

Mapping of major and modifying genes for high oleic acid content in safflower

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Abstract

Oils with high oleic acid content are in great demand because they have optimal properties for food and non-food uses. Two different levels of high oleic acid content (>75 and >84%) have been reported in safflower (*Carthamus tinctorius* L.). The trait is mainly controlled by partially recessive alleles at a major gene *Ol*, but the highest levels have been attributed to modifying genes. The objectives of this research were to map the *Ol* locus and modifying genes involved in oleic acid content of safflower seeds and to determine the nature of *Ol* through a candidate gene approach. Two F₂ mapping populations from the nuclear male-sterile line CL-1 and the high oleic acid lines CR-6 (>75% oleic acid) and CR-9 (>84%) were developed and phenotyped for oleic acid content at the F₂ and F₃ seed level. A genetic linkage map comprising 15 linkage groups and 116 random amplified polymorphic DNA, simple sequence repeat (SSR), and sequence-characterized amplified regions marker loci was constructed for the CL-1 × CR-9 population. The *Ol* gene was mapped to linkage group (LG) T3 tightly linked to the SSR marker ct365, which was confirmed in the CL-1 × CR-6 population. Additionally, a quantitative trait locus with a minor effect on increasing oleic acid content was identified on LG T2. The candidate gene approach indicated that an oleoyl-phosphatidylcholine desaturase *FAD2-1* locus underlies the *Ol* gene. Both the genetic information and the markers developed in this research will contribute to marker-assisted selection for high oleic acid content in safflower.