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Genetic Variability for quantitative traits in F₃ families of *Brassica juncea* L. (Czern & Coss.)

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Abstract

Genetic variability is an indicator for a plant breeder to proceed further for evolution of candidate genotypes with novel traits. Fifteen intra-species single crosses made during 2013-14 were evaluated along with their parents for the extent of genetic variability available for seven major yield contributing traits viz., days to first flowering, plant height, secondary branches, main shoot length, number of siliqua on main shoot, number of seeds siliquae⁻¹, days to maturity besides seed yield plant⁻¹ in F₃ segregating generation. The field evaluation trial was conducted during 2016-17 at the experimental area of department of Genetics and Plant Breeding, Birsa Agricultural University, Ranchi (Jharkhand), India. The range of variability, GCV, PCV, heritability (b.s.) and genetic gain as expressed in percent of mean were estimated for all the target traits from both parental as well as segregating populations. Wide range of variations for PCV and GCV were observed for all most all the quantitative traits in segregating populations as compared to their parental populations. The extent of heritability and genetic gain were higher in magnitude for most of the yield components except days to first flowering in F₃ families. Among seven yield contributing traits, secondary branches, main shoot length, number of clique on main shoot and number of seeds siliquae⁻¹ were identified as most desirable traits contributing maximum towards seed yield and controlled by additive gene action. Out of fifteen F₃ families, five populations viz., NRCHB-101x PM-21, NRCDR-2x PM-21, PM-25 xPM-21, NRCHB-101 xRLC-1 and Pusa Bold X Pm-21 were registered outstanding performance for most of the traits.

Keywords: *Brassica juncea*, Segregating generation, variability, heritability, Genetic gain

Introduction

Indian sub-continent is the natural repository of the oilseed crops, yet is importing about 40% of the edible oil in the country. Its vegetable oil import further raised by 14% and a sum of ` 32,000 crore was spent on this import during the oil year 2009-10 (Yadava *et al.* 2012). This makes India the world's largest oil importer. Thus, oilseed crop occupy a place of prime importance in Indian economy. Among the six *Brassica* species, *B. rapa*, *B. napus* and *B. juncea* are grown predominantly for oil and seed meal in the country. Out of the total area under different species of *Brassica*, more than 85% area is occupied by Indian mustard (*B. juncea* L.) alone. The reason behind this has been assigned to higher productivity and greater tolerance to aphids, frost, drought and salinity (Singh *et al.* 1974) and wider adaptability than the other oiliferous *Brassica* crops (Labana, 1979). However, the average yield of *B. juncea* (L.) in India is around 1176kg/ha as against the worlds average 1850kg/ha which is much below than that of the other *Brassica* growing countries (DRMR annual report, 2013). To meet the projected demand of 13.4mt (25% share) of rapeseed-mustard by the end of 2020 in the country, there is a need to increase the productivity to the tune of 1787kg/ha through varietal improvement would be of a great challenge to the agricultural scientist as a whole and the plant breeders in particular (DRMR vision -2030). The average productivity of rapeseed-mustard in the state of Jharkhand is varying between 7-8q/ha (*Rabi* workshop Report, Gov. of Jharkhand, 2013) which also needs to be increased as it is much below than the national average (1176kg/ha).

The success of any breeding programme in general and improvement of specific traits through selection in particular, totally depends upon the genetic variability present in the available germplasms of a particular crop. For the success of the crop improvement programme, the characters for which variability is present, should be highly heritable. The progress due to selection depends on heritability, selection intensity and genetic advance of the characters. Heritability and genetic advance estimates for different targeted traits helps the breeder to apply appropriate breeding methodology in the crop improvement programme. Keeping this in view, the present programme was carried out during *Rabi* 2016-17

to study the magnitude and extent of genetic variability available in fifteen F₃ families for seven major yield contributing traits besides seed yield out of fifty six different crosses made during 2013-14 by a previous worker following line x tester design at Department of Plant Breeding and Genetics, Birsa Agricultural University Ranchi, (Jharkhand) India.

Experimental Materials and Methods

The experimental materials for the present study were the part of 56 single crosses generated by a previous Ph.D. student following line x tester design with 7 lines and 8 testers in the year 2013-14. During the present course of investigation, out of 56 crosses, 15 single cross combinations were studied for the extent of genetic variability available for seven major yield contributing traits viz., days to first flowering, plant height, secondary branches, main shoot length, number of siliqua on main shoot, number of seeds siliquae⁻¹, days to maturity besides seed yield plant⁻¹ in F₃ segregating generation along with their 8 parents. The field evaluation trial was conducted at the experimental area of department of Genetics and Plant Breeding, Birsa Agricultural University, Ranchi (Jharkhand), India during *Rabi* 2016-17. The segregating populations were sown in single replication in rows of 5 meter length. Each F₃ family was sown in 15 rows keeping the spacing of 30 cm and 10 cm between row to row and seed to seed, respectively in a plot size of 4.5 m x 5m. Around seven hundred fifty F₃ plant population of each cross was maintained in each plot. However, parents were raised in randomised block design with three replications in a plot size of 1.5 x 5 m with maintaining same spacing between rows and plants as adopted for raising segregating families. Recommended agronomical practices were followed to conduct the field experimentation. Observations for plant height, secondary branches, main shoot length, number of siliqua on main shoot, number of seeds siliquae⁻¹, and seed yield plant⁻¹ were recorded from sixty individual plants selected randomly from each segregating family while the same were recorded based on five plants selected randomly from each replication of each parental population. However, the observations for days to first flowering and days to maturity were recorded on plot basis in both segregating as well as parental populations.

Data recorded for all the quantitative characters from each of 60 selected individual plant of each cross were subjected to statistical analysis as per the method suggested by Singh and Chaudhary (1979) and Nadarajan and Gunasekaran (2005). However observations recorded from parents for each quantitative trait were averaged and subjected for statistical analysis to compute the mean performance, assessment of variability and genetic estimates as described below:

Mean Performance

Mean performance of parental population was calculated for each trait under study for each parent on the basis of average value of selected plants. However, the observations recorded for each quantitative trait from each individual plant from each segregating family were presented as such.

Variability and Genetic Estimates

The information on the genetic variability with respect to economic characters in a population is essential for formulating an efficient breeding programme. Phenotypic variability is observable and includes both genotypic and environmental variations. Genotypic variation is heritable that

transmit from one generation to another, which remains unaltered by environmental conditions. This type of variability is more useful to a plant breeder for exploitation in selection or to use in hybridization programme. The genetic estimates viz., σ^2p , σ^2g , σ^2e , GCV and PCV were computed using the method suggested by Singh and Chaudhary (1979) and Nadarajan and Gunasekaran (2005) as described below:

Phenotypic variance: Phenotypic variance (σ^2p) was estimated by using the formula

$$\text{Var } p (\sigma^2p) = \frac{\sum(x - \bar{x})^2}{n}$$

Where \bar{x} is the sample mean and n is the sample size.

Environmental variance (σ^2e): Environmental variance is the sum of variances of both the parents divided by two.

$$\sigma^2e = p_1 + p_2 / 2$$

Genotypic variance: Genotypic variance (σ^2g) was estimated by subtracting the error variance (σ^2e) from the phenotypic variance (σ^2p) as per method suggested by.

$$\sigma^2g = \sigma^2p - \sigma^2e$$

Genotypic Coefficient of variation: The genotypic coefficient of variation (GCV) was computed by dividing the square root of the genotypic variance by population mean and was expressed in percentage.

$$\text{GCV} = \frac{\sqrt{\sigma^2g}}{\bar{x}} \times 100$$

Where, σ^2g is genotypic variance and \bar{x} is population mean.

Phenotypic coefficient of variation: The Phenotypic coefficient of variation (PCV) was computed by dividing the square root of the phenotypic variance by population means and expressed in percentage.

$$\text{PCV} = \frac{\sqrt{\sigma^2p}}{\bar{x}} \times 100$$

Where, σ^2p is phenotypic variance and \bar{x} is population mean.

Heritability (h^2) and Genetic Advance (G.A.)

Heritability is the ratio of genotypic variance to total variance. It is a good index of transmission of characters from parent to their offspring (Falconar, 1981). Heritability estimates facilitates the evaluation of genetic and environmental effect and also measures the value of selection of a particular character (Mehdi and Khan, 1994 and Khan *et al.* 2008). The estimates of heritability help the plant breeder in selection of elite genotype from diverse genetic population based on heritability of major yield and/or quality attributing traits. But, heritability itself does not provide any indication towards the amount of genetic progress that would result in selecting best individuals rather it depends upon the amount of genetic advance (Kumar and Sasivannan, 2006). Hence, heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (Johnson *et al.* 1955). These two estimates are also indicative of the mode of gene action operated in trait expression (Mahmood *et al.* 2003

and Akbar *et al.* 2003; 2007). Additive genes are said to control a trait having high heritability along with high genetic advance which highlight the usefulness of plant selection based on phenotypic performance (Akbar *et al.* 2003 and 2007; Aytac and Kinaki 2009 and Sadat *et al.* 2010) whereas, high heritability but low genetic advance is indicative of non-additive (dominant/epistasis) control over the expression of character and limit the improvement in that character only through selection (Akbar *et al.* 2003).

Heritability in broad sense and genetic advance were calculated as per the method suggested by Lush, 1949 followed by Johnson *et al.* (1955), Swarup and Chaugle (1962) and Gandhi *et al.* (1964) and Lal *et al.* (1983) as follow:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where, h^2 is heritability (broad sense), σ^2_g is genotypic variance and σ^2_p is phenotypic variance.

$$\text{Genetic Advance (G.A)} = k\sigma_p h^2$$

Where,

h^2 = heritability in broad sense

σ_p = phenotypic standard deviation

K = Standardized selection differential which is expressed in terms of standard deviation units and its value vary with the intensity of selection. For the purpose of present study, K has a value of 1.76 which is the value of 10 percent selection intensity.

Results and discussion

Analysis of variance revealed significant differences among genotype for most of the yield contributing traits including yield indicating thereby presence of sufficient genetic variability in the genotypes selected for this study. (table-1). High magnitude of variability have been reported in Indian mustard germplasm & varieties for various characters by many workers for days to 50% flowering, days to maturity, plant height, total silique per plant & seed yield (Kumar & Mishra 2007). The reason for high magnitude of variability in present study may be due to the fact that the genotype selected for the present study were diverse & have broad genetic base. The coefficient of variation (CV) ranged from 0.5 to 10.73% for various quantitative traits in parental populations (Table-2). The lowest coefficient of variation (0.5%) shows the best genetic potential and its genetic influence while the highest shows more influence of environmental fluctuations (Khan *et al.* 2008).

Mean performance of segregating population & parents.

The mean performance of each of the segregating family registered wide range of variation for most of the yield contributing traits indicating thereby release of sufficient genetic variability in all the crossed materials for this study (table-3). High magnitude of variability has been reported in Indian mustard germplasms and varieties for various characters by many workers for first flowering, days to maturity, plant height, and number of silique on main shoot and seed yield per plant (Kumar and Mishra, 2007). The reason for release of high magnitude of variability in the present study may be due to the fact that the parents used in the crossing programme were diverse in nature and evolved involving different pedigree and developed at different regions representing different agro-climatic conditions of the country.

Variability Assessment

A wide range of variability was observed for almost all characters viz; plant height, number of secondary branches per plant, main shoot length, silique on main shoot, days to maturity and yield per plant except days to first flowering in segregating populations (table-3). However, the range of variability were moderate to low for all the yield attributing traits in parental populations. (Table-2). This may be due to the fact that parental populations were fixed lines which give rise to greater extent of variations in segregating populations after involving them in crossing programme. Hence, the characters showing wide range of variability provide greater opportunities for selection as compared to those having narrow range of variability. Larik and Rajput (2000), Shalini *et al.* (2000), Ghosh and Gulati (2001), Ali *et al.* (2003), Ramesh (2011), Mahto and Haider (2012) had also found significant genetic variation for different seed yield contributing character in Indian mustard.

It is evident from the tables (Table 4 and 5(a to h)) that the PCV were invariably higher in magnitude than their corresponding GCV for all the traits studied from both parental as well as segregating populations. This is mainly due to the fact that phenotypic variance also consist of error variance in addition to genotypic variance. From parental population it could be observed that most of the yield attributing traits were recorded lower magnitude of phenotypic and genotypic coefficient of variation except secondary branches per plant and seed yield per plant (Table 4) as could be expected from the fixed lines.

However, on the other hand, in F_3 segregating families, wide to moderate PCV and GCV were recorded for almost all the quantitative traits except days to first flowering and days to maturity (Table-5a to h). The segregating populations of different crosses responded differentially for the expression for yield attributing characters as a result, the magnitude of variations for phenotypic and genotypic coefficient were different. The segregating population of PM-25 X PM-21 exhibited maximum GCV and PCV for secondary branches per plant whereas, NRCHB-101 X PM-21, SHIVANI X PM-21 and NRCDR-2 X PM-21 expressed greater extent of GCV for plant height, main shoot length and seed per silique respectively (Table-5a-5h). These characters having higher magnitude of GCV provides greater opportunity for selection and supposed to be main yield contributing traits in Indian mustard. Present findings were also in agreement of the previous findings reported earlier by many workers including Akbar *et al.* (2003); Mahla *et al.* (2003); Ali *et al.* (2003); Singh (2004); Patel and Patel (2005); Yadav *et al.* (2011); Singh *et al.* (2011) and Singh *et al.* (2013).

Heritability and Genetic Advance

The estimate of heritability revealed that seed yield per plant, number of seed per silique, days to first flowering, days to maturity, silique on main shoot, secondary branch per plant, & plant height recorded higher magnitude of heritability in parental populations (table-4). However, in segregating populations higher magnitude of heritability was recorded for secondary branch per plant, silique on main shoot, yield per plant, and days to maturity. Other yield attributing traits viz, days to first flowering, plant height, main shoot length, & seed per silique have also recorded high heritability in most of the segregating populations except some of the F_3 families but, the values were moderate (table-5a to h). These characters have been considered as major yield attributing traits and presence of high heritability indicated that variability in these

traits is mostly due to genetic component and transmissible to their offspring in succeeding generation hence, selection would be rewarding in further improvement of these characters (Singh et.al. 2011).

When heritability and genetic advance were considered together, it was observed that most of the traits recorded high heritability coupled with low genetic advance in parental population. On the other hand, in most of the F₃ families, secondary branch per plant, main shoot length, silique on main shoot, number of seed per silique & seed yield per plant had moderate to high heritability coupled with moderate to high genetic advance as expressed in percent of mean. This indicated that traits showing high heritability along with high genetic advance were governed by additive gene effect & selection for these traits would be effective for yield improvement. Similar findings were observed by Gowthami et.al. (2014). The characters, like plant height, days to maturity showing high heritability but coupled with low genetic advance are supposed to be controlled by non-additive gene effects indicating thereby improvement in these characters only through selection could be limited. Similar findings related to high heritability along with high genetic advance have been reported by several earlier workers for various traits (Singh et.al. 2003; Singh and Singh, 2004; Kumar and Mishra 2007; Singh et.al. 2011, Yadav et.al. 2011 and Mishra 2011).

Conclusion

On the basis of present studies and results obtained it may be concluded that (1) secondary branch per plant, main shoot length, number of siliqua on main shoot, number of seeds per siliqua besides seed yield per plant were identified as most important reliable traits based on which selection could be made from the segregation populations.(2) Out of 900 individual plant investigated from fifteen F₃ families, 113desirable segregants could be selected having excellent expression for six different yield attributing traits. It includes 15 for secondary branches (10-17 branch/Plant), 26 for main shoot length (80-95cm), 9 for number of siliqua on main shoot (55-65 siliqua/plant), 20 for number of seeds per siliquae (17-18 seeds/siliquae), 16 for yield for plant (8-14 gm /plant), and 27 for earliness (93-95 days) and (3) Out of fifteen F₃ populations, five families viz.,NRCHB-101x PM-21, NRCDR-2x PM-21, PM-25 xPM-21, NRCHB-101 xRLC-land Pusa Bold X Pm-21 were registered outstanding performance for most of the traits.

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Table 1: Analysis of variance (mean square values) for various important characters of parents.

Source of variation	DF	Mean Square values							
		DF	DM	PH (cm)	MSL (cm)	Sec. B/P	Siliqua On MS	Seed/ siliqua	Yield/ plant(g)
Replication	2	0.10	0.08	67.27	3.10	0.17	20	0.03	0.18
Genotype	7	1.32**	1.26**	57.75*	73.47*	0.60*	39.3*	1.77**	1.08**
Error	14	0.22	0.28	16.73	18.05	0.15	3.47	0.29	0.09

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

Table-2: Mean performance and range for eight quantitative traits of eight Parents involved in fifteen F₃ Families of Indian mustard.

Genotype	Mean/ Range	DF	Sec BPP	PH	MSL	Sili on MS	Seed/siliqua	Seed yield/ plant	DM
NRCHB-101	M	43.46	4.00	121.60	59.66	41.26	13.93	4.84	104.73
	R	43-44	3-5	110-142	50-70	39-52	12-15	3.44-5.8	104-106
NRCDR-02	M	43.80	3.93	115.06	43.73	37.53	14.20	4.25	103.53
	R	43-45	3-5	100-130	34-52	30-42	12-16	3.21-5.01	103-104
PUSA BOLD	M	44.13	4.80	115.20	50.53	40.33	12.73	4.08	104.80
	R	43-45	4-6	100-129	36-65	32-46	10-14	3.01-5.21	104-106
SHIVANI	M	43.80	4.33	119.46	50.93	39.60	12.53	4.31	103.80
	R	43-45	3-5	105-132	35-62	35-45	12-14	3.12-5.216	103-105
PM- 25	M	42.80	4.46	119.40	50.60	42.86	13.00	4.68	103.53
	R	42-44	3-6	100-135	39-61	38-48	10-16	3.01-6.01	103-105
PM - 21	M	44.86	4.20	121.13	57.26	40.00	12.40	4.05	104.73
	R	44-47	3-5	110-132	63-51	39-49	10-14	3.12-5.23	103-106
RLC -1	M	44.06	3.26	128.60	55.13	37.66	13.20	3.30	104.80
	R	43-45	2-4	110-150	39-65	35-50	12-15	2.01-4.01	103-106
JN-032	M	44.73	4.06	116.86	54.60	39.46	11.93	3.15	105.13
	R	44-46	3-5	102-130	39-62	38-48	11-13	2.01-4.03	104-106
Grand mean		43.95	4.13	119.66	52.80	39.84	12.99	4.08	104.38
C.V%		1.08	9.39	3.41	8.04	10.73	4.17	7.64	0.5
SEm±		0.27	0.22	2.36	2.45	2.47	0.31	0.18	0.3
C.D 5%		0.83	0.67	7.16	7.44	3.29	0.95	0.54	0.93

Table 3: Mean performance and range for eight characters of 15 F₃ families of Indian mustard.

Genotypes	Mean/ Range	DFE	Sec BPP	PH	MSL	Siliqua on MS	Seed/ siliqua	Yield/ plant	DM
NRCHB101 X PM21	M	43.33	3.96	117.61	52.28	32.10	12.23	3.09	98.20
	R	42-46	0-10	76-147	33-73	7-53	8-16	1.28-7.26	95-103
NRCHB-101XJN-032	M	43.71	3.86	119.95	53.98	32.41	12.21	3.87	100.03
	R	42-46	0-10	63-149	30-90	12-56	10-18	0.82-11.7	94-104
NRCDR-2XPM-21	M	43.93	4.68	126.88	61.35	35.36	12.96	3.61	99.05
	R	42-46	0-14	81-148	30-74	17-50	10-17	0.96-9.22	97-104
NRCDR-2XJN-032	M	44.26	4.38	118.81	50.78	30.00	13.28	3.21	99.00
	R	42-46	0-10	100-168	35-87	13-57	10-17	1.37-9.92	93-103
PUSA BOLD X PM-21	M	43.76	5.03	129.26	61.16	36.53	12.46	3.91	99.45
	R	43-47	0-12	85-169	14-85	18-41	10-17	0.45-12.05	95-104
PUSA BOLD XJN-032	M	43.93	4.68	126.88	61.35	35.36	12.96	3.61	99.05
	R	43-47	0-10	90-159	32-77	13-55	10-17	0.71-7.57	95-104
SHIVANI x PM-21	M	44.98	4.43	126.75	51.55	30.23	12.20	3.94	99.00
	R	43-46	0-17	84-160	25-75	16-61	10-17	1.24-13.16	94-105
SHIVANI x JN-032	M	43.96	4.11	126.38	55.80	31.58	12.21	3.62	100.18
	R	43-47	0-11	95-150	35-85	21-51	10-18	0.78-5.64	95-105
PM-25 x PM-21	M	44.96	5.10	125.33	53.75	33.90	12.56	3.45	99.40
	R	42-47	0-13	92-160	27-88	12-55	10-18	0.77-13.06	95-102
PM-25 X JN-032	M	43.86	5.40	123.48	53.48	33.73	12.28	3.85	99.90
	R	43-46	0-13	95-160	17-80	12-48	9-17	1.66-8.35	95-105
NRCHB-101 X RLC-1	M	43.96	4.73	126.50	59.45	33.98	11.58	3.46	99.61
	R	42-46	0-11	85-155	25-80	18-60	10-16	0.70-13.28	95-107
NRCDR-2 XRLC -1	M	44.63	4.61	123.70	58.45	34.95	13.05	3.21	98.58
	R	40-48	0-11	100-160	35-95	22-65	10-16	1.89-6.92	96-103
PUSA BOLD X RLC-1	M	44.20	3.51	124.78	53.88	33.00	12.38	3.08	99.13
	R	42-46	0-13	95-165	33-80	16-53	10-16	1.08-8.31	96-106
SHIVANI X RLC-1	M	43.80	4.86	123.00	54.91	34.03	12.88	4.02	99.45
	R	42-46	1-12	100-165	35-82	19-47	10-16	1.53-6.50	95-103
PM-25 x RLC-1	M	44.25	4.43	125.23	57.30	35.15	12.16	3.41	99.10
	R	43-46	0-12	95-147	7-90	19-50	10-17	0.79-8.81	95-103

Table 4: Estimation of σ^2_p , σ^2_g , σ^2_e , GCV, PCV, h^2 , GA, and GAM% for eight characters observed from parental populations of Indian mustard involved in 15 F₃ families

Characters	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h^2	GA	GAM%
DFE	0.44	0.36	0.07	1.51	1.37	82	1.13	2.58
sec BPP	0.2	0.15	0.05	10.87	9.42	75	0.69	16.82
PH	19.25	13.67	5.57	3.66	3.09	71	6.41	5.36
MSL	24.49	18.47	6.01	9.37	8.13	75	7.68	14.56
Siliqua on MS	3.1	-3	6.1	4.41	4.34	77	5.31	12.68
Seed/siliqua	0.59	0.49	0.09	5.91	5.41	83	1.32	10.16
Yield/ plant	0.36	0.32	0.03	14.67	13.99	90	1.12	27.49
DM	0.42	0.32	0.09	0.62	0.54	77	1.03	0.99

Table 5 a: Variability and genetic estimates for days to first flowering observed in F₃ families of fifteen cross combinations of Indian mustard.

DFE	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h^2	G.A	GAM%
NRCHB101XPM21	2.12	1.64	0.48	3.36	2.95	77.35	1.98	4.57
NRCHB-101XJN-032	1.69	1.18	0.51	2.95	2.46	69.65	1.59	3.62
NRCDR-2XPM-21	1.65	1.08	0.57	2.90	2.34	65.21	1.47	3.33
NRCDR-2XJN-032	1.45	0.97	0.47	2.74	2.25	67.22	1.42	3.24
PUSA BOLD X PM-21	1.03	0.48	0.55	2.26	1.54	46.55	0.83	1.85
PUSA BOLD XJN-032	0.81	0.36	0.45	2.00	1.33	44.31	0.70	1.56
SHIVANI X PM-21	0.79	0.21	0.57	2.03	1.06	27.56	0.43	0.98
SHIVANI X JN-032	1.28	0.81	0.47	2.54	2.01	63.00	1.25	2.81
PM-25 X PM-21	0.97	0.40	0.57	2.23	1.43	40.98	0.71	1.61
PM-25 X JN-032	0.49	0.62	0.47	2.35	1.77	56.77	1.04	2.35
NRCHB-101 X RLC-1	0.88	0.50	0.38	2.15	1.62	56.92	0.94	2.15
NRCDR-2 XRLC -1	2.08	1.60	0.47	3.29	2.89	77.10	1.95	4.47
PUSA BOLD X RLC-1	1.15	0.69	0.45	2.45	1.91	60.71	1.14	2.62
SHIVANI X RLC-1	1.15	0.67	0.47	2.44	1.86	58.64	1.10	2.51
PM-25 X RLC-1	0.77	0.29	0.47	2.00	1.24	38.38	0.59	1.35

Table 5 b: Variability and genetic estimates for secondary Branch/Plant observed in F₃ families of fifteen cross combinations of Indian mustard.

No of sec BPP	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h ²	G.A	GAM%
NRCHB101 X PM21	6.64	6.12	0.51	64.97	62.41	92.25	4.18	105.50
NRCHB-101 X JN-032	6.26	5.44	0.81	65.01	60.61	86.92	3.82	99.46
NRCDR-2 X PM-21	10.07	9.59	0.47	72.39	70.66	95.27	5.32	121.39
NRCDR-2 X JN-032	6.01	5.52	0.49	52.37	50.17	91.76	3.96	84.59
PUSA BOLD X PM-21	8.11	7.58	0.52	64.25	62.12	93.48	4.68	105.71
PUSA BOLD X JN-032	6.05	5.51	0.54	48.25	46.02	90.96	3.94	77.25
SHIVANI X PM-21	10.04	9.55	0.49	58.68	57.22	95.11	5.30	98.23
SHIVANI X JN-032	5.66	5.15	0.51	51.55	49.17	91.00	3.81	82.56
PM-25 X PM-21	6.79	6.22	0.57	74.13	70.92	91.52	4.19	119.41
PM-25 X JN-032	8.25	7.65	0.59	64.78	62.40	92.78	4.69	105.79
NRCHB-101 X RLC-1	7.77	7.31	0.46	72.12	69.95	94.06	4.61	119.40
NRCDR-2 X RLC -1	5.42	4.99	0.42	46.26	44.42	92.18	3.77	75.06
PUSA BOLD X RLC-1	6.30	5.83	0.47	49.90	47.97	92.45	4.08	81.19
SHIVANI X RLC-1	5.48	1.01	0.43	25.50	21.32	69.93	1.48	31.39
PM-25 X RLC-1	5.94	5.42	0.52	50.11	47.85	91.19	3.91	80.43

Table 5 c: Variability and genetic estimates for plant height observed in F₃ families of fifteen cross combinations of Indian mustard.

PLANT HEIGHT	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h ²	G.A	GAM%
NRCHB101XPM21	315.46	260.34	55.11	15.10	13.71	82.52	25.79	21.93
NRCHB-101XJN-032	342.89	245.07	97.81	15.85	13.40	71.47	23.29	19.94
NRCDR-2XPM-21	215.23	167.85	47.38	12.34	10.90	77.98	20.13	16.94
NRCDR-2XJN-032	231.96	175.73	56.23	12.00	10.44	75.75	20.30	16.00
PUSA BOLD X PM-21	314.80	262.29	52.50	13.99	12.77	83.32	26.01	20.52
PUSA BOLD XJN-032	232.02	170.66	61.36	12.15	10.42	73.55	19.71	15.73
SHIVANI X PM-21	203.57	148.45	55.12	11.55	9.86	72.92	18.31	14.83
SHIVANI X JN-032	235.50	171.52	63.98	12.40	10.58	72.83	19.67	15.90
PM-25 X PM-21	242.41	164.05	78.40	12.47	10.26	67.65	18.53	14.85
PM-25 X JN-032	239.87	152.61	87.26	12.36	9.86	63.62	17.34	13.84
NRCHB-101 X RLC-1	215.74	130.05	85.68	12.24	9.50	60.28	15.58	12.99
NRCDR-2 XRLC -1	165.28	87.33	77.94	9.94	7.23	52.84	11.95	9.24
PUSA BOLD X RLC-1	206.20	123.13	83.07	11.10	8.58	59.71	15.09	11.67
SHIVANI X RLC-1	197.16	111.47	85.69	11.10	8.34	56.54	13.97	11.04
PM-25 X RLC-1	182.33	73.36	108.97	10.97	6.96	40.23	9.56	7.77

Table 5 d: Variability and genetic estimates for main shoot length observed in F₃ families of fifteen cross combinations of Indian mustard.

MSL	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h ²	G.A	GAM%
NRCHB101 X PM21	110.61	88.10	22.51	20.11	17.95	79.65	14.74	28.19
NRCHB-101 X JN-032	144.85	96.34	48.51	20.37	16.61	66.51	14.08	23.84
NRCDR-2 X PM-21	108.61	85.68	22.92	20.52	18.22	78.89	14.47	28.49
NRCDR-2 X JN-032	154.90	121.96	32.94	20.28	18.00	78.73	17.24	28.11
PUSA BOLD X PM-21	144.86	94.12	50.73	23.34	18.82	64.97	13.76	26.70
PUSA BOLD X JN-032	123.03	62.27	60.76	20.63	14.68	50.61	9.88	18.38
SHIVANI X PM-21	140.05	101.91	38.13	22.12	18.87	72.76	15.15	28.33
SHIVANI X JN-032	149.03	100.86	48.16	20.88	17.18	67.68	14.54	24.88
PM-25 X PM-21	157.15	128.20	28.94	23.26	21.01	81.58	18.00	33.40
PM-25 X JN-032	138.28	99.31	38.97	20.52	17.39	71.81	14.86	25.94
NRCHB-101 X RLC-1	133.30	91.41	41.89	21.38	17.71	68.57	13.93	25.81
NRCDR-2 X RLC -1	130.10	87.79	42.31	18.64	15.31	67.48	13.54	22.14
PUSA BOLD X RLC-1	101.99	31.86	70.12	16.51	9.22	31.24	5.55	9.08
SHIVANI X RLC-1	111.09	53.57	57.52	17.73	12.31	48.22	8.94	15.04
PM-25 X RLC-1	176.62	128.28	48.33	24.20	20.62	72.63	16.98	30.93

Table 5 e: Variability and genetic estimates for number of siliqua on main shoot observed in F₃ families of fifteen cross combinations of Indian mustard.

SILIQUA ON MS	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h ²	G.A	GAM%
NRCHB101XPM21	81.82	72.34	9.47	28.17	26.49	88.41	14.07	43.85
NRCHB-101XJN-032	75.23	57.41	17.81	27.90	24.37	76.32	11.65	37.48
NRCDR-2XPM-21	57.89	48.77	9.12	25.36	23.27	84.23	11.28	37.60
NRCDR-2XJN-032	73.15	61.74	11.40	24.18	22.21	84.40	12.70	35.92
PUSA BOLD X PM-21	36.86	27.48	9.37	20.08	17.34	74.56	7.96	26.35
PUSA BOLD XJN-032	69.31	57.65	11.65	24.55	22.39	83.18	12.18	35.95
SHIVANI X PM-21	66.77	58.59	8.17	24.22	22.69	87.75	12.62	37.41

SHIVANI X JN-032	47.60	37.15	10.45	19.74	17.44	78.04	9.47	27.11
PM-25 X PM-21	80.64	73.03	7.60	27.21	25.89	90.57	14.31	43.37
PM-25 X JN-032	59.07	49.19	9.88	21.86	19.95	83.27	11.26	32.04
NRCHB-101 X RLC-1	78.01	62.66	15.34	27.24	24.41	80.32	12.48	38.51
NRCDR-2 XRLC -1	76.89	61.89	15.00	24.00	21.53	80.49	12.42	34.00
PUSA BOLD X RLC-1	62.82	47.57	15.24	21.69	18.88	75.72	10.56	28.91
SHIVANI X RLC-1	54.25	40.20	14.04	21.67	18.65	74.10	9.60	28.27
PM-25 X RLC-1	42.67	29.20	13.47	19.19	15.87	68.42	7.86	23.11

Table-5 f: Variability and genetic estimates for number of seeds per siliquae observed in F₃ families of fifteen cross combinations of Indian mustard.

SEED/SILQUA	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h^2	G.A	GAM%
NRCHB101XPM21	3.50	2.41	1.09	15.30	12.69	68.87	2.26	18.54
NRCHB-101XJN-032	4.01	3.05	0.95	14.89	13.00	76.15	2.68	19.96
NRCDR-2XPM-21	30.85	29.49	1.35	41.81	40.88	95.60	9.34	70.35
NRCDR-2XJN-032	3.35	2.52	0.83	14.12	12.24	75.16	2.42	18.68
PUSA BOLD X PM-21	3.04	1.45	1.59	14.30	9.88	47.75	1.46	12.01
PUSA BOLD XJN-032	3.47	2.40	1.06	14.82	12.33	69.26	2.27	18.07
SHIVANI X PM-21	2.95	1.90	1.04	13.98	11.23	64.51	1.95	15.88
SHIVANI X JN-032	4.25	3.72	0.52	15.80	14.79	87.68	3.18	24.38
PM-25 X PM-21	5.32	3.19	2.12	18.63	14.43	60.02	2.43	19.68
PM-25 X JN-032	2.95	1.35	1.60	14.12	9.55	45.69	1.38	11.36
NRCHB-101 X RLC-1	3.19	2.28	0.90	14.61	12.37	71.63	2.25	18.43
NRCDR-2 XRLC -1	2.79	1.62	1.17	13.41	10.22	58.09	1.71	13.71
PUSA BOLD X RLC-1	2.95	1.54	1.40	13.78	9.97	52.41	1.58	12.71
SHIVANI X RLC-1	2.11	1.25	0.86	12.54	9.65	59.18	1.51	13.06
PM-25 X RLC-1	3.90	1.95	1.94	15.33	10.86	50.20	1.74	13.54

Table-5 g: Variability and genetic estimates for seed yield per plant observed in F₃ families of fifteen cross combinations of Indian mustard.

YIELD/PLANT	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h^2	G.A	GAM%
NRCHB101XPM21	1.40	0.94	0.44	38.04	31.39	68.07	1.40	45.58
NRCHB-101XJN-032	3.76	3.21	0.54	51.46	47.56	85.42	2.91	77.37
NRCDR-2XPM-21	3.76	3.32	0.44	60.41	56.76	88.28	3.01	93.87
NRCDR-2XJN-032	3.39	3.05	0.34	50.98	48.35	89.96	2.91	80.72
PUSA BOLD X PM-21	5.51	5.05	0.45	59.54	57.02	91.71	3.79	96.11
PUSA BOLD XJN-032	2.61	2.26	0.35	46.86	43.55	86.37	2.45	71.23
SHIVANI X PM-21	3.86	3.46	0.40	51.00	48.27	89.57	3.10	80.40
SHIVANI X JN-032	1.18	0.88	0.30	33.79	29.14	74.39	1.42	44.25
PM-25 X PM-21	2.91	2.37	0.53	55.27	49.90	81.53	2.44	79.31
PM-25 X JN-032	1.81	1.38	0.43	39.46	34.39	75.93	1.80	52.74
NRCHB-101 X RLC-1	5.81	5.44	0.37	62.23	60.21	93.60	3.97	102.53
NRCDR-2 XRLC -1	1.66	1.29	0.37	33.02	29.12	77.75	1.76	45.19
PUSA BOLD X RLC-1	1.72	1.33	0.38	33.55	29.54	77.51	1.79	45.78
SHIVANI X RLC-1	1.72	1.39	0.33	37.93	34.08	80.70	1.86	53.88
PM-25 X RLC-1	2.05	1.58	0.46	35.55	31.23	77.17	1.94	48.29

Table 5 h: Variability and genetic estimates for days to maturity observed in F₃ families of fifteen cross combinations of Indian mustard.

DM	σ^2_p	σ^2_g	σ^2_e	PCV%	GCV%	h^2	G.A	GAM%
NRCHB101XPM21	3.34	2.64	0.71	1.86	1.65	78.81	2.53	2.58
NRCHB-101XJN-032	4.73	3.96	0.77	2.20	2.01	83.70	3.20	3.24
NRCDR-2XPM-21	2.67	2.01	0.66	1.65	1.43	75.10	2.16	2.18
NRCDR-2XJN-032	4.62	4.07	0.55	2.17	2.03	88.05	3.33	3.36
PUSA BOLD X PM-21	4.71	3.95	0.76	2.19	2.00	83.83	3.20	3.23
PUSA BOLD XJN-032	4.41	3.76	0.64	2.11	1.95	85.32	3.15	3.17
SHIVANI X PM-21	7.10	6.34	0.76	2.66	2.52	89.28	4.19	4.19
SHIVANI X JN-032	4.38	3.73	0.64	2.12	1.96	85.22	3.14	3.18
PM-25 X PM-21	2.93	2.19	0.73	1.72	1.49	74.81	2.25	2.27
PM-25 X JN-032	4.83	4.21	0.62	2.21	2.07	87.10	3.37	3.40
NRCHB-101 X RLC-1	9.42	8.87	0.54	3.06	2.97	94.18	5.08	5.08
NRCDR-2 XRLC -1	3.43	2.93	0.50	1.86	1.72	85.31	2.78	2.80
PUSA BOLD X RLC-1	4.76	4.16	0.60	2.19	2.05	87.40	3.35	3.37
SHIVANI X RLC-1	3.66	3.06	0.60	1.92	1.75	83.62	2.81	2.82
PM-25 X RLC-1	3.74	3.16	0.57	1.94	1.78	84.60	2.88	2.89

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