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Research Article

Genetic variability analysis in F_2/F_3 population derived through inter-specific hybridization in oilseed *Brassica*

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Abstract

The experiment was carried out to estimate genetic variability among thirty-five genotypes of oilseed *Brassica,* including 20 F_2s/F_3 populations derived through interspecific hybridization and 15 parents, during *rabi* 2015-16 and 2016-17. Pooled analysis showed that considerable variability was observed among F_2s/F_3s and parents for all the fourteen characters. Variation due to "location x treatment" was significant only for secondary branches & oil content. The estimates of GCV and PCV were comparatively higher for plant height, primary & secondary branches/plant, number of siliquae per plant, siliqua length, seeds per siliqua, test weight, seed yield per plant and oil yield per plant. High estimates of heritability were recorded for all the characters. The estimates of genetic advance (GA) were also recorded high for number of siliquae per plant and plant height. Number of siliquae per plant showed high heritability (92.4 %) together with high genetic advance (219.1%) and genetic advance as percentage of mean (78.8). Traits like siliquae per plant and plant height might be considered as high potential traits for effective selection for further crop improvement in Brassica spp.

Keywords

Brassica species, genetic variability, GCV, PCV, heritability

Introduction

India's edible oil consumption has grown at a 5% Compound Annual Growth Rate (CAGR) over the past decade to reach 23.1 million tonnes in 2017 as compared to 13.5 million tonnes in 2007. Rising demand and stagnant domestic vegetable oil supply will push India's vegetable oil imports to over 25 million tonnes by 2030. Among food commodities, edible oil import is the largest with a foreign exchange outgo of a humongous \$11 Billion (₹ 77,000 crore) towards import of about 15 million tonnes of various types of oils. Import is inevitable as consumption continues to far outstrip domestic production. Therefore, something different, somewhat disruptive, should be attempted to bridge gap between demand and supply of edible oil. Roughly, about 15 per cent of our annual imports can be comfortably reduced by way of developing high yielding varieties. The edible oil security of the country will have to pivot on rapeseed - mustard because of their high oil content (37-42%) and preference as a cooking medium across eastern and northern India (Report: Stagnant Supply To Push India's Vegetable Oil Imports: June 26, 2018).

Rapeseed-mustard is an important edible oilseed crop in India after soybean. It is grown over about 7.0 million ha with average productivity of about 10 q/ha. Most of rapeseed-mustard cultivars grown in India have very narrow genetic base and limits their further crop improvement. The improvement of this crop depends entirely on the extent of genetic variability existing in the characters and the magnitude of heritability. Thus, keeping this in view, the present research work was designed to create genetic variability through interspecific hybridization and determine the nature and extent of genetic diversity using ANOVA and estimates of variability parameters *viz.* GCV, PCV, GA, GAM and heritability among thirty-five genotypes.

Material and Methods

The experimental material was comprised of 20 segregating populations (F_2s / F_3s) and 15 parents (Nine *B. juncea* lines, two *B. napus* lines, one line each of *B. rapa* var toria, *B. rapa* var. yellow sarson, *B. carinata* and *B. nigra*) as presented in Table 1. These genotypes represented a very wide range of diversity available in the respective species. The segregating populations were derived through interspecific hybridization during *rabi* 2013-14. F_1s were planted during 2014-15 and Colchicine treatment was given to sterile interspecific F_1s. The F_1s were selfed to develop F_2 populations during *rabi* 2014-15. Likewise, F_2s were selfed to develop F_3s population in subsequent year. Twenty F_2s/ F_3s population along with fifteen parents were evaluated for two consecutive years, *rabi* 2015-16 and 2016-17 at research field, College of Agriculture Gwalior (MP) India. The experiments were laid out in randomized block design with two replications at spacing of 45 x 15 cm in paired rows. Ten plants from parent and 40 plants from F_2s/ F_3s were selected randomly for recording of various observations. Data for different traits *viz.* days to 50% flowering (DF), plant height (PH), nos. of primary branches per plant (PB), nos. of secondary branches per plant (SB), main shoot length (MSL), siliquae on main shoot (SOMS), siliquae per plant (SPP), siliqua length (SL), seeds per siliqua (SPS), test weight (TW), days to maturity (DM), seed yield per plant (SYPP), oil content (OC) and oil yield per plant (OYPP) were recorded from randomly selected plants. Pooled estimations of both years were considered for drawing inference.

Mean values of each parent and F_2/F_3 population were used for statistical analysis. All 35 genotypes were grown in two consecutive years *rabi* 2015-16 and 2016-17 and data were combined separately over years to get information on Genotype × Environment (G×E) interaction. The analysis of variance for pooled data was done utilizing the Bartlets method (Panse and Sukhatme, 1967). The mean, range components of variance, genotypic and phenotypic coefficient of variation and heritability in broad sense, genetic advance and expected genetic advance were calculated as per procedure described by Singh and Choudhary (1985).

Results and Discussion

Pooled analysis showed significant variation for all 14 characters. The variation due to "location x treatment" was non-significant for characters *viz.* days to 50% flowering, plant height, primary branch, main shoot length, siliquae on main shoot, siliquae per plant, siliqua length, seeds per siliqua, test weight, seed yield per plant and oil yield per plant. Characters like nos. of secondary branches & oil content exhibited significant variation at 5% level of probability while days to maturity showed significant variation at 1% level of probability (Table 2).

The days to 50% flowering (DF) ranged from 32.0 (V32) to 55.0 (V34) with the mean value of 43.4. Estimates of GCV (10.60) & PCV (11.43) were moderate, heritability (86%) & GAM (20.3) were high and GA (8.8) was low for this trait. Range and mean of plant height (PH) were 77.9 (V32) - 222.8 (V5) and 175.3, respectively. The estimates of GCV (21.13), PCV (21.99), heritability (92.4), GA (73.3) and GAM (41.8) were high. Nos. of primary branches (PB) ranged from 3.5 (V30) to 10.0 (V11, V34) with the mean value of 5.5. While estimates of GCV, PCV, heritability, GA and GAM were 25.87 (high), 28.57 (high), 82.0% (high), 2.7 (low) and 48.5 (high), respectively. Nos. of secondary branches per plant (SB) ranged from 2.5 (V33) to 24.2 V34) with the mean value of 9.6. The variability parameters *viz.* GCV, PCV, heritability and GAM were recorded very high i.e. 43.57, 45.12, 93.3% and 87, respectively. While the value of GA was found low 8.3 for this trait. The range of main shoot length (MSL) was recorded from 43.7 (V11) to 79.5 (V5) with the mean value of 65.3. The estimates of GCV, PCV, heritability, GA and GAM were found to be 14.13 (moderate), 16.66 (moderate), 72% (high), 16.1 (moderate) and 24.7 (high), respectively. Likewise, siliquae on main shoot (SOMS) varied from 35.3 (V11) to 72.8 (V35) with the mean value of 49.7. The estimates of GCV, PCV and GA were moderate with the values of 17.43, 19.72 and 15.8, respectively. While the estimates for heritability (78%) and GAM (31.8) were recorded high. Nos of siliquae per plant (SPP) ranged from 108.5 (V19) to 622.7 (V20) with mean of 278.2. Very high estimates of GCV (39.8), PCV (41.4), heritability (92.4), GA (219.8) and GAM (78.8) were recorded for this trait. Range of siliqua length (SL) was 1.3 cm (V35) to 7.1 cm (V11) and mean of character was 5.04 cm. Values of GCV, PCV, heritability and GAM were very high i.e. 20.40, 21.66, 88.7% and 39.5 respectively. While estimate of genetic advance was low 2.0. Range of seeds per siliqua varied from 4.3 (V35) to 37.8 (V19) with the mean value of 17.3. Estimates of GCV, PCV, heritability and GAM were recorded very high i.e. 44.9, 45.7, 96% and 90.7, respectively while GA was moderate (15.7). Test weight (TW) ranged from 1.2 g to 7.1 g with average value of 4.9 g. Estimates of GCV, PCV, heritability and GAM were high i.e. 23.4, 24.1, 94.1% and 46.5, respectively. While value of GA was low 2.3. Range and mean of days to maturity (DM) were 122.3 (V32) – 150.0 (V34) and 135.8 days, respectively. The values of GCV (2.94), PCV (3.08), GA (7.8) and GAM (5.8) were low for DM. While heritability of trait was very high (90.9%). Seed yield per plant (SYPP) ranged from 6.8 g (V30) to 27.4 g (V20) with mean seed yield plant of 13.8 g. The estimates of GCV (34.46), PCV (36.28), heritability (90.2%) and GAM (67.4) were recorded very high for SYPP. While estimate for genetic advance was low (9.3) for this trait. Range of oil content (OC) varied from 33.3% (V18) to 45.0% (V11) with mean OC of 39.2%. Variability parameters *viz.* GCP, PCV, heritability, GA and GAM were observed to be 6.3 (low), 6.55 (low), 92.4% (high), 4.9 (low) and 12.5 (moderate), respectively for OC. Range and mean of oil yield per plant (OYPP) was 2.6 g (V30) to 10.8 g (V20) and 5.4 g, respectively. Variability parameters *viz.* GCV, PCV, heritability and GAM were observed very high i.e. 34.48, 36.29, 90.3% and 67.4, respectively. While estimate of GA was observed very low 3.6 (Table 3).

The improvement in a character depends entirely on the extent of genetic variability and the magnitude of heritability existing in the character. The knowledge of the estimates of variability in the source population in respect of yield and its heritable components is a pre-requisite for any breeding programme aimed at improving the yield and other characters. The improvement of a character by selection has no relevance without the knowledge of heritability of a character. Thus, it is imperative to have information on both phenotypic and genotypic coefficient of variation to get an idea about the heritability of the character. The information on genotypic and phenotypic coefficient of variation as well as heritability could be an indicator of the genetic advance possible by selection for the character.

Analysis of variance for all fourteen characters showed significant variation for all the characters under study. However, variation due to “location x treatment” was significant only for secondary branches & oil content at 5% and for days to maturity at 1% level of probability, respectively. For rest of characters the variation was non-significant (Table 2).

The result indicated the existence of inherent variability among the population with possibility of high potential for selection. The variability for yield and related traits was reported by Pant and Singh (2001), Vijay Kumar *et al.* (2001), Mahla *et al.* (2003), Poonam and Singh (2004), Kumar and Mishra (2006), Afrin *et al.* (2011), Ali *et al.* (2013), Amsalu *et al.* (2017) and Sandhu *et al.* (2017) in different *Brassica* species. Abebe (2006) also observed existence of large amount of genetic variability for various agro-morphological characters in Ethiopian mustard. Interspecific hybridization generated considerable variability in the studied population. The variability was observed among the F_2s/F_3s population and between population & parents as well for all the fourteen characters. The results were in close agreement with the Ara *et al.* (2013) who also reported considerable variability among the genotypes and F_2 populations generated through inter-varietal crosses. Shen *et al.* (2002) observed significant differences between F_1s and their parents for yield per plant. Katiyar *et al.* (2004) also reported significant variability among parents and crosses which indicated the presence of adequate genetic variance in inter-varietal cross combinations of *Brassica campestris.*

Estimates of genetic variability revealed that GCV and PCV were comparatively higher for plant height, primary & secondary branches/plant, number of siliquae per plant, siliqua length, seeds per siliqua, test weight, seed yield per plant and oil yield per plant (Table 3). Similar findings were reported by Rai *et al*., (2005), Abebe (2006), and Singh *et al*., (2013). The estimates of GCV & PCV were moderate for days to 50% flowering, main shoot length and numbers of siliquae on main shoot. For oil content the estimates of both parameters *viz.* GCV and PCV were low which indicated that this character was highly influenced by environmental factors. The phenotypic coefficient of variation was found to be greater than genotypic coefficient of variation for all the characters indicating some degree of environmental influence on the traits. Narrow differences between PCV and GCV suggested negligible influence of extraneous factors which was recorded for days to 50% flowering, plant height, seeds per siliqua, test weight, days to maturity and oil content. It indicated the influence of environment for all the traits under study. Similar results were reported by Ghosh and Gulati (2001), Kumar and Mishra (2006) and Ara *et al*. (2013).

The coefficient of variation indicates only the extent of variability present for different characters, it does not indicate any idea about heritable portion. It could be known through heritability estimates for different characters. It separates the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by its phenotypic performance, thus making the selection more effective. High estimates of heritability were recorded for all the characters. High heritability for various yield and component traits was reported by Khulbe *et al.* (2000), Ghosh and Gulati (2001), Pant and Singh (2001), Abebe (2006), Upadhyay and Kumar (2009), Afrin *et al.* (2011), Yadav *et al.* (2012) and Sandhu *et al.* (2017). The highest broad sense heritability for thousand seed weight followed by days to flowering, linolenic acid, days to maturity, plant height, palmitic acid, linoleic acid, oil content, oil yield, seed yield per plot and primary branches was also recorded by Amsalu *et al.* (2017). Selection of character having high heritability is fairly easy and effective as selected character will be transmitted to its progeny. This is because there would be a close correspondence between genotype and phenotype due to a relatively similar contribution of the environment to the genotype.

High estimates of genetic advance (GA) was observed for number of siliquae per plant and plant height. Genetic advance was moderate for main shoot length, siliquae on main shoot and number of seeds per siliqua. Katiyar *et al.* (2004) reported high heritability for plant height and number of primary branches per plant. Poonam and Singh (2004) reported highest genetic advance in 1000 seed weight followed by seed yield per plot, days to 50 per cent flowering and siliquae per plant.

High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for numbers of seeds per siliqua followed by secondary branches per plant, number of siliquae per plant, oil yield per plant, seed yield per plant, primary branches, test weight, plant height and length of siliqua. This implied that, these traits were less influenced by environmental factors which in turn indicated that these traits were mostly controlled by additive and /or additive × additive gene interactions and was expected to respond to direct selection for improvement. These observations were in accordance with the results of Chowdhary and Goswami (1991), Khulbe *et al.* (2000) and Jaylala Mahto (2001). Mahla *et al.* (2003) also observed high heritability coupled with high genetic advance as per cent of mean for days to flowering followed by 1000 seed weight, days to maturity and plant height.

Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955). The traits such as days to 50% flowering, primary branches, secondary branches, length of siliqua, test weight, seed yield per plant, oil content and oil yield per plant, in which high heritability was accompanied by low genetic advance, indicated the effect of non- additive gene action and hence heterosis breeding were not rewarding for these traits. These results are in agreement with previous finding of Pant and Singh (2001). Similarly, Ara *et al*. (2013) also recorded high heritability with low genetic advance and high genetic advance in percentage of mean in eight F_2 populations generated through inter-varietal crosses of *Brassica rapa* for the number of branches per plant, days to 50% flowering, days to maturity and length of siliqua.

Number of siliquae per plant showed high heritability (92.4 %) together with high genetic advance (219.1%) and genetic advance in percentage of mean (78.8). Similarly, high estimates of these parameters *viz.*, heritability (92.4%), genetic advance (73.33%) and genetic advance in percentage mean (41.8) were recorded in plant height. As these traits possessed high genetic advance coupled with high heritability and high genetic advance in percentage of mean, these might be considered as high potential traits for effective selection for further crop improvement. Mahla *et al.* (2003) also observed high heritability coupled with high genetic advance as per cent of mean for days to flowering followed by 1000 seed weight, days to maturity and plant height.

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Table 1. List of F_2s/ F_3 population and parents used in research experiment

Genotype	Pedigree	Genomic constitution
V1	NGM-43 X PT-303	*B. juncea* x *B. rapa var toria*
V2	NGM-17 X PT-303	*B. juncea* x *B. rapa var toria*
V3	KM-11 X T-42	*B. juncea* x *B. rapa var yellow sarson*
V4	NGM-6 X T-42	*B. juncea* x *B. rapa var yellow sarson*
V5	NGM-17 X T-42	*B. juncea* x *B. rapa var yellow sarson*
V6	PL-58 X PT-303	*B. juncea* x *B. rapa var toria*
V7	PT-303 X GPM-O-5	*B. rapa var toria x B. juncea*
V8	(PT-303XGPM-O-5) X GPM-O-5	(*B. rapa var toria x B. juncea*) x *B. juncea*
V9	PT303 X GPM-O-5	*B. rapa var toria x B. juncea*
V10	T-42 X GPM-O-58	*B. rapa var yellow sarson x B. juncea*
V11	T-42 X NGM-17	*B. rapa var yellow sarson x B. juncea*
V12	PT-303 X *B. nigra*	*B. rapa var toria x B. nigra*
V13	PL-6 X BN-11	*B. juncea* x *B. napus*
V14	PL-6 X BN-10	*B. juncea* x *B. napus*
V15	PL-58 X BN-10	*B. juncea* x *B. napus*
V16	PL-58 X BN-11	*B. juncea* x *B. napus*
V17	BN-11 X PL-6	*B. napus x B. juncea*
V18	KM-11 X CRP-09	*B. juncea x B. carinata*
V19	T-42 X PL-58	*B. rapa var yellow sarson x B. juncea*
V20	GPM-O-1 X PT-303	*B. juncea* x *B. rapa var toria*
V21	NGM-43	*B. juncea*
V22	NGM-17	*B. juncea*
V23	KM-11	*B. juncea*
V24	NGM-6	*B. juncea*
V25	PL-58	*B. juncea*
V26	GPM-O-5	*B. juncea*
V27	GPM-O-58	*B. juncea*
V28	PL-6	*B. juncea*
V29	GPM-O-1	*B. juncea*
V30	BN-10	*B. napus*
V31	BN-11	*B. napus*
V32	PT-303	*B. rapa var toria*
V33	T-42	*B. rapa var yellow sarson*
V34	CRP-09	*B. carinata*
V35	Banarasi Rai	*B. nigra*

Table 2. Pooled analysis of variance for 14 characters in Brassica species during *rabi* 2015-16 and 2016-17.

Source	Degree of freedom	Days 50% to flowering	Plant height	Primary Branches	Secondary branches	Main shoot length	Siliquae on main shoot	Siliquae per plant	Length of siliqua	Seeds per siliqua	Test weight	Days to maturity	Yield per plant	Oil content	Oil yield
Year	1	23.22	1.00	0.18	1.61	19.94	91.2	2826.0	0.11	19.32	0.0007	825.7	22.9	19.8	1.74
Replication	1	24.87	995.0	0.86	0.35	141.06	46.87	2169.0	0.03	4.8	0.80	93.0	0.71	1.14	0.01
Treatment	34	86.96 **	5586.3 **	8.44 **	72.48 **	355.8 **	317.5 **	49527.6 **	4.2 **	243.6 **	5.3 **	70.3 **	93.4 **	25.3 **	14.4 **
YXT	34	2.38 NS	96.87 NS	0.24 NS	1.97 *	15.07 NS	16.81 NS	574.7 NS	0.04 NS	3.1 NS	0.1 NS	6.6 **	3.04 NS	0.99 *	0.55 NS
Error	68	3.47	113.7	0.45	1.27	331.9	21.0	1000.2	0.13	2.3	0.08	1.6	2.5	0.50	0.37
SEm ±	-	1.317	7.54	0.47	0.8	4.1	3.2	22.36	0.26	1.1	0.2	0.89	1.11	0.50	0.43
CV (%)	-	4.29	6.1	12.1	11.7	8.8	9.2	11.4	7.3	8.8	5.9	0.9	11.4	1.81	11.31

***,** Significant at 5% and 1% level**.

Table 3. Estimates of variability parameters for different yield & its contributing traits in 20 F_2s/F_3s and 15 parents of *Brassica* species under pooled analysis

Characters	Range	Mean	GCV	PCV	Heritability	GA	GAM
Days to 50% flowering	32.0 – 55.0	43.4	10.60	11.43	85.9	8.8	20.3
Plant height (cm)	77.9 – 222.8	175.3	21.13	21.99	92.4	73.3	41.8
No of primary branches	3.5 – 10.0	5.5	25.87	28.57	82.0	2.7	48.5
No of secondary branches	2.5 – 24.2	9.6	43.57	45.12	93.3	8.3	87.0
Main shoot length (cm)	43.7 – 79.5	65.3	14.13	16.66	72.0	16.1	24.7
No of siliquae on main shoot	35.3 – 72.8	49.7	17.43	19.72	78.1	15.8	31.8
No of siliquae per plant	108.5 – 622.7	278.2	39.77	41.36	92.4	219.1	78.8
Length of siliqua (cm)	1.3 – 7.1	5.04	20.40	21.66	88.7	2.0	39.5
No of seeds per siliqua	4.3 – 37.8	17.3	44.89	45.74	96.3	15.7	90.7
Test weight (g)	1.2 – 7.1	4.9	23.4	24.1	94.1	2.3	46.5
Days to maturity	122. 3 – 150.0	135.8	2.94	3.08	90.9	7.8	5.8
Yield per plant (g)	6.8 – 27.4	13.8	34.46	36.28	90.2	9.3	67.4
Oil content (%)	33.3 – 45.0	39.2	6.30	6.55	92.4	4.9	12.5
Oil yield per plant (g)	2.6 – 10.8	5.4	34.48	36.29	90.3	3.6	67.4