

INHERITANCE OF SEED OIL CONTENT IN LINSEED UNDER DIFFERENT ENVIRONMENTS

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ABSTRACT

In both the approaches, additive as well as non additive genetic variances were significant. However, additive genetic variance was of greater magnitude. Parents Chambal and Triveni had possessed maximum oil content along with high GCA effects over the environments. In pooled analysis about 1/3 crosses exhibited significant and positive SCA effects. The cross combination AKL 79 x Chambal depicted the highest SCA effect, however, the cross LCK 88062 x LW 28-9 had high oil content. For improvement of this trait pedigree selection method and diallel selection mating are suggested.

KEY WORDS: Additive, Non - additive, Inheritance, pedigree selection

Oil content of seed is essential component of oil yield in linseed. Studies on inheritance of oil content of linseed are very scanty. Therefore, present study was carried out to investigate the inheritance of oil content through combining ability analysis and genetic components of variation analysis from 10-parent diallel cross growth in three different environments.

MATERIALS AND METHODS

Ten linseed varieties (Table 2) differing in their oil content and other phenological as well as agronomic traits were crossed in all possible combinations, excluding reciprocals. Forty five F₁S along with parents, were grown in a randomised block design with three replications under unirrigated (E1, 1st Oct. 1994), as well as

Table 1 : Analysis of variance for combining ability of oil content in linseed

Source of variation	E1	E2	E3	Pooled
GCA	6.17**	6.74**	5.56**	13.32**
SCA	0.86**	1.36**	2.43**	1.68
Environment (E)	-	-	-	140.26**
GCA x Environment	-	-	-	2.57**
SCA x Environment	-	-	-	1.49**
Error	0.02	0.04	0.001	0.02

*,** Significant at 5 and 1 per cent probability levels respectively.

Table 2. Estimation of general combining ability effects and mean values of parents for oil content in different environments in linseed

Environment	LC 1048	LCK 88062	LCK 88511	LW 28-9	LCK 8605	AKL 79	RLC 29	RLC 35	Chambal	Triveni	SE ± (gi)	SED ± (gi-gi)
B ₁	-0.45** (44.60)	-0.12* (44.25)	-0.05 (44.99)	-0.50** (43.09)	-0.70** (43.13)	0.04 (43.62)	-0.07 (44.68)	-0.68** (42.99)	1.40** (47.52)	1.11* (47.78)	0.03	0.05
B ₂	0.31** (41.30)	-0.61** (41.59)	-0.18* (42.12)	-1.01** (39.81)	-0.92** (41.36)	0.28** (44.33)	0.16* (43.34)	-0.26** (41.39)	0.99** (45.32)	1.24** (45.21)	0.05	0.08
B ₃	0.32** (40.05)	0.19** (39.45)	-0.78** (39.55)	-0.51** (38.18)	0.03** (40.45)	0.44** (41.59)	-1.29** (37.94)	0.14** (39.83)	1.07** (43.03)	0.39** (43.19)	0.007	0.01
Pooled	0.06* (41.98)	-0.18** (41.77)	-0.34** (42.22)	-0.67** (40.36)	-0.53** (41.64)	0.26** (43.18)	-0.40** (41.96)	-0.27** (41.41)	1.15** (45.29)	0.91** (45.39)	0.022	0.09

*,** Significant at 5 and 1 per cent probability levels respectively.

irrigated (E2 21st Oct. 1994) condition at Udaipur and irrigated condition (E3, 10th Oct. 1994) at Anand. Each treatment was adjusted in a single was kept 25 and 10 cm respectively. Estimation of oil content was done with the use of NMR. The mean data were subjected to combining ability analysis according to Griffing (1956 b) Method - 2 and Model I and Singh (1979), whereas genetic component of variance analysis was followed as given by Hayman (1954).

RESULTS AND DISCUSSION

The anova of combining ability (Table 1) revealed that variance due to both GCA and SCA were highly significant in all the environments, whereas in pooled analysis only GCA variance was significant in individual environment, additive genetic variance was of greater magnitude compared to non-additive genetic variance. These findings are in agreement with those of Bhatnagar (1977) and Dhakar (1994). Mean squares due to

Table 3. Crosses sowing significant positive SCA effects and heterobeltiosis (in parenthesis) for oil content

Crosses	SCA effects and heterobeltiosis			
	E1	E2	E3	Pooled
LC 1048 x LCK 88062	-	2.01** (4.74**)	-	0.48** (1.91**)
LC 1048 x LCK 88511	-	1.35** (2.88**)	0.68** (3.39**)	0.50** (0.78**)
LC 1048 x LCK 8605	-	0.95**	1.71** (6.92**)	0.87** (2.00**)
LC 1048 x RLC 29	-	-	2.54** (6.76**)	0.49** (1.41**)
LC 1048 x Triveni	0.75**	-	2.00** (1.61**)	0.98**
LCK 88062 x LW 28-9	-	0.63*	3.38** (12.17**)	1.30** (2.61**)
LCK 88062 x RLC 29	0.83**	-	1.85** (6.29**)	0.80** (1.64**)
LCK 88511 x LW 28-9	0.72**	0.57**	0.96** (3.30**)	0.75**
LW 28-09 x RLC 35	0.88** (1.93**)	0.71*	0.84** (4.57**)	0.81** (2.13**)
LCK 8605 x RLC 29	0.65**	-	1.17** (1.60**)	0.36**
LCK 8605 x RLC 35	0.63**	0.90**	0.39** (3.19**)	0.64**
AKL 79 x Chambal	1.45**	-	2.73**	1.44**
AKL 79 x Triveni	1.53**	-	0.72**	0.71**
RLC 35 x Chambal	-	1.16**	0.88** (0.51**)	0.75**
RLC 35 x Triveni	-	1.16**	0.94**	0.33**
SE Sij	0.13	0.18	0.02	0.07
SE (Sij-Sik)	0.19	0.26	0.03	0.11
SE (Sij-Skl)	0.18	0.25	0.03	0.10

Table 4. Estimates of genetic components of variance for oil content in linseed in three environments

Components of variation	E1	E2	E3	Pooled
E	0.02	0.04	-	0.01
	0.13	0.11	-	0.04
D	2.97**	3.45**	-	2.70**
	0.44	0.36	-	0.12
F	1.54**	2.40**	-	1.88**
	1.02	0.84	-	0.28
H_1	3.59*	5.74**	-	2.50**
	0.94	0.78	-	0.26
H_2	3.05*	4.61**	-	2.00
	0.80	0.66	-	0.22
t^2	0.94	2.47*	-	0.05
	0.53	0.44	-	0.15
H_1/D	1.10	1.29	-	0.96
$H_2/4H_1$	0.21	0.20	-	-
K_D/K_R	1.62	1.74	-	2.13
h^2/H_2	0.31	0.54	-	-
h^2 (n)	58.30	49.70	-	80.54
r	0.442	0.756	-	0.512
i^2	0.91	0.57	4.03*	0.001
t for b-0	3.85**	4.21**	1.07	3.01**
t for b-1	-1.98	-1.68	-4.57**	-0.51

*. ** Significant at 5 and 1 per cent probability level respectively.

GCA X environment and SCA environment were highly significant with higher magnitude of former one suggesting that the additive variance was more variable over environments as compared to non-additive variance.

Per se performance and GCA effects of parents are given in Table 2. Parents, Chambal and Triveni and the maximum oil content along with high GCA effects over the environments, these parents showed consistency of GCA effects in each individual environment also. The parents LC 1048 and AKL 79 had significant and positive GCA effect in E2, E3 and in pooled analysis. Use of these genotypes in linseed crossing programme aimed at improving oil content is suggested.

About 1/3 crosses depicted significant and positive SCA effects in pooled analysis. Of which, seven crosses exhibited significant and positive

heterotic effect. Two crosses, LW 28-9 x RLC 35 and LCK 88511 x LW 28-9 had consistent performance in individual environment including pooled analysis. The cross combination AKL 79 x Chambal depicted the highest SCA effect. However, the cross LCK 88062 x LW 28-9 had high SCA effect with the highest heterotic effect. The crosses LC 1048 x Triveni, AKL 79 x Chambal and AKL 79 x Triveni involved both good general combiner parents, its exploitation in linseed breeding programme would be beneficial because of preponderance of additive gene effects. Most of the other promising crosses also had at least one parent as good general combiner, therefore, they are expected to give desirable segregants. Intermating between these hybrids is advocated to mop up additive genetic variance.

The components of genetic variance analysis was followed for E1, E2 and pooled over environments as t^2 value was non-significant. The t test indicated presence of epistatic and linkage for all the above analysis. The genetic component of variance which measured the variance due to additive gene effect (D) as well as non-additive components, H_1 and H_2 were significant in all the analysis except for H_2 in pooled analysis. Both fixable and non-fixable genetic variances were of equal magnitude in E and in pooled analysis, whereas in E2 non-fixable genetic variance was of greater magnitude. The ratio $(H_1 / D)^{1/2}$ also indicated presence of co-dominance in E2. The ratio KD/KR attained the value of more than unity, which revealed that the dominant genes were more frequently distributed than the recessive genes in the parental lines in all the analysis. The ratio, h^2/H_2 indicated involvement of one major gene group in the inheritance of oil content in all the environments. The heritability estimates were moderate in E1 and E2, whereat it was high in pooled analysis. $H_2/4H_1$ ratio revealed symmetrical distribution of increasing and decreasing alleles in parental population in E1 and E2. Above observations as a whole indicated equal importance of both additive and non-additive genetic components in the control of oil content, which is fully in agreement with earlier findings of Bhatnagar and Mehrotra (1980) and Nie *et al.* (1991). However, the significant values of additive components indicate that there is scope of oil improvement by predigree selection.

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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN BLACKGRAM

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ABSTRACT

Fifteen parents and 50 hybrids were evaluated at two locations. Variability, correlation and path coefficients were worked out on seven characters. High PCV and GCV were observed for seed yield and plant height. High heritability coupled with high genetic advance was observed for plant height, clusters per plant, pods per plant and seed yield per plant. Branches per plant, clusters per plant and pods per plant showed significant positive correlation with seed yield. Protein content was negatively correlated with seed yields. Pods per plant exerted positive direct effect on yield.

KEY WORDS: Blackgram, Variability, Correlation, Path analysis

The improvement of crop yield largely depends upon the magnitude of genetic variability and the extent to which the determining characters are heritable from generation to generation. A measure of heritability alone does not give an idea about the expected genetic gain in the next generation but it has to be considered with genetic advance. Correlation and path analysis will establish the extent of association between yield and its components and bring out relative importance of their direct and indirect effects on yield for simultaneous improvement of characters. The present investigation in blackgram (*Vigna mungo* (L.) Hepper) is an attempt in this direction.

MATERIALS AND METHODS

The materials consisted of 15 parents and their resultant 50 cross combinations obtained through L X T mating design. They were evaluated in a randomized block design with three replications at two environments *viz.*, National Pulses Research

Centre, Vainban and Coconut Research Station, Veppankulam during *Kharif* 1996. Observations were recorded on Plant height, number of branches per plant, number of clusters per plant, number of pods per plant, 100 seed weight, protein content and seed yield per plant on 10 randomly selected plants. Genotypic and phenotypic coefficient of variation (Burtan, 1951), heritability (Lush, 1940) Genetic advance (Burtan, 1952), correction Coefficients (Johnson *et al.*, 1955) and path analysis (Dewy and Lu, 1959) were worked out.

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among the genotype for all the seven characters studied in two locations. The mean, PCV, GCV, heritability and genetic advance as per cent of mean are presented in Table 1. A notable mean difference were observed among the locations for plant height, clusters per plant, pods per plant and seed yield per plant. The relative