

Segregation Analysis of SSR Markers in Safflower (*Carthamus Tinctorius L.*) for Oil Content

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ABSTRACT

In the present study, 176 F_{2:3} population of the cross A-1 (low oil content variety, ~26%) x EC-755673-1 (high oil content variety, ~38%) is genotyped with 250 polymorphic SSR markers. Out of which only a set of 30 (~12%) SSR have shown polymorphism among the parents. The mapping population was genotyped using 30 polymorphic markers. The Chi-square (χ^2) test revealed that, out of 30 polymorphic markers genotyped, 25 markers followed the Mendelian ratio of 1:2:1 whereas the remaining 5 markers deviated from the expected ratio. The genotypic data of the SSRs developed in this study can be used for augmenting the linkage maps developed in the previous studies. Further the polymorphic markers identified in the present study were not mapped in the previous studies.

Keywords: *Chi-square, Genotyping, Mapping, Polymorphism and SSRs.*