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# DETECTION OF EPISTATIC, ADDITIVE AND DOMINANCE VARIATION IN LINSEED (*LINUM USITATISSIMUM* L.)

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## ABSTRACT

**Three testers, Neelum, LHCK 222 and their hybrid Neelum x LHCK 222, were crossed to ten strains/varieties of linseed to detect the presence of epistatic, additive and dominance variation. Modified triple test-cross analysis was done for nine metric traits. Epistasis did not affect any of these traits. An additive–dominance model was fitted to all the traits. Both additive and dominance gene actions were found significant. However, additive gene action was predominant than dominance. Partial dominance was observed for all the traits studied.**

**Key words**: Modified triple test-cross, epistatic, additive dominance variance, linseed, *Linum usitatissimum* L.

A knowledge of the genetic system controlling the metric traits is important for devising an efficient selection programme through the use of an appropriate mating design. Ketata et al. [1] suggested modified triple test-cross analysis in which the parents, $L_1$, $L_2$, and their hybrid ($L_1$ x $L_2$) are crossed to a number of varieties instead of random $F_2$ individuals [2]. The present study has been undertaken to detect epistasis, additive and dominance components using the method of Ketata, with the objective of investigating the role of epistasis in determining inheritance of nine traits in linseed or its absence and to detect the extent of additive–dominance variance.

## MATERIALS AND METHODS

The material for the present study comprised two varieties, Neelum ($L_1$) and LHCK 222 ($L_2$) and their hybrid (Neelum x LHCK 222), designated as testers. These three testers were crossed to 10 strains of linseed. The characteristics of testers and lines are presented in

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Table 1. The experimental materials consisting of 2 testers, 10 lines, 21 single crosses, and 10 three-way crosses were grown in randomized block design with three replications at the Farm of Narendra Deva University of Agriculture and Technology, Narendranagar, Faizabad, during winter 1985-86. Each entry was sown in a single row of 3 m length. The inter- and intrarow spacings were 30 and 10 cm, respectively. The data were recorded on 5 random competitive plants for nine quantitative characters (Tables 2, 3).

**Table 1. Characteristics of linseed lines selected for crossing with testers**

| Parent or tester | Tillering | Stature | Time of flowering | 1000-grain weight | Oil content (%) |
|---|---|---|---|---|---|
| T 397 | Moderate | Medium tall | Medium | Medium | 44 |
| Mukta | Moderate–low | Short | Early | Heavy | 45 |
| DPL 21 | High | Tall | Late | Medium | 40 |
| DPL 17 | High | Tall | Late | Medium | 41 |
| CI 1889 | Moderate–high | Tall | Late | Light–medium | 40 |
| M 54 | Moderate | Medium | Medium late | Medium heavy | 40 |
| C 429 | Low | Short | Early | Medium | 44 |
| LS 2 | Moderate | Medium tall | Medium | Medium | 43 |
| LHCK 172 | High | Tall | Late | Light–medium | 38 |
| R 552 | Moderate | Medium tall | Medium | Medium–heavy | 42 |
| Neelum (tester, $L_1$) | Moderate | Medium tall | Medium | Heavy | 43 |
| LHCK 222 (tester, $L_2$) | High | Tall | Late | Medium | 38 |
| Neelum x LHCK 222 (tester) | Moderate–high | Medium tall | Early–medium | Medium heavy | 45 |

For detection of epistasis, modified triple test-cross analysis was done. Where epistasis was not significant, an additive–dominance model was fitted [3].

## RESULTS AND DISCUSSION

*Detection of epistasis.* The mean squares for epistatic deviation of the nine traits are given in Table 2. The variance due to epistasis was nonsignificant for all the traits, implying that epistasis was absent in the crosses and the parents. These results are in agreement with those reported in wheat and rice. It was thus concluded that the testers may have some common loci which do not segregate in the population. In the present study two testers, $L_1$ and $L_2$, are significantly different for all the characters studied. Despite these differences, it is still possible that the testers may not be divergent enough to enable detection of epistasis by this method.

Table 2. Mean square for epistatic deviation for the nine characters of linseed

| Source | d.f. | Days to flowering | Plant height | Tillers per plant | Capsules per plant | 1000-seed weight | Seed yield per plant | Oil content | Refractive index | HCN content |
|---|---|---|---|---|---|---|---|---|---|---|
| Epistasis | 9 | 88.1$^{ns}$ | 35.9$^{ns}$ | 13.6$^{ns}$ | 4138.3$^{ns}$ | 6.0$^{ns}$ | 4.7$^{ns}$ | 43.8$^{ns}$ | 0.004$^{ns}$ | 5744.7$^{ns}$ |
| Error | 20 | 127.0 | 313.4 | 52.0 | 4639.7 | 7.2 | 4.1 | 64.6 | 0.007 | 8565.8 |

ns—nonsignificant.

*Additive and dominance model.* In the absence of epistasis analysis of variance for sums ($L_{1i}$ + $L_{2i}$) and differences ($L_{1i}$ –$L_{2i}$) provide direct means of estimating the additive and dominance components, respectively (Table 3). These estimates may be confounded with location effect since the experiment was conducted at only one location. In other environments or with other sets of lines, the traits studied may show epistatic effects.

The additive and dominance components of genetic variance were significant for all the characters, except refractive index. This indicated that both additive and dominance gene effects are relevant in the inheritance of these characters. Dominance contributed to the variation in days to flowering, plant height, tiller No., capsules/plant, 1000-seed weight, seed yield/plant, oil and HCN content.

Table 3. Estimates of additive (D) and dominance (H) variance components and degree of dominance $(H/D)^{0.5}$ for traits not showing significant epistasis

| Component | Days to flowering | Plant height | Tillers per plant | Capsules per plant | 1000-seed weight | Seed yield per plant | Oil content | Refractive index | HCN content |
|---|---|---|---|---|---|---|---|---|---|
| D | 1073.6$^{**}$ | 1049.0$^{**}$ | 68.8$^{**}$ | 4888.2$^{**}$ | 12.1$^{**}$ | 96.3$^{**}$ | 145.2$^{**}$ | 0.04 | 30349.6$^{**}$ |
| H | 199.6$^{**}$ | 261.0$^{**}$ | 13.6$^{**}$ | 2281.6$^{**}$ | 2.27$^{*}$ | 1.1$^{**}$ | 124.8$^{**}$ | 0.01 | 8879.4$^{**}$ |
| $(H/D)^{0.5}$ | 0.4 | 0.5 | 0.4 | 0.7 | 0.5 | 0.1 | 0.9 | 0.40 | 0.5 |

$^{*,**}$Significant at 5% and 1% levels, respectively.

Average degree of dominance $(H/D)^{0.5}$ ranged from 0.11 for seed yield to 0.93 for oil content. Beside these characters, partial dominance was also observed for HCN content, plant height, 1000- seed weight, No. of tillers and capsules/plant, days to flowering, and refractive index. These results are in agreement with those reported earlier [4, 5] in linseed.

The present study shows the predominance of additive type of gene action for yield, its components and quality characters, although dominance variance was also detected. Under such circumstances, it is suggested that biparental mating design III [6] may be used to identify promising genotypes of linseed.

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