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ESTIMATION OF GENETIC VARIABILITY AMONG DROUGHT TOLERANT RIL POPULATION OF INDIAN MUSTARD (*BRASSICA JUNCEA* L.) DERIVED FROM ROHINI X RH819

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ABSTRACT

This investigation was aimed to study the patterns of genetic variation among 215 RILs derived from cultivars Rohini (drought susceptible) and RH819 (drought tolerant). The RILs were characterized and evaluated under stress as well as irrigated conditions along with parents and checks in augmented block design. Observations were recorded on plant height, main shoot length, fruiting zone length, siliqua length, seeds/siliqua, biological yield/plant, 1000-seed weight, harvest index, seed yield/plant, oil content glucosinolates, fiber and phenol content. Analysis of variance indicated that significant differences were found among RILs for all traits except oil content under irrigated conditions while under stress conditions they were non-significant for seed/siliquae and BY/plant. The range of seed yield/plant, harvest index, 1000-seed weight was 6.49-20.52 g, 11.83-48.86%, 2.34-5.74g and 7.93-32.26g, 10.85-60.34%, 2.36-5.59g under stress and irrigated conditions respectively. Genetic components such as GCV, PCV and high heritability estimates (>50) were also calculated. Seed yield/plant was significantly and positively correlated with plant height (0.243**), fruiting zone length (0.203*), seeds/siliquae (0.343**), BY/per plant (0.444**) and harvest index (0.790**) and negative with oil content (-0.224**) and fibre (-0.213**). Out of these 215 RILs, 25 were identified as most promising lines which may further be used for multi-location trials and in various brassica improvement programs to develop drought tolerant varieties.

INTRODUCTION

Brassicas are very important among the oilseed crops in our country and rank third after soybean and palm. Among Brassicas, Indian mustard (*B. juncea*) occupies approx. 80% of (Supriya *et al.,* 2014). However, its growth and seed yield production have greatly decreased during last two decades and thus it has become a major challenge for maintaining world food supplies for the growing population. For the synthesis of genetically superior rapeseed, variety/hybrids possessing harmonious combination of desirable parameters and increased adaptability to a wide range of climatic conditions is prerequisite. The success of any crop improvement program depends upon the presence of substantial amount of genetic variability and heritability (Sidra *et al.,* 2014; Laila *et al.,* 2014; Shah *et al.,* 2015). Thus, the measurement of genetic variation is important and understanding the extent and nature of this variation is essential for enhancing the breeding efforts such as selection and hybridization to improve breeding programs effectively. Brassicas possesses enormous genetic variability and several researches have worked on the extent and nature of genetic variation for Brassicass (Iqbal *et al.,* 2014; Shafari *et al.,* 2015; Verma *et al*., 2016). Heritability and genetic advance studies were also done by many researchers (Bind *et al.,* 2014; Synrem *et al.,* 2014; Ullah *et al.,* 2016). Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another in a population. It is important for biodiversity as without variability it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction. Indian mustard is mainly grown as a rainfed crop and thus later it results into drought stress during its reproductive stage (Kumar and Singh, 1998). Thus, production and productivity of the crop is adversely affected. In the context of changing global climatic scenario, breeders need to develop drought tolerant varieties to mitigate climate change which may further be helpful to increase area and yield of the oilseed crops under such adverse conditions (Zhao *et al.,* 2008). Morphological traits have been used to assess the genetic variation and relationships among populations of

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different oilseed species (Ullah *et al.,* 2015; Singh *et al.,* 2016). Seed yield as in other crops, is a complex character which is dependent on a number of other characters. Thus, to increase yield, the evaluation of direct and indirect effects of yield and its components provide the basis for successful breeding program (Gupta *et al.,* 2015). In this sense, increase of seed yield can be more effectively achieved on the basis of performance and selection for closely associated traits. However, these traits should be highly heritable as the progress through selection depends on heritability, selection intensity and genetic advance of the trait (Meena *et al.,* 2014). Hence, in the context of yield improvement, it is necessary to analyze the nature and extent of variation present within a set of breeding material and the interrelationships between yield and its components. Keeping all this in view, the present study was undertaken to (1) evaluate the RILs developed from a recombinant inbred line (RIL) population through cross between two high yielding commercial varieties Rohini and RH-819, and (2) to determine the extent of genetic variability, heritability, genetic advance and interrelationship of yield and yield components and identify superior drought tolerant lines.

MATERIALS AND METHODS

Plant material and assessment of RIL population

Commercially released Indian mustard cultivars Rohini and RH-819 were used to develop a RIL population of 215 individuals by single-seed-descent approach. These were evaluated along with four checks (RB-50, RH-819, PBR-97 and Rohini) during the *rabi* season of 2014-15 under rainfed and irrigated conditions in augmented block design. Drought was simulated by withholding water throughout the growing season, whereas, under normal conditions the crop was irrigated according to the standard practices. During irrigated conditions moisture content was 8.0% (0-15 cm depth), 9.5% (15-30 cm depth) and 7.7% (30-45 cm depth) at sowing time whereas it was 8.5 % (0-15 depth), 10.4% (15-30 cm depth) and 8.3% (30-45 cm depth) after 45 days and 8.2%, 9.9% and 8.0% after 120 days respectively. Moisture profiling of rainfed fields at sowing time was 6.8% (0-15 cm depth), 7.8% (15-30 cm depth) and 6.9% (30-45 cm depth). After 45 days, moisture content reduced to 6.4% (0-15 depth), 7.1% (15-30 cm depth) and 6.2% (30-45 cm depth) while after 120 days it was 6.1%, 6.8% and 6.0%, respectively. It is worthwhile to mention that crop received 574.4 mm rainfall during monsoon. Approx. 41.7 mm rain was recorded from October-February and 57.0 mm in March during 2014-2015.

Morphological Parameters

Plant height (PH), main shoot length (MSL), siliqua length (SL), fruiting zone length (FZL), seeds/siliqua, biological yield/plant (BY/plant), 1000-seed weight, harvest index (HI), seed yield/plant (SY/plant) were recorded for each RIL by selecting five plants randomly in both conditions. Harvest index (HI) was calculated by the formula: HI = grain yield/total above ground biomass × 100. Oil, glucosinolates, fiber and phenol contents were estimated using FT-NIR spectroscopy.

Statistical analysis

Analysis of variance was performed as per the method suggested by Federer (1956). Genotypic and phenotypic coefficient of variation, heritability, genetic advance and correlation coefficients were calculated using the standard statistical procedures.

RESULTS AND DISCUSSION

Morphological characterization

In the present study, RIL population was evaluated in augmented block design for yield and yield related components. The analysis of variance showed highly significant differences among RILs for these parameters indicating that RILs were differing for genes controlling yield and other traits (Golabdi *et al.,* 2006; Gholipouri *et al.,* 2009). Treatments were found to be significant for all the traits except days to flowering and seed/siliquae under irrigated and stress conditions, respectively. Similarly, RILs exhibited significant differences for PH, MSL, FZL, seed/siliqua, SL, BY/plant, HI, 1000-seed wt., SY/plant, fibre, phenol, RWC, days to flowering and SPAD while non-significant for oil content in well watered conditions (Table 1a, b).

On the other hand, RILs showed significant differences for all characters except seed/siliqua, and BY/plant under stress conditions. Under drought conditions, check versus RILs exhibited highly significant differences for PH, SL, 1000-seed wt., SY/plant, fibre, phenol, oil content, days to flowering and SPAD while they were significant for PH, SL, BY/plant, 1000-seed weight, SY/plant, fibre, phenol, oil content, days to flowering in irrigated conditions indicating that checks as a group differed significantly from RILs as a group (Table 1a, b). Various agro-morphological characteristics such as PH, FZL, SL, BY/plant, 1000-seed weight are considered as the most important characters contributing to seed yield and it has already been reported that the performance of most of these characters was reduced under drought conditions (Chauhan *et al.,* 2007; Tripathi *et al.,* 2015). Similarly, in this study we observed reduction in most of the characters under drought conditions as indicated in Table 2 and the major effect was on yield under stress conditions. The mean SY/plant was 15.48 g under irrigated conditions whereas it was 10.38 g under stress conditions. Thus, on average, yield was reduced under water deficit by 32.94%. Seed yield/plant of RILs under non-stress ranged from 7.93 to 32.26g while it was from 6.49-20.52 g under stress conditions (Table 2).

The estimates of mean for some other components such as PH, FZL, 1000-seed wt., BY/plant and OC were 199.18 cm and 169.09 cm; 80.38 cm and 63.38cm; 4.21g and 4.35g; 60.01g and 48.68g; 39.41% and 39.33% under irrigated and drought conditions, respectively as indicated in Table 2. Similarly, mean and range for other important morphological and biochemical parameters were also recorded among these RILs as shown in Table 2. Among the 25 best selected RILs, seed yield/plant ranged from 7.25g (RIL180) to 19.22g (RIL110) under stress condition while it ranged from 7.93-20.59g under irrigated conditions and the yield reduction was 2.20 to 6.26% (Table 3). Various other yield components and biochemical parameters were also recorded for these RILs under both conditions where PH ranged from 153.82-194.16 cm and 154.00-214.16 cm; siliqua length from 3.4-5.1cm and 3.4-5.4 cm; oil content from 38.25-40.15% and 37.41-40.63% under drought and normal conditions respectively. The details are shown in Table 3.

Table 1(a) Mean sum of squares for different morphological traits in RILs for irrigated condition

Source	d.f.	Plant height (cm)	Main shoot length (cm)	Fruiting zone length (cm)	Siliquae length (cm)	Seeds/ siliquae	Biological Yield / plant	1000 seed wt. (g)	Harvest index	Seed yield / plant (g)	Oil content (%)	Fiber	Phenol	DAF
Block	4	34.65	20.72	105.45*	0.67	10.32**	183.06**	0.51**	11.71	3.01	0.11	0.59	0.01	2.17
Treatment	218	235.10*	95.35*	90.20**	28.48**	3.53**	189.12**	0.26**	63.42**	22.82**	1.40*	1.12**	0.04**	33.84
Control	3	189.38	19.27	24.11	19.55	9.10**	50.33	0.84**	22.63	11.10	3.04**	1.77**	0.005	0.40
Progeny	214	231.07*	96.64**	91.50**	24.85**	3.45**	182.68**	0.24*	64.23**	22.87**	0.87	0.88**	0.02**	33.15**
Control v/s progeny	1	1234.54**	54.95	10.43	832.01**	3.67	663.32**	2.66**	13.43	47.81*	110.28**	51.17**	3.28**	281.30**
Error	12	89.38	41.47	32.05	8.90	1.09	42.45	0.09	22.85	7.89	0.54	0.39	0.009	2.77

* and ** significance levels represents at 0.05 and 0.01 respectively

Table (1b) Mean sum of squares for different morphological traits in RILs for stress condition

Source	d.f.	Plant height (cm)	Main shoot length (cm)	Fruiting zone length (cm)	Siliquae length (cm)	Seeds/ siliquae	Biological Yield / plant	1000 seed wt. (g)	Harvest index	Seed yield / plant (g)	Oil content (%)	Fiber	Phenol	DAF
Block	4	60.30*	9.72	16.57**	4.62	0.57	92.80*	0.24	1.97	2.31	0.58	1.58**	0.008	3.17
Treatment	218	103.25**	18.79**	22.13**	14.97**	1.26	64.60*	0.35*	29.18**	8.14**	0.63**	0.67*	0.02**	22.25**
Control	3	114.04*	18.21*	20.20**	5.17	6.04*	64.20*	0.21	29.36**	20.76**	2.60**	0.44	0.04**	0.45
Progeny	214	103.12**	18.89**	22.25**	11.47**	1.18	64.50	0.34*	29.20**	7.89**	0.60**	0.63*	0.02**	22.07**
Control v/s progeny	1	97.49*	0.17	2.83	794.28**	4.02	89.12	2.21**	23.75	23.74**	1.63**	9.45**	0.24**	126.47**
Error	12	17.39	4.41	3.49	3.74	1.67	26.53	0.15	8.30	2.39	0.19	0.27	0.006	1.24

* and ** significance levels represents at 0.05 and 0.01 respectively

Table 2. Overall mean value of RILs, their range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance.

Characters	Mean		Range		GCV		PCV		h^2		GA	
	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated
Plant height (cm)	169.09	199.18	146.62-199.34	144.72-236.92	5.47	5.97	6.00	7.63	83.14	61.32	10.28	9.63
Main shoot length (cm)	58.58	77.85	46.34-76.18	42.80-101.75	6.49	9.62	7.41	12.62	76.65	57.09	11.70	14.85
Fruiting zone length (cm)	63.38	80.38	47.82-80.48	46.44-102.08	6.83	9.59	7.43	11.9	84.31	64.97	12.91	15.92
Siliquae length (cm)	42.55	44.54	33.27-53.43	31.87-62.53	6.53	8.96	7.94	3.79	67.39	64.19	11.03	14.78
Seeds / siliquae	12.64	12.98	8.21-16.12	8.83-18.24	*	*	*	*	*	*	*	*
Biological yield / plant (g)	48.68	68.01	33.30-72.42	34.23-99.12	12.65	4.70	16.50	19.87	58.87	76.76	20.00	31.41
1000 seed weight (g)	4.35	4.21	2.34-5.74	2.36-5.59	9.89	9.19	13.33	11.63	55.88	62.50	15.35	14.68
Harvest index (%)	21.49	23.42	11.83-48.86	10.85-60.34	21.27	27.46	25.13	34.22	71.58	64.42	37.05	45.39
Seed yield per plant (g)	10.38	15.48	6.49-20.52	7.93-32.26	22.54	25.00	26.97	30.89	69.71	65.50	38.74	41.66
Oil content (%)	39.33	39.41	34.47-41.02	35.23-41.52	1.63	1.45	1.96	2.36	68.33	37.93	2.76	1.84
Fiber	8.60	9.57	4.46-10.99	6.58-12.52	6.98	7.31	9.19	9.8	57.14	55.68	10.81	11.15
Phenol	1.63	1.54	1.22-2.15	1.01-2.02	6.13	6.49	8.59	9.18	70.00	55.00	12.39	10.30
Days to flowering	41.45	45.38	36.01-57.21	40.64	11.00	12.14	11.31	12.68	94.38	91.64	22.00	23.92

* Genetic parameters could not be calculated because of non-significant progeny mean squares

Table 3. Characterization of promising RILs for important morphological and biochemical traits

S. No.	RIL No.	Seed yield per plant (g)		Plant height (cm)		Main shoot length (cm)		Fruiting zone length (cm)		Siliquae length (cm)		1000 seed weight (g)		Oil content (%)		Fibre (%)	
		Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated	Stress	Irrigated
1	165	11.49	11.59	168.98	192.72	62.18	75.14	66.68	78.60	4.44	4.45	3.99	4.18	38.88	39.84	8.84	9.34
2	101	13.25	13.43	194.16	211.78	66.51	77.40	67.94	80.14	4.28	4.51	3.71	4.29	39.38	39.96	9.19	9.16
3	64	18.14	18.42	159.02	209.22	55.36	83.88	58.92	82.58	3.48	4.66	5.09	4.37	40.11	40.37	8.59	8.64
4	209	8.28	8.53	155.12	182.71	51.34	68.80	56.20	75.84	4.62	3.46	4.41	3.98	38.55	39.64	9.55	11.40
5	205	8.23	8.48	153.82	154.01	60.94	51.38	65.64	57.94	3.40	4.54	4.71	3.45	39.29	40.55	8.78	10.56
6	199	8.15	8.46	191.90	207.92	57.04	82.20	62.04	85.24	4.42	4.44	5.21	4.46	39.35	37.84	8.43	9.72
7	121	10.21	10.62	163.96	213.51	55.84	75.80	61.24	76.38	4.22	4.60	4.52	2.36	39.57	40.48	9.32	9.51
8	164	9.13	9.53	180.80	197.48	70.44	89.35	74.11	91.86	4.44	4.80	3.65	3.69	39.39	40.21	7.28	9.07
9	182	9.19	9.62	182.31	185.66	60.26	72.93	67.12	76.94	4..4	4.64	4.60	4.58	40.03	37.44	9.71	9.08
10	189	8.07	8.46	158.94	186.02	61.64	58.72	58.68	56.94	4.46	4.44	5.09	5.21	39.61	40.30	8.53	10.01
11	153	10.89	11.42	179.14	203.66	56.76	70.66	59.33	69.14	4.50	4.41	3.87	2.76	38.32	40.52	8.44	10.53
12	214	9.34	9.83	156.82	172.81	51.42	52.85	54.86	56.72	4.47	4.52	4.52	3.97	39.33	38.58	8.49	10.57
13	123	10.64	11.23	172.08	214.16	57.32	77.73	61.98	76.56	4.46	5.26	4.00	3.55	38.95	40.11	9.74	9.14
14	120	10.60	11.19	163.94	213.33	56.9	77.78	62.08	81.34	3.46	4.45	5.31	4.01	39.58	39.94	8.78	9.04
15	185	7.96	8.43	173.68	160.38	58.11	47.10	62.72	47.32	4.50	4.56	3.54	4.92	39.32	39.78	8.32	10.97
16	113	12.51	13.36	174.58	204.88	58.98	73.08	62.51	88.96	3.48	4.34	5.29	3.41	39.62	37.54	9.57	9.07
17	110	19.22	20.59	180.46	202.42	63.56	83.03	68.58	85.98	3.60	4.33	4.57	4.48	39.65	39.56	7.45	8.97
18	85	7.62	8.19	161.76	182.44	56.32	59.84	65.46	64.64	4.46	5.44	5.74	4.26	38.29	37.41	7.69	8.46
19	94	12.36	13.36	171.24	204.58	66.54	84.05	65.94	86.98	4.36	5.42	4.21	4.72	39.42	40.01	7.61	9.26
20	206	9.76	10.58	159.86	182.62	60.90	78.15	66.32	73.56	4.42	3.98	3.15	3.22	38.62	39.33	8.74	9.54
21	72	10.16	11.04	160.68	187.90	56.42	80.98	62.92	75.96	4.50	4.60	3.59	4.28	38.25	38.79	9.63	9.82
22	75	9.29	10.13	158.51	200.42	56.72	73.50	62.90	75.02	4.46	4.36	4.21	5.04	40.15	39.59	9.64	9.53
23	180	7.25	7.93	180.58	207.32	69.34	80.78	79.14	86.86	5.12	3.66	5.49	2.96	39.23	39.55	7.81	9.45
24	196	10.53	11.55	172.50	207.46	56.12	73.08	62.72	77.24	4.46	4.36	3.93	4.25	39.90	40.13	8.58	9.34
25	162	10.42	11.46	176.52	167.21	57.30	78.70	60.34	86.74	4.40	4.42	4.93	4.16	39.98	40.63	8.27	10.94
	CD (5%)	3.99	7.24	10.75	24.37	5.41	16.60	4.81	14.59	4.98	7.69	1.002	0.78	1.13	1.91	1.35	1.61
	CV	14.91	18.14	2.46	4.74	3.58	8.27	2.94	7.04	4.54	6.69	8.94	7.23	1.11	1.87	6.12	6.53

Genotypic and phenotypic coefficient of variation

Here in this study, the phenotypic variances were found to be significantly higher than the genotypic variances under both conditions thus reflecting the role of environmental factors on character expression. In addition, the differences between the phenotypic and genotypic variances were found to be very narrow as expected in augmented designs and because of these narrow difference between the variances, high heritability values were recorded which further gave higher GA estimates (Table 2). Similar observations were also reported earlier in oilseed Brassicas by various workers (Singh *et al.,* 2013, Bind *et al.,* 2014; Synrem *et al.,* 2014). Besides genetic advance, variability and heritability are the two important factors for an effective selection programme which plays a crucial role in assessing the expected improvement in a character (Nadarajan and Gunasekaran, 2005). It is reported that genetic variability, high heritability assisted with high genetic advance are normally more helpful to improve seed yield (Aytaç and Kinaci, 2009).

Under normal conditions, GCV varied from 1.45 (oil content) to 27.46 (HI) while it was 1.63 (oil content) to 22.54 (SY/plant) for water deficit conditions. The maximum PCV was estimated for SY/plant (26.97%) while it was lowest for oil content (1.96%) under drought conditions whereas it ranged from 2.36% (oil content) to 34.22% (HI) in irrigated conditions (Table 2). In this study, high heritability estimates (>50%) were recorded for almost all the characters. High heritability and high genetic advance combinations were reported for seed yield/plant (65.50%, 41.66%) and HI (64.42%, 45.39%), in irrigated conditions while it was (71.58%, 37.05%) for HI and (69.71%, 38.74%) for SY/plant under stress conditions indicating that selection would be highly effective in the present material for these characters (Table 2). Similar levels of heritability and genetic advance for different characters have already been reported earlier in Brassicas (Bind *et al.,* 2014; Iqbal *et al.,* 2014; Semahegn and Tesfaye, 2016).

Correlation coefficient

As seed yield is a complex trait, interactions and inter-relationships between yield and its components are important for selection of germplasm (Grafius 1964). We reported significant and positive correlations between seed yield and other morphological characters which ranged from 0.150* to 0.886**. Seed yield per plant was significantly and positively correlated with plant height (0.243**), FZL (0.203*), BY/plant (0.444**), seed/siliquae (0.343**), MSL (0.232**) and HI (0.790*). Hence, selection for the higher values of these traits would be desirable for increasing the seed yield. SY/plant was significantly and negatively correlated with OC (-0.224**) and fibre (-0.213**). In addition, PH showed positive and significant correlations with MSL (0.463**), BY/plant (0.441**), FZL (0.556**), seed/ siliqua (0.463**), HI (0.195**) and Phenol (0.150*). MSL was found to be positively correlated with FZL (0.886**), seed/siliquae (0.431**) and BY/plant (0.384**). HI was significantly positively associated with seed/siliquae (0.255**), BY/plant (0.389**) and seed yield/plant (0.790**). Thus, such correlations between different yield attributing traits revealed the mutual relationship between two or more characters. Such type of reports have ben also observed earlier by many workers (Singh *et al.,* 2010; Yadav *et al.,* 2011; Misra 2012).

Conclusion

The yield and yield components were reduced significantly due to water deficit. Seed yield per plant under stress could be improved by improving siliqua length, no. of siliqua per plant, 1000-seed weight etc. The 25 promising lines identified can be further used in the brassica breeding programmes to develop drought tolerant brassica varieties with desirable traits which will ultimately further enhance breeding efficiency. Moreover, the RIL population developed in this study may serve as a useful genetic resource for mapping genes/QTLs for seed yield or other related traits.

REFERENCES

Aytac, Z. and Kinaci, G. 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). *Afr. J. Biotech*., 8(15): 3547-3554.

Bind, D., Singh, D., Dwivedi, V.K. 2014. Genetic variability and character association in Indian mustard [*Brassica juncea* (L.) Czerns & Coss]. *Agric. Sci. Digest,* 34:183-188.

Chauhan, J.S., Tyagi, M.K., Kumar, A., Nashaat, N.I., Singh, M., Singh, N.B., Jakhar, M.L., Welham, S.J. 2007. Drought effects on yield and its components in Indian mustard (*Brassica juncea* L.). *Plant Breed.,* 126: 399-402.

Federer, W.T. 1956. Augmented designs. *Hawaian Planters Record,* 20:191-207.

Gholipouri, A., Sedghi, M., Sharifi, R.S., Nazari, N.M. 2009. Evaluation of drought tolerance indices and their relationship with grain yield in wheat cultivars. *Recent Res. Sci. Technol.*. 1(4): 195-198.

Golabadi, M.A., Arzani, S.A., Maibody, M. 2006. Assessment of drought tolerance in segregating populations in durum wheat. *Afr. J. Agric. Res.,* 1(5): 62-171.

Grafius, J.E. 1964. A geometry for plant breeding. *Crop Sci.,* 4: 242-248.

Gupta, R.K., Dwivedi, V.K. and Meena, B. 2015. Genetic divergence analysis for seed yield parameters and oil content in Indian mustard [*Brassica juncea* (L.) Czern Coss]. *Indian Res. J. Genetics Biotech.,* **7**: 84-86.

Iqbal, S., Haque, S., Nath, U.K. and Hamim, I. 2014. Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes, *International J. Agril. Sci. Res.*, 3(8): 141-156.

Kumar, A. and Singh, D.P. 1998. Use of physiological indices as a screening technique for drought tolerance in oilseed *Brassica* species. *Ann. Bot.,* 8: 413-420.

Laila, F., Farhatullah, Shah, S., Iqbal, S., Kanwal, M. and Ali, S. 2014. Genetic variability studies in brassica F2 populations developed through inter and intra-specific hybridization. *Pak. J. Bot*., 46(1): 265-269.

Meena, H.S., Kumar, D. and Singh, R.P. 2014. Genetic variability and character association in bread wheat (*Triticum aestivum*). *Indian J. Agril. Sci.,* 84:487-491.

Misra, A.K. 2012. Genetic variability and correlation studies on germplasm of yellow *sarson* (*B. rapa* L. var. yellow *sarson*) for seed yield and its component traits. *Cruciferae Newsletter,* 31:46-50.

Nadarajan, N. and Gunasekaran, M. 2005. Quantitative genetics and biometrical techniques in plant breeding. Kalyani Publication Ludhiana. pp 258.

Semahegn, Y. and Tesfaye, M. 2016. Variability, Heritability and Genetic Advance Analysis for some Morphological Characters in Oilseed Brassica Breeding Lines. *Molecular Plant Breeding*, 7(20): 1-8 (doi: 10.5376/mpb.2016.07.0020).

Shah, K.A., Farhatullah, Shah, L., Ali, A., Ahmad, Q. and Zhou, L. 2015. Genetic variability and heritability studies for leaf and quality characters in flue cured virginia tobacco. *Acad. J. Agric. Res*., 3(3): 044-048.

Sharafi, Y., Majidi, M.M., Jafarzadeh, M. and Mirlohi, A. 2015. Multivariate analysis of genetic variation in winter rapeseed (*Brassica napus* L.) cultivars. *J. Agril. Sci. Tech*., 17(4): 1319-1331.

Sidra, I., Farhatullah, Shah, S., Kanwal, M., Fayyaz, L. and Afzal, M. 2014. Genetic variability and heritability studies in indigenous *Brassica rapa* accessions. *Pak. J. Bot*., 46(2): 609-612.

Singh, A., Avtar, R., Singh, D., Sangwan, O., Balyan, P. 2013. Genetic variability, character association and path analysis for seed yield and component traits under two environments in Indian mustard. *J. Oilseed Brassica,* 4:43-48.

Singh, V.V., Gurjar, N., Ambawat, S., Yadav, S., Singh, B.K., Ram, B., Meena, M.L., Singh, B.R., Singh, S., Singh, D. 2016. Morphological and molecular diversity among full-sib progenies of Indian mustard (*Brassica juncea* L.). *SABRAO J. Breeding Genet.,* 48(2): 180-188.

Singh, V.V., Meena, S.S., Yadav, R, Srivastava, N., Kumar, A. 2010. Genetic variation and character association in F_6 progenies of interspecific crosses between *Brassica juncea* and *B. carinata. Indian J. Plant Genet. Resour.* 23:168-171.

Supriya, Priyamedha, Singh, B.K., Ram, B., Kumar, A., Singh, V.V., Singh, M.L. and Singh, D. 2014. Development and evaluation of double low quality lines in Indian mustard (*Brassica juncea* L. Czern & Coss). *SABRAO J. Breeding and Genet.,* 46:274-283.

Synrem, G.J., Rangare, N.R., Myrthong, I. and Bahadure, D.M. 2014. Variability studies in Intra specific crosses of Indian mustard [*Brassica juncea* (L.) Czern and Coss.]

genotypes, *IOSR J. Agril. Veterinary Sci*., 7: 29-32 http://dx.doi.org/10.9790/2380-07932932

Tripathi, N., Kumar, K. and Verma, O.P. 2015. Genetic Variability, Heritability and Genetic Advance in Indian Mustard (*Brassica juncea* L. Czern and Coss.) for Seed Yield and it's Contributing Attributes Under Normal and Saline/Alkaline Condition. *International J. Sci. Res.* 4(8): 983-985.

Ullah, N., Farhatullah, Rahman, H., Fayyaz, and Amin, N. 2015. Genetic variability among advanced lines of brassica *Pak. J. Bot.,* 47(2): 623-628.

Ullah, U., Raziuddin, Fakharuddin, Ullah, I., Ul Haq, M.M., Ataullah, Razi, M.J., Qamaruddin and Ahmed, S. 2016. Genetic Variability, Correlations and Heritability Estimates for Various Biochemical Traits in Rapeseed (Brassica napus L.) *Am-Euras. J. Agric. & Environ. Sci.,* 16 (3): 594-559.

Verma, S., Singh, V.V., Meena, M.L., Rathore, S.S., Ram, B., Singh, S., Garg, P., Gurjar, N., Ambawat, S. and Singh, D. 2016. Genetic analysis of morphological and physiological traits in Indian mustard (B*rassica juncea* L.). *SABRAO J. Breeding Genet.*, 48 (4) 391-401.

Yadava, D.K., Giri, S.C., Vignesh, M., Vasudev, S., Yadav, A.K., Dass, B., Singh, R., Singh, N., Mohapatra, T. and Prabhu, K.V. 2011. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian J. Agri. Sci.* 81:712-716.

Zhao, C.X., Guo, L.Y., Jaleel, C.A., Shao, H.B. andYang, H.B. 2008. Prospects for dissecting plant-adaptive molecular mechanisms to improve wheat cultivars in drought environments. *Comptes. Rendus Biologies* 331: 579-586.

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