Development and characterization of genomic microsatellite markers in safflower (*Carthamus tinctorius* L.)

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Abstract

Specific and robust marker resources available for safflower breeding are scarce. The present research was aimed at developing a collection of genomic microsatellite (SSR) markers and to assess their informativeness. A genomic library enriched for AC- and AG-repeats was constructed from safflower DNA. Around 35% of the 768 clones that were isolated and sequenced contained SSR sequences. From these, 108 unique primer pairs were designed. The majority of the SSRs contained simple di-nucleotide motifs (77 of 108), most of them being perfect repeats (63 of 77). Reference allele length ranged from 95 to 414 bp, averaging 241.2 bp. The 108 SSRs were amplified in a set of ten safflower lines. From 88 SSR markers that amplified successfully, 64 of them detected polymorphism among the ten safflower lines genotyped. The number of alleles per locus ranged from 2 to 8 (mean value of 3.2), whereas heterozygosity ranged from 0.18 to 0.86 (mean value of 0.52). These genomic SSR markers will contribute to advance in safflower molecular breeding.