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GENETIC DIVERSITY FOR AGRO-MORPHOLOGICAL AND OIL QUALITY TRAITS IN INDIAN MUSTARD (*BRASSICA JUNCEA* L. CZERN & COSS)

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ABSTRACT
Identification of diverse parents in any crop species like Indian mustard is the pre-requisite and in any crop improvement programme aimed to obtain the desirable recombinants in segregating generations. Greater contribution of additive genetic component was reflected by main shoot length, siliqua on main raceme, siliqua length, palmitic acid, oleic acid and linolenic acid with pronounced range of variation, high heritability coupled with high genetic advance under selection, which may be exploited in early segregating generations for yield and quality enhancement of Indian mustard. Amongst eight, five mono-genotype and clusters III, IV, I with 18, 12 and 11 genotypes, respectively, maximum divergence exhibiting mono-genotype clusters (VII and VIII) may be utilized through inter varietal hybridization to exploit high degree of genetic diversity between them. Noteworthy is that cluster VII exhibiting high genetic diversity for siliqua length, 1000 seed weight, harvest index and seed yield per plant; cluster II and VII for secondary branches per plant, siliqua on main raceme, 1000 seed weight and biological yield per plant heritability coupled with high heritability and genetic gain under selection, may prove their worth in genetic enhancement of mustard for yield and oil quality.

INTRODUCTION

The genetic variability is of great value while planning an efficient breeding programme for the improvement in any crop species like Indian mustard. Germplasm, the sum of variability present in any crop species and relatives, is important for exploitation to fulfill most of the changing needs for developing improved crop varieties. Variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. Genetic diversity plays an important role in plant breeding because hybrid between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent plants to obtain the desirable recombination of the segregating generation. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra- and inter-cluster levels (Jatasra and Parada, 1978; Zahan *et al*. 2008). Therefore, the present study was undertaken to identify divergent parents for hybridization program, which would provide superior segregates in mustard genotypes.

MATERIALS AND METHODS

The experimental material comprising of forty six genotypes of Indian mustard were grown in Randomized Block Design with three replications at the research farm of Tirhut College of Agriculture, Dholi, Muzaffarpur (Rajendra Agricultural University-Pusa) Bihar during *rabi* season of 2010-11. Each genotype was sown in a plot consisting of three rows of 5m length in three replications with inter and intra row spacing of 30cm x 10cm. Recommended package of practices for Indian mustard ware followed to raise a healthy crop. Data were recorded on five randomly selected competitive plants of each genotype in all the replications for twenty characters *viz.,* Days to 50% flowering, Days to maturity, Length of main shoot (cm), Primary branches per plant, Secondary branches per plant, Siliqua length (cm), Number of seeds per siliqua, Number of siliqua on main raceme, Siliqua density, 1000 seed weight (g), Biological yield per plant (g), Harvest index (%),and seed yield per plant (g). Oil extraction and Fatty acid profile were assessed from field harvested seed samples and the quality characters *viz.,* Palmitic acid, Stearic acid, Oleic acid, Linoleic acid, Linolenic acid, Erucic acid, and Oil content (%) and their mean values were subjected to various statistical and biometrical analyses. Fatty acid methyl esters were prepared from the seeds of each line, following the procedure described by AOAC (1990). The esters were taken and analyzed using NUCON-5765 a gas chromatography fitted with column as follows, 2m, 1/8" 0.d, 2mm i.d, mesh 100-200, SP 2300+2310 with flame ionization detector (FID). Nitrogen gas used as a carrier gas. The temperature of injection port and detector were maintained at 230ºC and 240ºC and the temperature programming during the analysis, it was held initially at 120ºC for 1 minute and then to 230ºC @ of 10ºC/ min. The peaks were identified based on their retention time using standard fatty acid esters. The percentage oil content of rapeseed mustard seeds was analyzed using a Foss-tecator

Near Infrared Reflectance Spectroscopy (FT-NIRS). Over 4g seeds of each intact sample were scaned in a 36nm inner diameter ring cup. The oil content calibration equation was determined using a modified partial least square regression method (Wu *et al*. 2006) Test of significance for each character were analyzed as per methodology advocated by Panse and Sukhatme (1967). Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton and De Vane (1953) and genetic advance *i.e*. the expected genetic gain were calculated by using the procedure proposed by Johnson *et al*. (1955). The genetic divergence was estimated by Mahalanobis (1936) D^2 statistics and the grouping of the genotypes into clusters were done using Tochers method (c. f. Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance was highly significant among the divergent genotypes for all the twenty traits under study, which revealed the presence of considerable variability among the studied genotypes (Table 1). This suggested that adequate scope is available for selection of superior genotypes aimed at enhancing genetic yield potential of *Brassica juncea*. Genetic parameters (Table 2) were studied to examine genetic worth of yield and oil quality traits, based on genetic variability estimates *viz*., mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance(GA) and genetic advance as percent of mean (GAM). It was observed that all the character studied exhibited wide range of variation, with most pronounced range for secondary branches per plant, siliqua on main raceme, 1000 seed weight, palmitic acid, oleic acid, linolenic acid and erucic acid except Siliqua density, Siliqua length, Stearic acid and Oil content reflecting narrow range of variation. Higher estimates of phenotypic coefficient of variation than genotypic coefficient of variation for all the traits reflected influence of environmental factor on these traits with variable influence. The estimates of phenotypic coefficient of variation and genotypic coefficient of variation were high for, harvest index, stearic acid and seed yield per plant, was earlier reported by Kardam and Singh (2005). It was interesting to note that except for primary branches per plant, secondary branches per plant, siliqua on main raceme, siliqua length, 1000 seed weight, biological yield per plant, palmitic acid, oleic acid and linoleic acid were under moderately influenced by the environment. Main shoot length, number of seeds per siliqua, siliqua density, linoleic acid, erucic acid and oil content, which were least influenced by environment, may be considered as distinguishing characters for mustard. It is clear that, seed yield per plant, biological yield per plant, harvest- index, 1000 seed weight, primary branches per plant, secondary branches per plant, siliqua density and erucic acid were (highly influenced by the environment) environmentally sensitive characters and need careful consideration. Keeping in view that consideration of heritability and genetic advance together prove more useful in predicting the resultant effect of selection on phenotypic expression (Johnson *et al*., 1955) eight characters identified namely, main shoot length, siliqua on main raceme, siliqua length, palmitic acid, stearic acid, oleic acid, linolenic acid and seed yield per plant. These characters reflected greater contribution of additive genetic component may be exploited in selection in early segregating generations for the development of Indian mustard genotypes. The findings of Mahla *et al*. (2003), Singh (2004), Kumar and Mishra (2007) were in accordance with the present investigation. Forty six genotypes, the basis of Mahalanobis D^2 following Tocher method for clustering, were grouped into eight clusters with cluster-wise variable number of genotypes (Table 3) developed by various centres and located at different geographical locations suggesting considerable amount of genetic diversity in the material. Amongst eight clusters, II, V, VI, VII and VIII were mono-genotype clusters. Cluster III was the largest having 18 genotypes involving varieties/ strains from various centers. Similarly, cluster IV and I involved 12 and 11 genotypes, respectively. The pattern of distribution of genotypes in different

Table 1: Analysis of variance for 20 quantitative characters of 46 Indian mustard genotypes

SN	Characters	Mean sum of squares (Degree of freedom)		
		Replications	Treatments	Error
		02	45	90
1	Days to Flowering	4.717	39.680**	1.576
2	Days to Maturirty	7.507	38.578**	1.166
3	Main Shoot Length	2.694	354.265**	11.430
4	Primary Branches/ Plant	0.349	1.208**	0.305
5	Secondary Branches/ Plant	2.567	6.544**	0.787
6	Siliqua On Main Raceme	3.037	117.831**	1.915
7	Siliqua Length	0.107	0.813**	0.018
8	Seeds/ Siliqua	1.012	4.533**	0.364
9	Siliqua Density	0.009	0.030**	0.005
10	1000 Seed Weight	0.018	0.559**	0.038
11	Biological Yield/ Plant	72.051	269.336**	22.887
12	harvest Index	0.584	67.179**	4.801
13	Palmitic Acid	0.013	0.363**	0.003
14	Stearic Acid	0.009	0.146**	0.001
15	Oliec Acid	0.019	4.754**	0.003
16	Linoleic Acid	0.036	3.471**	0.007
17	Linolenic Acid	0.005	3.675**	0.002
18	Erucic Acid	0.413	38.169**	0.672
19	Oil Content (%)	0.011	2.244**	0.014
20	Seed Yield/ Plant	1.117	15.541**	0.694

Table 2: Estimation of mean, range, coefficient of variation (PCV and GCV), Heritability, Genetic advance and Genetic advance as percent of mean for twenty characters.

S.N.	Characters	Mean	Range		GCV	PCV	h^2	GA	GAM
			Min.	Max.					
1.	Days to Flowering	57.087	46.667	62.333	6.243	6.619	89.0	6.924	12.130
2.	Days to Maturirty	117.558	107.333	132.667	3.004	3.141	91.4	6.957	5.918
3.	Main Shoot Length	195.012	169.400	217.000	5.482	5.749	90.9	20.996	10.767
4.	Primary Branches/ Plant	4.962	3.933	6.867	11.059	15.687	49.7	0.797	16.059
5.	Secondary Branches/ Plant	8.487	4.333	11.200	16.321	19.384	70.9	2.403	28.309
6.	Siliqua On Main Raceme	42.663	31.733	55.400	14.570	14.927	95.3	12.499	29.297
7.	Siliqua Length	5.112	4.660	6.173	10.070	10.405	93.7	1.026	20.075
8.	Seeds/ Siliqua	129.916	9.567	14.933	9.126	10.253	79.2	2.161	16.734
9.	Siliqua Density	1.313	1.110	1.560	6.959	8.949	60.5	0.146	11.148
10.	1000 Seed Weight	3.008	1.840	3.793	13.856	15.298	82.0	0.778	25.855
11.	Biological Yield/ Plant	52.449	29.000	73.333	17.281	19.540	78.2	16.512	31.482
12.	harvest Index	20.669	13.757	33.427	22.062	24.477	81.2	8.467	40.964
13.	Palmitic Acid	2.448	1.815	3.412	14.141	14.369	96.9	0.702	28.668
14.	Stearic Acid	0.704	0.120	1.070	31.273	31.583	98.0	0.449	63.791
15.	Oliec Acid	12.078	9.009	14.365	10.418	10.429	99.8	2.590	21.439
16.	Linoleic Acid	16.673	14.399	20.142	6.445	6.464	99.4	2.207	13.237
17.	Linolenic Acid	9.727	6.490	12.918	11.377	11.384	99.9	2.278	23.420
18.	Erucic Acid	44.438	36.191	54.850	7.956	8.167	94.9	7.094	15.965
19.	Oil Content (%)	37.928	35.370	39.410	2.273	2.294	98.2	1.760	4.640
20.	Seed Yield/ Plant	10.566	7.400	19.533	21.055	22.483	87.7	4.292	40.617

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 (bs) = Heritability (broad sense) GA = Genetic advance, GAM = Genetic advance as 5% mean.

Table 3: Distributing pattern of 46 genotypes of Indian mustard into eight clusters based on tochers' D^2 statistics

Cluster group	No. of Genotypes	Name of Genotypes
Cluster I	11	RAURD-156, RAURD-154, RAJENDRA SUFLAM, RAURD-195, RAURD-164, RAURD-63, RAURD-212, KRANTI, RAURD-242, RAURD-32, RAURD-193
Cluster II	1	RAURD-78
Cluster III	18	RAURD-07, RH-30, RAURD-185, RAURD-246, RAURD-205, RAURD-273, PUSA BOLD, RAURD-221, VARDAN, RAURD-220, RAURD-214, RAURD 245, RAJ. RAI PICCHETI, RAURD-25, EC-399788, RAURD-166, JD-6 , RAURD-241
Cluster IV	12	RAURD-190, RAURD-200, VARUNA, EC- 401574, RAURD-153, RAJENDRA ANOOKUL, RAURD-23, RAURD-69, RAURD-89, RAURD-35, RAURD-170, RAURD-171
Cluster V	1	LAXMI
Cluster VI	1	RAURD-34,
Cluster VII	1	RAURD-168,
Cluster VII	1	RAURD-172

Table 4: Average intra and inter cluster D^2 values among the cluster for 46 Indian mustard genotypes.

CLUSTER	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	265.654	419.609	753.483	1051.520	1042.507	1258.415	1455.603	3596.263
Cluster II		0.000	461.023	1444.419	1448.274	988.978	1731.166	2770.942
Cluster III			560.028	1890.161	1954.722	1546.475	1607.277	3193.151
Cluster IV				1267.771	2462.236	2907.954	2406.060	6010.449
Cluster V					0.000	668.143	2775.261	2488.920
Cluster VI						0.000	3842.904	922.779
Cluster VII							0.000	6463.781
Cluster VIII								0.000

clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier findings of Verma and Sachan (2000), Jeena and Sheikh (2003) and Sutariya *et al.*, (2011). The intra and inter - cluster distances (Table 4) and the mean performance of the clusters (Table 5) were used to select genetically diverse genotypes. The highest intra -cluster distance was shown by cluster IV indicated presence of high diversity within cluster, hence revealing scope for exchange of genes among genotypes within these clusters. Maximum diversity based on inter-cluster distance was observed between Cluster VII and VIII followed by between cluster IV and VIII and cluster VI and VII can be utilized by hybridization- selection breeding programme by involving genotypes in these clusters which can through useful transgressive segregants. High cluster means, for primary branches per plant, secondary branches per plant, number of siliqua on main raceme, number of seeds per siliqua, 1000 seed weight, biological yield per plant and oil content (cluster II). Cluster IV show low linolenic acid which is used for the edible purpose. Early flowering with late maturity along with high siliqua length, 1000 seed weight, harvest index, stearic acid and seed yield per plant in cluster V, whereas in cluster VI showed early flowering with early maturity along

Table 5: Mean values of cluster and contribution of different characters towards genetic divergence of 46 Indian mustard genotypes.

SN	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
1	Days to Flowering	56.667	58.000	56.667	58.750	53.000	52.000	59.667	55.000
2	Days to Maturirty	116.545	118.667	117.667	118.389	120.667	114.667	117.000	116.000
3	Main Shoot Length	191.600	198.067	193.281	198.683	207.500	196.867	194.533	202.733
4	Primary Branches/ Plant	4.673	5.800	5.094	4.922	5.367	4.600	4.667	5.667
5	Secondary Branches/ Plant	8.794	10.867	8.230	8.467	8.933	6.933	8.533	8.667
6	Siliqua On Main Raceme	40.158	52.933	40.998	47.631	38.290	42.400	43.067	34.533
7	Siliqua Length	5.533	4.680	5.065	4.876	5.647	5.240	4.920	4.127
8	Seeds/ Siliqua	13.658	14.333	12.728	12.425	13.167	12.600	13.333	12.267
9	Siliqua Density	1.341	1.120	1.325	1.302	1.193	1.267	1.300	1.307
10	1000 Seed Weight	3.099	3.153	2.979	2.981	3.213	2.733	3.113	2.680
11	Biological Yield/ Plant	55.152	73.333	49.870	50.694	51.667	58.333	61.667	55.000
12	harvest Index	21.709	14.913	20.061	20.916	25.223	23.313	17.820	18.593
13	Palmitic Acid	2.407	2.622	2.508	2.389	2.724	2.118	3.040	1.823
14	Stearic Acid	0.769	0.914	0.746	0.555	0.926	0.800	0.917	0.290
15	Oliec Acid	11.712	12.077	12.765	11.866	9.706	9.611	14.217	9.009
16	Linoleic Acid	16.976	16.869	16.502	16.370	17.762	16.079	20.142	15.914
17	Linolenic Acid	9.557	10.224	10.381	8.442	10.325	11.208	9.495	12.918
18	Erucic Acid	44.615	46.460	43.642	45.681	43.510	43.188	36.797	49.734
19	Oil Content (%)	37.609	39.310	38.117	38.209	35.370	37.583	35.857	38.250
20	Seed Yield/ Plant	12.124	10.933	9.726	9.972	13.000	13.533	10.333	10.133

with high seed yield per plant and cluster VII for high seeds per siliqua, biological yield per plant, palmitic acid, stearic acid, oleic acid, linoleic acid and low linolenic and erucic acid reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme, which was in accordance as earlier reported by Singh *et al*. (2010) and Zaman *et al*. (2010) for earliest flowering, maturity and highest cluster mean for Primary branches per plant, Kumar *et al*. (2007) and Sathi *et al*. (2012) for Secondary branches per plant, seed yield per plant and 1000 seed weight. Linolenic acid and oleic acid pre- dominantly contributed maximum towards the genetic divergence (table 6) along with less contribution of oil content and days to maturity. Noteworthy is that cluster V and VI reflected high cluster means for early flowering, early maturity, siliqua length, 1000 seed weight, harvest index, stearic acid and seed yield per plant; cluster II and VII for primary branches per plant, secondary branches per plant, siliqua on main raceme, number of seeds per siliqua, 1000 seed weight, biological yield per plant and oil content and cluster IV additionally for minimum linolenic acid and also exhibited high heritability coupled with high genetic advance as percent of mean, might be utilized in hybridization-selection breeding programme for Indian mustard improvement.

Inter-mating of RAURD 168 and RAURD 172 from the mono-genotype clusters, cluster VII and VIII showing maximum inter-cluster distance for getting better recombinants in segregating generations and enhancing the yield and oil content and minimize the linolenic acid and erucic acid, whereas crossing between mono-genotype cluster (cluster VIII) with 12 genotypes from cluster IV suggested for the development of high erucic acid and high oil content and chances of getting better recombinants in segregating generations and enhancing the yield and oil content and minimize the linolenic acid and erucic acid.

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