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Genetic variability and character association studies for yield and yield traits in Indian mustard (*Brassica juncea*)

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Abstract

An experiment for genetic parameters and character association studies for yield and yield traits, was conducted during the *Rabi* season 2021-22. Twenty-four Indian mustard genotypes were grown in randomized complete block design with three replications and observations were recorded for 15 characters. The analysis of variance revealed that all the traits had significant differences between the treatments. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability coupled with genetic advance were recorded higher for the harvest index, biological yield, seed yield/plant, number of secondary branches, main raceme length, siliquae/plant. Genotypic correlation showed that the harvest index (0.93), seed yield q/ha (0.92), siliquae/plant (0.92), number of secondary branches (0.91) and biological yield (0.81) had positive significant correlation with seed yield/plant. So, more emphasis should be given to these traits for selection of genotypes. Genotypic path coefficient analysis revealed that the characters harvest index (0.74), biological yield (0.44), siliquae/plant (0.42), plant height (0.31) and length of main raceme (0.19) showed the positive direct effect on seed yield/plant.

***Keywords**: Correlation, genetic variability, Indian mustard, path analysis*

Introduction

India's vegetable oil economy is fourth largest after the USA, China and Brazil and it is occupying about 20% of world's oilseed production. Rapeseed-mustard group of crops are the third major oilseed crops after soybean and palm oil and globally, India occupies second position in cultivation with 6.70 million hectares after China and third position with 8.50 million tonnes in production next to China and Canada (USDA, 2020-21). Among the species of rapeseed and mustard, Indian mustard [*Brassica juncea* (L.) Czern & Coss.] belongs to the family Cruciferae or Brassicaceae, is an amphidiploid (AABB, 2n=4x=36) of turnip mustard (*Brassica rapa* L.) (AA, 2n=2x=20) and black mustard (*Brassica nigra* L.) (BB, 2n=2x=16). Mustard seeds have high energy content, with oil content 36-46 % and protein content 28-36%. Mustard oil is used in cooking and frying for human consumption throughout north India. In rapeseed-mustard group of crops, Indian mustard occupies maximum area (85-90%). Rajasthan stands in first place in production of mustard by 4.51 million tonnes on 2.72 million hectares of land followed by Madhya Pradesh with a production of 1.31 million tonnes and 0.77 million hectares area, in the year 2020-21 (Anonymous, 2021).

Even though there is a record in cultivation, India is importing the edible oils to meet the increasing consumption with increase in population and change in their lifestyle. As a result, the primary goal of today's breeding programs should be increased productivity and yield stability. Therefore, increased output through the development of new varieties of Indian mustard must be maintained. Consequently, while selecting desirable types, breeders look for genetic diversity among features. The proper assessment of important crop species aids in the identification and use of improved genotypes (Jan *et al*., 2016). High genetic variability in the base population increases the likelihood of creating desirable plant types. As a result, the most important stage is to identify desirable features or combinations in a population. Therefore, a plant breeder must measure the parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance to quantify variability. The correlation coefficient is a symmetrical evaluation of the degree of association between the traits that helps in determining the type and extent of the relationship between yield and its components. It is well known that correlation does not primarily serve the researcher's objective because it does not detect the traits that have indirect impact on seed yield. In such a condition, Wright's (1921) path coefficient analysis found significant role of partitioning the correlation coefficient into direct and indirect effects. The extent of association between seed yield and its components can be determined by using correlation and path analysis. The direct and indirect effects of independent component characteristics on yield are estimated by path coefficient analysis and effective for genetic improvement. Therefore, present study was focused on genetic diversity for several quantitative components and their associations with plant yield enhancement with 24 Indian mustard genotypes involving 15 quantitative traits.

Materials and Methods

An experiment was conducted during the *Rabi* season 2021-22 at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh. Twenty-four Indian mustard advanced lines/ genotypes (Table 1) were grown in randomized complete block design with three replications with each genotype representing one treatment. On October 8, 2021, genotypes were sown in five rows of twelve plots each. The spacing was 30 cm between rows and 10 cm between plants within each row. All recommended cultural practices were followed to raise a healthy crop of mustard.

Table 1: List of genotypes with pedigree

S. no.	Name of entry/ genotype	Pedigree
1.	HUJM(E)-21-1	Ashirwad × Pusa Bold
2.	HUJM(E)-21-2	Kranti ×Jatai Rai
3.	HUJM(E)-21-3	NRCHB 101 × Jatai Rai
4.	HUJM(E)-21-4	Varuna × Jatai Rai
5.	HUJM(E)-21-5	Kranti × NPJ 112
6.	HUJM(E)-21-6	Varuna × HUJM 99-03
7.	HUJM(E)-21-7	Varuna × Pusa Bold
8.	HUJM(E)-21-8	NRCHB 101 × SEJ 2
9.	HUJM(E)-21-9	Maya × Pusa Bold
10.	HUJM(E)-21-10	Vardan × SEJ 2
11.	HUJM(E)-21-11	Maya × RLM 1359
12.	HUJM(E)-21-12	NRCHB 101 × HUJM 07-06
13.	HUJM(E)-21-13	SEJ 2 × Kranti
14.	HUJM(E)-21-14	Divya × Kranti
15.	HUJM(E)-21-15	NPJ 112 × RH 8813
16.	HUJM(E)-21-16	Ashirwad × HUJM 9901
17.	HUJM(E)-21-17	HUJM 8-16-1-1
18.	HUJM(E)-21-18	HUJM 08-18-1-1-1
19.	HUJM(E)-21-19	HUJM(E) 20-4 (NPJ-141 ×Ashirwad)
20.	HUJM(E)-21-20	HUJM-16-8 (DRMR904 × HUJM99-03-2-1)
21.	HUJM(E)-21-21	HUJM-09-07 (RH30 ×Varuna)
22.	HUJM(E)-21-22	Giriraj
23.	HUJM(E)-21-23	PM 25
24.	HUJM(E)-21-24	JD 6

The Research farm is located at 83°03' E longitude and 25°18' N latitude, at an elevation of 128.9 meters above sea level in the northern Gangetic plain. The soil type is fertile alluvial loam, which is typical of the Indo Gangetic plains and suitable for growing the experimental material. Observations were recorded for fifteen quantitative characters *viz.,* plant height (cm), days to maturity, days to 50% flowering, number of primary branches/plant, number of secondary branches/plant, length of main raceme (cm), siliquae on main raceme, siliqua length (cm), seeds/siliqua, siliquae/plant, biological yield, test weight, harvest index, seed yield/plant and seed yield (q/ha) from five randomly selected plants and averaged. The significance differences of each character were calculated, as indicated by Panse and Sukhatme (1978). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using formula given by Burton (1952). While, the broad sense heritability and genetic advance were computed by using the formula given by Johnson *et al.* (1955). Correlation coefficient at genotypic level is calculated by using the formula given by Aljibouri *et al.* (1958) and genotypic path analysis was used to know direct and indirect effects of components on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Results and Discussion

Analysis of variance (Table 2) for mean sum of squares of treatment showed significant differences for all the characters. The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance (GA) as percent mean is presented in Table 3. The GCV, PCV, heritability coupled with GA are higher for the harvest index, biological yield and seed yield/plant, biological yield, number of secondary branches, main raceme length, siliquae per plant. Similar results were reported by Singh *et al*. (2017), Patel *et al*. (2019) and Rout *et al*. (2019) suggesting influence of environment on the traits under study. High heritability coupled with high GA as percent mean was observed for traits like harvest index, number of primary and secondary branches, seed yield/plant, biological yield, seed yield q/ha, siliquae on main raceme revealing that the role of additive gene action in the inheritance of these characters, implying that these characters can be improved through simple selection. Similar findings were discussed by Shekhawat *et al*. (2014), Rout *et al*. (2019) and Pradhan *et al*. (2021).

Table 2: Analysis of variance for yield and yield contributing traits in 24 genotypes of Indian mustard

SV	PH	DTF	DM	NPB	NSB	LMR	NSMR	SL	NSS	NSP	BY	TW	HI	SY	SYp
Replication (df=2)	428.2	1.2	371.3	0.2	0.3	49.0	19.2	0.2	2.9	1095.5	144.0	0.1	0.0	6.2	3.3
Treatment (df=23)	523.1**	27.5**	322.2**	3.1**	8.7**	51.6**	135.8**	0.1*	2.6**	4981.2**	20621.2**	0.3**	0.0**	63.4 **	62.0**
Error (df=46)	216.8	7.6	116.6	0.1	0.9	17.6	15.3	0.0	0.9	1033.2	947.7	0.0	0.0	4.2	2.7

Where; SV: source of variation, PH: plant height (cm), DTF: days to 50% flowering, DM: days to maturity, NPB: number of primary branches, NSB: number of secondary branches, LMR: length of main raceme (cm), NSMR: number of siliquae on main raceme, SL: siliqua length (cm), NSS: number of seeds/siliqua, NSP: number of siliquae/plant, BY: biological yield (g/plant), TW: test weight (g), HI: harvest index, SY: seed yield (q/ha), SYp: seed yield/plant(g), ,* : significant at 5% level of significance, **: significant at 1% level of significance

Table 3: Estimates of genetic parameters for 15 quantitative traits of 24 Indian mustard genotypes

Trait	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (Broad sense %)	Genetic advance	Genetic advance as % of mean at 5%
Plant height (cm)	4.8	6.3	58.6	15.9	7.6
Days to 50% flowering	6.0	7.0	72.3	4.5	10.5
Days to maturity	7.0	8.8	63.8	13.6	11.6
No. of primary branches	15.8	16.1	96.4	2.0	32.0
No. of secondary branches	14.8	15.6	89.2	3.1	28.8
Length of Main raceme (cm)	5.1	6.3	65.9	5.6	8.6
No. of siliquae on main raceme	13.3	14.1	88.7	12.2	25.9
Siliqua length (cm)	2.8	4.3	43.7	0.2	3.9
No. of seeds/ siliqua	5.6	7.0	64.0	1.2	9.2
No. of siliquae/plant	10.1	11.3	79.3	66.5	18.5
Biological yield (g)	25.3	25.9	95.4	162.9	50.9
Test weight (g)	6.6	7.2	83.2	0.6	12.4
Harvest index	36.8	37.1	98.2	0.1	75.2
Seed yield (q/ha)	18.1	18.7	93.4	8.8	36.0
Seed yield (g/plant)	23.9	24.4	95.6	44.	848.1

Genotypic correlation study of fifteen quantitative traits of Indian mustard has been presented in Table 4, which shows the association between two characters as well as seed yield and other parameters at 1% and 5% significance levels. Characters like harvest index (0.93), seed yield (0.92), siliquae/plant (0.92), number of secondary branches/plant (0.91), biological yield (0.81), test weight (0.46), and main raceme length (0.44) all had significant and positive correlations with seed yield/plant. Similar results were made by Kumar *et al.*

Table 4: Genotypic correlation coefficients of fifteen quantitative characters in 24 Indian mustard genotypes

Trait	PH	DTF	DTM	NPB	NSB	LMR	NSMR	SL	NSS	NSP	BY	TW	HI	SY
PH	1.00	0.08	-0.13	0.17	-0.17	0.52**	-0.33	-0.00	0.10	0.10	-0.29	0.33	-0.16	-0.09
DTF		1.00	0.02	-0.08	-0.41*	-0.37	-0.15	0.36	0.09	0.07	-0.42*	-0.15	-0.24	-0.26
DTM			1.00	0.05	-0.12	-0.37	0.03	-0.08	-0.01	-0.12	-0.09	0.33	-0.16	-0.12
NPB				1.00	0.22	0.71**	0.16	0.10	0.60**	0.32	-0.18	0.29	0.10	-0.07
NSB					1.00	0.58**	0.52**	0.02	-0.15	0.76**	0.74**	0.43*	0.82**	0.83**
LMR						1.00	0.42*	-0.08	0.21	0.54**	0.23	0.20	0.31	0.19
NSMR							1.00	0.27	-0.10	0.33	0.15	-0.06	0.26	0.35
SL								1.00	0.36	0.35	-0.15	-0.33	0.00	-0.08
NSS									1.00	0.06	-0.47*	-0.03	-0.05	-0.44*
NSP										1.00	0.47*	0.53**	0.87**	0.70**
BY											1.00	0.40*	0.74**	0.91**
TW												1.00	0.54**	0.57**
HI													1.00	0.91**
SY														1.00
SYp	-0.05-	0.37-	0.27	0.08	0.91**	0.43*	0.38	0.23	-0.22	0.91**	0.81**	0.45*	0.92**	0.92**

Where; SV: source of variation, PH: plant height (cm), DTF: days to 50% flowering, DM: days to maturity, NPB: number of primary branches, NSB: number of secondary branches, LMR: length of main raceme (cm), NSMR: number of siliquae on main raceme, SL: siliqua length (cm), NSS: number of seeds/siliqua, NSP: number of siliquae/plant, BY: biological yield (g/plant), TW: test weight (g), HI: harvest index, SY: seed yield (q/ha), SYp: seed yield/plant(g), ,* : significant at 5% level of significance, **: significant at 1% level of significance

Table 5: Genotypic path matrix showing direct and indirect effects of 15 yield associated traits of 24 Indian mustard genotypes

Trait	PH	DTF	DTM	NPB	NSB	LMR	NSMR	SL	NSS	NSP	BY	TW	HI	SY
PH	0.30	0.02	-0.04	0.05	-0.05	-0.10	-0.00	0.15	0.03	0.03	-0.09	0.10	-0.05	-0.03
DTF	-0.01	-0.14	-0.00	0.01	0.06	0.05	0.0	-0.05	-0.01	-0.01	0.06	0.02	0.03	0.04
DTM	-0.01	0.00	0.08	0.00	-0.01	-0.03	0.00	-0.00	-0.00	-0.01	-0.00	0.02	-0.01	-0.01
NPB	-0.01	0.00	-0.00	-0.08	-0.01	0.06	-0.01	-0.00	-0.05	-0.02	0.01	-0.02	-0.00	0.00
NSB	-0.01	-0.02	-0.00	0.01	0.06	0.03	0.03	0.00	-0.00	0.04	0.04	0.02	0.05	0.05
LMR	-0.06	-0.07	-0.07	0.13	0.11	0.19	0.08	-0.01	0.04	0.10	0.04	0.03	0.06	0.03
NSMR	0.0	00.00	-0.00	-0.00	-0.01	-0.01	-0.02	-0.00	0.00	-0.00	-0.00	0.00	-0.00	-0.01
SL	0.02	0.01	-0.00	0.00	0.00	-0.00	0.01	0.04	0.01	0.01	-0.00	-0.01	0.00	-0.00
NSS	-0.02	-0.02	0.00	-0.14	0.03	-0.05	0.02	-0.08	-0.24	-0.01	0.11	0.00	0.01	0.10
NSP	0.04	0.03	-0.05	0.13	0.32	0.22	0.14	0.15	0.02	0.42	0.20	0.22	0.36	0.29
BY	-0.13	-0.18	-0.04	-0.08	0.33	0.10	0.06	-0.07	-0.20	0.20	0.44	0.17	0.32	0.40
TW	-0.085	0.039	-0.085	-0.074	-0.112	-0.05	0.01	0.08	0.00	-0.13	-0.10	-0.25	-0.13	-0.14
HI	-0.119	-0.180	-0.121	0.076	0.610	0.23	0.19	0.00	-0.04	0.64	0.54	0.40	0.73	0.67
SY	0.04	0.13	0.06	0.03	-0.40	-0.09	-0.17	0.04	0.21	-0.34	-0.44	-0.27	-0.44	-0.48
SYp-	0.05	-0.37	-0.27	0.08	0.91	0.43	0.38	0.23	-0.22	0.91	0.81	0.45	0.92	0.92
Partial R^2	-0.01	0.05	-0.02	-0.00	0.05	0.08	-0.01	0.01	0.05	0.38	0.35	-0.11	0.68	-0.44

Where; SV: source of variation, PH: plant height (cm), DTF: days to 50% flowering, DM: days to maturity, NPB: number of primary branches, NSB: number of secondary branches, LMR: length of main raceme (cm), NSMR: number of siliquae on main raceme, SL: siliqua length (cm), NSS: number of seeds/siliqua, NSP: number of siliquae/plant, BY: biological yield (g/plant), TW: test weight (g), HI: harvest index, SY: seed yield (q/ha), SYp: seed yield/plant(g), ,* : significant at 5% level of significance, **: significant at 1% level of significance

(2013), Singh *et al*. (2017), Arpna *et al*. (2018) and Sipra *et al*. (2019). Harvest index showed strong positive significant correlation with number of secondary branches, number of siliquae/plant, biological yield, test weight. Test weight had positive significant correlation with number of secondary branches, number of siliquae/plant, biological yield. Siliquae on main raceme and siliquae per plant showed positive correlation with number of secondary branches and main raceme length. These results indicate that selection of plant based on these characters is beneficial for crop improvement. Similar findings were also reported by Kumar *et al*. (2019), Dinesh *et al.* (2020) and Chakraborty *et al*. (2021). While siliquae on main raceme (0.38), siliqua length (0.24), and number of primary branches (0.08) all have positive but non-significant values.

The impact of genotypic association on seed yield/plant were divided into direct and indirect effects (Table 5) indicated that, harvest index (0.74) showed highest positive direct effect on seed yield/plant followed by biological yield (0.44), siliquae/plant (0.42) and plant height (0.31) thus, selection of these characters results in enhancing the seed yield. Similar findings were reported by Dipti *et al*. (2016), Kumar *et al*. (2016) and Rauf and Rahim (2018). Negative direct effects of seed yield/plant were observed on seed yield (q/ha; -0.49), test weight (-0.25), seeds/siliqua (-0.24) and days to flowering (-0.15). Most of the traits under study have the positive indirect effects through siliquae per plant, followed by harvest index and biological yield.

Conclusion

Based on the above findings, the genotypic coefficient of variation, phenotypic coefficient of variation, heritability coupled with genetic advance and direct effects on seed yield/plant, were recorded higher for the harvest index, biological yield and seed yield/plant, biological yield, number of secondary branches, main raceme length, siliquae per plant, indicating more emphasis should be given for these traits while selection for crop improvement. At genotypic level harvest index, seed yield, siliquae per plant, no. of secondary branches, biological yield, test weight and main raceme length all had significant and positive correlations with seed yield/plant, indicating simple selection as beneficial for these traits. Path coefficient analysis for seed yield/plant reveals the traits plant height, number of secondary branches, main raceme length, siliqua length, siliquae per plant, harvest index, biological yield had positive direct effect where direct selection is useful for enhancing the seed yield. Thus, from the present study selection indices for crop development programs can be created by using the identified traits.

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