5. SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic analysis of terminal heat stress tolerance in chickpea (Cicer arietinum L.)” was undertaken to investigate genetic of heat stress tolerance through marker trait association study, gene action study and QTL mapping. The study was carried out at main farm at Indian Institute of Pulses Research, Kanpur (Uttar Pradesh). A total of seventy eight genotypes were evaluated during Rabi 2015-16, and Rabi 2016-2017 for capturing the genetic variability for heat tolerance. Analysis of variance for various morpho-physiological traits revealed highly significant difference under normal and late sown conditions under both years. This genetic variation could be utilized for improvement of various quantitative traits in chickpea for heat stress tolerance.

Wide range of genetic variability for days to first flowering, SCMR, MSI, yield/plant, pods/plant, and biological yield was recorded under normal and late sown condition under both years. This genetic variability could be potentially used for increasing the genetic base of chickpea for development of heat stress tolerance.

Based on yield related parameters such as plot yield and lower yield reduction (%) RVG 203, RVG 202, JAKI 9218, Pusa 372, JG 130, ICC 07110, Pusa 240, and ICC 1356 genotypes were identified. Thus, these genotypes could serve as an important resource for heat stress tolerance improvement and could be potentially utilized in crossing programme.

Likewise, based on various heat tolerance indices such as heat susceptibility index, yield index, geometric mean productivity index several promising genotypes viz., JG 130, JAKI 9218, PBG1, ICC 07110, ICC 1356 and Pusa 240 were identified.
Concurrently, to capture genetic diversity at molecular level eighty one SSR marker assay was done. A total of 328 alleles with an average of 4.0 alleles per locus were obtained from 78 chickpea genotypes. Neighborhood joining tree analysis clustered the all the genotypes into two major clusters. Likewise, the result of factorial analysis and principal coordinate analysis were consistent with result of neighborhood joining tree analysis. Moreover, population structure analysis also supported presence of two subpopulations. Further, several significant marker trait associations for various traits related to heat relevant physiological and yield traits such as yield/plant, pods/plant and plot yield were elucidated. Thus, these marker trait associations could be useful for molecular breeding for heat tolerance in chickpea.

A total of six parents were selected for unraveling the gene action for various phenological, physiological and yield related traits under heat stress through half diallel analysis. Genetic analysis revealed the presence of both additive and non-additive genetic variances. However, higher magnitude of general combining ability (GCA) variance than specific combining ability (SCA) variance, with predictability ratio > 0.5 for most of the traits studied under both normal sown and late sown conditions indicated preponderance of additive gene action. The estimates of GCA effects revealed that the parents ICC 92944 and KWR 108 were better general combiners for yield and yield-related traits, under both NS and LS conditions. Likewise, ICC4958 × ICC92944 (under both conditions) and DCP 92-3× KWR 108 (under LS) F₁ crosses were the most suitable cross-combinations for yield and yield related traits.

In parallel, a F₂ based mapping population developed from DCP92-3 (heat sensitive) × ICC92944 (heat tolerant) cross was chosen for identification of heat relevant QTL. Wide range of genetic variability for various morpho-physiological traits was recorded in the given mapping population grown under late sown condition. A total of 78 SSR markers were used for
genotyping of the mapping population. A QTL linked to primary branch number was identified on LG3 with LOD value of 4.7 and flanked by TA142 and ICCM281a markers. The QTL explained phenotypic variation of 2% for the trait and had positive effect with male parent contributing favorable allele. Likewise, for chlorophyll content, a major QTL explaining 17.4% PV with LOD score of 4.9 on LG6 flanked by NCPGR206 and H3G031 SSR marker was detected. Thus the genetic and genomic resource developed in the present study could further help in development of terminal heat stress tolerant chickpea cultivar.
FUTURE SCOPE OF RESEARCH

The genetic variability for various morpho-physiological traits studied could be potentially used in future chickpea breeding programme for development of heat tolerant variety. Moreover, the improved breeding lines exhibiting superior yield performance needs further rigorous testing under multi-locations and heat stress conditions for evaluating their worth for commercial cultivation as direct varieties.

Various heat stress indices can be efficiently employed in breeding programme for screening suitable genotypes to sustain chickpea yield under HS. Moreover, genotypes selected based on various heat stress indices could be used in crossing programme for transferring heat tolerance related trait in heat sensitive yet high yielding breeding lines.

Genetic diversity recorded among the cultivars and advanced breeding lines along with accessions could be utilized for broadening the genetic base of chickpea for breeding high yielding chickpea cultivars. The genetic diversity can be further studied through recruiting high-throughput SNP markers for better understanding of genetic difference in the studied genotypes. The preliminary results of association mapping for various morpho-physiological traits could be helpful for screening of HS tolerance genotype. The putatively linked genomic regions may be further investigated in greater detail for better understanding of heat stress tolerance in chickpea.

The selected F\textsubscript{1} crosses displaying superior performance under normal and late sown conditions could be further handled by growing them in F\textsubscript{2} generation to select desirable transgressive segregants possessing heat tolerant traits.
Primary branch number and chlorophyll content controlling QTL regions may be further fine mapped for uncovering the underlying candidate gene(s). This will help the chickpea breeding community to transfer these genomic regions into the elite yet heat sensitive high yielding cultivars through marker assisted breeding for sustainable chickpea yield under heat stress.