



**University of Zabol**

Graduate School

Faculty of Agriculture

Plant breeding group

Dissertation for obtaining a doctorate degree in genetics and plant breeding

**Title**

**Evaluation of inheritance and Mapping of genes  
controlling of seed oil content and oil quality in safflower**

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## **Abstract**

Safflower oil is the main source of edible oil, and fatty acids are the main component of its oil. Improvement of oil content and quality traits (high oleic acid and low linoleic acid) in safflower can be accelerated by exploiting related markers through molecular breeding. However, evaluation of oil quality is not frequently included in the selection of new breed cultivars. This could be due to analysis problems in oil quality in a large set of genotypes. Therefore, the identification of molecular markers related to the quality traits of safflower oil can facilitate the selection of genotypes in breeding programs of this species. Therefore, this study was conducted with the aim of identifying quantitative trait loci (QTL) related to seed oil, oleic acid and linoleic acid in F<sub>9</sub> population derived from safflower Mex 22-191/Goldasht in 2018 crop season. A new linkage map was constructed with 69 polymorphic AFLP and 45 ISSR markers covering 1472.441 cM of the safflower genome. Finally, 63 main QTLs with additive effects and 238 epistatic QTLs with additive × additive effects were determined for oleic acid traits, linoleic acid content and their ratio. These results indicate that epistasis is an important genetic basis for complex traits such as oil content and oil quality. Additive and epistatic QTL described 8.30 and 36.56 of the phenotypic changes of traits, respectively. 14 main genomic regions in linkage group LG 3, 4, 7, 8 and LG 9 were co-localized for different QTL traits. The highest negative correlation was observed between the amount of oleic acid and linoleic acid. Cluster analysis based on biochemical markers and ISSR differentiated RILs into two distinct clusters, respectively. Also, the existence of sub-populations in 98 RILs was investigated using Bayesian method, which shows that there are two sub-groups in this population. These results can be useful for increasing the efficiency of breeding programs with the aim of selecting new cultivars with high oil percentage and oleic acid content and can lead to the properties and oxidative stability of safflower oil.

In order to investigate the mode of gene action for some quantitatively important traits in safflower, a crossing was made between two cultivars (Goldasht\* American: American\* 93) and the parents along with the F<sub>1</sub>, F<sub>2</sub>, BC<sub>1.1</sub> and BC<sub>1.2</sub> generations resulting from the crossing. They were evaluated in the conditions of moisture stress and in the form of a complete block design with two replications. The characteristics of height, number of sub-branches, main diameter, number of bolls, yield of a single plant, etc. were recorded and the results of analysis of variance showed that the mean square of the generations was significant for all the traits in two crossings, so the analysis of the mean of the generations. It was done for each trait that, in addition to additive and dominance effects, epistasis effects also played a role in controlling the inheritance of most traits. In normal irrigation conditions (Goldasht\* American) most of the traits except Spad, number of bolls, diameter, plant dry weight, photostase and 10% tillering were affected by the three parameter model. Also, in the conditions of moisture stress (Goldasht\* American), additive effects, dominance and epistasis played a role in controlling the inheritance of most traits except the main diameter, secondary diameter and plant fresh weight. Also, in the condition of moisture stress (93\* American), additive effects, dominance and non-reciprocal allelic effects played a role in controlling the inheritance of most of the traits except for photosynthesis rate and transpiration rate.

**Key words:** linkage mapping, epistasis content, oil content, oleic content

**Key words:** heredity, moisture stress, average generation breakdown, gene action type