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Assessment of Genetic Parameters, Trait Association and Diversity Analysis in Indian Mustard [*Brassica juncea* (L.) Czern and Coss]

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ABSTRACT: The current study including twenty- seven genotypes was undertaken to assess the genetic parameters, correlation coefficient, path coefficient analysis and genetic divergence. Moderate heritability combined with high genetic advance was noticed for total aphid proliferation compared to initial, demonstrating the prevalence of additive gene effect. Analysis of variance revealed substantial amount of variability among the genotypes for all the traits, showed varied spectrum of variability between the genotypes. The 27 mustard genotypes were assembled into five clusters. Cluster II had the maximum number of genotypes. This predicted that the genotypes grouped within a particular cluster are more or less genetically similar to each other. Maximum inter-cluster divergence was amongthe cluster I and cluster IV. Genotypes belonging to these clusters wereconsidered as more divergent. Trait like primary branches per plant, seeds per siliqua and 1000 seed weight showed significant positive association with seed yield per plant. Accordingly, it very well may be surmised that by improving these attributes through selection either unaccompanied or in combination, will result in improvement of yield in mustard. Path coefficient analysis depicteda high positive direct effect on the influence of primary branches per plant on seed yield. It would merit focusing on these traits for development.

Keywords: *Brassica juncea*, heritability, genetic advance, genetic diversity, correlation and path analysis

INTRODUCTION

Indian mustard is one of the oldest spices of India according to various Sanskrit texts. It had been used in India since 300 BC (Mehra, 1968). There are150 species of genus *Brassica* which are annuals or biennial herbs (Thomas *et al.*, 2012). It was developed naturally by interspecific hybridization between *Brassica nigra* and *Brassica campestris*. The regular dissemination of these two species happened in South Western Asia and India and the essential focus of beginning of Indian mustard (Saucere, 1993). Indian mustard is an amphidiploid species with a chromosome number of 2n = 36. It is an annual, erect, herbaceous and much-branched plant. It is mostly a self-pollinated crop, however there might be an inclination of outcrossing which may fluctuate from 12 to 20 percent, which mostly relies upon the natural conditions and pollination by insects.The yield loss due to aphid may vary from 30% to 75% in mustard. It sucks the plant sap which ultimately causes water stress, wilting, reduction of the growth rate of affected crop and in yield. Genetic enhancement of a crop depends on the strength of genetic diversity and variability within the crop type. Genetic variability for yield attributing traits is a very important factor of breeding programs for widening the gene pool of the crop. The achievement of any crop breeding objective not only relies on the total of genetic variability present in the population, but it also depends on the level to which it is transmissible or heritable, which sets the boundary of advancement which can be achieved at the end of the program.

High heritable traits are responsive to selection and improvement (Khan *et al.*, 2008). Heritability estimates along is not satisfactory. Hence, heritability with genetic advances is generally more dependable in forecasting the genetic addition under selection. Yield is an extremely unpredictable attribute that is the consequence of the association of different components.Information about the interrelationship among yield and its components is the foremost

significance for utilizing the concerned quality traits (Hasan *et al.,* 2013 and Moosavi *et al.,* 2015). Simple correlation analysis of a single trait may not bring an absolute perception of the significance of individual factor in influencing seed yield (Kote *et al.,* 2014 Jadhav *et al.,* 2015 and Roy *et al.,* 2021). Path analysis gives us an opportunity of dividing correlation into various other factors. This study helps us to examine critically all the concerned factors that produce a given correlation which can be used efficiently in an current selection strategy (Sabaghnia *et al.,* 2010). Seed yield is a dependent trait controlled by several positive or negative effects of other traits. So, it is essential to check the contribution of each of the trait to emphasize the maximum influence on seed yield. Accordingly, the investigation of pathand correlation coefficient analysis together is a very important selection criterion for mustard breeding in terms of yield. Genetic diversity plays an important role in plant breeding. Generally, hybrids developed from diverse lines show superior heterosis than those between closely related parents. The distance between two clusters is the measure of the degree of diversification. More the distance between the two groups will have greater diversity and vice versa. The genotypes present in the same cluster are closely related to those belonging to different clusters (Singh, 1983). In this manner, in the current examination, endeavor has been made to distinguish the degree of hereditary fluctuation, heritability along with genetic advance, genetic diversity, correlation and path analysis among the 27 assorted genotypes of Indian mustard.

MATERIAL AND METHODS

The test was led with 27 genotypes of Indian mustard acquired from Central Soil and Salinity Research Institute (Karnal), Pulses and Oilseed Research Station, Baharampur, Directorate of Rapeseed Mustard Research, Bharatpur and Presidency University (Kolkata). The list of genotypes mentioned in (Table 1). The field preliminary was directed at Instructional Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal during the *rabi* period of the year 2018-19. The experimental materialswere grown in a Randomized Complete Block Design with three replications. Each plot is included a solitary column of 5.0 m long.The row to row spacing was kept 60 cm and plant to plant distance was kept up at 15 cm by appropriate thinning.All the recommended package of practices was followed for the effective raising of the yield. The land was brought to a fine tilth preceding to planting. The manure @ 60: 40: 40 Kg/ha of N: P: K was applied as a basal portion with half of the nitrogen applied later as a top dressing. Water system was given as and when required. An intercultural operation like thinning and weeding was done as and when necessary. Five individually chosen plants from each genotype in each replication were utilized to record the observations on the accompanying eight traits. The data wasrecordedforplant height (cm), height up to first branching (cm), primary branches per plant, seeds per siliqua, 1000 seed weight (g), seed yield per plant (g), real-time aphid proliferation (RTAP) and total aphid proliferation compared to initial aphid count (TAPI).

Table 1: List of Indian mustard genotypes.

Sr. No.	Genotype	Source
1	CS 52	Central Soil and Salinity Research Institute (Karnal)
2	Varuna	Pulses and Oilseed Research Station, Baharampur
3	CS2002-195	Central Soil and Salinity Research Institute (Karnal)
4	CS2009-142	Central Soil and Salinity Research Institute (Karnal)
5	CS2013-19	Central Soil and Salinity Research Institute (Karnal)
6	DRMR-15-5	Directorate of Rapeseed Mustard Research, Bharatpur
7	KM-126	Presidency University (Kolkata)
8	RH-0923	Pulses and Oilseed Research Station, Baharampur
9	RGN-384	Pulses and Oilseed Research Station, Baharampur
10	CS 54	Central Soil and Salinity Research Institute (Karnal)
11	RGN-389	Pulses and Oilseed Research Station, Baharampur
12	CS2004-114	Central Soil and Salinity Research Institute (Karnal)
13	CS2009-129	Central Soil and Salinity Research Institute (Karnal)
14	Kranti	Directorate of Rapeseed Mustard Research, Bharatpur
15	DRMR-15-16	Directorate of Rapeseed Mustard Research, Bharatpur
16	RB-77	Pulses and Oilseed Research Station, Baharampur
17	DRMR-15-47	Directorate of Rapeseed Mustard Research, Bharatpur
18	PRD-2013-9	Presidency University (Kolkata)
19	CS 56	Central Soil and Salinity Research Institute (Karnal)
20	Pusa Bold	Pulses and Oilseed Research Station, Baharampur
21	CS2009-105	Central Soil and Salinity Research Institute (Karnal)
22	CS2013-10	Central Soil and Salinity Research Institute (Karnal)
23	SKM-1313	Pulses and Oilseed Research Station, Baharampur
24	RW-4C-6-3	Pulses and Oilseed Research Station, Baharampur
25	RGN-385	Pulses and Oilseed Research Station, Baharampur
26	DRMR-4001	Directorate of Rapeseed Mustard Research, Bharatpur
27	Divya-88	Central Soil and Salinity Research Institute (Karnal)

Data was recorded plot basis for days to 50% flowering in each replication. 10 random siliquae from each replication was assessed for seeds per siliqua. Five samples were taken from each replication to asses the 1000 seed weight. RTAP was deliberated by dividing the aphid number in the present time point by the aphid number in the previous time point whereas TAPI wasestimated by dividing the present time point aphid number with initial aphid count. The recorded morphological attribute information was averaged and analysed for basic statistics*i.e.*, arithmetic means, range, analysis of variance, genetic parameters,correlation, path analysis and D^2 investigation utilizing computer programming WINDOW STAT 8.6 from INDOSTAT administrations, Hyderabad, India.The mean over replication of each trait was subjected to statistical analysis. The means associated with the RCBD examination were as depicted by Panse and Sukhatme (1969). The phenotypic and genotypic coefficients of variation (PCV, GCV) were registered according to the technique depicted by Burton (1952) and heritability was determined according to Allard (1960).

$\sigma^2 g$ = (MSG-MSE)/r, where MSG=Mean sum of square of genotype, MSE= Mean sum of square of error, and r=Number of replications.

$$\sigma^2 p = (\sigma^2 g) + (\sigma^2 e)$$

GCV = $[(\sqrt{\sigma^2 g})/\bar{x}] \times 100$, where $\bar{x}$= Mean of the sample

PVC = $[(\sqrt{\sigma^2 p})/\bar{x}] \times 100$

$H^2 = (\sigma^2 g / \sigma^2 p) \times 100$

$GA = K \times H^2 \times \sqrt{\sigma^2 p}$

For this evaluation K, the selection differential was 2.06 at 5% selection intensity.Genetic advance as percent of mean[GA (%)] was calculated as follows:

$$GA\ (\%) = (GA/\ \bar{x}) \times 10$$

The correlation at the genotypic level was assessed from the analysis of variance and covariance as recommended by Searle (1961).

Genotypic correlation between trait x and y

$$r_{xy}(g) = \frac{Cov_{xy}(g)}{\sqrt{Var_x(g) \times Var_y(g)}}$$

Where,

Cov_{xy} (g) = Genotypic covariance between two trait x and y

Var_x(g) = Genotypic variance for traits x

Var_y (g) = Genotypic variance for traits y

The significance of the correlation coefficient (r) was verified by associating the observed value of the correlation coefficient with the arranged value for (n-2) degrees of freedom where n is the number of genotypes. If the experiential value is more than the table value, the correlation coefficient is significant.

The direct and indirect effects were assessed at the genotypic level by taking seed yield as adependent variable utilizing way coefficient examination proposed by Sewall Wright (1921) and Dewey and Lu (1959). Path coefficient analysis was proposed by Sewall Wright (1921) and Dewey and Lu (1959). The direct and indirect effects were estimated at the genotypic level by taking seed yield as a dependent variable.

$$r_{ij} = p_{ij+} \sum r_{ik} p_{kj},$$

where r_{ij} = Common association between the independent trait (i) and dependent trait (j) as predictable by the correlation coefficient. p_{ij} = component of direct effects of the independent trait (i) and dependent trait (j) as measured by the path coefficient and, $\sum r_{ik} p_{kj}$ = summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) via all other independent trait (k).

The genetic divergence was estimated using Mahalanobis D^2 statistics (1936) followed by Rao (1952). Initially, the mean data for all the traits were analyzed and checked for normality.

The assessment of D^2 esteems by the equation *i.e.*, $D^2 = w^{ij}(\bar{x}_i^1 - \bar{x}_i^2)(\bar{x}_j^1 - \bar{x}_j^2)$extremely unpredictable since it needs the reversal of ahigh order matrix when the number of traits is huge.

As all the traits did not conform to normality, so log10(x) transformation for the mean data of traits with values above 10 was done. On account of characteristics with values under 10, log (x+1) transformation was done and subsequently, the analysis of variance for the eight attributes was done. P values as per the four different models for checking the normality of all the traits are signified in (Table 2) and log(x) and log(x+1) transformed values for the different traits in Indian mustard are represented in (Table 3).

Table 2: Computed P values as per the four different models for checking the normality of the different traits in Indian mustard.

Traits	Shapiro-Wilk	Anderson-Darling	Lilliefors	Jarque-Bera
Plant height (cm)	0.000	<0.0001	0.001	<0.0001
Primary branches / plant	0.047	0.105	0.243	0.269
Seeds / Siliqua	0.020	0.076	0.175	0.152
Height upto first fruiting branch (cm)	0.002	0.083	0.050	<0.0001
1000 Seed weight (g)	<0.0001	<0.0001	<0.0001	0.000
Real Time aphid proliferation	0.619	0.313	0.354	0.841
Total aphid proliferation compared to initial aphid count	0.024	0.010	0.025	0.155
Seed yield (g/plant)	0.005	0.002	0.000	0.200

Table interpretation:
Null Hypothesis H0: The samplefollowed the normal distribution
Alternative Ha: The sample does not follow a normal distribution.
As the figured p value is lower than the significance level alpha=0.05, one should reject the null hypothesis H0, and acknowledge the alternative hypothesis Ha.

Table 3: Log transformed values for the different traits in Indian mustard.

Transformation		log(x)	log(x+1)	log(x+1)	log(x)	log(x+1)	log(x+1)	log(x+1)	log(x+1)
Sr. No.	Genotype	Plant height (cm)	Primary branches per plant	Seeds per siliqua	Height uptofirst fruiting branch (cm)	1000 Seed weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
1	CS 52	2.12	0.78	1.05	1.76	0.67	0.43	0.87	0.91
2	CS 54	2.11	0.73	1.07	1.86	0.58	0.35	0.64	0.95
3	CS 56	2.10	0.73	1.10	1.86	0.59	0.43	0.87	0.91
4	Varuna	2.08	0.71	1.05	1.88	0.73	0.35	0.57	0.90
5	Kranti	2.03	0.70	1.11	1.84	0.74	0.34	0.41	0.95
6	Pusa Bold	2.10	0.70	1.09	1.79	0.74	0.39	0.64	0.95
7	CS2002-195	2.10	0.74	1.14	1.82	0.57	0.42	0.94	0.95
8	CS2004-114	2.00	0.71	1.10	1.82	0.75	0.31	0.51	1.13
9	CS2009-105	2.10	0.73	1.18	1.78	0.71	0.34	0.28	1.03
10	CS2009-142	1.99	0.74	1.13	1.76	0.75	0.35	0.67	1.17
11	CS2009-129	2.01	0.77	1.18	1.83	0.74	0.44	0.70	1.09
12	CS2013-10	2.18	0.76	1.19	1.86	0.67	0.41	0.84	1.08
13	CS2013-19	2.07	0.80	1.15	1.75	0.71	0.39	0.82	1.03
14	Kranti-NC	1.90	0.78	1.10	1.77	0.72	0.38	0.99	0.99
15	SKM-1313	2.05	0.76	1.06	1.71	0.67	0.38	0.89	0.98
16	DRMR-15-5	1.93	0.69	1.15	1.71	0.76	0.41	0.84	1.02
17	DRMR-15-16	2.07	0.76	1.14	1.63	0.74	0.35	0.37	1.01
19	RW-4C-6-3	2.01	0.75	1.08	1.62	0.80	0.39	0.83	1.01
20	KM-126	2.03	0.77	1.05	1.74	0.64	0.39	0.87	0.96
21	RB-77	1.95	0.78	1.16	1.72	0.72	0.39	0.79	0.99
22	RGN-385	1.90	0.84	1.13	1.67	0.73	0.36	0.69	1.03
23	RH-0923	2.07	0.83	1.05	1.72	0.74	0.35	0.57	1.03
24	DRMR-15-47	2.02	0.79	1.05	1.78	0.74	0.38	0.72	1.03
25	DRMR-4001	2.05	0.89	1.05	1.78	0.67	0.31	0.92	1.06
26	RGN-384	2.02	0.80	1.11	1.78	0.72	0.33	0.30	1.06
27	PRD-2013-9	2.06	0.76	1.13	1.67	0.72	0.35	0.55	1.00
	MEAN	**2.04**	**0.76**	**1.11**	**1.76**	**0.70**	**0.38**	**0.70**	**1.01**

RESULTS AND DISCUSSION

A. Analysis of variance (ANOVA)

Analysis of variance concerning 27 genotypes of mustard expressed significant differencesamong the genotypes utilized in the current examination,for every one of the eight attributes considered *viz*., plant height, primary branches per plant, seed per siliquae, height upto first fruiting branch, 1000-seed weight, real-time aphid proliferation, total aphid proliferation and seed yield per plant, showing the diverse scope of variation between the genotypes. The mean sum of the square for all the traits is mentioned in (Table 4). Such significant difference was earlier reported by Sandhu *et al*., (2017), Rout *et al*., (2019) and Ray *et al*., (2019) for primary branches per plant and seed yield per plant; Devi (2018), Sandhu *et al*., (2017), Tiwari (2019) for 1000 seed weight; Pal *et al*., (2019) for plant heightand seeds per siliqua.

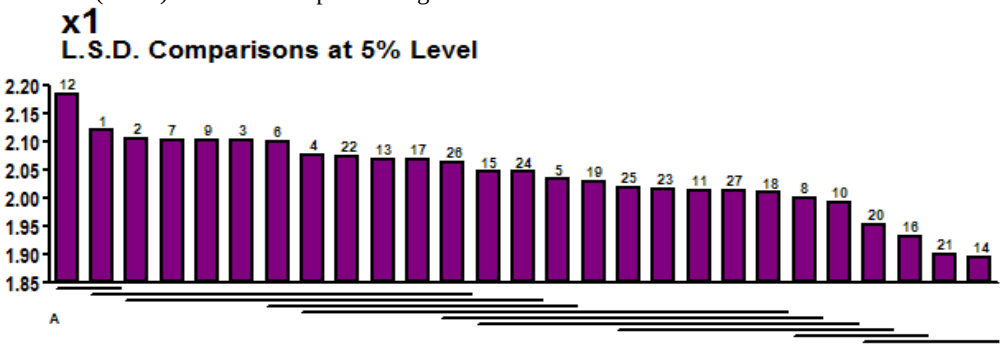
Table 4: ANOVA for seed yield and its attributing traits in mustard.

Sources of variation	Df	Mean Sum of Squares							
		Plant height (cm)	Primary branches per plant	Seeds per Siliqua	Height uptofirst fruiting branch (cm)	1000 Seed weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
Genotype	26	0.014**	0.007**	0.006**	0.020**	0.009**	0.004*	0.118**	0.012**
Replication	2	0.000	0.239	0.095	0.003	0.002	0.000	0.020	0.053
Error	52	0.002	0.002	0.001	0.003	0.002	0.002	0.014	0.005
Total	80	0.006	0.010	0.005	0.008	0.004	0.003	0.048	0.009

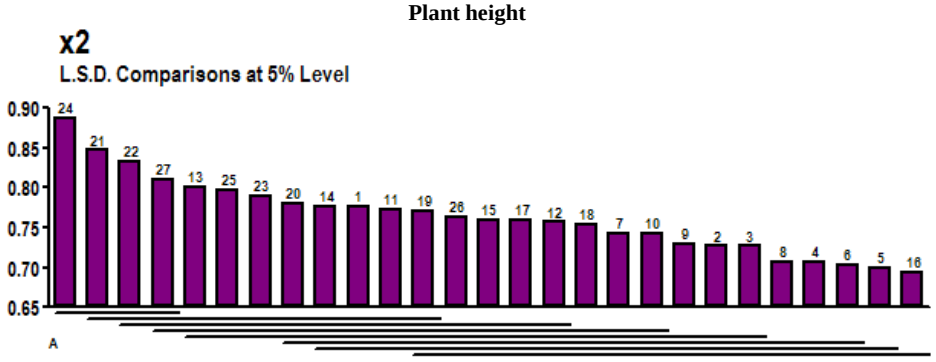
** Significant at 1% probability level

B. Mean performance of the mustard genotypes

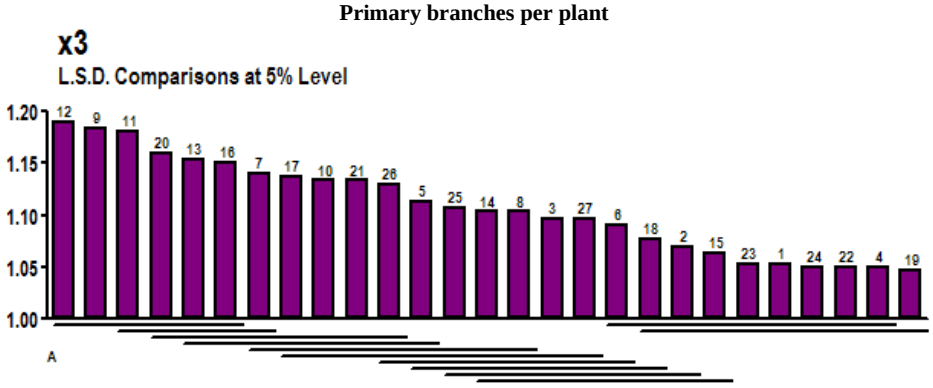
The mean performance of the mustard genotypes is presented in graphical way in (Fig. 1). In case of plant height genotype CS2013-10 (2.183) and genotype CS52 (2.120) was the best performing one which differed significantly from other genotypes but did not differ much from each other. The genotype Kranti-NC (1.897) and RB-77 (1.900) exhibited lowest plant height. However, it did not differ significantly from other genotypes namely DRMR-15-5 (1.933) and KM-126 (1.953); primary branches per plant genotype DRMR-15-47 (0.887) was the best performing one which did not differ significantly from other genotypes namely RB-77(0.847), RGN-385(0.833) and PRD-2013-9(0.810). Seeds per siliqua, genotype CS2013-10 (1.190) was the best performing one which did not differ significantly from other genotypes *i.e.* CS2009-105 (1.183), CS2009-129 (1.180), KM-126 (1.160), CS2013-19 (1.153), DRMR-15-5 (1.150) whereas lowest value observed for genotype RW-4C-6-3 (1.047). In case of height up to first fruiting branch genotype Varuna (1.883) was the best performing one which did not differ significantly from other genotypes namely CS2013-10 (1.863), CS 56 (1.860), CS 54 (1.860), Kranti-NC (1.770), CS2009-129 (1.830), CS2002-195 (1.820) and CS2004-114(1.820). Poor performance was showed by the genotype PRD-2013-9 (1.547); 1000 seed weight genotype RGN-389 (0.800) was the best performing one which did not differ significantly from other genotypes specifically DRMR-15-5 (0.760), CS2009-142 (0.750), CS2004-114 (0.747), Kranti- NC (0.720), Pusa Bold (0.740), CS2009-129 (0.740), DRMR-15-16 (0.740), RGN-385 (0.740) and RH-0923 (0.737) whereas low performing genotype was CS2002-195 (0.573). In case of real time aphid proliferation, genotype CS2009-129 (0.440) was the best performing one which did not differ significantly from other genotypes *viz.*, CS 56 (0.427), CS-52 (0.427), CS2002-195 (0.420), PRD-2013-9 (0.410), CS2013-10 (0.407), DRMR-15-5 (0.407), CS2013-19 (0.393), Pusa Bold (0.390), KM-126 (0.390), RGN-389 (0.390), RW-4C-6-3 (0.387), Karnti-NC (0.383), SKM-1313 (0.377) and RH-0923 (0.377).



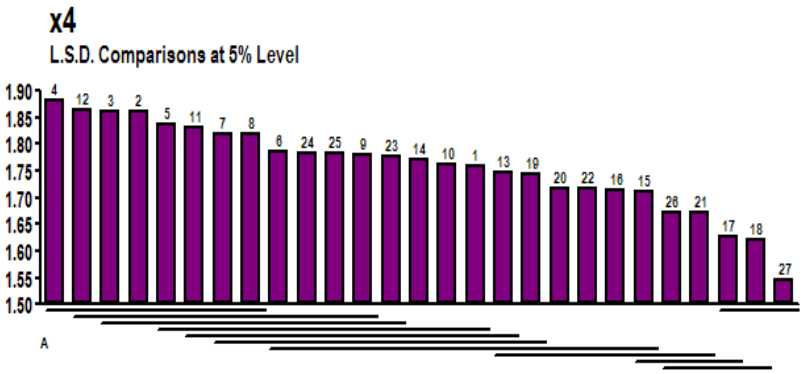
Plant height



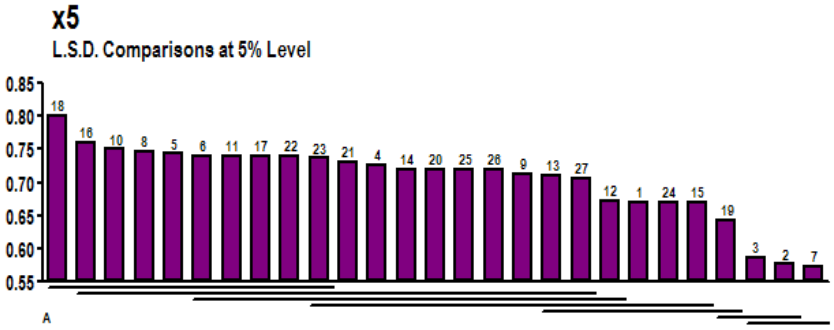
Primary branches per plant



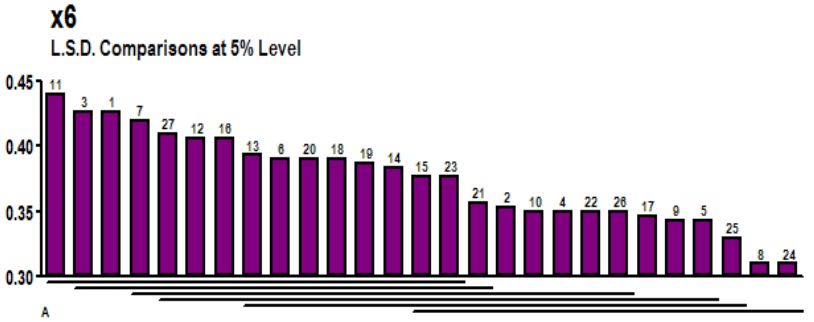
Seeds per siliqua



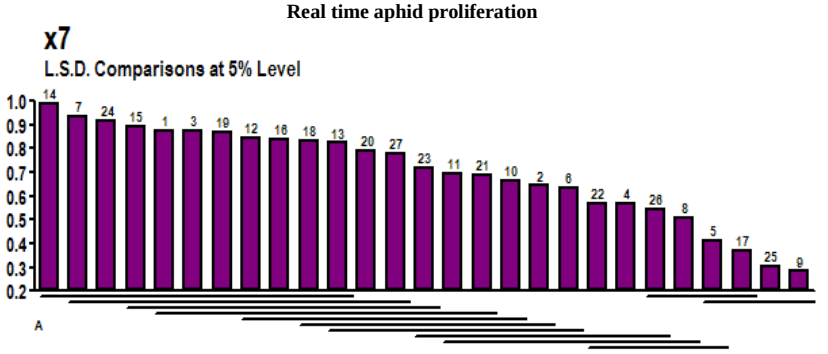
Height upto first fruiting branch



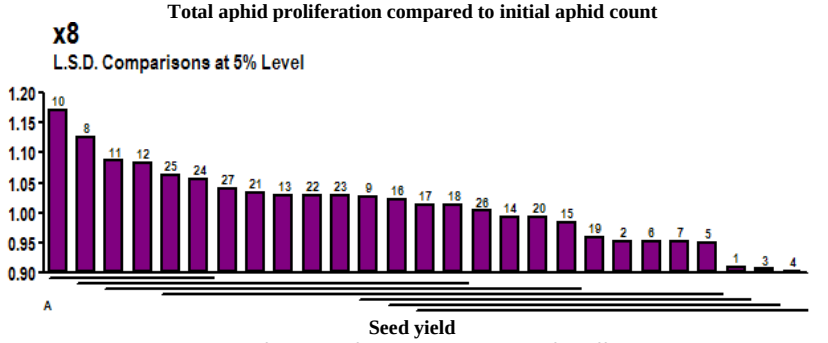
1000 seed weight



Real time aphid proliferation



Total aphid proliferation compared to initial aphid count



Seed yield

Fig. 1. Mean performance of the mustard genotypes for different traits.

Table 5: Mean table of the 27 Indian mustard genotypes.

Sr. No.	Name	Plant height (cm)	Primary branches per plant	Seeds per Siliqua	Height uptofirst fruiting branch (cm)	1000 Seed weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
1	CS 52	132.123 (2.120)	5.033 (0.777)	10.340 (1.053)	57.607 (1.760)	3.700 (0.670)	1.667 (0.427)	6.533 (0.873)	7.200 (0.910)
2	CS 54	127.413 (2.107)	4.417 (0.727)	10.787 (1.070)	72.360 (1.860)	2.833 (0.577)	1.260 (0.353)	3.533 (0.643)	8.030 (0.953)
3	CS 56	126.580 (2.103)	4.407 (0.727)	11.553 (1.097)	72.800 (1.860)	2.867 (0.587)	1.667 (0.427)	6.533 (0.873)	7.123 (0.907)
4	Varuna	118.987 (2.077)	4.180 (0.707)	10.187 (1.050)	76.587 (1.883)	4.333 (0.727)	1.237 (0.350)	2.833 (0.567)	7.023 (0.903)
5	Kranti	106.943 (2.033)	4.067 (0.700)	12.067 (1.113)	68.447 (1.837)	4.533 (0.743)	1.223 (0.343)	1.633 (0.413)	8.093 (0.950)
6	Pusa Bold	125.217 (2.100)	4.090 (0.703)	11.393 (1.090)	61.387 (1.787)	4.500 (0.740)	1.480 (0.390)	3.467 (0.637)	8.130 (0.953)
7	CS2002-195	126.560 (2.103)	4.597 (0.743)	12.953 (1.140)	66.580 (1.820)	2.767 (0.573)	1.637 (0.420)	7.767 (0.937)	8.170 (0.953)
8	CS2004-114	99.970 (2.000)	4.160 (0.707)	11.840 (1.103)	66.450 (1.820)	4.600 (0.747)	1.053 (0.310)	2.333 (0.507)	12.530 (1.127)
9	CS2009-105	127.407 (2.103)	4.423 (0.730)	14.413 (1.183)	60.833 (1.780)	4.167 (0.713)	1.220 (0.343)	0.933 (0.283)	9.713 (1.027)
10	CS2009-142	98.177 (1.993)	4.590 (0.743)	12.740 (1.133)	57.713 (1.763)	4.667 (0.750)	1.247 (0.350)	3.933 (0.667)	13.873 (1.170)
11	CS2009-129	102.867 (2.013)	5.103 (0.773)	14.393 (1.180)	67.980 (1.830)	4.500 (0.740)	1.767 (0.440)	4.133 (0.697)	11.237 (1.087)
12	CS2013-10	152.130 (2.183)	4.883 (0.757)	14.567 (1.190)	74.213 (1.863)	3.767 (0.673)	1.567 (0.407)	6.000 (0.843)	11.157 (1.083)
13	CS2013-19	118.017 (2.070)	5.463 (0.800)	13.547 (1.153)	56.040 (1.747)	4.167 (0.710)	1.490 (0.393)	5.667 (0.823)	9.830 (1.030)
14	Kranti-NC	78.517 (1.897)	5.103 (0.777)	11.827 (1.103)	58.727 (1.770)	4.300 (0.720)	1.423 (0.383)	8.733 (0.987)	9.013 (0.993)
15	SKM-1313	111.317 (2.047)	4.897 (0.760)	10.540 (1.063)	51.847 (1.710)	3.700 (0.670)	1.387 (0.377)	6.833 (0.893)	8.857 (0.983)
16	DRMR-15-5	85.727 (1.933)	3.997 (0.693)	13.213 (1.150)	51.833 (1.713)	4.733 (0.760)	1.540 (0.407)	6.233 (0.840)	9.700 (1.023)
17	DRMR-15-16	117.893 (2.070)	4.897 (0.760)	12.897 (1.137)	42.383 (1.627)	4.467 (0.740)	1.223 (0.347)	1.400 (0.370)	9.437 (1.013)

Table 5. (continued)

Sl. No.	Name	Plant height (cm)	Primary branches per plant	Seeds per Siliqua	Height upto first fruiting branch (cm)	1000 Seed weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
18.	RGN-389	103.097 (2.010)	4.847 (0.753)	10.980 (1.077)	42.133 (1.620)	5.300 (0.800)	1.463 (0.390)	5.800 (0.833)	9.443 (1.013)
19	RW-4C-6-3	108.027 (2.030)	5.047 (0.770)	10.153 (1.047)	55.787 (1.743)	3.433 (0.643)	1.440 (0.387)	6.967 (0.867)	8.473 (0.960)
20	KM-126	90.567 (1.953)	5.193 (0.780)	13.647 (1.160)	52.223 (1.717)	4.233 (0.720)	1.470 (0.390)	5.267 (0.790)	8.850 (0.993)
21	RB-77	83.260 (1.900)	6.177 (0.847)	12.840 (1.133)	47.073 (1.673)	4.333 (0.730)	1.287 (0.357)	3.967 (0.690)	9.877 (1.033)
22	RGN-385	117.767 (2.073)	5.923 (0.833)	10.227 (1.050)	51.993 (1.717)	4.467 (0.740)	1.237 (0.350)	2.833 (0.567)	9.760 (1.030)
23	RH-0923	104.277 (2.017)	5.290 (0.790)	10.253 (1.053)	59.753 (1.777)	4.500 (0.737)	1.387 (0.377)	4.433 (0.720)	9.783 (1.030)
24	DRMR-15-47	111.260 (2.047)	6.897 (0.887)	10.247 (1.050)	60.727 (1.783)	3.733 (0.670)	1.043 (0.310)	7.933 (0.917)	10.537 (1.057)
25	DRMR-4001	105.613 (2.020)	5.503 (0.797)	11.760 (1.107)	60.947 (1.783)	4.233 (0.720)	0.793 (0.330)	1.033 (0.303)	10.823 (1.063)
26	RGN-384	115.547 (2.063)	5.073 (0.763)	12.540 (1.130)	47.613 (1.673)	4.233 (0.720)	1.230 (0.350)	2.533 (0.547)	9.480 (1.003)
27	PRD-2013-9	103.010 (2.013)	5.683 (0.810)	11.620 (1.097)	36.447 (1.547)	4.100 (0.707)	1.583 (0.410)	5.300 (0.777)	10.110 (1.040)
	MEAN	111.047 (2.040)	4.961 (0.763)	11.982 (1.108)	58.462 (1.758)	4.117 (0.705)	1.371 (0.375)	4.614 (0.699)	9.491 (1.011)
	C.V. (%)	8.131 (2.049)	15.027 (6.150)	7.039 (2.226)	10.510 (2.902)	11.123 (5.878)	20.717 (11.895)	36.389 (16.937)	17.570 (7.114)
	C.D. (5%)	14.794 (0.068)	1.221 (0.077)	1.382 (0.040)	10.067 (0.084)	0.750 (0.068)	0.465 (0.073)	2.751 (0.194)	2.732 (0.118)

The values in parenthesis indicate the transformed values of the original data

Genotype Kranti-NC (0.987) showed best performance in case of total aphid proliferation compared to initial and did not differ significantly from other genotypes namely CS20002-195 (0.937), DRMR-15-47 (0.917), SKM-1313 (0.893), CS 52 (0.873), CS 56 (0.873), RW-4C-6-3 (0.867), CS2013-10 (0.843), DRMR-15-5 (0.840), RGN-385 (0.567) and CS2013-19 (5.667). In case of seed yield CS2009-142(1.170) was the best performing one which did not differ significantly from other genotypes namely CS2004-114 (1.127), CS2009-129 (1.087), CS2013-10 (1.083), DRMR-4001 (1.063) and DRMR-15-47 (1.057), whereas low performing genotype was Varuna (0.903).

C. Estimation of genetic parameters

The range of GCV and PCV was suggested by Sivasubramanian and Madhavamenon (1973). Results from the current investigation (Table 6), showedthat high (>25%) phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) wasnoticedfor total aphid proliferation compared to initial aphid count (31.60 and 26.68); moderate PCV (10-25%) was noticed for real-time aphid proliferation (13.55) and low PCV and GCV (<10%) was perceived for plant height (3.70, 3.09), primary branches per plant (7.92, 4.99), seeds per siliqua (4.45, 3.85), height up to first fruiting branch (5.21, 4.33), 1000 seed weight (9.28, 7.19) and seed yield (8.62, 4.87). Further, the current outcomes showed that assessments of PCV were for the most part higher than their identical GCV for all the attributes examined.

The PCV and GCV esteems for the various attributes didn't contrast alot, suggesting that there is a more influence of genetic factors for the outflow of these traits than environmental factors. Some traits like primary branches per plant, real-time aphid proliferation, total aphid proliferation compared to initial and seed yield per plant showed more considerable variation among GCV and PCV, which showed the more significant impact of the climate in the expression of these attributes.These results are in agreement with Islam *et al*., (2015) and Tripathi *et al*., (2019) for plant height; Rameeh*et al*., (2016) a Synrem *et al*., (2014) for seeds per siliqua.

The estimates of heritability (Table 6) were categorized into 3 major groups, *i.e.*, high heritability (> 60%), moderate heritability (30 to 60%), and low heritability (<30%). The range of low, medium and high was classified by Johnson *et al.* (1995). The traits under study showed moderate heritability (60-80%) *viz*., for plant height (69.40), the number of seed per siliquae (75.00), height up to first fruiting branch (69.00) and total aphid proliferation compared to initial aphid count (71.30) whereas, low heritability (<60%) was recorded for primary branches per plant (39.70), 1000 seed weight (59.90), real-time aphid proliferation (23.00) and seed yield (31.90). Moderate heritability was shown by plant height, the number of seed per siliquae, height up to first fruiting branch and total aphid proliferation compares to initial aphid count which signified that these traits were reasonably influenced by the environmental effects and may be accepted for improving seed yield. Bind *et al*., (2014), Tiwari *et al.*, (2017), Sandhu *et al*., (2017) and Abe*et al.*, (2019)observed moderate heritability *viz.*, for plant height, seed per siliquae and height upto first fruiting branch whereas Mahmood *et al*., (2003) observed low heritability for primary branches per plant.

The evaluation of genetic advance (Table 6) wereconsidered into three major sets, *i.e.* high (above 20%), moderate (10-20%) and low genetic advance (less than 10%). It was classified by Johnson *et al.* (1955). Genetic advance as percentage of mean was high (>20%) for only one trait *i.e.*,total aphid proliferation compared to initial aphid count (46.40); moderate (10-20%) for 1000 seed weight (11.46) and low genetic advance as percentage of the mean (<10%) was noted for plant height (5.29), primary branches per plant (6.48), number of seed per siliqua (6.87), height upto first fruiting branch (7.41), real-time aphid proliferation (6.42) and seed yield (5.66). For an effective selection, the data alone on the assessments of heritability isn't satisfactory and whenever genetic advance as percentage of mean concentrated together with heritability, it would be more significant. High genetic advance specified that the trait is governed by additive genes and selection will be worthwhile for the enhancement of such attributes. The trait 1000 seed weight displayed moderate genetic advance, thereby, signifying normal response for selection based on *per se* performance andheterosis breeding was considered for those trait which exhibited low GA as these traits showed non- additive gene action.

Table 6: Genetic parameters of 27 genotypes of Indian mustard.

Traits	Mean	Range	GCV	PCV	Heritability (Broad Sense %)	GA as percentage of Mean (%)
Plant height (cm)	2.04	1.81 – 2.20	3.09	3.70	69.40	5.29
Primary branches per plant	0.76	0.60 – 1.02	4.99	7.92	39.70	6.48
Seeds per Siliqua	1.11	1.00 – 1.27	3.85	4.45	75.00	6.87
Height uptofirst fruiting branch (cm)	1.76	1.37 – 1.93	4.33	5.21	69.00	7.41
1000 Seed weight (g)	0.71	0.49 – 0.82	7.19	9.28	59.90	11.46
Real time aphid proliferation	0.38	0.24 – 0.50	6.50	13.55	23.00	6.42
Totalaphid proliferation compared to initial aphid count	0.70	0.23 – 1.13	26.68	31.60	71.30	46.40
Seed yield (g/plant)	1.01	0.85 – 1.20	4.87	8.62	31.90	5.66

Comparable outcomes were accounted by Tiwari *et al*., (2017), Sikarwar *et al*., (2017) and Gupta *et al*., (2019). In the current investigation, moderate heritability combined with high genetic advance as percentage of mean was noticed for total aphid proliferation compared to initial (71.30 and 46.40) which showed that heritability is because of additive gene effect and selection might be effective. Plant height (69.40 and 5.29), the number of seed per siliqua (75.00 and 6.87) and height up to first fruiting branch (69.00 and 7.41)exhibited moderate heritability coupled with low genetic advance as percent of mean which uncovered the non-additive gene action. The high heritability was being displayed due to favourable effect of environment rather than genotype and selection for such traits may not be worthwhile.

D. Estimation of Genetic diversity

Clustering of genotype. In view of D^2 analysis all the 27 mustard genotypes were assembled into five groups. The clustering pattern of the genotypes is presented in (Table 7). Anaggregate of nine genotypes fell into cluster I (CS52, RW-4C-6-3, SKM-1313, Pusa Bold, CS 54, CS 56, RH-0923, Varuna, CS2013-19), ten genotypes in cluster II (Kranti, CS2004-114, CS2009-105, DRMR-4001, RGN-384, CS2009-129, DRMR-15-16, CS2009-142, DRMR-15-5, KM-126), two genotypes in cluster III (CS2002-195, CS2013-10) as well as in cluster V (RGN-385, DRMR-15-47) and four genotypes in cluster IV (Kranti-NC, RB-77, RGN-389, PRD-2013-9). Likewise, Naznin*et al*., (2015) attained five clusters by using 33 genotypes in their study and Kumari *et al*.,(2018) gotfour major groups of different sizes while assessing thirty-one *Brassica juncea* genotypes. The clustering pattern of these germplasm accessions uncovered that the germplasm gathered from a similar locale can likewise be assembled into various clusters,which demonstrated that geographic variety was not identified with the genetic diversity of the resources.

The intra and inter-cluster D^2 values were analyzed and are given in (Table 8). Maximum intra-cluster divergence value was found for cluster I (21.48) and cluster IV (21.48) followed by cluster II (21.22), cluster V (20.02) and cluster III (17.63). Genotypes having a place with groups having high intra-cluster distance are hereditarily more dissimilar and hybridization between dissimilar clusters is probably going to create wide variability with desirable segregants.

Table 7: Distribution of 27 Indian mustard genotypes in different clusters.

Cluster No.	Total no. of germplasm accessions	Source	Name of germplasm accessions
I	9	(CSSRI, Karnal) (PORS, Baharampur) (Presidency University, Kolkata) (BHU, Varanasi) (ICAR-DRMR, Bharatpur)	CS52, RW-4C-6-3, SKM-1313, Pusa Bold, CS 54, CS 56, RH-0923, Varuna, CS2013-19
II	10		Kranti, CS2004-114, CS2009-105, DRMR-4001, RGN-384, CS2009-129, DRMR-15-16, CS2009-142, DRMR-15-5, KM-126
III	2		CS2002-195, CS2013-10
IV	4		Kranti-NC, RB-77, RGN-389, PRD-2013-9
V	2		RGN-385, DRMR-15-47

Table 8: Average intra and inter-cluster D^2 values of Indian mustard genotypes

Cluster	I	II	III	IV	V
I	**21.48**	37.45	39.85	46.01	37.10
II		**21.22**	56.43	34.17	50.13
III			**17.63**	82.48	83.43
IV				**21.48**	36.30
V					**20.02**

Maximum inter-cluster D^2 value was noted between cluster V and III (83.43) followed by cluster IV and III (82.48), cluster III and II (56.43), cluster V and II (50.13), cluster IV and I (46.01), cluster III and I (39.85), cluster II and I (37.45), cluster V and I (37.10), cluster V and IV(36.3) and cluster IV and II (34.17). These findings were also similar to Mohan *et al.*, (2017) and Kumari *et al.*, (2018). To acquire the maximum desirable heterosis or valuable transgressive segregants it would be reasonable to go for crossing between the different genotypes having a place within the cluster contaning high inter-cluster distances proved by high D^2 esteems. The cluster mean values were calculated for 12 traits understudy and have been presented in Table 9. In light of cluster mean investigation, the most noteworthy cluster mean value for plant height was recorded in the case of cluster III (2.14) followed by cluster I (2.07), cluster V (2.06), cluster II (2.02) and cluster IV (1.96). The highest cluster mean value for primary branches per plant was notedon account of cluster V (0.86) followed by cluster IV (0.80), cluster III (0.75) as well as cluster I (0.75) and the lowest mean for cluster number II (0.74). High cluster mean for seeds per siliqua was recorded in the case of cluster III (1.17) followed by cluster II (1.14), cluster IV (1.10), cluster I (1.08) and cluster V (1.05). The highest cluster mean value for height up to first fruiting branch was recorded in the case of cluster III

(1.84) followed by cluster I (1.79), cluster II (1.75) as well as cluster V (1.75), cluster IV (1.65). The highest cluster mean value for 1000 seed weight was recorded in the case of cluster II & IV (0.74) followed by cluster V (0.71), cluster I (0.67), cluster III (0.62). The highest cluster mean value for real-time aphid proliferation was recorded in the case of cluster number III (0.41) followed by cluster I & IV (0.39), cluster II (0.36) and cluster V (0.33). The highest cluster mean value for total aphid proliferation compared to initial was recorded in the case of cluster number III (0.89) followed by cluster IV (0.82), cluster I (0.77), cluster V (0.74) and cluster II (0.54). The most noteworthy cluster mean value for seed yield per plant was noted if there should be an occurrence of cluster VII (22.90) followed by cluster III (21.63), cluster IV (18.90), cluster I (18.34), cluster II (17.92) and cluster I (15.63). The highest cluster mean value for 1000 seed weight was recorded in the case of cluster number II (1.05) followed by cluster V (1.04), cluster III & IV (1.02) and cluster I (0.96). Devi *et al.*,(2017)acquired the most elevated cluster mean values for plant height, shoot length, siliqua length, number of seeds per siliqua and seed yield per plant. If crossing involves parents from clusters V and III then there is a good chance of obtaining higher heterosis for plant height, primary branches per plant, seeds per siliqua, height upto first fruiting branch, real-time aphid proliferation and total aphid proliferation compare to initial. The contribution and expression of various traits understudy towards the genetic divergence are presented in (Table 9). It is obvious from the table that seeds per siliqua had a maximum contribution to divergence (27.35%) followed by height upto first fruiting branch (19.09%), total aphid proliferation compared to the initial (18.52%), plant height (14.25%), seed yield (9.12%), 1000 seed weight (8.83%), primary branches per plant (1.71%) and real-time aphid proliferation (1.14%). Hence, independently choosing genotypes from the clusters showing high inter-cluster distance for hybridization, one can likewise consider choosing parents dependent on the degree of divergence concerning the commitment of attribute towards absolute uniqueness. The present findings corroborate the earlier report of Shekhawat*et al.*, (2014), Kumar *et al.*, (2017) and Rout *et al*., (2018).

Table 9: Cluster means for 8 traits of Indian mustard genotypes and their contribution towards divergence.

Cluster	Plant height (cm)	Primary branches per plant	Seeds per siliqua	Height uptofirst fruiting branch (cm)	1000 Seed Weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
I	2.07	0.75	1.08	1.79	0.67	0.39	0.77	0.96
II	2.02	0.74	1.14	1.75	0.74	0.36	0.54	1.05
III	2.14	0.75	1.17	1.84	0.62	0.41	0.89	1.02
IV	1.96	0.80	1.10	1.65	0.74	0.39	0.82	1.02
V	2.06	0.86	1.05	1.75	0.71	0.33	0.74	1.04
Population Mean	2.04	0.76	1.11	1.76	0.71	0.38	0.70	1.01
Percent Contribution	14.25	1.71	27.35	19.09	8.83	1.14	18.52	9.12

Correlation analysis. Broad information on the interrelationship of plant attribute like seed yield and different traits of foremost significance to the breeders for improving complex quantitative traits for which direct selection isn't useful.The estimates of the genotypic correlation coefficient have been presented in (Table 10).

A positive significantcorrelation of seed yield was observed with primary branches per plant (0.633), seeds per siliqua (0.517) and 1000 seed weight (0.662). The significant negative correlation of seed yield with plant height (-0.378) and real-time aphid proliferation (-0.756) was observed. The findings of Kumar *et al.*, (2018) reported primary branches per plant exhibited a positive and significant correlation with seed yield, secondary branches per plant and siliqua per plant and Pal *et al.*, (2019) informed that 1000 seed weight and days to maturity showed a significantly positive correlation with seed yield per plant.

As per genotypic correlation study, it was found that plant height had a significant positive association with height up to first fruiting branch (0.451) and a significant negative association with 1000 seed weight (-0.556).

Primary branches per plant were positively associated with only one trait *i.e.*, total aphid proliferation compares to initial aphid count (0.366) and significant negative association with height upto first fruiting branch whereas height upto first fruiting branch was negatively associated with 1000 seed weight (-0.464). The trait 1000 seed weight had a negative association with real-time aphid proliferation (-0.460) and total aphid proliferation compared to initial aphid count (0.428), whereas real-time aphid proliferation had a positive significant association with total aphid proliferation compared to initial aphid count (0.828). In the present study, a significant positive correlation of seed yield was observed with primary branches per plant, seeds per siliqua and 1000 seed weight. Thus, it implies that the association between seed yield and the other traits showing positive significant association is high and improving these traits through selection would result in improvement of yield in mustard. These results are in agreementwith the findings of Chaurasiya *et al.*, (2019), Kumar *et al.*, (2019) and Pandey *et al.*, (2020).

Path coefficient analysis. The path coefficient analysis was mentionded in (Table 11). The correlation of plant height with seed yield per plant was negative and its

direct effect (-0.13292) was additionally negative. However, the coefficient of correlation was less than the direct effect. This indicates the presence of the indirect negative effect of plant height on seed yield via primary branches per plant (-0.509), seeds per siliqua (-0.037) and 1000 seed weight (-0.474). Primary branches per plant had a positive correlation with seed yield per plant and its direct effect (1.789) was positive. This direct effect was more than the coefficient of correlation which indicated the prevalence of indirect positive effects via other traits *i.e.*, plant height (0.037) and 1000 seed weight (0.018). The Association of seeds per siliqua with seed yield per plant was positive and its direct effect (0.582) was also high and positive. But the coefficient of correlation was lower than the direct effect.

Table 10: Estimates of correlation coefficient for genotypic correlation coefficient among 8 traits in Indian mustard.

Traits	Primary branches / plant	Seeds / Siliqua	Height uptofirst fruiting branch (cm)	1000 Seed weight (g)	Real time aphid proliferation	Total aphid proliferation compared to initial aphid count	Seed yield (g/plant)
Plant height (cm)	- 0.284	- 0.063	0.451*	- 0.556*	0.300	- 0.110	- 0.378*
Primary branches / plant		- 0.297	- 0.544*	0.021	- 0.168	0.366*	0.633*
Seeds / Siliqua			0.016	0.146	0.304	- 0.176	0.517*
Height uptofirst fruiting branch (cm)				-0.464*	0.025	- 0.020	- 0.237
1000 Seed weight (g)					- 0.460*	- 0.428*	0.662*
Real time aphid proliferation						0.828*	- 0.756*
Total aphid proliferation compared to initial aphid count							-0.294

* Significant at 5% probability level

Table 11: Direct and indirect effects of different traits on seed yield in Indian mustard.

Traits	Plant height (cm)	Primary branches / plant	Seeds / Siliqua	Height upto First Fruiting branch (cm)	1000 Seed Weight (g)	Real Time Aphid Proliferation	Total Aphid Proliferation compared to initial aphid count	Correlation with Seed yield (g/plant)
Plant height (cm)	**-0.130**	-0.509	-0.037	0.518	-0.474	0.154	0.099	- 0.378*
Primary branches / plant	0.037	**1.792**	-0.173	-0.626	0.018	-0.086	-0.329	0.633*
Seeds / Siliqua	0.008	-0.531	**0.584**	0.018	0.125	0.156	0.158	0.517*
Height upto first fruiting branch (cm)	-0.059	-0.974	0.009	**1.151**	-0.395	0.013	0.018	- 0.237
1000 Seed Weight (g)	0.072	0.038	0.085	-0.534	**0.851**	-0.236	0.385	0.662*
Real time aphid proliferation	-0.039	-0.301	0.177	0.028	-0.392	**0.513**	-0.744	- 0.756*
Total aphid proliferation compared to initial aphid count	0.014	0.655	-0.103	-0.023	-0.365	0.425	**-0.899**	-0.294

*= Significant at 5% probability level, ** = Significant at 1% probability level, Residual effect= 0.80

This indicated that the indirect positive effects of seeds per siliqua were enhanced via plant height (0.008), height upto first fruiting branch (0.018), 1000 seed weight (0.125), real-time aphid proliferation (0.156) and total aphid proliferation compared to the initial (0.158) of which the via effect through total aphid proliferation compared to initial was highest. The correlation of 1000 seed weight with yield was positive and its direct effect was also positive (0.849) but the direct effect was higher than the correlation. This was because of the indirect positive effect of 1000 seed weight via other traits like plant height (0.072), primary branches per plant (0.038), seeds per siliqua (0.085) and total aphid proliferation (0.385).

Real-time aphid proliferation showed a negative correlation with yield and its direct effect is positive whereas the direct effect was higher than correlation. This specifies the negative effect of real-time aphid proliferation through traits like plant height (-0.039), primary branches per plant (-0.301), 1000 seed weight (-0.392) and total aphid proliferation (-0.744).

Total aphid proliferation compared to initial aphid count showed a negative correlation with yield and its direct effect is also negative whereas the direct effect was lower than correlation. This specifies the indirect negative effect of total aphid proliferation compared to initial aphid count through traits seeds per siliqua (-0.103), height upto first fruiting branch (-0.023) and 1000 seed weight (-0.365). Path coefficient is a standardized partial regression coefficient, which splits the correlation coefficients into the measures of direct and indirect contributions of independent variables on dependent variables. In this study primary branches per plant showed the highest direct effect (1.792) followed by height up to first fruiting branch (1.151), 1000 seed weight (0.851), seeds per siliqua (0.584) and real-time aphid proliferation (0.513). Heretraits like primary branches per plant, seeds per siliqua and 1000 seed weight had a high positive direct effect on seed yield. It was supported by earlier findings of Roy *et al*., (2015), Solanki *et al*., (2017), Roy *et al*., (2018), Kumar *et al*., (2019).

It revealed that greater emphasis during the selection of traits should be given on those traits for improving seed yield whereas height up to first fruiting branch had a very high positive direct effect but this trait should not be taken directly for improvement of seed yield because it also showed very high negative indirect effect through primary branches per plant and 1000 seed weight. So restricted selection method should be imposed for improving yield for this trait. The contribution of residual effects that affected seed yield was very high at genotypic levels representing that the traits includedin the current investigation were deficient tointerpret for the complete variability in the dependent trait *i.e.*, seed yield per plant.An examination of the above outcomes uncovered that primary branches per plant, height up to first fruiting branch, 1000 seed weight, seeds per siliqua and real-time aphid proliferation showed a positive direct effect on yield indicating the proper relationship between trait and seed yield and direct selection for theseattribute will be rewarding for yield improvement. The indirect influence of the traits is mainly due to the indirect effects of the attribute through other component traits.

CONCLUSION

Consequently, it may be concluded that there is adequate genetic variability for most of the traits studied in the above genetic material and total aphid proliferation compared to initial aphid count showed maximum potential for effectiveness of selection. Because these traits showed high GCV as well as PCV, heritability and genetic advance as percentage of mean. This would help us design the selection methodology that can further be employedin the breeding programme to recoverseed yield in Indian mustard. The traits showing a significant positive correlation with the seed yield are primary branches per plant, seeds per siliqua and 1000 seed weight. These above said attributes could serve as marker traits for seed yield improvement in mustard. The high positive direct effect was showed by primary branches per plant indicating the proper relationship between trait and seed yield. Maximum inter-cluster D^2 value was noted among the clusters V and III which signifies that crossing would be obtained between the genotypes separated by considerable D-square distance to supply superior hybrid within the F_1 generation and promising segregating generation.

FUTURE SCOPE

The variability studies affirmed that the mustard genotypes varied altogether for the majority of the traits under investigation.The inheritances of some of the yield attributing characters were known from the values of h^2_b and GA as percentage of mean.Consequently, there is adequate opportunity for future improvement by utilizing these genotypes as breeding material. The association study about the traits by correlation and path analysis gave a clear picture regarding influence of the attributing characters on seed yield. In future, improvement in primary branches per plant, seeds per siliqua and 1000 seed weightlead to theimmediate improvement in the seed yield. As per genetic divergence study, the cross between the genotypesRGN-385 × CS2002-195, RGN-385 × CS2013-10, DRMR-15-47 × CS2002-195 and DRMR-15-47 × CS2013-10 would be worthwhile for getting desired segregants, from breeding point of view.

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Conflict of Interest. The author's declares that there is no conflict of interests regarding the publication of this article.

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