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## Study of heritability and genetic advance in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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### Abstract

The present research was carried out at the Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University during the year 2017-2019. Studies were undertaken to estimate the genetic advances and heritability for 15 characters among different generations (F1, F2, P1, P2, BC1 and BC2) of five families in Indian mustard. High estimates of both narrow sense heritability and expected genetic advances for the characters for primary branches per plant, secondary branches per plant, the effective length of the main branch, siliquae per plant, biological yield per plant, harvest index (%) and oil content (%) suggested the preponderance of additive/fixable gene effect. These characters could be improved through the direct selection of desirable segregants.

**Keywords:** Genetic advance, heritability, Indian mustard

### Introduction

Indian mustard (*Brassica juncea* L.) belong to family Brassicaceae or cruciferae with chromosome number  $2n=4x=36$ . Indian mustard is one of the most important edible oil with the lowest amount of saturated fats in the country and it occupies considerably large acreage among the brassica group oil seed, a leafy vegetable rich in minerals, antioxidants and tasteful condiment crop. It is a self-pollinating crop, however, due to entomophily, there is 2–15% cross-pollination. Nearly 5% of the Gross National Product and 10% of the value of agricultural goods in India are derived from oilseed crops. The second-largest indigenous oilseed crop in India is rapeseed mustard, which contributes 32% to the country's overall oilseed production. Important species like yellow sarson (*B. campestris*) and Indian mustard (*B. juncea*) are mostly farmed as oilseed crops in subtropical and tropical regions. In India, the rapeseed mustard group of crops is dominated (about 90%) by Indian mustard. The Indian cuisine includes a lot of mustard oil. Among rapeseed and mustard, rai (*B. juncea*) is very popular among farmers due to its higher yield and greater tolerance against lodging, shattering, drought conditions, heat and relative diseases as well as saline-sodic conditions. Brassica also performs well on neglected sites where problems like soil acidity, low available nutrient content, poor drainage, drought, and soils with topographical limitations exist germplasm, which is a prerequisite for any breeding programme, serves as a valuable source material as it provides scope for building for genetic variability. Estimating factors like heritability and genetic advance is a need for effective selection. Estimates of heritability and genetic advance are useful in assessing the suitability of a character for selection.

### Material and Methods

The present study was carried out at Agronomy Farm, B. A. College of Agriculture, Anand Agricultural University, Anand during the rabi season in 2017-2019. The experimental material is composed of five families each representing six generations (P1, P2, F1, F2, B1 and B2). Six families were developed from six parents viz. GM 1, GM 2, GM 3, Rayad 9602, NRCM 120 and NRCM 353. They were collected from different research centres according to morphological variation. These generations were grown in a Randomized Complete Block Design using three replication each. Each plot consisted of a single row of 3-meter length and 3.3-meter width (P1- 1 line, P2-1 line, F1-1 line, F2-4 line, BC1-2line & BC2-2line). The distance between plant to plant 10 cm and row-to-row 30 cm is maintained. All the recommended culture and plant protection practices were adopted for raising a good crop. Data were recorded on five Randomly selected plants from each line for fifteen characters viz., days

to flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, effective length of main branch (cm), siliquae per plant, siliqua length (cm), seeds per siliqua, 1000 seed weight (g), seed yield per plant (g), Biological yield per plant (g), Harvest Index (%), oil content (%), protein content (%).

**Heritability**

**Heritability in Broad Sense**

The broad sense heritability in percent was calculated by using formula suggested by Burton (1951) [3] as follows.

$$h^2_{bs} (\%) = \frac{VF_2 - VF_1}{VF_2}$$

**Heritability in Narrow Sense**

The narrow sense heritability (h<sup>2</sup><sub>ns</sub>) in percent from the estimates of basic generations was calculated by using formula suggested by Warner (1952) [15] as follows.

$$h^2_{ns} (\%) = \frac{2VF_2 - (VB_1 + VB_2)}{VF_2} \times 100$$

**Estimation of expected genetic advance under selection:**

The expected genetic advance at 5% selection intensity was estimated by using formula suggested by Allard (1960) [1]

$$G.A. = h^2_{ns} \times K \times \sigma_p$$

Where,

h<sup>2</sup><sub>ns</sub> = Heritability in narrow sense

K = Selection differential (K=2.06) at 5% selection intensity

σ<sub>p</sub> = Phenotypic standard deviation

Expected genetic advance as percent of population mean was obtained by using following formula.

$$\text{Genetic advance as percent of mean} = (G.A.)/X \times 100$$

Where,

$$X = \frac{P_1 + P_2}{2} \text{ (Base population mean)}$$

G.A. = Expected genetic advance

**Result and Discussion**

The estimates of heritability and genetic advance are important selection parameters. The metric traits are largely affected by the external environment; therefore, those limit its expression. To predict the selection response in case, where heritability is mainly due to non-additive gene effects, the expected genetic gain will low, but if it is due to additive gene effects, high gene advance is expected.

The broad sense heritability was high for days to flowering in families I (83.24), IV (74.20) and V (60.74); for days to maturity in family I (80.02), III (59.55), IV (77.13) and V (75.48); for siliqua length in family IV (52.25); for 1000 seed weight in family II (69.00) and V (66.08); for harvest index in family III (77.49), for oil content in family I (71.89), II (53.14), IV (78.99) and V (68.43), except this all other families and character exhibited low to moderate broad sense heritability, which indicating the predominant role of additive gene action. Respectively, these approximations of the current study were authorized with the outcome by Verma *et al.* (2016) [14], Maurya *et al.*, (2018) [7], Narlagadda and Pandey (2021) [9], Nandi *et al.* (2021) [8], Nishad *et al.* (2022) [10] and Pal *et al.* (2019) [11].

High estimates of narrow sense heritability coupled with high genetic advance observed for primary branches per plant in families I (40.43, 33.10), III (40.43, 21.99) and IV (42.70, 31.27), secondary branches per plant in family I (128.30, 21.99), effective length of main branch in family II (83.16, 30.08) and III (62.75, 20.95), siliqua per plant in family I (47.97, 38.06), biological yield per plant in family I (75.21, 139.53), harvest index (%) in family III (124.39, 175.07), oil content (%) in family I (132.47, 35.16), II (97.87, 23.90) and IV (97.24, 20.24) and similar results were also reported by Kumar *et al.* (2019) [6, 13], Prajapati *et al.* (2020) [12], Gadi *et al.* (2020) [4], Tripathi *et al.* (2019) [13], Awasthi *et al.* (2020) [2] and Jat *et al.* (2019) [5].

High narrow sense heritability and moderate genetic advance were observed for siliqua length in family I (93.19, 18.39) and seeds per siliqua in family II (73.83, 15.66). Therefore, improvement of these characteristics would be possible with use of the aforesaid through a simple selection approach in segregating generation (Narlagadda and Pandey 2021) [9].

**Table 1:** Estimates of heritability (Broad-sense and narrow sense) and expected genetic advance (% of mean) for yield attributing traits in Indian Mustard.

Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Days to Flowering					Days to Maturity				
h <sup>2</sup> <sub>bs</sub> (%)	83.24	-	37.12	74.20	60.74	80.02	16.32	59.55	77.13	75.48
h <sup>2</sup> <sub>ns</sub> (%)	-	34.34	19.79	60.32	5.36	-	17.91	-	-	67.88
G.A. (%)	-	3.76	2.67	8.90	0.64	-	1.21	-	-	4.56
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Plant Height					Primary Branches Per Plant				
h <sup>2</sup> <sub>bs</sub> (%)	-	37.28	-	-	25.20	39.92	9.72	-	-	-
h <sup>2</sup> <sub>ns</sub> (%)	-	-	7.58	-	-	40.43	-	40.43	42.70	-
G.A. (%)	-	-	0.92	-	-	33.10	-	21.99	31.27	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Secondary Branches Per Plant					Effective Length of Main Branch				
h <sup>2</sup> <sub>bs</sub> (%)	-	-	-	-	32.40	5.76	-	47.24	-	31.70
h <sup>2</sup> <sub>ns</sub> (%)	128.3	-	-	-	14.58	-	83.16	62.75	-	-
G.A. (%)	21.99	-	-	-	9.71	-	30.08	20.95	-	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Siliquae Per Plant					Siliqua Length				

$h^2_{bs}$ (%)	13.90	-	-	2.54	67.77	11.08	31.00	-	52.25	-
$h^2_{ns}$ (%)	47.97	-	-	-	-	93.19	10.75	32.54	39.90	-
G.A. (%)	38.06	-	-	-	-	18.39	2.00	4.36	7.29	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Seeds Per Siliqua					1000 Seed Weight				
$h^2_{bs}$ (%)	46.32	-	17.15	14.29	13.10	13.25	69.00	-	-	66.08
$h^2_{ns}$ (%)	7.40	73.83	-	-	-	-	24.92	15.88	-	-
G.A. (%)	1.59	15.66	-	-	-	-	9.86	3.89	-	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Seed Yield Per Plant					Biological Yield Per Plant				
$h^2_{bs}$ (%)	-	-	33.48	38.92	47.90	-	-	-	10.25	9.51
$h^2_{ns}$ (%)	-	-	-	-	-	75.21	-	-	8.10	-
G.A. (%)	-	-	-	-	-	139.53	-	-	16.77	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Harvest Index					Oil Content				
$h^2_{bs}$ (%)	30.97	-	77.49	18.42	8.01	71.89	53.14	41.34	78.99	68.43
$h^2_{ns}$ (%)	-	-	124.39	-	-	132.47	97.87	-	97.24	-
G.A. (%)	-	-	175.07	-	-	35.16	23.90	-	20.24	-
Family	I	II	III	IV	V	I	II	III	IV	V
Characters	Protein Content									
$h^2_{bs}$ (%)	-	-	-	-	-	-	34.09	-	-	-
$h^2_{ns}$ (%)	-	-	-	-	-	-	51.62	-	-	-
G.A. (%)	-	-	-	-	-	-	2.58	-	-	-

\*(-) Genetic variance not estimated because of the -ve values of heritability

## Conclusion

High estimates of both narrow sense heritability and expected genetic advances for the characters for primary branches per plant, secondary branches per plant, effective length of main branch, siliqua per plant, biological yield per plant, harvest index (%) and oil content (%) suggested the preponderance of additive/fixable gene effect. These characters could be improved through the direct selection of desirable segregants. For the majority of the traits in different families, low to moderate values of expected genetic advance were found in combination with high levels of narrow sense heritability. This suggested that both additive and nonadditive gene influences might affect the inheritance of these traits. Direct selection would not be advantageous for such features since strong narrow sense heritability implies high selection efficiency. Population improvement strategies would be more helpful for such characters' improvement.

The combination of low heritability estimates along with low expected genetic advance was detected for days to maturity and siliqua length with family II, and for seeds per siliqua with family I. Improvement of would be very difficult for such characters even with efficient population improvement approaches; therefore, such families may be eradicated from breeding populations, and more consideration could be diverted to promising families and /or responsive characters.

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