CHAPTER – VI
SUMMARY AND CONCLUSION

The present investigation was conducted to assess the genetic variability, correlation coefficient, path coefficient analysis, selection indices and genetic divergence in 60 kabuli chickpea genotypes taking twelve quantitative characters viz., days to 50 per cent flowering, plant height, number of primary branches per plant, number of secondary branches per plant, days to maturity, number of pods per plant, number of seeds per pod, biological yield per plant, seed yield per plant, 100-seed weight, harvest index and protein content. The experimental material of the present investigation comprised of 60 genotypes of chickpea. The pure seeds of these genotypes were obtained from germplasm maintained at Pulses Research Station, Junagadh Agricultural University, Junagadh. The study was carried out at Pulses Research Station, Junagadh Agricultural University, Junagadh during Rabi 2015-16 in a randomized block design with three replications.

The observations were recorded on five randomly selected plants from each replication except days to maturity and days to 50% flowering where plot means were used. The data were analysed at computer cell of Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh. The salient features of the findings are as under:

1) The analysis of variance revealed highly significant differences among the mean square due to genotypes for all the characters studied, suggesting the sufficient amount of variability present in the material used.

2) Seed yield per plant recorded maximum phenotypic range of variation followed by 100-seed weight, number of pods per plant, biological yield per plant, number of primary branches per plant, harvest index and number of secondary branches per plant. Number of seeds per pod, days to 50% flowering and plant height shows moderate phenotypic range of variation. There was narrow range of variation for days to maturity and protein content.

3) The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation indicating the influence of environmental factors.
The highest genotypic coefficient of variation was observed for 100-seed weight followed by seed yield per plant, biological yield per plant, number of pods per plant and number of primary branches per plant. This indicated the presence of wide variation for these characters.

4) High heritability coupled with high genetic advance as percent of mean was observed for 100-seed weight, seed yield per plant, biological yield per plant, number of pods per plant, days to 50% flowering and number of primary branches per plant suggesting the existence of sufficient heritable variation and wider scope for effective selection.

5) Significant and positive genotypic and phenotypic correlations of seed yield per plant were observed with days to maturity, number of seeds per pod, number of pods per plant, harvest index, 100-seed weight and biological yield per plant.

6) The genotypic and phenotypic path coefficient analysis revealed that number of pods per plant, number of seeds per pod, biological yield per plant, 100-seed weight, days to maturity and harvest index exhibited high and positive direct effects on seed yield per plant. While days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant and protein content exerted low and negative effect towards seed yield per plant.

7) The genotypic and phenotypic residual effects were of considerable magnitude suggesting that the all of the yield attributes have not been included in the study of path analysis.

8) The negative direct effect of low magnitude of number of primary branches per plant was nullified by high and positive indirect effects of number of seeds per pod and 100-seed weight.

9) The results of path coefficient analysis revealed that for improvement of seed yield in chickpea through selection programme, more emphasis should be given to number of pods per plant, number of seeds per pod, biological yield per plant, 100-seed weight and days to maturity.

10) The selection index comprised of seed yield per plant, biological yield per plant, harvest index, 100-seed weight and number of pods per plant was the most efficient one and for obtaining higher yielding lines, maximum weightage should be given to these functions while making selection.
11) $D^2$ analysis indicated genetic diversity among 60 genotypes of chickpea which were grouped into four clusters.

12) The genetic diversity was independent of geographic regions as genotypes from same area scattered into few clusters and genotypes of different areas were grouped in a same clusters. Hence, breeder must evaluate his material for genetic diversity instead of depending merely on their geographical diversity.

13) The attributes, viz., 100-seed weight, days to 50% flowering, number of primary branches per plant and seed yield contributed much to the total genetic divergence. Hence, selection for divergent parents based on these characters would be useful for exploitation of heterosis breeding in chickpea.

14) On the basis of cluster means, cluster IV was superior for seed yield per plant, 100-seed weight, number of seeds per pod, number of pods per plant, protein content, longer maturity phase duration, short plant height and earlier days to 50% flowering Whereas cluster II was desirable rating in respect of maximum mean value for harvest index and number of primary branches per plant. Cluster III was the high biological yield per plant and maximum mean value for the secondary branches per plant.

**CONCLUSION**

It can be concluded from the present findings that additive gene action was operating for seed yield per plant, biological yield per plant, harvest index, number of pods per plant and 100-seed weight; maximum contribution of these five traits on total genetic divergence as well as correlation study, path coefficient analysis and selection indices also revealed the importance of these traits. Therefore, due weightage should be given to these traits for genetic improvement in chickpea.