Chapter - 7

Summary and conclusion
7. SUMMARY AND CONCLUSION

7.1. SUMMARY

Grain legumes, commonly known as pulses, are nutritionally richer in protein and thus make an important component of the vegetarian diet. In addition to high protein content, it has the ability to fix atmospheric nitrogen in soil through root nodules. Pulses occupy a unique position in Indian agriculture but the productivity of the crop has remained more or less static as compared to cereal. Therefore, boosting up of yield trend becomes major objective of all the pulse improvement programmes. For achieving this objective, different approaches have been followed by research workers, of which the most important one is to breed high yielding varieties through various breeding programmes namely hybridization and selection.

Among pulses, blackgram \([Vigna mungo (L) Hepper]\) occupies third position in India. Likewise in Assam, blackgram has a significant importance in terms of area, production and popularity. In Assam, productivity of blackgram is found to be very low and major improvement is to be made to meet the need of the population.

The present investigation was undertaken to study the combining ability variances and effects for yield and yield attributing characters and to select superior plant types in the later generations in terms of yield and protein content.

Six parents of blackgram viz, PU-19, T-9, KU-3, KU-40, KU-49 and SB-121 were crossed in all possible combinations excluding their reciprocals in the experimental field of the Department of Botany, Gauhati University, Assam. There were a total of fifteen cross combinations. The different cross combinations were PU-19×T-9, PU-19×KU-3, PU-19×KU-40, PU-19×KU-49, PU-19×SB-121, T-9×KU-3, T-9×KU-40, T-9×KU-49, T-9×SB-121, KU-3×KU-40, KU-3×KU-49,
KU-3×SB-121, KU-40×KU-49, KU-40×SB-121 and KU-49×SB-121. These 15 hybrids (F₁) were grown along with their parents and one high yielding variety PU-30 as the check during Kharif (Aug. – Nov.) of 2004. The experiment was conducted in a Randomised Block Design (RBD) with three replications. Studies were made for the combining ability of the yield attributing characters as well as for the heterosis effects. The characters considered for this purpose were (i) Plant height (ii) Number of primary branches (iii) Pods per plant (iv) Number of seeds per pod (v) Pod length (vi) Yield per plant (vii) 100-seed weight (viii) Days to 50% flowering and (ix) Days to maturity. Besides seed yield per plant, observations were recorded for all the characters under consideration. For combining ability analysis data were analysed by following Griffing Method-2, Model- I. (Griffing, 1956).

The general combining ability (GCA) and specific combining ability (SCA) variance were significant for all the characters except for number of branches and days to maturity which indicates the role of both additive and non-additive types of variance in the inheritance of these characters. The characters pod length, number of seeds per pod and days to flowering were equally governed by additive as well as non-additive genetic system. The yield per plant and days to maturity were influenced by non-additive gene action while plant height, number of pods and seed weight indicate the predominance of additive gene action in inheritance of the concerned characters.

The parent T-9 was found to be the good general combiner for early flowering. The parent KU-3 was observed to be good combiner for tallness and number of pods. T-9, KU-40 and SB-121 were found to be the good general combiner for yield per plant. There was no good combiner for the characters number of branches, pod length, number of seeds and 100-seed weight. In the present study, none of the crosses was
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found to be the good specific combiner for all the characters collectively. The cross KU-40×KU-49 showed significant SCA effect for earliness in maturity. The cross KU-3×SB-121 was found to be the good specific combiner for dwarfness while KU-3×KU-49, KU-49×SB-121 and T-9×KU-40 were good specific combiner for tallness. The crosses PU-19×T-9, KU-3×KU-49 and KU-40×KU-49 were found to be good specific combiner for the character number of pods per plant.

Most of the characters showed higher mean values than their mid parental, better parental and standard variety in different crosses. The extent of heterosis varied with the characters along with crosses. Moreover, none of the crosses showed heterosis for all the characters together. The cross PU-19×T-9 was potential cross for grain yield. The cross KU-3×KU-40 and T-9×KU-49 showed significant heterosis over mid parent, better parent and check variety for yield and two other yield attributing characters. Simultaneous selection for at least two yield components is more efficient selection method than selection based on single component for the improvement programme of Blackgram.

Selection in any plant improvement programme depends upon the genetic variability prevalent in segregating population. In $F_2$ population mean, range of the characters were estimated. Further, genotypic variance and phenotypic variance, genotypic coefficient variance and phenotypic coefficient of variation heritability in broad sense and genetic advance as % of mean were estimated to obtain information on the nature and magnitude of genetic variation of the characters concerned. High genotypic and phenotypic variance were observed for number of pods per plant followed by yield per plant which indicated the existence of sufficient genetic variation for these characters in the segregating population.
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The phenotypic coefficient of variation was always higher than genotypic coefficient of variation for all the characters. In the present study, high genotypic coefficient of variation along with high phenotypic coefficient of variation was found for yield per plant, plant height and number of pods per plant. Also, high heritability with high genetic advance was recorded for number of pods per plant and yield indicating that these characters were governed by additive gene action. Selection for these characters is likely to be highly effective. High to moderate heritability with low genetic advance was recorded for plant height, pod length and days to maturity which revealed that these characters were more influenced by environment and hence less effective for selection.

In F₂ generation, individual plant selections from each cross were made on the basis of yield, plant height, number of branches, number of pods, number of seeds per pod, seed weight and days to flowering with an aim to obtain good recombinants for these characters. From fifteen crosses, a total of 125 plants (good recombinants) were selected for their further evaluation in F₃ and F₄ generations.

F₃ families were raised from the selected F₂ plants and evaluated for the performance of the characters under study. The range, mean and percentage of F₃ family mean for the considered characters were compared with those of their respective parental mean performance. It was observed that out of 125 families, only 35 families could show good performance over the better parent in terms of yield and other considered characters.

In the F₃ generation of fifteen crosses, both between and within family selection was exercised. Out of 125 families only 35 families were isolated and from 35 families, altogether 60 individual plant selection were made on the basis of yield. F₄ families were raised from 60 individual F₃ selections of the crosses. The F₄ families showed good performance and retained their parental characteristics under
considerations such as - plant height, number of branches, number of pods, seeds weight and yield per plant. Performance of promising families in comparison to their better parent was higher in F₄ generation than in F₃ generation. Thus selection for yield per plant become effective in later generations only. In F₄ generation, 24 promising families were selected and forwarded for quality analysis. In F₃ and F₄ generations, the extent of variability with respect to five characters were measured in terms of range, genotypic variation, phenotypic variation, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits under study. High heritability along with high genetic advance was observed for number of pods and yield per plant. It might be due to additive gene action and improvement could be possible through selection. High heritability with moderate genetic advance was exhibited by plant height implied that the additive and non-additive gene action influenced in the expression of the concerned character.

In F₄, reduction of difference between phenotypic coefficient of variation and genotypic coefficient of variation for number of pods, 100-seed weight and yield per plant may be due to stabilization of gene action with selection. Heritability estimates were increased as compared to F₃ for 100-seed weight and equal to F₃ for number of pods per plant.

The seed protein content of the 24 promising families were estimated following the Microjheldahl method. The protein content of the families ranged from 19.40% to 26.12%. Family No. 5 isolated from the cross PU-19×KU-40 showed highest protein value (26.12%). Family No 20 recorded the lowest protein content (19.40%) which also exhibited less value than its parental value.
7.2 CONCLUSION

In self pollinated crop like green gram and black gram, hybrid seed production is very difficult and can not be exploited due to limitations of hybrid seed production. In coming year there will be a demand of more production of black gram on account of population explosion and decreased agricultural land. To meet the need, hybrid black gram varieties have to be developed. In the present investigation a total of fifteen F₁ hybrids were obtained from six parents by crossing in diallel fashion without reciprocals. Out of 15 hybrids all showed better performance (mean value) than their better parental mean, mid parental mean for different characters. These hybrids may be adopted in the field of farmers of Assam.

Genetic divergence among parents is important because a cross involving genetically divergent parents increases the heterosis effect to obtain desirable recombinants in segregating generations. Identification of parents for crosses and their combining ability for the characters are tools for successful breeding. Use of genetic diversity for potentially yield attributing traits is a good technique in the present as well as in future breeding efforts. The different varieties of black gram used by the farmers are not able to yield up to a satisfactory level due to their less number of branches, less number of pods, less number of seeds per pod and low seed yield.

In order to identify the superior crosses and segregants, it is desirable to assess the response to selection in the initial segregating generations. Selection and isolation of good recombinant plants from large segregating population is a difficult task concerning both time and labour. In early generation when selected sequentially, a large number of undesirable segregants may be eliminated. Breeders may give emphasis in such type of selection procedure.
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The new variety which is high yielder has good demand for farmers as it gives more profit. The consumers as well as farmers prefer good cooking quality seeds with high nutritional value.

In the present investigation, chemical analysis of the selected families was done where percentage of protein content in the seed was determined. It was revealed that some selected families showed higher percentage of protein than their parents. Although protein content was not the selection criteria, it may be considered as selection criteria for improving nutritional status of the existing varieties of blackgram.

In the present investigation, only 24 best families were identified and out of these, only 8 families were found to be more promising in terms of yield. These families were also beneficial for plant height number of branch and seed weight. Family no 6 identified in the present study was found to be promising in terms of yield, dwarf in nature and had more branch number. This family also contains high percentage of protein. The other families are also promising in terms of yield as well as in certain considered characters.