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Genetic Divergence of *Brassica campestris*, *Brassica juncea* Parents and Their Hybrids

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Abstract: This study was conducted with varieties, inter-variety and inter-species hybrids of *Brassica* oil crop to determine genetic divergence. The divergence study indicated that parent, inter-variety and inter-species hybrids almost clearly forms five groups indicating that they are divergent and might be of value for future breeding programme. Based on the study on genetic divergence of the *Brassica*, the varieties having the performance and located in the distant clusters could be utilized for hybridization programme to develop desired high yielding varieties. The genotypes grouped together are less divergent than the ones which into different clusters.

Key words: Genetic divergence, inter variety and inter species hybrids

Introduction

The cultivated *Brassica* is generally represented by three elemental and three amphidiploid species. These are *Brassica campestris* L., *Brassica nigra* Koch, *Brassica oleracea L., Brassica napus* L. , *Brassica juncea* Czern and Coss and *Brassica carinata* Braun. The genomic constitutions of the three diploid elemental species of *Brassica* are 'AA' for *Brassica campestris*, 'BB' for *Brassica nigra* and 'CC' for *Brassica oleracea* having diploid chromosome number of 20, 16 and 18 respectively. On the other hand the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids. The cultivation of *B juncea* is mostly limited to the Indian Subcontinent, while that of *Brassica campestris* with different ecotypes and also sub-species has wider global distribution and is mostly cultivated in Europe, Scandinavian countries, Canada, India, Bangladesh and China. Due to wider distribution of the later, the genetic variations are also very high (Malik *et al.*, 1995; Nanda *et al.*, 1995; Chhanda, 2000).

In Bangladesh the oleiferous *Brassica* is a highly important edible oil crop. The country is facing huge shortage in edible oils. Almost two third of the total edible oil consumed annually are imported (BBS, 1999). On recommended dietary allowance (RDA) basis, Bangladesh requires 0.29 million tons of oils which is equivalent to 0.8 million tons of oilseeds; but it produces only about 0.254 million tons, which covers only 40% of the domestic need (FAO, 1998). In Bangladesh there is limited scope to increase acreage due to pressure of other crops and cropping pattern. Therefore, attempt should be taken to develop HYV and increase their adaptation in different areas for cultivation. Based on the study on genetic divergence of the *Brassica*, the varieties having the performance and located in the distant clusters could be utilized for hybridization programme to develop desired high yielding varieties. Clusters by D^2 statistics are useful in this manner.

The present investigation was performed for the following objectives: To I) choice of the particular cluster from which genotypes are to be used as parents. ii) selection of particular genotype from the selected clusters. iii) measure relative contribution of characters to total divergence.

Materials and Methods

In the rabi season of 2000; twenty six genotypes including six parents of both *Brassica campestris* and *Brassica juncea* namely Sampad, Dhali, Agrani, Safal, Shambol and Pucca rai and their 12 inter-variety and also their eight interspecies hybrids were grown in the Genetics and Plant Breeding farm of Bangladesh Agricultural University, Mymensingh. The RCBD trial was followed with three replications. The unit plot size was $5 \times 1.5 \, m^2$. The distance between rows was 15 cm and between plants was 5 cm. Plot to plot distance was 50 cm with 1-m distance between the blocks. Chemical fertilizers were applied @ 220 kg ha^{-1} urea, 125 kg ha^{-1} TSP, 80 kg ha^{-1} MP, 27 kg ha^{-1} ZnO, 112 kg ha^{-1} gypsum and 14 kg ha^{-1} borax. Data were collected on nine quantitative characters viz. germination percentage, number of siliquae/plant, number of seeds/siliqua, plant height, fruit setting density, fruit setting angle, 1000-seed weight and yield/plant Mahalanobis' D^2-statistics is applied for studying the genetic divergence suggested by Singh and Chaudhury (1985).

Results and Discussion

Using Mahalanobis (1928) D^2 statistics and Tocher method, the genotypes were grouped into distinct

Table 1: Distribution of 26 *Brassica* genotypes in 5 different clusters

Cluster number	No. of Genotypes	Genotypes
I	5	Shambol × Sampod (H_7)
		Shambol × Dhali (H_8)
		Shambol × Safal (H_9)
		Pucca rai × Sampod (H_{11})
		Pucca rai × Agrani (H_{14})
II	15	Sambol (V_1)
		Sampod (V_3)
		Dhali (V_4)
		Safal (V_5)
		Agrani (V_6)
		Sampod × Dhali (H_{15})
		Sampod × Agrani (H_{17})
		Dhali × Sampod (H_{18})
		Dhali × Agrani (H_{20})
		Safal × Sampod (H_{21})
		Safal × Dhali (H_{22})
		Safal × Agrani (H_{23})
		Agrani × Sampod (H_{24})
		Agrani × Dhali (H_{25})
		Agrani × Safal (H_{26})
III	3	Pucca rai (V_2)
		Pucca rai × Dhali (H_{12})
		Dhali × Safal (H_{19})
IV	2	Shambol × Agrani (H_{10})
		Pucca rai × Safal (H_{13})
V	1	Sampod × Safal (H_{16})

Table 2: Average intra and inter cluster D^2 and D values at five clusters formed by Tocher's method

Cluster number	I	II	III	IV	V
I	1490.044	2829.62	1357.61	1602.36	4798.58
	(38.60)	(53.19)	(36.84)	(40.03)	(69.27)
II		8287.43	2307.94	3245.67	3393.82
		(91.03)	(48.04)	(56.97)	(58.26)
III			1175.25	2946.17	6040.15
			(34.28)	(45.28)	(77.72)
IV				1450.56	3659.26
				(38.08)	(60.49)
V					0.00
					(0.00)

* Figures in parenthesis are the D-values (D = $\sqrt{D^2}$)
** The values on the diagonals are intra cluster and those on off diagnals are inter cluster distances.

clusters. The genotypes belonging to the same group had smaller D^2- values than between those belonging to different clusters. Based on D^2 values, the genotypes were grouped into five clusters (Table 1). Cluster V had only one genotype. Two genotypes were clustered in cluster IV. The cluster I, II and III contained 5, 15 and 3 genotypes respectively. Thus, cluster II was the largest followed by cluster I. The D^2-values ranged from 224.78 to 6942.07. It was observed that inter cluster distances were always higher than those of intra-cluster distances except cluster II. The distance between cluster III and cluster V (D = 77.72) was the highest (Table 2). Cluster II had the highest intra-cluster distance (D = 91.03), cluster IV (D = 38.08) and cluster III (D = 34.28). However, cluster V contained only one genotype and had no intra cluster distance. The mutual relationships among five clusters are presented in the diagram (Fig. 1). According to this classification, cluster I, which comprised of five genotypes showed high divergence from cluster II and V, low divergence from cluster III, but intermediate divergence from IV. Cluster II which comprised of 15 genotypes showed intermediate divergence from III, but showed high divergence from cluster IV and V. Cluster III showed intermediate divergence from IV but high divergence from cluster V. Cluster IV showed high divergence from cluster V.

The maximum inter cluster distance was observed between genotypes of cluster III and V (77.72) followed by cluster I and V (69.27). Thus, hybridization among genotypes drawn from these widely divergent cluster with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Mahto (1996) evaluated nineteen genotypes (crosses and parents) of Indian mustard (*Brassica*

Table 3: Contribution of each character to divergence

Character	Germination rate (%)	No. of siliquae/ plant	No. of seeds/ siliqua	Plant height	Fruit setting density	Fruit setting angle	Siliqua length	1000-seed weight	Yield/ plant	Total
Number of times appearing first in ranking	11	10	48	104	37	24	26	19	46	325
Percent contributing	3.38	3.07%	14.77	32	11.38	7.38	8.0	5.85	14.5	100.00

Table 4: Cluster means for nine quantitative characters in 26 genotypes of *Brassica*

Characters	Clusters				
	I	II	III	IV	V
Germination rate (%)	6.25l	58.05h	46.66h	10.41l	31.25i
No. of siliquae/plant	79.73l	84.17i	84.44i	79.83l	87.67h
No. of seeds/siliqua	2.04l	12.01h	7.02i	2.04l	12.7h
Plant height (cm)	153.79i	138.73l	151.06i	158.29h	134.6l
Fruit setting density/10 cm	10.74h	7.08l	8.08i	10.39l	10.67h
Fruit setting angle at 10 cm	35.59l	44.27i	29.09l	47.21i	67.21h
Siliqua length (mm)	29.87l	37.37h	32.67i	32.74i	18.84l
1000-seed weight (g)	3.52l	3.91l	4.08i	3.76l	5.04h
Yield/plant (g)	6.77l	7.48i	6.08l	7.79h	7.43i

H = High values;   I = Intermediate values and   L = Low values
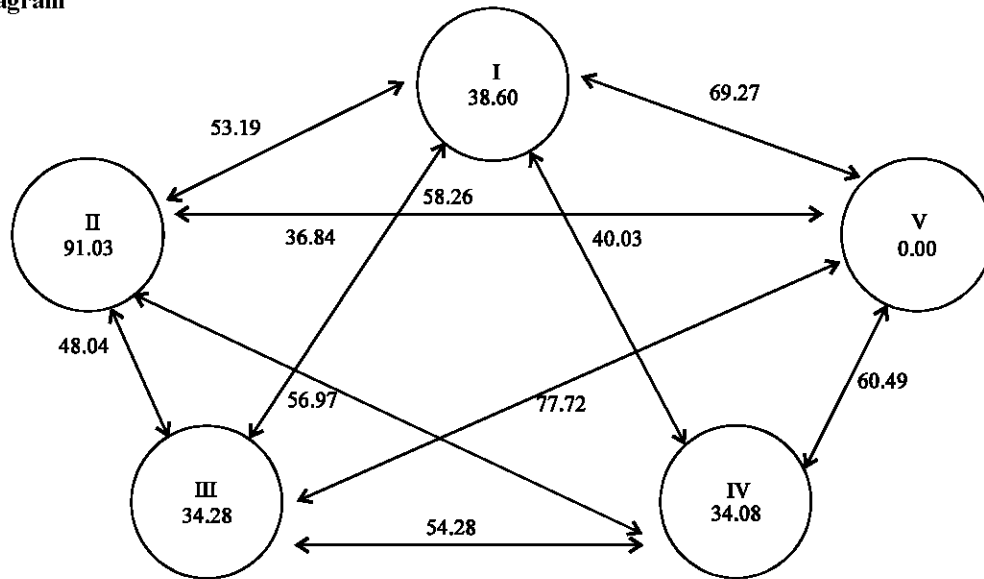
Cluster diagram

Fig.1: Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$) of 26 *Brassica* genotypes. The values along the lines indicate inter cluster distances and the values within the circle indicate intra cluster distances

juncea). Genotypes were grouped into 3 clusters based on D^2 analysis. Jagadev *et al.* (1991) evaluated 19-rape mustard (*B. campestris*) and genotypes were grouped into 5 clusters.

On the basis of priority in contribution, the order of the character were plant height, number of seeds/siliqua, yield/plant, fruit setting density, siliqua length, fruit setting angle, 1000-seed weight, germination percentage and number of siliquae/plant (Table 3). There was a wide range of variation in the cluster mean values except number of siliquae/plant and yield/plant (Table 4). The mean values of all clusters for the respective character were recognized into low (L), intermediate (I) and high (H) classes.

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