Fourth Article (Considered Single - Shared with another outside the specialization – Publish in International Journal**)**

Selections of donors depending on agronomic traits, seed yield components and fatty acid profile for genetic improvement of Carthamus using stepwise multiple regression. (2020) Oliseeds and fats, Crops and Lipids OLC 27-66

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Abstract

Safflower (*Carthamus tinctorius* L.) is of potential interest to agriculture due to mainly variability of fatty acid composition of seeds oil. The purpose of this study was to evaluate various exotic genotypes of safflower for agronomic traits, components of seed yield and fatty acid content. For this purpose, plant height (cm), number of first, second and third branches/plant, seed yield/plant (g), thousandseed weight (g), oil content (%), and composition of fatty acid were investigated. Stepwise multiple regression analysis was used to develop fitted equation to predicate seed yield/plant. Analysis of variance of agronomic traits showed high differences among genotypes. Although the safflower oil genotype K2 had the highest oil seed content (42.8%), K13 obtained the highest percentage of monounsaturated fatty acids (MUFA). Highest oleic type of safflower oil has been found in K13 and K26, which can be used as a source oil quality for plant breeding. Heritability as broad sense was high and ranged from 82% in number of secondary branches (NSB) and number of third branches (NTHB) to 99% in seed index (1000 seeds weight) and oil content. High genetic advance was found in plant height (PH), seed yield/plant (SYP) and 1000-seed weight, estimated at 43.41 cm, 21.34 g and 17.62 g, respectively. Stepwise multiple regression analysis indicated that, 99.2% of the total variation in seed yield/plant could be explained by variation in yield of secondary (YSB) branches, yield of first branches (YFB), yield of third branches (YTHB), plant height (PH) and spiny as dummy variable. 23.56% of the total variation in seed oil percent could be explained by variation in yield of first branches (YFB), seed index and spiny as dummy variable. The information detected here may be a useful tool for the selection of parents in safflower breeding program.