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Short Communication

Inheritance of fatty acids in linseed (*Linum usitatissimum* L.)

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Linseed (*Linum usitatissimum* L.) is an important non-edible oilseed crop of India grown widely under rainfed situation. Linseed oil is unique as it contains a fatty acid with three double bonds namely linolenic acid which is used mainly as drying oil. For the quantitative and qualitative improvement of linseed oil, it is imperative to know the genetics of fatty acid profiles and accordingly, the present investigation was undertaken.

The experimental material comprised three crosses *viz.*; Neela × Hira, Neela × J-23 and RLC (U)-2 × T-397 of linseed. Six basic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of each cross were grown in a randomized block design with three replications during *rabi*, 1998-99. The parents and F_1 populations were sown in one row each, whereas, the backcrosses and F_2 populations were represented by two and six rows, respectively. Five randomly selected plants from each of P_1, P_2 and F_1 generations, 30 plants from F_2 generations and 15 plants from backcrosses were used for the chemical analysis of quality traits. After the harvest, seed samples were collected from all the three replications of selected plants. Fatty acids were determined in triplicate by gas liquid chromatography [1]. Mather's scaling test was applied to detect the epistasis [2]. In case of significance of scaling tests, generation mean analysis was carried out using six parameter model as suggested by Hayman [3].

A perusal of Table 1 revealed that F_1^s means were either intermediate or closer to lower parent for all the three crosses in case of palmitic and oleic acid and one cross each for the contents of stearic (Neela × J-23) and linoleic acid (RLC (U)-2 × T-397) indicating dominance of genes towards lower values for these traits. Similarly, mean values of F_1^s for all the three crosses of linolenic acid and two crosses each of stearic and linoleic acid contents were found to be closer or higher than the higher parents suggesting dominance of genes for the high content of these fatty acids. BC_1 and BC_2 means for linolenic acid in cross, RLC (U)-2 × T-397 were invariably higher than those of parents and F_1. It may be suggested from this result that an additional backcrossing to either parent would lead to the accumulation of favourable alleles in this particular set of materials for linolenic acid content which is other wise desirable for industrial purposes.

The analysis of scaling tests indicated existence of non-allelic interactions in all the three crosses for fatty acid profiles in linseed (Table 2). The A, B and C scales across crosses were significant for all the characters. Partitioning of the genetic components of means revealed that mean values were highly significant for all the five quality traits irrespective of the crosses studied. Both fixable and non-fixable gene effects were important for the expression of palmitic acid in all the crosses, predominantly with duplicate type of gene interaction. However, the magnitudes of dominance (h) and dominance × dominance (l) components were high in the cross Neela × J-23 indicating predominance of non-additive gene effects. Stearic acid was predominantly under the control of non-additive gene effects in the cross Neela × Hira with duplicate type of gene interaction. The l component was positive and highly significant in the crosses Neela × J-23 and RLC (U)-2 × T-397 suggesting a role of dominance × dominance effects in the expression of this trait. Furthermore, significant mean differences between F_1^s and better parents also revealed the dominance of genes and consequently manifestation of considerable heterosis in these two crosses for stearic acid content. In the case of oleic acid, additive (d) gene effects was more important in all the three crosses with significant epistatic interactions (i, j, l) which is in conformity with the earlier reports [4]. The data indicated the possibility of duplicate gene interactions in two crosses i.e. Neela × Hira and RLC (U)-2 × T-397, whereas the cross Neela × J-23 indicated the possibility of the occurrence of complementary type of epistasis.

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Table 1. Generation means for fatty acid profiles in three crosses of linseed

Cross+	Generations					
	P_1	P_2	F_1	F_2	BC_1	BC_2
	Palmitic acid (%)					
C_1	6.18	8.04	6.26	7.96	12.92	6.01
C_2	13.28	5.57	5.54	6.92	10.43	8.60
C_3	6.43	6.07	5.45	7.19	6.22	7.89
	Stearic acid (%)					
C_1	5.28	3.82	7.56	1.59	11.82	2.07
C_2	13.25	3.86	6.24	5.19	4.17	1.45
C_3	2.97	1.87	3.64	5.74	4.15	2.59
	Oleic acid (%)					
C_1	29.63	24.20	21.56	28.07	25.61	21.21
C_2	27.70	25.76	21.11	25.95	29.75	21.59
C_3	22.51	23.29	22.73	26.20	19.31	22.76
	Linoleic acid (%)					
C_1	12.30	17.57	15.91	26.83	13.80	18.97
C_2	23.71	24.11	29.58	21.61	13.91	25.17
C_3	24.31	22.63	22.73	17.24	23.17	16.79
	Linolenic acid (%)					
C_1	46.90	45.90	48.73	35.19	35.82	51.72
C_2	22.09	40.71	37.69	40.35	41.73	43.58
C_3	43.77	46.15	45.45	43.60	47.15	49.97

occurrence of complementary epistasis. With respect to linolenic acid, an important constituent of this industrial oilseed crop, dominance gene effects were more pronounced. However, d and i (additive × additive) components were also important but still, the presence of duplicate epistasis across crosses may hinder the progress and gain in selection for linolenic acid content. Large scale detection of non-additive gene effects in the inheritance of fatty acids, except oleic acid pinpointed the problems faced by linseed breeders while fixing the desirable expression where simple pedigree selection may not yield desirable results. It may be concluded that biparental mating or reciprocal recurrent selection would be more useful through effective and efficient utilization of both additive and nonadditive types of gene actions for the improvement of fatty acid profiles in linseed.

References

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Table 2. Estimates of gene effects for fatty acid profiles in linseed

Cross+	Scale			Genetic Components						Type of ++ epistasis
	A	B	C	m	d	h	i	j	l	
				Palmitic acid (%)						
C_1	13.41**	−2.27**	5.11**	7.96**	6.91**	5.17**	6.02**	7.84**	−17.15**	D
C_2	2.05**	6.09**	−2.23**	6.92**	1.83**	6.49**	10.39**	−2.02**	−19.53**	D
C_3	0.57**	4.26**	5.37**	7.19**	−1.67**	−1.33**	−0.53**	−1.84**	−4.30	C
				Stearic acid (%)						
C_1	10.81**	7.33**	17.95**	1.59**	9.75**	24.92**	21.42**	9.02**	−24.99**	D
C_2	11.14**	−7.20**	−8.82**	5.19**	2.72**	−11.85**	−9.53**	−1.97**	27.87**	D
C_3	1.69**	−0.32**	10.84**	5.74**	1.55**	−8.23**	−9.47**	1.00**	8.09**	D
				Oleic acid (%)						
C_1	0.03	−3.34**	15.32**	28.07**	4.40**	−23.98**	−18.63**	1.68**	21.94**	D
C_2	10.68**	−3.69**	8.11**	25.95**	8.16**	−6.74**	−1.12**	7.19**	−5.87**	C
C_3	−6.62**	−0-49**	13.54**	26.20**	−3.45**	−20.92**	−20.66**	−3.06**	27.77**	D
				Linoleic acid (%)						
C_1	−0.61**	4.45**	45.60**	26.83**	−5.17**	−40.79**	−41.76**	−2.53**	37.92**	D
C_2	25.46**	3.35**	20.55**	21.61**	−11.25**	−2.60**	−8.27**	−11.06**	37.08**	D
C_3	−0.69**	11.78**	23.45**	17.24**	6.38**	10.23**	10.97**	5.54**	1.49**	C
				Linolenic acid (%)						
C_1	−24.00**	9.91**	47.91**	35.59**	−15.90**	35.05**	32.72**	−16.40**	−17.53**	D
C_2	36.69**	8.75**	23.22**	40.35**	−1.94**	15.51**	9.22**	7.47**	−41.66**	D
C_3	5.08**	8.33**	−6.41**	43.60**	−2.91**	20.32**	19.93**	−1.63**	−33.24**	D

**Significant at P = 0.01; +C_1 = Neela × Hira; C_2 = Neela × J-23; C_3 = RLC (U)-2 × T-397; ++ D = Duplicate, C = Complementary

For linoleic acid, both additive and dominance gene effects were important. Despite large magnitudes of h and l components for linoleic acid content, dominant genes alone may not get exploited because of the presence of possible duplicate gene interactions in the cross Neela × Hira, compared to the inheritance in the cross RLC (U)-2 × T-397 due to the possibility of the

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