



## MORPHOLOGICAL AND MOLECULAR DIVERSITY AMONG FULL-SIB PROGENIES OF INDIAN MUSTARD (*Brassica juncea* L.)

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### SUMMARY

*Brassica* species, belonging to the family Brassicaceae, comprise important sources of edible oil, vegetables and condiments across the globe. Among the different *Brassica* species, *Brassica juncea* is a major oilseed crop grown in India on approximately 6-7 million hectares of land during the winter season under rain-fed cropping system. Twenty-one full-sib progenies derived through 3 cycles of selection were evaluated for agromorphological traits in complete randomized block design during the *rabi* season of 2014-15. The analysis of variance revealed significant differences among the progenies for all the traits. High heritability estimates (broad sense) were observed for 1000-seed weight (83.5%), oil content (70.2%), seed yield per plant (57.0%) and biological yield per plant (55.4%). The coefficient of correlation between seed yield and morphological characters ranged from 0.54\* to 0.92\*\*. Seed yield per plant showed positive and highly significant correlations with biological yield per plant (0.80\*\*), number of secondary branches per plant (0.79\*\*), siliqua per plant (0.74\*\*), siliqua on main shoot (0.68\*\*), fruiting zone length, (0.66\*) and main shoot length (0.56\*). In summary, the study indicated that full-sib progeny selection creates ample variability after 3 cycles of selection which can be exploited by the plant breeders to develop high yielding cultivars.

**Key words:** *Brassica juncea*, full-sib progeny, genetic variability, molecular characterization

**Key findings:** Full sib progeny selection was effective in enhancing the mean performance by increasing frequency of desirable alleles and this information is very useful and can further be used in breeding programmes. Moreover, it generated sufficient variability after 3 cycles of selection for genetic improvement which was further confirmed by molecular analysis.

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### INTRODUCTION

Rapeseed-mustard, commonly referred as oilseed Brassicas, constitutes an important group of oilseed crops. Of these, Indian mustard (*Brassica juncea* L.), popularly known as 'raya' or 'laha' is a predominant *rabi* oilseed crop in India. The crop is mainly grown as a rainfed crop on conserved moisture

received from monsoon rains. Thus improvement for drought resistance becomes the prime objective for this crop (Singh and Choudhary, 2003). For improvement of drought resistance, several methods such as pedigree, bulk and backcross methods have been applied (Singh *et al.*, 2011). However, these conventional breeding procedures suffer from narrow genetic base and limited genetic

recombination in the crop. Although Indian mustard is predominantly a self-pollinated crop, but outcrossing exceeding 5% up to the extent of 18.1% has been reported (Ram Bhajan *et al.*, 1991; Abraham, 1994). This indicates that some extent of heterozygosity exists in the crop, and thus full-sib progeny selection can be used as a long term breeding strategy to expose hidden variability. However, information in this regard is lacking in Indian mustard. Therefore, the present investigation was undertaken to study the effect of 3 cycles of full-sib progeny selection in creating genetic variability for yield and its components under rain-fed conditions.

## MATERIALS AND METHODS

### Morphological characterization of full-sib progenies

The experiment commenced during the *rabi* season of 2006-07 at the experimental farm of the Directorate of Rapeseed-Mustard Research (DRMR), Bharatpur (Rajasthan) where a crossing programme involving Varuna and BPR-148 was initiated. Parents were selected on the basis of their adaptability, yielding ability and performance under rain-fed conditions. Varuna is a popular variety of Indian mustard which later became a National check in coordinated trials while, BPR-148 is an advanced entry having good performance under rain-fed conditions. During the *rabi* season of 2008-09, the  $F_2$  population (Varuna  $\times$  BPR-148) was sown in 50 rows each of 5 m length. From the  $F_2$  population, 5 sets each with 5 plants were selected randomly which constituted the male plants. Each male plant in each set was crossed to a set of 4 randomly selected plants from the population using them as females. Thus, a total of 100 crosses in the population were made to develop bi-parental progenies according to North Carolina Designs- I (NCD-I) (Comstock and Robinson, 1948). NCD is a crossing method for generating bi-parental progenies i.e. full sibs and helps in breaking linkages thus makes available for selection (Patel *et al.*, 2005). These full-sib progenies (100) were evaluated during the *rabi* season of 2009-10 in an augmented block design under rain-fed conditions. Significantly superior progenies on the basis of seed yield/plant in comparison to checks (RB-50, RH-819, RGN-48, RGN-229)

and base population ( $F_2$  variable population) were selected for initiating second cycle of selection. Total 18 progenies were selected from first cycle of selection and 500 seeds from these progenies were mixed and sown in crossing blocks during the *rabi* season of 2010-11. Similarly, full sib progenies were developed and evaluated for 3 cycles of selection as described by Singh *et al.* (2011). Finally, 120 full-sib progenies were generated and evaluated in augmented block design during the *rabi* season of 2013-14 under rain-fed conditions. From these 120 full-sib progenies, 21 superior progenies were selected and grown along with check varieties (RB-50, RH-819, RGN-48, RGN-229) during the *rabi* season of 2014-15 in completely randomized block design (RCBD) with 3 replications under rain-fed conditions. However, one pre-sowing irrigation was provided. Progenies and check varieties were sown in two-row plots of 5 meter length, spaced 30 cm apart with plant-to-plant spacing of 10 cm achieved by thinning during 15-20 days after sowing. Border effect was removed by taking observations on middle plants in a row. Recommended dose of fertilizer for rain-fed experiments was applied (40 Kg Nitrogen/ha, 20 Kg Phosphorus/ha) and weeds were removed from the field as and when they appeared to raise a healthy crop. Moisture content of experimental area at sowing time was 11.8% (0-15 cm depth), 16.7% (15-30 cm depth) and 16% (30-60 cm depth). After 45 days, moisture content reduced to 10.9% (0-15 depth), 12.4% (15-30 cm depth) and 11.2% (30-60 cm depth) while after 120 days it was 9.1%, 8.6% and 9.1%, respectively. Observations were recorded on 12 morphological characters *viz.*, plant height, primary branches per plant, secondary branches per plant, fruiting zone length, siliquae per plant, siliquae on main shoot, main shoot length, siliqua length, seeds per siliqua, biological yield, seed yield per plant, harvest index, 1000-seed weight and oil content.

The mean data was subjected to analysis of variance as per standard procedure using Windostat software version 8.5. Genetic parameters and simple correlations in all possible combinations were determined as per Burton (1952) and Johnson *et al.* (1955).

### Molecular characterization of full-sib progenies

### DNA extraction and SSR analysis

Genomic DNA was extracted from the 3 leaf stage of 27 genotypes using CTAB method (Murray and Thompson, 1980). A total of 150 genic-SSR markers developed at our laboratory using paired-end whole transcriptome sequencing of *Brassica juncea* cv CS-52 were used for parental screening (Singh *et al.*, 2016). Out of these, 65 genic-SSR markers showing polymorphism among the parental genotypes were PCR amplified in all the full-sib progenies and checks. The amplification reactions were carried out in a total volume of 10 µl containing 10X buffer (20 mM Tris HCl, pH 8.0; 100 mM KCl and 1.5 mM MgCl<sub>2</sub>), 200 mM each dNTP, 0.4 µM of forward and reverse primers, 1.0 unit *Taq* DNA polymerase and 20 ng of template DNA, using a Veriti 96-well Thermal Cycler (AB Applied Biosystems, USA). Thermal cycler was programmed at 94°C for 5.0 min for initial denaturation followed by 38 cycles of 30s at 94°C for denaturation, 40s of 58°C for annealing and 30s at 72°C for primer extension. Final extension was carried out at 72°C for 7 min. The reproducibility of PCR was checked twice for each marker.

### Cluster analysis

Variations in the DNA banding patterns were scored from gel photographs for presence (1) and absence (0) of bands assuming that each band represents a unique genetic locus and their sizes were determined by comparing with 100 bp DNA ladder. Based on the presence or absence of amplicons, a binary 1-0 data matrix was created and used to calculate Jaccard's similarity coefficient (Jaccard, 1908). Cluster analysis was carried out among the lines based on Jaccard's similarity coefficients using UPGMA (Sneath and Sokal, 1973) and SAHN-clustering algorithm in NTSYS-pc, version 2.02e (Applied Biostatistics) software. The confidence limit of the UPGMA-based dendrogram was determined by bootstrap analysis. One thousand bootstrap replicates were computed and bootstrap of 50% majority rule consensus tree was constructed using the WinBoot software (Yap and Nelson, 1996).

## RESULTS AND DISCUSSION

### Morphological diversity among full-sib progenies

The analysis of variance revealed highly significant differences among the full-sib progenies for all the traits studied, indicating sufficient amount of genetic variability in the materials. This suggests that selection of high-yielding progenies along with desirable morphological traits may be practiced in the generated breeding materials. Estimates of mean and range for all the characters exhibited wide range of variation (Table 1). The most pronounced range was obtained for siliquae per plant, fruiting zone length, biological yield per plant, plant height and seed yield per plant. On the other hand, characters like number of primary branches per plant, siliqua length and 1000-seed weight exhibited a narrow range of variation. Significant differences were also observed between the genotypes for seed yield per plant which ranged from 6.8 g (RB-50) to 15.6 g (DFS-41). However, biological yield per plant for these lines ranged from 32.5 g to 70.0 g. The plant height was highest for DFS-93 (190.0 cm) and lowest for DFS-95 (150.6 cm). Thousand-seed weight ranged from 3.9 g (Varuna) to 6.4 g (DFS-40) (Table 1). The number of primary branches was maximum for DFS-107 (6.0) and lowest for Varuna (3.4) while number of secondary branches varied from 2.8 (Varuna) to 6.8 (DFS-91). The fruiting zone length ranged from 61.0 cm (Varuna) to 90.2 (DFS-104) while main shoot length varied from 57.6 (RGN-48) to 77.0 (DFS-100). Significant estimates for siliqua traits were observed among the different lines. The siliqua on main shoot was highest for Varuna (48.0) and lowest for DFS-95 (33.3). The siliqua per plant ranged from 128.1 (DFS-90) to 226.6 (DFS-104) while siliqua length varied from 3.6 cm (DFS-107) to 4.5 cm (DFS-99). Similarly, seeds per siliqua ranged from 10.9 (BPR-148) to 26.8 (RGN-48). The harvest index (%) was highest for DFS-41 (29.5) and lowest for DFS-103 (17.1). The highest oil content was obtained in for RGN-229 (41.6%) while it was lowest in Varuna (38.4%) (Table 1).

DFS-41 (15.6 g), DFS-91 (14.8 g), DFS-40 (14.8 g), DFS-101 (13.8 g), DFS-93 (12.8 g) and DFS-107 (12.0 g) attained high seed yield per plant compared to checks RH-819, RGN-229, RGN-48, RB-50, BPR-148 and Varuna (Table 2). On the basis of morphological and yield data, these progenies hold promise for multi-location testing and generation advancement.

**Table 1.** Numerical values of statistical and genetic parameters for seed yield and yield contributing traits in full-sib progenies of Indian mustard.

Characters	Mean $\pm$ SE <sub>M</sub>	Range	GCV (%)	PCV (%)	Heritability (h <sup>2</sup> )	Genetic advance as percentage of mean
Plant height (cm)	167.8 $\pm$ 4.6	150.6-190.0	4.8	6.8	49.3	8.9
Number of primary branches	4.65 $\pm$ 0.3	3.4-6.0	10.0	14.4	47.6	18.1
Number of secondary branches	4.4 $\pm$ 0.7	2.8-6.8	18.1	33.2	29.6	26.0
Fruiting zone length (cm)	74.8 $\pm$ 4.8	61.0-90.2	6.1	12.9	22.4	7.6
Main shoot length (cm)	66.5 $\pm$ 4.7	57.6-77.0	2.7	12.8	4.3	1.5
Siliquae on main shoot	40.8 $\pm$ 2.4	33.3-48.0	7.1	12.6	32.1	10.7
Siliquae per plant	172.3 $\pm$ 16.4	128.1-226.6	10.8	20.0	29.0	15.3
Silique length (cm)	4.1 $\pm$ 0.2	3.6-4.5	3.6	7.4	23.5	4.6
Seeds per silique	13.5 $\pm$ 1.5	10.9-26.8	17.5	26.3	44.4	30.8
Biological yield per plant (g)	46.3 $\pm$ 4.2	32.5-70.0	17.8	24.0	55.4	35.1
Seed yield per plant (g)	10.1 $\pm$ 1.1	6.8-15.6	21.7	28.7	57.0	43.1
Harvest index (%)	22.3 $\pm$ 2.2	17.1-29.5	7.3	18.9	15.0	7.5
1000-seed weight (g)	5.5 $\pm$ 0.2	3.9-6.4	11.5	12.6	83.5	27.7
Oil content (%)	40.4 $\pm$ 0.2	38.4-41.6	1.5	1.8	70.2	3.3

The estimates of genotypic and phenotypic coefficients of variation were considerably high (> 15%) for seed yield per plant, number of secondary branches, biological yield per plant and seeds per silique. High genotypic coefficient of variation for seed yield per plant and number of secondary branches provide good opportunity for selecting desirable traits. High genotypic and phenotypic coefficients of variation for seed yield per plant, number of secondary branches, biological yield per plant, seeds per silique and 1000-seed weight were also reported by Singh *et al.* (2013) and Shekhawat *et al.* (2014) in Indian mustard.

High heritability estimates (broad sense) were observed for 1000-seed weight (83.5%), oil content (70.2%), seed yield per plant (57.0%) and biological yield per plant (55.4%). Results indicated that these characters are less influenced by the environmental factor and direct selection for these characters would be effective for further improvement. The high genetic advance was observed for seed yield per plant (43.1%) and for biological yield (35.1%) while the other characters showed moderate to low genetic advance. According to Hanson *et al.* (1956), heritability estimates along with genetic advance are of more value than the former

alone in predicting effect of selection. Further, Panse (1957) has reported that high genetic advance might be expected when heritability is mainly due to additive gene effect. In this study, heritability (broad sense) of seed yield per plant (57.0%) with maximum genetic advance (43.1%) was observed, which might be due to heritability with additive gene impact and therefore selection may be effective (Table 1). These results are in agreement with the results obtained by several workers including Adnan *et al.* (2013) and Shekhawat *et al.* (2014) in *Brassica*.

The genotypic correlations were estimated for yield and morphological characters in all possible combinations. The significant coefficient of correlation between seed yield and morphological characters ranged from 0.54\* to 0.92\*\* (Table 3). Seed yield per plant showed positive and highly significant correlations with biological yield per plant (0.80\*\*), number of secondary branches per plant (0.79\*\*), silique per plant (0.74\*\*), silique on main shoot (0.68\*\*), fruiting zone length, (0.66\*) and main shoot length (0.56\*). The same pattern of positive associations has also been reported earlier (Raut *et al.*, 2012; Adnan *et al.*, 2013; Shweta, 2014).

**Table 2.** Mean performance of selected full-sib progenies for yield attributes along with checks and parents.

No.	Progenies	Seed yield per plant (g)	Oil content (%)	1000-seed weight (g)	Biological yield (g)	Plant height (cm)	Number of primary branches	Number of secondary branches	Fruiting zone length (cm)	Main shoot length (cm)	Siliquae on main shoot	Siliqua per plant	Siliqua length (cm)	Seeds per siliqua	Harvest index (%)
1	DFS-41	15.6	40.5	5.4	55.0	166.5	4.7	6.5	79.6	69.1	42.5	193.9	4.1	14.1	29.5
2	DFS-91	14.8	40.4	5.0	70.0	173.2	5.1	6.8	72.8	59.1	43.2	192.0	4.3	13.5	21.6
3	DFS-40	14.8	40.4	6.4	57.5	160.4	5.0	6.7	79.0	66.8	45.7	192.0	4.3	13.6	25.7
4	DFS-101	13.8	40.9	6.2	65.0	171.1	4.3	5.2	75.5	69.6	41.1	197.4	4.4	12.7	22.7
5	DFS-93	12.8	40.9	5.3	47.5	190.0	5.7	5.3	81.7	67.7	44.5	209.0	4.1	12.7	27.2
6	DFS-107	12.0	40.2	6.4	57.5	176.0	6.0	4.8	77.8	67.1	40.3	214.0	3.6	12.1	21.4
7	DFS-100	11.7	40.8	5.6	55.0	175.5	4.0	5.1	84.3	77.0	44.9	193.7	4.1	13.2	20.5
8	DFS-70	11.5	40.8	6.1	50.0	156.0	4.7	4.5	73.1	64.7	38.1	172.1	4.2	13.2	23.4
9	DFS-104	10.7	39.5	5.3	42.5	168.1	4.6	4.0	90.2	73.5	39.4	226.6	4.2	13.8	25.2
10	DFS-102	10.2	40.5	5.8	42.5	174.6	4.6	5.3	75.1	65.6	39.5	180.9	4.3	13.1	24.2
11	DFS-108	10.0	39.7	6.2	52.5	176.2	4.0	4.3	81.6	66.1	43.9	144.8	3.9	11.4	19.0
12	DFS-105	9.8	39.8	6.3	47.5	163.3	4.0	4.0	78.8	65.9	39.5	147.3	4.2	11.9	20.6
13	DFS-106	9.4	40.4	5.4	40.0	162.7	3.9	3.8	81.4	72.6	44.9	142.3	3.9	11.8	23.5
14	DFS-92	9.0	39.7	4.5	42.5	165.7	4.9	5.4	76.9	64.9	35.4	175.8	4.3	13.6	22.6
15	DFS-74	9.0	40.8	5.8	42.5	160.6	5.0	4.1	70.8	60.2	38.8	150.6	4.1	14.1	21.1
16	DFS-95	8.7	41.3	5.2	57.5	150.6	4.3	4.0	67.1	58.5	33.3	154.9	3.9	15.1	24.2
17	DFS-103	8.6	40.6	5.3	50.0	169.5	3.9	4.0	77.2	73.0	44.8	177.1	4.4	12.6	17.1
18	DFS-90	8.2	40.8	4.8	37.5	152.0	4.7	3.1	68.4	61.7	35.7	128.1	3.8	13.4	23.3
19	DFS-81	7.9	40.2	6.3	42.5	163.0	4.0	4.0	76.1	66.3	41.4	157.5	4.3	13.9	19.9
20	DFS-76	7.7	41.1	6.2	45.0	157.0	4.2	3.7	69.5	60.7	34.9	143.8	3.9	13.4	17.3
21	DFS-99	7.5	40.2	5.3	32.5	164.2	4.3	4.2	77.5	65.9	42.3	167.1	4.5	12.1	23.7
22	RH-819	9.4	41.0	5.8	45.0	165.3	5.0	3.3	77.6	69.4	42.8	172.7	4.3	14.3	21.3
23	RGN-229	9.0	41.6	5.1	45.0	174.6	4.8	3.2	67.7	63.6	39.8	172.0	4.3	13.2	20.2
24	RGN-48	8.8	41.0	1.3	42.5	179.1	4.7	4.1	68.2	57.6	40.1	182.2	4.0	26.8	20.6
25	RB-50	6.8	40.3	6.1	35.0	159.5	4.7	3.9	69.5	65.2	34.2	135.2	4.3	12.3	21.0
26	BPR-148	8.3	39.8	4.3	34.7	175.3	4.6	3.4	62.3	67.9	41.9	172.9	4.1	10.9	24.0
27	VARUNA	7.4	38.4	3.9	34.6	181.3	3.4	2.8	61.0	76.8	48.0	177.6	4.4	12.4	21.3
	CV (%)	18.82	1.0	5.1	16.0	4.9	10.5	27.9	11.4	12.5	10.4	16.8	6.5	19.6	17.4
	CD	3.12	0.6	0.5	12.2	13.4	0.8	2.0	14.0	NS	6.92	47.5	0.4	4.3	NS
	(P=0.05)														

NS- Non significant

**Table 3.** Genotypic correlation coefficient (rg) between different pairs of morphological and quality traits of DFS progenies.

Character	Plant height (cm)	No. of primary branches	No. of secondary branches	Fruiting zone length (cm)	Main shoot length (cm)	Siliquae on main shoot	Siliqua per plant	Siliquae length (cm)	Seeds per siliquae	Bio-logical yield (g)	Har-vest index (%)	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)	
Plant height (cm)	Rg	1	-0.37	0.38	0.78**	0.74**	0.58*	0.47	0.88**	-0.05	0.71**	-0.53	0.03	0.34	0.31
Number of primary branches	rg	1	0.15	-0.14	-0.18	-0.05	0.32	-0.39	-0.06	-0.24	0.24	-0.12	-0.15	-0.09	
Number. of secondary branches	rg		1	0.54*	0.42	0.42	0.82**	0.31	0.21	0.65*	0.34	0.12	-0.01	0.79**	
Fruiting zone length (cm)	rg			1	0.92**	0.90**	0.75**	0.70**	-0.04	0.85**	-0.15	-0.02	0.25	0.66*	
Main shoot length (cm)	rg				1	0.77**	0.66**	0.66*	-0.22	0.75**	-0.13	-0.01	0.09	0.56*	
Siliquae on main shoot	rg					1	0.62*	0.54*	0.20	0.81*	-0.08	0.03	0.09	0.68**	
Siliquae per plant	rg						1	0.41	0.04	0.76**	0.14	0.46	0.24	0.74**	
Siliquae length (cm)	rg							1	-0.23	0.72**	-0.69	-0.46	0.39	0.23	
Seeds per siliquae	rg								1	0.25	0.32	-0.29	-0.04	0.47	
Biological yield per plant (g)	rg									1	-0.15	0.21	0.31	0.80**	
Harvest index (%)	rg										1	-0.41	-0.47	0.46	
1000-seed weight (g)	rg											1	0.07	-0.04	
Oil content (%)	rg												1	-0.01	
Seed yield per plant (g)	rg													1	

\* & \*\* represents significance levels at 0.05 and 0.01 respectively.

Similarly, biological yield showed positive and significant correlations with fruiting zone length (0.85\*\*), siliqua on main shoot (0.81\*\*), siliqua per plant (0.76\*\*), main shoot length (0.75\*\*), siliqua length (0.72\*\*), plant height (0.71\*\*) and number of secondary branches (0.65\*). Siliqua per plant was positively correlated with number of secondary branches (0.82\*\*), fruiting zone length (0.75\*\*), main shoot length (0.66\*\*) and siliqua on main shoot (0.62\*) while a positive and highly significant correlation was obtained between siliqua on main shoot and fruiting zone length ( $r = 0.90^*$ ). Fruiting zone length was significantly positively associated with plant height (0.78\*\*) and number of secondary branches (0.54\*).

Holland (2006) observed that genetic correlations between traits are due to linkage and/or pleiotropy indicating the magnitude and direction of correlated response to selection. He also emphasized the relative efficiency of correlations facilitating indirect selection. The present findings indicate that since the traits are highly correlated, selection based on correlations may be a useful breeding strategy for indirect selections for higher seed yield (Ojaghi and Akhundova, 2010). Therefore, it would be appropriate for selection of biological yield per plant, number of secondary branches, siliqua per plant, siliqua on main shoot, fruiting zone length and main shoot length for improving the seed yield per plant in this crop.

### SSR analysis of full- sib progenies

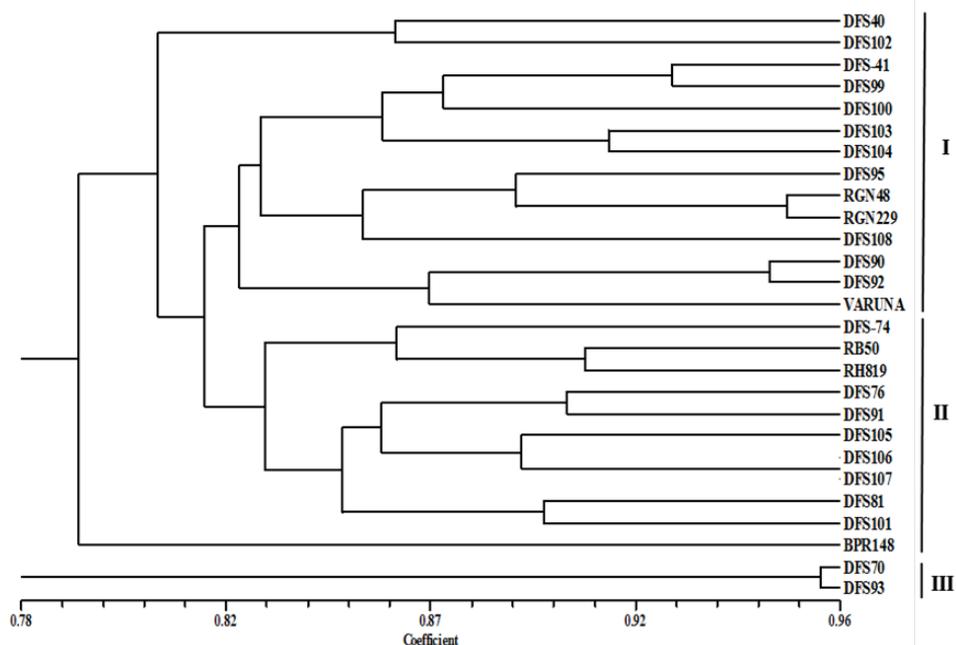
Out of the 150 genic-SSR markers used in this study, 65 markers (43.3%) were found to be polymorphic and amplified products of varying sizes in range of 100-400 bp while 85 SSRs (56.6%) were monomorphic. Though genic SSRs are less polymorphic compared with genomic SSRs in crop plants because of greater DNA sequence conservation in transcribed regions they were preferred because of some intrinsic advantages over genomic SSRs such as they are quickly obtained by electronic sorting, high transferability as these are designed from the more conserved coding regions of the genome,

public availability of large quantities of sequence data (Varshney *et al.*, 2005; Yue-peng *et al.*, 2012).

The cluster analysis of full-sib progenies based on genic-SSRs gave 3 major groups viz., I, II, III and the similarity coefficient ranged between 0.69 and 0.96. Cluster I contained 11 progenies along with 2 checks, RGN-48 and RGN-229 and grouped with parent Varuna. In this cluster, progeny DFS-90 exhibited highest similarity (89.4%) with parent Varuna followed by DFS-108 (86.4%) and DFS-40 (86.2%). The other progenies which were more close to varuna were DFS-95 (84.7%), DFS-92 (84.4%), DFS-104 (84.4%). DFS-90 and DFS-92 were more close to each other revealing 94.4% similarity. DFS-100 (77.0%) showed lowest similarity with parent Varuna. Cluster II consisted of 8 progenies and grouped with BPR-148 along with 2 checks RB-50 and RH-819. Here, 84.7% similarity was observed between DFS-101 and BPR-148. The other progenies which showed high similarity with parent BPR148 were DFS-81 (84.7%), DFS-106 (84.2%) and DFS-91 (83.9%) while DFS-74 (75.4%) exhibited lowest similarity. Further in this cluster, DFS-106 and DFS-107 were closely related having 96.1% similarity (Figure 1).

Two progenies namely, DFS-70 and DFS-93 were entirely separated and clustered together in cluster III and showed a very high level of genetic similarity (95.5%) The highest Nei's (1972) genetic distance (0.96) was observed in progenies DFS-106 and DFS-107 whereas the lowest genetic distance (0.69) was estimated in the 2 parents BPR-148 and Varuna.

In summary, this study indicated that full-sib progeny selection was effective in enhancing the mean performance by increasing the frequency of desirable alleles. Moreover, full sib progeny selection generated sufficient variability after 3 cycles of selection, which was also confirmed by genic-SSR analysis. This information will be useful to Brassica breeders as they can use full sib progeny selection as a long term breeding strategy in their Brassica improvement programme.



**Figure 1.** UPGMA dendrogram showing genetic relationships among full-sib progenies based on genic-SSR markers.

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