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| Title of Thesis | : | Characterization of mulberry genotypes (*Morus* spp.) of North-Western region using molecular markers |
| Name of the Student | : | Suraksha Chanotra |
| Registration No. | : | J-15-D-258-A |
| Name and Designation of Major Advisor | : | Dr. R.K. Bali  Professor, Division of Sericulture |
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**ABSTRACT**

Mulberry (*Morus* spp.) has prime importance in sericulture industry since its foliage is the only natural food of silkworm (*Bombyx mori* L.). In India, mulberry is cultivated mainly for sericulture and phase wise multipurpose uses are also tried for maximum exploitation of mulberry genetic resources. The present investigation was conducted on forty four mulberry genotypes to estimate the extent of genetic relationship by morphological and molecular characterization using SSR markers. Fourteen morpho-physiological traits viz. sprouting time, leaf shape, apex, base, margins, pubescence, leaf length, leaf width, actual leaf area, fresh leaf weight, dry weight, moisture percentage, inter-nodal distance and number of leaves per meter twig were studied and revealed significant variability among the genotypes. PCV was found to be higher than the respective GCV for all the characters denoting variability among genotypes. Estimates of phenotypic and genotypic coefficient of variation were high for fresh leaf weight (39.72, 35.06%) moderate for other traits (10-30%) and least in moisture percentage (9.24, 6.81% respectively). Maximum heritability percentage was recorded for fresh leaf weight (77.9%) and minimum in leaf width (36.7%). Highest genetic advance was recorded for fresh leaf weight (63.7%) and lowest in internodal distance (0.3%). Principal component analysis revealed maximum variation of 50.56 per cent was contributed by PC1 and least of 0.05 per cent by PC8. Cluster dendrogram grouped forty four genotypes under two main clusters A and B with sub-clusters and sub-sub clusters. The promising genotypes identified on the basis of morpho-physiological analysis included Behrampur, BhremC-776, Chinese white, Dhar local, LF-1, Miuraso, S-41, S-54, S-146, S-799, S-1608, S-1635, S-1708, Tr-4, Tr-8 and Kokuso-27. On molecular level Genetic diversity was assessed using set of 26 SSR primers which generated a total of 182 bands with an average of 6.96 alleles per locus. Primer M6 produced maximum of 15 alleles and minimum 3 alleles per locus in primer Mul3SSR91. Cluster dendrogram grouped 44 genotypes into three main clusters as A, B and C with sub-clusters and sub-sub clusters. Genotype Kokuso-27, S-146, Shimanouchi, KNG and V-1 were found to be the most diverse genotypes. NS-1 and NS-2 were recorded as duplicate accession. Behrampur and S-1 showed highest similarity index (0.48), closely followed by Chinese white and Ichinose, Miuraso and Dhar local (0.44 each), Kamabori and Chakmajra (0.40), while genotypes Shimanouchi and KNG showed least similarity index (0.10). Heterozygosity values ranged from 0.022 (Mul3SSR114) to 0.870 (Mul3SSR105) with an average of 0.200. Percentage of polymorphism ranged from 14.20 per cent (Mul3SSR80 and Mul3SSR97) to 100 per cent (Mul3SSR70, Mul3SSR74 and Mul3SSR114) with an average of 39.84 per cent. Highest PIC value was recorded for SSR marker M6 (0.901) and lowest for primer Mul3SSR91 (0.486) with an average of 0.724. This investigation suggested that the *Morus* germplasm is quite diverse and can be utilized for the development of promising genotypes.

**Keywords:** Mulberry, morpho-physiological traits, molecular markers, genetic diversity, simple sequence repeats