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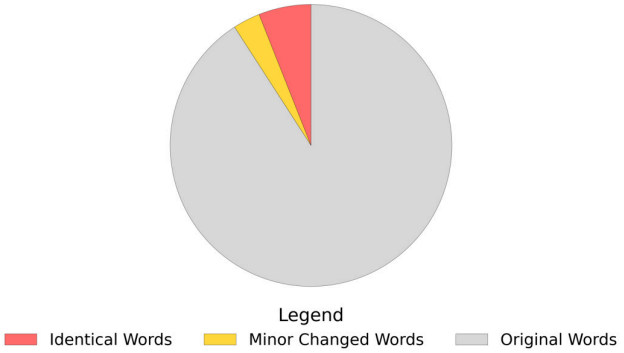

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Study of Genetic Variability and Yield Component Associations in Indian Mustard (Brassica juncea L.)

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Abstract

The present investigation was carried out to assess genetic variability and inter-relationships among yield and its component traits in Indian mustard (*Brassica juncea* L.). The experiment was conducted during the rabi season of 2023–24 at the research farm of J.V. College, Baraut, Baghpat (U.P.), which has clay-loam soil, annual rainfall ranging from 750 to 1190 mm, and temperature variation between 15°C and 30°C. Thirty mustard genotypes were evaluated in a randomized block design with appropriate replications. Observations were recorded on five randomly selected plants per replication for twelve agro-morphological traits, including flowering and maturity duration, plant height, branching pattern, siliqua traits, seed attributes, biological yield, seed yield, and harvest index. Analysis of variance revealed significant differences among genotypes for most of the traits, indicating the presence of substantial genetic variability. Genotypic and phenotypic coefficients of variation, heritability, genetic advance, correlation, and genetic divergence were estimated using standard statistical procedures. Higher estimates of variability, heritability, and genetic advance were observed for yield and its related traits, suggesting good scope for selection. Correlation and divergence analyses identified important yield-contributing characters, which can be effectively utilized in mustard breeding programs aimed at yield improvement.

Keywords: Genetic variability, Indian mustard, Yield components, Heritability

Introduction

Rapeseed and mustard (*Brassica* spp.) represent the third most important group of oilseed crops in India after soybean, contributing nearly 27% of the national oilseed production (DRMR, 2020; Meena et al., 2015). These crops are central to India's edible oil economy due to their high oil content, broader adaptability, and tolerance to diverse environmental conditions. Six *Brassica* species are cultivated in India, comprising three diploids—*B. rapa*, *B. oleracea*, and *B. nigra*—and three amphidiploids—*B. juncea*, *B. napus*, and *B. carinata* (Prakash et al., 2009). Among these, *Brassica juncea* is the dominant species, accounting for more than 80% of the total rapeseed–mustard acreage and production (Chauhan et al., 2011; DRMR, 2020). Its predominance is attributed to wider adaptability and better tolerance to major biotic and abiotic stresses compared to other *Brassica* oilseed species.

Indian mustard is widely cultivated in Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh, and Gujarat, and to a lesser extent in the non-traditional southern states of Karnataka, Tamil Nadu, and Andhra Pradesh (Shekhawat et al., 2012). Other *Brassica* forms such as yellow sarson, brown sarson, gobhi sarson, karan rai, and taramira are cultivated according to regional ecological conditions and contribute variably to oilseed supply (DRMR, 2020).

Understanding genetic diversity within rapeseed–mustard is crucial for strengthening breeding programs aimed at improving yield, stress tolerance, and seed quality. Genetic diversity exists at three levels—gene/germplasm level, species level, and ecosystem level—and forms the foundation of crop improvement (Gepts, 2006). Several approaches—including morphological characterization, biochemical markers, and molecular markers—are routinely employed to assess variability and identify promising genotypes (Rakow & Raney, 2005; Prakash et al., 2009).

For effective breeding, knowledge of genetic variability, interrelationships among yield components, and the direct and indirect effects of traits on yield is essential. Correlation analysis helps determine the strength and nature of associations among traits, while path coefficient analysis (Wright, 1921) partitions correlation coefficients to reveal direct and indirect contributions of individual traits. These tools together guide selection strategies for improving seed yield in *Brassica* crops. Hence, the present study aims to evaluate genetic variability, trait associations, and yield determinants in Indian mustard using agro-morphological traits to facilitate the selection of promising genotypes for future breeding interventions.

Materials and methods The experiment was conducted at J.V. College Baraut Baghpat U.P. in 2023-24. The area is also suitable for Mustard production with clay-loam type of soil, annual rainfall of 750-1190 mm and the highest and lowest temperature of the area are 30°c and 15°c, respectively. Thirty mustard genotypes were sown during the rabi season of 2023–24 in a randomized block design (RBD). The observations were recorded on individual plant basis on five randomly selected plants from each replication for 12 characters viz., days to 50 % flowering, days to maturity, plant height (cm), number of primary branch per plant, number of secondary branch

per plant, siliqua length (cm), number of siliquae on main shoot, number of seeds per siliqua, 1000-seed weight (g), biological yield per plant (g), seed yield per plant (gm), harvest index (%). Procedure adopted for recording the observations for each character is described as below. Analysis of variance was carried out as per standard procedure **(Fisher 1938).** Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) **(Burton 1952),** heritability **(Burton and Devane in 1978),** genetic advance **(Johanson *et al.*1955),** genetic divergence **(Beale, 1969; spark, 1973)** were estimated.

Results and discussion

Analysis of Variance

The analysis of variance for the12 characters studied is given in Table 1. There was a highly significant difference (P <0.061) among the tested genotypes for days to 50 % flowering, days to maturity, plant height (cm), No. of siliqua om main shoot, number of seed per siliqua (g), and harvest index. Significant differences (P<0.24) were observed for biological yield and grain yield. Non-significant differences were observed for traits like siliqua length (cm), flag leaf area (cm^2), and 1000- seed weight (Table 1).

Table 1: ANOVA table showing mean squares for genotypes, error mean square and replication mean squares

Characters	Replication	Treatment	Error
Degree of freedom	2	29	58
Days to 50% flowering	0.061	296.50**	11.47
Plant height	1.01	16.55**	3.89
no. of primary branch/plant	1.8	865.57**	1.01
No. of secondary branch/plant	0.08	16.11**	1.45
No. of siliqua om main shoot	8.71	67.68**	2.86
Length of siliqua	0.18	1.24**	0.04
No. of seed/siliqua	0.03	4.64**	0.28
Day to maturity	4.44	197.58**	1.62

1000-seed weight	0.03	0.65**	0.01
Biological yield/plant	0.24	2401.73**	0.85
Grain yield/plant	2.43	38.25**	0.58
Harvest index	0.99	44.30**	1.34

Where, Df= Degrees of freedom, ns=non-significant, * and ** indicates significant and highly significant respectively. **significant at 1% and *significant at 5% level

Variability parameters and per se performance:

Mean values of 30 genotypes for 12 characters were recorded carefully and presented in Table 2. The mean performance of different genotypes for the characters gave the first-hand information for the variability present in the materials under study and gives an opportunity to the plant breeders to select the diverse parents as per objective of the breeding in mustard crop. Among 30 genotypes of mustard M-57 (24.03g) genotype was observed highest mean performance for seed yield per plant followed by M-28 (24.00 g), PH-31 (23.30 g) and Kranti (23.17 g) indicating that these genotypes can be used in hybridization programs in order to achieve target environment in yield. The days to 50% flowering ranged from 34.00-69.00 days in genotype Giriraj (34.00) days to genotype Varuna (69.00) with a grand mean of 53.60 days. Days to maturity among all the genotypes about 22 day's variation was recorded at the maximum in respect of maturity. PM-30 was the earliest genotype for harvesting (123.67 days) and the genotype M-57 took maximum number of days (146.00 days) for harvesting. PM-30 genotypes can be used as a donor in hybridization programs for involving early maturity or short duration mustard varieties. Mean plant height was 186.38 cm and ranged between154.50-223.67 cm. The genotype Pusa Bold produced taller plants, while lowest height of plant was recorded in the genotype GM-1.The maximum number of primary branch per plant was found in the genotype Pusa Agrani (6.67) followed by the genotype Pusa Jagannath (6.33) PM-34, RH-775 (6.00) and PM-30, Pusa Vijay (5.67) while genotype M-58, GM-1 and GM-2 recorded lowest number of primary branch per plant (4.00) with a general mean of 5.19.The maximum number of secondary branch per plant was found in the genotype PM-25 (15.00) followed by the genotype Giriraj, GM-1 (14.67) while genotype PM-57 had lowest number of secondary branch per plant (7.00) with a general mean of 10.86.The maximum number of siliqua on main shoot was recorded in the genotype GM-2 (45.67) while the genotype GM-1, GM-3, M-59, NRCHB-101 had the lowest number of siliqua on main shoot (29.00) with mean number of siliqua on main shoot 38.58.The maximum siliqua length was

recorded in the genotype Pusa Tarak (5.87) while the genotypes M-58 had the lowest siliqua length (3.23) with mean siliqua length 4.05.The maximum number of seed per siliqua varied from Bullet (12.03) for while the genotype GM-1 (11.23), whereas lowest M-59 (7.07) with mean number of seed per siliqua was 9.03. The maximum number of 1000-seed weight varied from Pusa Bold, Pusa Jagannath (5.32) for while the genotype Pusa Agrani, Pusa Tarak (5.30) wears lowest genotypes PH-31(3.80) with means 1000-seed weight 4.86. The genotype produced highest biological yield per plant PM-33 (135.03 g) whereas, the genotype Pusa Vijay showed minimum biological yield per plant (35.17 g) with a grand mean of 80.13 g. The maximum harvest index from varied Varuna (34.27) for whiles the genotype RH-775 (26.00) wears lowest genotype Pusa Jagannath (15.13) with a grand mean of 27.70 per cent.

Higher seed yield is the ultimate goal of any breeding programme which is the product of different combinations of desirable and non-desirable traits. A wide range of grain yield per plant genotype M-57 produced highest seed yield per plant (24.03 g) whereas, the genotype Varuna produced minimum seed yield per plant (13.13g) has been observed in the present investigation wheat M-57 (24.03 g), M-28 (24.00 g), PH-31 (23.30g), Kranti (23.17 g) and Bullet (22.67 g) were found to be the top five yielders among the 30 genotypes with significant mean value (18.40) over average value.

Table. No. 2: Mean performance for 12 characters of mustard genotypes.

Genotypes	D50%F	PH	NPBPP	NSBPP	NSMS	SL	NSPS	DM	1000-SW	BYPP	SYPP	HI
PINEAR45S46	65.00	188.57	5.33	12.67	43.00	3.41	11.17	142.00	4.47	91.40	20.33	24.03
BULLET	48.33	196.07	4.67	13.00	36.00	3.77	12.03	140.67	4.54	102.83	22.67	23.20
GIRIRAJ	34.00	178.43	5.33	14.67	45.00	4.20	9.03	142.67	4.30	95.53	21.17	23.30
GM1	54.67	154.50	4.00	14.67	45.33	4.33	11.23	142.33	4.38	101.42	21.07	20.87
GM-2	52.00	198.77	4.00	11.67	45.67	4.31	10.37	144.00	5.07	89.67	19.20	22.27
GM-3	51.33	159.97	5.67	12.00	45.33	4.40	8.13	140.67	5.08	89.87	20.13	23.40
JAY KISAN	51.33	158.57	5.33	12.00	45.33	3.77	10.20	142.33	5.10	86.00	20.36	24.53
KRANTI	37.00	189.53	5.33	13.00	37.67	3.33	9.37	138.00	4.50	96.17	23.17	23.30
M-28	59.00	180.07	5.00	12.33	36.67	3.60	10.13	143.67	4.10	127.37	24.00	19.43
M-57	42.33	180.37	4.67	13.00	44.33	3.60	7.73	146.00	5.21	115.17	24.03	21.00
M-58	44.00	214.50	4.00	12.67	42.00	3.23	8.23	140.67	4.21	91.87	19.37	20.73
M-59	50.67	172.90	4.00	10.67	45.33	3.77	7.07	140.67	4.00	83.38	18.70	23.13
NRCHB-101	46.33	204.27	4.33	12.00	45.33	3.60	10.00	141.00	5.22	103.23	21.03	19.63
PH-31	36.33	187.47	5.33	12.00	37.33	3.72	9.43	143.67	3.80	115.53	23.30	22.97
PM-25	44.33	183.70	5.33	15.00	37.67	3.58	8.53	142.00	4.21	108.17	22.90	21.60
PM-26	56.67	179.20	6.00	9.00	35.33	3.90	9.90	126.00	5.10	39.25	18.08	19.07
PM-27	61.67	185.53	5.33	9.00	33.00	3.60	7.67	126.00	5.26	61.63	17.49	27.67
PM-30	64.67	184.27	5.67	7.00	35.00	4.00	8.83	123.67	5.20	73.40	14.08	19.27
PM-32	57.00	202.30	4.67	7.67	34.00	4.50	9.57	124.00	5.10	59.83	14.61	25.23
PM-33	65.67	216.73	5.00	10.00	37.00	4.20	9.50	123.67	5.15	135.03	13.76	20.27
PM-34	55.67	206.27	6.00	8.67	36.67	4.00	8.13	128.00	5.13	72.40	14.22	19.60
PM-57	63.33	190.27	5.33	7.00	33.67	4.10	8.07	124.00	5.08	81.63	16.74	19.03
PUSA AGRANI	65.33	163.57	6.67	8.00	34.33	4.83	7.87	126.33	5.30	65.77	14.28	22.13
PUSA BOLD	51.67	223.67	5.00	9.00	34.33	5.00	7.20	128.67	5.32	40.65	14.37	31.77
PUSA JAGANNATH	41.67	183.27	6.33	12.00	36.33	5.80	7.57	125.00	5.32	37.70	16.03	15.13
PUSA TARAK	48.33	165.43	5.33	9.00	36.67	5.87	8.93	125.67	5.30	53.17	14.08	25.55
PUSA VIJAY	59.33	185.90	5.67	10.00	36.67	4.20	9.77	127.67	5.00	35.17	18.27	23.37
RH0119	68.33	196.10	5.00	9.00	38.00	3.50	8.73	128.00	5.09	38.07	13.25	19.28
VARUNA	69.00	177.60	5.33	8.00	29.00	3.77	8.17	136.67	5.23	41.17	13.13	34.27
RH725	63.05	183.63	6.00	11.00	35.33	3.60	8.33	132.00	5.12	71.33	18.17	26.00
Mean	**53.60**	**186.38**	**5.19**	**10.86**	**38.58**	**4.05**	**9.03**	**134.52**	**4.86**	**80.13**	**18.40**	**22.70**
C.V.	6.32	0.54	27.99	11.08	4.38	5.10	5.88	0.95	1.80	1.15	4.13	5.10
S.E.	1.96	0.58	0.84	0.69	0.98	0.12	0.31	0.73	0.05	0.53	0.44	0.67
C.D. 5%	5.54	1.64	-	1.97	2.76	0.34	0.87	2.08	0.14	1.51	1.24	1.89
C.D. 1%	7.37	2.19	-	2.61	3.68	0.45	1.15	2.77	0.19	2.01	1.65	2.52
Min	**34.00**	**154.50**	**4.00**	**7.00**	**29.00**	**3.23**	**7.07**	**123.67**	**3.80**	**35.17**	**13.13**	**15.13**
MAX	**69.00**	**223.67**	**6.67**	**15.00**	**45.67**	**5.87**	**12.03**	**146.00**	**5.32**	**135.03**	**24.03**	**34.27**

It is understandable from the above discussion that the genotypes included in the study illustrated extensive range of variability in respect of all the eleven characters. Among 30 genotypes Giriraj (34.00) was found to be earliest day to 50% flowering, earliest maturity, shortest plant height and highest number of seed per siliqua. The genotype Pusa Tarak (5.87) was showed highest siliqua length. Genotype GM-2 (45.67) showed highest number of siliqua on main shoot. The mean performance Pusa Bold, Pusa Jagannath (5.32) was highest for 1000-seed weight whereas Varuna (34.27) for harvest index was the best performing genotypes for the respected characters. These results have been reported earlier by Chakraborty and Haque (2000), Rathi *et al.* (2002), Haddad (2004), Singh *et al*. (2005), Ahmad *et al.* (2021), sarkar *et al.* (2021) and Khatun *et al*. (2022) reported maximum variability for these traits. However, Low variability for yield and its contributing traits were reported by Ayaz *et al.* (2004). the minimum variance was recorded for number of seed per siliqua, 1000- seed weight, siliqua length and seed yield per plant. Result on these aspects was reported by Chakraborty and Haque (2000) and Rathi *et al.* (2002).

Heritability & Genetic Advance as per cent of mean:

Heritability is the proportion of phenotypic variance attributable to genetic variance and may be expressed in **broad or narrow sense**. Narrow-sense heritability reflects **additive gene effects**, whereas broad-sense heritability includes both **additive and non-additive effects**. In this study, heritability was estimated in the **broad sense**, which provides a general estimate and is often negatively correlated with narrow-sense heritability (Kempthorne, 1957). High heritability due to additive gene action results in **high genetic gain**, while non-additive gene action leads to **low genetic gain** (Panse, 1957). Heritability varies with population and environment and is important in crop improvement since only genetic variation is heritable. The Values of heritability in broad sense for all the characters studied were ranged from 0.49 per cent (number of primary branch/plant) to 1.00 per cent (plant height, biological yield/plant). High to heritability estimates observed for day to maturity (0.99), 1000-seed weight (0.99), seed yield/plant (0.99), siliqua length (0.97), harvest index (0.97), number of siliqua on main shoot (0.96), day to 50% flowering (0.96), while moderate heritability was estimated for number of seed per siliqua.

Genetic advance for various quantitative characters has been exhibited in table 3. The data reveals that number of primary branch per plant (0.69) showed lowest value of genetic advance followed by 1000-seed weight (0.95), siliqua length (1.28), number of seed per siliqua (2.41) and number of secondary branch per plant (4.34) whereas highest value of genetic advance at 5 per cent intensity of selection were biological yield per plant (58.27), plant height (34.96), day to 50%

flowering (19.67), day to maturity (16.58), number of siliqua on main shoot (9.37), harvest index (7.68) and seed yield per plant (7.25).

The genetic advance estimated as percentage of mean ranged from 12.33 to 72.72 per cent. The highest value of (72.72) per cent was exhibited by biological yield per plant followed by number of secondary branch/plant (40.03), seed yield per plant (39.37), day to 50% flowering (36.73), harvest index (33.82) and siliqua length (31.60). The moderate values were observed for number of seed per siliqua (26.65) and number of siliqua on main shoot (24.29). The lowest values were observed for 1000-seed weight (19.52) and plant height (18.76).number of primary branch per plant (13.32) and day to maturity (12.33).

Characters such as number of seeds per siliqua and number of siliqua on main shoot exhibited moderate genetic advance with high heritability, indicating reasonable scope for improvement through selection. Traits including biological yield per plant, number of secondary branches per plant, seed yield per plant, days to 50% flowering, harvest index, and siliqua length showed high heritability but comparatively lower genetic advance and GCV, suggesting limited response to selection. According to Johnson et al. (1955), characters with high heritability coupled with high genetic advance are more responsive to selection than those with high heritability but low genetic advance.

Traits such as days to maturity and number of primary branches per plant exhibited both high heritability and high genetic advance, indicating their improvement through pure line or mass selection. Moderate heritability and genetic advance observed for number of siliqua on main shoot and seed yield per plant suggest the predominance of additive gene action, making these traits amenable to selection, as also reported by Tyagi et al. (2010). Conversely, number of primary branches per plant showed low heritability with high genetic advance, indicating control by non-additive gene action, where selection may be less effective.

Among all traits, only seven characters—days to maturity, 1000-seed weight, seed yield per plant, siliqua length, harvest index, number of siliqua on main shoot, and days to 50% flowering—exhibited heritability exceeding 90%, suggesting minimal environmental influence. Similar findings of high heritability for important morphological traits in Indian mustard were earlier reported by Chakraborty and Haque (2000), Rathi et al. (2002), Bicer and Sakar (2004, 2010), Singh et al. (2004, 2005, 2007), Singh and Gupta (2008), Kakde et al. (2008), and Sharma et al. (2022).

Table. No. 3: Heritability, genetic advance and coefficient of variation for 12characters of mustard genotypes

Characters	Heritability (Broad Sense)	Genetic Advance 5 %	Genetic Advance Mean 5%	GCV (%)	PCV (%)

Days to 50% flowering	0.96	19.69	36.73	18.19	18.55
Days to maturity	0.99	16.58	12.33	6.01	6.03
Plant height (cm.)	1.00	34.96	18.76	9.11	9.12
Number of primary branch/plant	-0.49	-0.69	-13.32	9.26	13.25
Number of secondary branch/plant	0.91	4.34	40.03	20.37	21.35
Number of siliqua on main shoot	0.96	9.37	24.29	12.05	12.31
Siliqua length cm	0.97	1.28	31.60	15.61	15.89
Number of seed/siliqua	0.94	2.41	26.65	13.35	13.77
1000-seed weight g	0.99	0.95	19.52	9.53	9.59
Biological yield / plant g	1.00	58.27	72.72	35.31	35.31
Seed yield/plant g	0.99	7.68	39.37	19.26	19.41
Harvest index %	0.97	7.68	33.82	16.67	16.93

Genotypic and phenotypic coefficient of variation (GCV):

The data presented in Table 3. Reveals that the biological yield per plant had highest genotypic coefficient of variance (35.31) followed by number of secondary branch per plant (20.37) seed yield per plant (19.26), day to 50% flowering (18.19), harvest index (16.67) and siliqua length (15.61). While midrate genotypic coefficient of variance recorded for number os seed per siliqua (13.35) and number of siliqua on main shoot (12.05). The minimum genotypic coefficient of variation was observed for day to maturity (6.01), plant height (9.11), number of primary branch per plant (9.26) and 1000-seed weight (9.53).

The range of phenotypic coefficient of variation for various characters studied varied from 6.03 to 35.31 (Table 3). The highest value (35.31) was observed for biological yield per plant, whereas lowest value (6.03) was recorded for days to maturity. Number of secondary branch per plant (21.35), Seed yield per plant (19.41), day to 50% flowering (18.55), harvest index (16.93), siliqua length (15.89), number of seed per siliqua (13.77) number of primary branch per plant (13.25) and number of siliqua on main shoot (12.31) also showed high values of phenotypic coefficient of variation. The minimum phenotypic coefficient of variation was observed for day to maturity (6.03), plant height (9.12), and 1000-seed weight (9.59). Studies also revealed that the phenotypic coefficient of variations for all the characters were higher than their corresponding genotypic coefficient of variations.

The genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV) for all traits, indicating environmental influence on their expression, which is in agreement with earlier reports (Aich et al., 2007; Kumar et al., 2008; Sharma et al., 2022). The wide differences between GCV and PCV for most characters further suggest strong environmental effects. High GCV and PCV were observed for biological yield per plant, number of secondary branches per plant, seed yield per plant, days to 50% flowering, harvest index, and siliqua length, reflecting substantial genetic variability. Similar variability for yield and its components has also been reported by Hamdi et al. (2003), Bicer and Sakar (2004), and Kumar et al. (2020).

Identification of Parents for Different Characters

The following parents were identified superior for different component traits including yield per plant-

S.No.	Characters	Variety	Value
1.	Day to 50% flowering	GIRIRAJ	34.00 days
2.	Earliest Maturity	PM-30	123.67 days
3.	Lowest Plant height	GM-1	154.50 cm.
4.	Highest No. of primary branch/plant	PUSA AGRANI	6.67
5.	Highest No. of secondary branch/plant	PM-25	15.00
6.	Highest No. of siliqua on main shoot	GM-2	45.67
7.	Highest Siliqua length	PUSA TARAK	5.87
8.	Highest Number of seed/siliqua	BULLET	12.03 g.
9.	Highest 1000-seed weight	PUSA BOLD, P.JAGANNATH	5.32 g.
10.	Highest Biological yield per plant	PM-33	135.03 g.
11. 12.	High seed yield/plant High harvest index	M-57 VARUNA	24.03g 34.27%

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