

GENETIC ANALYSIS OF FATTY ACIDS PROFILE IN SUNFLOWER

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ABSTRACT

Genetic control of oil content and its fatty acids profile was studied in EC 68414 population of sunflower. A random sample of 32 males and 96 females was selected and mated in N.C. 1 design. Both additive and dominance components of variance were significant for stearic acid and oil content. Low h_n^2 was observed for these traits. The negative estimates of additive component of variance were observed for oleic acid, linoleic acid and palmitic acid content. Dominance component of variance was more important for all the quality characters.

Key words: Sunflower, fatty acids profile, oil content, N.C. 1 design, components of variance, heritability

Sunflower has a great potential for fulfilling the gap of production and requirement of edible oil in Indian diet. Diet with fat content containing a large percentage of oleic acid is effective to reduce plasma cholesterol, which is a risk factor for coronary heart disease [1]. The information is scanty on the genetic control of fatty acids profile in sunflower. This paper deals with the genetic control of fat content and fatty acids profile in EC 68414 population of sunflower.

MATERIALS AND METHODS

From EC 68414 population of sunflower, a random sample of 32 male plants were crossed with 3 randomly chosen female plants. No female was repeated with another male. In this way 96 full-sib and 32 half-sib progeny groups were produced. For field evaluation, the material was grouped into eight sets [2]. Each progeny was grown in a single row plot of 3 meter length accommodating 10 plants within a row. The distance between two rows was kept 60 cm.

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The oil content was estimated with the help of Nuclear Magnetic Resonance equipment. Fatty acids were determined using gas liquid chromatograph. Statistical analysis of sibs to estimate the genetic parameters was performed [2].

RESULTS AND DISCUSSION

Mean squares due to males in sets as well as females in males in sets were significant for all quality characters except males in sets for palmitic acid content (Table 1). This implied that sufficient genetic variability existed in the population

Table 1. Analysis of variance for quality characters in a sunflower population

Source	D.F.	Oil content in seed (%)	Oleic acid content (%)	Linoleic acid content (%)	Palmitic acid content (%)	Stearic acid content (%)
Sets	7	41.64	149.48	46.24	0.98	1.71
Replications in sets	8	0.52	3.19	0.78	0.22	0.36
Males in sets	24	17.75*	95.00*	32.76*	0.33	1.45*
Females in males in sets	64	16.76*	109.67*	37.01*	0.36*	0.97*
Pooled error	88	1.60	3.39	1.26	0.24	0.44

* = Significant at 5% level.

for most of the quality characters. Female as well as male components of genetic variance were significant for all the quality characters except male component for palmitic acid content (Table 2). Female component of variance exhibited higher magnitude than the respective male component for all the characters. consequently, the dominance component of genetic variance had higher magnitude than the additive component for all the quality characters. Only stearic acid and oil content showed the presence of both additive and dominance components of variance. Hence, narrow-sense heritability (h_n^2) and average degree of dominance (\bar{d}) could be estimated for these two characters only.

The magnitude of heritability was very low (0.02) for oil content and stearic acid content (0.25). The average degree of dominance was within over-dominance range for these characters. These results are corroborated by earlier study [3].

Table 2. Estimates of components of genetic variance and their ratio for quality characters in sunflower population

Items	Oil content in seed (%)	Oleic acid content (%)	Linoleic acid content (%)	Palmitic acid content (%)	Stearic acid content (%)
$\hat{\sigma}_f^2$	7.58*	53.14*	17.88*	0.06*	0.26*
$\hat{\sigma}_m^2$	0.17*	-2.45*	-0.71*	-0.01	0.08*
	±0.95	±5.42	±1.86	±0.02	±0.07
$\hat{\sigma}_A^2$	0.66	-9.78	-2.83	-0.02	0.32
	±3.82	±21.69	±7.43	±0.07	±0.29
$\hat{\sigma}_D^2$	29.66	222.35	74.34	0.27	0.74
	±6.99	±43.93	±14.88	±0.16	±0.46
\hat{h}^2 (n)	0.02	-	-	-	0.25
	±0.12	-	-	-	±0.23
\hat{d}	9.45	-	-	-	2.14

$\hat{\sigma}_f^2$ = female variance, $\hat{\sigma}_m^2$ = male variance, $\hat{\sigma}_A^2$ = additive variance, $\hat{\sigma}_D^2$ = dominance variance, \hat{h}^2 (n) = narrow sense heritability and \hat{d} = average degree of dominance.

The negative estimates of $\hat{\sigma}_m^2$ were observed for oleic acid, linoleic acid and palmitic acid content. A variance component is positive by definition [4]. However, estimates obtained from analysis of variance method can be negative. There is nothing intrinsic in the method to prevent it [5]. Negative estimates of variance components in N.C. 1 design have also been reported by Yunus [6] and Hooda [7]. Negative estimates may be obtained due to small sample size and inadequate experimental techniques i.e. competition among progenies [5]. Randomization theory also indicates that negative variance components can occur in randomized block design [8]. Such situation can arise when intra-block correlation of plots is less than the inter-block correlation. It has been suggested that the negative estimates of the components should be treated as zero for the true value of the component [4]. Considering this suggestion, the analysis of N.C. 1 progenies in the present investigation revealed that dominance component of genetic variance ($\hat{\sigma}_d^2$) was of higher magnitude for all quality characters. Role of dominance component of variance in sunflower had also been reported by several workers for oil content [9-10], oleic acid, linoleic acid and palmitic acid content [11]. On the other hand several workers have also demonstrated the importance of additive component of variance in sunflower for oil content [12,

13]. The discrepancy among results may be due to the differences in the reference populations. Also different mating design were used in different studies such as diallel, generation mean or line \times tester. North Carolina-1 mating design has been used sparingly in sunflower. The high magnitude of dominance component of variance suggested the use of inter-population improvement programmes such as reciprocal recurrent selection for genetic improvement of these quality characters. Finally the improved population may be used as a source material for developing promising inbred lines to be used subsequently in development of hybrids.

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