Original Research Article

Genetic Variability, Heritability, Genetic Advance and Cluster Analysis in Indian Mustard (*Brassica juncea* L. Czern & Coss.) Under Timely and late Sown Conditions

ABSTRACT

Two sets of field experiments were conducted at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology Kumarganj, Faizabad (U.P.), India during Rabi 2014-15 with 30 diverse genotypes of Indian mustard including three checks (Kranti, Vardan and RGN-73) to assess the genetic variability, heritability and genetic advance under timely (TS) and late sown (LS) conditions. The genotypes were evaluated for thirteen quantitative characters. The analysis of variance showed highly significant differences among the genotypes for all the characters. The maximum phenotypic and genotypic coefficient of variability was observed for biological yield plant^{-1} in timely sown condition while in late sown condition the maximum phenotypic and genotypic coefficient of variability was observed for seed yield plant^{-1}. High heritability coupled with high genetic advance was observed for biological yield plant^{-1} and seed yield plant^{-1} in both TS and LS conditions indicating the influence of additive gene effects. D^2 analysis grouped the 30 genotypes into six clusters. The distribution of genotypes in both the environments was different. Maximum genotypes (11) were present in cluster II in TS while maximum genotypes (12) were present in cluster IV in LS. The maximum inter cluster distance was observed between cluster IV and VI in TS while in LS the cluster II and VI showed maximum inter cluster distance. Hybridization among the genotypes separated by high inter-cluster distance will result in most heterotic crosses.

KEYWORDS: *Heritability, genetic variability, genetic advance, GCV, PCV, cluster, Indian mustard.*

1. INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is one of the major commercial oil yielding crops of India. Rapeseed-mustard has 38 to 42% oil & 24% protein. Oil is used in Northern India for cooking and frying purposes. India ranks first in the world in area and production for groundnut, castor, sesame and niger while second in safflower, rapeseed-mustard and third in linseed. Indian mustard (*Brassica juncea* L.) is a natural amphidiploid (2n=36) of *B. rapa* (2n=20) and *B. nigra* (2n=16). It is popularly known as rai or raya and belongs to the family Cruciferae (Brassicaceae) under the genus Brassica. It occupies considerably large acreage among the Brassica group of oil seed crops (Kaur *et al*., 2019). During the 2018-19 crop seasons, Indian mustard accounts for around 75-80 percent of the 6.23 million ha. Planting time is the single most important variable affecting the seed yield of rapeseed and mustard. Yield in Brassica crops, is a complex character and is the end product of a number of components, each of which is under polygenic control. All changes in yield must be accompanied by changes in one or more of its component traits (Grafius, 1964). The magnitude of genetic variability present in a population is essential for effective genetic improvement. Cluster analysis helps to understand the genetic relation between the genotypes and facilitate the selection of genetically diverse parents in hybridization programme. Hence, the present investigation was carried out to determine the genetic variability, heritability, genetic advance and genetic diversity in Indian Mustard under timely and late sown conditions.

2. MATERIAL AND METHODS

2.1. Experimental site and cultural practices

The present investigation was carried out at Research farm of Genetics and Plant Breeding, N.D. University of Agriculture and Technology, Kumarganj, Faizabad (U.P.), India during Rabi 2014-15. The climate of district Faizabad is semi-arid with hot summer and cold winter.Thirty diverse genotypes of Indian mustard including three checks (Kranti, Vardan and RGN-73) were taken for study obtained from Oilseed Section of Department of Genetics & Plant Breeding, NDUA&T Campus, Kumarganj (Faizabad). These genotypes were grown under timely sown (E1) and late sown (E2) conditions in a Randomized Block Design using three replications each. Each plot consisted of single row of 3 meter length, spaced at 45 cm apart. The distance between plant to plant 15 cm was maintained by thinning. All the recommended cultural practices were adopted for raising a good crop.

2.2. Characters studied

Data were recorded on five randomly selected plants from each plot for thirteen characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, length of main raceme (cm), silique on main raceme (cm), seeds silique^{-1}, 1000-seed weight (g), biological yield plant^{-1}(g), harvest index (%), oil content (%) and seed yield plant^{-1}(g), except days to 50% flowering and days to maturity where data were recorded on line basis.

2.3. Statistical analysis

Standard statistical procedure were used for the analysis of variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance. Cluster analysis was done based on Mahalanobis D^2 method (1936).

3. RESULT AND DISCUSSION

3.1 Analysis of variance and coefficient of variation

The analysis of variance for all the characters under TS (timely sown)and LS (late sown) conditions is presented in Table 1, indicating significant differences among the genotypes for all the characters under study. The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in E1 and E2 for various characters studied are presented in Table 2. Generally, the magnitude of PCV was higher than GCV for all the traits in both conditions *i.e.,* E1 and E2. High PCV and GCV values were observed for biological yield plant^{-1} (32.44) and (32.00), seed yield plant^{-1} (30.39) and (29.30), harvest index (19.65) and (17.95) under TS condition indicating better opportunity for improvement in these traits through selection. Primary branches/plant, secondary branches/plant, length of main raceme, harvest index, silique on main raceme and 1000-seed weight in E1 and E2 showed moderate values of phenotypic and genotypic coefficient of variability indicating the influence of environment in the expression of these traits. High values of PCV and GCV were observed for seed yield plant^{-1} (35.73) and (34.64), biological yield plant^{-1} (34.57) and (34.06), harvest index (23.68) and (21.73) under LS condition. The magnitude of PCV ranged from 2.61 for oil content to 32.44 for biological yield plant^{-1} while GCV ranged from 2.53 for oil content to 32.00 for biological yield plant^{-1} in E1. The characters which exhibited low values of PCV and GCV were oil content, days to maturity and days to 50% flowering in both E1 and E2. Similar results on variability for different characters were reported byRai *et al.* (2005), Sharma *et al.* (2014) Akabari and Niranjana (2015), Rout *et al*., (2019) and Kumar *et al*., (2023).

Table 01. Analysis of variance for 13 characters in Indian mustard under timely (E1) and late sown (E2) condition.

S.NO.	Character		Replications		Treatments		Error	
			E_1	E_2	E_1	E_2	E_1	E_2
		d.f.	**2**	**2**	**29**	**29**	**58**	**58**
1	Days to 50% flowering		2.43	1.07	56.77**	55.39**	2.39	3.05
2	Days to maturity		4.43	6.41	69.93**	68.47**	4.26	4.92
3	Plant height (cm)		71.02*	29.91	563.26**	483.99**	22.41	15.37

4	Primary branches/plant	0.73	0.86	3.53**	3.42**	0.49	0.46
5	Secondary branches/plant	5.71	5.34*	10.11**	10.78**	1.85	1.67
6	Length of main raceme (cm)	19.57	17.18	173.50**	173.72**	7.58	8.06
7	Siliquae on main raceme	4.79	2.98	94.33**	94.75**	7.95	7.72
8	Seeds/siliqua	1.43	1.01	4.79**	4.36**	0.60	0.74
9	1000 seed weight (g)	0.01	0.01	1.17**	0.68**	0.02	0.04
10	Biological yield/plant (g)	1.60	0.76	383.77**	381.15**	3.56	3.80
11	Seed yield/plant (g)	0.01	0.09	16.02**	14.52**	0.39	0.30
12	Harvest index (%)	1.00	2.22	52.38**	56.77**	3.25	3.33
13	Oil content (%)	0.15	0.08	3.14**	2.24**	0.06	0.05

***,** Significant at 5% and 1% probability levels, respectively**

3.2 Heritability and genetic advance

The heritability in broad sense and genetic advance in per cent of meanwere computed for all the characters and arepresented in Table 2. The heritability ranged from 59.78% (secondary branches/plant) to 97.26% (biological yield/plant) in E1 while in E2 it ranged from 61.89% (seeds/silique) to 97.06% (biological yield/plant). In general, higher estimates in broad sense were observed for all the characters in E1 and E2 except for primary branches/plant (67.08% in E1 and 67.75% in E2), secondary branches/plant (59.78% in E1 and 64.45% in E2) and seeds/silique (69.83% in E1 and 61.89% in E2) which showed moderate heritability in both E1 and in E2. High heritability indicated that the characters were least influenced by environmental factors.

The Genetic advance in % of mean ranged from 5.05% (oil content) to 65.01% (biological yield/plant) in E1 and in E2 it ranged from 4.40% (oil content) to 69.16% (seed yield/plant). In TS, biological yield plant^{-1} showed higher genetic advance in % of mean (65.01%) followed by seed yield plant^{-1} (58.19%), harvest index (33.78%), test weight (29.31%) and primary branches plant^{-1} (26.11%). In LS, seed yield plant^{-1} showed higher genetic advance in % of mean (69.16%) followed by biological yield plant^{-1} (69.12%), harvest index (41.09%), primary branches/plant (30.25%), secondary branches plant^{-1}(29.91%), length of main raceme (26.84%) and silique on main raceme (26.10%). Oil content showed low genetic advance in % of mean in both E1 (5.05%) and E2 (4.40%).

High heritability coupled with high genetic advance was observed for biological yield plant^{-1} and seed yield plant^{-1} in both E1 and E2 which suggested that these characters can be considered as favourable for improvement through selection. High heritability together with low genetic advance was noticed for days to 50% flowering, days to maturity, plant height and silique on main raceme both in TS and LS conditions indicating the role of non-additive gene for inheritance of these characters. Similar findings were also reported by Khulbe *et al.* (2000), Mahla *et al.* (2003) Pandey and Pandey (2014) and Maurya *et al*., (2018).

Table 2. Mean, range, genotypic and phenotypic coefficient of variability, heritability (% in broad sense) and genetic advance in % of mean for different characters in Indian mustard under timely (E1) and late sown condition (E2)

		Days to 50 % flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches/plant	Length of main raceme	Silique on main raceme	Seeds/silique	1000-seed weight (g)	Biological yield/plant (g)	Seed yield/plant (g)	Harvest index (%)	Oil content (%)
Range	E1 (Min)	52.00	109.66	111.90	4.07	6.66	42.65	29.81	9.54	2.90	21.36	4.75	14.29	38.26
	E1 (Max)	68.00	131.00	185.40	9.67	15.02	68.71	53.26	15.56	5.31	80.86	13.46	30.54	43.47
	E2 (Min)	42.33	106.33	107.14	3.38	4.62	39.31	27.47	8.57	2.55	19.48	3.45	11.81	37.31
	E2 (Max)	62.33	122.33	171.23	8.74	14.07	66.20	50.45	13.86	4.72	78.71	11.66	27.68	40.64
Mean	E1	60.83	123.43	152.01	6.50	10.65	56.01	39.37	12.80	4.24	35.18	7.79	22.54	40.07
	E2	51.81	114.54	142.66	5.56	9.63	53.28	37.77	11.75	3.80	32.93	6.28	19.42	38.73
GCV (genotypic coefficient of variability)	E1	7.00	3.79	8.83	15.48	15.57	13.28	13.63	9.23	14.62	32.00	29.30	17.95	2.53
	E2	8.06	4.02	8.76	17.84	18.09	13.95	14.26	9.35	12.08	34.06	34.64	21.73	2.21
PCV (phenotypic coefficient of	E1	7.45	4.14	9.37	18.89	20.14	14.16	15.39	11.05	15.03	32.44	30.39	19.65	2.61
	E2	8.74	4.46	9.18	21.67	22.53	14.93	16.04	11.88	13.35	34.57	35.73	23.68	2.29

variability)														
h^2 (broad sense) heritability (%)	E1	88.31	83.70	88.94	67.08	59.78	87.93	78.36	69.83	94.68	97.26	92.93	83.42	94.14
	E2	85.09	81.12	91.03	67.75	64.45	87.26	78.97	61.89	81.96	97.06	93.95	84.24	93.49
Gen.adv as % of mean	E1	13.55	7.14	17.16	26.11	24.80	25.65	24.85	15.90	29.31	65.01	58.19	33.78	5.05
	E2	15.32	7.45	17.22	30.25	29.91	26.84	26.10	15.15	22.54	69.12	69.16	41.09	4.40

E1= Timely sown condition (TS)
E2= Late sown condition (LS)

3.3 Genetic divergence

Timely sown:

On the basis of D^2 values, all the 30 genotypes were grouped in 6 clusters (Table 3) under timely sown condition. Cluster II had highest number of genotypes 11 followed by cluster I, V and III which had 8, 7 and 2 genotypes, respectively. Cluster IV and VI consisted of one genotype each (NDYR-8 and Divya-33, respectively). The intra and inter-cluster distance among different clusters are given in Table 4. The intra-cluster D^2 values ranged from 0.00 (cluster 4 and 6) to 168.292 (cluster 5). The inter cluster D^2 values indicated that the most diverse groups were IV and VI (2154.229) followed by V and VI (1962.074). The minimum inter cluster value was found between I and II (194.948) indicates that these groups are less diverse. The mean performance of all the characters in different clusters is presented in Table 5. Cluster II showed highest mean for primary branches plant^{-1}(6.938). Cluster III exhibited highest mean for length of main raceme (64.937) and seed yield plant^{-1} (12.998). Cluster IV showed highest mean for days to 50% flowering (66.000), secondary branches plant^{-1} (12.360), siliqua on main raceme (53.260), seeds/silique(14.553), harvest index (29.723) and oil content (43.470). Cluster VI showed highest mean for days to maturity (129.667), plant height (185.400), 1000-seed weight (4.873) and biological yield plant^{-1} (80.867).

Table 3. Distribution of 30 genotypes of Indian mustard in different clusters under timely sown condition

Cluster No.	Number of genotypes	Genotypes included
I	8	Kranti, NDR-8501(N.rai), Varuna, NDRS 2007-2, MCN 13-37, MCN 13-40, Ashirvad, MCN 13-44.
II	11	RGN-73, NDRS 2010-1-2, Vardan, NPJ-112, NDR-190, NDRE 11-3, JD-6, CS-54, NDRS 2008-1, NDRS 2011, QM 13-10.
III	2	Maya, NDRS 2001-1.
IV	1	NDYR-8
V	7	NDRE 08-4, QM 13-2, NDRS 2017, NDRE-4, MCN 13-41, NDRE-8213, NDRE-7.
VI	1	Divya-33.

Table 4. Intra-cluster and inter-cluster D^2 values among 6 clusters in Indian

mustard under timely sown condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**158.438**	194.948	273.414	448.658	351.755	1394.555
Cluster II		**118.104**	347.085	350.3	217.551	1685.545
Cluster III			**122.593**	415.688	604.955	1250.233
Cluster IV				**0.00**	588.794	2154.229
Cluster V					**168.292**	1962.074
Cluster VI						**0.00**

Bold figures indicate intra-cluster D^2 values

Table 5. Cluster mean for 13 characters in Indian mustard under timely sown condition

**** Highest**

	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Secondary branches /plant	Length of main raceme (cm)	Silique on main raceme	Seeds /silique	1000 seed weight (g)	Biological yield /plant (g)	Seed yield /plant	Harvest index (%)	Oil content (%)
Cluster I	59.833	124.458	148.723	6.322	11.203	49.872*	35.740*	12.988	4.810	36.261	7.388	20.720	40.036
Cluster II	63.515	125.273	154.617	6.938**	9.522*	58.355	41.714	12.868	4.176	31.500	7.492	23.849	40.321
Cluster III	58.167	123.333	167.763	6.493	12.275	64.937**	40.952	13.313	4.872	49.740	12.998**	26.387	39.762
Cluster IV	66.000**	117.000*	147.893	6.290	12.360**	64.933	53.260**	14.553**	4.493	41.343	12.380	29.723**	43.470**
Cluster V	59.048	119.429	142.990*	6.209	10.968	54.640	36.635	12.157*	3.389*	28.177*	6.039*	21.629	39.609
Cluster VI	52.000*	129.667**	185.400**	5.387*	11.660	62.233	44.910	12.460	4.873**	80.867**	11.563	14.290*	38.263*

***Lowest**

Late sown:

Thirty genotypes were grouped into 6 clusters (Table 6) under late sown condition. Cluster IV consisted of maximum number of genotypes (12) followed by cluster II which had 7 genotypes. Cluster V, I and III consisted of 5, 3 and 2 genotypes, respectively. The intra and inter-cluster distance among different clusters are given in Table 7. The intra-cluster D^2 values ranged from 0.00 (cluster VI) to 157.207 (cluster I). The inter-cluster D^2 values indicated that the most diverse groups were II and VI (1526.887) followed by I and VI (1510.943). The minimum inter-cluster value was found between IV and V (161.877) which indicates that these groups are less diverse. The mean performance for all the characters in different clusters is presented in Table 8. Cluster I showed highest mean for days to maturity (119.333) and harvest index (24.086). Cluster II exhibited highest mean for days to 50% flowering (55.667), siliqua on main raceme (42.994), seeds siliquae^{-1} (12.646) and oil content (39.775). Cluster III showed highest mean value for secondary branches plant^{-1} (11.415), length of main raceme (61.510), 1000-seed weight (4.378) and seed yield plant^{-1} (11.065). Cluster IV showed highest mean for primary branches/plant(5.983). Cluster VI showed highest mean for plant height (171.233) and biological yield plant^{-1} (78.710).

The estimates of genetic divergence for most of the characters under study are in accordance with earlier reports. Singh *et al*. (2007),Goswami and Behl (2006),Binesh *et al.* (2012), Ratnesh*et al*. (2013),Neelam *et al.* (2014) and Vanukuri and Pandey (2022) also studied genetic diversity in Indian Mustard.

Table 6. Distribution of 30 genotypes of Indian mustard in different clusters under late sown condition

Cluster No.	Number of genotypes	Genotypes included
I	3	Kranti, NDR-8501, NDRE-7.
II	7	Vardan, RGN-73, NDRE 11-3, NDR-190, CS-54, NDRS 2008-1, NDYR-8.
III	2	Maya, NDRS 2001-1.
IV	12	Ashirvad, MCN 13-40, Varuna, NDRS 2007-2, MCN 13-41, NDRE-8213, MCN 13-37, MCN 13-44, NDRS 2010-1-2, NPJ-112, JD-6, NDRE-4.
V	5	NDRS-2011, QM 13-10, NDRS-2017, QM 13-2, NDRE 08-4.
VI	1	Divya-33

Table 7. Intra-cluster and inter-cluster D^2 values among 6 clusters in Indian mustard under late sown condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**157.207**	228.851	447.965	218.041	298.347	1510.943
Cluster II		**133.906**	401.41	215.696	181.663	1526.887
Cluster III			**79.177**	278.919	377.18	799.896
Cluster IV				**124.193**	161.877	1191.577
Cluster V					**83.233**	1444.036
Cluster VI						**0.0000**

Bold figures indicate intra-cluster D^2 values

Table 8. cluster mean for 13 characters in Indian mustard under late sown condition

	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	Secondary branches /plant	Length of main raceme (cm)	Silique on main raceme	Seeds /silique	1000 seed weight (g)	Biological yield /plant (g)	Seed yield /plant	Harvest index (%)	Oil content (%)
Cluster I	49.444	119.333**	122.430*	4.092*	9.732	46.970*	32.792*	11.731	3.938	29.027	6.842	24.086**	39.533
Cluster II	55.667**	116.190	147.203	5.429	8.022*	53.552	42.994**	12.646**	3.717	29.240	6.269	21.263	39.755**
Cluster III	48.333	114.667	152.865	5.590	11.415**	61.510**	39.407	12.302	4.378**	47.483	11.065**	23.602	38.063
Cluster IV	50.917	114.611	139.749	5.983**	10.165	50.010	36.807	11.474	3.783	32.996	5.799	17.803	38.285
Cluster V	53.267	110.133	145.643	5.865	9.670	59.971	34.225	11.036*	3.641*	25.318*	4.457*	17.567	38.469
Cluster VI	42.333*	109.667*	171.233**	4.403	10.543	59.687	42.363	11.400	3.967	78.710**	10.137	12.870*	37.317*

**** Highest**

***Lowest**

3.4 Percent contribution of different characters towards genetic divergence

Per cent (%) character contribution towards divergence in Indian mustard under timely sown (TS) and late sown (LS) conditions is presented in Table 9.The maximum character contribution towards divergence was observed for1000-seed weight (31.03%) followed by biological yield plant^{-1} (22.99%) and oil content (15.86%) in TS. Under late sown condition maximum character contribution towardsdivergence was observed for biological yield plant^{-1} (29.20%) followed by oil content (25.52%) and length of main raceme (11.03%). Plant height (8.97%), 1000-seed weight (6.44%) and harvest index (5.98%) showed moderate character contribution.

Table 9. Percent (%) character contribution towards divergence in Indian mustard under timely and late sown condition

Character	Timely sown condition(%)	Late sown condition (%)
Days to 50% flowering	5.06	3.45
Days to maturity	1.38	2.30
Plant height (cm)	5.29	8.97
Primary branches/ plant	0.69	2.07
Secondary branches/ plant	0.00	0.23
Length of main raceme (cm)	6.90	11.03
Siliquae on main raceme	1.84	2.30
Seeds/ siliqua	2.76	0.92
1000 seed weight (g)	31.03	6.44
Biological yield/ plant (g)	22.99	29.20
Seed yield/ plant (g)	3.68	1.61
Harvest index (%)	2.53	5.98
Oil content (%)	15.86	25.52

4. CONCLUSION

From the present study it is concluded that sufficient genetic variability was present in the experimental material for most of the traits in both the environments. High heritability coupled with high genetic advance was observed for biological yield plant^{-1} and seed yield plant^{-1} in both TS and LS conditions. Cluster analysis revealed highest inter cluster distance between cluster IV and VI in TS while in LS the cluster II and VI showed maximum inter cluster distance indicating genetic diversity among the genotypes.

REFERENCES

1. Akabari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (Brassica juncea). International Journal of Agricultural Sciences. 2015 Jan;11(1):35-9.
2. Binesh G, Dhiraj S, Ram A, Amit S. Genetic divergence in elite gene pool of Indian mustard [Brassica juncea (L.) Czern & Coss.]. Research on Crops. 2012;13(3):1102-4.
3. Goswami PK, Behl RK. Genetic divergence in Indian mustard. Annals of Agricultural Research. 2006;27(2).
4. Grafius JE. A geometry for plant breeding. Crop Science. 1964;4:241-46.
5. Kaur S, Kumar R, Kaur R, Singh I, Singh H, Kumar V. Heterosis and combining ability analysis in Indian mustard (Brassica juncea L.). Journal of Oilseed Brassica. 2019 Apr 20;10(1):38-46.
6. Khulbe RK, Pant DP, Naveen S. Variability, heritability and genetic advance in Indian mustard [Brassica juncea (L.) Czern & Coss]. Crop Research (Hisar). 2000;20(3):551-2.
7. Kumar S, Bhardwaj R, Jhambhulkar SJ, Rai A. Assessment of genetic variability, heritability and genetic advance in Indian mustard (Brassica juncea L.). Journal of Oilseed Brassica. 2023 Feb 17;14(1):38-43.
8. Mahalanobis PC. On the generalized distance in statistics. National Institute of Science of

India.

9. Mahla HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability, correlation and path analysis in Indian mustard [Brassica juncea (L.) Czern and Coss.].
10. Maurya SK, Maurya KN, Lal K, Singh Y, Singh S, Dixit B, Singh S. Assessment of Genetic Variability, Heritability and Genetic Advance in Indian Mustard (Brassica juncea L. Czern & Coss.). Int. J. Curr. Microbiol. Appl. Sci. 2018;7(11):13-8.
11. Neelam S, Jadeja GC, Jogendra S. Genetic diversity analysis in relation to seed yield and its component traits in Indian mustard (Brassica juncea L. Czern & Coss). The Bioscan. 2014;9(2 Supplement):713-7.
12. Pandey SD, Anil P. Genetic variability, heritability and genetic advance for some characters in mustard [Brassica juncea (L.) Czern & Coss]. Annals of Agri Bio Research. 2014;19(3):467-73.
13. Rai SK, Verma A, Pandey DD. Genetic variability and character association analysis in Indian mustard (Brassica juncea (L.) Czern and Coss). Ann. Agri. Bio. Res. 2005;10(1):29-34.
14. Ratnesh P, Brajesh K, Manoj K. Genetic divergence for quantitative traits in Indian mustard (Brassica juncea L. Czern & Coss). American-Eurasian Journal of Agricultural & Environmental Sciences. 2013;13(3):348-51.
15. Rout S, Kerkhi SA, Gupta A. Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard [Brassica juncea (L.) Czern and Coss.]. Journal of Pharmacognosy and Phytochemistry. 2019;8(3):4119-23.
16. Sharma RM, Brijendra K, Kumar K, Chauhan MP. Variability analysis for yield and is component of Indian mustard [Brassica juncea (L.) Czern and Coss.]. Trends in Biosciences. 2014;7(17):2539-43.
17. Singh V, Bhajan R, Kumar K. Genetic diversity in indian mustard (Brassica juncea L. Czern and Coss.). Progressive Agriculture. 2007;7(1and2):105-9.
18. Vanukuri AR, Pandey MK. Genetic variability and genetic diversity studies in Indian mustard (Brassica juncea L.). The Pharma Innovation Journal. 2022;11(7):1357-60.