

Genetic Analysis in Local Collection of Indian Mustard (*Brassica juncea* L.)

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Abstract- The present study entitled “Genetic analysis in local collection of Indian Mustard (*Brassica juncea* L.)” for estimating the degree of genetic diversity in the parents' respective yield and quality metrics as well as to find superior parents. To achieve these objective parents were conducted *rabi* 2022-23. Spacing of 30 X 10 cm² was kept between row to row and plant to plant and 15 plants were raised in each row. Observations were made in days leading up to 50% flowering, plant height (cm), Numbers of primary branches per plant, Days to maturity, Numbers of silique per plant, Length of silique, Numbers of seed per silique, 1000 seed weight, Seed yield per plant. The results obtained were subjected to statistical analysis. All of the analyzed characters' mean squares resulting from genotypes were extremely significant i.e. 50% flowering, plant height (cm), Numbers of primary branches per plant, Days to maturity, Numbers of silique per plant, Length of silique, Numbers of seed per silique, 1000 seed weight, Seed yield per plant. This shows that the genotypes for these traits exhibit considerable genetic diversity.

The estimate of high PCV and moderate GCV was observed for length of silique and number of branches per plant in TAM-108-1 and BIO-902, suggesting influence of environment. These characters are not expression its genetic potential.

Moderate levels of PCV and GCV were obtained for days to flowering, 1000 seed weight, stem girth and average fruit weight indicating moderate level of variability for the said traits

The estimates of high heritability value were noticed for plant height, number of branches, days to flowering, average fruit weight, fruit yield per plot, fruit length, fruit diameter, and Days to maturity in Pusa Agrani. High heritability indicates, a large number of fixable additive genes are present for the traits. It is also supported by the ratio of GCV and PCV, which also

indicated the presence of additive genes for the characters.

INTRODUCTION

In the Cruciferae family, which has 338 genera and 3700 species, An amphidiploid species called *Brassica juncea* (AABB) (n=18) was created by crossing *Brassica nigra* (BB) (n=8) and *Brassica rapa* (AA) (n=10). The term *Brassica juncea*, which comes in several varieties, including Brown, Chinese, Indian, Leaf, Oriental, and Vegetable mustards, can be used to identify the crop. Many more species of *Brassica* that are members of this family are grown all over the world. These are Toria (*Brassica campestris* L. var. toria), Banarasi rai (*Brassica nigra*), Gobhi sarson (*Brassica napus*), brown mustard (*Brassica campestris* L. var. brown sarson) & *Brassica campestris* L. var. yellow sarson is known by this name. [*Brassica juncea* (L.) Czern] Coss. & Indian mustard is among the greatest significant oil seed harvest grown in the nation & ranks 2nd in Asia in terms of acreage & mustard output.

Rapeseed & mustard are the 2nd most produced oilseed crops in India, behind soybean. In India, oilseed crops were cultivated on 25.5 m ha or 13.33% of the total area, out of a variety of crops. 32.26 million tons of oilseeds were produced in total in 2018–19. Among oilseed crops, rapeseed and mustard came in second and third, respectively, has a 6.23 million hectare area and 9.34 million tons of produce in 2018–19 (Anon, 2019) [1]. More than 80% of the nation's total acreage and output of mustard is grown in the five states of Gujarat, Rajasthan, Uttar Pradesh, Haryana, and Madhya Pradesh.

The primary components of this crop, oil and fats, are utilized not just for food but also as vital materials for the sectors. Generally speaking, it contains 35–45% oil, 17–25% protein, 8–10% fiber, 6–10% moisture, and 10–12% extractable components. Terpenes, sterols, tocopherols, glycolipids, and phospholipids are examples of unsaponifiable hydrocarbons oil is mostly a triglyceride made of fatty acids. The antinutritional elements in the oil are glucosinolate and erucic acid. The foundation of genetic progress is genetic variety. It is generally acknowledged that a key component of plant breeding is knowledge of the genetic relatedness and diversity of the germplasm in elite breeding material (Mukhtar et al., 2002). Any scheme of hybridization with a focus on genetic yield enhancement must take genetic variety into consideration, especially regarding crops that self-pollinate (Joshi & Dhawan, 1966).

Genetic diversity among individuals or groups can be evaluated using morphological, biochemical & molecular techniques (Mohammadi and Prasanna, 2003). Using phenotypic traits, several studies have already evaluated the genetic diversity of *B. juncea*. (Gupta et al., 1991; Vaishnav et al., 2006; Alie et al., 2009; Singh et al., 2010). As sophisticated biometric techniques like multivariate analysis have evolved (Rao, 1952), Ward's no-hierarchical squared Euclidean distance & D2 statistics approach, which are based on Mahalanobis (1936), have made it feasible to quantify the amount of variety among germplasm for evaluation with regard to breeding programs. The current study was conducted with the aim of achieving the following goals: identifying the genetic diversity & variability of different mustard genotypes, calculating the genotype-environment (G×E) interaction in yield and yield-contributing traits of mustard genotypes, and choosing short duration genotype that increases crop yield. These

Table 4.1. Analysis of Variance for various attributes in tomato

Source of variance	Degree of freedom	PH	DF 50%	DtM	NPB/P	NS/P	LS	NS/S	1000 SW	SY/P
Replication	2	42.37	5.89	42.34	0.245	117.25	0.051	14.31	0.45	19.69
Treatment	23	1467.61**	56.26**	114.23**	2.40**	6536.12**	2.31**	14.49**	2.04**	29.38**
Error	46	23.66	1.44	1.16	0.053	0.12	0.15	4.97	0.071	3.14

** Significant at 1% level, *Significant at 5% level

Characters: -

- 1) PH - Plant height, 2) DF 50%- Days to 50% flowering, 3) DtM- Days to Maturity, 4) NPB/P – No. of primary branches / plant, 5) NS/P – No. of

objectives were undertaken in light of the widespread use of breeding programs and the genetic diversity that is currently accessible to produce variety for every attribute.

MATERIAL AND METHODS

The present investigation “Genetic analysis in local collection of Indian Mustard (*Brassica juncea* L.)” was conducted during *rabi* 2023 at Experiment will be carried out in the School of Genetics and Plant Breeding Department of agricultural Science, Saikheda

RESULT AND DISCUSSION

The experiment entitled, “Genetic analysis in local collection of Indian Mustard (*Brassica juncea* L.)” was undertaken at experimental area of the Department of Agril. Botany, College of Agriculture, GHRU Saikheda, Dist, PANDHURNA, Madhya Pradesh. during, 2022-2023. Three replications within the Randomized block layout were used to plant twenty promising genotypes in order to capture observations on various parameters. Based on Panse and Sukhatme (1965), a statistical analysis was conducted.

4.1 variance of analysis for various attributes in tomato

The variance of analysis for nine attributes studied presented in table 4.1a For each character, the genotype-based mean squares were highly significant studied i.e. Plant height (cm), No. of primary branches / plant, Days to 50% flowering, Days to 1st maturity, No. of silique / plant, length of silique, No. of seed / silique, 1000 seed weight, seed yield / plant this indicates the significant genetic diversity in these characteristics' genotypes.

- silique / plant, 6) LS – Length of silique, 7) NS/S – No. of seed / silique, 8) 1000 SW – 1000 seed weight, 9) SY/P – Seed yield / plant.

4.2 Mean performance of parents

The study helps in identifying good inbred lines for their use in genetic variability growth, yield and quality which ultimately can be involved in the development of single cross hybrid for commercial cultivation. Thus, study has broad scope, as it will help in developing new hybrid of brinjal with great potential yield.

The performance of parents for fifteen traits recorded in tomato are presented in table 4.2a and 4.2b. From each plot, the five plants were randomly selected for observation of every genotype in each replication for the following features (with the exception of days to 50% blooming & days to 1st flowering, which were documented according to a scheme).

1) Days to 50% flowering

Based on the average number of days required for 50% blooming, TAM-108-1 took the shortest amount of time (46 days), followed by Bio 902 (50.15 days) and Pusa Agrani (48 days). RH 1676 had the higher no. of days to 50% blooming (53.33 days), followed by NAVGOLD (IM) (55.57 days). For every genotype combined, the average number of days to 50% blooming was 50.61.

2) Days to Maturity

Based on mean days to maturity, TAM-108-1 took the shortest amount of time (85 days), followed by

Bio 902 (89.78 days) and Pusa Agrani (86.57 days). RH 1676 had the most documented days to maturity (90.55 days), followed by NAVGOLD (IM) (94.35 days). For every genotype combined, the average days to maturity was 89.25 days.

3) Plant height at (cm)

TAM-108-1 (90.32 cm) was the highest genotype ever measured; it was the earliest, followed by Pusa Agrani (88.57 cm) and Bio 902 (86.45 cm). RH 1676 (84.15 cm) had the smallest genotype, followed by NAVGOLD (IM) (80.59 cm). For every genotype combined, the average plant height was 86.01 cm.

4) Numbers of primary branches / plant

The greatest no. of main branches was noted. The earliest was TAM-108-1 (4.78), followed by Bio 902 (3.89) and Pusa Agrani (4.03). RH 1676 had the fewest main branches (3.45) and NAVGOLD (IM) had the fewest (3.39). Across all genotypes, the average number of branches was 3.90.

5) No. of Siliquae / plant

TAM-108-1 (165.89) had the highest amount of siliquae / plant & there was the earliest plant, followed by Bio 902 (164.85) and Pusa Agrani (159.86). RH 1676 (152.21) had the lowest number of siliquae per plant, whereas NAVGOLD (IM) (150.37) had the highest amount. 156.17 leaves were present in each plant for every genotype.

Table 4.2a. Average performance of various varieties for different traits

Sr.no.	Genotypes	Days to 50% Flowering	Plant height	Days to maturity	No. of primary branches / plant	No. of siliquae/ plant
1	D-4	47.65	119.34	86.50	6.37	159.29
2	GD-6	53.69	114.03	91.50	4.32	154.39
3	PM-26	47.33	118.70	86.50	6.04	158.98
4	PM-25	48.95	117.24	88.50	5.17	157.17
5	TAM-108-1	43.50	120.51	84.50	7.09	165.89
6	Kranti	53.97	114.03	93.50	4.16	154.14
7	Bio-902	46.25	119.63	85.50	6.62	164.85
8	ACN-9	49.58	116.99	92.50	4.91	157.11
9	SKM-1626	54.02	113.63	93.50	3.92	153.81
10	GM-2(LR)	48.49	118.38	87.50	5.72	158.45
11	NPT-224	54.57	113.39	94.50	3.69	153.05
12	GSC-7	51.52	115.25	91.50	4.68	155.80
13	RH-1676	56.61	111.57	95.50	2.93	152.21
14	Pusa Agrani	46.25	120.14	85.50	6.84	159.86
15	RH-1584	50.58	116.15	89.50	4.64	156.17
16	DRMR-1448	48.77	117.74	87.50	5.45	158.14
17	PM-21	54.57	112.65	94.50	3.36	157.73
18	PBR-297 (IM)	51.80	115.35	92.50	4.44	154.93
19	CS-60	56.01	112.00	95.50	3.21	151.71
20	NAVGOLD(IM)	58.16	110.59	96.50	2.68	150.37
	S.E (m)	0.17	0.11	0.15	0.84	0.11
	C.D (5%)	0.49	0.31	0.44	2.88	0.32

6)Length Siliquae

The maximum length of siliquae were recorded TAM-108-1 (6.96) was earliest followed by Pusa Agrani (6.44) and Bio 902 (6.12). The minimum no. of length silique were observed in RH 1676 (3.45) followed by NAVGOLD (IM) (3.39). The mean no. of length siliquae of all the genotype was 4.59.

7)Numbers of seed / Siliquae

The maximum no. of seed / siliquae were recorded TAM-108-1 (18.46) was earliest followed by Pusa Agrani (18.05) and Bio 902 (17.87). The minimum number of seed / siliquae were noted in RH 1676 (10.41) followed by NAVGOLD (IM) (11.14). The average number of seed / siliquae of all the genotype was 14.76.

8) 1000seed weight (g)

The maximum 1000 seed weight was observed in aTAM-108-1 (4.01) was earliest followed by Pusa

Agrani (3.89) and Bio 902 (3.65). While minimum 1000 seed weight was observed inRH 1676 (2.98) followed by NAVGOLD (IM) (2.81). The averagenumbers of 1000 seed weight of all the genotype was (3.46).

9)Total yield / plant (g)

The TAM-108-1 (11.31) had the highest total yield / plant, and it was the first to be seen. Pusa Agrani (9.89) and Bio 902 (8.65) were the next two. While RH 1676 (6.98) had the lowest amount total yield / plant, NAVGOLD (IM) came in second (5.81). Across all genotypes, the average total yield / plant was (8.52).

Table 4.2b. Average performance of various varieties for different traits

Sr.no.	Verities	Length of silique	No. of seed / silique	1000 seed weight	Seed yield / plant
1	GD-4	5.17	159.29	5.03	10.12
2	GD-6	4.15	154.39	3.50	8.17
3	PM-26	3.15	158.98	4.80	9.82
4	PM-25	4.55	157.17	4.87	9.28
5	TAM-108-1	6.96	165.89	5.71	10.66
6	Kranti	5.48	154.14	3.28	8.24
7	Bio-902	6.12	164.85	5.21	9.96
8	ACN-9	5.12	157.11	4.76	8.47
9	SKM-1626	5.66	153.81	3.06	7.76
10	GM-2(LR)	3.15	158.45	4.80	9.30
11	NPT-224	3.87	153.05	2.96	8.21
12	GSC-7	3.48	155.80	4.27	8.16
13	RH-1676	2.96	152.21	2.53	6.62
14	Pusa Agrani	6.44	159.86	5.41	9.40
15	RH-1584	4.76	156.17	4.53	8.40
16	DRMR-1448	5.33	158.14	4.84	9.09
17	PM-21	5.11	157.73	2.87	6.82
18	PBR-297 (IM)	4.54	154.93	4.03	8.46
19	CS-60	3.04	151.71	2.73	7.85
20	NAVGOLD(IM)	3.01	150.37	2.25	6.89
	S.E (m)	0.10	0.13	0.16	2.63
	C.D (5%)	0.31	0.39	0.49	5.74

4.3 Estimation of variability, genetic advance & heritability

4.3.1 Days to 50 % flowering

High PCV (8.91%) and GCV (8.58%) were paired with very high phenotypic and genotypic variations (19.71 and 18.27) in the data related plant height (Table 4.3). High genetic advance (8.47), high genetic heritability (92.67%) & This feature included strong genetic progress as a percent mean (17.01).

4.3.2 Days to Maturity

According to the data on the Days to maturity, there were Moderate PCV (5.13%) and GCV (4.57%) values and Moderate phenotypic and genotypic variances of 44.06 and 35.08, respectively. For this variable, it was also noted that the high heritability (79.59%) This characteristic exhibited strong genetic advance (10.88) and high genetic advance as a percent mean (8.41%).

4.3.3 Plant height (cm)

For the number of leaves per plant, there were high values for phenotypic and genotypic variation (504.97 and 481.32), moderate PCV and GCV (13.12% and 12.81%), high heritability (95.31%), moderate genetic advance (44.12) & strong genetic progress as a mean percentage (25.77%).

4.3.4 No. of primary branches / plant

For the character No. of primary branches / plant, moderate genotypic & phenotypic variances (0.83 and 0.78, respectively), GCV (16.54%) & moderate PCV (16.00%), high heritability (93.67%), medium genetic advance (1.76) & strong genetic advance as a percent mean (31.91%) were found.

4.3.5 Numbers of silique per plant

With modest PCV (23.81%) and GCV (23.69%), the results on the no. of siliques / plant demonstrated substantial phenotypic & genotypic variations (2193.09 and 2171.53, respectively). For this variable, there were estimations of moderate genetic advancement (95.5), strong genetic progress as a percent mean (48.57%) & high heritability (99.01%).

4.3.6 Length of silique

Very high phenotypic and genotypic variations (14.60 and 13.78, respectively) were observed in the data pertaining to the length of the silique, with very high PCV and GCV values of 22.44% and 21.78%. For this variable, there was extremely high

heritability (94.3%), very high genetic progress significant as a mean percentage (48.57%) and high genetic advance (7.42).

4.3.7 Fruit diameter (mm)

Extremely high PCV and GCV of 18.77% and 17.08% were observed in the fruit diameter data, which also showed extremely high genotypic & phenotypic variances of 0.72 & 0.87, respectively. For this variable, there was extremely high heritability (82.82 %) substantial genetic progress as a mean percentage (32.02%) and extremely high genetic advance (1.59%).

4.3.8 1000 seed weight

The statistics on the 1000 seed weight indicated genotypic & very high phenotypic genotypic variability of 0.65 & 0.73 respectively, with a very high PCV and GCV of 16.31% and 15.50% observed. High genetic advance (1.58), high heritability (90.22%) & high genetic advance as average percentage (30.33%) were found for this variable.

4.3.9 Seed yield per plant (g)

The results on average fruit weight showed significant phenotypic and genotypic variations (11.89 and 8.74), high PCV (28.00 %) and GCV (24.01 %), very high heritability (73.52 %), significant genetic progress (5.22) & high genetic progress as a mean percentage (42.41%) was discovered for this characteristic.

Table.4.3 Estimation of variability, heritability & genetic advance for twelve attributes in seven varieties of Mustard

Sr. No.	Characters	Mean	Range	Variance			G.C.V.	P.C.V.	h ² _{bs} (%)	G.A.	G.A. as % of mean
				Phenotypic	Genotypic	Environmental					
1.	Days to 50% flowering	49.81	43-59.5	19.71	18.27	1.44	8.58	8.91	92.67	8.47	17.01
2.	Days to maturity	129.3	111.5-138.5	44.06	35.08	8.98	4.57	5.13	79.59	10.88	8.41
3	Plant height	171.21	127.7-213.5	504.97	481.32	23.65	12.81	13.12	95.31	44.12	25.77
4	No. of primary branches / plant	5.53	3.96-7.0	0.83	0.78	0.053	16.00	16.54	93.67	1.76	31.91
5	No. of silique / plant	196.65	123.9-320.5	2193.09	2171.53	21.56	23.69	23.81	99.01	95.52	48.57
6	Length of silique	4.97	2.96-6.96	0.87	0.72	0.15	17.08	18.77	82.82	1.59	32.03
7	No. of seed / silique	14.37	10.41-18.46	8.14	3.17	4.97	12.39	19.86	38.96	2.29	15.94
8	1000 seed weight	5.23	3.80-6.89	0.73	0.65	0.071	15.50	16.31	90.22	1.58	30.33
9	Seed yield / plant	12.31	7.86-17.92	11.89	8.74	3.14	24.01	28.00	73.52	5.22	42.41

PCV and GCV: Phenotypic and genotypic coefficient of variation, h² bs: Heritability in broad sense, GA: Genetic Advanc

CONCLUSION

The present investigation entitled “Genetic analysis in local collection of Indian Mustard (*Brassica juncea* L.)” for estimating the degree of genetic diversity in

the parents' respective yield & quality metrics as well as to find superior parents. To achieve these objective parents were conducted *rabi* 2022-23. Twenty parents were obtained and grown at Department of

Agril. Botany, College of Agriculture, GHRU Saikheda, Dist, PANDHURNA, Madhya Pradesh in block design that is randomized and has three replications. A 30 by 10 cm² gap was maintained between each row and each plant & 15 plants were raised in each row. Observations were made in days leading up to 50% flowering, plant height (cm), No. of primary branches / plant, Days to maturity, no. of siliques / plant, Length of silique, no. of seed / silique, 1000 seed weight & Seed yield / plant. The results obtained underwent statistical examination. All of the analyzed characters' average squares resulting from genotypes were extremely significant i.e. 50% flowering, plant height (cm), no. of primary branches / plant, Days to maturity, no. of siliques / plant, Length of silique, no. of seed / silique, 1000 seed weight, Seed yield / plant. This shows that the genotypes for these characters exhibit considerable genetic diversity.

Each of the nine characteristics under investigation demonstrated significant genotype-related means squares, according to the analysis of variance for genetic advance estimates. Parental variance was further divided into variations resulting from genotypes. For every character, there was a considerable variance in the Means Square attributed to parents. With the exception of the length of the silique & the no. of main branches / plant, crosses noted important difference for every feature. For every character, there was a considerable variance in the Means Square attributed to the parents. With the exception of the no. of seeds / silique & the days until 50% blooming, the mean square resulting from genetic variability and reciprocal combining ability were significant for every feature under study.

The result performance as a whole showed that the parent TAM-108 & Pusa agrani was discovered to be significantly better than for total yield / plant & other yield contributing traits. Among the twenty parents, the TAM-108-1, Pusa agrani, Bio-902, kranti and RH-1676 found significantly better in terms of plant yield overall and in a few specific yield components.

The response of genetic variability for each trait that is being examined was found by estimating phenotypic and genotypic traits across all parents. In both generations, the coefficient of variance for phenotypic traits was often somewhat larger than corresponding varietal estimates, suggesting that the population's actual genetic potential was being

expressed. Height of Plant, the no. of branches / plant, the no. of fruits / plant, average fruit weight & the yield / plant all showed high (>20%) genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) differences across growth and yield characteristics. Fruit diameter, fruit length, and phenol content all showed high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (>20%) among quality indicators, suggesting the greatest potential for selection and character enhancement.

The estimate of high PCV & moderate GCV was noted for the silique's length & no. of branches / plant in TAM-108-1 and BIO-902, suggesting influence of environment. These characters are not expression of its genetic potential.

Moderate levels of GCV & PCV were obtained for days to flowering, 1000 seed weight, stem girth and average fruit weight indicating moderate level of variability for the said traits.

Plant height, no. of branches, days to flowering, average fruit weight, fruit production / plot & fruit length were all estimated to have strong heritability values. Fruit diameter & Days to maturity in Pusa Agrani. High heritability indicates, a large number of fixable additive genes are present for the traits. It is also supported by the ratio of PCV & GCV, which also revealed the existence of additive genes for the characters.

In terms of plant height, no. of siliques / plant & days to maturity, highest levels of GA have been seen in DRMR-1448. The single seed decent technique of breeding has resulted in minimal levels of GA for all other characteristics, however moderate amounts have been seen for seed output per plant. There was little to no selection, which explains the apparent genetic progress. With the exception of days to blooming in, for which a modest amount a significant degree of genetic advancement was seen in each trait, as shown by the percent mean. People with elevated GAM estimates imply that selecting for these qualities might be cost-effective.

The material evaluated for this inquiry was found to have a broad range of variance for the different features that were detected. There was plenty of room for improvement in the handled population of mustard's growth, yield, and quality characteristics, as evidenced by genetic progress, heritability &

coefficients of variation for genotype & phenotype as percent mean.

REFERENCE

- [1] Md. Shahin Iqbal, Md. Shamiul Haque, Dr. Ujjal Kumar Nath and Islam Hamim (2014). Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes. *International Journal of Agricultural Science Research* Vol. 3(8), pp. 141-156.
- [2] Singh D, Arya RK, 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 Oilseeds Brassica*, 1, 19-22.
- [3] Singh, P R. K. Arya, N. Chandra. R. Niwas and P. Salisbury, 2010. Genetic divergence studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L.) (Zem and coss). *J. Oilseed Brassica*, 1 (1): 19 - 22
- [4] A. M. Pradhan, M. Roy Choudhury, A. Sawarkar and S. Das (2021). Genetic Analysis of Some Genotypes of Indian Mustard (*Brassica juncea* L.) for Yield and Yield Attributing Traits. *Current Journal of Applied Science and Technology* 40(35): 51-60, 2021; Article no.CJAST.72924 ISSN: 2457-1024.
- [5] Akoju Saikrishna, Arunkumar B, Hasan Khan, Kuchanur PH and AyyanagoudaPatil (2021). Genetic diversity studies in Indian mustard [*Brassica juncea* (L.) Czern&Coss.] For yield and its component traits. *The Pharma Innovation Journal* 2021; 10(10): 534-538
- [6] Patel, J. M. and K. M. Patel. 2006. Genetic divergence in Indian mustard (*Brassica juncea* (L.) Czern and Coss). *Indian J. Pl. Breed.* 66 (1): 49-50.
- [7] Vaishnava A, Sachan JN, Tewari SK (2006). Genetic divergence for important quantitative traits in Indian mustard (*Brassica juncea* (L.) Czern and Coss). *Agricultural Science Digest*, 26, 269-272.
- [8] Sathi. D. A.. M. Arifuzzama, B. K. Biswas. M. Hasanuzzaman and A K. Azad. 2012. Genetic divergence in mustard. *Afr. J. Plant Sci.*(8) . 239-243.