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Short Communication

Development and evaluation of full sib progenies of Indian mustard (*Brassica juncea* L.) for moisture stress conditions

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Indian mustard (*Brassica juncea* L.) popularly known as mustard or Raya or Laha is an important *rabi* oilseed crop of India where it is grown on an area of approximately 6.5 mha, of which about 2.0 mha is rainfed. Because of its suitability to marginal and rainfed areas, Brassica improvement programmes were initiated long back to improve its grain yield potential under these conditions. However, genetic improvement is mainly based on pedigree, bulk and backcross methods. These conventional breeding procedures suffer from narrow genetic base and limited genetic recombination [1]. Application of population improvement procedures such as development and utilization of full sib progenies for such crops broaden genetic base, increase genetic advance through accumulation of desirable alleles and expose the hidden variability through breaking of linkages [2, 3]. Further, outcrossing in this crop has been reported to vary between 10-15% [4]. This extent of outcrossing indicates that a certain level of heterozygosity is prevailing naturally which can be exploited through full sib progeny selection. With this background, the present investigation was planned to increase the yield potential of Indian mustard under moisture stress conditions through full sib progeny development and utilization in breeding programme.

Present investigation was started during *rabi* 2006-07 at NRCRM (Presently DRMR), Bharatpur where a crossing programme involving Varuna and BPR-148 was started. Hybridization was done so as to get sufficient seeds for raising F_1. During 2007-08 F_1s were advanced to F_2 and during 2008-09, F_2 seeds were sown in 50 rows each of 5m length. From this F_2 variable population, 5 sets of five plants were selected randomly. This constituted the male plants. Each male plant in each of the set was crossed to a set of 4 randomly selected plants from the population using them as females. Care was taken that no male or female plant repeated in the whole crossing programme. Thus, a total of 100 crosses in the population were made to develop biparental progenies according to NCD-I [5]

The full sib progenies (100) thus developed from the population were evaluated during *rabi* 2009-10 in an augmented block design. The material was divided into 5 blocks; each block consisted of 20 progenies and 4 check varieties namely RH-819, Geeta, RB-50 and PBR-97. In each block, progenies and check varieties were sown in a plot size of 4x0.60 m accommodating two rows spaced 30 cm apart with plant to plant distance of 10 cm. The experiment was sown on conserved moisture and was kept unirrigated throughout the season. Observations were recorded on ten randomly selected plants for plant height, primary branches per plant, siliquae per plant, seeds per siliqua, seed yield per plant, 1000-seed weight, oil content and protein content. While, data on days-to flower and days-to maturity were recorded on whole plot basis. Data on physiological characters i.e. SPAD reading at flowering stage, SPAD reading at grain formation stage, transpiration at flowering stage and transpiration at grain filling stage were also recorded to quantify physiological efficiency of progenies. The unitless measurement

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obtained from the SPAD chlorophyll meter (SPAD-502, Minolta Corp., Ramsey, NJ) is based on the differences between light attenuation at 430 nm (the peak wavelength for chlorophyll a and b) and that at 750nm (near-infrared) with no transmittance. Thus, the SPAD chlorophyll meter reading (SCMR) represent the chlorophyll concentration in the leaf. The SCMRs were made on full flowering and grain filling stage in the field trials. The leaves were sampled from the nodal position three and four below the apex on the main axis of three randomly selected plants from each variety. The transpiration was recorded with the help LICOR-LI1600 steady state porometer on 3rd and 4th fully expanded leaf from the top of three randomly taken plants. The mean data were subjected to analysis of variance as per the method suggested by Fedrer [6]. Genetic parameters and simple correlations in all possible combinations were worked out as per standard procedure.

Since, no literature is available on development and utilization of full sib progenies in Indian mustard, the results are discussed with possible reasoning. In present investigation analysis of variance revealed significant differences among full sib progenies for most of the characters under study except days-to-flowering and transpiration at grain filling stage (data not presented). This indicates that full sib progenies have sufficient variability for these traits and response to selection may be expected in the breeding programme which may be used for further cycles of selection. The block effects were non significant for most of the traits except days-to-flowering and plant height indicating non-sensitivity of the material to the environment for these characters. Estimates of genotypic and phenotypic variances indicated that in general, magnitude of the PCV was higher as compared to GCV for all the characters in the present investigation indicating a positive effect of environment on the character expression. Transpiration at flowering stage followed by seed yield per plant exhibited comparatively higher estimates of genotypic as well as phenotypic coefficient of variation (Table 1). Genotypic variation in transpiration among mustard genotypes was also reported by Singh [7]. It indicated that simple selection for transpiration at flowering stage might be advantageous. With the help of GCV and PCV alone, it is not possible to determine the amount of variation. Thus, the heritability estimate along with genetic advance is more meaningful.

The estimates of heritability in present investigation were of higher magnitude (>50%) for all the characters studied. The characters days-to-maturity, oil content, protein content and SPAD at flowering stage showed more than 90 % heritability. The genetic advance was highest for transpiration at flowering stage followed by seed yield per plant, protein content, oil content and SPAD at flowering stage. These findings indicate that there is good scope for development of populations having high transpiration rates at flowering

Table 1. Over all mean value of full sib progenies, their range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance expressed as percent of mean

Character	Mean	Range	GCV	PCV	h^2	GA
Days-to-flowering	47.77	39.2-54.8	NS	NS	NS	NS
Days-to-maturity	138.37	114-176	9.25	9.70	90.83	18.15
Plant height (cm)	167.74	128.8-202.1	4.9	6.3	61.43	7.9
Primary branches per plant	3.84	2.55-5.2	13.27	16.26	66.66	22.31
Siliquae/plant	42.15	18.3-62.2	9.9	13.09	56.96	15.34
Seeds/siliquae	14.79	9.4-17.7	7.37	9.32	62.63	12.02
1000-seed weight (g)	4.93	3.7-6.4	14.76	19.56	56.98	22.93
Seed yield/plant (g)	9.72	1.1-20.8	28.58	36.03	77.77	57.16
Oil content (%)	40.14	38.9-44.2	18.75	19.05	96.88	37.99
Protein content (%)	19.58	14.9-21.6	19.31	19.49	98.08	39.35
SPAD (FS)	45.85	3.54-53.94	18.25	19.20	90.38	35.72
SPAD (GFS)	38.59	27.19-49.84	17.44	22	62.85	28.46
Transpiration (FS)	5.75	0.20-11.97	34.65	40.37	73.65	61.21
Transpiration (GFS)	0.92	–0.06-2.67	NS	NS	NS	NS

Table 2. Characterization of selected full sib families for morpho-physiological characters in Indian mustard

Progeny	Seed yield/ plant	Days to flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Siliquae/ plant	Seeds/ siliquae	1000-seed weight (g)	Oil content (%)	Protein content (%)	SPAD reading at FS	SPAD reading at GFS	Transpi-ration at FS	Transpi-ration at GFS
DFS-45	20.85	44.95	136.3	156.9	3.2	49.7	16.29	4.78	41.39	21.26	49.14	41.3	3.84	0.75
DFS-77	20.25	47.20	139.5	165.3	3.5	39.06	15.79	5.57	39.99	20.62	46.94	42.3	8.19	1.30
DFS-35	18.32	47.45	130.3	182.1	5.0	43.16	13.92	5.76	40.44	21.37	46.09	41.8	8.23	1.39
DFS-34	15.72	51.45	129.3	194.9	5.1	46.76	15.37	5.34	42.52	20.76	46.99	37.8	4.49	1.31
DFS-5	15.45	48.70	141.0	172.4	4.8	46.81	17.66	5.32	41.47	19.72	46.47	42.1	2.74	0.49
DFS-11	15.45	44.70	133.0	148.8	3.4	30.41	14.38	5.61	40.68	19.28	43.07	27.9	9.39	1.79
DFS-78	14.95	49.20	142.5	165.7	3.5	39.66	14.31	5.06	41.26	14.95	45.74	40.1	5.77	0.84
DFS-66	14.65	41.20	129.5	202.1	4.1	51.46	16.79	4.92	41.35	19.11	43.84	28.4	8.61	1.46
DFS-85	14.64	44.70	137.0	172.6	4.8	44.66	13.58	5.35	41.94	20.78	46.47	39.8	4.62	0.09
DFS-8	14.45	51.70	141.0	176.4	4.8	47.21	17.14	4.78	40.99	20.07	45.77	37.3	3.96	0.74
DFS-23	14.22	46.45	133.3	155.3	3.8	42.96	13.93	5.1	41.20	20.50	47.69	43.3	11.97	1.33
DFS-58	14.15	48.95	153.3	163.5	3.2	43.10	14.17	5.18	41.79	20.90	49.54	40.8	4.34	0.84
DFS-2	14.05	50.70	143.0	165.2	3.4	33.01	14.38	5.37	39.12	20.39	50.77	43.4	1.84	0.47
DFS-61	13.75	41.20	132.5	182.5	4.5	38.86	15.99	5.00	39.92	20.67	47.54	43.6	8.71	0.85
DFS-29	13.72	45.45	131.3	163.9	3.6	47.56	14.05	5.94	41.73	21.04	47.19	40.7	8.05	1.44
DFS-40	13.72	47.45	132.3	160.5	3.6	40.37	15.81	4.94	42.42	21.18	52.49	47.0	5.61	0.67
DFS-63	13.65	41.20	131.5	178.9	4.1	44.46	15.71	4.97	41.63	20.74	45.64	38.9	6.71	1.01
DFS-13	13.55	52.70	140.0	162.6	3.4	37.81	17.3	4.99	39.99	20.42	50.67	44.6	8.06	1.58
Best check	8.05	54.8	144.4	177.8	3.76	38.6	15.07	5.15	40.57	20.01	49.58	42.76	6.41	0.79
Base population	4.37	49.21	128.21	174.20	3.47	37.64	14.43	4.26	41.94	20.35	45.35	42.30	3.30	0.85

CD (5%) for seed yield/plant 5.5

stage and high chlorophyll content along with high oil and protein content which would perform better in water stress conditions. These characters also accompanied with high heritability values. This indicates that selection will be more effective for these characters in comparison to other in present material.

The correlations were worked out for yield and its component characters. Seed yield per plant showed positive and significant correlation with plant height (0.256), seeds per siliqua (0.258), 1000-seed weight (0.335), oil content (0.311) and protein content (0.286). Among physiological characters, seed yield per plant showed positive and significant association with SPAD reading at both flowering (0.319) and grain filling (0.335) stage and transpiration at flowering stage (0.216). Positive significant relationship of SPAD with grain yield was also reported by Fanaei *et al.* [8] in mustard. Therefore, high yielding drought tolerant populations can be developed with high chlorophyll and high transpiration rates at flowering stage. 1000-seed weight also showed similar pattern of association as exhibited by seed yield per plant. This indicates that physiological parameters have same impact on seed yield per plant and bold seed formation. Therefore, genotypes with bold seed size have to be selected for maximizing the yield/unit area in drought conditions. Oil content revealed significant positive correlation with plant height (0.484), siliquae per plant (0.340), protein content (0.962), SPAD (0.947 and 0.817 at flowering and grain filling stage, respectively, and transpiration at flowering (0.461) and grain filling (0.219) stage. Protein content also showed more or less similar pattern of association with these characters as shown by oil content. Physiological parameters i.e. SPAD and transpiration were significantly positively correlated with each other. This means that more photosynthetic activity will be expected from more transpiring material. Further, higher transpiration during flowering stage leads to high rate of assimilate translocation from source to sink (siliquae). Among other characters days-to-flowering showed significant positive association with days-to-maturity (0.205) only. Plant height showed significant positive association with most of the characters except days to maturity and days to flowering.

Transpiration at flowering and grain filling stage showed negative correlation with days-to-maturity (–0.100, –0.114) and days-to-flowering (–0.284, –0.025) indicating role of more transpiration in escape mechanism at later stages of moisture stress. However, days-to-flowering showed negative association with most of the traits except days-to-maturity and primary branches per plant (0.04). Adams [9] has shown that component compensation and negative correlation arise in response to competition between developmentally flexible components.

Association between some characters was non-significant which implies that the two variables are not linearly related [10]. It is also noted that characters which exhibited positive association with seed yield per plant also exhibited positive association among themselves thus these characters could be simultaneously improved to increase the seed yield.

The conclusion from present study indicates that 1000-seed weight, oil content, protein content, SPAD reading and transpiration at flowering stage are important characters that should be considered in selection procedure because all these characters had high heritability, moderate genetic advance and also exhibited positive association with seed yield, hence these characters would result in enhancement of yield in moisture stress conditions. The high yielding full sib progenies were selected and characterized for morphological and physiological characters (Table 2). The remnant seeds of these progenies shall be used for initiating second cycle of full sib progeny selection through controlled crossing between best plants of selected families. The results indicated that full sib progeny selection method is quite effective in generating genetic variability in self pollinated crops like *Brassica juncea.* The results also suggested that full sib progenies developed from broad based population can be selected that have yields superior to base population and existing check varieties under moisture stress conditions. Furthermore, mustard breeder can utilize full sib progeny selection method for development of high yielding, broad base genotypes.

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