DISCUSSION
CHAPTER V

DISCUSSION

Mungbean or grean gram (*vigna radiata* (L.) Wilczek) has emerged as a highly important and popular pulse crop in India by virtue of possessing several agronomically and economically valuable characteristics. Mungbean is very rich in protien (25%) that is digestable, so it has ability to serve an important source of portein in the diet of predominantly vegetarian population of India. Mungbean plants are also utilized as nutrition green fodder for cattle and green manuring. Being a short duration crop it can be cultivated as a pure culture as well as mixed crop in different seasons, i.e. *Rabi*, *Zaid* and *Kharif*. In addition to its ability to improve soil fertility by fixing atmospheric nitrogen, mungbean is highly suitable for many types of cropping systems. Though cultivated on large area, this crop is characterized by very low productivity due to lack of high yielding varieties adapted to different seasons and due to poor agronomic conditions such as mixed culture and stress environments. The identification of donor parents for important characters, assesment of genetic variation in the available germplasm, knowledge of genotype X environment interaction and stability of genotypes and the information about character associations are required for divising a succesful breeding programme. Keeping this in view, the present investigation has been undertaken to obtain information on genetic variation in the germplasm collection, genotype x environmental
interaction and stability, direct and indirect Selection parameters and, genetic divergence for yield and yield components in mungbean.

Considering the above aspects, the present investigation was undertaken i), to evaluate germplasm for important characters in relation to their suitability to different environments (ii) to assess the extent of variability, heritability genetic advance for various characters (iii) to estimate correlation coefficients among different characters (iv) to study the direct and indirect effects of yield component on seed yield by path coefficient analysis (v) to examine genetic divergence existing in the germplasm collections (vi) to understand the role of genotypes x environmental interactions in expression of various character and stability of genotypes.

In present study, 80 genotypes of mungbean germplasm collections, showing wide spectrum of variation for various characters, were evaluated during Kharif 1999. Zaid and kharif 2000. The characters studied were days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, clusters per plant, pods per cluster, pods per plant, seeds per pod, 100-seed weight, biological yield per plant, seed yield per plant and harvest index (%).

The pooled analysis of variance revealed significant differences among the environments, replications in environment, environment x replication, treatments (genotypes) and environment x treatment (genotypes) of almost all the characters which validated further statistical and genetical analysis (Table 4.2).

5.1 Coefficient of variation

The genetic variability is the raw material of plant breeding
industry on which selection acts to evolve superior genotypes. Thus, higher the amount of variation present for a character in the breeding materials, greater is the scope for its improvement through selection.

The genotypic, phenotypic and environmental coefficients of variation were computed to assess the existing variability in the germplasm (Table 4.5). The high magnitude of coefficient of variation at genotypic as well as phenotypic level was observed only for pods/plant. This indicated possibility of obtaining very higher selection response in respect of pods/plant. The high estimates of PCV and GCV for pods/plant was also reported earlier (Sawarker, 1978; Natarajan et al, 1988; Malik and Singh, 1991; Sharma et al, 1996; Byregowada et al, 1997; Das and Charkaborty, et al. 1998:) The high estimate of PCV with moderate GCV was recorded for clusters/plant, seed yield/plant and pods/cluster. The occurrence of high PCV with moderate GCV values for the three characters mentioned above reveals reasonable scope of improvement through selection. However, the existence of low value of GCV along with moderate PCV estimate for harvest index, biological yield/plant, primary branches/plant, plant height and 100-seed weight. It suggest that these traits are likely to show less response under selection. The low estimates of PCV as well as GCV found for seeds/pod, day to maturity and days to 50% flowering indicated that their was very lettle scope of improvent in these three character through direct selection due to apparent lack of variability. The low or moderate estimates of PCV and GCV for the characters mentioned above have also been reported by Pundir et al. (1992) and Sharma et al. (1996).
In respect of environmental coefficient of variation, the high order estimates were recorded for pods per plant, clusters per plant and seed yield per plant indicating thereby substantial role of environmental factors in their performance. Harvest index, biological yield per plant, pods per cluster, primary branches per plant and plant height showed moderate estimates of environmental coefficient of variation. The ECV estimates for above mentioned characters reveal considerable influence of environment in the expression of these traits. Rest of the characters viz, 100-seed weight, seeds/pod, and days to 50% flowering showed low ECV estimates representing lesser role of environment in expression of these traits.

5.2 Heritability and genetic advance.

Heritability estimate provides the assessment of amount of transmissible genetic variability to total variability and happens to be most important basic factor that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. The parameter, genetic advance in per cent of mean (Ga) is a more reliable index for understanding the effectiveness of selection in improving the traits because its estimate is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, heritability and genetic advance in per cent of mean, in combination, provide more clear pecture regarding the effectiveness
of selection for improving the plant characters.

Pods/plant, seed yield/plant, clusters/plant and pods/cluster exhibited moderate heritability and high estimate of genetic advance in per cent of mean along with high PCV and moderate GCV values. These four traits possessing very high genetic advance and phenotypic coefficient of variation PCV in combination moderate estimate of heritability and GCV appear suitable traits for improvement through selection due to their high variability and transmissibility. Thus the four characters mentioned above are likely to show high response to selection practised in the breeding populations involving the germplasm collections evaluated under present investigation.

The occurrence of high estimates of Ga with moderate PCV and heritability and low GCV for harvest index, biological yield/plant, 100-seed weight, primary branches/plant, and plant height indicated that these characters may also provide considerable response to selection owing to their moderate transmissibility and variability. Moderate Ga and h² estimates in combination with low PCV & GCV values were recorded for days to 50% flowering, days to maturity and seeds/pod except high Ga noted for seeds/pods. The moderate transmissibility with low genetic variation observed for above these three characters suggested that their is little scope of improvement through selection following the breeding efforts based on the germplasm lines evaluated.

5.3 Correlations

The seed yield or economic yield, in almost all the crops, is referred to as super character which results from multiplicative
interaction of several other characters that are termed as yield components. Thus, genetic architecture of grain yield in mungbean as well as other crops, is based on the balance or over all net effect produced by various yield components directly or indirectly by interacting with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient breeding strategy for evolving high yielding variety. In this respect, the correlation coefficient which provides symmetrical measurement of degree of association between two variables or characters, helps us in understanding the nature and magnitude of association among yield and yield components.

The genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficients in the experiment. However, genotypic correlation were larger in magnitude than the corresponding phenotypic values. Sawarker (1978) has also reported higher estimates of genotypic correlations than the corresponding phenotypic correlations between yield and yield components in mungbean.

In the present study, a very strong positive association of seed yield per plant was observed at genotypic, phenotypic and environmental level with biological yield/plant and harvest index. Thus biological yield per plant and harvest index emerged as most important associates of seed yield in mungbean. The available
literature has also indicated positive correlations between seed yield and the characters mentioned above in mungbean (Sawarkar, 1978; Choudhary, 1985; Singh et al., 1988; Lakshmaiah et al., 1989; Satyan et al., 1989; Pundir et al., 1992; Singh and Pathak, 1993; Sharma and Talukdar, 1996). However, seed yield showed nonsignificant phenotypic and environmental correlation along with low values of genotypic correlation with remaining nine characters except significant positive environmental correlation with clusters/plant and pods/plant and high order negative genotypic correlation with days to 50% flowering. The lack of association between yield and most of the yield components under study is contrary to reports of earlier workers indicating strong positive association of seed yield with most of the yield components studied. (Singh, et al., 1988; Lakshmaish, et al., 1989, Satyan, et al., 1989; Pundir, et al.; 1992; Sharma and Gupta, 1994; Sarma and Talukdar, 1996; Yaquob et al.; 1997, Naizi et al.; 1999.)

The existence of nonsignificant correlations of yield with most of the yield components in present study may be attributed to highly diverse nature of germplasm and environments used in the present study. Since the nature and magnitude of associations are reported to change with change in materials and environments, it is likely that contrasting nature of associations across genotypes and environments might have played a crucial role in cancelling one and another leading to low or non-significant estimates of correlations.

Primary branches/plant, clusters/plant pods/cluster and pods/plant were found to be positively associated at genotypic, phenotypic
and environmental levels baring non significant correlation between primary branches/plant at environmental level. The strong positive association among the four characters mentioned above, signifies a favourable situation. Thus, selection practised for improving these traits individually or simultaneously is likely to bring improvement in other due to correlated response. This suggests that selection would be quite efficient in improving such yield components in mungbean, especially in context of the germplasni collections evaluated. Positive correlation among the yield components, such as those above, have also been reported previous workers. (Chaudhary, 1985; Singh, et al.; 1988; Pundir et al.; 1992; Byregowda et al.; 1997)

The significant positive correlation at phenotypic, genotypic were also observed between pods/cluster and seeds/pod and between pods/plant and harvest index was also found. In addition, days to 50% flowering had positive association with days to maturity at phenotypic and genotypic level. Such association between flowering and maturity duration looks logical. However, the correlations of days to 50% flowering and days to maturity with yield and other yield component under study were found to be non significant barring positive and significant environmental correlation between seeds/pods and day to 50% flowering. The lack to positive and significant association of flowering and maturity duration with yield and yield component suggests that there is good possibility of combining early flowering and maturity with high mean performance for yield and yield component for developing early maturing high
yielding varieties using the germplasm material evaluated in present study.

In order to take care of occurrence of negative as well as positive correlations between important yield components, reasonable compromise is required for attaining their proper balance for maximum combined contribution towards manifestation of seed yield. The phenotypic and genotypic correlation coefficients between important yield components were either positively significant or nonsignificant, barring a few high order negative genotypic or environmental correlations. This reveals a less complex situation in attaining a proper balance between yield and its important components in context of mungbean germplasm used in present study as compared to complexities that arise due to existence of strong negative and positive associations between various characters in this as well as in many other crops. Most of the correlation coefficients obtained in present study are in conformity with previous reports in mungbean (Choudhary, 1985; Natarajan and Palanisamy, 1988 and Pundir et al., 1992).

5.4 Path coefficient analysis.

Path coefficient analysis is a biometrical tool to partition the observed correlation coefficient into direct and indirect effects of yield components on seed yield to provide more clear picture of character associations for formulating efficient selection strategy. Path analysis differs from simple correlations in that it points out the causes and their relative importance where as, the latter measures simply
the mutual associations ignoring the causation.

In the present study, the path coefficient analysis was carried out at phenotypic as well as genotypic level (Table 4.8). Biological yield per plant was the only character which exerted high order positive direct effects on seed yield per plant at phenotypic as well as genotypic level. Thus, biological yield per plant emerged as most important direct yield contributing trait in present study. Sharma and Gupta, (1994) have also identified biological yield as most important direct yield component.

The direct effects of remaining characters on seed yield at phenotypic level were not consistent in nature to corresponding direct effects at genotypic level. In phenotypic path analysis harvest index showed high order positive direct effect on seed yield while its direct effect at genotypic level was considerably negative. At genotypic level, clusters per plant, 100-seed weight, seeds per pod and days to 50% flowering exhibited high order positive direct effects on seed yield but their direct effects at phenotypic level were very low order positive in nature except days to 50% flowering which had low negative value. Thus, clusters per plant, 100-seed weight and seeds per pod also appeared as important direct yield components at least at genotypic level. These characters were identified as important yield components earlier. (Chaudhary, 1985; Nafade, 1988; Patil and Deshmukh, 1988; Sharma and Gupta, 1994; Byregowda et al.; 1997)

Clusters per plant and pods per plant exerted considerable
positive indirect effects at phenotypic level on seed yield via harvest index. Negative indirect effects at phenotypic level on seed yield via harvest index were exhibited by days to 50% flowering and plant height which also had considerable positive effects on seed yield via biological yield.

At genotypic level, primary branches per plant, pods per cluster, pods per plant, seeds per pod and harvest index exerted high order positive indirect effects on seed yield via clusters per plant while their indirect effects via pods per plant were high order negative. In contrast, indirect effects of days to 50% flowering and days to maturity were high order positive via pods per plant and high order negative via clusters per plant. Similarly, all the eleven characters showed contrasting positive and negative indirect effects on seed yield via one or another characters at genotypic level. Harvest index recorded positive indirect effects via plant height and biological yield per plant and negative indirect effects via days to 50% flowering on seed yield per plant. Biological yield per plant had considerable positive and negative indirect effects on seed yield via pods per plant and plant height, respectively. Days to 50% flowering days to maturity and primary branches per plant showed high order negative indirect effects on seed yield via plant height. Days to maturity and primary branches per plant via days to 50% flowering and plant height and primary branches via biological yield also had substantial positive effects on seed yield.

Considering the indirect path effects at phenotypic and
genotypic level, as described above, clusters per plant and pods per plant appeared as important indirect components at genotypic as well as phenotypic level. At genotypic level, primary branches per plant, seeds per pod, biological yield and harvest index also emerged as important indirect contributors despite having negative indirect effects via some other characters.

In overall consideration of results of phenotypic and genotypic path analysis, it may be concluded broadly that biological yield per plant followed by clusters per plant, 100-seed weight and seeds per pod emerged as most important direct yield contributor. Biological yield, clusters per plant and seeds per pod also identified themselves as important indirect yield components. Primary branches per plant, pods per plant and harvest-index were other characters which were also indicated as important indirect components of seed yield per plant.

At phenotypic level, most of the substantial estimates of direct and indirect effects of important yield components were positive except negative indirect effects of days to 50% flowering and plant height via harvest index. The genotypic and phenotypic correlations among the majority of characters studied were also significantly positive. The above observations indicate that the character associations and cause and effect inter-relationships in respect of the yield and its components were not complex. However, results of path analysis using genotypic correlations exhibited several high order direct and indirect effects of yield components in negative
direction which were contrary to substantial positive indirect effects at phenotypic level. This suggests that inter-relationships and direct and indirect effects among various characters were much more complex than that inferred from the results of genotypic and phenotypic correlations and path analysis at phenotypic level. Hence, for deeper insight in underlining inter relationships between various characters of mungbean, the path analysis at genotypic level appears more informative.

The above discussions also reveals the fact that important direct and indirect components such as, biological yield, harvest-index, pods per plant and clusters per plant as well as all other characters under study, exhibited substantial positive effects via some characters along with considerable negative effects of some other characters. The occurrence of negative as well as positive indirect effects by yield components on seed yield via one or other characters simultaneously, presents a complex situation where a compromise is required to attain a proper balance of different yield components for determining the ideotype for high seed yield in mungbean.

5.5 Genetic divergence.

The parental diversity in optimum magnitude is required to obtained superior genotypes in the segregating generations (Moll et al. 1962). Furthermore, the evaluation of data obtained on any germplasm collections represents many duplicate accessions. These objects, although desirable genetically, create a difficult task in recognition from data tables. Such duplicate accessions which differ
from each other in one or two characters significantly pose a difficult situation for resolving distinct types. Thus, for characterization of germplasm for genetic diversity, the genetic divergence analysis is very useful as it provides classification of materials in to different homogeneous groups. Mahalanobis' D² statistic, recognised as a very effective method of assessment of genetic divergence since long has been widely used for analysis of genetic diversity in mungbean as well as in many other crops (Mehndiratta and Singh 1971; Sindhu et al., 1984; Chandra et al., 1993; Sharma et al., 1996; and Raje and Rao, 2001).

In the present study, eighty genotypes of mungbean were grouped into eleven distinct non-overlapping clusters using Mahalanobis' D² statistic. This indicated that considerable diversity existed in the germplasm collections evaluated in the present study (Table 4.9) which is in agreement with earlier reports indicating substantial diversity in mungbean material (Natarajan et al. 1988; Gupta and Singh 1989; Naidu and Satyanarayana, 1991; Chandra et al., 1993 and Sharma et al., 1996; and Raje and Rao, 2001).

Clusters I, had 38 genotypes which were characterized by low mean performance for plant height, primary branches/plant, biological yield/plant and seed yield/plant along with medium performance for rest of the characters. Cluster II, comprising 16 entries, was also characterized by low means for plant height, primary branches/plant, biological yield/plant and harvest index in combination with medium mean for remaining characters. The eleven genotypes present in
remaining characters barring very low means for seed yield/plant and biological yield/plant. Highest cluster means for days to maturity, plant height, and primary branches/plant along with lowest means for pods/cluster and second lowest mean for 100-seed weight were recorded for cluster X, which had low to medium performance for remaining characters. Cluster XI, containing VL 363 had lowest cluster means for days to 50% flowering, primary branches/plant seeds/pod and biological yield/plant. Cluster XI showed low means for rest of the character except medium means for pods/plant, 100-seed weight and harvest index. The above discussion clearly underlines that different clusters showed wide variation from one another in respect of cluster means. This indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The above observation confirms that the Mahalanobis $D^2$ statistic is an efficient tool for classification of genotypes on the basis of genetic divergence as emphasized by earlier workers (Mehndiratta and Singh, 1971; Sindhu et al., 1989; Natarajan and Palanisamy, 1990; Holkar and Yadava, 1995).

The major clusters in the aforesaid genetic divergence analysis contained frequently the genotypes of heterogeneous origin (Table 4.9). Although, the genotypes of same origin or geographic region were also found to be grouped together in same cluster, the instances of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This suggests that there is no parallelism between genetic and geographic diversity. Therefore,
the selection of parental material for hybridization programme simply based on geographic diversity may not be a successful exercise. The choice of suitable diverse parents selected on the basis of genetic divergence analysis would be more rewarding than the choice made on the basis of geographic diversity. This finding is in agreement with the reports of Gupta and Singh (1970), Natarajan et al. (1988) Naidu Satyanarayana (1991) and Raje and Rao, (2001) advocating lack to definite relationship between genetic and geographic diversity in mungbean.

An examination of the estimates of within and between cluster genetic diversity presented by intra and inter cluster D^2 values revealed that genotypes of the same cluster had little divergence from each other with respect to aggregate effect of twelve characters under study (Table 4.10). Therefore, the chances of obtaining good recombinants in segregating generations by crossing the members of the same cluster are very low. It is, therefore, suggested that crosses should be attempted between the genotypes belonging to clusters separated by large inter-cluster distances. In this respect, the highest inter-cluster distance was observed between cluster VII and IX, followed the inter-cluster distance recorded between IX and X. The inter-cluster D^2 values between cluster VIII and IX and cluster VI and XI were also very high. High inter cluster distance were also noted between cluster VI and IX, cluster VI and VII and cluster VI and X. Thus, the crossing between the genotypes belonging to clusters pairs seperated by very higher inter-cluster distances, as mentioned above
may throw desirable transgressive segregates. The lowest inter-cluster distance was observed between cluster I and II, followed by cluster I and III, cluster I and IV, cluster III and V and cluster I and VI, which indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter-cluster distances are unlikely to throw promising recombinants in the segregating generations. Gupta and Singh (1970), Ramanujam et al. (1974), Natarajan and Palanisamy (1990), Sharma et al. (1996); and Raje and Rao, (2001) also proposed hybridization between lines belonging to clusters separated by large inter-cluster distances in mungbean.

The 100-seed weight followed by seeds/pod exhibited highest contribution towards total genetic divergence (Table 4.12). Days to 50% flowering, plant height, pods/cluster, days to maturity and biological yield/plant also played considerable role in determining the clustering pattern and overall genetic diversity. The earlier reports of genetic divergence studies in mungbean have also identified high contribution of 100-seed weight.

Primary branches/plant, clusters/plant and seed yield/plant played little role in group constellations while contribution of rest of the characters, viz., harvest index and pods/plant in conditioning the genetic divergence was almost negligible.

A perusal of Table 4.12, reveals that considerable differences existed between different clusters in respect to intra-cluster group means for twelve characters. The crossing between entries belonging
to cluster pairs separated by large inter-cluster distances and having high cluster means for one or other clusters to be improved is likely to be more traitful. Thus, during the selection of parent, the advantage of characters that played greater role in group constellations and the cluster pairs showing higher inter-cluster distances could be considered according to the objectives.

5.6 Stability analysis

A specific genotype may not exhibit the same phenotype characteristics under all the environments, and different genotypes respond differently to different environments. One of the major objectives in any plant breeding programme is, therefore, to develop stable varieties so that effects of environment on yield can be minimized. Allard and Bradshaw (1964) opined that a variety may achieve stability either through individual buffering or population buffering. The importance of G x E interaction in mungbean has been recognised by several workers.

The initial attempts to scale out G x E interaction were based on conventional analysis of variance technique (Sprague and Federer, 1951) and univariate stability parameters. These method, however, do not provide precise information on adaptation responses of individual genotypes. The regression analysis originally suggested by Yates and Cochran (1938) and developed by Finley and Wilkinson (1963), Eberhart and Russell (1966), Perkins and Jinks (1968, b) and Freeman and Perkins (1971), has been extensively used for characterizing the genotypic responses.
Eberhart and Russell's model (1966), based on regression of mean performances on environmental index, has been extensively used in mungbean. The analysis of variance for three environments individually, revealed significant differences among the genotypes for all the characters under study except pods/cluster in E1 with those E2 & E3 primary branches/plant in E2 and E3 and 100-seed weight in all the three environments. The pooled analysis of variance across three environments also showed significant differences among the genotypes for all the characters except days to 50% flowering and biological yield/plant. The results of individual as well as pooled analysis of variance indicated presence of substantial genetic variability among 80 genotypes for most of the characters under study. Pooled analysis also indicated significant variation among the environments and their influences on the expression of all the twelve characters as mean squares due to Environmental (Linear) component were significant in all cases. Significant mean squares due to genotype x environment (GxE) interaction for all the characters revealed that the genotypes interacted considerably with environmental conditions that existed in different environments. Important role of environment and genotype x environment interactions in expression of different characters in mungbean has also been reported by Naidu et al. (1991), Gill et al. (1995); Patil and Narkhede (1995); Renganayaki (1995), Godawat and Choudhary (1996), Manivannan et al. (1996) Singh and Nanda (1997) and Manivannan (1999).

Both linear and non-linear components of GxE interaction
were significant for primary branches/plant, 100-seed weight and seed yield/plant which suggested that GxE interaction was shared by both predictable and non predictable components. However, linear component was higher than the non-linear portion of the GxE interaction for these three traits. The linear component was significant against the pooled deviation, which indicated that a large portion of GxE interaction was accounted for by the linear regression although non-linear component (pooled deviation) was also found significant. The predominance of linear component noticed would help in predicting the performance of the genotypes across environments.

The significance of only linear component of GxE interaction in case of days to maturity, primary clusters/plant, pods/cluster, and seeds/pod suggested that these traits were mainly under control of predictable component of GxE interaction and performance of genotype across environments can be reasonably predicted. The pooled deviation or non-linear component of GxE interaction was significant for days to 50% flowering, plant height, pods/plant, biological yield/plant, and harvest index, indicating their by importance of non-linear functions which makes predictions of performance of genotypes very difficult. The results of the pooled analysis obtained in the present study are broadly in agreement with findings of the earlier workers (Aquilar and Villareal, 1989; Pathak et al., 1990; Malik and Singh 1991; Naidu et al., 1991; Gill et al., 1995; Ranganayaki, 1995; Godawat and Choudhary, 1996; Manivannan, 1996, Singh and Nanda; 1997).

The grain yield of mungbean fluctuates considerably with the
change in environmental conditions. Hence, a variety possessing reasonable stability for grain yield is desirable. Different measures of stability have been used by various workers. Finly and Wilkinson (1963) considered linear regression as a measure of stability, where as Eberhart and Russell (1966) emphasized that both linear ($S^2_{di}$) and non-linear ($S^2_{di}$) components of genotype x environment interaction should be considered while judging the phenotypic stability of a genotype. The linear regression ($b_l$) is simply regarded as measure of response of a particular genotype, whereas, deviation from regression ($S^2_{di}$) should be considered as measure of stability. Accordingly, the mean ($x$) and deviation from regression ($S^2_{di}$) of each genotype were considered for stability and linear regression ($b_l$) was used for testing the varietal response. The genotypes with lowest or non-significant $S^2_{di}$ are the most stable and vice-versa. The three parameters $X$, $b_l$ and $S^2_{di}$ together provide an idea of adaptability of genotypes across the environments. A variety with unit regression coefficient ($b_l=1$) and the deviation from regression not significantly different from zero ($S^2_{di}=0$) is said to be stable one.

5.6.1 Mean performance of genotypes.

The pooled mean performance of 80 mung bean genotypes for 12 characters across three environments is presented in Table 4.14.

The entry, WOGHALI- produced highest seed yield (20.42g) and significantly outyield the general mean for seed yield. It was present in top nonsignificant group for seed yield per plant, days to 50% flowering, plant height, primary branches per plant and
biological yield/plant. Among the five entries present in top non significant group of higher seed yield per plant DMG 1048, which ranked second (16.74g) behind WOGHALI in seed yield, was found in top-non significant group for days to 50% flowering, primary branches/plant, clusters/plant, pods/plant and harvest index besides showing above average mean performance for 100-seed weight. EC-319035 (16.72g), which ranked third highest in seed yield, emerged in top-non-significant group for high performance in case of days to 50% flowering, day to maturity clusters/plant and harvest index. The forth ranking genotype, LAGGOAN, showed very high mean performance for primary branches/plant biological yield and harvest index besides having above average performance for pods per cluster.

The fifth ranking yielder, ROJON (15.66g) appeared in top non significant for days to 50% flowering and harvest index.

The genotypes mentioned above may serve as promising parents/donors for seed yield and other characters for which they showed high performance. Similarly, some other genotypes showing very high mean performance for other characters can be used as donors for improving those characters in a component breeding approach even if they have medium or low seed yield. In this respect the genotypes exhibiting highest mean performance for different characters such as VL-363 and LM-484 for days to 50 flowering, DMG-1058 and STV-2696 for days to maturity, LM-303 and DMG-1080 for plant height, LM-285 and STV-2613 for primary branches/plant, M-45 and LM-484 for clusters/plant, Pusa Bold and LM-522 for pods/clusters,
Pusa Bold and STV-2836 for pods/plant, EC-30401 and PAYAR for seeds/pods, LM-1 and CHIKKHALI for 100-seed weight, P-342 and LM-43-1 for biological yield/plant, STV-2691 and PIM-531 for harvest index, may be mentioned as a few lines for their genetic worth and used in hybridization programme. These lines maybe useful for improving the characters for which they showed high mean performance, in a breeding programme based on component breeding approach.

5.6.2 Stability Parameters

The stability parameter analysis revealed that the four lines, namely, VL 363, LM 484, EC 3194.04 and DMG 1121-1, were highly stable for days to 50% flowering as they possessed bi=1 or <1 and S^2di=0. The line LM-1 had negative bi value. Even though its performance could not be predicted over the environments because the value of S^2di was more than zero. The nonlinear component of G X E. interaction was higher than zero, in case of the lines, namely, LM 527, STV 2779, STV 2768, DMG-1082, STV-2753, DMG-1084, STV-2695, DMG-1080, PHULAN, EC-319035, V-4619, STV-2610, DMG-1048 and DMG-1060 due to which the performance of these lines for days to 50% flowering could not be predicted over the environments.

Most of the lines exhibited non-significant values for the linear and non linear components of the GxE interaction for days to maturity, therefore, it may be suggested that the performance of the lines for this trait may be predicted over the environments. The three lines viz, LM-484, STV-2779 and VL 363 possessed bi=1 and S^2di=0.
hence these lines were most stable over the environments for days to maturity.

The observations on stability parameters revealed that the non linear component of GxE interactions was significant for plant height for most of the lines, therefore, the performance of most of lines, is not predictable. The most stable genotypes for this characters were P-342, LM-303 and CHOLDEV as the, showed $bi=1$ and $S^2di=0$. The line, DMG-1082 was also stable with negative $bi$ values. The five genotypes, LM 484, DMG-1111, LM-351, DMG-1082 and LM-335 were found to possessed $bi>1$ hence their performance is predictable in the varying environments for plants heights.

From the analysis of stability parameters it could be observed that the non linear component of GxE interaction was grater than zero for primary branches/plant in the lines, namely, LM-484, WOGHOLI, P-280, D-45-6, UPM-58, Pusa Bold, TAP-7, LM-303, LM-23, STV-2613, LM-313 and DMG-1060 indicating the unpredicatability of the performance of these lines over the varying environments. Six genotypes viz, STV-2696, DMG-1133-1, LM-335, STV-2626, V-4626 and LM-126 possessed the high values of linear component of GxE interaction, therefore, performance of these lines can be predicted over the varying environments. Only one genotype, LM-285 could be identified as most stable for primary branches per plant over the environments. Allthough the lines viz, Pusa Bold, LM-303 and STV-2613 were among the best lines even though their performance is not predictable because of the high values of non linear component
of GxExE interaction for number of primary branches plant.

The analysed stability parameters indicated that the most stable line for clusters/plant was STV-2691 which possessed bi=1 and S²di=0. The lines viz. M-45, LM-484, P342, STV-2626, STV-2613, STV-2836 and DMG-1065-1 exhibited the higher than one linear components of GxExE interaction which indicated that the performance of these lines are predictable for clusters/plant in varying environments. The non linear component of GxExE interaction was non significant for most of the lines for this trait.

The analysis of stability parameters for pods/cluster indicated that the linear components of GxExE interaction was significant for the lines viz, VL-113, DMG-1111, DMG-1058, LM-522, ROJON, EC-319404, UPM-58, LM-387, Pusa Bold-1, LM-23, LM-344, PIM-3, STV-2836, NDM-1, V-460, LM-46-1, VL-363 and LM-1. Therefore, it may be suggested that the performance of those eighteen lines is predictable in the varying environments. The three genotypes namely DMG-1065-1, LM-197 and PIM-531 were observed as most stable as they exhibited bi=1 and S²di=0. The significant value of non linear component of GxExE interaction made it impossible to predict the performance of LM-387 for pods/cluster.

The analysis of stability parameters indicated that linear components of GxExE interaction was non-significant for most of the genotypes for pods/plant. The non linear component of GxExE interactions was significant for pods/plant for 8 genotypes viz., LM-522, DMG-1081, ROJON, LM-285, LM-387, Pusa Bold, STV-2836 and
VL 363 which indicated that the performance of these lines is unpredictable in the varying environments. The linear responses of 72 genotypes were equal to unity, therefore, it may be suggested that these genotypes do not respond to the varying environments. Out of 80 genotypes studied for this character, nine namely, M-45, LM-484, P-342, DMG-1052, STV-2691, EC-319404, STV-2613, V-4620 and PIM 531 were highly stable genotypes. From the analysis of parameters of stability it was recorded that the linear component of GxE interaction was significant for seeds/pod for the lines viz., VL-113, LM-484, STV-2779, IC-20305, DMG-1081, EC-30401, PAYAR, D-45-6, EC-319404, STV-2785, TAP-7, PDM-55-1-6, MAIGAW, LM-344, ST-2626, PIM-3, STV-2836, DMG-1084, CHIKKHALI, PIM-646 and VL-363 therefore it may be concluded that the performance of these lines may be predicted in the varying environments. The non-linear component of all the genotypes for this trait was non-significant.

Five entries with above average performance namely DMG-1111, T-1-2-2, STV-2696, UPM-58 and Pusa Bold were observed as the most stable genotypes for seeds/pod as they possessed $b_i=1$ and $S^2d_i=0$.

The analysis of stability parameters for 100 seed weight, revealed that the linear sensitivity coefficients of 8 genotypes namely, DMG-1081, STV-2691, LM-387, DMG-1082, LM-23, STV-2613, Langon and ML-126, was significant which indicated that the performance of these genotypes is unpredictable in the varying environments. The genotype DMG-1084 was observed as highly stable for 100-seed
weight. In the varying environments the entries viz, EC-3040000, STV-2756 and LM-531 with $bi > 1$ (non-significant) and $S^d_1=0$ were also stable. The linear component of the genotypes, namely, LM-527, DMG-1080, T-1-2-2, LM-285, PAYAR-D-45-6, EC-319404, LM-387, STV-2785, STV-2684, EC-304000, TAP-7, PIM-3, STV-2756, NDM-1, STV-2753, LM-43-1, PIM-53-1 and PIM 46-4, was significant indicating that the performances of these genotypes are predictable for 100 seed weight in varying environments.

The analysis of stability parameters for biological yield/plants that indicated the non linear component of GxE interaction was highly significant for the genotypes namely. STV-2695, WOGHOLI, P-593, DMG-1081, EC-319035, ROJON, STV-2691, D-45-6, STV-2710, LM-387, Pusa Bold, DMG-1133-1, STV-2684, MAGAW, LM-23, NDM-1, LM-12, DMG-1084, CHIKKHALI, LM-1, PIM-6 and LAGGOAN. Therefore, it may be suggested that the performance of these genotypes is unpredictable in the varying environments. The genotype, LM-527, possessed significant linear component of GxE interaction. Out of 80 lines, none of the line was observed as stable for biological yield/plant which might be due to the dependence of this character on different yield traits.

From the analysis of stability parameters for seed yield/plant it was observed that non linear component of GXE interaction was significant for genotypes, namely, LM-527, P-342, DMG-1052, EC-319035, ROJON, DMG-1048 CHIKKHALI and LAGGOAN which suggested that the performance of these entries can not be predicted
in the varying environments. Out of 80 entries evaluated for seed yield/plant only one genotype, PM-280 could be identified that most stable. Since seed yield/plant is a very complex character and it depends upon so many components, therefore, it is very difficult to get a highly stable genotype for this trait.

From the analysis of stability parameters for harvest index it is evident that 8 genotypes viz., LM-484, LM-527, STV-2695, DMG-1081, DMG-1052, PDM-43-143, PIM-6 and LM-126, possessed highly significant values of non linear component of GxE interaction, therefore it may be concluded that the performance of these genotype can not be predicated in the varying environments for this trait. The most stable genotype indentified for this character was T-1-2-2 as it posessed bi=1 and S^2di=0 with low average mean performance. Here in the case of this character again two component characters (biological yield/plants and seed yeild/plant ) are responsible for the stability of the genotype. Therefore, it is easy to get the genotypes stable for this trait.

The over all result of the stability analysis indicated that none of the genotypes was stable for more than two character at a time. The genotypes stable for two characters were, VL-363 for days to 50% flowering and maturity, LM-484 for days to 50% flowering and days to maturity, EC-319404 for days to 50% flowering and pods/plant, P-342 for plant height and pods/plant, STV-2691 for clusters/plant and pods/plant, PIM-531 for pods/cluster and pods/plant. The lines which showed stability for two traits may be used in hybridization
programme for developing the new recombinants which may possess stability for more than two characters under study.