

Development of gSSRs in safflower through microsatellite enriched library

A microsatellite enriched genomic library was constructed from an Indian cultivar, A-1. A total of 750 SSR-positive clones was generated; of which, 617 were identified as unique sequences and sequencing of them revealed 238 SSR motifs. 79.5% of the SSRs identified were perfect, 1.5% were imperfect and 19% were compound (Table 1, 2). Primer-pairs were designed and validated in a panel of 24 genotypes of cultivated safflower. 164 primer-pairs produced clearly scorable amplicon; of which 42 showed polymorphism among genotypes. Number of alleles at polymorphic SSR locus ranged from 2 to 4 with an average of 2.7. The polymorphic information content (PIC) value ranged from 0.08 to 0.61 with an average of 0.33. The sequences obtained in this study have been deposited in the GeneBank (NCBI) viz., accession numbers KJ586129 to KJ586228 and KX914750 to KX914860. The SSR markers reported in this study would be useful for characterization of genetic diversity and trait mapping purposes in safflower.

Table 2 Summary of the microsatellite enriched library constructed for safflower

S. No.	Characteristic	Number
1	Clones sequenced	750
2	Number of redundant clones	133
3	Unique clones	627
4	Number of sequences containing more than one SSR Repeats	238
5	Primers developed	200
6	Primers standardized/lous specific amplification	164
7	Polymorphic markers	42