VI. SUMMARY

The wide genetic patrimony and the large germplasm of synonyms in jasmine require precise method of discrimination for cultivar identification and classification. Molecular markers by their potential are more reliable as they are not influenced by environmental factors. Diversity analyses through molecular markers will be very useful for genetic improvement of the crop as it can help in development of mapping populations. DNA markers associated with economically important characters can greatly aid in jasmine improvement efforts. Though markers linked with traits are conventionally discovered using linkage mapping strategy, this approach is having many disadvantages, mainly, poor resolution in detecting QTL, laborious and high cost. The power of association mapping is exploited in recent years for plant improvement.

The major focus of the present study was to determine diversity among jasmine germplasm accessions collected from different parts of India, determine its population structure and association studies with AFLP and SSR markers with some economically important traits of jasmine.

Wide ranges of variations among 56 jasmine genotypes for all the fourteen quantitative traits studied were seen. All quantitative characters except no. of calyx teeth have leptokurtic and positively skewed distribution. Phenotypic coefficient of variation (PCV) was high for all the characters studied. In the present study, 56 jasmine genotypes were classified using UPGMA based on 14 quantitative characters. Accordingly jasmine genotypes were grouped into seven major clusters. PCA for 56 jasmine genotypes was carried out using 14 quantitative characters and in this case also seven major clusters were seen. Nine qualitative traits of jasmine were also studied and wide variation was seen among all jasmine genotypes for all the traits.
Standardisation of DNA extraction method from leaf was done. CTAB method with few modifications was found to give high quality and quantity of DNA. It was also revealed that the DNA extracted from dry leaf sample and that of fresh leaf sample had no difference in respect of quality and quantity. AFLP protocol has been standardized for jasmine with few modifications. Five AFLP primer combinations generated 220 AFLP markers with 81.81% polymorphism. Diversity analysis among 56 jasmine genotypes was done using AFLP data. Shannon-weaver diversity index, average phenotypic genetic diversity and average gene diversity were calculated for each primer combination. SSR protocol was also standardized.

Fifty six SSR primers from an ornamental species in the family Oleaceae, Chionanthus retusus (Arias et al., 2011), were used to screen 56 jasmine germplasm accessions. Out of 56 primers, 26 primers gave amplification and 24 gave polymorphic band. Diversity analysis among 56 jasmine genotypes was done using SSR data. Per cent heterozygosity, allele diversity, allele frequency, allelic PIC was calculated for all the 26 SSR primers. The cluster analysis was done using Squared Euclidean Distances (SED) for 56 jasmine germplasm accessions with SSR and AFLP data. A dendrogram was also constructed by UPGMA method. Nine clusters were formed based on molecular data and the clusters formed based on AFLP and SSR data were not in agreement with the clusters formed based on morphological data. Morphological and molecular data could have applications in identifying unknown origins of germplasm sources, plant variety protection, and/or cultivar identification.

SSR marker StvChR_9a showed specific amplification of an amplicon of 250 bp in J. auriculatum species comprising jasmine genotypes J. auriculatum-1(code-16) and J. auriculatum-2(code-17). This marker can be helpful in jasmine species identification. However, this has to be confirmed with more number of genotypes belonging to the species.
Population structure analysis was carried out using both distance based and model based approach. Population structure analysis revealed the presence of four subgroups in the jasmine germplasm accessions. Q-matrix was calculated assuming four subgroups. K-matrix was calculated using SPAGEDI software. Both Q-matrix and K-matrix were used as inputs for assessing marker trait association using the software TASSEL by Mixed Linear Model. Tree construction by Neighbour-joining method also confirmed presence of four sub groups in jasmine germplasm.

The population stratification (Q-matrix) and family relatedness (K-matrix) among jasmine germplasm accessions were used for association analysis using the software TASSEL. Markers associated significantly (p < 0.05) and with r² value 10% or more were selected. A total of 42 markers were found to be associated with nine economically important characters. Among the associated 42 markers, 14 are SSR markers and rest 28 are AFLP markers.

Diversity analysis done in the present study through morphological and molecular markers can be useful in identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection in breeding programme. Introgression of desirable genes can also be done from the diverse jasmine germplasm into the commercially cultivated genetic base. In the present study, many molecular markers were tagged to QTLs governing economically important traits. These markers can be valuable tool in identification and selection of lines with economic traits in improvement of the crop.