

## Assessment of Genetic Divergence in *Brassica* Germplasm

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The objective of this study was to assess the genetic divergence available in *Brassica* germplasm based on Euclidean distances for the identification of genetically diverse and agronomically superior accessions from different *Brassica* species which may generate putative transgressive segregates on hybridization. Based on results obtained in field experiments, designed in compact family block, for two consecutive years, wide physio-morphological divergence were obtained for all the traits under study, both within and between species (though the inter-specific variation was higher than intra-specific one). Principal component analysis, which transformed all the metric traits into single index of similarity, yielded eight eigen vector and eigen roots. Based on first five principal components (which accounted for 97.83% of the total variation), non-hierarchical Euclidean cluster analysis grouped the 36 *Brassica* genotypes into five well characterized groups (based on aggregate effect of similarity in traits). Genotypes of each *Brassica* species grouped separately, depicting characteristic differences among species.

**Key Words:** *Brassica*, Cluster Analysis, Divergence, Germplasm

Rapeseed mustard crops account for almost 14% of the edible vegetable oil supply of the world. In spite of the competition from soybean and palmolive oils, the rapeseed mustard oil is expected to retain its current share in the international trade. The importance of oil seeds in Indian agricultural economy is well recognized. The oil seed productivity has increased almost three times since 1950-51 through inter-specific hybridization among desirable parents. Systematic improvement in any crop species depends upon the variability available in the germplasm. Numerous species have been recognized in the genus *Brassica*. *Brassica juncea* (L.) Czern and Coss (*raya*;  $2n = 36$ ) is the most commonly cultivated species with high productivity and greater resistance to insects and diseases. *B. napus* (*ghobi sarson*;  $2n = 38$ ) has high potential productivity, resistance to white rust and higher oil content. *B. carinata* (Ethiopian mustard;  $2n = 34$ ), with a high seed yield potential, has particular promise as an oil crop under dry land conditions. In order to further upgrade the yield potential of these crops and to impart resistance to biotic and abiotic stresses, it is imperative to introduce desirable attributes in a good agronomic base. For this, an inevitable requirement is to genetically characterize the available variability in the germplasm.

The ordination techniques like principal component analysis followed by cluster analysis was found to be useful tool for getting multi-correlated variables into another set of uncorrelated variables which can be utilized for classification of genotypes into homogenous groups.

Hence, the genotypes from diverse clusters can be earmarked for different objectives. The use of non-hierarchical Euclidean cluster analysis to estimate genetic divergence and for classification of germplasm is suggested (Arunachalam, 1981). In view of the above, the present studies were taken up with 36 genotypes of *Brassica* to (i) assess within and between variability in the germplasm based on morphological and yield attributes and (ii) perform natural classification in the germplasm accessions for their characterization based on cluster analysis for identification of genetically diverse and agronomically superior genotypes.

### Materials and Methods

Twelve *Brassica juncea* genotypes viz., Kranti, Prakash, Pusa-bold, RH-765, RH-8304, RLC-1359, RLM-29, RLM-198, RLM-185, RLM-234, RLM-619 and Varuna; 12 genotypes of *B. napus* namely, ABU, NB-215, BN-225, BN-510, GS-119, GS-124, GS-203, GSL-1, GLS-1501, HN-5-1, K-1 and Marinus, and 12 genotypes of *B. carinata* namely BIC-3, BS-260M, BS-70-1, DIC-2, DIC-3, HC-1, HC-2, HC-6, HC-7, HC-6-7, HC-6-7, HC-S-1 and PC-5 were grown in a compact family block design with three replications over two years. These genotypes were diverse collection of local selections, breeding lines, cultivars and commercial varieties. Recommended cultural practices and plant protection measures were followed to raise the crop. Data were recorded for two years on plant height (measured from the base to the tip of the plant at maturity in cm), number of primary branches (number of branches on the main stem), siliquae/plant. These observations were recorded on five randomly selected plants of each genotype. Other characters viz., 1000-seed weight, seed yield/plant, oil

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yield/plant (4g of oven dried seeds were taken and oil content was measured using NMR spectroscopy and multiplied by respective seed yield to calculate oil yield) and days to 50% flowering of genotypes were recorded on plot basis.

The principal component analysis was carried out to transform the inter-dependent variables into a set of independent variables (Hotelling, 1933; Mardia, 1971). These principal component scores were used to compute Euclidean distances based on non-hierarchical cluster analysis through SPAR 1 (Beale, 1969; Spark, 1973). This method characterizes genetic divergence on the basis of similarity and dissimilarity denoted by aggregate effects of agronomic traits under study.

## Results and Discussion

The pooled analysis of variance for morphological and quality traits in 36 genotypes showed the existence of distinct genetic differences among the genotypes in respect of all the characters studied (Table 1). The species-wise analysis of variance to assess inter-specific variation for 12 genotypes of each *Brassica* species showed significant differences among the genotypes (Table 2). Perusal of these studies indicated the presence of sufficient variability demonstrating the agronomic potential in crop *Brassic*as, which could be exploited for further improvement programme. Presence of variability for physio-morphological traits in *Brassica* species (Sandhu and Gupta, 1996) and in *Gobhi sarson* (*B. napus*) for

**Table 1. Pooled analysis of variance for morphological and quality traits in *Brassica* germplasm**

Source	df	Mean squares							
		Plant height	Primary branch number	Siliqua number	Siliqua length	1000 seed weight	Days to 50% flowering	Seed yield	Oil yield
Genotype	35	2077**	14.2**	4824**	4.18**	1.27**	780**	14.02**	
Error	70	31.5	2.23	34.5	0.23	0.19	6.26	1.76	0.39

\*\* Significant at 1%

**Table 2. Species-wise analysis variance for morphological and quality traits in *Brassica* species**

### *Brassica juncea*

Source	df	Mean squares							
		Plant height	Primary branch number	Siliqua number	Siliqua length	1000 seed weight	Days to 50% flowering	Seed yield	Oil yield
Genotype	11	4827**	4.13**	881**	0.48**	1.09**	99.1**	17.95**	2.99**
Error	22	45.5	0.57	30.3	0.09	0.19	7.22	2.85	0.72

\*\* Significant at 1%

### *Brassica napus*

Source	df	Mean squares							
		Plant height	Primary branch number	Siliqua number	Siliqua length	1000 seed weight	Days to 50% flowering	Seed yield	Oil yield
Genotype	11	532**	15.9**	1881**	4.18**	1.94**	0.796**	780.29**	14.02**
Error	22	14.6	3.30	20.3	0.23	0.55	0.26	1.76	0.39

\*\* Significant at 1%

### *Brassica carinata*

Source	df	Mean squares							
		Plant height	Primary branch number	Siliqua number	Siliqua length	1000 seed weight	Days to 50% flowering	Seed yield	Oil yield
Genotype	11	934**	13.6**	7369**	0.76	1.86**	85.3**	14.8**	2.09**
Error	22	28.5	2.46	50.6	0.51	0.11	3.06	0.88	0.15

\*, \*\* significant at 1 and 5 % level, respectively

seed and oil yield is assessed in previous studies (Singh *et al.*, 1991)

The mean, range and heritability (in broad sense) estimates for different characters are given in Table 3. A wide range was observed for all the traits except 1000-seed weight where value range from 2.1 to 4.3 g. The heritability was high for seed yield (95.5%), oil yield (94.5%), plant height (92.7%) and days to 50% flowering (98.3%). This suggests that these traits are least affected by the environment and, therefore, can be effectively used as selection criteria. High variability for these traits has also been reported in Swede rape (Li and Guan, 1981).

Correlation matrix was used to transform all the metric traits into a single index of similarity in the form of principal components, which yielded eight Eigen vectors and Eigen roots. The per cent variation explained by eight roots, 1 to 8, was 46.34, 26.37, 15.09, 6.51, 3.53, 1.08, 0.96 and 0.13, respectively. Further, maximum eigen root value was 3.707 obtained by eigen vector 1, followed by 2.110, 1.207, 0.520, 0.283, 0.086, 0.007

and 0.010, respectively, for rest of the vectors. The first five principal components calculated by using standard variables accounted for 97.84% of total variation, hence used for non-hierarchical cluster analysis. The first component was measure of primary branch number, second of seed yield/plant, third of siliqua length, fourth of 1000-seed weight and fifth of plant height and days of 50% flowering, as the coefficients associated with these traits have the largest magnitude (Table 4). The first five principal components were used for cluster analysis. Based on this, 36 accessions were grouped into five well-characterized group (I-V) based on similarity in traits (Table 5). The maximum number of genotypes (12) fell in cluster I, while minimum number (3) was observed in cluster II. This grouping indicated considerable diversity in the germplasm. The important finding in this regard is that all the 12 *B. napus* genotypes gathered into Cluster I, *B. juncea* genotypes converged to cluster II (3) and cluster IV (9) whereas *B. carinata* genotypes grouped into cluster III (5) and cluster V (7). This demonstrates the presence of characteristic differences

**Table 3. Estimate of variability parameters for quantitative traits of Brassica species**

Characters	Mean	Range	C.V. (%)	Heritability*
Plant height (cm)	161.45	110.8 -224.2	15.88	92.7
Primary branch number (cm)	8.21	3.31 - 13.4	26.65	72.7
Siliqua length (cm)	5.25	3.56 - 8.2	22.52	89.6
Siliqua number	138.05	71.6 -195.8	25.89	88.5
1000-seed weight (g)	3.22	2.1 - 4.0	16.62	73.6
Days to 50% flowering	101.23	62.3 -132.9	23.34	98.3
Seed yield (g)	12.49	5.26 - 21.4	38.19	95.5
Oil yield (g)	5.13	1.33 -10.26	45.78	94.5

\*Heritability in broad sense

**Table 4. Eigen vectors for eight standardized variables for the first five principles**

Variables	Principal				
	1	2	3	4	5
1	0.0470	-0.011	-0.037	-0.144	0.493
2	0.0628	-0.612	-0.384	-0.233	0.104
3	-0.0110	-0.123	-0.673	0.713	0.009
4	0.1300	-0.378	0.614	0.48	0.182
5	-0.7150	0.645	-0.093	-0.034	0.098
6	-0.1960	-0.217	-0.242	-0.138	0.684
7	-0.1810	0.0840	-0.300	-0.151	-0.177
8	-0.0620	0.0000	-0.072	0.032	-0.091

1-Plant height, 2-Primary branch number, 3-Siliqua length, 4-1000-seed weight, 5-siliqua number, 6-Days to 50% flowering, 7-seed yield.

among *Brassica* species for morphological and yield traits which could be exploited for improvement programme. Inter-and intra-cluster distances, which provided index of genetic diversity among and within the clusters, revealed that intra-cluster distances were of lower magnitude as compared to inter-cluster distances. It suggested that genotypes of same cluster had little divergence from each other. Therefore, the hybridization among the accessions of same cluster is not desirable. The intra-cluster distance ranged from 1.025–1.835. The minimum inter-cluster distance was observed between II and IV (2.984) followed by II and V (2.992). Maximum inter-cluster distance was between IV and V (5.050) followed by II and III (5.017) (Table 6). The crosses between the genotypes from the clusters may give putative transgressive segregates. It is suggested that better recombinants can be obtained by selecting genotypes with their phenotypic dissimilarity (Sharma *et al.*, 1998).

Cluster-wise mean values for each character under study are given in Table 7. The cluster IV genotypes (*B. juncea*) were characterized with high seed yield and oil yield. *B. carinata* genotypes (Cluster V & VII) had the highest plant height and primary branch number but they are late maturing (as indicated by high values for days of 50% flowering) and also the poorest yielders with lowest oil yield. The screening of germplasm helped in identifying promising genetic stocks, on the basis of their mean performance for important physiological traits and genetic divergence (Table 8). Use of these genotypes in *Brassica* breeding programme is suggested as multiple crossing among them may result in segregates with commercially desirable attributes. A similar approach was also followed for large collections of wheat (Garg and Gautam, 1997), and maize (Katiyar *et al.*, 1998) germplasm for selection of diverse and superior genotypes.

**Table 5. Distribution of genotypes of different clusters**

Cluster No.	No. of genotypes	Name of genotypes
I	12	GSL-1, GSL-1501, ABU, BN-215, Marinus, GS-119, BN-225, K-1, GS-203, HN-5-1, NH-510 and GS-124
II	03	Pusa-bold, RLC -1359 and RH-765
III	05	HC-1, DIC-2, PC-5, DIC-3 and HC-6
IV	09	Varuna, HR 8304, RLM-29, Prakash, RLM-198, Kranti, RLM-619, RLM-185 and RLM-234
V	07	HC-2, HC-7, BIC-3, HC-6-7, BS-26-M, HC-S-1, and BS-70-1.

**Table 6. Estimates of average intra- and inter-cluster distance**

Cluster number	I	II	III	IV	V
I	<b>1.835</b>	3.485	3.761	3.882	2.901
II		<b>1.025</b>	5.017	2.984	4.053
III			<b>1.298</b>	4.214	2.992
IV				<b>1.113</b>	5.051
V					<b>1.064</b>

Diagonal (bold face) values are average intra-cluster distances and under lined values are the highest (5.051) and the lowest (2.901) inter-cluster distances.

**Table 7. Average performance of different clusters for morphological, yield and yield contributing traits**

Cluster number	No. of genotypes	Plant height (cm)	Primary branch number	Siliqua number (cm)	Siliqua length	1000-seed weight	Days to 50% flowering	Seed yield (g)	Oil yield (g)
I	12	144.35	7.25	6.67	3.12	121.18	11.5.16	11.17	4.67
II	3	1234.93	6.32	4.28	3.94	160.93	73.4	14.73	6.11
III	5	201.76	11.74	4.29	2.77	137.18	112.58	9.87	3.63
IV	9	168.17	8.06	4.92	3.01	182.76	66.86	19.26	8.23
V	7	169.01	8.35	4.36	3.69	100.33	125.36	6.97	2.44

**Table 8. Important genetic donors identified from germplasm for different characters**

Plant height (>182cm)	HC-1, HC-2, DIC-2, DIC-3, PC-5
Primary branch number (>9.6cm)	HC-1, HC-6, HC-7, DIC-2, DIC-3, PC-5
Siliqua length (>6.67 cm)	ABU, BN-215, GS-2043, GSL-1501, HN-5-1
1000-seed weight (>3.30g)	Pusa bold, RH-765, RLC-1359, RLM-29, Varuna
Siliqua number (>170)	Prakash, RH-765, RH-8304, RLM-29, RLM-185, RLM-198, RLM-234, Varuna
Days to 50% flowering ( $\leq 63$ )	Kranti, RLM-234, Varuna
Seed yield (>18.0g)	RH-8304, RLM-29, RLM-185, RLM-234, Varuna
Oil yield (>8.00g)	RH-8304, RLM-29, RLM-185, RLM-234, Varuna

### Conclusions

The study depicted the relative divergence in morphological and quality traits. The screening of genotypes helped in identifying the promising genotypes for different traits, which may serve as good genetic donors for exploitation in further breeding programme. The genotypes occupying the top position in superior clusters may further be assessed for their combining ability and gene effects following suitable mating designs.

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