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Phenotypic Evaluation of Genetic Diversity of Diverse Indian Mustard (*Brassica Juncea* L. Czern and Coss) Genotypes using Correlation and Path Analysis

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Abstract

The present investigation was undertaken at experimental field, department of plant breeding and genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu, Jammu & Kashmir state, India for phenotypic evaluation of genetic diversity in a group of Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes. For this study we have chosen twenty Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes with respect to thirteen different characters for assessment of genetic diversity. The analysis of variance indicated significant differences among genotypes for all the traits. High heritability coupled with high genetic advance was observed for seed yield per plant (g) followed by number of siliqua per pant, days to 50% flowering, siliqua length (cm). Results revealed that in some genotypes seed yield had high heritability so it would show very good response on selection, so selection of such promising genotypes would be rewarded. The overall mean performance of genotypes was comparatively higher for days to 50% flowering, days to maturity, plant height (cm), primary branches plant^{-1}, secondary branches per plant, number of siliqua plant^{-1}, siliqua length (cm), number of seeds silique^{-1}, test weight (g), percent oil content,seed yield plant^{-1} (g). This study further can be useful for selection of desirable genotypes of Indian Mustard to fulfil the various breeding objectives.

Keywords: *Brassica juncea*, genetic variability, heritability, genetic advance

1. Introduction

In India, rapeseed-mustard is the second most important group of edible oilseed crops after groundnut sharing 27.8% in the Indian oilseed economy. *Brassica juncea* contributes more than 80% to the total rapeseed-mustard production in the country and is an important component in the oilseed sector (Vinu et al., 2013). It is cultivated over an area of 6.70 million hectare with a total production of 8.78 MT and average yield of 1310 kg ha^{-1} as per advance estimate (Anonymous, 2019). In Jammu division of J&K state, rapeseed-mustard is grown in an area of 0.028 mha with an average productivity of over 8 q ha^{-1}. Genetic diversity serves as a way for populations to adapt to changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals. In all populations, genetic drift occurs constantly—species gradually lose genetic variation. Genetic variation can be measured in a number of different ways. Various methods such as Euclidean distance, Manhattan distance, Pearson correlation, partial correlation, point correlation, linkage coefficients, Jaccard's coefficients etc. are used for studying genetic similarities or distances (Zhang et al., 2007). (Gupta et al.*,*1991), (Vaishnava et al*.,* 2006), (Ray et al., 2014) and (Singh et al., 2010**)** using D2 analysis classified 48,50,30 and 33 genotypes, respectively, for seed yield and its important component traits in Indian mustard. Hu et al., 2007 assessed genetic diversity of B. napus germplasms from China and Europe by using agronomically important traits. Shannon Diversity index based on the k-means clustering and inertia score was used by (Yadava et al., 2009) for the selection of diverse accession from 286 germplasm collections, ensuring higher evenness as well as richness in the sample. (Kumar et al*.,* 2008) evaluated 11 Indian mustard genotypes and found significant difference among them for different traits. He recorded high GCV and PCV for seed yield/ plant (GCV=42.5%, PCV=42.21%) and secondary branches/plant (GCV=41.53%, PCV=42.07%). Since plant breeding research and cultivar development are integral components of improving food production, therefore, availability of and access to diverse genetic sources will ensure that the global food production network becomes more sustainable.

2. Materials and Methods

The study was carried out at experimental field, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu, Jammu & Kashmir state, India during rabi season, 2017-18 (15 October 2017 to June 2018). The experimental material was grown in Randomized Blocked Design with 3 replications under normal conditions Each treatment was sown in 3 rows of 5 m length 30 cm and 15 cm spacing. The recommended dose of fertilizers was applied and also the recommended Plant Protection measures were adapted for raising a good crop. Analysis of variance and correlation analysis done using Statistical Analysis System (SAS) Software version 9.3.

The simple correlation coefficients between different characters at genotypic and phenotypic level was worked out between characters as suggested by al- (Jibouriet al.,1958).

i. Phenotypic correlation coefficients (r_p)

$$r_p = \frac{\text{Cov. XY(p)}}{\sqrt{\text{Var. X(p). Var. Y(p).}}}$$

ii. Genotypic correlation coefficients(r_g)

$$r_g = \frac{\text{Cov. XY(g)}}{\sqrt{\text{Var. X(g). Var. Y(g).}}}$$

Where, Cor. XY (p) and cov. XY (g) denote phenotypic and genotypic covariances between character X and Y, respectively. Var. X (p) and var. X (g) denote variance for characters X and Y, at phenotypic and genotypic levels, respectively. The significance of different correlation coefficients was tested against (v-2) degrees of freedom at 5% and 1%, where v is the no. of varieties on which the observations were recorded.

The path coefficient was done following the procedure outlined by Dewey and Lu (1959) using genotypic correlation of 'cause' with 'effects' was calculated by following simultaneous equations:

rmp=pmp+rmnpnp+rmo pop ...1

rnp= rnmpmp+ pnp+rno pop ...2

rop=romp mp+ ronpnp+pop ...3

where,

Pmp, Pnp, Pop are direct affects of m, n and o on cause P, and rmp, pnp, rmo, Pop… are indirect affects on cause. These simultaneous equations are solved by using matrix method expressed below:

$$\begin{array}{lllll} \text{rmp} & \text{rmp} & \text{rmn} & \text{rmo} & \text{Pmp} \\ \text{rnp} = & \text{rnm} & \text{rnn} & \text{rno} & \text{Pnp} \\ \text{rop} & \text{rom} & \text{ron} & \text{roo} & \text{Pop} \end{array}$$

or A = B.C. Here, A and B vectors are known. For calculation of C vectors, the formula used is:

$C = B^{-1}, A$

Here, B^{-1} is the inverse matrix of B vector. Pivotal condensation method was used for matrix inversion.

3. Results and Discussion

The data obtained for each of the eleven characters from the 20 genotypes evaluated in three replications under normal was subjected to standard methods of analysis of variance. Table 1 clearly shows significant differences among all the 20 genotypes of Indian mustard for all the characters under normal conditions. The mean value of 20 genotypes of Indian mustard for various characters under normal and rain fed conditions are presented in Appendix I and II. While, general mean, range, variances, coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean for different characters under normal and rain fed conditions are given in Table 1. The estimates of coefficients of variation (GCV and PCV) were found to be high for seed yield per plant followed by number secondary branches per plant and number of siliqua plant^{-1} under normal condition. High estimates of heritability (>93%) were observed for the characters namely seed yield per plant**,** followed by, days to 50% flowering, number of siliqua plant^{-1} (Table 2) Mean sum square due to genotypes were significant for all traits. This is show the presence of clear significant difference among the genotypes in normal conditions. Similar, findings have also been reported in mustard by (Matho et al*.,* 2002), (Singh et al., 2003), (Moondal et al*.,* 2000), and (Singh et al*.,* 2010).

The highest estimate of expected genetic advance was

Table 1: Analysis of variance for seed yield and its related traits under irrigated condition (E_1)

Source of variation	d.f.	DF	DM	PH	PBP	SBP	NSP	SL
Replication	2	2.617	0.867	137.335	0.428	9.874	1016.180	0.142
Genotypes	19	79.084**	60.702**	501.177**	1.839*	29.994**	10988.922**	0.543**
Error	38	3.687	4.902	126.259	0.968	8.825	689.316	0.142

Table 1: Continue...

Source of variation	NSS	TW	OC	SYP	RL	HI
Replication	2.792	0.106	2.668	1.383	1.502	1.547
Genotypes	3.822**	0.459**	7.190**	19.949**	12.504**	3.130**
Error	1.501	0.074	2.419	0.457	4.626	0.673

DF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); PBP: Primary branches plant^{-1}: SBP: Secondary branches plant^{-1}; NSP: Number of siliqua plant^{-1}; SL: Siliqua length (cm); NSS: Number of seeds siliqua^{-1}; TW: Test weight (g); OC: Oil content (%); SYP: Seed yield plant^{-1} (g); RL: Root length (cm); HI: Harvest index (%); *, ** Significant at 5% and 1% level of significance, respectively

Table 2: Range, Mean, Variance, Coefficient of variation, Heritability in broad sense, Genetic advance and Genetic advance as percentage of mean for different characters in Indian mustard genotypes under normal condition (E_1)

Characters	Mean	Range	GV	PV	Coefficient of variation		Heritability (%)	Genetic Advance	G.A PM
					Genotypic	Phenotypic			
Days to 50% flowering	59.03	48.67-69.00	25.30	28.81	8.492	9.093	87.20	9.64	16.30
Days to maturity	128.33	121.00-138.00	18.60	23.50	3.360	3.777	79.14	7.90	6.15
Plant height (cm)	218.32	197.56-238.00	124.97	251.23	5.120	7.260	49.74	16.24	7.43
Primary branches plant^{-1}	5.23	3.01-6.78	0.290	1.258	10.291	21.432	23.05	0.53	10.18
Secondary branches plant^{-1}	17.33	12.56-25.00	7.056	15.88	15.330	22.998	44.43	3.64	21.04
Number of siliqua plant^{-1}	365.96	266.00-462.67	3433.20	4122.51	16.011	17.544	83.27	110.15	30.09
Siliqua length (cm)	5.00	4.22-5.76	0.133	0.275	7.300	10.498	48.42	0.52	10.47
Number of seeds siliqua^{-1}	14.76	12.56-16.56	0.773	2.274	5.958	10.215	34.02	1.05	7.15
Test weight (g)	5.27	4.90-6.20	0.128	0.202	6.438	8.079	63.49	0.588	10.56
Oil content (%)	39.77	36.96-42.42	1.590	4.009	3.171	5.035	39.66	1.636	4.14
Root length (cm)	21.11	17.57-24.31	2.625	7.252	7.675	12.755	36.20	2.08	9.51
Harvest index (%)	7.06	5.62-9.13	0.819	1.492	12.817	17.300	54.88	1.38	19.56
Seed yield plant^{-1} (g)	15.60	12.33-19.62	6.490	6.95	16.337	16.903	93.42	5.07	32.53

GV: Genotypic variance; PV: Phenotypic variance; G.A PM: G.A. as percentage of mean

recorded for number of siliqua plant^{-1} under normal condition under normal condition and under rain fed condition highest genetic advance was recorded for plant height.The genetic advances expressed as percentage of mean were high for seed yield plant^{-1} followed by number of silique plant^{-1} and secondary branches plant^{-1} under normal condition.

3.1. Correlations between different characters

Under normal condition days to 50 per cent flowering had a significant positively correlation with plant height (r=0.596**), while significant negative correlation were observed for oil content (r=-0.554**), harvest index (r=-0.567*) and seed yield (r=-0.412**) at phenotypic level and same situation was observed at genotypic level except oil content (Table 3). Days to maturity had significant positive correlation with oil content (r=-0.450**) and significantly negative correlation for plant height (cm) (r=-0.405**), at phenotypic level under normal condition. Plant height had a significantly positive correlation with secondary branches plant^{-1} (r=0.523**), while siliqua length (cm) (r=-538**) and primary branches

Table 3: Correlation coefficients at phenotypic and genotypic levels between different characters of Indian mustard genotypes under normal condition (E_1)

Characters		DF	DM	PH	PBP	SBP	NSP	SL	NSP	TW	OC	RL	HI	SYP
DF	r_p	1.00	-0.308	0.596**	-0.041	0.228	0.250	-0.174	-0.004	0.521	-0.554**	0.184	-0.567**	-0.412**
	r_g	1.00	-0.322	0.431**	-0.009	0.081	0.243	-0.081	0.002	0.421	-0.264	0.090	-0.443**	-0.380**
DM	r_p		1.00	-0.405**	-0.271	-0.319	0.192	0.107	-0.199	-0.290	0.450**	-0.112	0.254	0.146
	r_g		1.00	-0.310	-0.233	-0.221	0.188	-0.052	-0.051	-0.247	0.201	0.069	0.141	0.142
PH	r_p			1.00	-0.399**	0.523**	0.226	-0.538**	-0.068	0.240	-0.215	0.082	-0.174	-0.162
	r_g			1.00	0.011	0.346**	0.108	-0.133	-0.175	0.165	-0.194	-0.056	-0.0003	-0.072
PBP	r_p				1.00	-0.487**	-0.108	0.241	0.188	0.175	0.923**	-0.045	-0.074	0.149
	r_g				1.00	0.148	0.038	0.279	0.126	0.131	0.239	-0.053	0.139	0.039
SBP	r_p					1.00	0.348**	-0.270	0.186	-0.328*	0.171	0.565**	-0.154	0.136
	r_g					1.00	0.269	-0.161	0.044	-0.155	-0.137	0.009	0.086	0.085
NSP	r_p						1.00	-0.155	-0.113	0.167	0.109	-0.173	0.137	0.0003
	r_g						1.00	-0.165	0.014	0.120	0.067	-0.126	0.058	-0.0006
SL	r_p							1.00	0.421	0.174	0.312	0.455**	0.182	0.371**
	r_g							1.00	0.195	0.202	0.246	0.075	0.146	0.266
NSS	r_p								1.00	0.319	-0.068	0.804**	-0.627**	-0.595**
	r_g								1.00	0.164	-0.043	0.377**	-0.370**	-0.402**
TW	r_p									1.00	-0.316	0.434**	-0.313	-0.458**
	r_g									1.00	-0.075	0.129	-0.146	-0.322*
OC	r_p										1.00	0.027	0.745**	0.660**
	r_g										1.00	-0.012	0.130	0.397**
RL	r_p											1.00	-0.351**	-0.304
	r_g											1.00	-0.233	-0.159
HI	r_p												1.00	0.884**
	r_g												1.00	0.664**
SYP	r_p													1.00
	r_g													1.00

plant^{-1} (r=-0.399**), negative correlation at phenotypic level. Primary branches plant^{-1} had a significant positive correlation with oil content (%) (r= 0.923**), while significant negative correlation was observed for secondary branches per plant (r=-0.487**) at phenotypic level under normal condition. Under normal condition secondary branches per plant had a significant positive correlation with number of siliqua per plant (r=0.348**), root length (cm) (r= 0.565**) at phenotypic level. Number of siliqua per plant had a significant positive correlation with test weight (g) (r=0.590**) at phenotypic level and genotypic level. Siliqua length had significant positive correlation with root length (cm) (r= 0.455**) and seed yield per plant (r=0.371**) at phenotypic level under normal condition. Number of seeds per siliqua had significant positive correlation with root length (cm) (r= 0.804**) and significant negative correlation with harvest index (%) (r=0.-627**) seed yield per plant (r=-0.595**) at genotypic and phenotypic level under normal condition. Under normal condition test weight had significant positive correlation with root length (cm) (r=0.377**) at genotypic and phenotypic level, while negatively correlated with harvest index (%) (r=-0.370**) at phenotypic level and negatively correlated seed yield plant^{-1} (r=-0.402**) at phenotypic level with genotypic levels under normal condition. Oil content had significant positive correlation with harvest index (%)(r=0.745**) and seed yield per plant (g) (r=0.660**) at phenotypic level and genotypic levels under normal condition. Root length (cm) had a significant positive correlation with seed yield per plant. Harvest index had significant positive correlation with seed yield per plant at phenotypic level and genotypic levels. In present study the number secondary branches per plant exhibited strong positive correlation with seed yield under normal condition. The results confirm the earlier research findings of (Labana et al., 1980), (Kumar et al*.,* 1984), (Singh et al., 1985), (Mishra et al*.,* 1987), (Kumar et al*.,* 1987) and (Chowdhary et al*.,* 1987), observed positive significant correlation of seed yield with number of secondary branches.

3.2. Path coefficient analysis

The genotypic and phenotypic correlation coefficients of seed yield with its contributing characters were partitioned into direct and indirect effects through path coefficient analysis. In general, there was good co-ordination between the direct and indirect effects observed at phenotypic and genotypic levels under normal conditions. In this study we found that Seed yield is dependent variables on many number of independent variables such as number of tillers per plant, number of silqua per tiller and number of seed per siliqua in Rapeseed-mustard crop plant. This is the similar results found by many researchers.

4. Conclusion

The analysis of variance indicated significant differences among genotypes for all characters under normal condition. Means they possess significant variation for different traits. Phenotypic variances were generally higher than genotypic variances for all the traits indicating positive effect of environment on variation under normal conditions. The maximum phenotypic coefficient of variation was observed for secondary branches per plant and minimum was observed for days to maturity under normal condition. This study further useful in efficient selection of genotypes for breeding purpose.

5. References

Anonymous, 2019. Indiastat 2018-19. Available at www.indiastat.com. Accessed on June, 2019.

Chowdhary, M.A., Miah, A.J., Rahman, L., Rahman, A., 1987.Correlation and path coefficient analysis of nine important characters of Mustard (*Brassica juncea* L. Czern and Coss). Bangladesh Journal of Agriculture 12, 149–154.

Gomez, K.A., and Gomez, A.A., 1984. Statistical procedures for agricultural research (Ed II). Wiley Interscience*,* New York.

Gupta, V.P., Sekhon, M.S., Satija, D.R., 1991. Studies on genetic diversity, heterosis and combining ability in Indian mustard [*Brassica juncea* L. (Czern and Coss)]. Indian Journal of Genetics 51, 448–453.

Hu, S., Yu, C., Zhao, H., Sun, G., Zhao, S., Vyvadilova, M., Kucera, V., 2007. Genetic diversity of *Brassica napus* L. Germplasm from China and Europe assessed by some agronomically important characters. Euphytica 154, 9–16.

Kumar, P.R., Arora, P.K., Yadav, R.C., Singh, N.P., Kumar, P., 1987. Association and path analysis of economic traits in Yellow Sarson. Journal of Oilseeds Research 4, 257–260.

Labana, K.S., Churasia, B.D., Singh, B., 1980. Genetic variability and inter-character associated in the mutants of Indian Mustard. Indian Journal of Agricultural Sciences, 50, 257–260**.**

Matho, J.L., Haeder, Z.A., 2002. Variability studies in Indian mustard under six different environment in acidic soil. Cruciferae Newsletter 24, 13–14.

Mishra, R., Singh, P., Singh, I., Kumar, S., 1987. Path analysis of factors contributing to seed yield in yellow seeded Indian mustard. Farm Sciences Journal 2, 88–91.

Mondal, S.K., Khajuria, M.R., 2000. Genetic analysis for yield attributes in mustard. Environmental and Economics 18(1), 1–5.

Ray, K., Pal, A. K., Banerjee, H., Phonglosa, A., 2014. Correlation and path analysis studies for growth and yield contributing traits in Indian mustard (*Brassica juncea* L.). International Journal of Bio-resource and Stress Management 5(2), 200–206.

Singh, D., Arya, R.K., Chandra, N., Niwas, R., Salisbury, P., 2010. Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). Journal of Oilseed Brassica 1(1), 19–22.

Singh, H., Yadav, A.K., Yadava, T.P., Lather, V., 1985.Morpho-physiological attributes in relation to seed yield in Indian Mustard. Haryana Agricultural University Journal of Research 15, 295–299.

Singh, P., Singh, D.N., Chakraborty, M., 2003. Variability, heritability and genetic advance in Indian mustard (*Brassica juncea* L.). Journal of Research- Birsa Agricultural University 15(1), 45–47.

Vaishnava, A., Sachan, J.N., Tewari, S.K., 2006.Genetic Divergence for Important quantitative traits in Indian mustard (*Brassica juncea* (L.) Czern and Coss). Agricultural Sciences Digest 26(4), 269–272.

Vinu, V., Singh, N., Vasudev, S., Yadava, D.K., Kumar, S., Naresh, S., Bhat, S.R., Prabhu, K.V., 2013. Assessment of genetic diversity in *Brassica juncea* (Brassicaceae) genotypes using phenotypic differences and SSR markers. Review of Biological Tropics 61(4), 1919–1934.

Yadava, D.K., Sapra, R.L., Sujata, V., Dass, B., Prabhu, K.V. 2009. Selection of high diversity with a minimal set of accessions from Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] germplasm collection. Indian Journal of Agricultural Sciences 79(7), 552–554.

Zhang, W., 2007. Computer inference of network of ecological interactions from sampling data. Environmental Monitoring and Assessment 124 (1–3), 253.

Zhang, X., Lu, G., Long, W., Zou, X., Li, F., Nishio, T., 2014. Recent progress in drought and salt tolerance studies in Brassica crops. Breeding Science 64, 60–73.