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Genetic variability studies in doubled haploids of Ethiopian mustard (*Brassica carinata* A. Braun)

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Abstract

The doubled haploids of Ethiopian mustard (*Brassica carinata* A. Braun) were evaluated along with mustard under two environments during *rabi*, 2010-11. Analysis of variance for different traits such as days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, length of main shoot, siliquae on main shoot, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant, biological yield per plant, harvest index and per cent oil content revealed the presence of sufficient genetic variability for all characters except siliqua length and per cent oil content in Env. I. On the other hand in Env. II, the presence of sufficient genetic variability for most of the traits was observed. Pooled analysis over environments revealed the presence of *g x e* interactions for all characters except days to flower initiation and per cent oil content. The estimates of PCV were found to be higher than their corresponding GCV for all characters. In pooled over the environments, high PCV values were observed for siliquae per plant and harvest index. The estimates of GCV were found to be moderate for siliquae per plant. High heritability values were observed for days to 50 per cent flowering followed by days to 75 per cent maturity and days to flower initiation. Expected genetic advance expressed as per cent of mean were moderate for siliquae per plant followed by 1000-seed weight, days to flower initiation and plant height.

Keywords: Ethiopian mustard, GCV, PCV, heritability, genetic advance

Introduction

Oilseed crops are the backbone of Indian agricultural economy and occupy an important position in daily diet, being a rich source of fats and vitamins. India is the second largest rapeseed-mustard growing country and accounts for 21.7% area in the world after China. Among oilseeds, rapeseed-mustard is the second most important oilseed crop of the country after groundnut and plays a significant role in Indian oil economy by contributing about 28.6% to the total oilseed production (Shekhawat *et al.*, 2014) ^[10].

Rapeseed-mustard is the third important oilseed crop in the world after soybean (*Glycine max*) and palm (*Elaeis guineensis* Jacq.). The crop occupies an area of 33.58 million ha with a total annual production of 67.76 million tonnes and productivity 2018 kg/ha. In production, India ranks third after China (22.9%) and Canada (19.7%). The global production of rapeseed-mustard oil is around 12-14 million tonnes. In India, the crop occupies an area of 6.50 million ha with a total production of 6.80 million tonnes and productivity of 1046 kg/ha (Anonymous 2016) ^[1].

Rapeseed-mustard in general, has shown a declining trend both in acreage and production largely due to lack of suitable cultivars for different ecosystems, fluctuations in weather conditions, cultivation in marginal and sub marginal lands and prevalence of various abiotic and biotic stresses. The present day varieties are more susceptible to *Alternaria* blight and white rust. Hence, the most suitable alternate way to increase productivity is by adoption of high yielding, input responsive genotypes having resistance against various biotic and abiotic stresses. The success of any breeding programme depends upon the nature and magnitude of variability present in the germplasm stock. The chances of initiating an effective breeding programme are greater if more genetic variability is available with the plant breeder. Thus, studies on parameters of genetic variability *viz.*, phenotypic and genotypic coefficients of variation, heritability and genetic advance are of paramount importance. Therefore, an attempt was made in the present study to estimate the nature and extent of genetic variability on Ethiopian mustard.

Materials and Methods

The materials for the present investigation comprised of 33 genotypes including 28 doubled haploids (DH) obtained through anther culture technique, one advanced breeding line (P-138)

And four (3 mustard and 1 Karan Rai) check varieties viz., Nav Gold, RCC-4, Pusa Jaikisan and Jayanti. The doubled haploids were obtained from the cross Jayanti x RCC-6-1 developed in the Department of Agricultural Biotechnology, CSK HPKV, Palampur. All the genotypes were raised at the experimental farm of Department of Crop Improvement, CSK HPKV, Palampur in randomized complete block design with three replications in the plot size of $3.0 \times 0.60 \text{ m}^2$ on two different sowing dates viz., 12th October, 2010 (Env. I) and 29th October, 2010 (Env. II). The row to row and plant to plant spacings were kept at 30cm and 15cm, respectively. The recommended cultural practices were followed to raise the crop. Data were recorded on various traits viz., days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, siliquae per plant, length of main shoot (cm), siliquae on main shoot, siliqua length (cm), seeds per siliqua, 1000-seed weight, seed

yield per plant, biological yield per plant, harvest index (%) and percent oil content. The data were analysed statistically as per the method of Panse and Sukhatme (1985) [7]. Genetic parameters (PCV, GCV, H²bs and GA) were calculated as suggested by Burton and De Vane (1953) [2] and Johnson *et al.* (1955) [4].

Results and Discussion

Analysis of variance indicated the presence of sufficient genetic variability for all characters except siliqua length and per cent oil content in Env. I (Table 1). In Env. II, the presence of sufficient genetic variability for days to flower initiation, days to 50 per cent flowering, days to 75 per cent maturity, plant height, number of primary branches per plant, number of secondary branches per plant, siliquae per plant, 1000-seed weight, seed yield per plant and harvest index was observed.

Table 1: Analysis of variance for different characters of *Brassica carinata* in Env. I and Env. II

Sr. No.	Characters	Env. I		Env. II		
		Mean Squares				
		Source	Genotypes	Error	Genotypes	Error
		df	32	64	32	64
1	Days to flower initiation		153.08**	10.87	203.82**	37.03
2	Days to 50% flowering		68.91**	8.33	198.81**	8.43
3	Days to 75% maturity		189.79**	8.94	119.96**	44.47
4	Plant height (cm)		2318.26**	207.41	226.03*	117.46
5	Number of primary branches /plant		2.60**	0.57	2.19**	1.08
6	Number of secondary branches /plant		7.44**	0.97	7.8**	3.92
7	Siliquae/ plant		3703.66**	666.21	8929.05**	2579.37
8	Length of main shoot (cm)		127.24**	23.73	48.36	37.67
9	Siliquae on main shoot		180.78**	35.26	45.55	41.95
10	Siliqua length (cm)		0.263	0.217	0.23	0.160
11	Seeds /siliqua		2.36*	0.87	2.43	2.08
12	1000-seed weight (g)		1.15**	0.10	0.20*	0.11
13	Seed yield /plant (g)		7.36**	1.42	3.54**	1.47
14	Biological yield /plant (g)		140.18**	34.49	68.41	64.92
15	Harvest index (%)		44.47**	19.81	71.77*	39.51
16	Oil content (%)		11.54	12.56	12.75	15.50

* And **indicate significance at $P \leq 0.05$ and 0.001 , respectively

Pooled analysis over environments revealed the presence of g x e interactions for all characters except days to flower initiation and per cent oil content (Table 2).

Table 2: Analysis of variance for different characters of *Brassica carinata* in pooled over the environments

Sr. No.	Characters	Mean Squares				
		Source	Genotypes	Environments	Genotype x Environment (g x e)	Pooled error
		Df	32	1	32	128
1	Days to flower initiation	337.18**	255.68**	17.72	23.95	
2	Days to 50% flowering	235.09**	147.68**	32.63**	8.38	
3	Days to 75% maturity	264.37**	6.55	45.38**	10.21	
4	Plant height (cm)	1322.76	15254.73**	1221.53**	162.43	
5	Number of primary branches / plant	1.52	20.97**	3.27**	0.82	
6	Number of secondary branches / plant	7.57	250.26**	7.67**	2.44	
7	Siliquae /plant	7940.97	1426.19	4691.74**	1622.49	
8	Length of main shoot (cm)	90.82	955.68**	84.79**	30.70	
9	Siliquae on main shoot	93.19	3224.25**	133.14**	38.60	
10	Siliqua length (cm)	0.23	0.44	0.323*	0.20	
11	Seeds /siliqua	2.21	52.08**	2.58**	1.47	
12	1000-seed weight (g)	0.86*	0.19	0.48**	0.11	
13	Seed yield /plant (g)	3.64	0.05	7.25**	1.44	
14	Biological yield /plant (g)	105.19	251.16	103.41**	46.70	
15	Harvest index (%)	47.92	199.20	68.29**	29.70	
16	Oil content (%)	18.31**	81.08**	6.10	13.62	

* And **indicate significance at $P \leq 0.05$ and 0.01 , respectively

The presence of g x e interaction has greatly influenced the variation due to genotypes to the extent that genotypic differences recorded in individual environments have vanished for these characters. Zehra and Gukan (2009) [14] observed significant differences for plant height, number of branches per plant, number of pods per plant, pods per main stem, pod length, 1000-seed weight, seed yield per plant and per cent oil content in two environments. Yared *et al.* (2012) [13] also observed highly significant differences for days to flower initiation and days to maturity in Ethiopian mustard.

A wide range of variability was observed for all the characters studied. The high estimates of PCV (>30%) were recorded for harvest index followed by siliquae per plant (Table 3). Moderate estimates (10-30%) were observed for seed yield per plant followed by siliquae on main shoot, number of secondary branches per plant, biological yield per plant, and number of primary branches per plant, plant height, and 1000-seed weight, length of main shoot, seeds per siliqua and siliqua length. However, PCV estimates were low for the remaining characters. Moderate GCV (10-30%) estimates were recorded for siliquae per plant followed by 1000-seed weight, plant height and number of secondary branches. The GCV estimates were observed to be low for the remaining

characters. Ghosh and Gulati (2001) [3] observed high estimates of PCV and GCV for all characters except plant height. The lower estimates of PCV and GCV were observed for days to 75 per cent maturity. This result is in confirmation to the earlier findings of Shalini *et al.* (2000) [9], Singh *et al.* (2003) [11] and Singh and Singh (2004) [12]. Heritability estimates were high (>60%) for days to 50 per cent flowering followed by days to 75 per cent maturity and days to flower initiation. High heritability estimates for days to 75 per cent maturity were also observed by Khulbe *et al.* (2000) [5] and Pant and Singh (2001) [8]. Moderate (30-60%) heritability estimates were observed for 1000-seed weight. Similar results have also been observed earlier (Shalini *et al.* 2000) [9]. Expected genetic advance expressed as per cent of mean was moderate (10-30%) for siliquae per plant followed by 1000-seed weight, days to flower initiation and plant height. All the remaining characters exhibited low estimates of expected genetic advance. High heritability coupled with low genetic advance was observed for days 50 per cent flowering and days to 75 per cent maturity. Lalta *et al.* (2001) [6] also reported high heritability coupled with low genetic advance for days to maturity.

Table 3: Estimates of different parameters of variability for various characters in pooled over the environments

Sr. No.	Characters	PCV (%)	GCV (%)	h^2_{bs} (%)	Genetic advance (%) of mean
1	Days to flower initiation	9.82	8.18	69.4	14.03
2	Days to 50% flowering	5.54	4.76	73.6	8.41
3	Days to 75% maturity	4.56	3.83	70.5	6.62
4	Plant height (cm)	20.35	11.09	29.7	12.45
5	No. of primary branches /plant	20.91	3.84	2.6	1.27
6	No. of secondary branches /plant	25.21	10.18	16.3	8.47
7	Siliquae /plant	32.18	17.58	29.8	19.78
8	Length of main shoot (cm)	16.58	6.74	16.5	5.64
9	Siliquae on main shoot	25.75	7.88	9.4	4.97
10	Siliqua length (cm)	12.33	2.02	2.7	0.68
11	Seeds /siliqua	12.68	2.79	4.8	1.26
12	1000-seed weight (g)	20.28	12.61	38.7	16.16
13	Seed yield /plant (g)	26.97	6.72	6.2	3.45
14	Biological yield /plant (g)	23.38	7.75	11.0	5.30
15	Harvest index (%)	34.01	7.19	4.5	3.14
16	Oil content (%)	9.94	2.69	7.3	1.50

PCV: Phenotypic Coefficient of Variation; GCV: Genotypic Coefficient of Variation; h^2_{bs} (%): Heritability in broad sense; GA: Genetic Advance (%) of mean

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