



## Genetic variability, correlation and path analysis in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]

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Indian mustard (*Brassica juncea*) is one of the most important oilseed crops of India. In order to incorporate desirable characters to maximize economic yields, the information on the nature and extent of genetic variability present in a population for desirable characters, their association and relative contribution to yield constitutes the basic requirement. The present study was under taken to find out the genetic variability available, heritability and genetic advance, the association of different characters and their contribution to define seed yield.

The material of the present study consisted of 55 genotypes including mutants and inter-specific derivatives along with released varieties and selections. These were grown in randomized block design with three replications, at Agricultural Research Station, Rajasthan Agricultural University, Bikaner (raj.). Each plot consisted of single row of 5 m length with row to row and plant to plant spacing of 40 cm and 15 cm, respectively. At maturity the data were recorded on 5 randomly selected plants for eight quantitative traits. Analysis of variance was performed following the standard procedures. The phenotypic and genotypic coefficient of variability (PCV, GCV) were computed according to the method suggested by Burton [1], heritability ( $h^2$ ) and genetic advance (GA) as per Johnson *et al.* [2]. Path coefficient analysis was done using genotypic correlation coefficients following Dewey and Lu [3].

The variance analysis showed that the genotypes differ significantly among themselves for all the characters under study except seeds per pod, indicating the presence of adequate variability. The phenotypic coefficients of variation (PCV) were invariably slightly higher than their corresponding genotypic coefficient of variation (GCV) due to the environmental influence (Table 1). The higher estimates of heritability coupled with higher genetic advance for yield per plant, test

**Table 1.** Mean, variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ( $h^2$ ) and genetic advance (GA) in mustard

Character	mean	Variance	GCV	PCV	$h^2$	GA	GA (% of mean)
Plant height (cm)	183.0	2696.3*	16.2	16.7	93.6	59.1	32.3
Length of main branch (cm)	80.0	448.1*	14.8	16.3	82.7	22.1	27.7
Branches/ plant	6.7	10.0*	24.8	31.5	61.6	2.7	39.9
Pods on main branch	43.6	319.5*	22.4	26.1	73.5	17.2	39.5
Seeds/ siliqua	14.6	10.8	9.6	17.9	29.0	1.6	10.7
Yield/ plant (g)	23.4	847.7*	71.4	72.6	96.8	33.9	144.7
test weight (g)	5.2	5.3*	25.3	26.3	90.5	2.6	49.6
Oil content (%)	33.8	38.3*	9.7	12.1	64.4	5.4	16.1
Days to flowering	54.8	123.9*	11.7	3.7	96.7	12.9	23.6
Days to maturity	133.7	73.6*	11.9	3.8	92.5	9.7	7.3

\*Significant  $p = 0.05$

weight, siliqua on main branch, and branches per plant indicated that heritability of the trait is mainly due to additive effects and selection is effective for such traits. High heritability accompanied with medium to low genetic advance for plant height, length of main branch, days to flowering is indicative of non-additive gene action and the high heritability is being exhibited due to favourable influence of the environment rather than genotypes [4].

Correlation studies showed that for most character pairs, genotypic and phenotypic associations were in the same direction and the genotypic estimates were higher than the phenotypic ones, indicating an inherited association between the characters. Yield per plant the most important economic trait, exhibited highest positive association with branches per plant (0.813), followed by siliqua on main branch (0.463), plant height (0.413), seeds per siliqua (0.392), and length of main branch (0.296). The negative correlation of oil content with test weight (-0.050) indicated that bolder seeded genotypes have less oil content.

The characters plant height, length of main branch, branches per plant, siliqua on main branch, seeds per siliqua and yield per plant were positively associated with each other, also reported by many authors [5, 6].

The path analysis revealed that the number of branches per plant is most pronounced character contributing directly to yield and most other characters associated to yield are contributing indirectly through this character. Similar results were reported by Satyavati et al. (6)

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