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Genetic Diversity Analysis in Rapeseed-Mustard using Quality Characters

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Abstract: A two-year study was carried out during 2003-04 and 2004-05 using 40 varieties of rapeseed-mustard to assess genetic divergence by Mahalanobis statistic, on the basis of oil and seed meal quality characters. Highly significant differences among the genotypes for the total 9 characters (X^2 = 752.2 at 351 degree of freedom) were revealed by the analysis using V statistics of dispersion for the test of significance of differences in the mean values based on Wilke's criterion. Based on the relative magnitude of D^2 values, 40 rapeseed-mustard varieties were grouped into 8 clusters, I being the largest having 29 varieties. The cluster I accommodated 23 mustard, 4 toria and 1 karan rai and 1 yellow sarson varieties. Cluster VI contained 4 gobhi sarson varieties. Clusters II, IV, V, VII and VIII were mono-genotypic. Except cluster I, the rest of the clusters were crop-specific. The intra-cluster distance ranged from 0.0-4.6 and the inter cluster distance varied between 4.3-8.9. The contribution of different quality characters towards divergence indicated that eicosenoic acid contributed the least (2.8%) and the protein content contributed maximum (26.5%) to the total divergence among the varieties investigated. The implications of these results in quality improvement program are discussed in this paper.

Key words: Rapeseed-mustard, *Brassica* species, quality characters, D^2 statistic, genetic divergence.

Rapeseed-mustard is an important group of oilseed crops of India contributing 26.1% and 29.1% to the total oilseed area and production, respectively, during 2005-06 (Anonymous, 2007). Rapeseed-mustard is an important source of edible oil in Indian diet especially in eastern and north-western parts of the country. Rapeseed-mustard breeding program in India aims at improving quality of oil by reducing erucic acid up to 2% and increasing oleic acid which is quite low (5.7-32.1%) in Indian cultivars and decreasing glucosinolate content in seed meal up to internationally accepted norms (<30 μ moles g^{-1} defatted seed meal) from 50-120 μ moles g^{-1} defatted seed meal present in the prevalent Indian rapeseed-mustard varieties. Recently, two double low rapeseed (*B. napus*) varieties, TERI-Uttam-Jawahar and GSC 5 have been released for Madhya Pradesh and Punjab states, respectively. Further, a low erucic acid Indian mustard (*B. juncea*) variety, Pusa Karishma has also been released for Delhi state (Chauhan *et al.,* 2006). Success of the conventional breeding program is largely dependent on the selection of appropriate genetically divergent parents for utilization in the hybridization program. Knowledge of the nature and degree of divergence is very useful in the characterization of genotypes and selection of desirable parents for breeding program. Mahalanobis D^2 statistic (Mahalanobis, 1930) is a powerful technique in assessing the genetic divergence among the groups based on multivariate analysis. Information on genetic diversity for oil and seed meal quality characters in

rapeseed-mustard is scanty (Singh *et al.*, 2000). Therefore, in the present investigation multivariate analysis using quality characters was carried out to assess the degree of diversity in rapeseed-mustard varieties using Mahalanobis D^2 statistic.

Materials and Methods

In the present study 40-released rapeseed-mustard varieties (Indian mustard [*Brassica juncea*] 25; gobhi sarson [*Brassica napus*] 4; toria [*B. rapa var.* toria] 6; yellow sarson [*B. rapa var.* yellow sarson] 2; karan rai [*B. carinata*] 2 and taramira [*Eruca sativa*] 1) were grown in randomized complete block design with two replications during 2003-04 and 2004-05 cropping seasons (October-April). There were 5 rows of 5 m length for each variety in a block, spaced 45 cm apart with plant-to-plant distance of 15 cm. The experiments were conducted at 80:40:40 kg ha^{-1} (N: P_2O_5: K_2O). Half dose of N and full doses of P_2O_5 and K_2O were given as pre-sowing and the remaining dose of N was top dressed after first irrigation (35 days after sowing). The crop was also irrigated 60 days after sowing. The observations were recorded on composite sample from central three rows. The characters studied were oil, protein, glucosinolate content, palmitic + stearic, oleic, linoleic, linolenic, eicosenoic and erucic acid.

The oil and protein contents were estimated using NIR Analyzer (Oicky John Instalab 600). Fatty acid profiles were analyzed by gas liquid chromatograph (Nucon model 5765) using SP 2300 + 2310 SS columns. Hyola 401, a double low hybrid of gobhi sarson (*B. napus*) and Varuna, non-canola variety of Indian mustard (*B. juncea*) were used as checks for the analysis of fatty acid profiles and glucosinolate content. The detailed method for fatty acid analysis has been described earlier (Chauhan *et al.*, 2002). ELISA reader at 405 nm was used to analyze the glucosinolate content of the seeds following tetrachloropalladate method (Kumar *et al.*, 2004). The mean values were used for analysis of variance of multiple randomized complete block design. Wilke's criterion and Mahalanobis D^2 statistic (Mahalanobis, 1936) were estimated using Indostat Computer Package to study genetic divergence among the varieties. The varieties were grouped into clusters following Tocher's method (Rao, 1952). The relative contribution of different characters towards divergence was also estimated.

Results and Discussion

Analysis of variance indicated significant differences for all the quality characters studied. The environmental effects were significant for erucic acid, oleic acid, glucosinolate and protein content. The interaction effects between genotype x environments were non-significant. Therefore, data from both the years were pooled for further analysis. Highly significant differences among the varieties for the total 9 characters (x^2 = 752.2 at 351 degree of freedom) were revealed by the analysis using V statistic of dispersion for the test of significance of differences in the mean values based on Wilke's criterion. Based on the relative magnitude of D^2 values, the 40 rapeseed-mustard varieties were grouped in to 8 clusters, I being the largest having 29 varieties. The cluster I accommodated 23 mustard, 4 toria

Table 1. Group constellation of the rapeseed-mustard varieties

Cluster	No. of genotypes	Genotypes
I	29	Bio 902, CS 52, GM 1, GM 2, Kranti, Krishna, Pusa Bahar, Pusa Bold, Pusa Jagannath, PBR 91, PBR 97, PCR 7, RCC 4, RH 781, RH 8113, RH 819, RH 30, RL 1359, RH 8812, Rohini, Sej 2, Vardan, Varuna, Bhawani, JT 1, PT 507, TH 68, Jhumka, Kiran
II	1	Sanjucta Asech
III	2	PT 303, TL 15
IV	1	Basanti
V	1	PC 5
VI	4	GSL 1, GSL 2, Neelam, Sheetal
VII	1	RTM 314
VIII	1	Pusa Gold

and 1 variety each of karan rai and yellow sarson. Cluster VI contained 4 gobhi sarson varieties and Cluster III had 2 varieties of toria. Cluster II, IV, V, VII and VIII were mono-genotypic (Table 1). Except cluster I, the rest of the clusters were crop specific.

The intra-cluster distance ranged from 0.0-4.6 and the inter-cluster distance varied between 4.3-8.9, which suggested that the clusters were homogeneous within themselves, but were heterogeneous among them. The minimum inter-cluster distance was between clusters I and IV while cluster VI and VIII were quite divergent as indicated by the maximum inter-cluster distance (Table 2).

The mean values for the 9 quality characters in different clusters (Table 3) revealed that clusters I, II, III and IV had varieties with low saturated fatty acids (palmitic + stearic acids). The cluster VI comprising gobhi sarson varieties had relatively high oleic acid content followed by RTM 314 variety of taramira in cluster VII. Cluster IV was mono-genotypic having Basanti variety of *Brassica juncea* which showed high linoleic acid content and the lowest was observed in variety RTM 314 of taramira in cluster VII. Basanti had low level of linolenic acid, a desirable character. Although all the rapeseed-mustard varieties investigated had high erucic acid, but magnitude varied among the clusters. The

Table 2. Average intra-(diagonal values) and inter-cluster distances among the eight clusters

Cluster	I	II	III	IV	V	VI	VII	VIII
I	3.3	4.4	5.9	4.3	5.4	7.0	5.9	5.3
II		0.0	7.3	4.8	5.6	7.9	5.5	5.6
III			2.3	7.2	8.1	5.8	8.1	7.0
IV				0.0	5.4	7.6	7.0	7.5
V					0.0	6.9	4.4	6.1
VI						4.6	7.5	8.9
VII							0.0	6.4
VIII								0.0

Table 3. Means of 9 quality characters in different clusters and their contribution to divergence

Character	I	II	III	IV	V	VI	VII	VIII	Contribution towards divergence (%)
Palmitic + stearic acid (%)	3.2	2.5	2.7	2.3	7.2	4.4	4.8	6.8	6.7
Oleic acid (%)	15.9	12.3	19.0	16.4	20.9	36.7	24.4	3.3	15.4
Linoleic acid (%)	20.8	21.6	23.8	31.8	19.5	22.6	9.5	15.0	15.4
Linolenic acid (%)	12.8	10.7	16.4	11.9	7.1	6.5	11.5	16.7	5.9
Eicosenoic acid (%)	6.5	6.4	9.9	6.5	8.7	9.7	10.3	5.7	2.8
Erucic acid (%)	41.0	46.4	46.3	38.7	37.9	37.5	39.4	47.5	6.3
Oil content (%)	39.6	40.2	40.3	39.8	37.9	39.7	35.3	39.8	10.5
Protein content (%)	19.8	21.4	18.9	20.3	21.1	20.2	21.7	19.7	26.5
Glucosinolate content (μ moles g^{-1} defatted seed meal)	95.9	94.0	90.5	106.8	101.9	87.5	79.5	89.1	10.5

clusters IV, V and VII had varieties with relatively less erucic acid as compared to those of the other clusters (Table 3). Except mean oil content of clusters V and VII, the rest of the clusters had similar oil content. The mean protein content was high in clusters II and VII. The glucosinolate content of gobhi sarson varieties in cluster VI was relatively lower but RTM 314 variety of taramira had the least glucosinolate content, among the varieties. The contribution of different quality characters towards divergence indicated that eicosenoic acid contributed the least (Table 3). Protein content followed by oleic and linoleic acid contributed maximum to the total divergence among the varieties. In earlier study (Singh *et al.,* 2000) oleic acid followed by erucic acid were the major contributors to diversity in *Braasica* species. The contribution of oil and glucosinolate content was similar (10.5%) to genetic divergence.

Ideally utilization of parents from divergent clusters in breeding program should result in wide variability and transgressive segregants in F_2 generation, but in the present study the rapeseed-mustard varieties investigated differed in their mating system and extent of cross ability. For example, toria varieties are self-incompatible and hence highly out-crossed and gene flow from toria to Indian mustard or vice versa are difficult. But toria varieties from divergent clusters, III and I could be successfully utilized for population improvement. Similarly, yellow sarson varieties from cluster I and VIII may be used in the breeding program. They could also be used in hybridization program with toria varieties to accumulate important traits from toria in high yielding genetic background. Gobhi sarson varieties from cluster VI may be utilized in the breeding program to improve Indian mustard

varieties, as both are crossable. Nevertheless, use of Indian mustard varieties from cluster II, IV and I will lead to high heterotic effects and better segregants.

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