

GENETIC ANALYSIS OF SEED YIELD AND ITS COMPONENTS IN YELLOW SARSON UNDER ARID CONDITIONS

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The lack of high yielding varieties of *Brassica campestris* var. *yellow sarson* has led to its gradual vanishing from its traditional areas in favour of Indian mustard. Efforts are, therefore, needed to evolve better cultivars in this crop to check its complete elimination. For developing the superior varieties through breeding efforts, it was necessary to analyse the genetic control of various characters to launch a systematic breeding approach.

The experimental material consisted of 28 F_1 crosses (excluding reciprocals) developed from an 8 x 8 diallel set of yellow sarson. The parents were 'YSC 86', 'YSC 5', 'YSC 96', 'YSC 128', 'YSC 84', 'YST 151', 'YSPb 24', and 'YSIK 80-BL'. The parents and their 28 F_1 crosses were raised in a Randomized Block Design with three replications under rainfed conditions of regional Research Station, Bawal (Mahendergarh), Haryana during winter season of 1985-86. Each entry was represented by a single row of 4-metre length. The soil was fertilized with 40 kg N/ha and the crop was protected from aphids. Observations on days to 50% flowering, plant height (cm), primary branches (no.), siliquae on main shoot (no.), seeds per siliqua (no.), oil content (%) and seed yield per plant (g) were recorded on five plants in each replication. Data were analysed following Hayman (1954) to calculate genetic components of variance such as D, H_1 , H_2 , h^2 , F and E. Various ratios were also computed after Askel and Johnson (1963).

Five II degree statistics were used for the estimation of the genetic components of variation (Table 1). Variation due to additive effects of genes (D) was significant for days to 50% flowering. Variation due to dominance effects of genes (H_1) was significant and higher than D for all the characters, suggesting more of the dominance action involved in the expression of these characters. Covariation of additive and dominance effect was positive for all the characters and it was significant for days to 50% flowering, primary branches, seeds per siliqua and oil content indicating an excess of dominant alleles. (Crumpacker and Allard, 1962). Asymmetry of positive and negative effects of genes (H_2) was high but less than H_1 in all the characters. Net dominant effect (h^2) was low and non-significant. The component of variation (E) was non-significant except for days to 50% flowering indicating absence of environmental variation for rest of the characters.

Table 1. Estimation of genetic variance for yield and other characters in 8 x 8 diallel crosses of yellow sarson

Components	Days to 50% flowering	Plant height	No. of primary branches	Siliquae on main shoot	No. of seeds per siliqua	Oil content	Yield/plant
D	8.34*	1.46	2.19	13.46	3.84	2.00	4.16
H ₁	8.47*	3.19*	20.50*	130.30*	18.00*	13.59*	106.07*
H ₂	5.95*	2.07*	13.08	110.88*	13.38*	10.53*	101.59
F	6.76*	0.81	8.07*	13.47	6.50*	3.65*	1.91
h ₂	1.87	0.69	0.92	0.21	0.38	0.13	26.73*
E	0.86*	0.06	0.61	2.53	0.29	0.02	5.19
(H ₁ /D) ^{0.5}	1.08	1.47	3.05	3.11	2.16	2.60	5.04
H ₂ /4H ₁	0.17	0.16	0.15	0.21	0.18	0.19	0.23
$\frac{(4DH)^{0.5} + F}{(4DH)^{0.5} - F}$	2.34	1.46	4.02	1.38	2.28	2.07	1.09
h ² /H ₂	0.31	0.33	0.07	0.002*	0.02	0.01	0.26
H ₁ -H ₂	2.52*	1.12*	7.42*	19.42	4.62*	3.06*	4.48*
r	-0.09	-0.43	-0.58	-0.03	0.15	-0.71	0.62
r ²	0.81	0.18	0.33	0.09	0.02	0.50	0.38

* P = 0.05

Overall degree of dominance H_1/D was 1.0 for all the characters. Average frequency of positive (u) versus negative (v) alleles in the parents, expressed as $H_2/4H_1$, was 0.25 for all the seven characters indicating more of positive alleles. The ratio of the total number of dominant to recessive genes in the parents, $(4DH)^{0.5} + F / (4DH)^{0.5} - F$, was positive for all the characters, again indicating an excess of dominant genes involved in the control of these characters. The ratio of h^2/H_2 was below unity for all the characters indicating that these characters were under the control of a single gene group. Deviation of H_2 from H_1 indicated distribution of genes in the direction of dominance.

REFERENCES

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