



Genetic analysis of F₂ Indian mustard (*Brassica juncea* L.) lines for drought tolerance

Shivam Raina*, SK Rai, Bupesh Kumar, Ashish Sheera, Radheshyam Kumawat

Division of Plant Breeding and Genetics, She-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Main Campus, Chatha, 180009, Jammu (J&K), India.

*Corresponding author: shivamisrk96@gmail.com

(Received: 25 December 2022; Revised: 28 December 2022; Accepted: 30 December 2022)

Abstract

The genetics of morphological and biochemical determinants of drought tolerance in sixteen genotypes and their F₂ population was investigated. Analysis of variance revealed significant differences among parents and F₂ population for all the traits recorded in both E₁ and E₂. Estimates of genetic parameters for traits viz., main shoot length, number of siliquae per plant for E₁ and days to 50% flowering, number of secondary branches for E₂ environments were found to have high heritability coupled with high genetic advance. Estimates of genetic parameters from the pooled data of the environments also revealed that traits like plant height, main shoot length and number of siliquae per plant have high heritability coupled with high genetic advance thereby, indicating effectiveness of these traits in selection. Estimation of proline content in leaves at flowering stage was analysed to evaluate the maximum stress tolerant cross combinations. Similarly, results for Drought Susceptibility Index (DSI) revealed that parents RB-77, RB-24, RB-69 and cross combinations DRMR-4006 x RB-24 followed by PM-25 x RB-24 and RH-749 x PM-25 were found to be tolerant. Hence, these lines may be used for further improvement of drought tolerance breeding program in Oilseed Brassica.

Keywords: Drought Susceptibility Index, Heritability, Indian Mustard, Proline

Introduction

Rapeseed-mustard group of crops belongs to the family Brassicaceae are the third most important oilseed crop after soyabean and palm in terms of oil seed production. Globally, it accounts for an estimated area of 36.59 million hectares with production and yield of 72.37 million tonnes and 1980 kg/ha, respectively (USDA, 2018-19). In India, being the second most important oilseed crop, next to soybean it accounts for 19.8% and 9.8% of the total area and production (Anonymous, 2020-21). In J&K UT total area is 51870 ha with production of 37000 metric tonnes which shares a 0.43% of the total production in India (Anonymous, 2020-21). Among all cultivating species of rapeseed-mustard, Indian mustard (*Brassica juncea* L.) covers about 80% of the total cultivated area in India because of its wider adaptability and high yielding performance (Priyamedha *et al.*, 2014). Genome wise it is an amphidiploid (2n= 36; AABB) derived from inter specific crossing and natural chromosomal doubling of *B. nigra* (2n= 16; BB) and *B. rapa* (2n=20; AA) (Srivastava *et al.*, 2001). As predominantly consumed for edible oil and livestock feed it has a huge potential for cultivation in semi-arid regions because it is known for more drought tolerant and shattering resistant crop than *B. napus* and *B. rapa* (Vinu *et al.*, 2013). Due to increase in per capita oil consumption, growing population and rising living

standards it is urgently necessary to use genetic interventions to boost yield potential of *B. juncea* in order to meet the current oil demand. Among all the abiotic stress, drought plays a significant role in reducing the physiological growth and restricts complete expression of the genes. Mustard genotypes which have drought tolerant traits, will perform better under water limited conditions as compare to genotypes which do not have desired drought tolerant traits. Indian mustard, is mostly grown as rainfed crop, resulting in occurrence of drought stress results in productivity loss ranging from 17-94 % (Luo *et al.*, 2014). For increasing yield in of mustard under adverse climatic conditions, drought tolerant varieties need to develop, which are least effected by drought and can survive well in abiotic stress conditions (Zhao *et al.*, 2008). Keeping all in view, an investigation was carried out with the aim to study the genetics of morphological and biochemical determinants in Indian mustard.

Materials and Methods

The experimental material includes 45 genotypes of Indian mustard, including 16 genotypes used as parents and 29 F₂ segregants of different cross combinations. Parental material used in the experimental material were brought from different sources. The experimental study was carried

out at Advanced Centre for Rainfed Agriculture (ACRA), Dhiansar in rainfed environmental conditions (E_1) and Experimental Research Area of Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu (SKUAST-J) in irrigated conditions (E_2) during 2021-22. Recommended package of practice was followed for raising good crop. The morphological observations *viz.*, days to 50 percent flowering, number of primary branches per plant, number of secondary branches, plant height, main shoot length, number of siliquae on main shoot, siliqua length, number of seeds per siliqua, days to maturity, seed yield per plant, 1000 seed weight, harvest index and Drought Susceptibility Index (DSI) were observed for the different traits in two different environments according to Fischer and Maurer (1978) to differentiate the average performance of yield of different cultivars in stress and non-stress environment. Moreover, biochemical estimation of proline content was measured for each genotype using the method given by Bates *et al.*, 1973.

Results and Discussion

The observations of morphological and biochemical were recorded and statistically analyzed to estimate analysis of variance, estimation of genetic variability parameters, estimation of proline and estimation of Drought Susceptibility Index (DSI).

Analysis of variance: Analysis of variance for different traits for environments E_1 , E_2 and Pooled. In E_1 all traits were found significant at 5% significant level except for 1000 seed weight and in E_2 except plant height, main shoot height and 1000 seed weight all were found significant at 5% significant level (Table 1). Similarly, pooled analysis of variance for all the traits of genotypes were found significant at 5% significant level. The presence of significant amount of genetic variations among lines may be due to inherent variations in the parents being hybridized. Similar results were obtained in study of Vinu *et al.*, 2013; Chaurasiya *et al.*, 2018 and Hyder *et al.*, 2021.

Genetic variability parameters: For estimation of genetic parameters, genotypic and phenotypic coefficient of variation was calculated, results revealed maximum genotypic and phenotypic coefficient of variation was observed for number of secondary branches in both the environment E_1 and E_2 indicating that equal influence of these in the expression of this trait (Table 2). Similar results were found by Yadav *et al.*, 2011 and Anand *et al.*, 2020. Moderate estimates of coefficient of variation (PCV and GCV) were observed for traits *viz.*, number of primary branches per plant and number of siliquae in E_1 and number of primary branches, number of seeds per siliqua and 1000 seed weight in E_2 , indicating additive gene action

Table 1: ANOVA for different morphological traits in Indian Mustard (*Brassica juncea*)

Environ-ment	Source	Degree of freedom	Days to 50% flowering	Number of primary of branches per plant	Number of secondary branches per plant	Plant height (cm)	Main shoot length (cm)	Number of siliquae on main shoot	Siliqua length (cm)	Seed per siliqua	Days to maturity	Seed yield per plant (g)	1000 Seed weight (g)	Harvest index (%)
E1 Rainfed	Replication	2	3.11	0.36	3.78	15.11	2.30	2.60	0.87	1.86	3.58	2.69	0.83	0.56
	Genotype	44	3.64*	2.34*	2.61*	99.42*	26.56*	14.05*	0.40*	6.71*	20.75*	4.87*	0.89**	6.30*
	Error	88	1.05	0.47	0.58	26.71	3.73	3.38	0.12	2.56	5.44	1.59	0.29	2.01
E2 Irrigated	Replication	2	0.27	0.42	0.09	82.81	14.06	89.82	0.09	7.31	3.31	1.29	0.05	0.96
	Genotype	44	17.79*	3.45*	15.40*	191.09**	78.54**	68.55*	0.15*	12.07*	14.81*	5.77*	0.42**	8.01*
	Error	88	2.88	0.83	1.95	70.46	27.11	15.76	0.03	3.06	3.84	1.19	0.15	2.67
Pooled (E1+E2)	Replication	2	0.91	0.54	2.23	83.03	2.97	31.58	0.22	6.95	6.71	0.32	0.48	1.42
	Genotype	44	30.37*	5.37*	55.24*	9212.15*	1263.46*	612.40*	0.22**	9.00*	20.38*	39.52*	2.30*	12.08*
	Error	220	3.57	0.78	1.73	104.71	27.63	18.34	0.08	3.2	6.74	1.74	0.21	3.24

**, * represents significance level at 1% and 5 % respectively

Table 2: Estimates of genetic parameters for different morphological traits under rainfed, irrigated & pooled basis

Environ- ment	Genetic Parameters	Days to 50% flowering	Number of primary branches	Number of secondary branches per plant	Plant height (cm)	Main shoot length (cm)	Number of siliquae on main shoot (cm)	Siliqua length (cm)	Seed per siliqua	Days to maturity	Seed yield per plant	1000 Seed weight (g)	Harvest index (%)
E1 (Rainfed)	PC.V.	1.30	14.13	20.03	4.9	6.3	10.31	7.01	9.88	1.91	8.67	9.31	6.80
	GCV.	0.78	11.36	17.63	3.1	5.8	8.99	4.37	6.67	1.64	3.36	6.29	4.65
	Heritability (%)	36.18	64.61	77.49	41.19	85.93	75.94	38.88	45.66	73.75	63.56	70.01	62.14
	Genetic Advance	0.55	0.89	1.49	4.36	5.26	3.38	0.20	1.17	3.99	0.24	0.39	1.15
	Genetic Advance (%) Mean	0.97	18.8	31.97	4.22	11.21	16.13	5.61	9.29	2.91	2.68	8.75	6.55
	PC.V.	4.02	10.99	23.08	4.34	6.61	7.96	4.09	15.90	1.61	9.98	10.70	8.34
E2 (Irrigated)	GCV.	3.68	7.19	21.56	3.37	5.05	3.40	3.00	13.75	1.38	8.89	9.41	6.81
	Heritability (%)	83.77	42.85	87.28	60.31	58.25	46.90	53.56	74.59	74.01	79.35	77.26	66.67
	Genetic Advance	4.20	0.61	4.07	9.75	5.98	1.22	17.64	3.08	3.38	2.26	0.59	2.24
	Genetic Advance (%) Mean	6.94	9.70	41.50	5.39	7.94	3.00	4.52	24.43	2.45	16.31	17.04	11.45
	PC.V.	3.83	17.08	41.92	27.58	23.72	32.73	5.11	9.76	1.34	22.30	15.37	7.63
	GCV.	3.60	15.79	41.26	27.42	23.46	32.24	3.96	7.37	1.09	21.80	14.62	6.52
Pooled (E1+E2)	Heritability (%)	88.22	85.42	96.85	98.86	97.81	97.00	59.94	58.05	66.96	95.58	90.50	73.15
	Genetic Advance	4.08	1.66	6.05	79.80	29.23	20.18	0.24	1.46	2.54	5.05	1.15	2.13
	Genetic Advance (%) Mean	6.96	30.06	83.65	56.16	47.80	65.42	6.32	11.57	1.84	43.91	28.65	11.50

Table 3: Concentration of proline accumulation ($\mu\text{mol g}^{-1}\text{FW}$) under rainfed and irrigated conditions

S.No.	Genotypes	Irrigated (IR)	Rainfed (RF)	S.No.	Genotypes	Irrigated (IR)	Rainfed (RF)
1	DRMR-4006	0.86	1.19	24	PM-195x RB-24	0.85	1.22
2	RH-1209	0.84	1.16	25	PM-25x RB-24	0.78	1.19
3	RSPR-01	0.79	1.09	26	RB-77xRB-24	0.81	1.14
4	RB-24	0.74	1.12	27	DRMR-541-46x RB-24	0.82	1.18
5	JM12-6	0.72	1.07	28	PM-28x RB-24	0.85	1.23
6	DRMR541-46	0.82	1.11	29	DRMR-541xRH-761	0.77	1.11
7	Tawari	0.74	0.92	30	JM12-6xRH-761	0.88	1.22
8	RL-1359	0.75	1.09	31	RB-77x RH-761	0.84	1.2
9	RB-77	0.84	1.03	32	RH-1206x RH761	0.81	1.07
10	PusaBold	0.69	0.98	33	PusaBoldxRH-761	0.79	1.12
11	RH-761	0.78	1.16	34	PM-25x RH-761	0.74	1.09
12	PM-28	0.82	0.97	35	RSPR-01xRH-761	0.79	1.21
13	RH-749	0.83	1.08	36	JM-12-6xRH-761	0.81	1.07
14	Kranti	0.79	1.17	37	RB-69x RH-761	0.78	1.04
15	RB-66	0.77	1.03	38	RH-761x RB-69	0.78	1.15
16	PM-195	0.80	1.21	39	PM-28x RH-749	0.88	1.19
17	DRMR-4006x RB-24	0.9	1.3	40	Krantix RH-749	0.69	1.01
18	TawarixRB-24	0.89	1.22	41	Tawarix RH-749	0.77	1.12
19	RB-69xRB-24	0.88	1.25	42	RH-1209x RH-749	0.88	1.14
20	Krantix RB-24	0.78	1.09	43	RSPR-01xRH-749	0.86	1.17
21	RSPR-01xRB-24	0.81	1.21	44	RH-749x PM-25	0.79	1.11
22	DRMR-659x RB-24	0.87	1.23	45	PusaBoldxRH-741	0.75	1.06
23	PM-25x RB-24	0.76	1.06				

in such traits. Similar results were found by Singh *et al.*, 2004; Gupta *et al.*, 2019 and Anand *et al.*, 2020. Low value estimates of PCV and GCV in E_1 were present in days to 50% flowering, plant height, main shoot length, siliqua length, number of seeds per siliqua, seed yield per plant, 1000 seed weight and harvest index. Similarly, lowest PCV & GCV were observed in E_2 for traits *viz.*, days to 50% flowering, plant height, main shoot length, siliqua length, seed yield per plant and harvest index indicates that there is limited scope for improvement through selection. Similar findings were reported by Nandi *et al.*, 2021 and Tripathi *et al.*, 2019 for plant height. High estimates of broad sense heritability were observed in E_1 for the traits *viz.*, number of primary branches per plant, number of secondary branches per plant, main shoot length, number of siliquae, days to maturity, seed yield per plant and 1000 seed weight while in E_2 high heritability was observed in traits *viz.*, days to 50% flowering, number of secondary branches per plant, plant height, seeds per siliqua, days to maturity, seed yield per plant, 1000 seed weight and harvest index, indicates reasonable variation for these traits thus suggesting that selection can be practiced by using these traits. Similar findings were reported by Rai *et al.*, 2005; Singh *et al.*, 2013 and Gupta *et al.*, 2019. Moderate estimates of heritability were reported in traits *viz.*, plant height and seed per siliqua in E_1 . Similarly, in E_2 traits *viz.*, number of primary branches, main shoot length and number of siliquae on main shoot showed moderate heritability. Results showed similar

findings to Sandhu *et al.*, 2017; Tiwari *et al.*, 2017; Abe *et al.*, 2019 and Nandi *et al.*, 2021. In E_1 number of secondary branches show high genetic advance as percent of mean. In E_2 traits like number of secondary branches and seed per siliqua show high heritability with high genetic advance. These results are found similar with previous findings of Pant and Singh *et al.*, 2001; Ara *et al.*, 2013 and Gupta *et al.*, 2019. Moderate genetic advance as percent of mean was found in traits *viz.*, number of primary branches, main shoot length and number of siliquae in E_1 . Similarly, in E_2 traits like seed yield per plant, 1000 seed weight and harvest index also recorded with moderate genetic advance as percent of mean. Similar findings were reported by Anand *et al.* 2020. This suggested that these characteristics were less affected by environmental influences, which in turn suggested that these characteristics were largely under the control of genes that have either additive or additive x additive gene action and was expected to respond to direct selection for improvement means selection can be effective.

Estimation of proline: The proline content of 45 cultivars, under irrigated conditions ranged from 0.69 (Krantix RH-749) to 0.9 (DRMR-4006 x RB-24), whereas under rainfed conditions it ranged from 0.97 (PM-28) to 1.3 (DRMR-4006 x RB-24) (Table 3). Similar findings were recorded by Din *et al.*, 2011; Ali *et al.*, 2022.

Drought Susceptibility Index (DSI): DSI was calculated for using yield data of both the environments. DSI value of different cultivars was ranged from 0.77 (RB-77) to 1.26 (RB-77 x RH-761). Thirteen lines came under the category

of drought tolerant on the basis of categorization of DSI value; tolerant, moderate and susceptible (Table 4). Similar method to determine DSI was used by Singh *et al.*, 2003; Chauhan *et al.*, 2007; Singh *et al.*, 2018 and Ali *et al.*, 2022.

Table 4 Drought Susceptibility Index (DSI) of different cultivars of *Brassica juncea*

Cultivars	Rainfed (RF)	Irrigated (IR)	DSI Ascending order	DSI range	Remarks
RB-77	0.84	1.03	0.45	<0.6	Tolerant
DRMR-4006x RB-24	0.9	1.30	0.46		
RB-24	0.74	1.12	0.53		
RB-66	0.84	1.16	0.56		
RH-1209	9.63	13.63	0.56		
PM-25x RB-24	0.78	1.19	0.61		
RH-749x PM-25	0.79	1.11	0.61		
DRMR-54x RB-24	0.87	1.23	0.63		
JM-12-6	0.72	1.07	0.64		
RB-66xRB-24	0.88	1.25	0.64		
PM-195	0.80	1.21	0.65		
PM-28	0.82	0.97	0.65		
JM-12-6xRH-761	0.81	1.07	0.67		
PM-195x RB-24	0.85	1.22	0.69	0.7-1.10	Moderate
JM12-6xRH-761	0.88	1.22	0.70		
RB-24XPM-25	0.76	1.06	0.70		
PusaBoldxRH-741	0.75	1.06	0.72		
TawarixRB-24	0.89	1.22	0.74		
RSPR-01xRH-749	0.86	1.17	0.75		
RSPR-01xRH-749	0.86	1.17	0.75		
DRMR-659-46x RB-24	0.82	1.18	0.78		
RH-749	0.83	1.08	0.79		
KrantixRB-24	0.78	1.09	0.81		
Tawarix RH-749	0.77	1.12	0.82		
RSPR-01xRH-761	0.79	1.21	0.85		
RH-761	0.78	1.16	0.86		
PusaBoldxRH-761	0.79	1.12	0.88		
RSPR-01xRB-24	0.81	1.21	0.89		
Kranti	0.79	1.17	0.91		
PM-28x RH-749	0.88	1.19	0.92		
RH-1206x RH761	0.81	1.07	0.98		
PM-28x RB-24	0.85	1.23	0.98		
PM-25x RH-761	0.74	1.09	0.99		
RH-761x RB-66	0.78	1.15	0.99		
RL-1359	0.75	1.09	1.01		
RB-77xRB-24	0.81	1.14	1.01		
DRMR4006	0.86	1.19	1.10		
Krantix RH-749	0.69	1.01	1.04		
RH-1209xRH-749	0.88	1.14	1.17		
RH-1209x RH-749	0.88	1.14	1.17		
DRMR-51xRH-761	0.77	1.11	1.18		
Tawari	0.74	0.92	1.19		
RB-66x RH-761	0.78	1.04	1.26	dd1.2	Susceptible
RB-77x RH-761	0.84	1.20	1.26		
RB-77x RH-761	9.69	15.54	1.26		
PusaBold	9.23	15.27	1.37		

Conclusion

On the basis of parameters taken into consideration parents RB-77, RB-24, RB-66, PM-195, PM-28 and crosses DRMR-4006 x RB-24, PM-25 x RB-24, RH-749 x PM-25, DRMR-51 x RB-24, RB-66 x RB-24 and JM-12-6 x RH-761 can further be exploited after ascertaining their drought tolerant ability in future generations.

References

- Abe A and Adelegan CA. 2019. Genetic variability, heritability and genetic advance in shrunken-2 super-sweet corn (*Zea mays* L. *saccharata*) populations. *J Plant Breed Crop Sci* **11**:100-105.
- Ali Z. and Rai SK. 2022. Drought susceptibility index analysis in Indian mustard (*B. juncea*). *J Oil seeds Res* **13**:136-142.
- Anand L, Girish T, Aditi E and Kartikeya S. 2020. Genetic variability and trait associated studies in Indian mustard (*B. juncea*) using microsatellite markers. *Int. J Curr Microbiol Appl Sci* **9**: 2556-2563.
- Anonymous. 2020-21. Directorate of Economics & Statistics. Ministry of Agriculture and Farmers Welfare, Govt. of India
- Ara S, Afroz S, Noman MS, Bhuiyan, MSR and Zia MIK. 2013. Variability, correlation and path analysis in F₂ progenies of inter-variety crosses of *Brassica rapa*. *Int J Environ Sci Nat* **6**: 217-220.
- Bates LS, Waldren RA and Teare ID. 1973. Rapid determination of free proline for water-stress studies. *Plant Soil Environ* **39**: 205-207.
- Chauhan JS, Tyagi MK, Kumar A, Nashaat NI, Singh M, Singh, NB, Jakhar ML and Welham SJ. 2007. Drought effects on yield and its components in Indian mustard (*B. juncea*). *Plant Breed* **126**:399-402.
- Chaurasiya JP, Singh M, Yadav RK, Singh L and Yadav HC. 2018. Genetic analysis for estimates components of genetic variance in Indian mustard (*B. juncea*). *J Pharm Innov* **7**:104-107.
- Din J, Khan SU, Ali I and Gurmani AR. 2011. Physiological and agronomic response of Canola varieties to drought stress. *J Anim Plant Sci* **21**:78-82.
- Fischer RA and Maurer R. 1978. Drought resistance in spring wheat cultivars. I. Grain yield responses. *Aust J Agric Res* **29**:897-912.
- Gupta MC, Roy HS and Bhadauria SS. 2019. Genetic variability analysis in F₂/F₃ population derived through inter-specific hybridization in oilseed *Brassica*. *Electron J Plant Breed* **10**:1275-1282.
- Hyder A, Iqbal AM, Sheikh FA, Wani MA, Nagoo S, Khan MH and Dar ZA. 2021. Genetic variability studies for yield and yield attributing traits in Gobhi Sarson (*B. napus*) genotypes under temperate ecology of Kashmir. *J Oilseeds Res* **12**:44-48.
- Luo G, Zhang J and Guo W. 2014. The role of Sec3p in secretory vesicle targeting and exocyst complex assembly. *Mol Biol Cell* **25**:3813-3822.
- Nandi S, Rout S, Sur B, Chakraborty M, Hijam L, Roy SK and Gupta A. 2021. Assessment of genetic parameters, trait association and diversity analysis in Indian mustard (*B. juncea*). In *Biological Forum–An Intl J* **13**:95-109.
- Pant SC and Singh P. 2001. Genetic variability in Indian mustard. *Agric Sci* **21**:28-30.
- Priyamedha S, Singh BK, Ram B, Kumar A, Singh VV, Meena ML and Singh D. 2014. Development and evaluation of double low quality lines in Indian mustard (*B. juncea*). *Sabrao J Breed Genet* **46**: 274-283.
- Rai SK, Verma A, and Pandey DD. 2005. Genetic variability and character association analysis in Indian mustard (*B. juncea*). *Ann Agri Bio Res* **10**:29-34.
- Singh A, Avtar R, Singh D, Sangwan O and Balyan P. 2016. Genetic variability, character association and path analysis for seed yield and component traits under two environments in Indian mustard. *J Oilseeds Res* **1**:43-48.
- Singh B. 2004. Character association and path analysis under dry land condition in Indian mustard (*B. juncea*). *Cruciferae Newsl* **25**:99-100.
- Singh SP and Choudhary AK. 2003. Selection criteria for drought tolerance in Indian mustard (*B. juncea*). *Indian J Genet Plant Breed* **63**:263-264.
- Singh VV, Garg P, Meena HS and Meena ML. 2018. Drought stress response of Indian mustard (*B. juncea*) genotypes. *Int J Curr Microbiol App Sci* **7**:2519-2526.
- Srivastava A, Gupta V, Pental D and Pradhan AK. 2001. AFLP-based genetic diversity assessment amongst agronomically important natural and some newly synthesized lines of *B. juncea*. *Theor Appl Genet* **102**:193-199.
- Tiwari AK, Singh SK, Tomar A and Singh M. 2017. Heritability, genetic advance and correlation coefficient analysis in Indian mustard (*B. juncea*). *J Pharmacogn Phytochem* **6**:356-359.
- Tripathi N, Kumar K, Tiwari R and Verma OP. 2019. Assessing genetic variability in Indian mustard (*B. juncea*) for seed yield and its contributing attributes under normal and saline/alkaline condition. *J Pharmacogn Phytochem* **8**:1322-1324.
- Vinu V, Singh N, Vasudev S, Kumar Yadava D, Kumar S,

- Naresh, S., Ramachandra Bhat, S. and Prabhu KV. 2013. Assessment of genetic diversity in *B.juncea* Brassicaceae genotypes using phenotypic differences and SSR markers. *Rev Biol Trop* **61**:1919-1934.
- Yadava DK, Giri SC, Vignesh M, Vasudev S, Kumar Yadav A, Dass B, Singh R, Singh N, Mohapatra T and Prabhu KV.2011. Genetic variability and trait association studies in Indian mustard (*B.juncea*). *Indian J Genet Plant Breed* **81**:712.
- Zhao CX, Guo LY, Jaleel CA, Shao, HB and Yang HB, 2008. Prospectives for applying molecular and genetic methodology to improve wheat cultivars in drought environments. *C R Biol* **331**:579-586.