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Research Article

Comparison of variability in early segregating generations of Indian Mustard [*Brassica juncea* (L.) Czern & Coss.] crosses

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Abstract
Eight parents and the 28 crosses of Indian Mustard (*Brassica juncea* (L.) Czern & Coss.) in two segregating generations, *viz*., F_2 and F_3 were studied for their genetic variability during the *rabi* seasons of 2020-21 and 2021-22, respectively. Observations were recorded for six morphological characters such as plant height (cm), primary branches per plant, secondary branches per plant, siliquae per plant, 1000 seed weight (g) and seed yield per plant (g). The PCV was found to be greater than the GCV and the difference between them was high in all the characters in both F_2 and F_3 generations. Most of the characters revealed a medium range of GCV and PCV. Moderate heritability was expressed by all the characters except primary branches per plant in F_3 generation. The Genetic Advance as a percentage of Mean (GAM) was higher in most characters except in plant height. The character plant height was found to be positively correlated with seed yield per plant in both F_2 and F_3 generations, with secondary branches per plant in the F_3 generation and negatively correlated with primary branches per plant in F_3 generation. A high direct effect on seed yield per plant was exhibited by plant height and 1000 seed weight in both F_2 and F_3 generations and by Secondary branches per plant in the F_2 generation and Siliquae per plant in the F_3 generation.

Keywords: Mustard, Genetic variability, Heritability, Correlation, Path analysis, Box plot, Segregating generation

INTRODUCTION

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] belongs to the family *Brassicaceae* (Cruciferae). *Brassica juncea* is an amphidiploid (2n=36) that evolved from an interspecific cross between *B. rapa* (2n=20) and *B. nigra* (2n=16). The Brassica comprises of six species, of which three are primary diploid species (*B. rapa*, n = 10; *B. oleracea*, n = 9; *B. nigra*, n=8), and the rest three are amphidiploids (*B. napus*, n=19; *B. carinata*, n=17; *B. juncea*, n=18) that have naturally come into existence through interspecific hybridization between the primary species. *B. juncea* is an annual herbaceous plant with brown to dark brown coloured rough seeds and predominantly self-pollinated and self-compatible (Labana *et al*., 1992).

Indian mustard is economically essential not only in the Indian market but also worldwide. After soybean and oil palm, it is the world's third most important source of edible

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oil (Indian Council of Agriculture and Research: http://www.icar.org.in). Canada is the largest producer of Indian mustard followed by China. However, India, Bangladesh, Nepal, Sweden etc. are also important mustard-growing countries. Indian mustard is the key source of oil seed crop in India that helps in addressing the demand-supply gap of edible oil of the country. Of the total area and production under the nine oilseed crops grown in India, rapeseed-mustard accounts for 23.2% of the acreage and 26.2% of the production (2014-15 to 2018-2019). The average rapeseed-mustard yield in India is about 1499 kg/ha compared to the combined oilseeds crops average of 1265 kg/ha (2018-19). Indian mustard accounts for about 80% of the total area under these crops in the country, and nearly 74% of the area under the crop is irrigated. In India, Rajasthan is the largest producer of Rapeseed-Mustard followed by Haryana, Madhya Pradesh, Uttar Pradesh and West Bengal (National Bulk Handling Corporation Pvt. Ltd http://www.nbhcindia.com).

To improve such important oilseed crop through breeding process, study on genetic variability of important characters responsible for seed yield is necessary. The knowledge of heritability and genetic advance of a particular character helps in increasing the scope for the improvement of a trait through selection. The genetic variability study on segregating populations will yield an effective selection tool that helps develop inbred lines (Ghosh *et al.,* 2010). However, very few studies have been reported on the genetic variability in segregating populations. Therefore, the present study is an attempt to assess the genetic variability that can be present in F_2 and F_3 populations of Indian mustard for further utilization in the breeding process.

MATERIALS AND METHODS

The experiment was conducted at the Agricultural Instructional Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal, during the *rabi* seasons of 2020- 21 and 2021-22. The experimental material for the study comprised eight parents and 28 crosses of Indian mustard [*Brassica juncea* (L.) Czern & Coss.] in two generations, namely, F_2 and F_3. The crosses were derived through intervarietal hybridization during *rabi* 2018-19 from an earlier study by Rout *et al*. (2019) and Rout (2021). The seeds of F_2 generation were sown to develop F_2 populations during *rabi* 2020-21. Then the F_3 seed harvested from the F_2 population was bulked separately for each of the crosses, to proceed to the F_3 generation in the subsequent year 2021-22. The F_2 and F_3 populations and the eight parents, were evaluated in two consecutive years, *rabi* 2020-21 and *rabi* 2021-22 in Randomized Block Design with three replications. Recommended cultural practices and plant protection measures were adopted in all the experimental plots during the experimentation. The data from randomly selected plants from each treatment (parents along with F_2 in 2020-21 and F_3 in 2021-22) per replication were recorded for six morphological characters namely, plant height (cm), primary branches per plant, secondary branches per plant, siliquae per plant, 1000 seed weight (g) and seed yield per plant (g). Twenty plants for the F_2 population in 2020-21 and 10 plants for F_3 population in 2021-22 from each plot were randomly selected for recording observations on a per plant basis for all the quantitative characters except 1000 seed weight which was recorded from seed samples. The means of the plant data in each replication was used for statistical analysis

The genotypic and phenotypic variance and heritability were estimated as suggested by Johnson *et al*. (1955). Genotypic and phenotypic coefficient of variation (GCV and PCV) was estimated according to Burton and Devane (1953) and categorized according to Sivasubramanian and Menon (1973). Estimation of Genetic advance (GA) was done using the formula suggested by Robinson *et al*. (1949) and GA as percentage of mean was calculated by the formula suggested by Johnson *et al.* (1955). Correlation and path analysis were done according to Dewey and Lu (1959). According to Krzywinki and Altman (2014), box plots and scattered plots were generated and the results were interpreted as suggested by Mcleod (2019). The software used in the present study were the IRRI software - STAR (version 2.0.1, January 2014) and GENRES (1994).

RESULTS AND DISCUSSION

The ANOVA **(Table 1)** revealed that the mean squares of the 36 entries consisting of eight parents and 28 F_2 populations in 2020-21 and eight parents and 28 F_3 populations in 2021-22 differed significantly for all the six characters studied, indicating the presence of wide variability among the entries in both F_2 and F_3 generations. The variability for yield and its attributing characters in *Brassica* species was also reported by Afrin *et al.* (2011), Sandhu *et al.* (2017) and Amsalu *et al.* (2017). The considerable variability among parents and segregating populations was also reported by Ara *et al.* (2013) in inter-varietal crosses of *Brassica* species.

The mean values **(Table 2)** for the six characters differed in F_2 and F_3 generations to a different extent, implying the segregation of the genes resulting in differential phenotypic expressions of the characters in F_2 and F_3. Evaluation of mean value is a basic indicator of better performance of any entry. On comparing the character means of both the F_2 and F_3 generations, an immense shift in the mean values were observed for all the characters under study. Similar findings were reported by Byadagi *et al*. (2018). Some of the crosses mentioned below showed a high mean performance for a given character in a desirable direction, which may be used to improve the particular character. As mentioned by Khan *et al.* (2007) and Sabesan *et al.* (2016), the segregating generations having extraordinary performance can boost the yield.

Table 1. Analysis of variance (ANOVA) for seed yield and its attributing characters in Indian Mustard in the F$_2$ (2020-21) and the F3 (2021-22) generations

Sources of variation	Degrees of freedom	Generation	Mean sum of squares					
			Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	1000 Seed Weight	Seed yield per plant
Replication	2	F2	1227.715**	0.456	21.175**	3548.591**	1.072	5.828**
		F3	339.360	0.227	3.473	342.578	0.135	1.550
Genotype	35	F2	263.789**	0.953**	12.727**	1272.174**	1.491**	2.346**
		F3	1051.315**	4.094**	7.480**	2712.316**	0.814**	4.613**
Error	70	F2	76.024	0.241	2.904	373.024	0.382	0.610
		F3	245.627	0.697	3.191	846.026	0.188	1.845

**Significant at 1% probability level

Table 2. Mean performance of the parents and the respective F2 and F3 segregating populations of Indian mustard

S.No.	Treatment	Plant height (cm)		Primary branches per plant		Secondary branches per plant		Siliquae per plant		1000 Seed weight (g)		Seed yield per plant (g/plant)	
		F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3
1	Npj-194 [Parent-1]	136.00	158.58	5.53	2.57	7.93	7.17	132.86	113.12	4.33	3.25	5.06	5.06
2	RW-85-59(Sarma) [Parent-2]	131.60	119.87	4.33	3.00	7.67	9.70	137.26	143.53	3.16	3.61	4.06	3.76
3	DRMR-15-16 [Parent-3]	141.13	148.53	4.53	2.18	6.13	6.97	115.20	105.38	3.76	2.28	3.13	2.46
4	SKJM-05 [Parent-4]	145.60	109.30	4.27	2.50	3.80	5.60	117.53	103.95	5.73	3.33	3.21	4.96
5	Kranti [Parent-5]	143.53	157.78	4.27	2.58	4.53	7.42	113.06	124.53	3.56	3.40	2.46	5.94
6	Giriraj [Parent-6]	154.13	148.70	3.60	2.75	4.73	11.30	123.86	112.77	4.67	3.71	4.66	6.34
7	RNWR-09-3 [Parent-7]	138.53	175.53	4.33	3.77	4.27	7.17	112.86	111.90	5.00	3.53	2.20	6.26
8	PHR-2 [Parent-8]	163.73	186.82	6.47	2.20	10.33	8.67	129.60	115.00	3.35	3.60	3.00	6.50
9	(1×2)	129.13	112.80	4.60	4.87	4.00	6.87	123.60	234.93	3.76	3.89	3.00	6.34
10	(1×3)	155.27	118.73	4.40	7.00	3.60	9.20	112.20	174.60	4.26	3.71	4.53	6.65
11	(1×4)	137.00	136.53	4.93	4.00	2.73	8.75	102.20	199.97	3.20	4.94	1.60	6.63
12	(1×5)	131.07	121.80	3.47	3.20	2.53	7.13	107.30	149.40	4.10	3.28	2.00	5.35
13	(1×6)	144.60	127.40	4.00	4.53	2.80	6.08	103.76	118.85	4.73	4.17	2.46	4.32
14	(1×7)	135.00	115.67	4.33	4.80	4.27	6.13	121.73	121.70	3.90	2.89	2.93	4.68
15	(1×8)	150.53	122.13	4.07	4.78	3.20	8.22	104.33	122.42	2.70	3.64	1.86	5.60
16	(2×3)	136.53	116.45	4.00	4.45	3.87	6.23	98.00	164.93	4.13	3.47	2.86	3.40
17	(2×4)	136.40	109.40	4.20	4.75	3.40	5.00	99.13	128.83	3.43	3.13	2.73	5.05
18	(2×5)	133.87	118.87	3.93	5.18	6.60	6.03	137.26	105.20	3.18	2.53	2.40	3.02
19	(2×6)	142.20	120.67	4.87	5.53	7.87	7.40	139.90	100.95	3.43	3.77	3.33	3.56
20	(2×7)	139.53	119.20	4.13	4.08	5.13	5.77	113.93	116.65	2.60	3.78	2.40	3.67
21	(2×8)	135.93	113.47	4.47	3.13	5.67	5.26	108.86	95.03	2.94	3.30	2.00	4.34
22	(3×4)	139.80	111.27	4.53	5.47	6.20	7.43	147.13	134.33	3.50	3.42	2.00	3.33
23	(3×5)	168.87	117.27	4.00	4.07	7.90	6.17	125.80	107.10	4.73	2.91	4.06	4.61
24	(3×6)	135.40	120.87	4.13	4.20	5.67	7.20	123.93	129.73	3.06	3.58	2.06	7.23
25	(3×7)	134.40	107.53	4.40	2.75	5.20	7.10	126.26	133.22	3.36	3.72	1.73	5.80
26	(3×8)	147.27	112.93	4.47	2.27	7.20	6.38	138.26	85.82	3.70	3.44	2.60	3.22
27	(4×5)	144.40	115.07	4.13	3.80	7.07	5.13	150.26	136.02	3.26	3.48	3.46	4.57

Table 2. continued.

S.No.	Treatment	Plant height (cm)		Primary branches per plant		Secondary branches per plant		Siliquae per plant		1000 Seed weight (g)		Seed yield per plant (g/plant)	
		F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3	F_2	F_3
28	(4×6)	140.00	114.27	3.67	3.53	5.53	4.08	124.53	96.48	4.30	4.97	1.93	5.95
29	(4×7)	135.27	121.33	3.93	5.08	6.13	7.12	120.00	167.60	3.53	4.01	1.80	5.65
30	(4×8)	147.67	112.33	4.87	5.87	6.87	7.87	155.53	133.90	3.30	3.33	2.80	3.91
31	(5×6)	144.93	121.56	4.60	5.07	7.87	9.20	188.73	142.47	4.60	3.54	3.13	4.50
32	(5×7)	143.40	120.60	5.00	4.13	7.93	3.87	152.53	105.62	4.38	4.00	3.53	6.91
33	(5×8)	153.80	121.53	4.87	4.20	11.53	6.07	171.73	133.92	3.03	3.51	2.86	6.34
34	(6×7)	122.67	118.00	3.80	3.07	4.73	6.10	128.06	112.23	3.43	3.41	1.46	5.03
35	(6×8)	146.33	117.80	4.67	3.60	5.00	5.00	137.40	144.84	3.67	3.90	2.20	4.39
36	(7×8)	145.93	115.87	5.07	3.89	6.80	6.09	156.26	160.02	4.43	3.66	2.60	4.79
Mean		141.99	125.12	4.41	3.97	5.67	6.87	127.81	132.23	3.78	3.55	2.78	5.01
CV (%)		6.140	12.52	11.14	21.02	30.06	25.99	15.11	22.00	16.36	12.23	28.05	27.13
SEm (±)		5.03	9.05	0.28	0.48	0.98	1.03	11.15	16.80	0.36	0.25	0.45	0.78
CD (P=0.05)		14.20	25.52	0.80	1.36	2.78	2.91	31.45	47.37	1.01	0.71	1.27	2.21

The box plot and the scatter plot descriptions of the F_2 and F_3 generations of the 28 mustard crosses revealed the same **(Fig. 1, Fig. 2, Fig. 3** and **Fig. 4)**. Box plots are used to show the overall patterns of response for a group. They are useful to depict the result in the data as they show outliers within a data set. The box plots generated for all the six characters in F_2 generation exhibited a slight deviation from the normal distribution (Skewness of quartile from the center of the box). On looking into the box plot of F_2 generation **(Fig. 1)**, when compared to other traits, plant height and primary branches per plant boxes were narrow, indicating that the characters did not differ much. It was also observed that all characters (Boxes, 50% of cores which are ranged between 25th and 75th percentile) were skewed towards the minimum score (left whisker, the lowest score excluding outliers). This indicated that most of the values fell in the minimum range. The median (line dividing the box), was slightly skewed towards the positive side for the character plant height and highly skewed for the character seed yield per plant. It was also observed that all the characters exhibited the outliers (an observation that is numerically distant from the rest of the data). In F_3 generation **(Fig. 2)**, there was a deviation from the normal distribution except for 1000 seed weight. Among all the characters, plant height showed a very narrow range of variation and all the characters were skewed towards the minimum value except 1000 seed weight. The median showed a slight positive skewness for primary branches per plant, siliquae per plant and seed yield per plant, whereas, in 1000 seed weight, the median was negatively skewed.

Scatter plots are used to plot data points on a horizontal and vertical axis in the attempt to show how much one character is affected by the other character. The scatter plot generated for F_2 generation for all the characters are given in **Fig. 3**. The scatter plot revealed the weak correlation between the residuals and fitted values and all Q-Q plots showed a perfect positive correlation between residual and fitted values for primary branches per plant and secondary branches per plant whereas other traits showed a positive weak correlation with a slight skewness in the data. The scatter plots generated for F3 generation are depicted in **Fig. 4** and revealed a weak correlation between the residuals and fitted for all the traits except primary branches per plant. The Q-Q plots revealed an almost perfect correlation between residual and fitted for siliquae per plant and weak correlation for the other characters with a high skewness indicating that the characters were not following the normal distribution.

The genetic parameters for the six characters under the present study of F_2 and F_3 generations are presented in **Fig 5**. The presence of genetic variability is a prerequisite for any plant breeding programme. The GCV and PCV ranged from medium (10 – 20) to high (>20) in both F_2 and F_3 generations for all the characters, except in F_2 generation for plant height, where the GCV and PCV were low (<10). The PCV was greater than the GCV and the difference between them was high in all the characters in both F_2 and F_3 generations, indicating the greater role of the environment in the phenotypic expression of the characters **(Fig. 6)**. Similar findings regarding the huge difference between the GCV and PCV was also reported by Kumar and Mishra (2006) and Ara *et al.* (2013). The minimum PCV and GCV was observed for plant height in F_2 generation, indicating that the opportunity for improvement through selection for the character was limited. The difference between the PCV and the GCV was higher in the F_3 generation in all the characters except in 1000 seed weight, where the difference between PCV and GCV was higher in F_2 than in F_3. The

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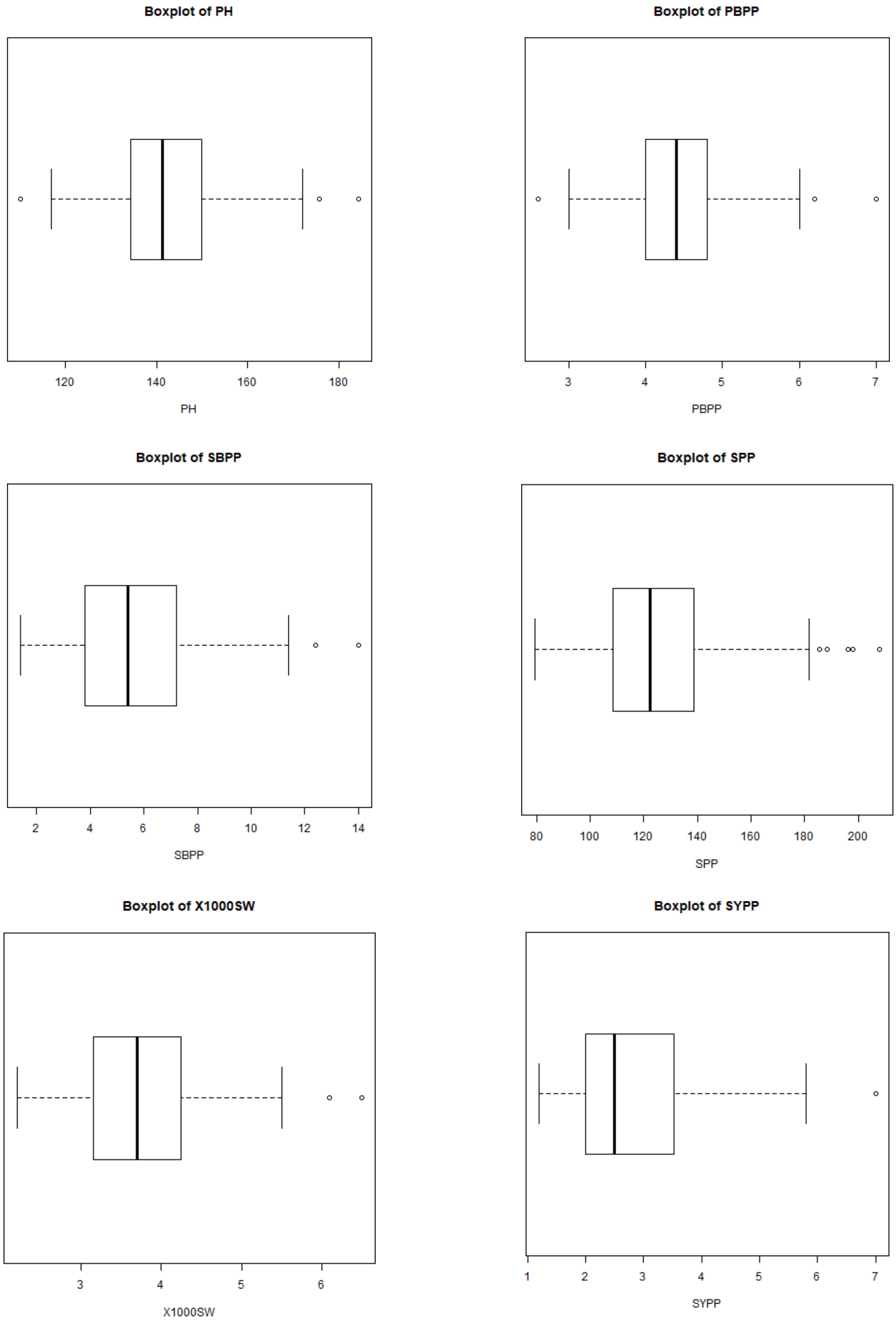

Fig. 1. Box plot depiction of the F_2 population

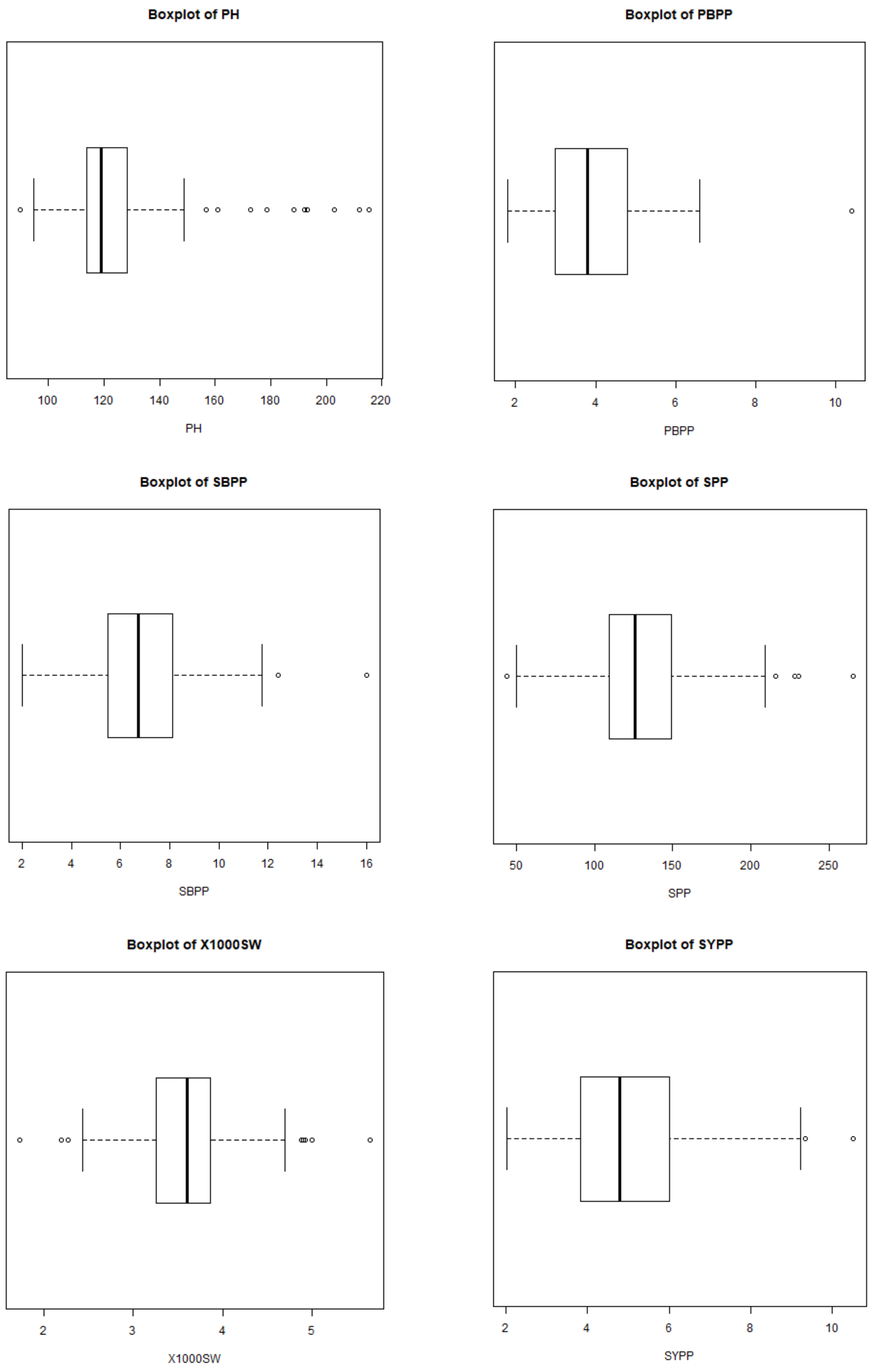

Fig. 2. Box plot depiction of the F_3 population

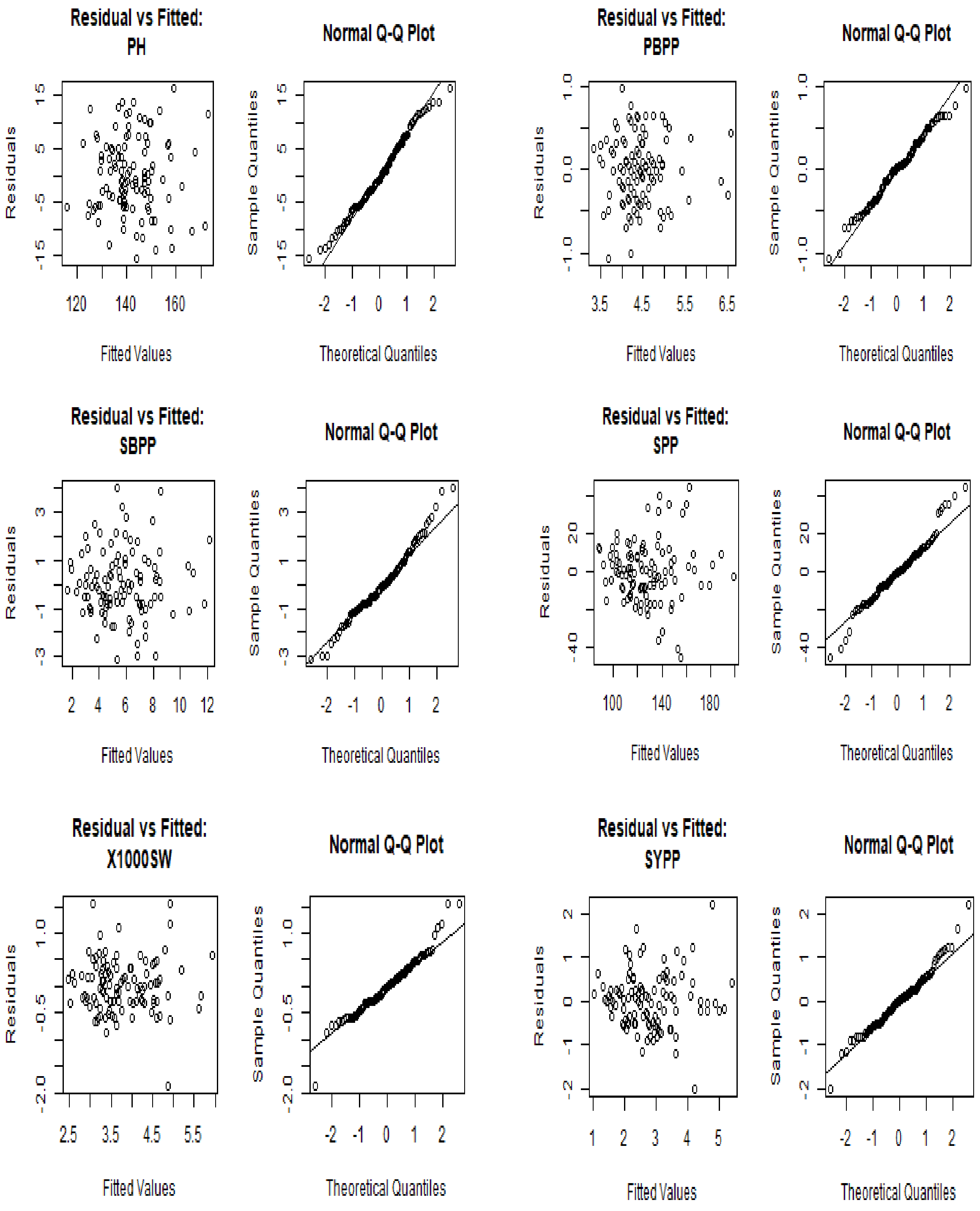

Fig. 3. Scatter plot depiction of the F_2 generation

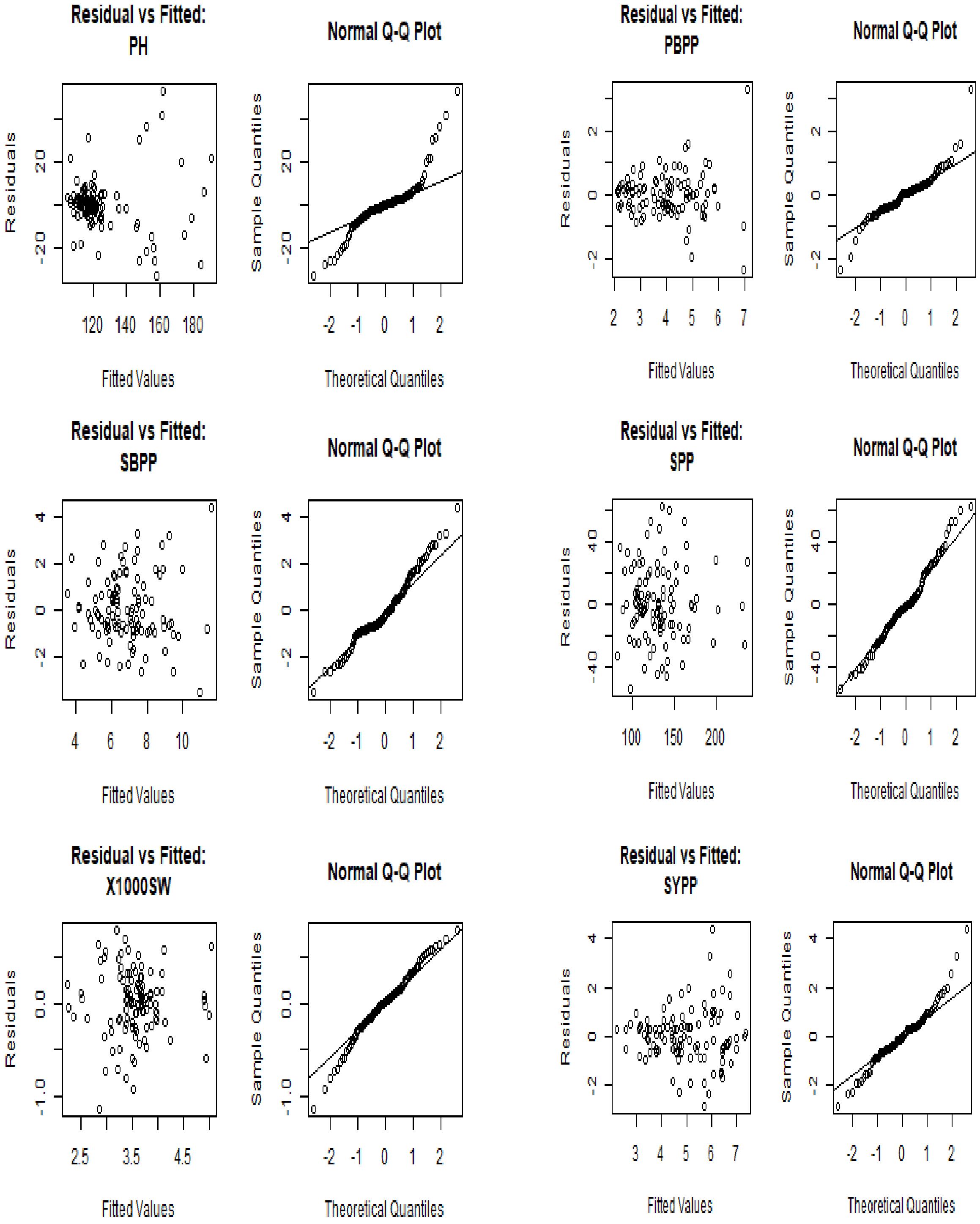

Fig. 4. Scatter plot depiction of the F_3 generation

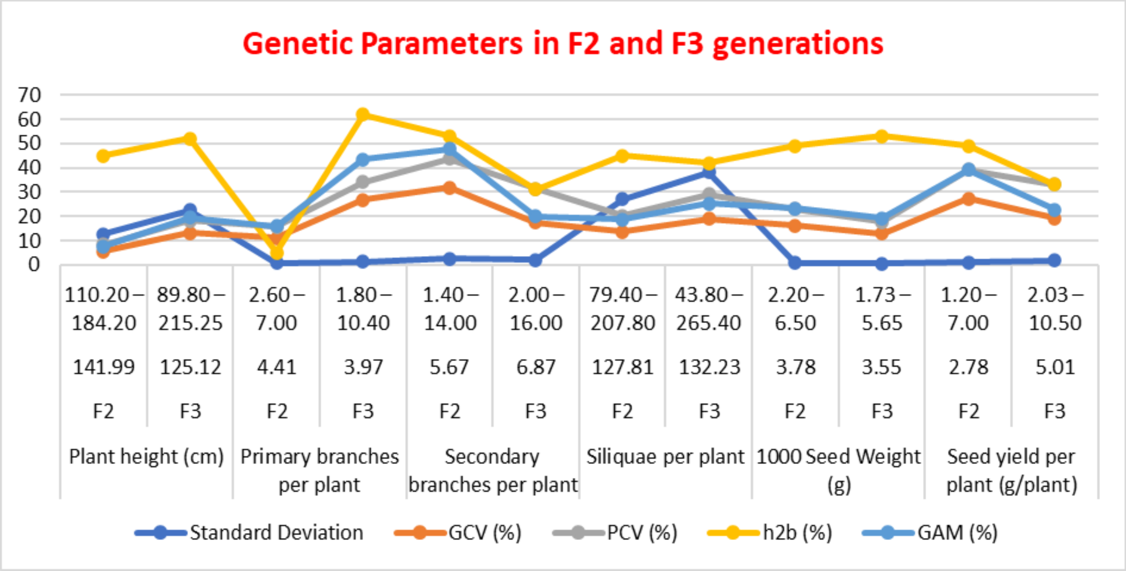

Fig. 5. Genetic parameters of seed yield and its attributing traits in Indian Mustard in the F_2 and F_3 generations

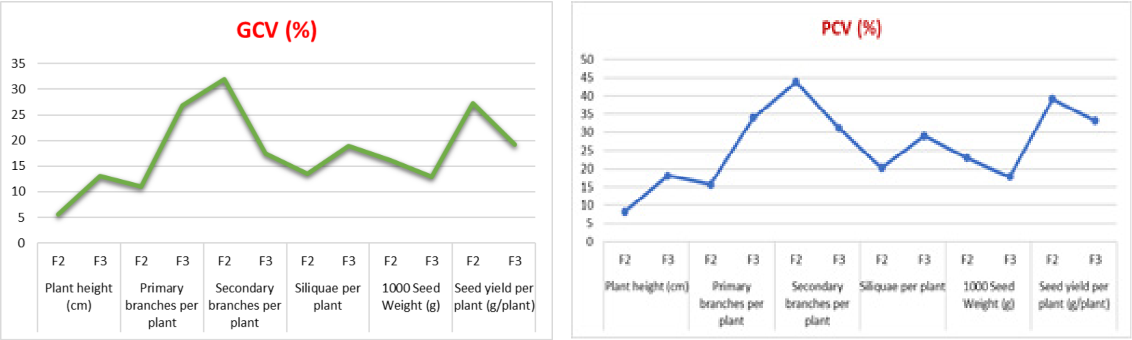

Fig. 6. GCV (%) and PCV (%) in the F_2 and F_3 generations

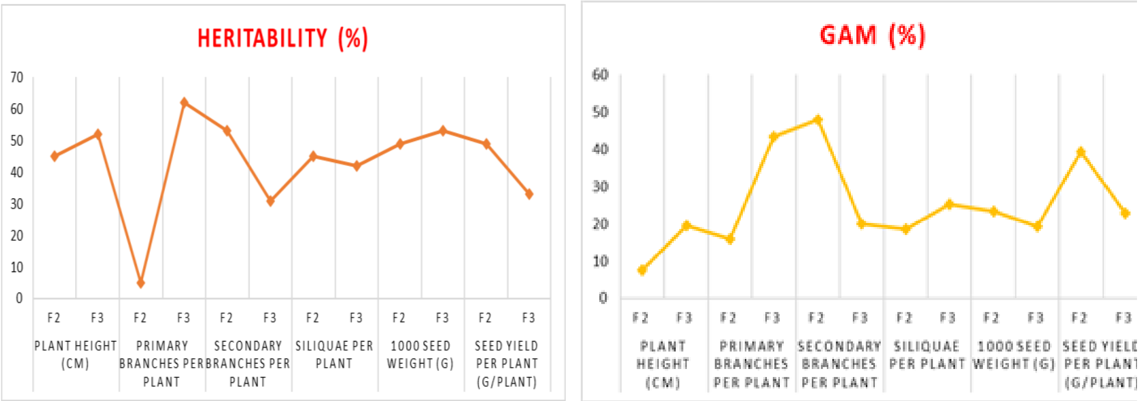

Fig. 7. Heritability (%) and GAM (%) in the F_2 and F_3 generations

variability increased further in F_3 generation giving hope that the character can be improved by selecting entries from the further segregating generations. The remaining characters showed a medium range of genotypic and phenotypic variability in both generations, indicating that the characters can be selected for improvement programmes after assessing them in further generations. The heritability in broad sense was medium for all the characters in both F_2 and F_3 generations except in case of primary branches per plant in F_3 generation, which ascertained that the environment interfered with the phenotypic expression of the characters, resulting in lower contribution of the genotype to the phenotype **(Fig. 7)**. The seed yield per plant which is a complex character dependent on several other attributing characters had expressed medium heritability, which means that seed yield per plant can be improved by improving other attributing characters like primary branches per plant, which expressed higher heritability. The Genetic advance as a percentage of the mean (GAM) was found to be higher in most of the characters except in plant height, where it was found to be low (7.71) in F_2 and medium (19.49) in F_3. The GAM was found to be moderate in primary branches per plant in F_2 (16.01), in secondary branches per plant in F_3 (19.94), in siliquae per plant in F_2 (18.63) and in 1000 seed weight in F_3 (19.26).

High heritability and high genetic advance were expressed by primary branches per plant in F_3, indicating the preponderance of additive gene action in the genetic inheritance of this character, which suggests that selection would be rewarding. Similar findings for the high heritability and high genetic advance were recorded by Gupta *et al.* (2019). In most of the other characters in F_2 and F_3, moderate genetic advance was expressed along with high or moderate GAM which also indicated additive genetic control of the mustard characters in the present study. Therefore, it is suggested to follow recombinant breeding for the improvement of the character, primary branches per plant. In most of the other characters in F_2 and F_3 moderate genetic advance was expressed along with high or moderate GAM, which also indicated additive genetic control of the characters in the present study and selection in the early generation would lead to the identification of better entries.

The character plant height was found to be positively correlated with seed yield per plant in both F_2 and F_3 generations, with secondary branches per plant in F_3 generation and negatively correlated with primary branches per plant in F_3 generation **(Table 3)**. Primary branches per plant was found to be positively correlated with secondary branches per plant in F_2 generation and siliquae per plant in both F_2 and F_3 generations. Secondary branches per plant was positively correlated with siliquae per plant only in F_2 generation. Siliquae per plant was found to be positively correlated with 1000 seed weight and seed yield per plant in F_3 generation. The 1000 seed weight was positively correlated with seed yield per plant in both F_2 and F_3 generations. The correlation of any particular character differed from F_2 to F_3 due to the segregation of genes and new genetic recombination taking place during the transmission of the characters from F_2 to $F_{3.}$

High direct effect on seed yield per plant was exhibited by plant height and 1000 seed weight in both F_2 and F_3 generations and by secondary branches per plant in the F_2 generation and siliquae per plant in the F_3 generation **(Table 4)**. Similar findings of the correlation of plant height, siliquae per plant and test weight with seed yield were reported by Yadav *et al*. (1992), Roy *et al*. (2015) and Kumar *et al*. (2018). The correlation coefficient between plant height and seed yield per plant (0.439) in

Table 3. Genotypic correlation between seed yield and its attributing characters in Indian Mustard in the F_2 and F_3 generations

Characters	Generation	Primary branches per plant	Secondary branches per plant	Siliquae per plant	1000 Seed Weight	Seed yield per plant
Plant height (cm)	F2	0.393	0.263	0.071	0.194	0.439**
	F3	-0.511**	0.552**	-0.182	-0.034	0.406*
Primary branches per plant	F2		0.741**	0.382*	-0.171	0.300
	F3		-0.076	0.504**	0.136	-0.164
Secondary branches per plant	F2			0.799**	-0.281	0.218
	F3			0.315	-0.000	-0.085
Siliquae per plant	F2				-0.054	0.115
	F3				0.442**	0.374*
1000 Seed Weight (g)	F2					0.444**
	F3					0.706**

**Significant at 1% probability level, *Significant at 5% probability level

Table 4. Direct (diagonal) and indirect (off-diagonal) effect of different characters on seed yield of Indian mustard in F$_2$ and F$_3$ generations

Characters	Generation	Plant height	Primary branches per plant	Secondary branches per plant	Siliquae per plant	1000 Seed Weight	Correlation with Seed yield per plant
Plant height (cm)	F2	0.194	0.005	0.156	-0.024	0.108	0.439**
	F3	0.907	0.084	-0.447	-0.122	-0.016	0.406*
Primary branches per plant	F2	0.076	0.012	0.438	-0.132	-0.095	0.300
	F3	-0.464	-0.164	0.062	0.339	0.063	-0.164
Secondary branches per plant	F2	0.051	0.009	0.592	-0.277	-0.157	0.218
	F3	0.501	0.013	-0.810	0.212	-0.00004	-0.085
Siliquae per plant	F2	0.014	0.005	0.473	-0.347	-0.030	0.115
	F3	-0.165	-0.083	-0.255	0.672	0.204	0.374*
1000 Seed Weight (g)	F2	0.038	-0.002	-0.166	0.019	0.557	0.444**
	F3	-0.031	-0.022	0.00007	0.297	0.462	0.706**

**Significant at 1% probability level, *Significant at 5% probability level, Residual effect for F2 = 0.758, Residual effect for F3 = 0.204

F$_2$ generation was higher than all the direct and indirect effects of the attributing characters. In contrast, in F$_3$, the correlation coefficient was lower than the direct effect of the plant height on seed yield per plant due to the negative indirect effects of plant height via secondary branches per plant, siliquae per plant and 1000 seed weight. The correlation coefficient between siliquae per plant and seed yield per plant (0.374) was lower than the direct effect in F$_3$ generation due to the negative indirect effect of siliquae per plant on seed yield per plant via plant height, primary branches per plant and secondary branches per plant which indicated that selection for these characters would not increase the seed yield. Such a negative correlation with seed yield was also reported by Islam and Haque (2015).

In F$_2$ generation, the correlation coefficient between 1000 seed weight and seed yield per plant (0.444) was lower than the direct effects of 1000 seed weight on seed yield per plant due to the negative indirect effect of 1000 seed weight on seed yield per plant via primary branches per plant and secondary branches per plant. Also, the correlation coefficient between 1000 seed weight and seed yield per plant in F$_3$ was higher than the direct effect of 1000 seed weight on seed yield per plant due to the high indirect effect of 1000 seed weight on seed yield per plant via siliquae per plant. The correlations and the direct and indirect effects of the different attributing characters on seed yield per plant varied from F$_2$ to F$_3$, indicating the segregation of the genes controlling the characters. Similar findings were reported by Tahira *et al.* (2014), Kumar *et al.* (2016) and Kumar *et al.* (2018). A higher residual effect in both F$_2$ and F$_3$ generations indicated that the characters included in the present study were not able to account for all the variability observed and more characters were needed to be included for better conclusions.

The experiment revealed that the variability present among the segregating populations such as F$_2$ and F$_3$ can be helpful for the improvement of mustard genotypes. Among all, the character siliquae per plant was found to show high range, high standard deviation, medium genotypic and phenotypic variances, medium heritability in broad sense, medium genetic advance as per cent of mean (GAM) in F$_2$ and a high GAM in F$_3$, significantly positive correlation with seed yield per plant and a high direct effect on seed yield per plant. This provides us evidence that by improving siliquae per plant, the seed yield per plant can be improved in the present set of mustard crosses in their segregating generations.

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