

Effect of Genetic variability on seed yield and oil content in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

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Ten parents of wide phenotypic differences and their 45F₁S and 45F₂S progenies were studied to assess the genetic variability among the parents and progenies for seed yield and oil content attributes for improvement in Indian mustard. The seed yield and oil content related to days to flowering, number of primary and secondary branches / plant, 1000 grain weight, length of main fruiting branches, harvest index exhibited significant differences among parents and the progenies but 1000 grain weight did not show any significant difference among F₁S and F₂S. Therefore, the direct and indirect selection efficiency through desirable characters is to be fixed for high yield. The range and variability are the measurements of parents and progenies, which will be supporting analogs for selection.

Key words : Variability, *Brassica juncea*, Oil content

INTRODUCTION

Rapeseed - mustard crops occupy a prominent place being next in importance to groundnut. India has about 6 million hectares for rapeseed-mustard cultivation with an average yield of 1150 Kg/ha. The yield of Asian Countries are below the world average (1613 Kg/ha). In order to increase the seed yield and oil content it is essential to develop high yielding potential varieties along with better oil content. The knowledge of genetic system is important for the improvement programme in any crop. Hence, the present investigation was, carried out to find out the seed yield and oil content improvement contributed by different hybrids of Indian mustard.

MATERIALS AND METHODS

The base material comprised of ten widely diverse Indian mustard genotypes namely, CSR-1017, RL-18, LAHA-101, T-6342, RK-8901, RK-8601, RK-8608, RK-8701, A-11 and B-85. All possible single cross combinations were among all the parents in a diallel fashion. The experiment was sown in Randomized Block Design with three replications at Research farm of C.S.A. Univ. of Agriculture and Technology, Kanpur. All the treatments were grown in 5 m. long three rows plots. Twenty plants were taken at random from each of F₁S and F₂S and ten plants each of parent in each replication and data were collected and compiled for biometrical analysis.

RESULTS AND DISCUSSION

The data obtained from the present investigation on

seed yield and oil content improvement for eight character viz., days to flowering, number of primary and secondary branches / plant, length of main fruiting branch, seed yield / plant, harvest index, 1000 grain weight and oil content. The analysis of variance (Table 1) for all the characters were subjected for 'F' test to know the significant differences among the parents and offspring's for different attributes. The parent, F₁S and F₂S showed significant variation among all the traits except number of primary branches / plant for parent and 1000 grain weight for F₁S and F₂S. Parents vs crosses did not show any significant difference for the characters days to flowering, 1000 grain weight and oil content. F₁S and F₂S showed differences significantly for all the characters except 1000 grain weight and oil content. The data presented in Table 2 revealed the range and variability in the traits. The high variation in days to flowering in F₁S population was 45.27-69.83 as compared to parent and F₂S, which indicated presence of both additive and non - additive gene interactions (Asthana and Pandey, 1977). The maximum number (6.43-10.63) of primary branches in F₁S and secondary branches / plant (20.70-37.67) in F₁S indicated involvement of non-allelic gene interactions in the expression of this character. The large variations in length of main fruiting branch in F₁S (70.17 - 96.03) and F₂S (66.19 - 90.02) were observed. Such type of variability occurs due to non-additive gene effects (Anand and Rawat, 1978). The seed yield / plant exhibited higher mean values (36.24g) in F₁S populations over the F₂S (26.37g) and parents (21.21g). Such type of genetic variability is additive gene effects in the progenies (Varshney *et al.*, 1990). The