	$2\bar{B}_1 + 2\bar{B}_2 - 4\bar{F}_2$
j	=	Additive x Dominance
	=	$\bar{B}_1 - \frac{1}{2}\bar{P}_1 - \bar{B}_2 + \frac{1}{2}\bar{P}_2$
l	=	Dominance x Dominance
	=	$\bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{B}_1 - 4\bar{B}_2$
V _m	=	V(\bar{P}_2)
V _d	=	V(\bar{B}_1) + V(\bar{B}_2)
V _h	=	V(\bar{F}_1) + 16 V(\bar{F}_2) + $\frac{1}{4}$ V(\bar{P}_1) + $\frac{1}{4}$ V(\bar{P}_2) + V(\bar{B}_1) + 4 V(\bar{B}_2)
V _i	=	4V(\bar{B}_1) + 4 V(\bar{B}_2) + 16 V(\bar{F}_2)
V _j	=	V(\bar{B}_1) + $\frac{1}{4}$ V(\bar{P}_1) + V(\bar{B}_2) + $\frac{1}{4}$ V(\bar{P}_2)
V _l	=	V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16 V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)
S.E.(m)	=	(V _m) ^{1/2}
S.E.(d)	=	(V _d) ^{1/2}
S.E.(h)	=	(V _h) ^{1/2}
S.E.(i)	=	(V _i) ^{1/2}
S.E.(j)	=	(V _j) ^{1/2}
S.E.(l)	=	(V _l) ^{1/2}

't' values are obtained as follows :

$$t(m) = m/S.E.(m)$$

$$t(d) = d/S.E.(d)$$

$$t(h) = h/S.E.(h)$$

$$t(i) = i/S.E.(i)$$

$$t(j) = j/S.E.(j)$$

$$t(l) = l/S.E.(l)$$

Heterosis

(1) Heterosis : It was estimated as per cent increase or decrease in the mean values of F_1 hybrids over better parent (BP) and check (CP).

(a) Heterosis over better parent

$$= \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100$$

Where,

$$\bar{F}_1 = \text{mean performance of } F_1$$

$$\bar{BP} = \text{mean value of better parent}$$

(b) Heterosis over check parent (Economic Heterosis)

$$= \frac{\bar{F}_1 - \bar{CP}}{\bar{CP}} \times 100$$

Where,

$$\bar{F}_1 = \text{mean performance of } F_1$$

$$\bar{CP} = \text{mean value of check parent}$$

Test of significance of Heterosis

't' test was applied to determine the significance of heterosis by using the formulae :

$$t' \text{ (MP)} = \frac{\bar{F}_1 - \underline{MP}}{\overline{MP}} \times 100$$

$$t' \text{ (BP)} = \frac{\bar{F}_1 - \bar{Bp}}{\text{S.E. (heterosis over Bp)}}$$

$$t' \text{ (CP)} = \frac{\bar{F}_1 - C_p}{\text{S.E. (heterosis over } C_p)}$$

Where,

$$\text{S.E. (heterosis over MP)} = 2(me/r)^{1/2}$$

$$\text{S.E. (heterosis over Bp)} = (2 Me/r)^{1/2}$$

$$\text{S.E. (heterosis over } C_p) = (2 Me/r)^{1/2}$$

$$Me = \text{mean error variance for parents and } F_1 \text{'s}$$

$$R = \text{number of replications}$$

The calculated 't' value was compared with the table value of 't' at error degree of freedom for test of significance.

Estimation of Inbreeding Depression

$$\text{Inbreeding depression} = \bar{F}_1 - \bar{F}_2 = \text{reduction in } F_2 \text{ from } F_1$$

$$\text{Per cent inbreeding depression} = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1} \times 100$$

Where,

$$\bar{F}_1 = \text{Mean value of } F_1 \text{ generation}$$

$$\bar{F}_2 = \text{Mean value of } F_2 \text{ generation}$$

Standard error of inbreeding depression was calculated as follows :

$$SE (I) = \sqrt{S^2_2 \left(\frac{1}{r} + \frac{1}{10r} \right)}$$

Where,

$$S^2_2 = \text{error variance obtained by using parents } F_1 \text{'s and } F_2 \text{'s together.}$$

Test of Significance

Significance of inbreeding depression was tested by 't' test.

$$t = \frac{\bar{F}_1 - \bar{F}_2}{SE (1)}$$

Where,

SE (I) = Standard error of inbreeding depression the 't' value was compared at 5per cent and 10per cent level of significance .

Chi-square

$$X^2 = \frac{\Sigma (O-E)^2}{E}$$

Where,

O = Observed value

E = Expected value

□□□□□

EXPERIMENTAL FINDINGS

Six intra and four inter specific crosses of *Vigna* were generated involving three of each *Vigna mungo* and *Vigna radiata* MYMV resistant varieties as well as one of each MYMV susceptible variety Barabanki local and LGG 450 respectively to have the P₁, P₂, F₁, F₂, BC₁ and BC₂ population. The generated population of all ten crosses were grown in Randomized Block Design (RBD) with three replications and observations were made for thirteen quantitative agronomical traits alongwith MYMV susceptible/resistant reactions. The obtained data subjected to different statistical analysis in two parts (i) including the parents (P₁, P₂, F₁, F₂, BC₁ and BC₂) (ii) excluding parents (F₁, F₂, BC₁ and BC₂) and the results of present investigation are presented in following sub heads :

- 4.1 Analysis of variance
- 4.2 Mean and range
- 4.3 Genetic variability
- 4.4 Character association
- 4.5 Direct and indirect effect
- 4.6 Estimation of gene effects
- 4.7 Heterosis and inbreeding depression
- 4.8 Inheritance pattern of Mungbean Yellow Mosaic Virus.

4.1 Analysis of variance

Analysis of variance for thirteen characters of *Vigna* viz., days to 50 per cent flowering, Plant height (cm), Number of primary branches, Number of cluster per plant, Pod per cluster, Number of Rod per plant, days to maturity, pod length (cm), number of grains per pod, 100 seed weight (g), Harvest index (HI), Phenol content mg/g of fresh leaf and grain yield per plot (kg) has been presented in table 3a and 3b In the design of experiment mean sum of squares due to genotypes were found to be highly significant for all the characters in including as well as excluding parents.

Table 3a : Analysis of variance for thirteen characters including parent of *Vigna*

Sl. No.	Characters	Mean sum of squares		
		Replication	Treatment	Error
1.	Days to 50% flowering	0.188	20.02**	0.821
2.	Plant height (cm)	0.093	322.04**	4.61
3.	No. of Primary branches	0.197	4.62**	0.22
4.	No. of cluster per plant	3.078	106.13**	4.28
5.	Pod per cluster	1.807	1.56**	0.26
6.	No. of pod per plant	2.027	512.71**	8.56
7.	Days to maturity	5.906	58.39**	2.93
8.	Pod length (cm)	0.009	7.53**	0.16
9.	No. of grain per pod	0.469	7.90**	0.18
10.	100-seed weight (g)	0.005	1.03**	0.004
11.	Harvest index (HI)	0.002	0.03**	0.001
12.	Phenol content mg/g	0.014	0.18**	0.001
13.	Grain yield/plot (kg)	0.003	0.07**	0.001

* Significant at P = 0.05

** Significant at P = 0.01

Table 3b : Analysis of variance for thirteen characters excluding parent of *Vigna*

Sl. No.	Characters	Mean sum of square		
		Replication	Treatment	Error
1.	Days to 50% flowering	0.130	18.868**	0.913
2.	Plant height (cm)	0.037	349.988**	4.849
3.	No. of Primary branches	0.298	4.979**	0.233
4.	No. of cluster per plant	3.647	120.736**	4.795
5.	Pod per cluster	1.492	1.700**	0.288
6.	No. of pod per plant	0.748	520.477**	9.565
7.	Days to maturity	4.495	54.615**	3.079
8.	Pod length (cm)	0.003	6.562**	0.176
9.	No. of grains per pod	0.282	7.592**	0.198
10.	100-seed weight (g)	0.006	0.843**	0.005
11.	Harvest index (HI)	0.002	0.035**	0.001
12.	Phenol content mg/g	0.011	0.193**	0.001
13.	Grain yield/plot (kg)	0.002	0.059**	0.001

* Significant at P = 0.05

** Significant at P = 0.01

4.2 Mean and range (including/excluding parent)

The mean and range of the genotype for thirteen characters have been enlisted in table 4a (including, parent) and in Table 4b (excluding parent) as well as mean performance of the genotypes for thirteen quantitative characters are given in table 5a (including parent) and in Table 5b (excluding parent).

4.2.1 Days to 50% flowering

The range of days to 50% flowering varied from 25.5 (Samrat) to 36.0 days (Samrat x LGG 450 – BC₂) with the general mean of 30.8 ± 0.52 days in including the parents.

The range of 50% flowering varied from 26.00 (TMB 37 x Barabanki F₁) to 30.0 (Uttara x LGG 450) days comprising the general mean of 31.5 ± 0.55 days in excluding the parent. Whereas all the genotypes in both the set of experiment had shown non significant superiority except Samrat in including parents over check.

4.2.2 Plant height

The range varied for plant height among the genotypes from 17.9 (PU 31 x Barabanki, BC₁) to 52.7 cm (HUM 16 x LGG 450, BC₂) including as well as excluding the parent comprising the general mean of 32.74 ± 1.24 and 32.63 ± 1.27 cm. respectively. Whereas, 32 and 34 genotypes exhibited significant superiority for dwarfness over the check SML 668 respectively.

4.2.3 Number of Primary branches

Range varied for number of primary branches from 1.60 (Uttara x LGG 450, BC₂) to 7.33 (TMB 37 x LFF 450 F₁) including as well as including parent comprising the general mean of 4.17 ± 0.27 and 4.30 ± 0.28 respectively. Most of the genotypes had shown significant superiority over the check variety except eight genotypes both in including as well as excluding parent.

Table 4a : Mean and range of thirteen characters including parent of *Vigna*

Sl. No.	Character	Mean	Range	
			Minimum	Maximum
1.	Days to 50% flowering	30.83	25.50 (Samrat)	36.00 (BC ₂ Samrat x LGG 450)
2.	Plant height (cm)	32.74	17.90 (BC ₁ PU ₃₁ x Barabanki)	52.700 (BC ₂ HUM 16 x LGG 450)
3.	No. of Primary branches	4.17	1.60 (BC ₂ Uttra x LGG 450)	7.3333 (F ₁ TMB ₃₇ x LGG 450)
4.	No. of cluster per plant	17.81	9.43 (BC ₁ Uttra x LGG 450)	39.5000 (BC ₂ HUM 16 x LGG 450)
5.	Pod per cluster	3.15	1.87 (BC ₂ HUM16 x LGG 450)	5.23 (F ₁ TMB ₃₇ x LGG 450)
6.	No. of pod per plant	45.37	22.27 (F ₂ HUM 16 x LGG 450)	84.43 (F ₁ Uttara x Barabanki)
7.	Days to maturity	71.76	62.17 (PU31)	80.67 (BC ₂ Uttra x LGG 450)
8.	Pod length (cm)	5.99	3.63 (BC ₂ Uttra x Barabanki)	10.50 (SML 668 check)
9.	No. of grains per pod	6.89	4.60 (BC ₂ Uttra x Barabanki)	11.00 (F ₁ TMB ₃₇ x LGG 450)
10.	100-seed weight (g)	3.68	2.49 (BC ₂ Samrat x LGG 450)	4.87 (Sekhar)
11.	Harvest index (HI)	0.28	0.10 (BC ₂ Samrat x LGG 450)	0.54 (PU ₃₁ x Barabanki)
12.	Phenol content (mg)	0.93	0.55 (BC ₂ HUM 16 x LGG 450)	2.03 (Uttra x LGG 450)
13.	Grain yield/plot (kg)	0.49	0.17 (Barabanki)	0.82 (F ₁ HUM 16 x LGG 450)

Table 4b : Mean and range of thirteen characters excluding parent of *Vigna*

Sl. No.	Character	Mean	Range	
			Minimum	Maximum
1.	Days to 50% flowering	31.45	26.00 (F ₁ TMB ₃₇ x Barabanki)	36.00 (F ₁ Uttara x LGG 450)
2.	Plant height (cm)	32.63	17.90 (BC ₁ PU ₃₇ x Barabanki)	52.70 (BC ₁ HUM 16 x LGG 450)
3.	No. of Primary branches	4.30	1.60 (BC ₂ Uttara x LGG 450)	7.33 (F ₁ MM ₃₇ x LGG 450)
4.	No. of cluster per plant	18.33	9.43 (BC ₁ Uttara x LGG 450)	39.50 (BC ₂ HUM 16 x LGG 450)
5.	Pod per cluster	3.23	1.87 (BC ₂ HUM 16 x LGG 450)	5.23 (F ₁ MM ₃₇ x LGG 450)
6.	No. of pod per plant	47.17	1.60 (F ₂ HUM 16 x LGG 450)	84.43 (F ₁ Uttara x Barabanki)
7.	Days to maturity	72.13	64.00 (BC ₁ PU ₃₁ x LGG 450)	80.67 (BC ₂ Uttara x LGG 450)
8.	Pod length (cm)	5.97	3.63 (BC ₂ Uttara x Barabanki)	10.50 (SML 668 check)
9.	No. of grain per pod	6.90	4.60 (BC ₂ Uttara x Barabanki)	11.00 (F ₁ TMB ₃₇ x LGG 450)
10.	100-seed weight (g)	3.62	2.49 (BC ₁ Samrat x LGG 450)	4.52 (Sekhar x Barabanki, F ₂)
11.	Harvest index (HI)	0.29	0.100 (BC ₁ Samrat x LGG 450)	0.54 (F ₁ PU ₃₁ x Barabanki)
12.	Phenol content (mg)	0.93	0.55 (BC ₁ HUM 16 x LGG 450)	2.03 (BC ₁ Uttara x LGG 450)
13.	Grain yield/plot (kg)	0.49	0.24 (BC ₂ PU ₃₁ x LGG 450)	0.82 (F ₁ HUM 16 x LGG 450)

4.2.4 Number of cluster per plant

Number of cluster per plant ranged from 9.43 (Uttara x LGG 450, BC₁) to 39.5 (HUM 16 x LGG 450, BC₂) in including as well as excluding parent, comprising the general mean 17.81 ± 1.19 and 18.33 ± 1.26 respectively. For this trait significant superiority over the check was observed in thirty six and thirty one genotypes including as well as excluding parent respectively.

4.2.5 Number of pod per cluster

Pod per cluster ranges from 1.87 (HUM 16 x LGG 450, BC₂) to 5.23 (TMB 37 x LGG 450, F₁) both the including as well as excluding parent comprising the general mean of 3.15 ± 0.29 and 3.23 ± 0.31 respectively. For the trait significant superiority over the check was observed in including and excluding parent in 17 and 16 treatments respectively.

4.2.6 Number of pod per plant

For this trait range varied from 22.27 (HUM 16 x LGG 450, F₂) to 84.43 (Uttara x Barabanki, F₁) in including and excluding parent obtaining the general mean of 45.37 ± 1.69 and 47.17 ± 1.79 respectively. For this trait 30 and 34 genotype had shown significant superiority over the check variety in including as well as excluding parent respectively.

4.2.7 Days to maturity

Days to maturity varied from 62.17 (PU 31) to 80.67 (Uttara x LGG 450, BC₂) in including parent, whereas by excluding the parent minimum range of days to maturity was observed 64 day (Pant U 31 x LGG 450, BC₁) having the same maximum range along with the general mean of 71.76 ± 0.99 and 72.13 ± 01.01 days respectively in including as well as excluding parent. Significant superiority over the check variety was observed for 32 genotype in including parent and in 30 genotypes excluding parent.

4.2.8 Pod length

Pod length ranged from 3.63 (Uttara x Barabanki, BC₂) to 10.50 (SML 668) both in including as well as excluding parent exhibited the general mean 5.99

Table 5a : Means performance of thirteen characters including parent of *Vigna*

Sl. No.	Characters	Days to 50% flowering	Plant height (cm)	Primary branches	Cluster per plant	Pods per cluster	Pods per plant	Days to maturity
	Genotypes	1	2	3	4	5	6	7
1.	Barabanki	29.00	27.84	3.99	17.65	3.07	46.69	73.13
2.	HUM 16	28.00	34.27	3.47	14.20	2.37	24.87	69.00
3.	LGG 4500	30.87	45.30	3.03	15.63	2.83	44.60	75.40
4.	PU 31	29.00	23.57	4.05	16.13	2.27	31.03	62.17
5.	Samrat	25.50	45.48	2.20	14.38	3.08	29.33	65.83
6.	Sekhar	32.33	27.03	4.33	14.80	2.67	35.60	74.00
7.	TMB 37	26.67	34.47	3.23	11.98	3.32	33.17	65.33
8.	Uttara	32.17	28.33	3.79	16.42	2.61	44.07	73.83
9.	F ₁ (HUM 16 x LGG 450)	34.00	46.53	4.80	24.67	3.00	71.17	75.33
10.	F ₂ (HUM 16 x LGG 450)	31.00	44.60	1.63	9.53	2.75	22.27	67.00
11.	BC ₁ (HUM 16 x LGG 450)	32.67	43.88	4.42	18.80	2.73	50.00	73.00
12.	BC ₂ (HUM16 x LGG 450)	35.00	52.70	4.57	39.50	1.87	57.50	75.67
13.	F ₁ (Samrat x LGG 450)	28.67	40.57	4.10	12.83	4.13	52.47	72.33
14.	F ₂ (Samrat x LGG 450)	28.33	46.10	5.07	19.53	4.07	31.07	72.00
15.	BC ₁ (Samrat x LGG 450)	27.00	51.30	4.13	18.33	2.30	43.50	67.33
16.	BC ₂ (Samrat x LGG 450)	29.67	37.93	3.60	14.13	3.17	41.43	73.00
17.	F ₁ (TMB 37 x LGG 450)	31.67	51.00	7.33	30.33	5.23	52.73	78.00
18.	F ₂ (TMB 37 x LGG 450)	30.33	25.13	2.97	10.77	4.03	29.67	75.33
19.	BC ₁ (TMB 37 x LGG 450)	29.00	31.33	5.27	15.17	3.13	45.33	70.33
20.	BC ₂ (TMB 37 x LGG	33.33	42.33	3.07	16.90	4.20	55.93	73.33

	450)							
21.	F ₁ (PU 31 x Barabanki)	29.00	21.00	4.40	20.60	2.80	54.07	78.00
22.	F ₂ (PU 31 x Barabanki)	30.67	21.33	3.53	17.73	2.02	34.03	77.33
23.	BC ₁ (PU 31 x Barabanki)	31.00	17.90	3.78	16.27	1.93	34.70	64.33
24.	BC ₂ (PU 31 x Barabanki)	32.67	22.97	3.67	19.47	2.32	37.10	78.33
25.	F ₁ (Sekhar x Barabanki)	35.00	25.40	6.63	24.00	3.67	48.00	77.33
26.	F ₂ (Sekhar x Barabanki)	30.67	26.77	5.60	19.07	2.90	48.07	71.00

Contd....

Table 5a : Contd...

Sl. No.	Characters	Days to 50% flowering	Plant height (cm)	Primary Branches	Cluster per plant	Pods per cluster	Pods per plant	Days to maturity
	Genotypes	1	2	3	4	5	6	7
27.	BC ₁ (Sekhar x Barabanki)	31.67	26.00	6.40	30.87	3.27	67.33	72.67
28.	BC ₂ (Sekhar x Barabanki)	33.00	29.53	4.63	16.23	3.57	46.80	72.67
29.	F ₁ (Uttara x Barabanki)	33.67	31.20	6.03	27.13	3.55	84.43	74.00
30.	F ₂ (Uttara x Barabanki)	31.00	27.00	5.07	17.67	2.83	50.27	73.33
31.	BC ₁ (Uttara x Barabanki)	35.00	18.33	4.43	17.17	2.70	25.33	67.00
32.	BC ₂ (Uttara x Barabanki)	32.67	23.10	4.97	17.93	3.40	50.67	65.00
33.	F ₁ (Samrat x Barabanki)	37.67	50.60	4.70	17.83	3.63	54.27	69.67
34.	F ₂ (Samrat x Barabanki)	29.33	45.87	4.20	15.50	3.87	51.57	66.00
35.	BC ₁ (Samrat x Barabanki)	27.00	44.30	2.70	15.43	2.40	34.40	69.67
36.	BC ₂ (Samrat x Barabanki)	32.00	35.20	4.50	18.70	3.80	53.00	73.67
37.	F ₁ (TMB 37 x Barabanki)	26.00	33.87	3.00	28.87	2.80	69.00	72.33
38.	F ₂ (TMB 37 x Barabanki)	29.00	21.50	4.07	12.13	3.16	31.83	67.33
39.	BC ₁ (TMB 37 x Barabanki)	31.33	23.33	5.17	18.83	2.54	45.00	67.00
40.	BC ₂ (TMB 37 x Barabanki)	33.33	23.60	5.60	16.50	2.81	43.03	65.00
41.	F ₁ (PU 31 x LGG 450)	31.67	23.53	6.07	24.83	3.93	61.67	77.00
42.	F ₂ (PU 31 x LGG 450)	29.00	24.07	3.93	10.13	2.83	61.57	72.33

43.	BC ₁ (PU 31 x LGG 450)	32.00	20.43	4.57	16.23	4.30	31.53	64.00
44.	BC ₂ (PU 31 x LGG 450)	34.00	42.60	3.27	13.37	3.57	52.63	74.00
45.	F ₁ (Uttara x LGG 450)	36.00	33.50	4.33	18.60	4.67	49.53	74.00
46.	F ₂ (Uttara x LGG 450)	32.00	22.37	4.17	18.47	3.63	46.07	74.67
47.	BC ₁ (Uttara x LGG 450)	33.67	21.47	1.93	9.43	2.85	44.57	74.33
48.	BC ₂ (Uttara x LGG 450)	29.67	27.64	1.60	10.83	3.30	42.50	80.87
49.	SML 668 (Check)	27.00	39.93	2.53	11.07	2.57	27.73	72.00
	Mean	30.83	32.74	4.17	17.81	3.15	45.37	71.76
	S.Em (\pm)	0.52	1.24	0.27	1.19	0.29	1.69	0.99
	C.D. at 5%	1.47	3.48	0.76	3.35	0.82	4.74	2.78

Cont...

Table 5a : Contd...

Sl. No.	Characters	Pod length (cm)	Grains	100 seed weight (g)	Harvest index	Phenol content (G)	Grain yield per plot (kg)
	Genotypes	1	2	3	4	5	6
1.	Barabanki	4.00	5.06	3.24	0.21	0.69	0.17
2.	HUM 16	10.33	10.40	4.59	0.38	1.10	0.79
3.	LGG 4500	6.21	6.13	3.23	0.11	0.79	0.23
4.	PU 31	4.72	5.33	3.98	0.38	1.06	0.56
5.	Samrat	7.20	7.43	2.90	0.31	0.93	0.60
6.	Sekhar	4.43	6.07	4.87	0.19	0.95	0.52
7.	TMB 37	7.47	8.90	4.61	0.28	1.25	0.60
8.	Uttara	4.43	5.67	4.64	0.19	0.77	0.46
9.	F ₁ (HUM 16 x LGG 450)	7.80	8.67	3.72	0.41	1.13	0.82
10.	F ₂ (HUM 16 x LGG 450)	4.50	5.73	4.24	0.43	0.75	0.59
11.	BC ₁ (HUM 16 x LGG 450)	7.37	7.93	3.71	0.36	0.55	0.52
12.	BC ₂ (HUM16 x LGG 450)	7.70	7.80	2.93	0.28	1.15	0.40
13.	F ₁ (Samrat x LGG 450)	6.53	10.33	3.07	0.34	0.82	0.60
14.	F ₂ (Samrat x LGG 450)	6.30	5.53	3.27	0.11	0.78	0.42
15.	BC ₁ (Samrat x LGG 450)	7.43	8.93	2.49	0.10	1.05	0.46
16.	BC ₂ (Samrat x LGG 450)	6.63	7.80	2.79	0.14	1.25	0.33
17.	F ₁ (TMB 37 x LGG 450)	7.57	11.00	3.57	0.21	0.92	0.67
18.	F ₂ (TMB 37 x LGG 450)	7.73	6.67	4.15	0.20	1.02	0.46
19.	BC ₁ (TMB 37 x LGG 450)	6.50	6.40	4.16	0.28	1.02	0.50
20.	BC ₂ (TMB 37 x LGG 450)	7.33	9.33	2.95	0.29	0.68	0.37
21.	F ₁ (PU 31 x Barabanki)	5.10	7.00	3.52	0.54	0.88	0.70
22.	F ₂ (PU 31 x Barabanki)	5.87	6.27	3.17	0.40	0.79	0.40
23.	BC ₁ (PU 31 x Barabanki)	5.47	6.20	3.50	0.40	1.05	0.49

24.	BC ₂ (PU 31 x Barabanki)	4.77	6.33	2.83	0.22	0.88	0.29
25.	F ₁ (Sekhar x Barabanki)	5.43	8.07	3.97	0.15	0.84	0.56
26.	F ₂ (Sekhar x Barabanki)	5.20	7.07	4.52	0.31	0.68	0.29
27.	BC ₁ (Sekhar x Barabanki)	6.07	5.53	4.20	0.14	1.10	0.42
28.	BC ₂ (Sekhar x Barabanki)	6.67	7.80	3.62	0.35	0.94	0.35

Cont....

Table 5a : Contd...

Sl. No.	Characters	Pod length (cm)	Grains	100 seed weight (g)	Harvest index	Phenol content (G)	Grain yield per plot (kg)
	Genotypes	1	2	3	4	5	6
29.	F ₁ (Uttara x Barabanki)	4.93	6.53	3.54	0.29	0.94	0.68
30.	F ₂ (Uttara x Barabanki)	4.30	5.80	4.32	0.19	0.76	0.47
31.	BC ₁ (Uttara x Barabanki)	3.97	5.27	4.20	0.26	1.12	0.63
32.	BC ₂ (Uttara x Barabanki)	3.63	4.60	3.81	0.38	0.86	0.34
33.	F ₁ (Samrat x Barabanki)	7.87	6.47	3.63	0.29	0.82	0.67
34.	F ₂ (Samrat x Barabanki)	7.63	10.47	3.33	0.29	0.73	0.48
35.	BC ₁ (Samrat x Barabanki)	7.57	6.60	3.42	0.33	1.25	0.51
36.	BC ₂ (Samrat x Barabanki)	5.67	6.20	3.72	0.19	0.82	0.44
37.	F ₁ (TMB 37 x Barabanki)	5.57	6.60	3.56	0.36	1.13	0.67
38.	F ₂ (TMB 37 x Barabanki)	4.63	5.73	3.97	0.39	0.75	0.46
39.	BC ₁ (TMB 37 x Barabanki)	4.87	5.87	4.30	0.39	0.55	0.40
40.	BC ₂ (TMB 37 x Barabanki)	4.67	5.27	2.84	0.47	1.15	0.28
41.	F ₁ (PU 31 x LGG 450)	7.00	6.87	3.56	0.14	0.96	0.56
42.	F ₂ (PU 31 x LGG 450)	5.53	4.80	3.12	0.29	0.76	0.38
43.	BC ₁ (PU 31 x LGG 450)	4.40	5.27	3.62	0.34	0.92	0.46
44.	BC ₂ (PU 31 x LGG 450)	6.40	5.07	3.08	0.17	0.89	0.24
45.	F ₁ (Uttara x LGG 450)	4.17	6.13	3.93	0.22	0.66	0.69
46.	F ₂ (Uttara x LGG 450)	5.60	7.40	3.92	0.25	0.64	0.52
47.	BC ₁ (Uttara x LGG 450)	4.00	6.13	4.15	0.28	2.03	0.46
48.	BC ₂ (Uttara x LGG 450)	4.10	6.00	3.18	0.15	1.13	0.36
49.	SML 668 (Check)	10.50	9.60	4.81	0.47	1.00	0.76
	Mean	6.0	6.90	3.68	0.28	0.93	0.49

	S.Em (\pm)	0.23	0.25	0.04	0.02	0.02	0.01
	C.D. at 5%	0.64	0.69	0.10	0.06	0.05	0.04

Table 5b : Means Performance of thirteen characters excluding parent of *Vigna*

Sl. No.	Characters Genotypes	Days to 50% flowering	Plant height (cm)	Primary Branches	Cluster per plant	Pods per cluster	Pods per plant	Days to maturity
		1	2	3	4	5	6	7
1.	F ₁ (HUM 16 x LGG 450)	34.00	46.53	4.80	24.67	3.00	71.17	75.33
2.	F ₂ (HUM 16 x LGG 450)	31.00	44.60	1.63	9.53	2.75	22.27	67.00
3.	BC ₁ (HUM 16 x LGG 450)	32.67	43.88	4.42	18.80	2.73	50.00	73.00
4.	BC ₂ (HUM 16 x LGG 450)	35.00	52.70	4.57	39.50	1.87	57.50	75.67
5.	F ₁ (Samrat x LGG 450)	28.67	40.57	4.10	12.83	4.13	52.47	72.33
6.	F ₂ (Samrat x LGG 450)	28.33	46.10	5.07	19.53	4.07	31.07	72.00
7.	BC ₁ (Samrat x LGG 450)	27.00	51.30	4.13	18.33	2.30	43.50	67.33
8.	BC ₂ (Samrat x LGG 450)	29.67	37.93	3.60	14.13	3.17	41.43	73.00
9.	F ₁ (TMB 37 x LGG 450)	31.67	51.00	7.33	30.33	5.23	52.73	78.00
10.	F ₂ (TMB 37 x LGG 450)	30.33	25.13	2.97	10.77	4.03	29.67	75.33
11.	BC ₁ (TMB 37 x LGG 450)	29.00	31.33	5.27	15.17	3.13	45.33	70.33
12.	BC ₂ (TMB 37 x LGG 450)	33.33	42.33	30.7	16.90	4.20	55.93	73.33
13.	F ₁ (PU 31 x Barabanki)	29.00	21.00	4.40	20.60	2.80	54.07	78.00
14.	F ₂ (PU 31 x Barabanki)	30.67	21.33	3.53	17.73	2.02	34.03	77.33
15.	BC ₁ (PU 31 x Barabanki)	31.00	17.90	3.77	16.27	1.93	34.70	64.33
16.	BC ₂ (PU 31 x Barabanki)	32.67	22.97	3.67	19.47	2.32	37.10	78.33
17.	F ₁ (Sekhar x Barabanki)	35.00	25.40	6.63	24.00	3.67	48.00	77.33
18.	F ₂ (Sekhar x Barabanki)	30.67	26.77	5.60	19.07	2.90	48.07	71.00
19.	BC ₁ (Sekhar x	31.67	26.00	6.40	30.87	3.27	67.33	72.67

	Barabanki)							
20.	BC ₂ (Sekhar x Barabanki)	33.00	29.53	4.63	16.23	3.57	46.80	72.67
21.	F ₁ (Uttara x Barabanki)	33.67	31.20	6.03	27.13	3.55	84.43	74.00
22.	F ₂ (Uttara x Barabanki)	31.00	27.00	5.07	17.17	2.83	50.27	73.33
23.	BC ₁ (Uttara x Barabanki)	35.00	18.33	4.43	17.17	2.70	25.33	67.00
24.	BC ₂ (Uttara x Barabanki)	32.67	23.10	4.97	17.93	3.40	50.67	65.00
25.	F ₁ (Samrat x Barabanki)	27.67	50.60	4.70	17.83	3.63	54.27	69.67
26.	F ₂ (Samrat x Barabanki)	29.33	45.87	4.20	15.50	3.87	51.57	66.00
27.	BC ₁ (Samrat x Barabanki)	27.00	44.30	2.70	15.43	2.40	34.40	69.67
28.	BC ₂ (Samrat x Barabanki)	32.00	35.20	4.50	18.70	3.80	53.00	73.67

Cont...

Table 5b : Contd...

Sl. No.	Characters	Days to 50% flowering	Plant height (cm)	Primary Branches	Cluster per plant	Pods per cluster	Pods per plant	Days to maturity
	Genotypes	1	2	3	4	5	6	7
29.	F ₁ (TMB 37 x Barabanki)	26.00	33.87	3.00	28.87	2.80	69.00	72.33
30.	F ₂ (TMB 37 x Barabanki)	29.00	21.50	4.07	12.13	3.16	31.83	67.33
31.	BC ₁ (TMB 37 x Barabanki)	31.33	23.33	5.17	18.83	2.54	45.00	67.00
32.	BC ₂ (TMB 37 x Barabanki)	33.33	23.60	5.60	16.50	2.81	43.03	65.00
33.	F ₁ (PU 31 x LGG 450)	31.67	23.53	6.07	24.83	3.93	61.67	77.00
34.	F ₂ (PU 31 x LGG 450)	29.00	24.01	3.93	10.13	2.83	61.57	72.33
35.	BC ₁ (PU 31 x LGG 450)	32.00	20.43	4.57	16.23	4.30	31.53	64.00
36.	BC ₂ (PU 31 x LGG 450)	34.00	42.60	3.27	13.37	3.57	52.63	74.00
37.	F ₁ (Uttara x LGG 450)	36.00	33.50	4.33	18.60	4.67	49.53	74.00
38.	F ₂ (Uttara x LGG 450)	32.00	22.37	4.17	18.47	3.63	46.07	74.67
39.	BC ₁ (Uttara x LGG 450)	33.67	21.47	1.93	9.43	2.85	44.57	74.33
40.	BC ₂ (Uttara x LGG 450)	29.67	27.64	1.60	10.83	3.30	42.50	80.67
41.	SML 668 (Check)	27.00	39.93	2.53	11.07	2.57	27.73	72.00
	Mean	31.15	32.63	4.30	18.33	3.23	47.17	72.13
	S.Em (\pm)	0.55	1.27	0.28	1.26	0.31	1.79	1.01
	C.D. at 5%	1.55	3.58	0.78	3.56	0.87	5.03	2.85

Cont....

Table 5b : Contd...

Sl. No.	Characters	Pod length (cm)	Grains	100 seed weight (g)	Harvest index	Phenol content (G)	Grain yield per plot (kg)
	Genotypes	1	2	3	4	5	6
1.	F ₁ (HUM 16 x LGG 450)	7.80	8.67	3.72	0.41	1.13	0.82
2.	F ₂ (HUM 16 x LGG 450)	4.50	5.73	4.24	0.43	0.75	0.59
3.	BC ₁ (HUM 16 x LGG 450)	7.37	7.93	3.71	0.36	0.55	0.52
4.	BC ₂ (HUM 16 x LGG 450)	7.70	7.80	2.93	0.28	1.15	0.40
5.	F ₁ (Samrat x LGG 450)	6.53	10.33	3.07	0.34	0.82	0.60
6.	F ₂ (Samrat x LGG 450)	6.30	8.53	3.27	0.11	0.78	0.42
7.	BC ₁ (Samrat x LGG 450)	7.43	8.93	2.47	0.10	1.05	0.46
8.	BC ₂ (Samrat x LGG 450)	6.63	7.80	2.79	0.14	1.25	0.33
9.	F ₁ (TMB 37 x LGG 450)	7.57	11.00	3.57	0.21	0.92	0.67
10.	F ₂ (TMB 37 x LGG 450)	7.73	6.67	4.15	0.20	1.02	0.46
11.	BC ₁ (TMB 37 x LGG 450)	6.50	6.40	4.16	0.28	1.02	0.50
12.	BC ₂ (TMB 37 x LGG 450)	7.33	9.33	2.95	0.29	0.68	0.37
13.	F ₁ (PU 31 x Barabanki)	5.10	7.00	3.52	0.54	0.88	0.70
14.	F ₂ (PU 31 x Barabanki)	5.87	6.27	3.17	0.40	0.79	0.40
15.	BC ₁ (PU 31 x Barabanki)	5.47	6.20	3.50	0.40	1.05	0.49
16.	BC ₂ (PU 31 x Barabanki)	4.77	6.33	2.83	0.22	0.88	0.29
17.	F ₁ (Sekhar x Barabanki)	5.43	8.07	3.97	0.15	0.84	0.56
18.	F ₂ (Sekhar x Barabanki)	5.20	7.07	4.52	0.31	0.68	0.29
19.	BC ₁ (Sekhar x Barabanki)	6.07	5.53	4.20	0.14	1.10	0.42
20.	BC ₂ (Sekhar x Barabanki)	6.67	7.80	3.62	0.35	0.94	0.35
21.	F ₁ (Uttara x Barabanki)	4.93	6.53	3.54	0.29	0.94	0.68
22.	F ₂ (Uttara x Barabanki)	4.30	5.80	4.32	0.19	0.76	0.47
23.	BC ₁ (Uttara x Barabanki)	3.97	5.27	4.20	0.26	1.12	0.63

24.	BC ₂ (Uttara x Barabanki)	3.63	4.60	3.81	0.38	0.86	0.34
25.	F ₁ (Samrat x Barabanki)	7.87	6.47	3.63	0.29	0.82	0.67
26.	F ₂ (Samrat x Barabanki)	7.63	10.47	3.33	0.29	0.73	0.48
27.	BC ₁ (Samrat x Barabanki)	7.57	6.60	3.42	0.33	1.25	0.51
28.	BC ₂ (Samrat x Barabanki)	5.67	6.20	3.72	0.19	1.82	0.44

Cont.....

Table 5b : Contd...

Sl. No.	Characters	Pod length (cm)	Grains	100 seed weight (g)	Harvest index	Phenol content (G)	Grain yield per plot (kg)
	Genotypes	1	2	3	4	5	6
29.	F ₁ (TMB 37 x Barabanki)	5.57	6.60	3.56	0.36	1.13	0.67
30.	F ₂ (TMB 37 x Barabanki)	4.63	5.73	3.97	0.39	0.75	0.46
31.	BC ₁ (TMB 37 x Barabanki)	4.87	5.87	4.30	0.39	0.55	0.40
32.	BC ₂ (TMB 37 x Barabanki)	4.67	5.27	2.84	0.47	1.15	0.28
33.	F ₁ (PU 31 x LGG 450)	7.00	6.87	3.56	0.14	0.96	0.56
34.	F ₂ (PU 31 x LGG 450)	5.53	4.80	3.12	0.29	0.76	0.38
35.	BC ₁ (PU 31 x LGG 450)	4.40	5.27	3.62	0.34	0.92	0.46
36.	BC ₂ (PU 31 x LGG 450)	6.40	5.07	3.08	0.17	0.89	0.24
37.	F ₁ (Uttara x LGG 450)	4.17	6.13	3.93	0.22	0.66	0.69
38.	F ₂ (Uttara x LGG 450)	5.60	7.40	3.92	0.25	0.64	0.52
39.	BC ₁ (Uttara x LGG 450)	4.00	6.13	4.15	0.28	2.03	0.46
40.	BC ₂ (Uttara x LGG 450)	4.10	6.00	3.18	0.15	1.13	0.36
41.	SML 668 (Check)	10.50	9.60	4.81	0.47	1.00	0.76
	Mean	5.97	6.90	3.62	0.29	0.93	0.49
	S.Em (±)	0.24	0.25	0.04	0.02	0.02	0.01
	C.D. at 5%	0.68	0.72	0.11	0.06	0.05	0.04

± 0.23 and 5.97 ± 0.24 respectively in including as well as excluding parent. None of the genotypes had shown significant superiority over the SML 668.

4.2.9 Number of grains per pod

For this trait ranged varied from 4.60 (Uttara x Barabanki, BC₂) to 11.00 (TMB 37 x LGG 450, F₁) in both the experiment comprising the general mean 6.89 ± 0.25 and 6.90 ± 0.26 in including as well as excluding parent. Four genotypes exhibited significant superiority in including parents and only three genotypes in excluding parents over the check variety.

4.2.10 100-seed weight

The range of 100-seed weight lies from 2.49 g (Samrat x LGG 450, BC₂) to 4.87 g (Sekhar) in including parent, whereas in excluding parent maximum range 4.52 of (Sekhar x Barabanki, F₂) having the same minimum range along with the grand 3.66 ± 0.04 and 3.62 ± 0.04 respectively. None of the genotypes were found to be significant superior than the check SML 668.

4.2.11 Harvest index

Harvest index ranged from 0.10 (Samrat x LGG 450, BC₂) to 0.54 (Pant U31 x Barabanki, F₁) in both set of experiments having the general mean of 0.28 ± 0.02 and 0.29 ± 0.02 in including as well as excluding parent, respectively. Only one genotype (Pant U31 x Barabanki, F₁) exhibited significant superiority over the SML 668.

4.2.12 Phenol content

Phenol content ranged between 0.55 (HUM 16 x LGG 450, BC₂) to 2.03 mg/g of fresh leaf (Uttara x LGG 450, BC₁) in both set of experiment along with the general mean of 0.93 ± 0.02 mg/g of fresh leaf. Significant superiority over the check was observed in fourteen genotype including parent and twelve genotype by excluding parent.

4.2.13 Grain yield per plot

For this trait ranged obtained from 0.17 (Barabanki) to 0.82 kg (HUM 16 x LGG 450, F₁) in including parent, whereas in excluding the parent minimum

range was observed 0.24 kg (PU 31 x LGG 450, BC₂) comprising the similar value of maximum having the similar mean of 0.49 ± 0.01 . In both sets of experiment same genotype (HUM 16 x LGG 450, F₁) exhibited the significant superiority over the check SML 668.

4.3 Genetic Variability

Genetic variability of thirteen character studied with the help of genetic parameters viz., genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), heritability in broad sense (h^2/bs), Genetic advance (GA), as per cent of mean as presented in table 6a and 6b.

Measures of variation

The character having more than 25% GCV have been grouped high genetic variability, those having 15-24% group in moderate genotypic variability and one having GCV less than 15% kept in low genotypic variability class; phenotypic coefficient of variance was observed slightly higher than genotypic coefficient of variance for all the traits under studied.

High GCV was observed for the traits viz., plant height, number of primary branches, number of cluster per plant, number of pod per plant, pod length, harvest index, phenol content and grain yield per plot, moderate genotypic coefficient of variability was observed for the trait pod per cluster and 100-seed weight, whereas, low genotypic coefficient of variance was observed for days to 50 per cent flowering and days to maturity.

Heritability and Genetic advance

Heritability (h^2) and genetic advance (GA) in broad sense estimated for thirteen characters. On the basis, they were classified in three groups.

- i. Highly heritable h^2 more than 80%
- ii. Moderately heritable- h^2 60-80 %
- iii. Poorly heritable- h^2 less than 60%

Table 6a : Genetic parameter for thirteen characters including parent of *Vigan*

Sl. No.	Character	PCV	GCV	Heritability (h ²)	GA as per cent mean
1.	Days to 50% flowering	8.72	8.21	89.0	15.91
2.	Plant height (cm)	32.11	31.42	96.0	63.36
3.	No. of Primary branches	31.11	29.02	87.0	55.75
4.	No. of cluster per plant	34.72	32.72	89.0	63.51
5.	Pod per cluster	26.40	20.89	63.0	34.07
6.	No. of pod per plant	29.29	28.57	95.0	57.42
7.	Days to maturity	6.45	5.99	86.0	11.47
8.	Pod length (cm)	26.97	26.15	94.0	52.23
9.	No. of grain per pod	24.05	23.25	93.0	46.30
10.	100-seed weight (g)	15.99	15.90	99.0	32.56
11.	Harvest index (HI)	38.79	36.83	90.1	72.05
12.	Phenol content (mg)	26.16	25.96	98.0	53.09
13.	Grain yield/plot (kg)	30.91	30.56	98.0	62.26

Table 6b : Genetic parameter for thirteen characters excluding parent of *Vigna*

Sl. No.	Character	PCV	GCV	Heritability (h²)	GA in per cent of mean
1.	Days to 50% flowering	8.43	7.85	87.0	15.07
2.	Plant height (cm)	33.56	32.87	96.0	66.34
3.	No. of Primary branches	31.31	29.24	87.0	56.23
4.	No. of cluster per plant	35.96	33.92	89.0	65.91
5.	Pod per cluster	27.01	21.27	62.0	34.51
6.	No. of pod per plant	28.44	27.87	95.0	55.46
7.	Days to maturity	6.24	5.75	85.0	10.90
8.	Pod length (cm)	25.41	24.42	92.0	48.36
9.	No. of grain per pod	23.00	22.73	93.0	45.06
10.	100-seed weight (g)	14.73	14.60	98.0	29.83
11.	Harvest index (HI)	38.94	36.85	89.0	71.85
12.	Phenol content (mg)	27.38	27.21	99.0	55.68
13.	Grain yield/plot (kg)	28.97	28.29	97.0	58.11

High heritability was observed for all the traits except pod per cluster having moderate, heritability in both the set of experiment.

Genetic advance (GA) was estimated in terms of absolute figure and GA in per cent of mean. GA as pre cent of mean has been classified in the following groups.

- i. High Genetic advance – more than 20%
- ii. moderate genetic advance – 15-20%
- iii. Low genetic advance - less than 15%

All the characters exhibited high genetic advance as per cent of mean while, moderate genetic advance was observed for days to 50% flowering and low genetic advance for days to maturity.

4.4 Character association

Genotypic as well as phenotypic correlation coefficient were calculated and enlisted in the table 7a and 7b in including parent and excluding parent respectively. All the character combinations exhibited slightly higher or on par of magnitude of genotypic correlation coefficient than phenotypic correlation coefficient value.

Days to 50% flowering exhibited significant and positive correlation with primary branches; whereas with pod length significant and negative correlation was observed in including as well as excluding parent experiment.

Plant height showed highly significant and positive correlation with pod length and grain per pods in both sets of experiment, whereas for 100-seed weight significant and negative correlation was observed.

Number of primary branches highly significantly and positively correlated with cluster per plant and pods per plant in both the sets of experiment.

Cluster per plant showed highly significant and positive correlation with pod per plant in both set of experiment; whereas significant and positive

Table 7a : Correlation between the traits of thirteen characters including parents of *Vigna*

Character		Days to 50% Flowering	Plant Height (cm)	Primary Branches	Clusters/ Plant	Pods/ Cluster	Pods/ Plant	Days to Maturity	Pod Length (cm)	Grains/ Pod	100 Seed Weight (g)	harvest Index	Phenol Content (mg/g)	Grain Yield /Plot (kg)
Days to 50% Flowering	G	1.0000	-0.2311	0.3782	0.3278	0.1909	0.2855	0.3172	-0.3914	-0.2084	0.0468	-0.1306	-0.0474	-0.1648
	P	1.0000	-0.2144	0.3156*	0.2799	0.1430	0.2628	0.264	-0.3581*	-0.1852	0.0467	-0.1155	-0.0466	-0.1551
Plant Height (cm)	G		1.0000	-0.1110	0.1922	0.1920	0.1337	0.0485	0.6255	0.5312	-0.3170	-0.1726	-0.0628	0.1861
	P		1.0000	-0.1003	0.1792	0.1300	0.1331	0.0498	0.5924**	0.5045**	-0.3122*	0.1580	-0.0561	0.1808
No. of Primary Branches	G			1.0000	0.6581	0.3779	0.4753	0.0785	-0.0772	0.0529	0.0734	-0.1405	-0.2700	0.0557
	P			1.0000	0.5700**	0.2555	0.4394**	0.0650	-0.0632	0.0399	0.0694	-0.1347	-0.2473	0.0551
No of Clusters/ Plant	G				1.0000	0.0637	0.6133	0.3032	0.0719	0.1318	-0.1580	-0.1299	-0.0451	0.1502
	P				1.000	0.0374	0.5741**	0.2914*	0.0732	0.1170	-0.1504	-0.1129	-0.0430	0.1287
No. of Pods/ Cluster	G					1.0000	0.2789	0.2115	0.0382	0.2547	-0.0647	-0.3541	-0.2480	0.1196
	P					1.0000	0.2086	0.1445	0.0201	0.1758	-0.0464	-0.2702	-0.1925	0.0863
No. of Pods/ Plant	G						1.0000	0.4014	-0.0314	0.0640	-0.2356	-0.1199	-0.0717	0.0477
	P						1.0000	0.3744**	-0.0377	0.0563	-0.2257	-0.1137	-0.0652	0.0448
Days to Maturity	G							1.0000	0.0445	0.1298	-0.1275	-0.3895	-0.0319	-0.0435
	P							1.0000	0.0233	0.1149	-0.1225	-0.3651**	-0.0300	-0.0452
Pod Length (cm)	G								1.0000	0.7394	-0.0382	0.0697	0.0834	0.3850
	P								1.0000	0.7190**	-0.0358	0.0694	0.0801	0.3699**
Grains/ Pod	G									1.0000	-0.0406	0.0799	0.0373	0.4559
	P									1.0000	-0.0406	0.0734	0.0333	0.4350**
100 Seed Weight (gm)	G										1.0000	0.1547	0.0196	0.3901
	P										1.0000	0.1479	0.0186	0.3845**
harvest Index	G											1.0000	-0.0036	0.3537
	P											1.0000	-0.0028	0.3278*
Phenol Content (mg)	G												1.0000	0.1382
	P												1.0000	0.1368

* Significant at P= 0.05

** Significant at P = 0.01

Table 7b : Correlation between the traits of thirteen characters excluding parent of *Vigna*

Character		Days to 50% Flowering	Plant Height (cm)	Primary Branches	Clusters/ Plant	Pods/ Cluster	Pods/ Plant	Days to Maturity	Pod Length (cm)	Grains/ Pod	100 Seed Weight (gm)	harvest Index	Phenol Content (mg/g)	Grain Yield/ Plot (kg)
Days to 50% Flowering	G	1.0000	-0.2090	0.2992	0.2882	0.1821	0.1755	0.1805	-0.3559	-0.1485	0.0604	-0.0999	0.0156	-0.1141
	P	1.0000	-0.1927	0.2487	0.2411	0.1308	0.1595	0.1383	-0.3228	-0.1288	0.0602	-0.0866	0.0124	-0.1067
Plant Height (cm)	G		1.0000	-0.0485	0.2272	0.1842	0.1688	0.0508	0.6700	0.5655	-0.2986	-0.1660	-0.0660	0.2333
	P		1.0000	-0.0440	0.2083	0.1272	0.1664	0.0527	0.6299**	0.5368**	-0.2949	-0.1542	-0.0594	0.2271
No. of Primary Branches	G			1.0000	0.6482	0.3696	0.4400	0.0073	-0.0118	0.1071	0.0908	-0.1842	-0.2860	0.0921
	P			1.0000	0.5600**	0.2562	0.4110**	0.0042	0.0026	0.0904	0.0866	-0.1757	-0.2602**	0.0902
Clusters/ Plant	G				1.0000	0.0199	0.5944	0.2826	0.1421	0.1960	-0.1077	-0.1549	-0.0133	0.2272
	P				1.0000	0.0076	0.5570**	0.2742	0.1373	0.1731	-0.1038	-0.1374	-0.0140	0.2000
No. of Pods/ Cluster	G					1.0000	0.2120	0.1875	0.0590	0.2899	0.0469	-0.4055	-0.2646	0.1912
	P					1.0000	0.1522	0.1203	0.0334	0.1972	0.0413	-0.3054	-0.2085*	0.1395
No. of Pods/ Plant	G						1.0000	0.3248	0.0843	0.1677	-0.1680	-0.0997	-0.0098	0.2068
	P						1.0000	0.3065	0.0689	0.1537	-0.1588	-0.0965	-0.0069	0.1973
Days to Maturity	G							1.0000	0.1654	0.2451	-0.1153	-0.3445	0.0777	0.1243
	P							1.0000	0.1210	0.2104	-0.1125	-0.3234*	0.0708	0.1050
Pod Length (cm)	G								1.0000	0.6756	-0.1019	-0.0268	-0.0137	0.2741
	P								1.0000	0.6543**	-0.0958	-0.0179	-0.0134	0.2600
Grains/ Pod	G									1.0000	-0.1492	-0.0029	-0.0684	0.3664
	P									1.0000	-0.1447	-0.0001	-0.0671	0.3461*
100 Seed Weight (gm)	G										1.0000	0.2062	-0.0749	0.3599
	P										1.0000	0.1960	-0.0753	0.3534*
harvest Index	G											1.0000	-0.0795	0.2673
	P											1.0000	-0.0770	0.2446
Phenol Content (mg)	G												1.0000	0.0180
	P												1.0000	0.0185

* Significant at P= 0.05

** Significant at P = 0.01

correlation was observed for days to maturity only in one set of experiment i.e. including parent.

Pods per plant exhibited highly significant and positive correlation with days to maturity only present in including parent.

Days to maturity highly significantly and positive, correlated with harvest index in including the parent; whereas significantly and negatively correlated in excluding the parent with harvest index.

Pod length showed highly significant and positive correlation with grains per pod in both the set of experiments.

Grain yield exhibited highly significant and positive correlation with pod length, grains per pod and 100-seed weight as well as positive and significant correlation with harvest index in including the parent; whereas in excluding the parents this trait exhibited significant and positive correlation with grains per pod and 100 seed weight only.

4.5 Direct and indirect effect

The path analysis offers an opportunity to portioning of correlation coefficient into direct and indirect effects to understand the causes of association.

Genotypic path analysis being free from environmental effect can give a better pictures of cause and effect relationship than phenotypic path analysis. The direct and indirect effects of causal variables on the resultant variable is grain yield (kg/plot) have been presented in table 8a for including parent as well as in table 8b for excluding parent.

From the table it is evident that pod length exhibited positive direct effect (0.035) on grain yield as well as positive indirect effect (0.073) via days to 50% flowering only in including parent.

Grain per pod has positive and high direct effect (0.188) with grain yield as well as positive and high indirect effect (0.139) via plant height in including parent; whereas in excluding the parent. positive and high direct effect (0.156)

Table 8b : Direct & indirect effect of the traits on grain yield excluding parent of *Vigna*

Character		Days to 50% Flowering	Plant Height (cm)	Primary Branches	Clusters/ Plant	Pods/ Cluster	Pods/ Plant	Days to Maturity	Pod Length (cm)	Grains/ Pod	100 Seed Weight (g)	harvest Index	Phenol Content (mg/g)	Grain Yield/ Plot (kg)
Days to 50% Flowering	G	-0.2258	0.0472	-0.0676	-0.0651	-0.0411	-0.0396	-0.0408	0.0804	0.0335	-0.0136	0.0226	-0.0035	-0.1141
	P	-0.1535	0.0296	-0.0382	-0.0370	-0.0201	-0.0245	-0.0212	0.0496	0.0198	-0.0092	0.0133	-0.0019	-0.1067
Plant Height (cm)	G	-0.0355	0.1697	-0.0082	0.0385	0.0313	0.0286	0.0086	0.1137	0.0959	-0.0507	-0.0282	-0.0112	0.2333
	P	-0.0465	0.2412	-0.0106	0.0502	0.0307	0.0401	0.0127	0.1520	0.1295	-0.0712	-0.0372	-0.0143	0.2271
Primary Branches	G	-0.0574	0.0093	-0.1919	-0.1244	-0.0709	-0.0845	-0.0014	0.0023	-0.0205	-0.0174	0.0354	0.0549	0.0921
	P	-0.0017	0.0003	-0.0067	-0.0037	-0.0017	-0.0028	0.0000	0.0000	-0.0006	-0.0006	0.0012	0.0017	0.0902
Clusters/ Plant	G	0.1185	0.0934	0.2665	0.4111	0.0082	0.2444	0.1162	0.0584	0.0806	-0.0443	-0.0637	-0.0055	0.2272
	P	0.0386	0.0333	0.0896	0.1600	0.0012	0.0891	0.0439	0.0220	0.0277	-0.0166	-0.0220	-0.0022	0.2000
Pods/ Cluster	G	0.0703	0.0711	0.1427	0.0077	0.3860	0.0818	0.0724	0.0228	0.1119	0.0181	-0.1565	-0.1021	0.1912
	P	0.0209	0.0203	0.0409	0.0012	0.1595	0.0243	0.0192	0.0053	0.0315	0.0066	-0.0487	-0.0333	0.1395
Pods/ Plant	G	0.0060	0.0057	0.0150	0.0202	0.0072	0.0340	0.0110	0.0029	0.0057	-0.0057	-0.0034	-0.0003	0.2068
	P	0.0170	0.0178	0.0439	0.0595	0.0162	0.1068	0.0327	0.0074	0.0164	-0.0170	-0.0103	-0.0007	0.1973
Days to Maturity	G	0.0208	0.0059	0.0008	0.0326	0.0216	0.0375	0.1155	0.0191	0.0283	-0.0133	-0.0398	0.0090	0.1243
	P	0.0168	0.0064	0.0005	0.0333	0.0146	0.0372	0.1212	0.0147	0.0255	-0.0136	-0.0392	0.0086	0.1050
Pod Length (cm)	G	0.0264	-0.0496	0.0009	-0.0105	-0.0044	-0.0062	-0.0122	-0.0741	-0.0500	0.0075	0.0020	0.0010	0.2741
	P	0.0293	-0.0572	-0.0002	-0.0125	-0.0030	-0.0062	-0.0110	-0.0908	-0.0594	0.0087	0.0016	0.0012	0.2600
Grains/ Pod	G	-0.0232	0.0884	0.0167	0.0306	0.0453	0.0262	0.0383	0.1056	0.1563	-0.0233	-0.0005	-0.0107	0.3664
	P	-0.0296	0.1233	0.0208	0.0398	0.0453	0.0353	0.0483	0.1503	0.2296	-0.0332	0.0000	-0.0154	0.3461*
100 Seed Weight (gm)	G	0.0258	-0.1274	0.0388	-0.0459	0.0200	-0.0717	-0.0492	-0.0435	-0.0637	0.4267	0.0880	-0.0320	0.3599
	P	0.0270	-0.1325	0.0389	-0.0466	0.0186	-0.0713	-0.0505	-0.0430	-0.0650	0.4491	0.0880	-0.0338	0.3534*
harvest Index	G	-0.0423	-0.0703	-0.0780	-0.0656	-0.1717	-0.0422	-0.1459	-0.0114	-0.0012	0.0873	0.4235	-0.0337	0.2673
	P	-0.0267	-0.0475	-0.0541	-0.0423	-0.0941	-0.0297	-0.0997	-0.0055	0.0000	0.0604	0.3081	-0.0237	0.2446
Phenol Content (mg/G)	G	0.0024	-0.0100	-0.0435	-0.0020	-0.0402	-0.0015	0.0118	-0.0021	-0.0104	-0.0114	-0.0121	0.1521	0.0180
	P	0.0016	-0.0079	-0.0344	-0.0019	-0.0276	-0.0009	0.0094	-0.0018	-0.0089	-0.0100	-0.0102	0.1323	0.0185

Residual effect : Genotypic (G) = 0.6762
Phenotypic (P) = 0.7409

including parent of *Vigna*

Genotypical Path Diagram for Grain Yield/ Plot (kg)

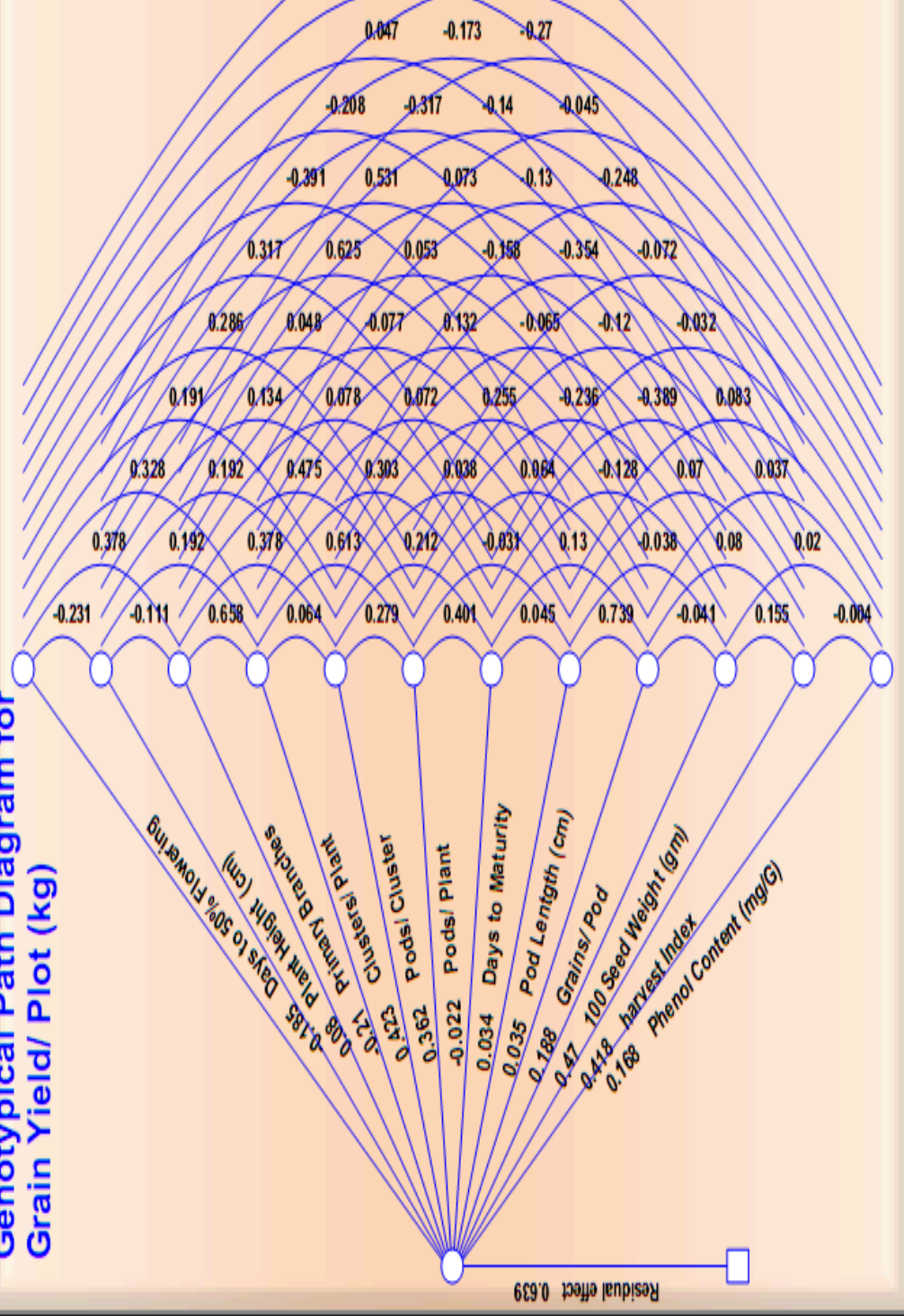


Fig. 4. Phenotypic path coefficient diagram for grain yield and its contributing characters excluding parent of *Vigna*

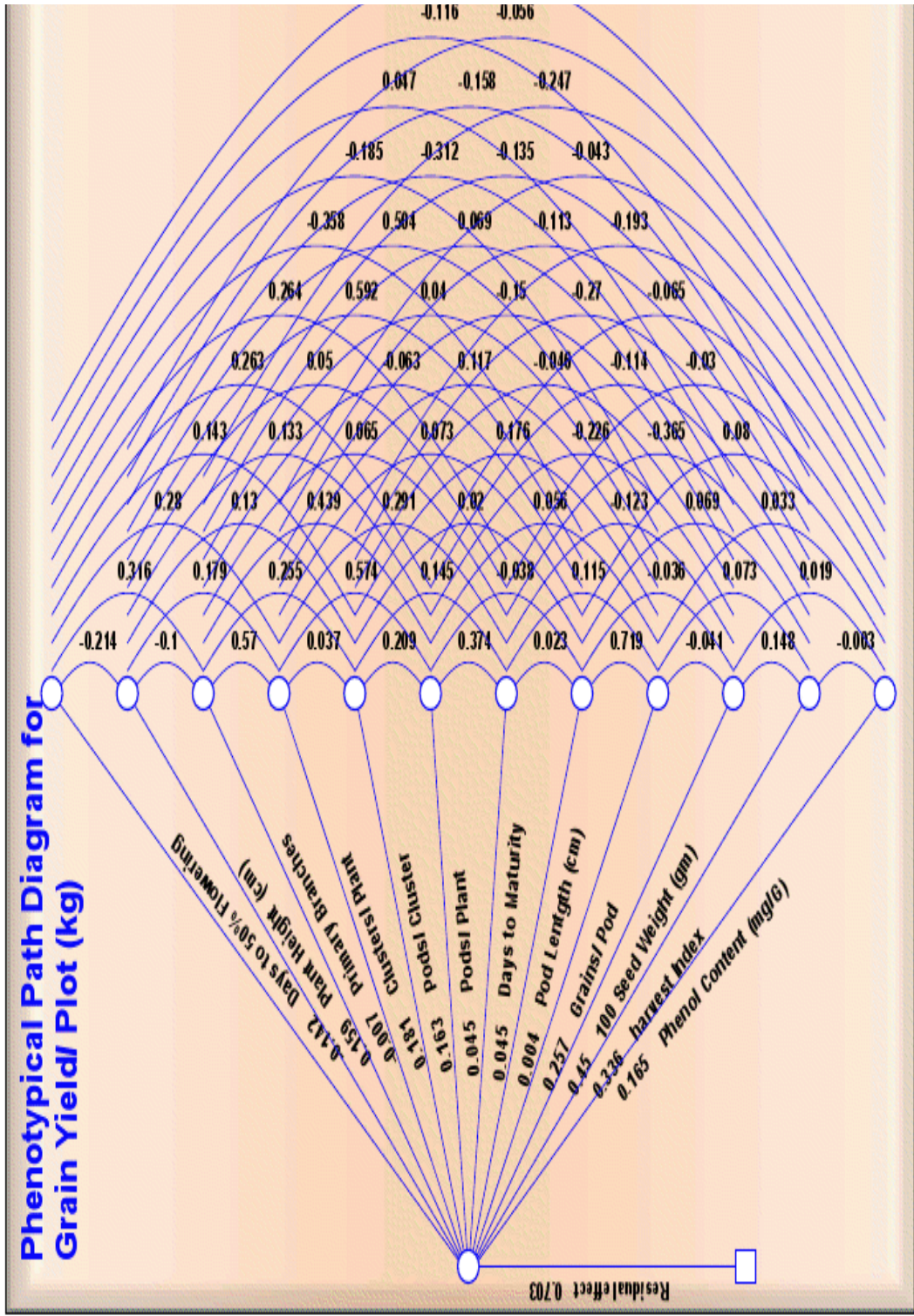


Fig. 3 : Genotypic path coefficient diagram for gram yield and its contributing chara excluding parent of *Vigna*

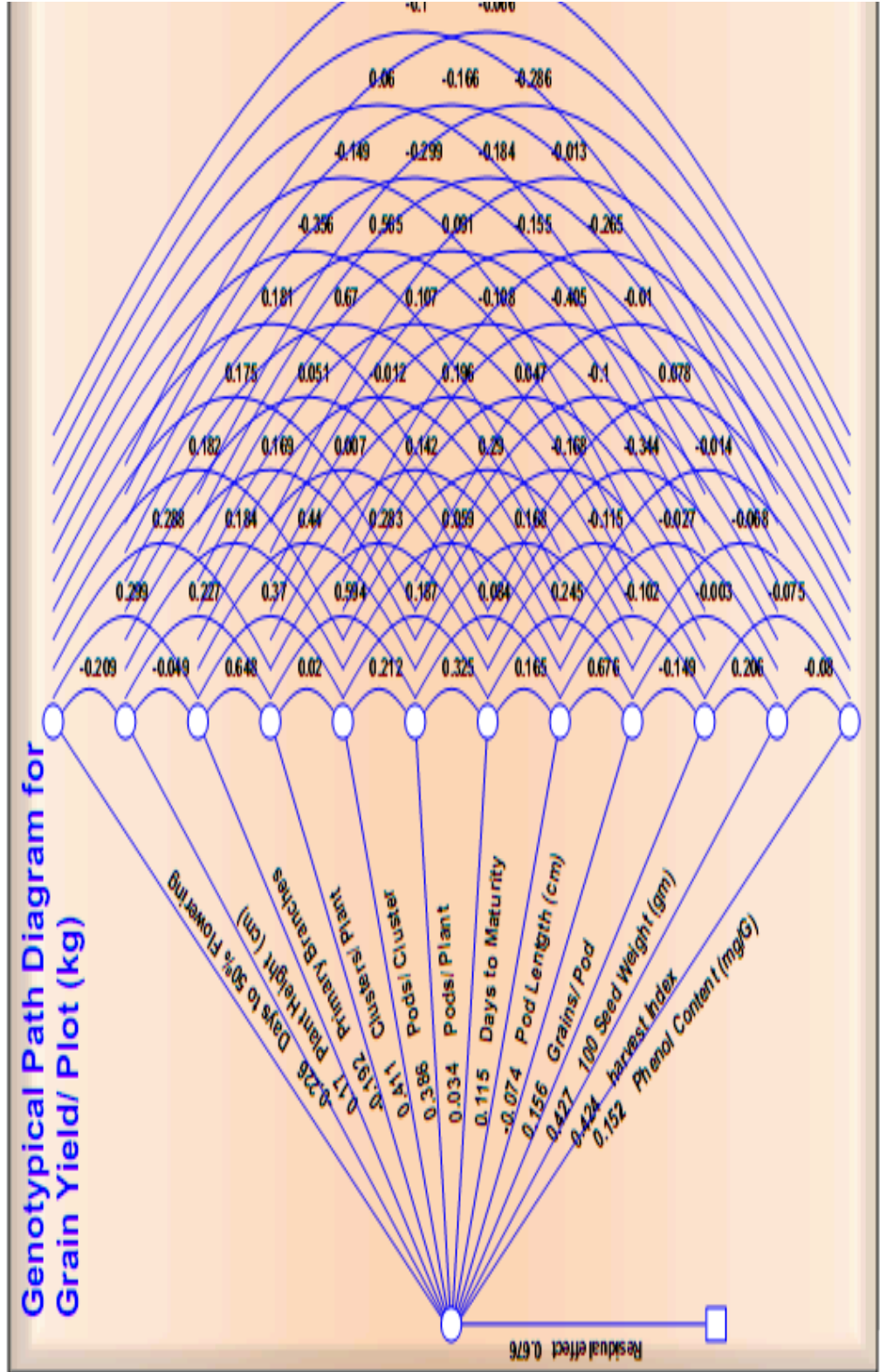
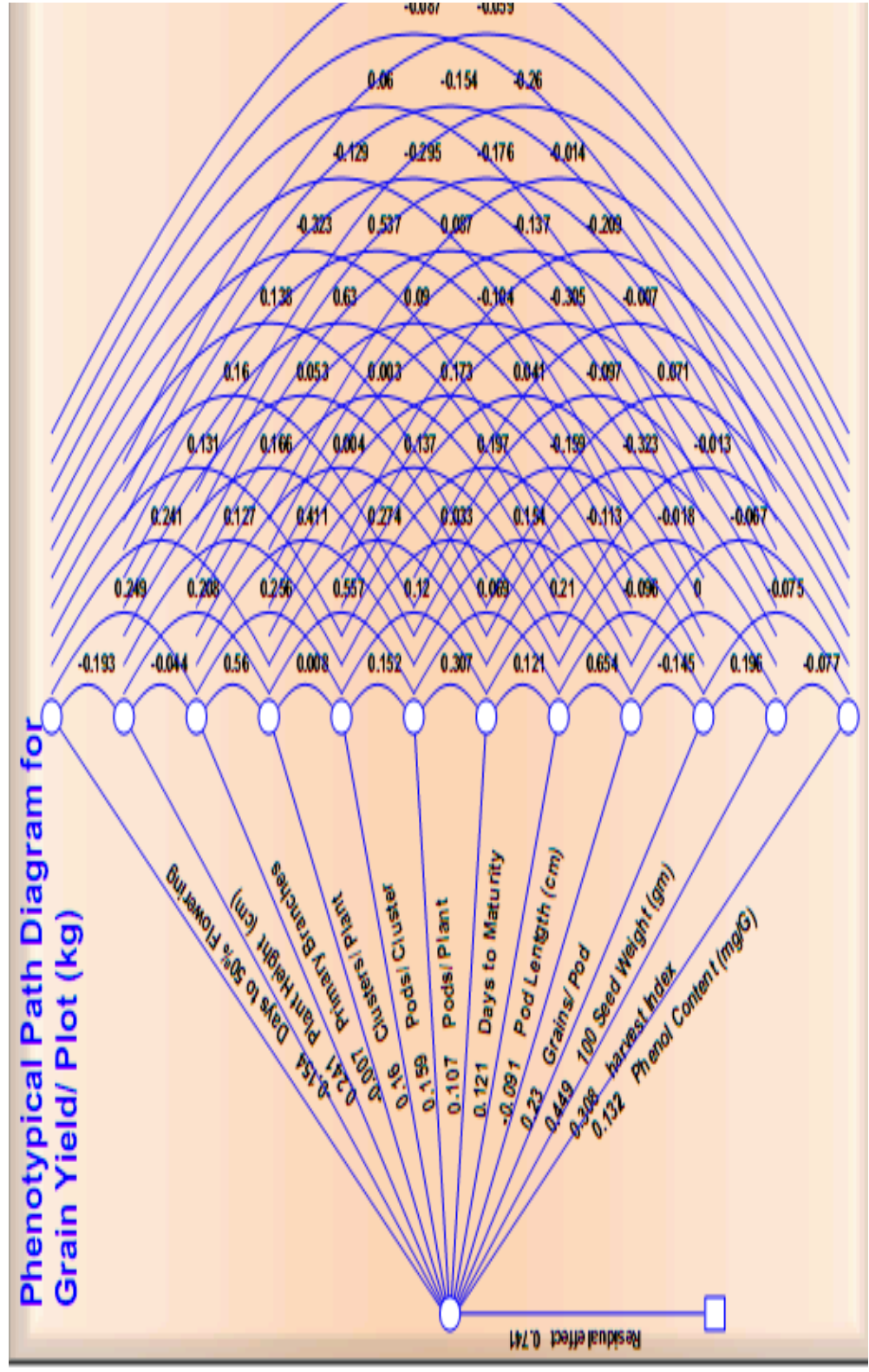


Fig. 4: Phenotypic path coefficient diagram for gram yield and its contributing character excluding parent of *Vigna*



with grain yield as well as coupled with positive and high indirect effect (0.106) via pod length.

100 seed weight exhibited high and positive direct effects (0.470) and (0.427) in including/excluding, parents respectively with grain yield.

Harvest index showed high and positive direct effect (0.418) with grain yield in including the parent only.

4.6 Estimation of gene effect

4.6A Joint scaling test

All the six intra specific and four inter specific crosses were analyzed using joint scaling test (Cavalli, 1952) to estimate the main gene effects [m] [d] [h] and also to seek the evidence of epistasis, if present for different traits studied. Analysis for genetic parameter to account for the genetic variability in terms of mean for thirteen characters have been presented in table 9a and 9b for intra and inter specific crosses respectively.

4.6.A.1 Intra specific crosses

4.6.A.1.1 Days to 50% flowering

For this trait, out of six crosses, X^2 value were found to be significant in four crosses, indicating the evidence of epistasis and hence, the analysis was extended excluded for this cross for six parameter model. Whereas two crosses were found adequate for m [d] [h] model.

Only two crosses showed negative significant addition component Samrat x LGG 450 and TMB 37 x LGG 450. While three crosses illustrated negative significant dominant component.

4.6.A.1.2 Plant height

Four crosses exhibited significant X^2 value among six crosses resulting the adoption of six parameter model. Significant positive additive component was found in Samrat x LGG 450; whereas negative significant additive gene effects were observed in cross HUM 16 x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki.

Table 9a : Estimation of gene effects based on joint scaling test of three parameter model for thirteen characters in interspecific crosses of *Vigna*

Cross			HUM 16 x LGG 450	Samrat x LGG 450	TMB 37 x LGG 450	Sekhar x Barabanki	PU 31 x Barabanki	Uttara x Barabanki
Characters			1	2	3	4	5	6
1.	Days to 50% flowering	m	29.88**	28.43**	29.61**	30.64**	30.42**	30.83**
		d	-1.89	-2.56*	-3.41**	0.80	-1.21	1.01
		h	4.88**	-0.09	2.59**	2.52	1.42	3.39**
		x ²	8.97*	1.97	16.14**	20.40**	0.00	32.64**
2.	Plant height (cm)	m	41.21	49.23	39.77	28.71	22.46	27.74
		d	-8.93**	5.47**	-9.17**	-3.40**	-1.46	-3.96**
		h	10.91**	-4.75**	-9.37**	-3.58**	-1.18	-9.07**
		x ²	34.93**	1.80	33.99**	2.18	24.93**	26.92**
3.	Number of primary branches	m	2.74**	2.89**	3.85**	4.62**	3.57**	4.54**
		d	-0.06	-0.18	0.87	0.23	0.05	-0.28
		h	1.45	1.66	-0.43	2.12	0.36	0.64
		x ²	17.15*	30.02**	0.22	0.65	4.47	7.34
4.	Number of cluster per plant	m	14.54**	18.87**	15.61**	16.36**	16.16**	17.36
		d	-0.82	1.53	-2.47*	0.22	-2.26	-0.29
		h	-2.13*	-5.53**	-4.81**	1.25	3.25**	0.93
		x ²	0.004	3.99	0.83	0.25	0.13	287.15**
5.	Number of pod per cluster	m	2.47*	2.13*	2.63**	2.48*	2.29*	2.85**
		d	0.44	-0.50	-0.12	-0.04	-0.66	0.34
		h	0.22	1.68	2.11*	1.11	-0.19	0.41
		x ²	11.34**	5.16	4.02	2.06	7.74	0.01
6.	Number of pod per plant	m	19.04**	34.09**	36.68**	47.14**	33.24**	30.82**
		d	-6.67**	-5.83**	-6.84**	4.74**	-2.67**	4.36**
		h	49.67**	14.38**	8.74**	2.32	5.95**	52.23**
		x ²	3.76	13.71**	44.52**	0.75	2.05	29.08**

Cont....

Table 9a : Contd...

Cross			HUM 16 x LGG 450	Samrat x LGG 450	TMB 37 x LGG 450	Sekhar x Barabanki	PU 31 x Barabanki	Uttara x Barabanki
Characters			1	2	3	4	5	6
7.	Days to maturity	m	68.96	71.09	70.21	72.96	67.46	68.72
		d	-1.25	-6.80**	-5.65**	-1.67	-12.26**	1.58
		h	0.25	0.27	7.68**	-1.49	12.56**	-0.75
		x ²	0.31	3.31	28.02**	0.75	654.62**	0.00
8.	Pod length (cm)	m	4.88**	7.03**	6.69**	4.62**	5.43**	3.78**
		d	-1.89	0.25	-0.26	0.01	0.90	0.32
		h	-0.12	-0.02	0.86	1.12	-0.26	0.72
		x ²	125.76**	2.00	41.28**	0.18	49.17**	0.00
9.	Number of grains per pod	m	7.68**	6.43**	6.87**	5.91**	5.90**	4.57**
		d	1.27	1.28	-0.76	-0.69	-0.07	0.58
		h	-2.25*	0.26	2.89**	1.80	0.85	1.27
		x ²	0.95	4.76	4.55	1.97	3.65	69.21**
10.	100-seed weight (g)	m	3.89**	3.42**	4.04**	4.41**	3.60**	4.38**
		d	0.69	0.17	0.72	0.80	0.36	0.37
		h	-0.19	-0.31	-0.32	-0.19	-0.08	-0.73
		x ²	16.40**	21.30**	1730.21**	20391.34**	0.99	131.64**
11.	Harvest Index (HI)	m	0.31	0.11	0.18	0.48	0.25	0.16
		d	0.20	0.002	0.06	-0.20	0.16	-0.09
		h	0.16	0.002	0.09	-0.22	0.24	0.29
		x ²	42.12**	12.47**	69.40**	0.48	79.31**	8.75*
12.	Phenol content (mg)	m	0.50	0.90	0.98	0.78	0.82	0.71
		d	-0.43	0.02	0.32	0.13	0.13	0.07
		h	0.64	-0.08	-0.08	-0.04	0.02	0.33
		x ²	11.08*	139.95**	25.58**	1.14	0.12	279.10**
13.	Grain yield per plot (kg)	m	0.48	0.35	0.38	0.21	0.34	0.32
		d	0.22	0.13	0.16	0.08	0.21	0.19
		h	0.22	0.12	0.16	0.28	0.11	0.30
		x ²	655.79**	4.50	116.11**	8.55*	26.86**	2.14

Table 9b : Estimation of gene effects based on joint scaling test of three parameter model for thirteen characters in interspecific crosses of *Vigna*

Cross			Samrat x Barabanki	TMB 37 x Barabanki	PU 31 x LGG 450	Uttara x LGG 450
Character			1	2	3	4
1.	Days to 50% flowering	m	28.82**	30.65**	29.86**	30.70**
		d	-3.02**	1.61	-0.87	2.82**
		h	0.06	0.65	2.20	2.73**
		x ²	1.68*	25.55**	28.00**	5.35
2.	Plant height (cm)	m	39.13	29.75	35.41	23.95
		d	5.52**	0.64	-17.23**	-12.05**
		h	10.34**	-12.60**	-6.15**	7.43
		x ²	20.27**	38.33**	23.35**	4.85
3.	Number of primary branches	m	3.45**	3.49**	3.38**	1.71
		d	-1.49	0.33	0.88	-1.38
		h	0.50	1.15	1.17	2.54*
		x ²	75.38**	24.18**	0.08	1.70
4.	Number of cluster per plant	m	14.42**	12.35**	13.29**	13.25**
		d	-1.61	-1.44	1.55	1.74
		h	3.16**	5.54**	-3.19**	-1.62
		x ²	2.42	14.90**	0.001	0.43
5.	Number of pod per cluster	m	3.04**	3.25**	2.55*	2.67**
		d	-0.65	0.09	-0.30	-0.19
		h	-0.11	-0.30	1.36	1.49
		x ²	24.95**	25.45**	100.59**	9.03*
6.	Number of pod per plant	m	41.60**	14.02**	39.30**	42.52**
		d	-11.93**	-4.34**	-19.80**	1.84
		h	15.26**	54.78**	17.16**	5.17**
		x ²	425.94**	0.01	320.36**	1.34
7.	Days to maturity	m	68.00	68.12	65.89	75.65
		d	-2.94**	-2.79**	-6.51**	-3.52**
		h	0.50	0.66	10.04**	-0.57
		x ²	19.75**	21.86**	107.25**	83.35**

Cont.....

Table 9b : Contd...

Character			Samrat x Barabanki	TMB 37 x Barabanki	PU 31 x LGG 450	Uttara x LGG 450
			1	2	3	4
8.	Pod length (cm)	m	5.53**	4.46**	4.10**	5.35**
		d	1.78	0.84	-1.17	-0.66
		h	2.74**	0.54	2.51*	-1.35
		x ²	0.30	31.50**	0.81	436.04**
9.	Number of grains per pod	m	6.39**	5.33**	4.10**	6.64**
		d	-0.52	1.42	-0.23	-0.26
		h	1.38	1.09	1.60	-0.39
		x ²	0.64	4.91	3.60	78.75**
10.	100-seed weight (g)	m	3.07**	4.10**	3.50**	3.93**
		d	-0.11	0.95	0.36	0.71
		h	0.64	0.39	-0.05	-0.01
		x ²	3163.29**	120.06**	0.28	217.13**
11.	Harvest Index (HI)	m	0.24	0.26	0.31	0.22
		d	0.09	0.08	0.14	0.10
		h	0.04	0.16	-0.17	0.30
		x ²	13.83**	0.66	10.12*	8.54*
12.	Phenol content (mg)	m	0.77	0.50	0.87	0.71
		d	0.16	-0.43	0.10	0.07
		h	0.06	0.64	-0.10	-0.04
		x ²	2694.30**	11.24*	70.18**	536.87**
13.	Grain yield per plot (kg)	m	0.39	0.25	0.33	0.34
		d	0.12	0.12	0.20	0.11
		h	0.16	0.25	0.08	0.26
		x ²	12.96**	486.11**	19.84**	3.37

Positive significant dominance component was observed in only one cross HUM 16 x LGG 450, while negative significant dominance component was observed in Samrat x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki.

4.6A.1.3 Number of primary branches

Only two crosses out of six crosses were found adequate for six parameter model i.e. HUM 16 x LGG 450 and Samrat x LGG 450. None of additive as well as dominant component were found significant.

4.6A.1.4 Cluster per plant

Out of six crosses Uttara x Barabanki showed X^2 significant and fit for six parameter model. Negative significant additive component was found in TMB 37 x LGG 450; whereas negative dominance component observed in HUM 16 x LGG 450, Samrat x LGG 450 and TMB 37 x LGG 450. Positive significant dominant component was found only in PU 31 x Barabanki.

4.6A.1.5 Pods per cluster

Among six intra specific crosses only one exhibited significant X^2 value, and extended for six parameter model. Only positive significant dominant was observed in cross TMB 37 x LGG 450.

4.6A.1.6 Pods per plant

Three crosses among six were found significant X^2 value for pod per plant resulting the adoption of six parameter model. Out of six crosses five crosses showed positive significant dominance component except Sekhar x Barabanki cross. All crosses exhibited significant and additive value, while four of them showed negative significant additive component as well as others for were observed positive significant additive component namely Sekhar x Barabanki and Uttara x Barabanki.

4.6.A.1.7 Days to maturity

Only two crosses exhibited significant X^2 value among six crosses namely TMB 37 x LGG 450 and PU 31x Barabanki. None was having positive significant additive value while three crosses showed negative significant additive gene effect viz., Samrat x LGG 450, Sekhar x Barabanki and PU 31 x Barabanki. Two crosses namely TMB 37 x LGG 450 and PU 31 x Barabanki showed positive significant dominant component.

4.6A.1.8 Pod length

Three intra specific crosses illustrated the significant X^2 value, which were subjected to six parameter model namely HUM 16 x LGG 450, TMB 37 x LGG 450 and PU 31 x Barabanki. None of additive as well as PU 31 x Barabanki. For one of the cross additive as well as dominance component was found significant.

4.6A.1.9 Grains per pod

Uttara x Barabanki was only cross exhibited significant X^2 model, so adequate for six parameter model. Significant dominant component was not observed for grains per pod, whereas two crosses exhibited significant additive value, one of them was negative significant i.e. (HUM 16 x LGG 450) and other was positive significant of (TMB 37 x LGG 450).

4.6A.1.10 100 seed weight

Among six intra specific crosses one cross exhibited non significant x^2 value i.e. PU 31 x Barabanki. In 100 seed weight significant dominant as well as significant additive component was not observed.

4.6A.1.11 Harvest index

Among six crosses only one cross exhibited non significant X^2 value i.e. Sekhar x Barabanki. Significant dominant as well as additive component was not found for this trait.

4.6A.1.12 Phenol Content

For this trait only two crosses among six were found non significant x^2 and not adequate for six parameter model namely Sekhar x Barabanki and PU 31 x Barabanki. None of additive and dominant component were found for this trait.

4.6A.1.13 Grain yield per plot

Among six crosses only in two crosses were found non significant X^2 value and fit for [m] [d] [h] model. For grain yield per plant additive as well as dominant components were not found.

4.6A.2. Inter specific crosses

4.6A.2.1 Days to 50% flowering

Among four inter specific crosses two were found significant X^2 value, indicating adequate for six parameter model namely TMB 37 x Barabanki and PU 31 x LGG 450. Cross Uttara x LGG 450 showed positive significant additive as well as dominant component. Negative significant additive component was found only in Samrat x Barabanki cross.

4.6A.2.2 Plant height

X^2 significant value was observed in three crosses among four i.e. Samrat x Barabanki, TMB 37 x Barabanki and PU 31 x LGG 450. For Samrat x Barabanki both additive and dominant component were observed positive and significant. Negative significant value was observed for in additive as well as dominant component for PU 31 x LGG 450 cross. Uttara x LGG 450 showed positive significant value for dominant and negative significant for additive component. TMB 37 x Barabanki showed only negative significant dominant component.

4.6A.2.3 Number of primary branches

Two crosses showed significant X^2 value viz., Samrat x Barabanki and TMB 37 x Barabanki and extended for Hayman's six parameter model. Only positive significant dominant was found in Uttara x LGG 450 while additive component was not exhibited significant value.

4.6A.2.4 Cluster per plant

Only TMB 37 x Barabanki exhibited significant value of X^2 and subjected to for six parameter model. For this trait positive significant dominant component was observed in Samrat x Barabanki and TMB 37 x Barabanki whereas negative significant dominant component for PU 31 x LGG 450 was observed.

4.6A.2.5 Pod per plant

This trait exhibited in all inter specific crosses significant X^2 value. While dominant and additive components were absent.

4.6A.2.6 Pod per plant

Two crosses Samrat x Barabanki and PU 31 x LGG 450 showed significant X^2 value among four crosses and adequate for six parameter model. Three crosses showed negative significant additive component except Uttara x LGG 450 whereas positive significant dominant value exhibited by all four interspecific crosses.

4.6A.2.7 Days to maturity

For this trait all of four crosses showed X^2 significant value and adequate for six parameter model. Negative significant additive value showed by all crosses whereas positive significant dominant value exhibited by only PU 31 x LGG 450 cross.

4.6A.2.8 Pod length

Among four inter specific crosses only two crosses showed significant X^2 value namely TMB 37 x Barabanki and Uttara x LGG 450. These two crosses were found adequate for six parameters model. Positive significant dominant component was found in two crosses viz. Samrat x Barabanki and PU 31 x LGG 450, while significant additive component was not found in there crosses.

4.6A.2.9 Grains per pod

Uttara x LGG 450 only one cross showed X^2 value significant and indicating adequate for six parameter model. Significant additive and dominant components were not observed for any cross.

4.6A.2.10. 100-seed weight

Samrat x Barabanki, TMB 37 x Barabanki and Uttara x LGG 450 were showed significant X^2 value except PU 31 x LGG 450 cross. These three crosses were adequate for six parameter model. whereas, significant additive and dominant component was not observed for 100-seed weight.

4.6A.2.11 Harvest index (HI)

Except TMB 37 x Barabanki three other crosses showed significant X^2 value namely Samrat x Barabanki, PU 31 x LGG 450 and Uttara x LGG 450 indicating adequate for six parameter model. Significant additive and dominant component were absent for harvest index trait.

4.6A.2.12 Phenol content

All four interspecific crosses showed significant X^2 value, resulting the adoption of six parameter model. Significant additive and dominant component were not observed for this trait.

4.6A.2.13 Grain yield per plot

The value of X^2 showed significant for all interspecific crosses except Uttara x LGG 450 while significant dominant and additive components were not found. All crosses showed adequacy for six parameter model of gene effect.

4.6B Estimation of Gene effects from the Analysis of Generation Mean

Joint scaling test (Cavalli, 1952) was applied to short out the interacting and non-interacting crosses and accordingly the six parameter model following Hayman (1958) was applied to understand the nature of genetic component of means governing the different yield traits in the interacting crosses.

The six parameters were mean (m), the main gene effects, additive (d) and dominance (h) and their inter allelic interactions those are dominance x dominance (l), additive x additive (i) and additive x dominance (j). Type of epistasis (complementary or duplicate) for different characters are presented in table 10a and 10b for intra and interspecific crosses respectively. The character wise results are presented below :

Table 10 a : Estimation of gene effects through generation mean analysis for thirteen characters in interspecific crosses of *Vigna*

			m	d	h	i	l	j	Epistasis
1.	Days to 50 % flowering	HUM 16 x LGG 450	31.00**	-2.33**	11.33**	15.33**	-19.67**	-0.32**	D
		TMB 37 x LGG 450	30.33**	-4.33**	3.33**	6.33**	-7.33**	-2.00**	D
		Sekhar x Barabanki	30.67**	-1.33**	4.67**	4.67**	-16.00**	1.67**	D
		Uttara x Barabanki	31.00**	2.33**	11.33**	15.00**	-19.33**	1.33**	D
2.	Plant height (cm)	HUM 16 x LGG 450	44.60**	-8.82**	14.77**	22.50**	-37.27**	-4.28**	D
		TMB 37 x LGG 450	25.13**	-11.00**	46.80**	57.33**	-11.20**	-5.40**	D
		PU 31 x Barabanki	21.33**	-5.07**	-3.60**	-5.02**	8.70**	-6.48**	D
		Uttara x Barabanki	27.00	-4.77**	-25.13**	-20.85**	58.50**	-7.25**	D
3.	Number of primary branches	HUM 16 x LGG 450	1.63**	-0.15	11.43**	13.13**	-13.60**	0.52**	D
		Samrat x LGG 450	5.07**	0.53**	-4.80**	-3.23**	2.60**	0.67**	D
4.	Number of cluster per plant	Uttara x Barabanki	17.67**	0.77**	-0.47	8.77**	20.33**	-0.03	C
5.	Number of pod per cluster	HUM 16 x LGG 450	2.75**	0.87**	-1.79**	-1.30**	3.62**	1.02**	D
6.	Number of pod per plant	Samrat x LGG 450	31.07**	2.07*	45.60**	63.55*	-41.50**	9.45**	D
		TMB 37 x LGG 450	29.67**	-10.60**	83.87**	96.40**	-100.53**	-5.80**	D
		Uttara x Barabanki	50.27**	-25.33**	-49.07**	-10.33**	157.33**	-23.03**	D
7.	Days to maturity	TMB 37 x LGG 450	75.33**	-3.00**	-14.00**	-6.17**	23.00**	2.83**	D
		PU 31 x Barabanki	77.33**	-14.00**	-24.00**	-15.00**	32.67**	-7.00**	D

Cont.....

Table 10 a : Contd...

			m	d	h	i	l	j	Epistasis
8.	Pod length (cm)	HUM 16 x LGG 450	4.50**	-0.33**	12.13**	11.52**	-9.83**	0.01	C
		TMB 37 x LGG 450	7.33**	-0.83**	-3.27**	-2.68**	4.70**	0.77**	D
		PU 31 x Barabanki	5.87**	0.70**	-3.00**	-2.93**	2.8**	-0.53**	D
9.	Number of grains per pod	Uttara x Barabanki	5.80**	0.67**	-3.47**	-1.48**	5.90**	-0.53**	D
10.	100 seed weight (g)	HUM 16 x LGG 450	4.24**	0.78**	-3.70**	-3.88**	5.70**	0.10**	D
		Samrat x LGG 450	3.24**	-0.30**	-2.52**	-2.51**	4.23**	-0.12**	D
		TMB 37 x LGG 450	4.15**	1.21**	-2.38**	-2.73**	3.14**	0.52	D
		Sekhar x Barabanki	4.52**	0.58**	-2.45**	-2.41**	2.62**	-0.36**	D
		Uttara x Barabanki	4.32**	0.39**	1.25**	-2.03**	0.96**	-0.06**	D
11.	Harvest Index (HI)	HUM 16 x LGG 450	0.43**	0.08**	-0.41**	-0.23**	0.39**	-0.06**	D
		Samrat x LGG 450	0.11**	-0.04**	0.05**	0.16**	0.62**	-0.16**	C
		TMB 37 x LGG 450	0.19**	-0.01	0.34**	0.36**	-0.60**	-0.08**	D
		PU 31 x Barabanki	0.39**	0.18**	-0.37**	-0.15**	0.86**	0.08**	D
		Uttara x Barabanki	0.19**	-0.11**	0.51**	0.615**	-0.83**	-0.10**	D
12.	Phenol content (mg)	HUM 16 x LGG 450	0.75**	-0.59**	0.42**	0.59**	0.36**	-0.74**	C
		Samrat x LGG 450	0.78**	-0.19**	1.49**	1.43**	-2.67**	-0.24**	D
		TMB 37 x LGG 450	1.02**	0.34**	-0.68**	-0.87**	1.34**	0.04**	D
		Uttara x Barabanki	0.76**	0.26**	0.91**	1.15**	-1.56**	0.19	D
13.	Grain yield per plot (g)	HUM 16 x LGG 450	0.59**	0.11**	-0.52**	0.23**	1.38**	-0.15**	C
		TMB 37 x LGG 450	1.46**	0.13**	-0.11**	0.14*	0.57**	-0.04**	C
		Sekhar x Barabanki	0.29**	0.67**	0.37**	0.60**	-0.12**	-0.12**	D
		PU 31 x Barabanki	0.39**	0.20**	-0.03**	0.31**	0.59**	-0.02**	C

Table 10 b : Estimation of gene effects through generation mean analysis for thirteen characters in intraspecific crosses of *Vigna*

Character			m	d	h	i	l	j	Epistasis
1.	Days to 50 % flowering	TMB 37 x Barabanki	29.00**	-2.00**	13.33**	11.33**	-34.67**	-1.00**	D
		PU 31 x LGG 450	29.00**	-2.00**	16.00**	13.00**	-25.33**	-1.33**	D
2.	Plant height (cm)	Samrat x Barabanki	45.87**	9.10**	24.77**	-12.73**	44.46**	3.03**	D
		TMB 37 x Barabanki	21.50**	0.27	7.87**	10.37**	28.73**	-2.97**	D
		PU 31 x LGG 450	24.07**	-22.17**	29.80**	18.40**	-38.93**	-10.53**	C
3.	Number of primary branches	Samrat x Barabanki	4.20**	-1.80**	-2.40**	-0.92**	3.83**	-0.78**	D
		TMB 37 x Barabanki	4.07**	-0.43**	5.27**	5.17**	-14.60**	-0.80**	D
4.	Number of cluster per plant	TMB 37 x Barabanki	12.13**	2.33**	22.13**	37.33**	-7.73**	5.87**	D
5.	Number of pod per cluster	Samrat x Barabanki	3.87**	-1.40**	-3.07**	-2.57**	4.20**	-1.17**	D
		TMB 37 x Barabanki	3.16**	-0.27**	-1.92**	-2.17**	2.91**	-0.63**	D
		PU 31 x LGG 450	2.83**	0.73**	4.40**	5.67**	-6.93**	1.27**	D
		Uttara x LGG 450	3.63**	-0.45**	-2.23**	-0.31	4.75**	-0.33**	D
6.	Number of pod per plant	Samrat x Barabanki	51.57**	-18.60**	-31.47**	-18.52**	47.83**	-8.82**	D
		PU 31 x LGG 450	61.57**	-21.10**	-77.93**	-56.23**	112.87**	-10.80**	D
7.	Days to maturity	Samrat x Barabanki	66.00**	-4.00**	22.67**	23.33**	-32.00**	-2.00**	D
		TMB 37 x Barabanki	67.33**	2.00**	-5.33**	-2.17**	24.33**	4.83**	D
		PU 31 x LGG 450	72.33**	-10.00**	-13.33**	-3.33**	25.32**	-5.33**	D
		Uttara x LGG 450	74.67**	-6.33**	11.33**	10.17**	-23.00**	-3.50**	D

Cont.....

Table 10 b : Contd...

			m	d	h	i	l	j	Epistasis
8.	Pod length (cm)	TMB 37 x Barabanki	4.63**	0.20**	0.53**	0.52**	2.70**	-1.88**	D
		Uttara x LGG 450	5.60**	-0.10*	-6.20**	-7.70**	9.67**	0.93**	D
9.	Number of grains per pod	Uttara x LGG 450	7.40**	0.13**	-5.33**	-5.23**	5.40**	0.63	D
10.	100 seed weight (g)	Samrat x Barabanki	3.33**	0.29**	0.94**	1.61**	-2.05**	-0.26**	D
		TMB 37 x Barabanki	3.97**	1.45**	-1.58**	-1.82**	2.04**	0.64**	D
		Uttara x LGG 450	3.92**	0.97**	-1.04**	-1.05**	2.13**	0.26**	D
11.	Harvest Index (HI)	Samrat x Barabanki	0.29**	0.14**	-0.12**	0.06*	0.13**	0.11**	D
		PU 31 x LGG 450	0.29**	0.16**	-0.15**	-0.26**	-0.009**	0.07**	C
		Uttara x LGG 450	0.25**	0.13**	-0.17**	-0.10**	-0.07**	0.09**	D
12.	Phenol content (mg)	Samrat x Barabanki	0.73**	0.44**	1.22**	1.26**	-2.14**	0.29**	D
		TMB 37 x Barabanki	0.75**	-0.59**	0.42**	0.59**	0.36**	-0.74**	C
		PU31 x LGG 450	0.76**	0.23**	0.58**	0.58**	-0.36**	-0.11	D
		Uttara x LGG 450	0.64**	0.90**	3.76**	3.70**	-7.31**	0.85**	D
13.	Grain yield per plot (kg)	Samrat x Barabanki	0.48**	0.07**	-0.03**	0.19**	0.39**	-0.14**	C
		TMB 37 x Barabanki	0.46**	0.12**	-0.47**	-0.19**	1.21**	-0.11**	D
		PU 31 x LGG 450	0.38**	0.22**	-0.12**	0.10**	0.53**	0.03**	C

4.6B.1 Intra specific crosses

4.6B.1.1 Days to 50 per cent flowering

Out of six crosses in four crosses were found interactions for this trait. The relative contribution of additive gene effect (d) to parameter (m) was significantly negative in three crosses namely HUM 16 x LGG 450, TMB 37 x LGG 450 and Sekhar x Barabanki; whereas, (Uttara x Barabanki) which was comprising positively significant additive component gene effect.

In addition, dominance component (h) was found to be positively significant in all four crosses. Of the non allelic interaction, all four crosses exhibited negative and significant dominant x dominant and positive and significant additive x additive gene effects along with reducing (negative) and enhancing (positive) effects respectively for all four crosses wise HUM 16 x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki. In two crosses HUM 16 x LGG 450 and TMB 37 x LGG 450 negative and significant as well as in two other crosses Sekhar x Barabanki and Uttara x Barabanki significant and positive additive x dominance component was observed.

For this trait duplicate type of epistasis was observed for all the above four crosses.

4.6B.1.2 Plant height

Of the six crosses, in four non-allelic interaction was observed. The significant and negative additive gene effects was observed in HUM 16 x LGG 450, TMB 37 x LGG 450, PU 31 x Barabanki and Uttara x Barabanki; whereas for dominant components two crosses HUM 16 x LGG 450 and TMB 37 x LGG 450 comprising significant and positive as well as other two crosses PU 31 x Barabanki and Uttara x Barabanki comprising negative and significant component for this trait.

Regarding the epistasis negative and significant dominant x dominant as well as positive and significant additive x additive gene effects were observed in HUM 16 x LGG 450 and TMB 37 x LGG 450. In other two crosses PU 31 x Barabanki and Uttara x Barabanki exhibited positive and significant dominant x

dominant component as well as negative significant additive x additive type gene effects, while all four crosses having the significant and negative additive x dominant component. Duplicate epistasis was observed in all four crosses.

4.6B.1.5 Number of primary branches

Out of six crosses only in two crosses non allelic interaction was observed Samrat x LGG 450 was comprising the significant and positive relative contribution of additive gene effect (d) to parameter (m). HUM 16 x LGG 450 and Samrat x LGG 450 showed positive and significant as well as negative and significant dominant components respectively. HUM 16 x LGG 450 exhibited negative and significant dominance x dominance component whereas positive and significant additive x additive and additive dominance component, while in Samrat x LGG 450 observed significant and positive dominance x dominance and additive x dominant as well as negative significant additive x additive component were observed. For both the crosses duplicate epistasis was observed.

4.6B.1.4 Number of cluster per plant

Non-allelic interaction was observed only in one cross in Uttara x Barabanki with positive and significant (d x h) additive x dominance gene effect with relative contribution to the parameter (m).

In this cross positive and significant dominant x dominant component was observed alongwith the complementary type epistasis.

4.6B.1.5 Number of pod per cluster

Out of six crosses only in one cross HUM 16 x LGG 450 [m] [d] [h] model was not adequate. Significant and positive additive (d) component and negative and significant dominant components were observed for this trait. In this particular cross positive and significant dominant x dominant component as well as additive x dominance components were observed; while negative and significant additive x additive gene effect was found. Duplicate type of epistasis was estimated for this trait.

4.6B.1.6 Number of pod per plant

Out of six crosses, in three crosses non allelic interaction was observed. Significant and positive additive and dominant components were observed for Samrat x LGG 450 to the relative contribution for parameter (m). In TMB 37 x LGG 450 negative and significant additive and positive significant dominance components were observed; whereas, Uttara x Barabanki exhibited negative and significant additive as well as dominance components.

In Samrat x LGG 450 negative and significant dominance x dominance, positive and significant additive x additive as well as additive x dominance components were observed. TMB 37 x LGG 450 showed positive and significant additive x additive negative and significant dominance x dominance and additive x dominance gene action. In cross Uttara x Barabanki the and significant in dominance x dominance whereas negative and significant additive x additive as well as dominance x additive components were observed. For this trait among all crosses duplicate epistasis were observed.

4.6B.1.7 Days to maturity

Of the six crosses, two exhibited non-allelic interaction. In both the crosses viz., TMB 37 x LGG 450 and PU 31 x Barabanki negative and significant additive as well as dominant components were observed.

In both the crosses positive and significant dominance x dominance whereas, negative and significant additive x additive components were observed. In TMB 37 x LGG 450 positive and significant whereas in PU 31 x Barabanki negative and significant additive x dominance gene effects was observed. For this trait duplicate epistasis was observed for both the crosses.

4.6B.1.8 Pod length

Out of six crosses, only in three crosses [m] [d] [h] model was not found adequate. Negative and significant additive as well as positive and significant dominance components were observed in HUM 16 x LGG 450 in TMB 37 x LGG 450 negative and significant additive and dominance component were found;

whereas PU 31 x Barabanki exhibited positive and significant additive and negative and significant dominance components.

Negative and significant dominance x dominance as well as positive and significant additive x additive components were found in HUM 16 x LGG 450. Positive and significant dominant x dominant and negative and significant. Additive x additive gene effects were found in TMM 37 x LGG 450 and PU 31 x Barabanki; while positive and significant additive x dominance component in TMB 37 x LGG 450 and negative and significant additive x dominance component in PU 31 x Barabanki were observed along with the duplicate type of epistasis. In the cross HUM 16 x LGG 450 complementary epistasis was found.

4.6B.1.9 Number of grain per pod

Among the six crosses, only one cross gave non allelic interaction in Uttara x Barabanki positive and significant additive as well as negative and significant dominance components were found. Significant and positive dominance x dominance, negative and significant, additive x additive as well as additive x dominance gene effects comprising the duplicate type of epistasis were observed.

4.6B.1.10 100-seed weight

Of the six crosses, five crosses showed non allelic interaction. Significant and positive additive and negative and significant dominant components were observed in HUM 16 x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki; whereas Samrat x LGG 450 exhibited negative and significant additive as well as dominance components.

Positive and significant dominance x dominance as well as negative and significant additive x additive gene effects were observed in all four crosses except Uttara x Barabanki which is comprising positive and significant dominance x dominance and additive x additive components. Significant and positive additive x dominance component was observed in HUM 16 x LGG 450 and Uttara x Barabanki; whereas, negative and significant additive x dominance component

was observed in Samrat x LGG 450 and Sekhar x Barabanki. Duplicate epistasis was observed in all five crosses for 100-seed weight.

4.6B.1.11 Harvest index

Out of six crosses five crosses showed non allelic interaction. Positive and significant additive as well as negative and significant dominant component were observed in HUM 16 x LGG 450 and PU 31 x Barabanki; whereas, negative and significant additive followed by positive significant dominance components were observed for two crosses viz., Samrat x LGG 450 and Uttara x Barabanki. TMB 37 x LGG 450 comprised of positive and significant dominance component.

Two crosses namely HUM 16 x LGG 450 and PU 31 x Barabanki having the positive and significant dominant x dominant followed by negative and significant followed by negative and significant additive x additive type of gene effects; whereas other two crosses viz., TMB 37 x LGG 450 and Uttara x Barabanki comprising negative and significant dominant x dominant followed by positive and significant additive x additive type of genetic components. In Samrat x LGG 450 positive and significant dominance x dominance and additive x additive gene effects were observed. For harvest index out of five crosses, four exhibited negative and significant additive x dominance gene action except PU 31 x Barabanki which was having the positive and significant additive x dominance effect.

Out of five crosses in four crosses duplicate epistasis was observed except Samrat x LGG 450 had the complementary epistasis.

4.6B.1.12 Phenol content

Out of six crosses, in four [m] [d] [h] model was not found adequate. Cross HUM 16 x LGG 450 and Samrat x LGG 450 found to be negative and significant additive followed by the positive and significant dominance components, whereas, TMB 37 x LGG 450 exhibited positive and significant additive followed by negative and significant dominance components. In Uttara x Barabanki cross positive and significant additive as well as dominance component were observed.

In two crosses, namely Samrat x LGG 450 and Uttara x Barabanki negative and significant dominance x dominance followed by positive and significant additive x additive components were observed; whereas, TMB 37 x LGG 450 showed positive and significant dominance x dominance followed by negative and significant additive x additive type of genetic components. In the cross HUM 16 x LGG 450 positive and significant dominance x dominance and additive x additive gene effects were observed.

For the phenol content in three crosses namely Samrat x LGG 450, TMB 37 x LGG 450 and Uttara x Barabanki observed duplicate epistasis; whereas, HUM 16 x LGG 450 showed complementary type of epistasis.

4.6B.1.13 Grain yield per plot

For this trait out of six crosses, four crosses showed non-adequacy of [m] [d] [h] model. All four crosses viz. HUM 16 x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and PU 31 x Barabanki having the positive and significant additive as well as dominance components.

HUM 16 x LGG 450 and TMB 37 x LGG 450 exhibited positive and significant dominance x dominance followed by negative and significant additive x additive gene effects, whereas Sekhar x Barabanki negative and significant dominance x dominance followed by positive and significant additive x additive components. PU 31 x Barabanki showed positive and significant dominance x dominance followed by negative and significant additive x additive gene effects. In all four crosses negative and significant additive x dominance component was observed.

In three crosses complementary epistasis was observed except Sekhar x Barabanki which was having duplicate type of epistasis.

4.6B.2 Inter specific crosses

4.6B.2.1 Days to 50 % flowering

Of the four crosses, two crosses were unable to attend the adequacy of [m] [d] [h] model. These two crosses namely TMB 37 x Barabanki and PU 31 x LGG

450 comprised of negative and significant additive followed by positive and significant dominant components.

Negative and significant dominant x dominant as well as additive x dominant followed by significant and positive additive x additive type of gene action along with the duplicate epistasis for this were observed for both crosses.

4.6B.2.2 Plant height

Out of four crosses, three crosses did not show the adequacy of the [m] [d] [h] model. Samrat x Barabanki exhibited positive and significant additive component followed by negative and significant dominance component; whereas PU 31 x LGG 450 exhibited negative and significant additive followed by positive and significant dominance component. In TMB 37 x Barabanki cross only positive and significant dominance component was observed.

Samrat x Barabanki and TMB 37 x Barabanki comprised of positive and significant dominance x dominance as well as additive x additive gene effects; whereas in PU 31 x LGG 450 negative and significant dominance x dominance followed by positive and significant additive x additive components were observed. Significant and negative additive x dominance component was observed in PU 31 x LGG 450 whereas, Samrat x Barabanki showed positive and significant dominance component alongwith duplicate epistasis; while TMB 37 Barabanki had complementary epistasis.

4.6B.2.3 Number of primary branches

Of the four crosses, two crosses not fulfilled the adequacy of [m] [d] [h] model. In Samrat x Barabanki negative and significant additive as well as dominance components were observed; while in TMB 37 x Barabanki negative and significant additive followed by positive and significant dominance components were observed.

In Samrat x Barabanki significant and positive dominant x dominant followed by significant and negative additive x additive; whereas in TMB 37 x Barabanki negative and significant dominance x dominance followed by positive and significant additive x additive components were observed. In both the crosses

negative and significant additive x dominance component was found alongwith duplicate epistasis.

4.6B.2.4. Number of cluster per plant

Out of six crosses, only one cross TMB 37 x Barabanki was found adequate for six parameter model, which exhibited positive and significant additive as well as dominance component. In this cross negative and significant dominance x dominance and positive and significant additive x additive gene effects were observed having the positive significant additive x dominance component.

This cross showed duplicate type of epistasis.

4.6B.2.5 Number of pod per plant

Of the six crosses, four crosses showed epistasis. Samrat x Barabanki, TMB 37 x Barabanki and Uttara x LGG 450 gave the negative and significant additive as well as dominance components in contrary to this PU 31x LGG 450 had positive and significant additive as well as dominance components. Significant positive dominance x dominance and negative significant additive x additive gene actions were observed in Samrat x Barabanki, TMB 37 x Barabanki and Uttara x LGG 450 alongwith the negative and significant additive x dominance gene action in all three crosses; while in PU 31 x LGG 450 negative and significant dominance x dominance followed by positive and significant additive x additive as well as additive x dominance components were observed.

In all four crosses duplicate epistasis was found.

4.6B.2.6 Number of pod per plant

Out of six crosses, only in two crosses namely Samrat x Barabanki and PU 31 x LGG 450 epistasis interaction were observed comprising the negative and significant additive as well as dominant component. In these two crosses significant and positive dominance x dominance and negative and significant additive x additive as well as additive x dominance component were observed alongwith duplicate epistasis.

4.6B.2.7 Days to maturity

In all the four crosses [m] [d] [h] model was not found adequate. Negative and significant additive followed by positive and significant dominance components were observed in Samrat x Barabanki and Uttara x LGG 450 in contrary to this TMB 37 x Barabanki exhibited positive and significant additive and negative significant dominance components. In PU 31 x LGG 450 negative and significant additive and dominance components were observed. In the cross Samrat x Barabanki and Uttara x LGG 450 negative and significant dominance x dominance as well as additive x dominance followed by positive and significant additive x additive gene actions were observed. In TMB 37 x Barabanki and PU 31 x LGG 450 positive and significant and PU 31 x LGG 450 positive and significant dominance x dominance followed by negative and significant additive x additive components were observed. In TMB 37 x Barabanki positive and significant while PU 31 x LGG 450 negative and significant additive x dominance components was observed. All the crosses exhibited duplicate epistasis.

4.6B.2.8 Pod length

Out of four crosses, only two crosses showed the epistasis. In TMB 37 x Barabanki positive and significant additive as well as dominance components were observed. In other cross, Uttara x LGG 450 both additive and dominance component were negative and significant in nature.

Both crosses showed positive and significant dominance x dominance gene action whereas TMB 37 x Barabanki had positive significant additive x additive alongwith negative and significant additive x dominance gene action comprising complementary epistasis. In Uttara x LGG 450 cross positive and significant dominance x dominance as well as additive x dominance gene action were observed; whereas negative and significant additive x additive with duplicate epistasis was observed.

4.6B.2.9 Number of Grains per pod

Only one cross was found to be adequate for non-allelic interaction Uttara x LGG 450 showed positive significant additive and negative significant dominance components. In this cross positive and significant dominance x

dominance as well as additive x dominance gene actions were observed alongwith with duplicate epistasis.

4.6B.2.10 100-seed weight

For this trait three crosses exhibited non-allelic interaction. The cross Samrat x Barabanki showed positive and significant additive and dominance components' whereas TMB 37 x Barabanki and Uttara x LGG 450 exhibited positive and significant additive as well as negative and significant dominance components. Samrat x Barabanki showed positive and significant additive x additive; whereas negative and significant dominance x dominance as well as additive x dominance component were observed. In other two crosses, TMB 37 x Barabanki and Uttara x LGG 450 negative and significant additive x additive in contrary to this positive and significant dominance x dominance as well as additive x dominance components were found.

All these crosses showed duplicate type of epistasis.

4.6B.2.11 Harvest Index

Out of four, only three crosses showed epistasis namely Samrat x Barabanki, PU 31 x LGG 450 and Uttara x LGG 450. In all the three crosses were observed positive significant additive components, whereas Samrat x Barabanki showed positive significant dominance component and rest two crosses comprised of negative significant dominance component. In Samrat x Barabanki cross positive and significant dominance x dominance and additive x dominance in contrary to this negative and significant interactions were observed along with duplicate epistasis.

For PU 31 x LGG 450 and Uttara x LGG 450 exhibited negative and significant additive x additive as well as dominance x dominance followed by positive and significant additive x dominance gene actions alongwith complementary and duplicate type of epistasis, respectively.

4.6B.2.12 Phenol content

All the crosses showed epistasis gene action comprising the positive and significant dominance as well as component except TMB 37 x Barabanki having the negative and significant additive component.

All three crosses had duplicate type of epistasis; whereas TMB 37 x Barabanki showed complementary gene action.

4.6B.2.13 Grain yield per plot

Among four crosses, three crosses illustrated epistasis viz., Samrat x Barabanki, TMB 37 x Barabanki and PU 31 x LGG 450. All the three crosses showed positive and significant additive as well as dominance components except in TMB 37 x Barabanki having negative significant dominance component.

Negative and significant additive x additive as well as positive and significant dominance x dominance components were observed for all three crosses while Samrat x Barabanki exhibited negative and significant and PU 31 x LGG 450 positive and significant additive x dominance component alongwith complementary type of epistasis. TMB 37 x Barabanki showed negative and significant additive x dominance component having the duplicate epistasis.

4.7 Heterosis and Inbreeding depression

The quantum and magnitude of heterosis in percentage over mid-parent (MP), better parent (BP), SML 668 the standard check (EH) and inbreeding depression (ID) in F₂ only tested for thirteen characters are presented in table 11a and 11b for intraspecific and interspecific crosses respectively. The mean performance of parent, crosses of F₁ and F₂ are presented.

4.7.1 Days to 50% flowering

4.7.1.a Intraspecific crosses

The estimates of heterosis ranged from 0.00 (PU 31 x Barabanki) to 21.43 (HUM 16 x LGG 450) over better parent. The mid parent heterosis ranged from 0.00 (PU 31 x Barabanki) to 15.25 (HUM 16 x LGG 450) per cent, 6.17 (Samrat x LGG 450) to 25.93 (HUM 16 x LGG 450) per cent over standard variety.

None of the cross combination was found desirable for early flowering. Out of six intra specific crosses four crosses viz., HUM 16 x LGG 450, TMB 37 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki exhibited positive and

Table 11a : Heterosis over Better parent (BP), Mid parent (MP), Economic Heterosis (EH) and Inbreeding Depression (ID) for thirteen characters in intraspecific crosses of *Vigna*

Sl. No.	Crosses	Over	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of cluster per plant	Pod/ cluster	No. of pod per plant	Days to maturity
			1	2	3	4	5	6	7
1.	HUM-16 x LGG 450	BP	21.43**	35.80**	75.61**	73.30	12.50	62.73	9.18
		MP	15.25**	19.93**	54.84**	73.51**	19.21**	107.48**	5.86
		EH	25.93**	16.53**	122.89**	122.89**	16.58*	156.61**	4.63
		ID	8.82*	4.16	65.97***	61.36**	8.44**	68.71***	11.06**
2.	SAMRAT x LGG 450	BP	10.26**	-11.88**	86.36**	-25.96*	26.53	25.22**	11.85**
		MP	0.59	-12.45**	61.84**	-19.29	39.33	52.00**	1.40
		EH	6.17	1.59	61.84**	15.96	60.62	89.18**	0.46
		ID	1.63	-13.64*	-23.58	-52.21**	1.61	40.79*	0.46
3.	TMB 37 x LGG 450	BP	20.25**	46.27**	105.61**	66.67**	61.86**	17.19*	21.24**
		MP	10.47**	26.03**	123.35**	89.39**	75.42**	31.18**	11.16**
		EH	17.28**	27.71	189.47	174.10**	103.37**	90.14**	8.33**
		ID	4.21	50.72***	59.55**	64.51**	22.93	43.74	3.42
4.	SEKHAR x BARABANKI	BP	20.69*	-6.04	40.14	26.09	37.50*	14.92**	4.51*
		MP	14.13**	-14.38*	46.32*	41.87	41.94**	24.08**	3.57*
		EH	29.63**	-36.39**	161.84**	116.87**	42.49**	73.08**	7.41**
		ID	12.38**	-5.38	15.58	20.55	20.91	-0.14	8.19**
5.	PU 31 x BARABANKI	BP	0.00	0.00	20.00	13.18**	-17.65**	48.67**	25.81
		MP	0.00	-6.32**	21.66*	20.00**	-3.50	57.25**	13.04**
		EH	7.41*	-47.41**	73.68**	86.15**	8.81	94.95**	8.33**
		ID	-5.75	-1.59	19.70	13.92**	27.74***	37.05**	0.86
6.	UTTARA x BARABANKI	BP	16.09**	27.69*	29.29**	45.62**	4.51	75.90**	3.74*
		MP	12.22**	15.913	33.09**	51.58**	18.77**	84.76**	0.91
		EH	24.69**	-12.87**	138.16**	145.18**	38.08**	204.45**	2.78
		ID	7.92*	13.46	16.02	34.89**	20.26**	40.47**	0.90

Conti...

Table 11a : Contd...

Sl. No.	Crosses	Over	Pod length	No. of	100-seed	Harvest	Phenol	Grain yield per
			(cm)	grain/pod	weight (g)	Index	content	plot (kg)
			8	9	10	11	12	13
1.	HUM-16 x LGG 415	BP	-24.52**	-16.67**	-18.78**	10.43**	3.03	3.79
		MP	-7.33	4.21	4.68*	75.87**	18.06**	54.23**
		EH	-25.71**	-9.72*	-22.54**	-11.69*	13.33**	7.42**
		ID	42.31**	33.85**	-13.85**	-3.47	34.12***	28.05***
2.	SAMRAT x LGG 450	BP	-7.11	17.42**	-5.26**	0.98	-10.85**	12.58**
		MP	-6.667	37.17**	0.46	55.71**	-6.24**	55.65**
		EH	-37.78**	7.64**	-36.13**	-26.59**	-17.60**	-21.83
		ID	3.57	46.45	-6.37***	67.67***	5.74**	29.61**
3.	TMB 37 x LGG 450	BP	4.13	23.13*	-22.51**	-17.79	-34.62	14.12**
		MP	8.35	40.43**	-8.64**	13.44	-17.17**	58.43**
		EH	-27.94**	14.58*	-25.72**	-54.88**	-8.33*	-11.79
		ID	-2.20	39.39**	-16.20***	5.85	-10.10**	31.19***
4.	SEKHAR x BARABANKI	BP	18.98	21.70**	-18.42**	-34.50**	-11.58	8.33*
		MP	20.74*	30.81**	1.14**	-28.89**	4.78	68.16**
		EH	-48.25**	-15.97**	-17.37**	-68.07**	-16.00	-26.20**
		ID	4.29	12.40	-13.81***	-111.83***	19.05**	47.93***
5.	PU 31 x BARABANKI	BP	-4.38*	15.39**	-11.64**	30.59**	-13.77**	19.43**
		MP	1.33	16.02**	-2.44**	69.05**	3.54	91.74**
		EH	-51.43	-27.08**	-26.76**	15.61**	-12.33*	-8.73**
		ID	-15.03**	10.48	9.94***	26.17**	9.51**	43.06***
6.	UTTARA x BARABANKI	BP	16.54**	12.64	-23.78**	45.36	22.35**	46.43**
		MP	26.50**	43.59**	-17.99**	52.43**	32.77**	125.28**
		EH	-53.02**	-31.94**	-26.38**	-37.42**	-5.67**	-10.48**
		ID	12.83*	11.22	-21.89***	34.40**	19.44**	31.71***

Table 11b : Heterosis over Better parent (BP), Mid parent (MP), Economic Heterosis (EH) and inbreeding depression (ID) for thirteen character in interspecific crosses of *Vigna*

Sl. No.	Crosses	Over	Days to 50% flowering	Plant height (cm)	No. of primary branches	No. of cluster per plant	Pod/ cluster	No. of pod per plant	Days to maturity
			1	2	3	4	5	6	7
1.	SAMRAT x BARABANKI	BP	10.67*	54.27**	11.02	17.33**	7.92	6.19	3.98
		MP	2.47	30.19**	46.11**	20.90**	15.96	31.34**	0.97
		EH	2.47	26.71**	85.53**	61.15**	41.19**	95.67**	-3.24
		ID	-6.02*	9.35	10.64	13.08*	-6.42**	4.98	5.26*
2.	TMB 37 x BARABANKI	BP	-3.70	18.14**	-13.46	67.83**	-17.97	22.78**	9.05
		MP	-7.19**	7.97	-3.23	111.22**	-8.10	58.38**	4.58*
		EH	-3.70	-15.19**	18.42	160.84**	8.81	148.80**	0.46
		ID	-11.54*	36.52**	-35.56*	57.97***	-12.74	53.87***	6.91*
3.	PU 31 x LGG 450	BP	9.19**	1.00	36.84**	53.93**	22.92**	22.68**	23.53**
		MP	6.74*	-32.63**	63.23**	75.71**	47.50**	54.30**	14.93**
		EH	17.28**	-41.07**	139.47**	124.40**	52.85**	122.36**	6.94**
		ID	8.42*	-2.27	35.17*	59.20**	27.97***	0.16	6.06
4.	UTTERA x LGG 450	BP	16.13**	22.86*	36.41*	14.58	62.79**	16.73**	2.30*
		MP	11.92**	-5.86	41.07**	16.61	69.70**	14.09**	-1.55
		EH	33.35**	-16.11*	71.05**	68.07**	81.35**	78.61**	2.78
		ID	11.11**	33.23***	3.85	0.72	22.14	6.10	0.90

* Significant at P = 0.05

** Significant at P = 0.01

Cont....

Table 11b : Contd...

Sl. No.	Crosses	Over	Pod length	No. of	100-seed	Harvest	Phenol	Grain yield per
			(cm)	grain/pod	weight (g)	Index	content	plot (kg)
			8	9	10	11	12	13
1.	SAMRAT x BARABANKI	BP	6.79*	5.44	21.14**	10.59	-10.71**	0.00
		MP	43.03**	6.01	22.56**	27.26**	5.05**	46.91**
		EH	-25.08**	-32.64**	-24.62**	-36.78**	-17.50**	-11.79**
		ID	2.97	-61.86***	8.09***	1.47	11.52***	28.71**
2.	TMB 37 x BARABANKI	BP	-27.39**	-25.56**	-22.77**	17.90	2.88	7.53
		MP	-0.30	5.88	-6.32*	48.71	17.88**	72.41**
		EH	-46.98**	-31.25**	-25.93**	-23.95	13.17**	-12.66**
		ID	16.77**	13.13	-11.29***	-7.87	34.02***	31.50**
3.	PU 31 x LGG 450	BP	66.67**	41.10**	-10.59**	-59.54**	-13.03**	5.62
		MP	68.68**	45.07**	-1.35*	-45.19**	-0.69	65.69**
		EH	-33.33**	-28.47**	-25.99**	-70.99**	-4.33	-26.20**
		ID	20.95***	30.10**	12.44***	-114.50**	20.56**	32.54**
4.	UTTERA x LGG 450	BP	-37.81**	-6.12	-15.35**	14.98	-14.51**	51.83**
		MP	-20.47**	1.66	-0.19	44.74**	-8.46	98.10**
		EH	-60.32**	-36.11**	-18.25**	-52.96**	-34.00**	-9.17**
		ID	-34.40***	-20.65***	0.23***	-15.15*	3.54	24.52**

* Significant at P = 0.05

** Significant at P = 0.01

significant BP, MP and EH; whereas two crosses Samrat x LGG 450 and PU 31 x Barabanki showed positive and significant heterosis over BP and EH respectively.

ID ranged from -5.75 (PU 31 x Barabanki) to 12.38 (Sekhar x Barabanki) and significant as well as positive ID was observed only in three crosses HUM 16 x LGG 450, Sekhar x Barabanki and Uttara x Barabanki.

Interspecific

The estimates of heterosis ranged from -3.70 (TMB 37 x Barabanki) to 16.13 (Uttara x LGG 450) per cent over BP, -7.14 (TMB 37 x Barabanki) to 11.92 (Uttara x LGG 450) per cent over MP, -3.70 (TMB 37 x Barabanki) to 33.33 (Uttara x LGG 450) per cent over standard variety, positive and significant heterosis were observed in three crosses over BP except TMB 37 x Barabanki two crosses PU 31 x LGG 450 and Uttara x LGG 450 had shown positive and significant heterosis over MP as well as check. Whereas TMB 37 x Barabanki had shown desirable (negative) significant heterosis only over MP.

ID ranged from -11.54 (TMB 37 x Barabanki) to 11.11 (Uttara x LGG 450) per cent. Two crosses (PU 31 x LGG 450) and (Uttara x LGG 450) exhibited positive and significant were observed.

4.7.2 Plant height

4.7.2.a Intraspecific crosses

As it is obvious that dwarfed plants are comparatively high yielder than the tall traditional variety hence negative heterosis for this trait would be desirable.

Estimates of heterosis ranged from -11.88 (Samrat x LGG 450) to 46.27 (TMB 37 x LGG 450) over BP, -14.38 (Sekhar x Barabanki) to 26.03 (TMB 37 x LGG 450) over MP and -47.41 (PU 31x Barabanki) to 27.71 (TMB 37 x LGG 450) over standard variety.

Significant and negative heterosis for plant height was observed in Samrat x LGG 450; whereas in HUM 16 x LGG 450 and Uttara x Barabanki observed positive and significant heterosis over BP, Negative and significant heterosis was

observed in Samrat x LGG 450, Sekhar x Barabanki and PU 31 x Barabanki; whereas in other two crosses showed positive and significant heterosis over MP. Desirable and significant heterosis was observed in three crosses Sekhar x Barabanki, PU 31 x Barabanki and Uttara x Barabanki; whereas in two crosses significant and positive were observed over standard variety.

Inbreeding depression ranged from -13.64 (Samrat x LGG 450) to 50.72 (TMB 37 x LGG 450) Per cent. Samrat x LGG 450 exhibited negative and significant inbreeding depression for plant height.

4.7.2.b Interspecific crosses

Estimates of heterosis varied from 1.00 (PU 31 x LGG 450) to 54.27 (Samrat x Barabanki) Per cent over BP, -32.63 (PU 31 x LGG 450) to 30.19 (Samrat x Barabanki) over MP and comprising the significant value -41.67 (PU 31 x LGG 450) to 26.71 (Samrat x Barabanki) over standard variety. Significant and positive heterosis were observed in three crosses except PU 31 x LGG 450. Three crosses had shown desirable (negative) significant heterosis except Samrat x Barabanki having the positive and significant heterosis over standard variety.

ID lies between -2.27 (PU 31 x LGG 450) to 36.52 (TMB 39 x Barabanki), positive and significant inbreeding depression was observed only in two crosses viz., TMB 37 x Barabanki and Uttara x LGG 450.

7.3 Number of primary branches

4.7.3.a Intra specific crosses

The estimates of heterosis ranged from 20.0 (PU31 x Barabanki) to 105.61 (TMB 37 x LGG 450) per cent over BP, 21.66 (PU 31 x Barabanki) to 123.35 (TMB 37 x LGG 450) per cent over MP and 61.84 (Samrat x LGG 450) to 189.47 (TMB 37 x LGG 450) over standard variety were observed.

Positive and significant heterosis over BP in four crosses; whereas in all six crosses positive and significant heterosis over MP as well as over standard variety were observed.

ID ranged -23.58 (Samrat x LGG 450) to 65.97 (HUM 16 x LGG 450) only two crosses (HIM 16 x LGG 450) and (TMB 37 x LGG 450) having the positive and significant ID.

4.7.3.b Interspecific cross

The magnitude of heterosis varied from -13.46 (TMB 37 x Barabanki) to 36.84 (PU 31 x LGG 450) per cent over BP, -3.23 (TMB 37 x Barabanki) to 63.23 (PU 31 x LGG 450) per cent over MP and 18.42 (TMB 37 x Barabanki) to 139.47 (PU 31 x LGG 450) over standard variety. Only two crosses exhibited positive and significant heterosis over BP, MP and standard variety; whereas cross Smart x Barabanki showed positive and significant heterosis over MP and standard variety (SML 668).

ID ranged from -35.56 in the cross (TMB 37 x Barabanki) to 35.17 in PU 31 x LGG 450 comprising the negative and positive significant heterosis respectively.

4.7.4. Number of cluster per plant

4.7.4.a Intraspecific

Out of six crosses, only in three crosses positive and significant as well as in one was negative and significant heterosis over BP. Which was observed, and ranged from -25.96 to (Samrat x LGG 450) to 73.30 (HUM 16 x LGG 450). Five crosses were showed positive and significant heterosis over MP, except one which was having negative, non-significant. Range of MP heterosis was observed from -19.29 to (Samrat x LGG 450) to (TMB 37 x LGG 450) 174.10 per cent. Among six crosses only one cross exhibited non significant heterosis over standard variety having the range from 15.96 (Samrat x LGG 450) to 174.10 (TMB 37 x LGG 450) per cent.

ID was observed significant in five crosses except one. Out of five significant four showed positive; whereas one showed negative ID which ranged from -52.21 (Samrat x LGG 450) to 64.51 (TMB 37 x LGG 450) per cent.

4.7.4.b Interspecific

Among four crosses, three showed positive and significant heterosis over BP and ranged from 14.58 (Uttara x LGG 450) to 67.83 (TMB 37 x Barabanki) per cent MP. Heterosis varied between 16.61 (Uttara x LGG 450) to 111.12 (TMB 37 x Barabanki) whereas; three crosses showed positive significant heterosis. All the crosses showed positive and significant heterosis over standard variety, having the range between 61.15 (Samrat x Barabanki) to 160.84 (TMB 31 x LGG 450) per cent.

ID ranged from 0.72 (Uttara x LGG 450) to 59.20 (PU 31 x LGG 450) three crosses showed positive significant heterosis.

4.7.5 Pod per cluster

4.7.5.a Intraspecific

BP heterosis ranging from -17.65 (PU 31 x Barabanki) to 37.50 (Sekhar x Barabanki) per cent; while two crosses illustrated positive significant and one negative significant value. Four crosses showed positive significant heterosis among six over MP and value lies between -3.50 (PU 31 x Barabanki) to 75.42 (TMB 37 x LGG 450). EH heterosis ranged from 8.31 (PU 31 x Barabanki) to 103.37 (TMB 37 x LGG 450) per cent, while four crosses showed positive and significant economic heterosis.

ID ranged from -12.74 (TMB 37 x Barabanki) to 27.97 (PU 31 x LGG 450) and showed significant ID having one positive and other with negative value.

4.7.5.b Interspecific

BP heterosis ranged from -17.97 (TMB 37 x Barabanki) to 62.79 (Uttara x LGG 450) per cent, and in two crosses heterosis were observed significant and positive. Two crosses showed positive significant value ranged from -8.10 (TMB 37 x Barabanki) to 69.70 (Uttara x LGG 450) per cent over MP. Out of four cross, three were exhibited desirable economic heterosis ranged from 8.81 (TMB 37 x Barabanki) to 52.85 (PU 31 x LGG 450).

ID ranged from -12.74 TMB 37 x Barabanki to 27.97 PU 31 x LGG 450. Significant negative and positive ID was observed in Samrat x Barabanki and Uttara x LGG 450 respectively.

4.7.6. Number of pods per plant

4.7.6.a Interspecific

BP heterosis ranging from 17.19 (TMB 37 x LGG 450) to 75.90 (Uttara x Barabanki) and obtained significant positive heterosis in five crosses. All the crosses showed significantly positive heterosis over MP and stander variety. MP and economic heterosis varied from 31.18 (TMB 37 x LGG 450) to 107.48 (HUM 16 x LGG 450) and 73.08 (Sekhar x Barabanki) to 204.45 (Uttara x LGG 450) per cent respectively.

ID in three crosses were significantly positive and ranged from 0.16 (PU 31 x LGG 450) to 53.87 (TMB 37 x Barabanki) per cent.

4.7.6.b Interspecific

All the crosses showed significant positive BP, MP and economic heterosis, which ranged from 6.19 (Samrat x Barabanki) to 22.78 (TMB 37 x Barabanki), 14.09 (Uttara x LGG 450) to 58.38 (TMB 37 x Barabanki) and 78.61 (Uttara x LGG 450) to 148.80 (TMB 37 x Barabanki) respectively.

ID was ranged from 0.16 (PU 31 x LGG 4500) to 53.87 (TMB 37 x LGG 450) and only one cross showed significantly positive value for the trait.

4.7.7 Days to maturity

Negative heterosis indicates early maturity, would be considered as desirable.

4.7.7.a Intraspecific crosses

Five crosses exhibited significantly positive heterosis over BP, range varied from 3.74 (Uttara x Barabanki) to 25.81 (PU 31 x Barabanki) per cent. MP heterosis was observed significantly positive among three crosses and ranged from 0.91 (Uttara x LGG 450) to 13.04 (PU 31 x LGG 450) per cent. Three crosses observed significantly positive heterosis over standard variety.

Only two crosses showed positively significant ID, which ranged from 0.46 (Samrat x LGG 450) to 11.06 (HUM 16 x LGG 450)

4.7.7.b Interspecific crosses

BP heterosis among four interspecific crosses ranged between 2.30 (Uttara x LGG 450) to 23.53 (PU 31 x LGG 450) and two crosses showed significantly positive value. MP heterosis found significantly positive in two crosses and ranged between -1.55 (Uttara x LGG 450) to 14.93 (PU 31 x LGG 450). Only two crosses showed positive significant heterosis over standard variety, which ranged from -3.24 (Samrat x Barabanki) to 6.94 (PU 31 x LGG 450).

ID ranged from 0.90 (Uttara x LGG 450) to 6.91 (TMB 37 x Barabanki); while significantly positive value were observed among two crosses.

4.7.8 Pod length

4.7.8.a Intraspecific crosses

Out of six crosses, three crosses exhibited negative significant and one cross showed positive significant BP heterosis. It ranged from -24.52 (HUM 16 x LGG 450) to 18.98 (Sekhar x Barabanki) per cent. Mid parent heterosis ranging from -7.33 (HUM 16 x LGG 450) to 26.50 (Uttara x Barabanki); while in two crosses positive significant, heterosis were observed.

Negative significant heterosis were observed for five crosses out of six over standard variety, which ranged from 53.02 (Uttara x Barabanki) to -25.71 (HUM 16 x LGG 450) per cent.

ID ranged from -15.03 (PU 31 x Barabanki) to 42.31 (HUM 16 x LGG 450); while three crosses showed significant value, two of them showed positive and one had negative value.

4.7.8.b Interspecific crosses

MP heterosis ranged from -20.47 (Uttara x LGG 450) to 43.03 (Samrat x Barabanki); while two crosses showed significant positive and other two had negative value. BP heterosis was observed significant for all crosses, while two of

each had negative as well as positive value. All the crosses exhibited negative significant value, which ranged from -60.32 (Uttara x LGG 450) to -25.08 (Samrat x Barabanki) per cent over check variety.

ID was observed positive significant for two crosses, which ranged from -34.40 (Uttara x LGG 450) to 20.95 (PU 31 x LGG 450) per cent.

4.7.9 Number of grains per pod

4.7.9.a Intraspecific crosses

All the six crosses showed significant value; while five of them exhibited positive and one had negative value, which ranged from -16.67 (HUM 16 x LGG 450) to 23.13 (TMB 37 x LGG 450) per cent over BP. MP heterosis observed in five crosses with positive and significant value, which ranging from 4.21 (HUM 16 x LGG 450) to 43.59 (Uttara x Barabanki). EH was found significant in all crosses had four negative and two were positive value over standard check, comprising with -31.25 in TMB 37 x Barabanki and 28.47 in PU 31 x LGG 450 with minimum and maximum per cent, respectively.

ID ranged from 10.48 (PU 31 x Barabanki) to 46.45 (Samrat x LGG 450) while two crosses showed significant positive value.

4.7.9.b Interspecific crosses

BP heterosis ranged -6.12 (Uttara x LGG 450) to 41.10 (PU 31 x LGG 450) per cent. In two crosses heterosis observed significant with one negative and in one positive value only cross showed positive significant heterosis over MP, which ranged standard heterosis 1.66 (Uttara x LGG 450) to 45.07 (PU 31 x LGG 450) per cent. All the crosses exhibited negatively significant; with the minimum -36.11 (Uttara x LGG 450) and maximum -28.47 (PU 31 x LGG 450) value.

ID observed significant for three crosses, whereas two crosses had negative and one with positive value. ID ranged from -61.86 (Samrat x Barabanki) to 30.10 (PU 31 x LGG 450) per cent.

4.7.10. 100 seed weight

4.7.10.a Intraspecific crosses

All the six crosses showed significantly negative heterosis which ranging from -23.78 (Uttara x LGG 450) to -5.26 (Samrat x LGG 450) per cent over BP. MP heterosis ranged from -17.99 (Uttara x Barabanki) to 1.14 (Sekhar x Barabanki) per cent and five crosses exhibited significant value among them four were negative while one with a positive value. For 100 seed weight, all the crosses showed significantly negative economic heterosis, which ranged from -36.13 (Samrat x LGG 450) to -17.37 (Sekhar x Barabanki) per cent over check variety.

ID exhibited significant for all crosses; while five crosses showed negative and only one had positive value. ID observed between -21.89 (Uttara x Barabanki) to -6.37 (Samrat x LGG 450) per cent.

4.7.10.b Interspecific crosses

BP heterosis exhibited between -22.77 (TMB 37 x Barabanki) to 21.14 (Samrat x Barabanki); while all the crosses showed significant with three negative and one positive value. MP heterosis varied from -6.32 (TMB 37 x Barabanki) to 22.53 (Samrat x Barabanki) per cent. Three crosses were observed significant had one positive and two negative value. Negative and significant crosses were observed, which ranged from -25.98 (PU 31 x LGG 450) to -18.25 (Uttara x LGG 450) per cent over check variety (SML 668).

ID varied from -11.29 (TMB 37 x Barabanki) to 12.44 (PU 31 x LGG 450) per cent. Three crosses exhibited significant positive and one cross with negative value.

4.7.11 Harvest Index

4.7.11.a Intraspecific crosses

BP heterosis was observed significantly in two crosses one comprising with positive and another with negative value. BP heterosis lies between -34.50 (Sekhar x Barabanki) to 45.36 (Uttara x Barabanki) per cent. Four crosses showed significant and positive heterosis over mid parent; while one cross showed

significant negative. MP heterosis varied between -28.89 (Sekhar x Barabanki) to 75.87 (HUM 1 heterosis was observed significantly in two crosses had one with positive and another with negative value. BP heterosis lies between -34.50 (Sekhar x Barabanki) to 45.36 (Uttara x Barabanki) per cent. Four crosses showed significant and positive heterosis over mid parent while one cross showed significant negative MP heterosis varied between -28.89 (Sekhar x Barabanki) to 75.87 (HUM 16 x LGG 450) per cent. EH was found significant in all crosses, five had negative and one had positive value, which ranging from -68.07 (Sekhar x Barabanki) to 15.61 (PU 31 x LGG 450) per cent.

ID varied between -111.83 (Sekhar x Barabanki) to 67.67 (Samrat x LGG 450) per cent; whereas three crosses showed positive and two were negative significant.

4.7.11.b Interspecific crosses

Only one cross exhibited negative significant over BP; while range varied from -59.54 (PU 31 x LGG 450) to 17.90 (TMB 37 x Barabanki) per cent. MP heterosis were observed significant in three crosses; while two had positive and one had negative value and ranged between -45.19 (PU 31 x LGG 450) to 48.71 (TMB 37 x Barabanki) EH were observed significantly negative among three crosses, which ranged from -70.99 (PU 31 x LGG 450) to -23.95 (TMB 37 x Barabanki) per cent over standard variety.

ID ranged between -114.50 (PU 31 x LGG 450) to 1.47 (Samrat x Barabanki) per cent, while two crosses exhibited significant negative value.

4.7.12 Phenol content

4.7.12.a Intraspecific

BP heterosis ranged from -34.68 (TMB 37 x LGG 450) to 22.35 (Uttara x LGG 450) per cent; whereas two crosses showed significant negative and one cross with positive value. Four crosses showed significant, each of the two were having negative and positive value; while ranged between -17.17 (TMB 37 x LGG 450) to 32.77 (Uttara x Barabanki) per cent over MP. EH showed five crosses with significant negative and one significant positive; while range

observed between -17.60 (Samrat x LGG 450) to 13.33 (HUM 16 x LGG 450) per cent over check.

ID found significant in all six crosses, while only one showed negative value along with the range -10.10 (TMB 37 x LGG 450) to 34.12 (HUM 16 x LGG 450) per cent.

4.7.12.b Interspecific

BP heterosis obtained significant negative in three crosses, and ranged from -14.51 (Uttara x LGG 450) to 2.38 (TMB 37 x Barabanki) per cent. Two crosses showed positive significant heterosis over MP and ranged from -8.46 (Uttara x LGG 450) to 17.88 (TMB 37 x Barabanki) per cent. EH was observed significant among three crosses, two showed positive and one negative value over check variety and it ranged between -34.00 (Uttara x LGG 450) to 13.17 (TMB 37 x Barabanki) per cent.

ID range varied between 3.54 (Uttara x LGG 450) to 34.02 (TMB 37 x Barabanki) per cent, whereas three crosses were observed with significant and positive value.

4.7.13 Grain yield per plot

4.7.13.a Intraspecific crosses

Range varied from 3.79 (HUM 16 x LGG 450) to 46.43 (Uttara x Barabanki) per cent over BP; and five crosses showed significant positive value. All six crosses showed significant positive heterosis and varied between 54.23 (HUM 16 x LGG 450) to 125.28 (Uttara x Barabanki) per cent over MP. Out of all six significant crosses five crosses had negative and only one cross had positive significant value over check variety. EH lies between -26.20 (Sekhar x Barabanki) to 7.42 (HUM 16 x LGG 450) per cent.

ID range varied between 23.05 (HUM 16 x LGG 450) to 47.93 (Sekhar x Barabanki) per cent; whereas all six crosses showed positive and significant, ID.

Table 12 : Reaction of Mungbean Yellow Mosaic Virus in parents of *Vigna*

Sl. No.	Crosses	Total no. of plant	Diseases score					Weighted mean	Disease Reaction
			1	3	5	7	9		
1.	HUM-16	118	47	71	-	-	-	2.20	Resistant
2.	TMB 37	110	56	54	-	-	-	1.98	Resistant
3.	SAMRAT	121	85	36	-	-	-	1.59	Resistant
4.	Pant U 31	119	96	23	-	-	-	1.38	Resistant
5.	UTTARA	116	77	39	-	-	-	1.67	Resistant
6.	SEKHAR	112	92	20	-	-	-	1.35	Resistant
7.	LGG 450	108	-	-	-	10	98	8.35	Susceptible
8.	BARABANKI	114	-	-	-	26	89	8.62	Susceptible
9.	SML 668	117	35	82	-	-	-	2.40	Resistant

Table 13 : Reaction of Mungbean Yellow Mosaic Virus in intra and inter specific crosses of *Vigna*

Sl. No.	Crosses	Generations	Total no. of plant	Diseases score					Disease Reaction	
				1	3	5	7	9	Susceptible	Resistant
1.	HUM-16 x LGG 450	F ₂	147	3	8	13	58	65	136	11
		BC ₁	63	5	9	3	26	20	49	14
		BC ₂	69	-	-	5	29	35	69	-
2.	SAMRAT x LGG 450	F ₂	149	5	7	9	59	69	137	12
		BC ₁	66	6	9	2	27	22	51	15
		BC ₂	74	-	-	8	29	37	74	0
3.	TMB 37 x LGG 450	F ₂	127	2	4	7	60	54	121	6
		BC ₁	59	5	8	4	19	23	46	13
		BC ₂	71	-	-	5	37	32	74	0
4.	SEKHAR x BARABANKI	F ₂	159	7	6	11	66	69	146	13
		BC ₁	72	7	10	3	22	30	55	17
		BC ₂	61	-	-	6	19	26	61	0
5.	PU 31 x BARABANKI	F ₂	127	2	4	13	49	59	121	6
		BC ₁	65	5	8	4	21	27	52	13
		BC ₂	56	-	-	6	22	28	56	0
6.	UTTARA x BARABANKI	F ₂	154	4	7	14	62	67	143	11
		BC ₁	67	5	10	7	21	24	52	15
		BC ₂	74	-	-	9	29	36	74	0

Cont....

Table 13 : Contd...

Sl. No.	Crosses	Generations	Total no. of plant	Diseases score					Disease Reaction	
				1	3	5	7	9	Susceptible	Resistant
7.	SAMRAT x BARABANKI	F ₂	114	2	9	17	47	39	103	11
		BC ₁	67	3	12	3	23	26	52	15
		BC ₂	66	-	-	6	28	32	66	0
8.	TMB 37 x BARABANKI	F ₂	132	2	9	11	59	51	121	11
		BC ₁	71	3	11	6	28	23	57	14
		BC ₂	76	-	-	13	24	29	76	0
9.	PU 31 x LGG 450	F ₂	100	2	6	9	46	37	92	8
		BC ₁	59	4	8	2	26	19	47	12
		BC ₂	47	-	-	6	25	16	47	0
10.	UTTARA x LGG 450	F ₂	126	2	5	17	53	49	119	7
		BC ₁	68	5	11	2	22	28	52	16
		BC ₂	53	-	-	5	20	28	53	0

4.7.13.b Interspecific crosses

BP heterosis ranged between 0.00 (Samrat x Barabanki) to 51.83 (Uttara x LGG 450) per cent comprising positive and significant value in two crosses. All crosses showed positive and significant MP, which ranging from 46.91 (Samrat x Barabanki) to 98.10 (Uttara x LGG 450) per cent. EH ranged between -26.20 (PU 31 x LGG 450) to -9.17 (Uttara x LGG 450) per cent and all crosses showed negative significant heterosis over the check.

ID exhibited ranged between 24.52 (Uttara x LGG 450) to 32.54 (PU 31 x LGG 450) per cent while all crosses showed positive and significant, ID.

4.8 Inheritance Pattern of Mungbean Yellow Mosaic virus (MYMV)

As per the results revealed by Table 12 for the disease reaction against Mungbean Yellow Mosaic Virus of resistant as well as susceptible parents are quite evident to identify resistance and susceptible parents based on the score of frequencies of the plants.

Since the disease reaction was scored in 1-9 scale as a quantitative trait but based on the frequencies of the plants towards both the extremes (resistance/susceptible) score 1 and 3 as resistant and score 5,7, and 9 as susceptible based on the frequencies of the plant as 5 score worked as threshold level consequently it has been grouped into two discrete phenotypic classes as susceptible which is evident from Table 13.

The segregating pattern for resistance to MYMV in the F_2 , BC_1 and BC_2 generation in has been presented in Table 12 F_2 population in all the crosses showed digenic inheritance with 15 (susceptible) : 1 (resistant) ratio. The BC_1 population was observed in three classes (susceptible, resistant and segregating) and showed 3:1 (susceptible : resistant) ratio while BC_2 had 100 per cent susceptible population.

DISCUSSION

Basic objective of Plant Breeding is to evolve varieties that perform certain functions better than the existing varieties. The superiority of the improved type is manifested by certain specific gene combinations and how rapidly these specific gene combinations can be obtained in single crop variety, much depends on the system into which the genes available improvement was restricted to the use of various selection methodology coupled with introgression and/or selection of favourable plant type in autogamous plant limited to utilization of fixable genes effect only.

The knowledge regarding the estimations of relative magnitude of various gene effects including epistasis is of great importance in formulating the most appropriate breeding procedure in crop improvement programme.

Among the crop species pulse also known as grain legumes are valued for their protein rich grains and soil fertility restoration as well as comprising the soil amelioration property. India has be pride of being the world's largest producer of pulses contributing 13-15 m tonnes to the global basket. The important Indian pulses crop are chick pea (38%), *Vigna* (22%), pigeonpea (16%), lentil (7%) field pea (5%) are being grown across the length and breadth of the country on 22-24 m ha of area.

As *Vigna* is comprising highest area next to chickpea in India. But their production and productivity is very meager due to the unavailability of high yield genotype alongwith the proper resistance against the disease and insects. While this crop is comprising high and quality protein alongwith the sulphur containing amino acids.

Keeping in view the above facts the present investigation was undertaken to find out the components of gene effects of yield and yield traits. It was envisaged that parameter estimated as well as heterosis study would be helpful in

formulating suitable breeding programme to bring rapid and rational improvement in *Vigna*.

The knowledge of the extent and nature of phenotypic as well as genotypic variability holds the key to the success of a plant breeder desirous of improving the character of interest. But yield of a crop plant is a dependable variable on the other attributes, so it is difficult to predict the expected improvement in the yield on the bases of variability study alone. The study of genotypic and phenotypic coefficients of variation along with heritability estimates provides the vivid picture of the progress that can be expected from selection (Burton, 1952). Information on the association of yield attributes and their direct and indirect effects on yield bears paramount significance thus it is necessary to have such information, while analysing these traits for bringing out its improvement.

For sorting out interacting and non-interacting crosses, joint scaling test was applied. The interacting crosses were subjected to generation mean analysis to study the main gene effects and their interactions. It was envisaged that the parameters estimated would be helpful in formulating suitable breeding plans to bring about rapid and rational improvement in *Vigna* productivity. [Similar results were also observed by Sadiq and Abbas (2007) Rahim *et al.* (2010)].

The breeder in autogamous crop is primarily interested in identifying parental combinations that are likely to produce superior homozygous segregants, but identification of specific parental combinations capable of producing highest level of F_1 , transgressing effects are of great value in the present context as female parents involved in the present study. The magnitude of heterosis, expressed as superiority of the F_1 s over better parent, mid parent and over commercial variety (economic heterosis) and inbreeding depression from F_1 's to F_2 's of intra and interspecific crosses were also worked out and their implications on increasing mungbean productivity were examined. Mungbean Yellow Mosaic Virus (MYMV) is one and one bottle neck for making the yield improvement in mungbean, so study the inheritance Pattern of MYMV for knowing the genetics of resistance for the adoption of suitable breeding methodology to incorporate the resistant gene/genes, would be helpful to commensurate the total potential of *Vigna*.

5.1 Analysis of variances

The analysis of variance of thirteen characters of sixty, one treatments including parents crosses and check revealed highly significant differences among genotypes for all the characters studied. The material taken under study was having comprising sufficient variability, which helps to the breeder for the identification of suitable high yielding genotypes to be used for the exploitation of heterosis to improve the yield of the crop.

5.2 Mean and Range performance

The mean value of different quantitative traits including the days to maturity, number of cluster per plant, number of grains per pods and grain yield per plot performance in available treatment suggested that selection of high yielding desirable treatments (genotype/crosses) from the material may be possible and would be effective.

1. Days to 50% flowering

Among all the treatments none of the parent as well as crosses was found earlier than the Samrat. Suggesting that Samrat may be used in crossing programme for developing the earliness.

2. Plant height

A wide range of variation from 17.9 to 52.7 cm. among the treatments for plant height was observed. All the treatments were dwarfer than the check. Treatment number 23, 31, 43, 21, 22, 47 were found superior for dwarfness indicating that to have the dwarfer genotypes. These six treatment may be exploited in crop improvement programme.

3. Number of primary branches

A considerable range varied from 1.6 to 7.33 primary branches per plant. For this trait most superior treatment 17, 25, 27, 41 and 29 were identified. To have the more number of primary branches per plant these crosses may be utilized in crop improvement programme.

4. Number of cluster per plant

A wide range of variability (9.43-39.5) cluster per plant were observed among all the treatments. The higher magnitude of cluster density was observed in treatment 12, 17, 27, 37 and 29. To have the higher number of cluster per plant these cross combinations may be utilized in breeding programme.

5. Number of pod per cluster

For this character, range was observed from 1.87 to 5.23 among the treatment. The most superior treatments were 17, 45, 43, 20, 18, 13 and 14 were identified for pod per cluster.

6. Number of pod per plant

A considerable range of variability was observed among the treatment variability from 22.27 to 84.42 among the treatment. The most promising treatment were found 29, 9, 37, 27, 41 and 42 for this trait. So, these treatment may be included for further utilization.

7. Days to maturity

Range for days to maturity was found 61.27 to 82.67. The most early maturing treatments were 31, 32, 33, 34 and 35. Suggesting that these treatment may be further utilized in improvement programme to have the early maturing variety in mung as well as urd.

8. Pod length

A considerable range of variability from 3.63 to 10.50 was observed for pod length but none of the treatment had shown the superiority over the check variety SML 668. So, it is very much evident for increasing the pod length SML 668 is used as a parent in hybridization programme.

9. Number of grains per pod

A wide range of variation from 4.602-11.00 number of grains per pod was observed. Four treatments exhibited significant superiority viz., 17, 13, 34 and 2 over check variety SML 668. Suggesting the importance of these treatment to get exploited in breeding programme for enhancing the number of grains per pod.

10. 100-seed weight

Within this trait range was observed 2.49 to 4.87. None of treatment shown significant superiority over the check variety (SML 668) for 100-seed weight. So, it is very much evident that to enhance the 100-seed weight SML 668 may be used for crop improvement programme.

11. Harvest index

A considerable range of variation from 0.102 to 0.54 was observed for harvest index. Only one treatment (PU 31 x Barabanki) exhibited the significant superiority over the check variety for harvest index. Suggesting that this cross combination may be further exploited to increase the harvest index.

12. Phenol content

A considerable range of variation from 0.55 to 2.03 mg/g of phenol content in fresh leaf weight was observed among the treatment. It is evident from the table susceptible variety Barabanki and LGG 450 is comprising significant lower phenol content in comparison to improve variety HUM 16, PU 31 and TMB 37. Which are showing the resistant to moderate resistant disease reaction against MYMV. Similar result were also observed by Kosauge, T. (1979), Singh and Bedi (1975), Sharma *et al.* (1983) and Reddy *et al.* (2002). Treatment number 24, 79, 12, 15, 16, 23, 27, 31, 25, 37, 40, 47 and 48 had shown the significant superiority over the check SML 668 for phenol content. Suggesting that these treatments may be utilized to enhance the phenol content for producing the higher magnitude of resistance against disease.

13. Grain yield per plot

A wide range of variability was obtained from 0.17-0.82 kg per plot among the treatments. Only one treatment (HUM 16 x LGG 450) had given the significant superiority for grain yield per plot over the check; indicating that, this treatment may be further exploited to have the higher grain yield per plot.

3. Genetic variability

Measures of variability and selection are indispensable in any plant breeding programme. Variability provide the material resources to breeder for restructuring the plant genotype as well as provides wider genetic base for selection. Wide range of variability was observed amongst the available material for the characters taken under study. For all the character PCV was slightly higher than GCV, which indicated very meager effect of environment on the expression of the traits. This finding also get confirmed by the Konda *et al.* (2009), Venkateswarle (2001), Reddy *et al.* (2003) and Dikshit *et al.* (2002).

High GCV alongwith PCV was observed for the traits viz. plant height, number of primary branches, number of cluster per plant, number of pod per plant, pod length, harvest index, phenol content and grain yield per plot. Similar result were also observed by Konda *et al.* (2009), Venkateswarlu (2001), Reddy *et al.* (2003), Prakash Singh and Khedar (2007), Dhananjay *et al.* (2009) and Dikshit *et al.* (2002). While moderate GCV followed by PCV was observed for pod per cluster and 100-seed weight. It is also reported by Peerajade *et al.* (2009), Sadiq and Abbas (2007). The estimates of GCV indicated that traits like grain yield, harvest index, number of cluster per plant and plant height may be used as a selection criteria, because these trait showed comparatively very high GCV.

The GCV provides a measures for comparison of genetic variance and sometimes gives indication regarding the suitability of the traits for selection. The effectiveness of selection for any character depends on variability present as well as heritability of the characters concerned. The higher importance of heritability estimates of character have been pointed out by Lush (1940) in animal and Johnson *et al.* (1955) in plant. Hanson (1963) stated that heritability estimates are influence by method of estimation, generation of study, sample size and environment.

Genetic advance, though a not independent entity has added advantage over heritability. Johanson *et al.* (1955) reported the importance of both the heritability and genetic advance in selection under breeding programme. Hanson (1963) stated that heritability and genetic advance are complementary concept.

According to Kung (1977) GA would be overestimated in either of the following situation (i) low selection proportion with high heritability and (ii) high selection proportion with low heritability. Genetic gain would be under estimated where both the selection proportion and heritability were high and low.

Appraisal of table revealed high heritability estimate coupled with high GA observed for in all the traits under study except days to 50 per cent flowering and days to maturity. Similar results was also obtained by Nazir *et al.* (2005), Pandey *et al.* (2007), Prakash Singh and Kheder (2007), Sadiq and Abbas (2007), Perajade *et al.* (2009), Dhananjay *et al.* (2009) and Rahim *et al.* (2010).

It indicates preponderance of additive and fixable genetic variance suggesting that if these characters are subjected to any selection scheme, wide adopted genotype can be developed and selection pressure should be exercised in early generation.

4.1 Character Association

The indirect selection is more effective than direct selection procedure, when in attributes in question has low heritability and/or is not easily or precisely measurable. The aim of correlation studies is primarily to know of the suitability of various characters for indirect selection. Because selection for one or more trait results in correlated response for several of the traits (Searle, 1965) and the pattern of variation will also be changed (Waddington and Robertson, 1966) therefore, the knowledge of genetic correlation existing between yield and its component is essential.

The magnitude of genotypic correlation was greater than phenotypic correlation hence, the significant phenotypic association between the character were primarily due to genetic course, which might be due to pleiotropic effect rather than linkage between gene affecting different characters. The self pollinated mechanism is a pre-laid to the fixation of blocks of genes as well as due to limited chances for breaking linkage compare with the random mating system, prevailing cross pollinated crops (Johanson *et al.* 1955).

In present investigation 50 per cent flowering exhibited significant and positive correlation with number of primary branches. Similar results were also observed by Obaidullah *et al.* (2006), Sadiq and Abbas (2007), Verma and Garg (2007), Arshad *et al.* (2009).

Days to 50 per cent flowering revealed significant and negative correlation with pod length in including as well as excluding the parent. This finding got also confirmed by Arsher *et al.* (2009).

Plant height positive and significant correlation with pod length and grains per pod. Similar result were also obtained by Islam *et al.* (1999).

Number of primary branches showed positive and significant correlation with cluster per plant and pod per plant. This finding was in agreement with the observation of Joseph and Kumar (1999) in including as well as excluding the parents.

Cluster per plant exhibited positive and significant correlation with pods per plant in both sets of experiment; whereas it also showed the positive and significant correlation with days to maturity only in including the parents. Similar results were also observed by Srivastava *et al.* (2008) and Singh *et al.* (1995).

Pods per plant positively and significantly associated with days to maturity only in set I (including Parent).

Negative and significant association was observed for days to maturity with harvest index in both sets of experiment.

Pod length exhibited positive and significant correlation with grains per pod in both sets of experiment. This finding is in confirmity of the reports Hegde *et al.* (1996) and Srivastava *et al.* (2008).

Grain yield per plot was positively and significantly correlated with 100 seed weight and grains per pod in both set of experiment. While this trait showed the positive and significant association with pod length and harvest index only in first set of experiment. Similar result were observed by Srivastava *et al.* (2008). Arshad *et al.* (2009), Peerajade *et al.* (2009) and Singh *et al.* (2009).

5. Direct and Indirect effects

The coefficient of correlation does not give the three picture under complex situations. Under such situations, path coefficient analysis provides a means to determine the direct influence of one variable (cause) upon another variable (effect). For establishment of cause and effect relationship path coefficient analysis offers an opportunity to partition correlation coefficient into component of direct and indirect effects (Wright, 1921) and Path coefficient is standardized partial regression coefficient, which measures the influence of independent variables on dependent variables (Dewey and Lu, 1959).

In present investigation, grains per pod and 100 seed weight exhibited positive and high direct effect with grain yield in both sets of experiment; whereas pod length and harvest index showed positive and high direct effect with grain yield only in first set of experiment. Similar results were reported by Sharma (1999), Sabaghopur *et al.* (1999), suggesting that for enhancing the yield in case of *Vigna* during the course of selection first and for most importance should be given to these traits.

For all the characters residual effect was very high in both sets of experiment referring to very few of the yield contributing characters taken under study would attribute towards the grain yield and it also indicates that there are some other traits which also contribute to grain yield of *Vigna*.

6. Generation mean analysis

Adequacy and Genetic model

Joint scaling test was applied to test the adequacy of additive dominance model. Significance of X^2 value indicated the evidence of epistasis in respective crosses for the trait under study. Therefore, data from all the crosses (when X^2 value significant) were further analysed using six parameter model for their practical application.

The estimation of additive, dominance as well as presence of epistasis were done by joint scaling test and consequently significance of three parameter [m] [d] [h] were evaluated.

In intra specific, few crosses exhibited the presence of epistasis, further importance of additive components was realized for days to 50 % flowering, plant height, number of pods per plant, number of cluster per plant and days to maturity. In contrast dominance component was found to play an important role in the expression of days to 50% flowering, number of cluster per plant, number of pod per plant, days to maturity, number of grains per pod. However, both additive and dominant component were equally important for the inheritance of days to 50% flowering, plant height, number of cluster per plant, number of pod per plant and days to maturity in the several crosses namely TMB 37 x LGG 450, HUM 16 x LGG 450, Samrat x LGG 450, Sekhar x Barabanki and Uttara x Barabanki. Days to 50% flowering, number of cluster per plant and days to maturity in the cross TMB 37 x LGG 450, whereas, for plant height in all six crosses except PU 31 x Barabanki.

For number of pod per plant, all six crosses exhibited equally significant additive as well as dominant components for the expression of the character except Sekhar x Barabanki. Cross PU 31 x Barabanki had also indicated the importance of additive and dominant components for days to maturity.

In interspecific crosses, epistasis was evident in most of the crosses for different traits under study. Further preponderance of additive components was noticed for days to 50% flowering, plant height, number of pods per plant, days to maturity; whereas, dominance component was found to play an important role in the expression of days to 50% flowering, plant height, number of primary branches, number of cluster per plant, number of pod per plant, days to maturity, pod length. Both additive and dominance components were equally important for the inheritance of days to 50% flowering in the cross Uttar x LGG 450, for plant height in all three crosses except TMB 37 x Barabanki, for number of pods per plant in all three crosses except Uttara x LGG 450; whereas for days to maturity namely PU 31 x LGG 450. It is pertinent to emphasize here that, when we compare the significance of gene interaction involving the inheritance of yield and yield attributing components studied in intra specific and inter specific crosses, it is quiet obvious that epistasis was frequently evident in inter specific crosses as compare to intra specific crosses. It is clearly indicates that inheritance of yield

components become more complex when the crosses involved distantly related parent. However, the relative estimates of two types of gene actions varied from cross to cross for same character because of the limitations of this procedure. Firstly, X^2 estimates cannot be compared at zero degree of freedom and secondly sequential elimination technique would not be carried out to estimate the actual significant components, contributing to the traits in present set of materials.

From the analysis of three parameter model it appears that additive and/or dominance components seemed to play an important role in the inheritance of few yield components, such as days to 50% flowering, number of cluster per plant, number of pod per plant, days to maturity and pod length, which are assumed to have less complex inheritance. Conversely for complex traits likes plant height, number of pods per plant besides dominance or additive, epistatic gene interaction was also found to play significant role in the expression of these traits in the majority of the crosses. It indicates that as the inheritance of quantitative character become more complex, the contribution of epistatic gene effects to their inheritance becomes greater.

The Estimates of gene effect through generation mean analysis in relation to *Vigna* improvement

The knowledge regarding the estimates of relative magnitude of various gene effects including epistasis is of great importance in formulating the most appropriate breeding procedure for further improvement, when the cross combinations are considered individually. Although linkage affects the epistatic components in generation mean (Hayman, 1958) additive and dominance gene effects are also likely to be biased in the presence of epistasis (Hayman, 1960). Therefore, for those crosses where the joint scaling test suggested the presence of epistasis, six parameter model gives reliable estimates of main gene effects as well as epistatic gene inter action. Thus, in present investigation, attempts has been made to examine whether epistatic gene effect exist in the materials involving diverse parents belonging to same species that is intra specific crosses and even to different species i.e. inter specific crosses and if so what is their relative importance.

Intra specific crosses

In intra specific crosses, the estimates of six parameter for various gene effect considered, revealed the significant reducing (-ve) additive gene effects for the expression of almost all the characters except number of cluster per plant and number of pod per cluster while grain yield per plot exhibited significant enhancing (+ve) additive gene effects. Similar results were also observed like Seenaiyah *et al.* (1993), Rosaiah *et al.* (1994) and Manivannan (2002). Significant and positive dominant gene effects were observed for the traits days to 50 % flowering, phenol content, harvest index and grain yield and thus exhibiting the enhancing (+ve) effects for the inheritance of the traits which was inconformity with earlier report (Shanmugasundaram and Rangaswamy, 1994; Joseph and Kumar, 2000) while significant reducing (-ve) dominant gene effect were observed for number of pod per cluster, days to maturity, number of grains per pod and 100 seed weight for the expression of the traits under study. Similar results were also obtained by Singh *et al.* (2006). The relative magnitude of dominant gene effect were higher than the additive gene effect for inheritance of all the traits studied, which was in conformity with the earlier reports of Shanmugasundaram and Rangaswamy (1994) and Joseph and Kumar (2000).

Among epistatic interaction, additive x additive gene effect for days to 50% flowering and dominant x dominant gene effect for 100 seed weight were evident in all four crosses except Samrat x LGG 450 and PU 31 x Barabanki exhibited the significant enhancing (+ve) effects for the inheritance of these traits in respective crosses. In contrast significant reducing (-ve) additive x additive gene effect for 100 seed weight and dominant x dominant gene effects for days to 50% flowering were observed in four crosses except Samrat x LGG 450 and PU 31 x Barabanki. Which was inconformity with earlier worker Ammavasai *et al.* (2005).

Among the digenic interactions, additive x additive, and dominance x dominance were found equally important for the traits viz. plant height, number of primary branches, number of pods per plant, pod length, harvest index, phenol content and grain yield.

Additive x dominance significant reducing (-ve) gene effect were observed for days to 50% flowering, plant height, number of cluster per plant. For all the traits except number of primary branches and number of pods per cluster for the expression of these traits.

Duplicate type of epistasis was found in eight traits namely days to 50% flowering, plant height, number of primary branches, number of pod per cluster, number of pod per plants, days to maturity, number of grains per pod and 100-seed weight. Inconterary to this complementary epistasis was observed for only one trait number of cluster per plant; whereas, for rest four traits viz. pod length, harvest index, phenol content, and grain yield per plot, few crosses showed duplicate as well as complementary type of epistasis. These finding suggest that few cycles of recurrent selection followed by pedigree method will be effective and useful to utilize all the three types of gene effects. It will also lead to increased variability in later generation for effective selection by maintaining considerable heterozygosity through mating of selected plants in early segregating generation. Epistasis was mostly of duplicate type which will reduce variation in F₂ and subsequent generation, consequently it hinders the pace of progress through selection.

The complementary type of non allelic interaction for number of cluster per plant was observed suggesting that intercrossing of F₂ plants may be recommended to produce superior recombinants having the complex genetic behaviour and selection in the later generation of segregating population for enhancing the number of cluster per plant of the *Vigna* genotypes.

Inter specific crosses

In inter specific crosses, though both additive and dominant gene effect (ignoring, sign) were almost equally important and the relative magnitude of dominant gene effect were even higher than the additive gene effects for inheritance of all the traits under study, which was inconfirmary with the earlier reports of Tyagi and Srivastava (2001), Singh *et al.* (2006), Saxena and Sharma (1993) and Jhangirda (2001).

Among epistatic interaction positive and significant additive x additive gene effects were observed for the enhancing of the expression of days to 50% flowering, Plant height and Phenol content.

In contrast to this negative and significant additive x additive gene effects were found responsible for reducing (-ve) the expression of number of pod per cluster number of pods per plant, harvest index (HI) and grain yield per plant. Dominant x Dominant gene effects exhibited significant enhancing (+ve) effect for the inheritance of number of pods per plant, number of grains per pod and grain yield per plant. In contrast significant and reducing (-ve) effects for the inheritance of traits days to 50% flowering and phenol content for most of the crosses. Additive x dominance gene effect showed reducing (-ve) effects for the expression of most of the traits except number of grains per pod and harvest index (HI). For almost all the characters duplicate type of epistasis was observed in Samrat x Barabanki, PU 31 x LGG 450 and Uttara x LGG 450, while for the cross TMB 37 x Barabanki complementary type of gene effect was observed for the traits pod length and phenol content as well as PU 31 x LGG 450 also showed complementary type of gene effects for the traits harvest index (HI) and grain yield per plot.

Thus to exploit all the three types of gene action present in most of the crosses for most of the characters, recurrent selection has been suggested followed by modify pedigree method or and pedigree method as well as intermating of superior selected plants in segregating generation will be useful. It will help in breaking gene constellation and will lead to release of free variability for effective selection. This is in agreement with the earlier findings of Patil *et al.* (1996), Naidu and Satynaryana (1993), Khattak *et al.* (2002), Brar (1985), Srinivas *et al.* (1991), Saxsena and Sharma (1993).

7. Heterosis

The breeder in autogamous crop is Primarily interested in identifying parental combinations that are likely to produce superior homozygous segregant, but identification of specific parental combinations capable of producing highest level of F₁, transgressive effects are of great value in the present context. The superiority of cross combination is of not availed unless it is economical. The

affords, therefore, have been made to compare and adjudged the superiority of F₁ crosses over their mid-parental, better parental and on standard variety (SML 668).

From the perusal of the table it is obvious that desirable heterosis would not be obtained for days to 50% flowering in any of the intra/inter specific crosses; whereas, for the plant height desirable heterosis was obtained in intraspecific crosses viz., Uttara x Barabanki, PU 31 x Barabanki and Sekhar x Barabanki as well as inter specific crosses namely TMB 37 x Barabanki and PU 31 x LGG 450. Suggesting that in out of five crosses, in four crosses Barabanki was involved as male parent and none of the crosses exhibited significant inbreeding depression. Thus it is evident that there is a involvement of additive type of gene action, so Barabanki may be used as one of the parent for developing the dwarfness in *Vigna* and that could be fixable in nature.

For most of the yield attributing traits viz., number of primary branches, number of cluster per plant, pod per cluster, number of pod per plant and days to maturity in intraspecific crosses TMB 37 x LGG 450 and Sekhar x Barabanki; whereas in inter specific cross PU 31 x LGG 450 were found promising, so it is very much obvious that these cross combinations may be further exploited in *Vigna* improvement programme. Which was in confirmity with the results of the earlier worker Patil *et al.* (1996), Sharma (2000), Jahagirdar (2001) and Singh and Dikshit (2003).

All intra as well as inter specific crosses exhibited significant and undesirable heterosis for pod length, number of grain per pod, 100 seed weight, harvest index (HI), phenol content and grain yield per plot; whereas, only one cross HUM 16 x LGG 450 showed significant and desirable heterosis for phenol content and grain yield per plot alongwith the significant and high magnitude of inbreeding depression. Suggesting that there is preponderance of non additive type of gene action. Therefore, in hybridization programme suitable breeding methodology may be used and selection can be practiced in later generation for the improvement of phenol content to produce resistance against the MYMV alongwith the higher yield potential.

8. Inheritance pattern of mungbean yellow mosaic virus (MYMV)

The F₁ generation of all crosses exhibited susceptible reaction to MYMV. This indicates dominance of susceptibility over resistance which was in confirmity with earlier report of Singh and Patel (1977), Singh (1980), Solanki *et al.* (1982), Verma and Singh (1989), Reddy and Singh (1993), Singh *et al.* (2002) and Ammavasai *et al.* (2004). In contrast, Dahiya *et al.* (1971) reported that resistance was dominant over susceptibility.

The segregation for resistance in the F₂ generation showed digenic inheritance with 15 (susceptible) : 1 (resistant) ratio, which was further confirmed by BC₁ and BC₂ segregating progenies. It clearly indicates that resistance to MYMV is under control of digenic recessive genes. Two recessive genes for resistance to MYMV have also been reported by Singh, (1980); Solanki *et al.* (1982); Verma and Singh (1989); Singh *et al.* (2002); Sierohi *et al.* (2002); Ammavasi *et al.* (2004). However, a single recessive gene for MYMV resistance has also been reported by Kaushal and Singh (1988), Saleem *et al.* (1998), Khattak *et al.* (1999) and Khattak *l.* (2000). In Contrast, Reddy and Singh (1993) suggested one dominant and one recessive gene for resistance to MYMV. The differences in the nature of gene(s) contributing resistance to MYMV might be attributed due to differences in the sources of resistant genotypes used in the investigation and/or variation in the virus strain. The possibility of environmental factors in relation to penetrance and expressivity of the genes also cannot be ruled out.

Since two recessive genes for MYMV resistance are involved in the resistance donors genotypes of mungbean, it will be desirable to grow a large segregating populations to recover a number of resistant plants coupled with other desirable traits to have a successful breeding programme.

Implication of Result for Vigna Improvement Programme

On the basis of genetic variability study characters viz plant height, number of primary branches per plant, number of cluster per plant, number of pod per plant, pod length, harvest index, phenol content and grain yield exhibited high GCV, heritability as well as genetic advance suggesting that preponderance of additive gene action selection based on these traits will be rewardive in case of Vigna improvement programme. Number of grains per pod , 100-seed weight and harvest index had shown positive and highly significant correlation alongwith their high positive direct effect with grain yield suggesting that these three parameter may be considered as important trait during the course of selection to have the higher yield in case of Vigna.

In most of the crosses for most of the characters additive x additive, additive x dominance, dominance x dominance gene actions were observed suggesting that in Vigna improvement programme few cycles of recurrent selection followed by modified pedigree method and/or pedigree method as well as intermating superior selected plants in segregating generation will be rewardive and also it will help in breaking gene constellation and will lead to release of free variability for effective selection.

Three crosses namely TMB37 X LGG450, Sekhar x Barabanki and PU31XLGG450 were found promising for most of the yield attributing traits like number of primary branches, number of cluster per plant, pod per cluster, number of pod per plant and days to maturity. Suggesting that these cross combinations may be further exploited to have the higher yield.

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SUMMARY

In present investigation on “Generation Mean Study for Yield Components and Inheritance Pattern of MYMV in *Vigna*.” was carried out at Research Farm of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar during Summer 2008, Kharif 2010 and Summer 2011. The experimental material six intra and four interspecific crosses of *Vigna* were generated involving three varieties of urdbean viz. Sekhar, Uttara and PU 31 and three varieties of mungbean viz. HUM 16, Samrat and TMB 37 of *Vigna radiata* a resistant source as well as one of each MYMV susceptible variety i.e. LGG 450 for (mungbean) and Barabanki local (Urdbean) to have the P₁, P₂, F₁, F₂, BC₁ and BC₂ population. The generated material of all the crosses were grown in randomized block design with three replications having the row to row and plant to plant distances 30 x 10 cm under the optimal agronomical practices.

The observations were recorded for thirteen different quantitative as well qualitative traits viz., Days to 50 flowering, Plant height (cm), Number of primary branches, Cluster per plant, Pods per cluster, Number of pod per plant, Days to maturity, Pod length (cm), Grains per pod, 100 seed weight (g), Harvest index, Phenol content (mg) and Grain yield per plot (kg).

The observed mean data of ten plant each of P₁, P₂, F₁, BC₁, BC₂ and forty plants from F₂ were randomly selected from each treatment for all the characters were subjected to various statistical analysis for the study of Analysis of variance, Mean and Range, Genetic variability, Character association, Direct and indirect effect, Estimation of gene effects, Heterosis and inbreeding depression, Inheritance pattern of mungbean yellow mosaic virus.

The results of investigations are summarized as under :

Analysis of variance indicated significant differences among all the treatment for all character in the study for both sets of experiment.

On the basis of mean performance for phenol content fourteen genotypes had shown significant superiority over the check SML 668, among them Uttara x LGG 450 was having the highest phenol content (2.03 mg/g of fresh leaf). Whereas for the grain yield only one treatment i.e. HUM 16 x LGG 450 (0.82 kg/plot) exhibited the significant superiority over the check SML 668 (0.76 kg/plot).

For all the traits PCV was bit higher than the GCV, which indicated the very meager influences of environment on the expression of the character in both sets of experiment.

All the characters exhibited high heritability coupled with high genetic advance except pod per cluster, days to 50% flowering and days to maturity indicating the preponderance of additive gene action. Thus selection may be rewarding based on these traits.

As evident from the character association study grain yield exhibited positive and highly significant correlation with 100-seed weight, grains per pod alongwith their the positive and high direct effects in both sets of experiment, whereas pod length and harvest index also exhibited positive and significant correlation alongwith positive and high direct effect in 1st set (including parent) of experiment.

The estimation of additive and dominance as well as presence of epistasis were performed by joint scaling test. Interacting crosses were further subjected to six parameter model to estimate the nature of gene effect. In intraspecific crosses few combinations exhibited the presence of epistasis; whereas in interspecific crosses epistasis was evident in most of the crosses for different trait under study.

From the analysis of three parameter model it appears that additive and/or dominance components seemed to play an important role in the inheritance of few yield components such days to 50% flowering, Number of cluster per plant, Number of pod per plant, days to maturity and pod length, which are assumed to have less complex inheritance in intraspecific as well as interspecific crosses. Conversely for complex traits like plant height, number of pods per plant besides dominance or additive, epistasis gene interaction was also found to play

significant role in the expression of these traits in the majority of the crosses. It indicates that as the inheritance of quantitative character become more complex, the contribution of epistatic gene effects to their inheritance becomes greater.

In intraspecific crosses the estimates of six parameter for various gene effect revealed the significant reducing (-ve) additive gene effect for expression of almost all the characters except number of cluster per plant and number of pod per cluster, while grain yield per plot, which exhibited significant enhancing (+ve) additive gene effect. Among epistatic interaction additive x additive gene action for days to 50 per cent flowering and dominate x dominant gene effect for 100 seed weight were evident in all four intra specific crosses except Samrat x LGG 450 and PU 31 x Barabanki.

Barring the crosses in most of the crosses duplicate type of epistasis was observed. Suggesting that, few cycles of recurrent selection followed by pedigree method will be effective for *Vigna* improvement.

In interspecific crosses, though both additive and dominant gene effect were almost equally important and relative magnitude of dominant gene effect were even higher than the additive gene effect for inheritance of all the traits under study. In most of the interspecific crosses for yield attributing traits comprise additive x additive, dominant x dominant and additive x dominant gene effects (ignoring the sign) alongwith the duplicate type of epistasis.

Thus to exploit all the three types of gene action present in most of the crosses for majority of the characters, recurrent selection has been suggested followed by modify pedigree method or and pedigree method as well as intermitting of superior selected plants in segregating generation will be useful. It will help in breaking gene constellation and will lead to release of free variability for effective selection.

For most of the yield attributing traits viz., number of primary branches, number of cluster per plant, pod per cluster, number of pod per plant and days to maturity in intra specific crosses TMB 37 x LGG 450 and Sekhar x Barabanki; whereas in inter specific crosses PU 31 x LGG 450 were found promising, so it is

very much obvious that these cross combinations may be further exploited in *Vigna* improvement programme.

All intra as well as inter specific crosses exhibited significant and undesirable heterosis for pod length, number of grain per pod, 100-seed weight, harvest index (HI), Phenol content and grain yield per plot, whereas, only one cross HUM 16 x LGG 450 showed significant and desirable heterosis for phenol content and grain yield per plot alongwith the significant and high magnitude of inbreeding depression, suggesting that there is preponderance of non-additive type of gene action. Therefore, suitable breeding methodology may be used for hybridization and selection may be done in later generation for the improvement of phenol content to produce resistance against the MYMV alongwith the higher yield potential.

The F₁ generation of all crosses showed susceptible reaction to MYMV suggesting that resistance is governed by recessive gene the segregation for resistance to MYMV in the F₂ generation showed digenic inheritance with 15 :1 (susceptible : resistance), which was confirmed by ratio by BC₁ (3 : 1) and BC₂ (1 : 0) segregating progenies. It clearly indicates that resistance to MYMV is under the control of digenic recessive genes.

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REFERENCES

- Aher, R.P. and Dahat, D.V. (1999). Heterosis and inbreeding depression in mungbean (*Vigna radiata* (L) Wilczek). *Agricultural Science Digest Karnal*, **19** (3): 155-158.
- Aher, R.P. Sonawane, V.P. and Dahat, D.V. (2000). Heterosis in mungbean [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Agricultural Research*, **34** (2): 134-137.
- Aher, R.P. Surve, P.P. and Dahat, D.V. (2000). Heterosis for yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Agricultural Science Digest*, **20** (1): 5-8.
- Ahmad, N. M. Abbasi Waseem, S. Shaukat Sahid and Zaki Javed, M. (2009). Physiological changes in leaves of mungbean plants infected with *Meloidogyne javamica*. *Phytopathol. Mediterr*, **48** : 262-268.
- Ali, M.N. Gupta, S. Das, A.K. Bhattacharyya, S. and Sarkar, H.K. (2008). Character association study in urdbean (*Vigna mungo* L.). *Environment-and-Ecology*, **26** (2A): 952-954.
- Al-Jibouri, H.A., Miller, P.A. and Robin, U.K. (1958). Genotypic and environmental variances and co-variances in a upland cotton cross of inter specific origin, *Agro. J.* **50** : 633-637.
- Ammavasai, S. Phogat, D.S. and Solanki, I.S. (2005). Genetics of some quantitative traits in mungbean. *Indian Journal of Pulses Research*, **18** (2) : 127-130.
- Ammavasai, S.; Phogat, D.S. and Solanki, I.S. (2004). Inheritance of resistance to mungbean yellow mosaic virus (MYMV) in green gram [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Genetics and Plant Breeding*, **64** (2): 146.
- Arshad, M. Aslam, M. and Irshad, M. (2009). Genetic variability and character association among morphological traits of mungbean, *Vigna radiata* L. *Journal of Agricultural Research Lahore*, **47** (2) : 121-126.
- Bray, H.G. and Thorpe, W.V. (1954). *Methods in Biochemistry Analysis*, **1** : 27-52.
- Burton, G. W. (1952) Quantitative inheritance in Grasses. Ptoc. VI Int. Grassland Cong. I. 277-283.
- Cavalli, L.L. (1952). An analysis of linkage in quantitative inheritance. (eds. E.C.R. Rieve and C.H. Waddington), pp. 135-144, HMSO, London.

- Chand, P. and Verma, J.P. (1980). Some characteristics of mungbean and urdbean varieties resistant and susceptible to Yellow mosaic virus. *Indian Phytopathology* **33** : 48-53.
- Dahiya, B.S., Singh, K. and Brar, J.S. (1977). Incorporation of resistance to mungbean yellow mosaic virus (MYMV) in black gram (*Vigna mung* L.). *Tropical grain legumes Bulletin*, **9** : 28-32.
- Datta, S. and Gupta, S. (2009). Use of genomic resources in improvement of *Vigna* species. *Journal of Food Legumes*, **22** (1) : 1-10.
- Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of created wheat grass for seed production. *Agron. J.*, **51** : 515-518.
- Dhananjay, Rama Kant Singh, B.N. Singh, G. and Salimath, P.M. (2009). Studies on genetic variability, correlations and path coefficients analysis in mungbean. *Crop Research Hisar.*, **38** (1/3) : 176-178 .
- Dikshit, H.K. Singh, B.B. and Dua, R.R. (2002). Genetic variation in mungbean. *Indian J. Pulses Res.*, **15** (2) : 125-127.
- Directorate of Economics and Statistics Department of Agriculture and Cooperation. 2010. **7**(2) : 1-2.
- Donald, C.M. (1962). In search of yield. *J. Aust. Inst. Agric. Sci.*, **28** : 171-178.
- Elangaimannan, R. Anbuselvam, Y. Venkatasan, M. and Karthikeyan, P. (2008). Heterosis and inbreeding depression for yield and yield attributes in urdbean *Madras Agricultural Journal*, **95** (7/12) : 453-457.
- Fisher, R.A. (1918). The correlation between relatives on the supposition of mendelian inheritance. *Trans. Roy. Soc. edn.*, **52** : 399-433.
- Fisher, R.A. (1936). The use of multiple measurement in taxonomic problems. *Ann Eugen.* **7** : 179-189.
- Fisher, R.A. and Yates, F. (1938). Statistical tables for biological, agricultural and medical research (3rd ed.) London : Oliver & Boyd. Pp 26-27.
- Gartan, S.L. and Sood, B.C. (1996). Relative contribution of various yield components in urdbean . *Indian Journal of Pulses Research*, **9** (1) : 11-13
- Gawande, V.L. and Patil, J.V. (2005). Gene action for seed yield and its components in mungbean (*Vigna radiata* (L) Wilczek). *Journal of Maharashtra Agricultural University*, **30** (3) : 285-288.
- Gawande, V.L. Patil, J.V. Kute, N.S. Dhole, V.J. and Patil, D. K. (2001). Heterosis studies in mungbean [*Vigna radiata* (L.) Wilczek]. *New Botanist*, **28** (1/4) : 127-13

- Gayen, P.; Chattopadhyay, P. (2000). Variability and association of pod and seed characters in urdbean. *Annals of Agricultural Research*, **21** (4) : 575-576.
- Ghafoor, A. Ahmad, Z. Qureshi, A.S. and Iqbal, S.M . (2000). Significance of mungbean yellow mosaic virus on yield and its components in *Vigna mungo* L. Hepper. *Pakistan Journal of Phytopathology*, **12** (2): 74-78.
- Ghafoor, A. Zubair, M. and Malik, B.A. (1993). Harvest index in mungbean. *Pakistan Journal of Agricultural Research*, **14** (4) : 309-313.
- Ghafoor, A. Zubair, M. Bakhsh, A. and Bashir, M .(1990). Heterosis among seven parents and their crosses in mungbean. *Pakistan Journal of Agricultural Research*, **11** (3): 169-173.
- Ghavami, F. and Rezai, A. (2000). Variation and relation of morphological and phenological traits in mungbean *Iranian Journal of Agricultural Sciences*, **31** (1) : 147-158.
- Gupta, S. Kumar, S. Singh, R.A. and Chandra . (2005). Identification of a single dominant gene for resistance to Mungbean Yellow Mosaic Virus in blackgram (*Vigna mungo* (L.) Hepper). *SABRAO Journal of Breeding and Genetics*, **37** (2) : 85-89.
- Hanson, W.D. (1963). Heritability statistical genetics and plant breeding NASRRC. Washington, Publ., **982** : 125-140.
- Haque, M.F. Ganguli, D.K. and Mishra, A.K. (1988). Combining ability and heterosis in urdbean. *Indian Journal of Pulses Research*, **1** (1) : 6-11
- Hayman, B.I. (1958). The separation of epistasis from additive and dominance variation in generation means. *Heredity*, **21** : 371-390.
- Hayman, B.I. (1960). Maximum likelihood estimation of genetic components of variation. *Biometrics*, **16** : 369-381.
- Hedge, V.S., Parameshwappa, R. and Goud, J.V. (1996). Association analysis in F₂ populations of inter-variety crosses in mungbean. *Legume Res.*, **19** (2) : 107-110.
- Hegde, V.S., Parameshwarappa, R. and Goud, J.V. (1996). Heterosis and inbreeding depression in mungbean (*Vigna radiata* (L.). *Mysore Journal of Agricultural Sciences*, **30** (2) : 101-105.
- Indian Statistics at a Glance (2008). **7** (3) : 1-2.
- Islam , M.T. Haque, M.M. Islam, M.O. Malek, M.A. and Hoque, M.E. (1999). Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* L. Wilczek). *Bangladesh Journal of Scientific and Industrial Research*, **34** (1): 103-107.

- Jahagirdar, J.E. (2001) . *Heterosis* and combining ability studies for seed yield and yield components in mungbean. *Indian Journal of Pulses Research*, **14** (2): 141-142.
- Jink, J. L. and R.M. Jones. (1958). Estimation of the components of heterosis. *Genetics* **43** : 223-234.
- Johanson, H.W. Robinson, H.F. and Comstock, R.E. (1955). Genotypic and Phenotypic correlation in Soyabean and their implication in selection. *Agron. J.*, **47**: 477-483.
- Joseph, J. and Kumar, A.V. (1999). Character association and cause effect analysis in some F₂ population of green gram *Vigna radiata* (L.), *Legume Res.*, **22** (2) : 99-103.
- Kalia, R.K. Gupta, V.P. and Kalia, N.R. (1988). Estimates of heterosis and inbreeding for seed yield over locations in urdbean. *Indian Journal of Pulses Research*, **1** (1) : 43-49
- Kasuage, T.(1969). The role of phenols in host response to infection. *Annual Review of Phytopathology*, **7** : 195-222.
- Khan, M.G. Ahmad, W. Khattak, G.S.S. and Siraj-ud-Din Ahmad, H. (2007). Studies on detection of epistasis and estimates of gene effects for secondary yield characters in *Vigna radiata* (L) Wilczek. *Sarhad Journal of Agriculture*, **23** (4): 1013-1017.
- Khan, M.G. Ahmad, W. Khattak, G.S.S. Siraj-ud-Din and Ahmad, H. (2007). Mode of inheritance of resistance to Mungbean Yellow Mosaic Virus (MYMV) in mungbean (*Vigna radiata* (L.) Wilczek). *Sarhad Journal of Agriculture*, **23** (4) : 1071-1074
- Khan, M.S.S. Abdul-Latif, Tahir-Sajjad, and Latafat-Parveen (2005). Expression of heterosis in mungbean for yield and yield components in semi-arid region. *Indus Journal of Plant Sciences*, **4** (4): 530-53
- Khan,M.N. (1998). Character association and component analysis in urdbean . *Advances in Plant Science*, **11** (2): 269-272
- Khattak, G.S.S. Haq, M.A. Rana, S.A. Srinives, P. and Ashraf, M. (1999). Inheritance of resistance to mungbean yellow mosaic virus (MYMV) in mungbean (*Vigna radiata* (L.) Wilczek). *Thai Journal of Agricultural Science*, **32** (1): 49-5
- Khattak, G.S.S. Ashraf, M. and Khan, M.S. (2004). Assessment of genetic variation for yield and yield components in mung bean [*Vigna radiata* (L) Wilczek] using generation mean analysis. *Pakistan Journal of Botany*, **36** (3): 583-588.
- Khattak, G.S.S. Haq, M.A. Rana, S.A. and Abass, G.I. (2000). Effect of mungbean yellow mosaic virus (MYMV) on yield and yield components

- of mungbean (*Vigna radiata* (L.) wilczek) *Kasetsart Journal Natural Sciences*, **34** (1): 12-16
- Khattak, G.S.S. Haq, M.A. Ashraf, M. Elahi, T. (2000). Genetics of Mungbean Yellow Mosaic Virus (MYMV) in mungbean (*Vigna radiata* L.) Wilczek. *Journal of Genetics and Breeding*, **54** (4): 237-243
- Khattak, G.S.S.; Ashraf, M. and Zamir, R. (2004). Gene action for synchrony in pod maturity and indeterminate growth habit in mung bean [*Vigna radiata* (L.) Wilczek]. *Pakistan Journal of Botany*, **36** (3): 589-594.
- Kingshlin, M. and Vanniarajan, C. (2000). Association of yield attributes and component analysis among the quantitative characters of rice fallow urdbean genotypes. *Crop Research Hisar*, **19** (1): 102-105
- Konda, C.R., Salimath, P.M. and Mishra, M.N. (2009). Genetic variability studies for productivity and its components in Black gram [*Vigna mungo* (L) Hepper]. *Legume Res.*, **32** (1): 59-61.
- Krishnan, A.G. Reddisekhar, M., Reddy, K.R. and Reddy, K.S. (2003). Heterosis and combining ability studies in urdbean {*Vigna mungo* (L.) Hepper}. *Legume Research*, **26** (4): 280-283
- Kuldeep Tyagi; Tomer, A.K. Singh; V.K. Rajeshwar Nandan. (2006). Research on crops. **7** (2) : 458-460.
- Kumar Sanjay; Sharma, V; NaikM; Vashi, P.S. (2007). *J. of Food Legumes* **20** (2) : 203-204.
- Kumar, R. Rathi, A.S. and Singh, A. (1999). Association analysis in *Vigna mungo* (L.). *Annals of Agricultural Research*, **20** (4): 468-471
- Kumar, S. Sharma, V. Naik, M.R. Vashi, P.S. (2007). Heterosis for yield and yield attributes in mungbean . *Journal of Food Legumes*. **20** (2): 203-204
- Kumar, U. Singh, S.P. and Vikas (2005). Variability and character association in mungbean [*Vigna radiata* (L.) *New Agriculturist*, **16** (1/2): 23-28
- Kung, F.H. (1977). Error in predicting genetic gain from mass selection. *Proc. Intl. Confr. Quant. Genet. Iowa State. Univ. Press. A. Mes. Iowa*, 859-864.
- Kute, N.S. Deshmukh, R.B. (2002). Genetic analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*, **25** (4): 258-261.
- Lush, J.L. (1940). Inter rice correlation of off spring an dams as a method of estimating heritability of characters. *Proc. 23rd Ann. Amer. Soc. Anim. Prod.*, **38**: 293-301.
- Malik, B. A., Tahir, M., Khan, I.A., Zubair, M. and Choudhary, A.H. (1987). Genetic variability, character correlaton and path analysis of yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Pakistan Journal of Botany*, **19** (1) : 89-97

- Manivannan, N. (2002). Line x tester analysis in Kharif green gram, *Legume Res.*, **25** (2): 127-130.
- Manivannan, N. Viswanathan, P. Sethuraman, K. and Dhanakodi, C.V. (1999). Genetic variability, correlation and path analysis in urdbean. *Indian Journal of Pulses Research*, **12** (1): 110-111
- Marappa, N., Savithamma, D.L. and Prabuddha, H.R. (2010). Correlation coefficient and path coefficient analysis in mungbean. *Vigna radiata* (L.) Wilczek. *Environment and Ecology*, **28** (2A): 1104-1107
- Mathur, K. 1949. Biometrical genetics. Dover Publication, Inc, New York.
- Mishra, D.K. (2003). Inheritance of yellow mosaic virus in mung bean. *JNKVV Research Journal*, **37** (2): 40-45
- Mishra, R.K. and Yadav, R.K. (1992). Path analysis of component factors influencing economical yield, harvest index and biological yield of mungbean. *Advances in Plant Sciences*, **5** (2) : 578-584
- Naidu, N.V. and Satyanarayana, A. (1993). Heterosis and inbreeding depression for yield and yield components of mungbean (*Vigna radiata* (L.) Wilczek). *Annals of Agricultural Research*, **14** (1): 30-34
- Naidu, N.V. and Satyanarayana, A. (1993). Heterosis and combining ability in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Pulses Research*, **6** (1): 38-4
- Naidu, N.V., Satyanarayana, A. (1993). Heterosis for yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Pulses Research*, **6** (1): 102-105
- Naraini, T.K. (1960). Yellow mosaic of mungbean (*Phaseolus aureus* L.) *Indian Phytopathology* **13** : 24-29.
- Nariani, T.K. (1959). Yellow Mosaic of mung (*Phaseolus aureus* L.). *Indian Phytopathology*, **13**: 24-29.
- Nazir; A. Sadiq, M.S. Hanif, M. Abbas, G. and Haidar, S. (2005). Genetic parameters and path analysis in mungbean, *Vigna radiata* (L.) Wilczek. *Journal of Agricultural Research Lahore*, **43** (4): 339-347.
- Nelder, J.A. (1960). The estimation of various components in certain types of experiment on quantitative genetics. *Biom. Genet.* (ed. O. Kempthorne). pp. 139-158, Pergaman Press, London.
- Nene, Y. L., Srivastava, S.K. and Naresh, J.S. 1972. Evaluation of urdbean (*Phaseolus mungo*) and mungbean (*P. aureus*) germplasm and cultivars against mungbean yellow mosaic virus. *Indian Journal Agricultural Genetics* **42** : 251-254.

- Nene, Y.L. (1973). Viral disease of some warm wealthy pulse crops in India. *Pl. Dis. Repr.* **57** : 463-464.
- Netam, R. Netam, C.R. Pandey, R.L. and Khan, R.U. (2010). Estimation of relationship of seed yield with its attributing traits in Urdbean [*Vigna mungo* L (Hepper)]. *Advances in Plant Sciences*, **23** (1) : 97-100.
- Obaidullah, S. Munawar, Khan and Abdul, Qayyum (2006). Correlation coefficient and path coefficient analysis in green gram genotypes. *Indus Journal of Plant Sciences*, **5** (1): 693-697.
- Ostle (1975). Statistics in research, 3rd ed. USA : Iowa State University Press. page 193-202.
- Pandey, A.K. and Singh, S.P. (2000). Growth pattern in relation to yield in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Genetics and Plant Breeding*, **60** (2): 237-238.
- Pandey, M.K. Srivastava, N. and Kole, C.R. (2007). Selection strategy for augmentation of seed yield in mungbean (*Vigna radiata* L. Wilczek). *Legume Research*, **30** (4): 243-249.
- Pandiyani, M. Senthil, N. Ramamoorthi, N. Muthiah, A.R. Tomooka, N. Duncan, V. and Jayaraj, T. (2010). Interspecific hybridization of *Vigna radiata* x 13 wild *Vigna* species for developing MYMV donar. *Electronic Journal of Plant Breeding*, **1** (4): 600-610.
- Panse, V.G. and Sukhatme, P.V. (1967). Statistical analysis for Agricultural Workers, ICAR, New Delhi.
- Patel, M.B., Patel, B.N., Savaliya, J.J. and Tikka, S.B.S. (2009). Heterosis and genetic architecture of yield, yield contributing traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*, **32** (4): 260-264.
- Patil, A.J. Wanjari, K.B. Patil, A.N. Raut, B.R. and Ghawghawe, P.B. (1992). Studies on heterosis in mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Soils and Crops*, **2** (1) : 1-4.
- Patil, V.S. Deshmukh, R.B. and Patil, J.V. (1996). Heterosis and inbreeding depression in mungbean. *Journal of Maharashtra Agricultural Universities*, **21** (1): 152-154.
- Payasi, D. Pandey, S. Nair, S.K. and Pandey, R. (2010). Generation mean analysis for yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *International Journal of Plant Sciences Muzaffarnagar*, **5** (2) : 485-493.
- Peerajade, D. and Ravikumar, R.L. (2009). Genetic variability and character association in local green (*Vigna radiata* (L.) Wilczek.) genotypes of Karnataka. *Environment and Ecology*, **27** (1): 165-169

- Prakash, V. Singh, R.V. and Khedar, O.P. (2007). Genetic parameters, correlation and path analysis among yield and yield characters in mungbean. *Journal of Arid Legumes*, **4** (1): 6-8.
- Priya, M.S. and Reddy, K.H.P. (2008). Character association and path analysis in twenty one F₃ progenies of mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Research ANGRAU*, **36** (1): 16-20
- Pundir, S.R. Gupta, K.R. and Singh, V.P. (1992). Studies on correlation coefficients and path-coefficient analysis in mungbean (*Vigna radiata* (L.) Wilczek). *Haryana Agricultural University Journal of Research*, **22** (4): 256-258
- Rahim, M.A. Mia, A.A. Mahmud, F. Zeba, N. and Afrin, K.S. (2010) Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiata* L. Wilczek). *Plant Omics*, **3** (1) : 1-6.
- Rajan, R.E.B. Wilson, D. Vijayaraghava, K. and Kumar, V. (2000). Correlation and Path analysis in the F₂ generation of greengram (*Vigna radiata* L.). *Madras Agri. J.*, **87** (10-12) : 590-593.
- Raje, R.S.; Rao, S.K. (2000). Association analysis for yield and its components in mungbean (*Vigna radiata* L. Wilczek). *Legume Research*, **23** (1) : 42-48
- Ram, T. (1997). Gene action for certain quantitative characters in greengram [*Vigna radiata* (L.) Wilczek]. *Indian Journal of Genetic and Plant Breeding*, **57** (2): 143-148.
- Rao, S.K. and Suryawanshi, R.K. (1988). Analysis of yield factors in urdbean (*Vigna mungo*). *Legume Research*, **11** (3): 134-138
- Rao, S.S. (1991). Heterosis and inbreeding depression in urdbean. *Indian Journal of Pulses Research*, **4** (1): 23-27
- Rasaiah, G. Kumari, D.S., Satyanarayana, A. and Naidu, N.V. (1994). Combining ability studies on sport quality traits in mungbean. *Indian J. Puls. Res.*, **7** (1): 1-6.
- Reddy, K.R. and D.P. Singh. (1993). Inheritance of resistance to mungbean yellow mosaic virus. *Jour Madras Agric.* **60** : 199-201.
- Reddy, V. Lakshmi, Narayana, Reddisekhar, M. Reddy, K. Raja Reddy K. Hariprasad (2003). Genetic variability for yield and its components in Mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Res.*, **26** (4): 300-302.
- Reddy, V.L.N. Reddisekhar, M. Reddy, K.R. and Reddy, K.H. (2003). Heterosis for yield and its components in mungbean {*Vigna radiata* (L.) Wilczek}. *Legume Research*, **26** (4): 248
- Reddy, Jayrami P. Rao, Narasimha Rao, D.V. and Suba. (2002). Effect of phenolic compounds growth and yield of mungbean. *Indian J. Pulses Res.*, **15** (2): 188-189.

- Rout, K. Mishra, T.K. Bastia, D.N. and Pradhan, B. (2010). Studies on heterosis for yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Research on Crops*, **11** (1): 87-90
- Sabaghpour, H. Moghddam, M. Grami, A. and Sadri, B. (1998). Path analysis of yield components in mungbean varieties of Iran. *3rd European conference on grain legumes Opportunities for high quality, healthy and added value crops to meet European demands Valladolid, Spain*, 14-19 November. 1998; 219.
- Sadiq, M.S. and Abbas, G. (2007). Selection indices for seed yield in mungbean. *International Journal of Biology and Biotechnology*, **4** (4) : 421-423.
- Saleem, M. Haris, W.A.A. and Malik, I.A. (1998). Inheritance of yellow mosaic virus in mungbean (*Vigna radiata* L. Wilczek). *Pakistan Journal of Phytopathology*, **10** (1): 30-32.
- Santha, S. and Veluswamy, P. (1999) .Heterosis in urdbean. *Indian Journal of Pulses Research*, **12** (2): 239-242.
- Sawale, V.S. Patil, J.V. Desmukh, R.B. and Kute, N.S.(2003). Heterosis and Inbreeding depression for yield and its components in Mungbean. *Legume Res.*, **26** (2): 134-136.
- Saxena, R.R.; Singh, P.K.; Saxena, R.R. (2007). Correlation and path analysis in mungbean cultivars (*Vigna radiata* (L.) Wilczek). *Journal of Interacademia*, **11** (2) : 143-148.
- Searle, S.R. (1965). The value of indirect selection. *Mass selection Biometrics*, **21**: 682-708.
- Senaiah, P. Satyanarayana, A. Naidu, N.V. Murthy, S.S.N. and Kodandaramaiah, D. (1993). Combining ability in urdbean [*Vigna mungo* (L) Hepper]. *Indian J. Puls. Res.*, **6** (1): 10-14.
- Sekhar, M.R. Reddy, K.R. and Reddy, C.R. (1994). Heterosis for yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Genetics and Plant Breeding*, **54** (1): 1-5.
- Shanmungasundaram, P. and Rangaswamy, S.R. (1994). Combining ability for yield and its components in black gram [*Vigna mungo* (L) Hepper] *Indian J. Genet.*, **54** (1): 6-9.
- Shantipriya, M. and Reddy, K.H.P. (2008). Character association and Path analysis in twenty one F₁ progenies of mungbean (*Vigna radiata* L.). *J. Res. NAGRAU*, **36** (1): 16-20.
- Shantipriya, M. and Reddy, K.H.P. (2008). Character association and Path analysis in twenty one F₁ progenies of mungbean (*Vigna radiata* L.) *J. Res. NAGRAU*, **36** (1): 16-20.

- Sharma, D.J. (1995). Path coefficient analysis of yield attributes in mungbean. *Advances in Plant Sciences*, **8** (1): 115-117
- Sharma, D.J. and Yadav, R.K. (1993). Heterosis and inbreeding depression in mungbean. *Indian Journal of Pulses Research*, **6** (2): 191-193
- Sharma, J.D. and Gupta, V.P. (1994). Selection parameters in inter-specific derivatives of urdbean x mungbean. *Indian Journal of Pulses Research*, **7** (2) : 174-176
- Sharma, R. N. (1999). Heritability and character association in non segregating populations of mungbean (*Vigna radiata* (L.) Wilczek). *Journal of Interacademia*, **3** (1): 5-10
- Sharma, R.N. (2000). Exploitation of heterosis in urdbean (*Vigna mungo* L. Hepper). *Journal of Interacademia*, **4** (1): 9-12
- Sharma, S.G. Narayan, R. Sangam, L. and Chaturvedi C. (1983). Role of phenolic compounds in Resistance of Maize to leaf blight caused by *Drechslera* State of *Cochliobolus Hetersterophus*. *Indian Phytopath*, **36** (1): 43-46.
- Shinde, N.V.; Deshmukh, R.B. (1989). Heterosis in urdbean. *Indian Journal of Pulses Research*, **2** (2) : 119-124
- Shrivastava, Anjali, Panday, R.L., and Sahu, Mayuri (2008). Correlation studies in parents and segregating populations of different crosses of field pea (*Pisum sativum* L.) *Legume Res.*, **31** (3): 157-163.
- Shukla, G.P. (1977). Studies on the inheritance of resistance to mungbean yellow Mosaic virus in green gram. Unpub. Ph.D. Thesis, G.B. Pant Univ. of Agric. and Tech., Pantnagar, India, pp. 1-47.
- Shukla, G.P. Pandya, B.P. and Singh, D.P. (1978). Inheritance of resistance to yellow Mosaic in mungbean. *Indian J. Genet.*, **38** : 358-360.
- Sirohi, A. Singh, A. and Bishnoi, S.S. (2000). Inheritance of mungbean yellow mosaic virus resistance in blackgram (*Vigna mungo*). *Crop Improvement*, **29** (2): 173-176
- Sirohi, S.P.S. Gaurav, S.S. Singh, S.P. and Yadav, R. (2008). Heterosis in mungbean (*Vigna radiata* L. Wilczek). *Progressive Research*, **3** (1): 35-37
- Singh, S.K. Singh, M.N. (2006). Inheritance of resistance to mungbean yellow mosaic virus in mungbean. *Indian Journal of Pulses Research*, **19** (1) : 21-23
- Singh, A. Sirohi, A. and Panwar, K.S. (1998). Inheritance of mung bean yellow mosaic virus resistance in urdbean (*Vigna mungo* (L.) Hepper). *Indian Journal of Virology*, **14** (1): 89-90
- Singh, A.B. (2001). Influence of Phenolic compounds on yield and protein quality of green gram (*Vigna radiata* L. Wilozek). *Leg. Res.*, **24** (4): 260-263.

- Singh, Gurdip and Bedi, P.S. (1975). Phenolic and sugar constituent of gram cultivars resistant and susceptible to *operaculla padwickii*. *Indian Phytopathology*, **29** .
- Singh, Inderjit Gill, M.S. and Bains, T.S. (2006). Generation mean analysis for yield attributing traits in mungbean [*Vigna radiata* (L) Wilczek]. *Indian Journal of Genetics and Plant Breeding*, **66** (1) : 47-48.
- Singh, Inderjit, Gill, M.S. Bains, T.S. and Brar, J.S. (2006). Genetic analysis of yield and other quantitative characters in mungbean. *Indian Journal of Pulses Research*, **19** (1) : 26-30.
- Singh, M. Sharma, S.K. Chahota, R.K. (2003). Heterosis in urdbean [*Vigna mungo* (L.) Hepper]. *Crop Research Hisar*, **26** (1) : 131-134.
- Singh, R.P. Pathak, M.M. (1992). Heterosis in mungbean (*Vigna radiata* (L.) Wilczek). *Agricultural Science Digest Karnal*, **12** (1): 4.
- Singh, S.B. and Singh, S.P. (2000). Study of correlation in segregating and non-segregating populations of mungbean (*Vigna radiata* (L.) Wilczek). *Applied Biological Research*, **2** (1/2): 111-112.
- Singh, S.K. Singh, I.P. Singh, B.B. and Singh, onkar (2009). Correlation and path coefficient studies for yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). *Legume Research*, **32** (3): 180-185.
- Singh, T. Sharma, A. and Alie, F.A. (2009). Morpho-physiological traits as selection criteria for yield improvement in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Research*, **32** (1): 36-40.
- Soehendi, R. and Srinives, P. (2005). Significance of heterosis and heterobeltiosis in an F₁ hybrid of mungbean (*Vigna radiata* (L.) Wilczek) for hybrid seed production. *SABRAO Journal of Breeding and Genetics*, **37** (2): 97-10
- Sohal, B.S. and Bajaj, K.L. (1993). Effects of yellow mosaic virus on polyphenol metabolism in resistant and susceptible mungbean (*Vigna radiata* L. Wilczek) leaves. *Biochemie und Physiologie der Pflanzen*, **188** (6): 419-423
- Srivastava, A. Lavanya, G.R. Pandey, R.K. and Rastogi, M.C. (2008). Association and cause and effect analysis in F₂ generation of mungbean (*Vigna radiata* (L.) Wilczek) . *Madras Agricultural Journal*, **95** (1/6): 195-199.
- Tomooka, N. Kashiwaba, K. Vaughan, D.A. Ishimoto, M. and Egawa, Y. (2000). The effectiveness of evaluating wild species: searching for sources of resistance to bruchid beetles in the *Vigna* genus subgenus *Ceratotropis*. *Euphytica*, **115** (1): 27-41.
- Tyagi, K. Tomer, K. Singh, V.K. and Nandan. R. (2006). Heterosis and inbreeding depression in mungbean [*Vigna radiata* (L.) Wilczek]. *Research on Crops*, **7** (2): 458-460.

- Venkateswarlu, O. (2001), Genetic variability in green gram [*Vigna radiata* (L) Wilczek]. *Legume Research*, **24** (1): 69-70.
- Verma, P. and Garg, D.K. (2007). Correlation and path coefficient studies in mungbean (*Vigna radiata* (L.) *Journal of Arid Legumes*, **4** (2) : 88-91.
- Vijaylaxmi Bhattacharya, A. (2006). Mung bean seed yield: III. Effect of yield attributing traits and phenology. *Legume Research*, **29** (1) : 11-17.
- Vikas ,Singh, S.P. and Tyagi, V.K. (1998). Phenotypic correlation in segregating and non-segregating populations of mungbean (*Vigna radiata* (L.) Wilczek). *Annals of Biology Ludhiana*, **14** (2) : 181-183.
- Vikas, Paroda, R.S. Singh, S.P. (1999). Phenotypic correlation and direct and indirect relation of component characters with seed yield in mungbean (*Vigna radiata* L. Wilczek) over environments. *Annals of Agricultural Research*, **20** (4): 411-417.
- Vyas, P Vishwakarma, D.N. and Singh, P.K. (2008). Heterosis and combining ability for grain yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *Progressive Research*, **3** (2) : 123-125.
- Waddington, C.H. and Robertson, E. (1966). Selection for development canalization. *Genet. Res.*, **7** : 303-312.
- Wright, S. (1992). Correlation and causation. *J. Agri. Res.*, **20**: 557-558.
- Yadav, G.C. Singh, P.K. Singh, B.B. and Verma, Ritu (2001). Genetic variability and path coefficients in urdbean. *Indian Journal of Pulses Research*, **14** (2): 143-144 .

