Chapter-V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Characterization and evaluation of *Perilla frutescens* (L.) Britton germplasm collected from North-eastern region of India.” was undertaken with the following objectives: (1) to study the extent of genetic variability in terms of yield and its attributes within the available germplasm collected from the northeastern region. (2) To determine the extent of correlation and their causal relationships among different quantitative traits. (3) To group constellation and cataloging the available *Perilla* germplasm by multivariate analysis to study the genetic divergence among them. (4) To determine the oil, fatty acid profiling, protein and total phenol content of the germplasm under investigation. (5) To identify superior genotypes for commercial cultivation in this region and for utilizing in further breeding programmes.

The experiment was conducted at the experimental farm of the ICAR-National Bureau of Plant Genetic Resources (NBPGR) Regional Station, Umiam, Meghalaya during *Kharif* season of the year 2012 and 2013. The experimental materials were 62 germplasm accessions and four local checks collected from different states of the northeastern region of India. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications.

The field data was subjected to analysis of variance for randomized block design (Panse and Sukhtame, 1967), estimation of correlation coefficients (Searle, 1961), path-coefficient analysis (Dewey and Lu, 1959) and multivariate analysis. Oil protein, total phenol and fatty acids were studied from harvested seeds. Molecular characterization by STMS markers of all the collected accessions was also conducted.
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The salient results of present study along with the conclusions are summarized below:

1. The highest mean performance for seed yield per plant along with some of the component traits was exhibited by IC599238, IC599235, IC599251, IC599254, IC599246, IC599240, IC521281 and IC599257. The above mentioned genotypes may be used directly for commercial growing and/or as donor parents in hybridization programme for further improvement.

2. The most desirable genotypes for improving characters other than seed yield per plant are IC006446 for days to 50% flowering and days to maturity; IC599246 and IC599238 for primary branches per plant and number of inflorescence per plant; IC599254 for main inflorescence length and days to 50% flowering; IC599257 and IC599254 for leaf length, leaf breadth and petiole length. Similarly, the promising genotypes for 1000-seed weight were IC599254, IC599251, IC599257, IC599252 and IC006440; for plant height IC003942, IC006441, IC003908, IC003955 and IC006442; and for seed size IC599257, IC599254, IC006441, IC599251 and IC599231. These lines merit consideration as promising parents for hybridization programme for bringing over-all improvement in plant architecture in a component breeding approach for development of high yielding Perilla genotypes even if they have moderate or low seed yield.

3. Highest phenotypic as well as genotypic coefficient of variation was observed for number of inflorescence per plant followed by plant height, 1000 seed weight, main inflorescence length and yield per plant. The present study showed that high heritability values coupled with moderate genetic advance as per cent of means were recorded
for plant height, number of inflorescence per plant, leaf length, main inflorescence length and 1000 seed weight, indicating the scope of selection for improvement of these traits. High heritability values coupled with low genetic advance as per cent of means were observed for primary branches per plant, days to 50% flowering, days to 80% maturity and seed size. The characters showing high heritability with low genetic advance indicated the presence of non-additive gene action in the inheritance of these traits; hence in this case selection may not be effective and heterosis breeding may be rewarding.

4. Seed yield per plant showed highly significant and positive correlation with number of inflorescence per plant, number of primary branches per plant, days to 50% flowering, petiole length and 1000-seed weight, while significant and negative correlation with plant height. Therefore, these five characters emerged as most important characters contributing seed yield in *Perilla*.

5. The highest positive direct effect on seed yield per plant was exerted by leaf length followed by 1000-seed weight, petiole length and days to 80% maturity, which indicated that these traits were most important for direct seed yield components in *Perilla*. The remaining seven characters exhibited negative direct effects on seed yield per plant.

6. The Hierarchical clustering using wards method on the basis of 22 morphological traits grouped total accessions and 4 checks in two major clusters A and B. Cluster-A included a total of 18 accessions including one check. Cluster-B was further divided in three sub cluster B-I, B-II and B-III. The sub cluster B-I, B-II and B-III comprised 26 accessions including 3 checks, 8 accessions and 14 accessions, respectively.
7. The highest mean performance for oil percentage along with some of the other biochemical traits was exhibited by IC006444, IC524504, IC275959, IC524455, IC422885, IC006442, IC524554 and IC599246. These accessions may be used as donor parents in hybridization programme for developing high oil yielding varieties of respective groups. For fatty acid profiling, the desirable lines found for palmitic acid, stearic acid and oleic acid were IC524504, IC275959, IC524551 and IC006441, respectively.

8. The Pearson’s correlation was significantly and positively correlated for linoleic acid, protein percentage and palmitic acid with seed oil percentage. Therefore, these three characters emerged as most important traits for seed oil percentage in Perilla.

9. Multivariate analysis revealed the diversity for biochemical traits in two major clusters, cluster-A and B. Cluster-B is further divided in sub-clusters B-I, B-II, B-III, B-IV and B-V. Cluster-A included a total of 11 accessions with high values for oleic acid, linoleic acid, palmitic acid, stearic acid, oil as well as protein percentage. The cluster B-I, B-II, B-III and B-IV comprised 20, 3, 4 and 4 accessions, respectively. Maximum 22 accessions including three checks are in cluster B-V. Since there is no released variety available in the country in this crop, therefore representative accessions may be chosen from particular groups for release as variety or for use as parents in hybridization programme.

10. The $Na$ value obtained in the current study was 6.57. The average PIC value of present study was 0.61 per marker. Highest expected heterozygosity ($He$) value was recorded for the STMS loci such as
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KWPE57, KWPE26, KWPE53, GBPFM204 and KWPE58 with a mean 0.669.

11. The genetic distance based on neighbour-joining-based phylogeny divided the accessions into two major clusters A and B. Cluster-A had the promising accessions for biochemical traits and cluster-B for morphological traits. At sub-cluster level, sub-cluster A-I consisted of 11 accessions out of total of 20 accessions collected from Nagaland. Sub-cluster A-II had the accessions having long main inflorescence length and greater 1000-seed weights. Sub-clusters A-I and B-II mainly consisted of the accessions collected from Arunachal Pradesh, Mizoram and Nagaland revealed that the accessions of these groups are genetically similar or seeds of accessions were exchanged by the farmers at local level, which is very common in Northeast India. Sub-cluster B-III had 21 accessions and all the accessions collected from Manipur and Meghalaya were in this sub-cluster. Though, at the cluster level there was no strong association observed between geographical origin and genetic diversity, yet at sub cluster level this association was better revealed particularly in sub-cluster A-I and B-II. The genetic similarity observed among the *Perilla* landraces may be useful for future *Perilla* crop variety identification, conservation, and improvement programs.

On the basis of the experiments conducted over two years in a particular location and the analyses of different qualitative and quantitative agro-morphological and biochemical characters, the accessions IC599238 and IC599235 (forming separate morphological and molecular cluster) could be used directly for commercial cultivation and cross-breeding programme for further improvement. The other accessions, *viz.*, IC599240
for early maturity, IC524504, IC275959 and IC006444 for higher oil per cent, better oil quality and higher protein per cent, IC599251 and IC599254 for larger seed size and attractive seed characters, which are of growers’ choice and consumers’ preference, could be used in recombination breeding programme for development of superior genotypes by combining superior characters through accumulation of favourable alleles of different genes from different accessions. IC599257 which is a distinct accession in morphological and molecular clustering and also recorded good yield with moderate maturity and some other accessions on the basis of cluster analysis can be used in transgressive breeding programme.

The conclusions drawn from the present investigations, however, are based on two years trials from a particular location, which may have wide implications. The experiments need to be conducted in different locations under different crop management practices over years for drawing better conclusions.

**Future scope for research**

*Perilla* is one of the potential oilseed crops of Northeastern hill (NEH) Region of India and there is no released variety of this crop. Therefore the promising accessions can be sent to AICRP for potential crop for further trials for release of variety. Exploration to remote and difficult-to-reach areas may be conducted for collection of indigenous germplasm. Moreover procurement for exotic germplasm from the centre of diversity outside India like China and Korea may be done. Rigorous and extensive testing of germplasm should be done under different locations over growing seasons for assessing the agronomic worth/potential and identification of climate proofing genotype in the context of climate change. The total biochemical profiling of oil can be done to explore the other nutritive values of this
crop. Study of nutraceutical properties including vitamin E and other antioxidants of this orphan crop could be an important area. Tailoring of this under-utilized crop through classical and modern breeding methods for modification of agronomic traits for higher yield and better fitting in lay farming and multiple cropping and alteration of fatty acid profile and improvement of other quality traits for better health would be very important. Some other molecular markers like ISSR, CAPS, SCAR, EST, SNP’S etc can be developed for better and more authentic molecular characterization of crop. Decoding the *Perilla* genome may be an important task for exploring the genome sequence and in-silico research for better understanding the variations within the DNA sequence and its interaction with environment which will ultimately help to develop new improved lines.