Studies on Genetic Variability and Divergence in Relation to Heterosis for Some Metric Traits in Indian Mustard

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Genetic variability and divergence were studied for some metric traits in 23 Indian mustard genotypes under timely and late sown conditions to assess the impact of environments. The results revealed presence of wide exploitable variability in the material. The high values of phenotypic coefficient of variation closely followed by genotypic coefficient of variation for seed yield per plant in both the conditions while, all the characters except oil content, days to flowering and days to maturity showed moderate to high estimates of genetic advance in (%) of mean coupled with high heritability. The genotypes were grouped into 9 clusters under timely sown (E_1) and 6 clusters under late sown conditions (E_2), where cluster I was the largest and contained 5 genotypes in E_1, 13 genotypes in E_2. Maximum inter cluster distance was noticed between the clusters IV and IX in E_1 and cluster II and VI in E_2, which could be made use of in heterosis and recombination breeding. Plant height and days to maturity contributed maximum to genetic diversity in both the conditions. The genotypes NDYR-32 and NDRE-4 genotypes do not cluster in a single cluster in both the environments, therefore could be used in breeding programme for obtaining the desirable recombinants.

Key Words: Coefficient of variability, Genetic advance, Genetic divergence, Heritability, Heterosis, Indian mustard

Introduction

Rapeseed-mustard oil is the third largest edible oil produced in the world after Soy oil and Palm oil. It accounts for about 12% of the total world's edible oil production. Indian mustard is the pre-dominant crop occupying nearly 80% of the rapeseed-mustard cropped area in the country. India is estimated to have a total mustard seed output of 5 million tons while oil is around 1.3 million tons (Damodaran and Hegde, 2005). The country also generates 2.4 million tons of oil cake. However, India exports around 400,000 tons of oil cake. Hence, increasing yield potential of the crop is imperative to enhance oilseed production. Knowledge of genetic diversity and utilization of divergent genotypes in breeding programme is the key to success in developing heterotic gene pool in Indian mustard (Chauhan *et al*., 2007; Patel and Patel, 2006; Pradhan *et al*., 1993). Genetic diversity in breeding is of paramount importance as evidenced by earlier workers (Murty and Arunachalam, 1966). Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence among biological population. Change in environments alters clustering patterns due to genotype-environment interaction (Raut *et al*., 1985). Inter crossing between more divergent parents is expected to generate a broad spectrum of variability. Therefore, study was undertaken to identify suitable stable donors having wider genetic distance among Indian mustard.

Materials and Methods

Twenty-three genotypes of Indian mustard from different geographical regions of the India were grown in two environments *viz*., timely (E_1) and late (E_2) sown conditions during *Rabi* season, 2004-05 at farm of N.D. University of Agriculture and Technology, Kumarganj, Faizabad. Eighty crosses were made during *Rabi* season, 2005-06 with 20 varieties/strains using as lines and 4 testers namely NDYR-32, Narendra Rai, NDRE-4 and a hybrid NDYR-32 x Narendra Rai for triple test cross analysis. These diverse elite strains were selected from the collection of the genetic stock available in oilseeds breeding section of Genetics & Plant Breeding of this University. The F_1 (hybrid) of NDYR-32 x Narendra Rai was produced by hand emasculation and pollination. The trials were conducted in Randomized Block Design with three replications under uniform cultural practices. Observations were recorded on 10 randomly selected plants for plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae/plant, seeds/siliqua, seed yield/plant,

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1000-seed weight and oil content (%) while, data on days to flowering and days to maturity were recorded on whole plot basis. Multivariate analysis of genetic divergence among varieties was done using Mahalanobis D^2 statistics (1936) and grouping of varieties into clusters by Toucher method (Rao, 1952). The character wise rank totals were used to calculate the per cent contribution of each character to the total divergence. Averages inter-and intra-cluster distance, coefficient of variation, heritability in broad sense and genetic advance were estimated as per the method given by Singh and Chaudhary (1985). Heterosis expressed as per cent increase or decreases of hybrids (F_1) over better-parent (heterobeltiosis) and standard variety (standard heterosis) were calculated according to the method suggested by Hayes *et al.* (1955).

Results and Discussion

The results revealed presence of wide exploitable variability in the materials examined with respect to various morphological traits in both the environments indicating, thereby, immense scope of genetic up-gradation in Indian mustard. High values of phenotypic coefficient of variation closely followed by genotypic coefficient of variation for plant height, primary branches/plant, secondary branches/plant, length of main raceme, siliquae/plant, seeds/siliqua, 1000-seed weight and seed yield/plant indicated greater opportunities for desired gain through phenotypic selection. Earlier studies by Chaudhary *et al.* (2003) and Ahlawat *et al.* (2006) also exhibited the existence of greater natural variability for seed yield and secondary branches per plant. The high magnitude of phenotypic and genotypic coefficient of variations for 1000-seed weight has also been reported by Akbar *et al.* (2007). Simultaneously, high PCV and GCV for plant height, siliquae/plant and seed yield/plant were found by Khan *et al.* (2006). The low magnitude of phenotypic and genotypic coefficient of variations for days to flowering, days to maturity and oil content recorded in both the environments, indicated lesser opportunities for improvement through selection for these characters in the present set of material. For days to flowering, low coefficient of variability has also been reported by Pant and Singh (2001). In present study, genetic advance expressed as per cent of mean showed a wide range in its magnitude and in general, high heritability (broad sense) estimated were associated with the high genetic advance in per cent of mean (Table 1). All the

Table 1. Mean, range, coefficient of variation, heritability and genetic advance for eleven characters in Indian mustard (E_1 & E_2)

Characters	Environments	General mean ± SE	Range		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in per cent of mean
			Minimum	Maximum	Genotypic	Phenotypic		
Days to flowering	E_1	42.49 ±0.64	34.33	47.67	5.93	6.21	91.3	11.68
	E_2	43.06 ±0.49	39.67	46.67	4.05	4.28	89.5	7.90
Days to maturity	E_1	115.79 ±0.88	105.67	139.67	5.61	5.68	97.3	11.39
	E_2	119.21 ±0.64	108.67	127.33	2.80	2.87	94.7	5.61
Plant height (cm)	E_1	157.74 ±1.82	105.31	197.67	12.29	12.37	98.7	25.16
	E_2	174.69 ±3.13	105.00	237.67	16.70	16.84	98.3	34.10
Primary branches/plant	E_1	5.30 ±0.32	3.20	7.02	18.24	19.57	85.9	34.63
	E_2	5.55 ±0.46	4.24	7.33	9.74	14.07	87.9	13.88
Secondary branches/plant	E_1	10.96 ±0.52	2.99	16.93	30.07	30.63	96.4	60.80
	E_2	10.44 ±0.49	6.37	13.90	16.68	17.66	89.2	32.45
Length of main raceme (cm)	E_1	61.63 ±1.53	34.00	82.29	17.43	17.69	97.0	35.37
	E_2	59.12 ±2.33	41.81	79.09	14.10	14.91	89.5	27.49
Siliquae/plant	E_1	176.99 ±8.43	102.76	241.53	17.20	18.16	89.7	33.56
	E_2	180.29 ±8.35	112.93	252.73	13.18	14.35	84.4	24.95
Seeds/siliqua	E_1	12.48 ±0.26	9.67	16.82	16.69	16.89	97.7	33.98
	E_2	13.24 ±0.52	10.11	15.79	9.49	10.63	79.7	17.46
Seed yield/plant (g)	E_1	9.10 ±0.51	4.46	13.92	23.93	24.91	92.3	47.36
	E_2	9.84 ±0.93	5.61	16.54	20.88	23.88	86.5	37.62
1000-seed weight (g)	E_1	3.99 ±0.09	2.65	5.40	15.63	15.91	96.5	31.63
	E_2	3.98 ±0.12	2.52	5.88	20.09	20.44	96.6	40.67
Oil content (%)	E_1	40.01 ±0.23	37.88	43.24	2.57	2.66	92.9	5.09
	E_2	39.55 ±0.15	33.56	42.79	3.67	3.69	98.4	7.49

E_1: Timely sown condition; E_2: Late sown condition

characters except days to flowering, days to maturity and oil content in both the conditions and seeds/siliqua in E_2 demonstrated to high estimates of genetic advance in per cent of mean coupled with high heritability values. Similar results for days to flowering and oil content found by Pant and Singh (2001). Though contrast result was observed by Akbar *et al*. (2007). High heritability (broad sense) coupled with the high genetic advance in per cent of mean for 1000-seed weight and seed yield/plant was reported by Singh *et al*. (2003).

Based on D^2 values, the varieties were grouped in to 9 distinct non-overlapping clusters under E_1 and 6 under E_2. Cluster I and II contained approximately 22% of total varieties under E_1 and 56% under E_2. Interestingly, only one variety each was constituted by last three clusters in both the environments (Table 2). Similar results were reported by Vaishnava *et al*., (2006) and Khan *et al*. (2005). In both the environments, clusters included genotype from different region of India, indicating that clustering of the genotype did not follow their geographic distributions. The absence of correlation between genetic diversity and geographic diversity suggests that forces other than geographic origin, such as exchange of breeding material, genetic drift, variation, selection are responsible for diversity, as reported earlier (Alie *et al*., 2009).

The statistical distances represent the extent of genetic diversity amongst clusters. D^2 values were, in general, higher in E_2 than E_1. The average D^2 value within and between clusters revealed that intra cluster divergence was maximum in cluster IV (D^2 406.68) which include three entries in E_1 and cluster I (D^2 288.40) which comprised of 13 entries in E_2. The inter cluster distance was maximum between cluster IV and IX (1652.69) followed by IV and VII (1369.08) in E_1 and between cluster II and VI followed by III and VI (1593.44) in E_2 (Patel and Patel, 2006), while, closest cluster I and II (451.69) in E_1 and cluster II and III (373.27) in E_2 indicates that genotypes of these clusters had maximum number of common gene complexes. High statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates.

Days to maturity contributed maximum to total divergence followed by plant height in E_1 while, plant height appeared most important contributor towards divergence in E_2 (Pradhan *et al*., 1993). The developmental traits like days to maturity and plant height are known to have substantial contribution to genetic divergence in several crops (Singh *et al*., 2010). The genetic differences between the clusters were reflected in cluster means. Considering the cluster means for different characters under E_1, it was observed that cluster IV possessed dwarf plant stature, with short maturity duration, high values for length of main raceme, while, cluster IX had only one genotype (NDYR-32), with the highest values for primary branches/plant, siliquae/plant, seed yield/plant, plant height and oil content. However, under E_2, cluster III had high values for the primary branches/plant, seed yield/plant and oil content, while cluster V had highest values for length of main

Table 2. Distribution of 23 genotypes of Indian mustard in different clusters (E_1 & E_2)

Cluster No.	Environments	Number of genotypes	Genotypes included
I	E_1	5	BPR-558, RK-02-2, RAURDL-02-01, RGN-101, PR-2001-62
	E_2	13	BPR-558, RAURDL-02-01, KLM-145, Narendra Rai, RGN-101, HUJM-0202, RK-02-2, CS-611-1-3-1, JMWR-946-3-13, SEJ-2, JGM-15-02, RK-03-2, BAUSM-92-1-1
II	E_1	5	JGM-15-02, HUJM-0202, JMWR-946-3-13, RGN-74, SEJ-2
	E_2	4	NDM-87-1, PR-2001-62, RGN-74, PBR-253
III	E_1	3	RK-03-2, Narendra Rai, BAUSM-92-1-1
	E_2	3	SKM-9928, RH-0202, NDYR-32
IV	E_1	3	CS-33-4-9, NDRE-4, Kranti
	E_2	1	CS-33-4-9
V	E_1	2	NDM-87-1, CS-611-1-3-1
	E_2	1	Kranti
VI	E_1	2	SKM-9928, KLM-145
	E_2	1	NDRE-4
VII	E_1	1	PBR-253
VIII	E_1	1	RH-0202
IX	E_1	1	NDYR-32

E_1: Timely sown condition; E_2: Late sown condition

Table 3. Heterosis over better parent (BP) and standard variety (SV) for yield and yield contributing characters in Indian mustard (E_1 and E_2)

Crosses	Environments	1000-seed weight		Seed yield/plant (g)		Oil content	
		BP	SV	BP	SV	BP	SV
BPR-558 x NDYR-32	E_1	4.20*	-6.98**	17.69**	22.44**	-3.09**	3.30**
	E_2	2.14	-9.19**	1.73	6.91	-2.97**	6.56**
BPR-558 x N. Rai	E_1	2.39	2.39	25.74**	25.74**	-2.61**	3.81**
	E_2	1.44	1.44	27.58**	27.58**	2.04**	2.04**
BPR-558 x NDRE-4	E_1	-30.97**	-38.37**	-7.01	-11.83*	-1.00	3.53**
	E_2	-5.54*	-16.02**	33.47**	7.90	-0.65	1.58**
RAURDL-02-01 x NDYR-32	E_1	-2.28	-19.77	-0.27	3.81	-3.08**	2.58**
	E_2	-1.08	-9.98	-6.93	-2.91	-7.09**	2.04**
RAURDL-02-01 x N. Rai	E_1	-25.26**	-25.26**	-7.61	-7.61	-4.32**	0.92
	E_2	-7.55**	-7.55**	-12.31	-12.31	2.60**	2.60**
RAURDL-02-01 x NDRE-4	E_1	13.38**	-6.91**	37.29**	-8.03	-2.70	2.63**
	E_2	10.75**	0.79	9.68	-3.55	3.10**	-0.93*
RGN-101 x NDYR-32	E_1	-22.67**	-33.66**	-17.34**	13.92**	-1.30*	4.45**
	E_2	-12.35	-20.29**	-12.24	-7.78	2.12**	7.50**
RGN-101 x N. Rai	E_1	-0.90	-0.90	16.92**	16.92**	1.09	3.24**
	E_2	15.76**	15.76**	25.92*	25.92**	1.61**	5.39**
RGN-101 x NDRE-4	E_1	9.64**	-5.94**	-11.86**	19.00**	-4.40**	0.84
	E_2	10.32**	0.33	44.60**	-4.57	-0.82*	2.87**
RK-02-2 x NDYR-32	E_1	8.16**	-16.09**	23.24**	28.27**	-5.03**	2.88**
	E_2	-32.30**	-45.76**	-21.23	-17.22	-3.68**	5.78**
RK-02-2 x N. Rai	E_1	-20.35**	-20.35**	15.57**	15.57**	-4.13**	3.85**
	E_2	-37.69**	-37.69**	-18.98*	-18.98*	2.90**	5.10**
RK-02-2 x NDRE-4	E_1	-16.93**	-37.86**	3.47	1.04	-5.18	2.72**
	E_2	-37.95**	-50.30**	4.67	-20.46*	-2.87**	0.70

raceme, seeds/siliqua and siliquae/plant and substantial high values for seed yield/plant. Interestingly, cluster VI constituted with NDRE 4 possessed low values for seven characters *viz*., days to flowering, days to maturity, plant height, secondary branches/plant, seeds/siliqua, seed yield/plant and 1000-seed weight. In view of late sown condition, NDRE 4 serves as good donor for short duration and stature.

The genotypes like BPR-558, RK-02-2, RAURDL-02-01 and RGN-101 were found stable diverse varieties because these genotypes were grouped in the same cluster under both the environments. Noteworthy observations were that above said stable genotypes in different cross combinations, recorded significant heterosis for seed yield/plant, oil content and other characters in both the environments (Table 3). The variety Narendra Rai was used as standard variety (SV) to calculate standard heterosis. Significant levels of heterosis with respect to seed yield and its component attributes have been reported with hybrids showing greater advantage under adverse environmental conditions (Banga, 2005). The selections of the crosses based on heterotic response over standard variety could be more realistic under such a situation. There was high manifestation of heterosis over standard variety for seed yield/plant as evidenced by the significant superiority of hybrids of stable parents ranging from 13.92 to 28.27% in 7 crosses in E_1 and 2 crosses in E_2. Ten crosses in each environment, registered significant heterosis over standard variety for oil content. Results of heterobeltiosis for oil content indicated that the pool of material studied was, in general, poor combiner for oil content. Thus, there exist hardly any opportunity for transgressive segregates, beyond the better parents.

Manifestation of high amount of heterosis by a large number of crosses, thus, indicate the presence of substantial parental diversity at genetic level. The crosses of divergent genotypes in present study exhibited significant desirable heterosis for yield and yield components in both the environments (Table 4). Similar findings were reported by Pradhan *et al*. (1993) and Goswami *et al*. (2006). Furthermore, NDYR-32 and NDRE-4 genotypes do not cluster in a single constellation in any environment and crosses between these strains are expected to give promising segregates in the segregating generations.

Table 4. Prospective cross combinations of divergent genotypes based on heterosis (BP & SV) for different characters in Indian mustard (E_1 and E_2)

S.No.	Cross Combinations	Significant heterosis for different characters
E_1		
1	CS 33-4-9 x NDYR 32	PH, PB/P, SB/P and OC
2	PBR 253 x NDRE 4	DF, PH, PB/P, SB/P, S/S and OC
3	Kranti x NDYR 32	PH, PB/P, SB/P, LMR, S/P, SY/P, TW and OC
E_2		
1	NDM 87-1 x NDRE 4	PH, LMR and OC
2	PR 2001-62 x NDRE 4	S/P, S/S, DF and DM
3	RGN 74 x NDRE 4	DF, DM, LMR and S/S
4	PBR 253 x NDRE 4	DF, PH, SB/P, S/P and S/S
5	SKM 9928 x NDRE 4	DF and PH
6	RH 0202 x NDRE 4	DF, DM, SB/P, LMR and S/S

DF: Days to flowering; DM: Days to maturity; PH: Plant height (cm); PB/P: Primary branches per pant; SB/P: Secondary branches per plant; LMR: Length of main raceme (cm); S/P: Siliquae per plant; S/S: Seeds per siliqua; SY/P: Seed yield per plant (g); TW: 1000-seed weight (g), OC: Oil content (%)
E_1: Timely sown condition; E_2: Late sown condition

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