

Microsatellite based Genetic Linkage Map in Medicinal Legume

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Abstract—Development of genetic linkage map using microsatellite markers can provide great impetus for marker assisted crop improvement programs. We report here first such attempt in *M.pruriens*. One hundred and sixty one RIL lines (F_6) derived from a single seed descent of F_2 individuals raised from cross between genotype: 500108KA and 500113MH was used for genotyping. Following marker screening, we obtained usable data from 32 markers which was used for map construction. Linkage analysis was performed using JoinMap 4.0 software. A minimum LOD score of 3.0 and maximum recombination fraction (θ) of 0.50 were set as thresholds for linkage group (LG). Recombination fractions were converted into map distances in centimorgans using the Kosambi mapping function. Using the above threshold, 32 SSR markers were mapped into 11 linkage groups which covered a total distance of 837.04 cM in length. Linkage groups ranged from 4.49 cM to 186.48cM in length with average of 76.04 cM per linkage group. While most linkage groups consisted of only two to three linked markers, two linkage groups showed five linked markers. The largest linkage group spanned 186.48 cM. However, due to y limited data obtained from this study, the map attained is of lower resolution than expected. Work is in progress to use large number of markers from extended SSR collection to convert this into a workable genetic linkage map.