Estimation of Variability and Genetic Diversity in Indian Mustard Germplasm (*Brassica juncea* L.)

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ABSTRACT

The genetic variability and divergence among 41 Indian mustard (*Brassica juncea* L.) genotypes were assessed for 12 characters. High to moderate estimates of GCV and PCV were exhibited by siliqua plant $^{-1}$, harvest index and biological yield plant $^{-1}$. High estimates of heritability and genetic advance were observed for plant height and harvest index. High estimate of genetic gain was observed for siliqua plant $^{-1}$, harvest index and biological yield plant $^{-1}$. Forty one genotypes were grouped into seven clusters. The cluster II had the maximum number of genotypes. The maximum inter-cluster distance was observed between cluster III and VI and cluster VI and VII and cluster III and VII. Thus, genotypes present in cluster III and VI and VII like Raya, CS54, Sivalik, Krishna, NDRE 4, Urvasi, Ganga Kaveri Vijay may be used in hybridization programme to obtain superior segregants for yield improvement in Indian mustard.

Key words : Heritability, GCV, Genetic Diversity, Genetic Gain, PCV, Mustard, Variability

Mustard (*Brassica juncea* L.) is the third most important edible oil source of the world after Soybean and Palm. In India, it ranks second in acreage superseded by only groundnut. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. The D^2 statistic is useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam, 1966). An Attempt has been made in this study with an objective to assess the variability and diversity in Indian mustard germplasm to identify divergent parents for hybridization.

MATERIAL AND METHODS

The present experiment was conducted comprising 41 genotypes collected from National Research Center for Rapeseed and Mustard, Bharatpur, Rajasthan at Crop Research Farm, Department of Genetics and Plant Breeding, Allahabad during *rabi*, 2007-08. The seeds of each entry were sown in two row plot with 30 x 10 cm of inter- and intra-row spacing. Fertilizers were applied @ 60: 40: 40 NPK kg ha^{-1}. The other intercultural operations were done to raise the crop uniformly. Data were recorded on five randomly selected competitive plants or on plot basis for each treatment in each replication for twelve characters viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of secondary

branches, number of siliqua branch^{-1}, number of siliqua plant^{-1}. number of seeds siliqua^{-1}, biological yield plant^{-1} (g), harvest index, test weight (g) and seed yield plant^{-1} (g). The genetic parameters were estimated following Burton (1952) and Johnson *et al*., (1955). Further, the data were subjected to multivariate analysis as suggested by Mahalanobis (Mahalanobis, 1936) and genotypes were grouped into different clusters by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

High magnitude of phenotypic coefficient of variation was recorded for siliqua plant^{-1} (45.36) followed by harvest index (41.59) and biological yield (39.94). Number of primary branches (24.64) and siliqua branch^{-1} (20.87) showed moderate value and days to 50% flowering (7.75) depicted least phenotypic coefficient variation. Das et al., (1998) also observed high phenotypic coefficient of variation for siliqua plant^{-1} among 12 yield component characters while evaluating 41 genotypes of *Brassica juncea*. High magnitudes of GCV were recroded for siliqua plant $^{-1}$ (44.80) followed by harvest index (40.86) and biological yield plant^{-1} (39.79) while days to do 50% flowering (6.60) exhibited least genotypic coefficient of variation (Table 1).

High heritability was recorded for biological yield plant^{-1} (99.26%) followed by plant height (97.84%) and harvest index (96.52%) and low heritability was calculated for primary branches

Table 1. Estimates of genetic parameters for different quantitative characters in Indian mustard gumplasm.

Characters	Genotypic coefficient of variation	Phenotypic coefficient of Variation	Heritability (%)	Genetic advance	Genetic gain
Days to 50% flowring	6.60	7.75	72.53	5.67	11.58
Plant height (cm)	8.67	8.77	97.84	35.26	17.67
Primary branches	17.14	24.64	48.42	1.26	24.57
Secondary branches	30.47	33.05	85.03	5.83	57.86
Siliqua branch^{-1}	20.17	20.87	93.44	15.97	40.17
Siliqua plant^{-1}	44.80	45.36	87.53	29.24	91.15
Days to maturity	3.07	3.20	92.03	7.63	6.07
Seeds siliqua^{-1}	12.22	13.86	87.88	2.87	22.18
Biological yield plant^{-1}	39.79	39.94	99.26	61.90	81.66
Harvest index%	40.86	41.59	96.52	22.99	82.70
Test weight (g)	12.84	13.58	88.88	1.46	25.00
Seed yield plant^{-1}(g)	29.03	30.62	89.80	9.45	56.70

Table 2. Distribution of 41 genotypes of Indian mustard into different clusters

Cluster	No.of genotypes	Genotypes included
I	8	Kranti, C.S 52, Shivani, GM 1, Nitya Vishal, Swom Jyoti, Rohini, Pusa Mahak
II	13	GM-3, Aravali, T-59, Sourabh, G.K. Abhay, RH 30, Aruti Kranti, Can Satavdi, Maya, Gloriya, Sarpanch, Dev (Desi), Rohini Chipka
III	4	Raya, C S 54, Sivalik, Krishna
IV	6	Pusa Jaikishan, RLM-619, Patan Mustard - 67, PBR 210, Narendra Rai, Sajucta Asech
V	7	GM2, Aruti 4001, RLM 1359, Victory, Lafer Kranti, Madhuri, Geeta
VI	1	NDRE 4
VII	2	Urvasi, Ganga Kaveri Vijay

(48.42%). High values indicated that heritability may be due to higher contribution of genotypic component (Table 1). Low heritability estimates were also reported for primary branches by Prasad et al., (2003).

High values of genetic advance were recorded for biological yield (61.90) followed by the plant height (35.26) and siliqua plant^{-1} (29.24). Moderate estimate siliqua per branch (15.97) and low value for primary branches plant^{-1} (1.16) were recorded. High genetic gain estimates were registered for siliqua per plant (91.15), harvest index (82.70) and biological yield plant^{-1} (81.66) (Table 1)

In the present study, the significant 'V' statistic at 480 degree of freedom revealed the presence of differences among the genotype means for all character. Forty one mustard genotypes were grouped into seven clusters. Cluster II had maximum number of genotypes (13) followed by cluster 1 (8), cluster V (7), cluster IV (6), cluster III (4), Cluster

Table 3. Intra (diagonal) and inter-cluster average distances in Indian mustard

Cluster number	I	II	III	IV	V	VI	VII
I	228.30	360.93	730.69	651.77	415.47	1836.01	1405.57
II		241.79	526.91	847.12	573.01	1550.20	1303.25
III			237.57	1886.35	1376.19	2809.44	2134.39
IV				151.56	321.64	825.18	1523.42
V					173.84	1266.94	1040.28
VI						0.000	2625.07
VII							494.85

Table 4. Cluster mean values for seven clusters for different quantitative characters in Indian mustard.

S.No	Characters \ Cluster no	I	II	III	IV	V	VI	VII
1	Days to 50% flowring	49.83	50.61	50.33	44.72	49.00	38.33	50.50
2	Plant height (cm)	217.42	193.14	204.41	192.15	203.18	130.22	203.22
3	Primary branches	4.99	4.90	5.19	6.08	4.52	5.33	5.71
4	Secondary branches	10.66	10.68	7.74	9.82	7.86	11.55	16.16
5	Siliqua branch^{-1}	37.38	41.85	40.13	29.70	46.20	32.55	45.83
6	Siliqua plant^{-1}	303.74	341.55	320.24	208.24	292.47	113.44	295.94
7	Days to maturity	125.66	126.89	127.50	122.61	124.33	112.66	134.66
8	Seeds siliqua^{-1}	13.10	12.44	13.94	12.01	13.29	11.77	15.44
9	Biological yield plant^{-1}	82.17	90.49	133.16	38.12	52.52	33.77	55.56
10	Harvest index%	23.96	19.54	17.03	35.61	38.78	29.35	55.62
11	Test weight (g)	5.74	5.83	5.31	5.80	6.17	5.38	6.68
12	Seed yield plant^{-1} (g)	18.49	15.65	14.32	13.09	18.40	11.02	28.53

VII (2) and cluster VI (1) (Table 2.). The inter-cluster distance ranged from 321.64 to 2809.44. The inter-cluster D^2 value was maximum between cluster III and VI (2809.44) followed by cluster VI and VII (2625.07) and cluster III and VII (2134.39), suggesting that the genotypes present in these clusters may be used as parents for hybridization programme to develop desirable types. Minimum inter-cluster distance was observed between IV and V (321.64) (Table 3). Kumar *et al.*, (2007) distributed 29 genotypes of Indian mustard into seven clusters.

Wide range of variation was observed in cluster mean performance for all twelve characters studied, indicating the presence of appreciable amount of variability among the genotypes. Cluster VII had high mean values for secondary branches plant^{-1} (16.16), seeds siliqua^{-1} (15.44), harvest index (55.62), test weight (6.68) and seed yield plant^{-1} (28.53). Cluster VI had low mean value for days to maturity (112.66), indicating early maturity. Cluster V had maximum mean value for siliqua per branch (46.20), Cluster IV had the

maximum mean values for primary branches per plant (6.08), cluster III had the maximum mean values for biological yield per plant (133.16) and cluster II had the maximum mean values for days to 50% flowering (50.6) and siliqua per plant (341.55). Cluster I had the maximum mean values for the plant height (217.42) followed by the cluster III (204.41) and cluster VI (203.22) (Table 4). Kumar *et al*., (2007) reported that Cluster VII registered the highest seed yield plant[-1], 1000 seed weight, number of secondary branches, length of the main shoot, number of pods on the main shoot and number of pods on secondary branches. Cluster VI showed the highest mean values for number of days to 50% flowering and maturity.

It has been well established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. The genetically divergent genotypes present in cluster VI (NDRE-4) and VII (Urvashi and Ganga Kaveri Vijay) as cluster III (Raya, Sivalik, CS-54 and Krishna) may be utilized as parents in future breeding programme. The characters silique plant[-1], harves index, biological yield plant[-1] which exhibited high GCV and PCV, heritability and gentic advance should be given top priority during selection.

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