Abstract

Mulberry is the most important crop of sericulture industry. The major constraint in realizing the potential mulberry leaf yield is due to prevalence of soil moisture stress in vast sericultural zones of the country. Development of mulberry varieties with moisture stress tolerance is one of the rewarding strategies to address the problem. Many investigations have revealed that water use efficiency (WUE) and root characters play a pivotal role in drought tolerance mechanism in plants. However, it has been also understood that WUE and root traits are complex characteristics and governed by many genes. In this context, the present study is an effort towards understanding of moisture stress tolerance in mulberry by development of trait specific (WUE and root) linkage maps and then to map QTLs controlling the traits for utilization in directional improvement through marker assisted selection.

Characterization of about 300-mulberry germplasm using growth traits, rooting and $\Delta^{13}C$ resulted in the identification of contrasting accessions for WUE (5 Nos.) and root trait (4 Nos.). Parent specific linkage maps were constructed by genotyping WUE mapping population (200 Nos.) from the cross Himachal Local x MS-3 using 76 RAPD primers (196 polymorphic markers). Based on phenotypic data of two different seasons, QTL analysis resulted in identification of loci governing average shoot length and inter-nodal distance on female (LG7) and male (LG3) map respectively. The mapping population from the cross Dudhia White x UP were utilized for linkage analysis and QTL mapping of root traits. Composite Interval Mapping analysis of the female parent based on the trait values of two seasons identified many putative QTLs on LG9. Shoot weight (in saplings) and length of the longest root were mapped on female LG5 by Interval Mapping (IM) with LOD score > 3.0 which was concurrent with Composite Interval Mapping analysis. Introgression of WUE and root trait in mulberry was undertaken by crossing Dudhia White (high root type) x MS-3 (high WUE type) and about 1104 lines were established in an experimental plot. Based on visual grading, $\Delta^{13}C$ and gas exchange parameters, five promising introgressed lines (IL - 126, 280, 309, 311 and 314) were identified for field evaluation of moisture stress tolerance and utilization.

The study is one of the first of its kind in mulberry, where construction of linkage maps of mulberry using a segregating population for both WUE and root traits have been achieved and also QTLs governing the traits and associated characters were identified on the map. Relatively sparse ‘framework’ maps of two parental lines have been constructed. From this point, there is need for saturation of maps consisting of evenly spaced markers, which is adequate enough for most of the genetic analysis including identification of QTLs controlling associated traits. The maps can be further saturated specifically using co-dominant markers like SSRs, SNPs, SCARs etc., to find markers tightly linked to the genomic regions of interest. This will help in a long way in utilization of identified major QTLs through marker assisted breeding and understanding the complexities of phenotypic expressions in terms of gene x environmental interactions in mulberry.