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Genetic diversity for yield and its contributing components in Indian mustard [*Brassica juncea* (L.) Czern & Coss]

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Abstract

Seventy three varieties/strains of Indian mustard [*Brassica juncea* (L.) Czern. and Coss.] were evaluated during Rabi 2017–18 under irrigated condition. Analysis of variance on 11 quantitative traits was carried out. The mean, range, phenotypic, genotypic and environmental variance, genotypic and phenotypic coefficient of variation, divergence were calculated. Path coefficient analysis was carried out using correlation coefficients to know the yield-contributing traits having true associations with seed yield. Improvement in seed yield can be achieved by selection using the correlation and path analysis data generated in this study. The genotypes QM 16-2, QM 16-3, QM 16-4, NDRE 7 and NDRS 2008 produced high seed yield per plant and these five lines constituted significant group for higher seed yield per plant. The above mentioned genotypes also showed high to very high mean performance for several other yield components. Seed yield per plant showed positive association with number of siliqua on main raceme followed by number of primary branches per plant. Path analysis identified number of siliqua followed by number of primary branches per plant as major direct contributors towards expression of seed yield per plant while number of seeds per siliqua, test weight and plant height emerged as most important indirect yield component. The material used in the study is of diverse nature and can be used in the breeding programme for development of improved genotypes in mustard.

Keywords: Genetic divergence, correlation, path coefficient, Indian mustard [*Brassica juncea* (L.) Czern. and Coss.]

Introduction

Brassica juncea L. commonly known as Indian mustard is globally used as vegetable, oilseed and condiments (Saleem *et al.*, 2017) [21]. Mustard belongs to family Brassicaceae and with *Brassica* genus. Indian mustard is a natural amphidiploids ($2n = 36$) of *B. rapa* ($2n = 20$) and *B. nigra* ($2n = 16$). Mustard is the premier oilseed Brassica which covers about 85 to 90% of the total area under cultivation of all oilseed crops (Rao *et al.*, 2017) [19]. It among rapeseed and mustard, which is grown in about 6.7 m ha in the Indian subcontinent. Indian mustard is an agriculturally important oilseed crop with a long history of cultivation in India, China and increasingly in Australia. In India, it is predominantly cultivated in Rajasthan, Uttar Pradesh, Haryana, Madhya Pradesh and Gujarat, which contribute 81.5% area and 87.5% production. The mean performance of 73 mustard genotypes along with three checks for 11 characters varied wide range of variation in mean performance of genotypes was observed for all the characters under study. The comparison of mean performance of 73 mustard entries for 11 quantitative traits using least significant differences revealed existence of very high level of variability in germplasm collections. Oil content showed highly significant and negative correlation with secondary branches per plant whereas significant and positive correlation with days to 50% flowering. The high positive direct contribution towards seed yield per plant. The highest positive direct effect on seed yield per plant was exerted by number of siliqua on main raceme followed by primary branch per plant whereas plant height, number of siliqua per plant, oil content and secondary branches per plant showed positive direct effect. The highest intra-cluster distance was observed in case of cluster I (16.940), followed by cluster VIII (15.313). The maximum inter cluster distance was observed between cluster I and IX (38.024) followed by cluster I and VII (36.332). The genotypes of cluster VII were responsible for highest cluster mean for days to 50% flowering (50.23 days) followed by entries of cluster VI (48.81 days). The proper evaluation of important crop species helps in the identification and

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utilization of improved genotypes (Jan *et al.*, 2016) ^[10]. Identifying parental material with strong heterosis use for yield and obtain genetic parameters are the important steps in the development of new cultivars. The present investigation was planned to access variability, genetic divergence, and association between traits and defines suitable selection criteria for mustard yield improvement.

Materials and Methods

The experiments were conducted at Genetics and Plant Breeding Farm of N. D. University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.) during *Rabi* 2017-18 under irrigated situations. The material for present study consisted of 73 varieties/strains of Indian mustard (*Brassica juncea* L.) comprising indigenous genotypes. The experimental plot was divided into 7 blocks of equal size, each block had 13 plots in which 3 plots were randomly allotted to three checks while, remaining 10 plots of block was used for accommodating the unreplicated test genotypes. The row to row distance and plant to plant spacing was maintained at 30cm x 10cm by thinning. To avoid the border effects the experimental plot was surrounded from all sides by non-experimental rows. Recommended cultural practices were used to raise a good crop.

Five competitive plants were randomly selected from each entry in each replication and were tagged for recording detailed field observations. Data on various quantitative characters such as days to 50 per cent flowering, days to maturity, plant height (cm), length of main raceme (cm), primary branches per plant, secondary branches per plant, number of siliquae on main raceme, number of seeds per siliqua, 1000 seed weight (g), seed yield per plant (g) and oil content (%) were recorded on the basis of five randomly selected plants, while data on two characters such as days to 50 percent flowering, days to maturity were recorded on plot basis.

Analysis of variance (ANOVA) for Augmented Block Design for all attributes was done using statistical software. Analysis of variance and the genetic parameters were computed by following standard statistical procedure. The mean data were subjected to analysis of Variance for Augmented Block Design by Federer, 1956 ^[6]. The Correlation Coefficient was calculated using the formula suggested by Searle, 1961 ^[22]. Path coefficient analysis was performed according to the method described by Dewey and Lu, 1959 ^[4]. Non-hierarchical Euclidean Analysis was calculated by the method suggested by Beal, 1969 ^[2] and Spark, 1973 ^[28].

Table 1: Adjusted mean, range and coefficient of variation of genotypes and checks mean for 11 characters in mustard

S. N.	Name of line	50% days to flowering (Days)	Plant height (cm)	No. of primary branch/plant	No. of secondary branch/plant	Length of main racheme (cm)	No. of siliqua on main racheme	No. of seed /siliqua	Maturity (days)	Test weight (gram)	Oil content %	Yield /plant (in gram)
1	WR-16-1	51.25	164	5.6	10.25	40.5	36.4	11.32	122	5.20	39.52	16.55
2	WR-16-2	51	142.2	5.1	10.5	39.81	34	13.4	126	3.87	38.76	21.55
3	WR-16-3	52.375	151.2	5.5	10.35	44	37.5	12.5	119	4.95	39.41	16.56
4	WR-16-4	51.75	135.6	5.4	10.25	44.5	36.8	12.3	112	4.55	40.27	16.75
5	WR-16-5	54	147.2	5.3	10.55	43.5	32.4	14.5	113	3.03	39.63	17.90
6	WR-16-6	56	147	5.6	10.45	42.7	35	11.4	114	4.18	40.45	18.25
7	WR-16-7	54	152	5.8	10.6	48	41.1	14.4	116	4.14	40.45	19.25
8	WR-16-8	51	151.4	5.3	10.75	49.85	40	12.5	122	4.96	40.05	20.5
9	WR-16-9	55	154	5.4	10.65	49	50.55	13.5	118	3.92	40.64	18.75
10	WR-16-10	56	146.2	5.1	11.58	49.75	33.5	12.5	124	3.77	40.72	17.85
C1	Narendra Rai	54	146.8	6.5	10.5	50	42.5	13.4	112	4.50	39.34	18.90
C3	Vardan	53	148	5.5	10	52	44	11.6	111	4.52	40.42	19.85
C2	Kranti	52	150	6	11	54	43.5	14.3	114	4.2	39.61	19.65
11	WR-16-11	57	144.8	5.3	10.45	55	39.5	12.2	113	3.64	40.65	18.45
12	MCN 16-1	52.57	145.8	5.3	10.3	43	32.25	11.6	115	4.1	39.73	18.95
13	MCN 16-2	53.55	146.8	4.9	11	43.75	33	12.6	113	3.06	38.45	19.26
14	MCN 16-3	61	152.5	5.6	10.2	44.95	34.8	12.4	115	4.87	42.80	19.05
15	MCN 16-4	63	145	4.8	8.56	53.75	42	13.3	116	4.86	40.03	17.85
16	MCN 16-5	66	155	4.6	10.75	49	37.5	14.4	117	2.95	39.94	18.95
17	MCN 16-6	54	149.5	5	8.56	48.45	36.75	12.3	113	3.95	42.80	19.75
18	QM 16-1	56	154	5.3	10	50.5	40	11.5	113	3.77	40.38	21.55
19	QM 16-2	65	147.8	5.6	10.75	51	41.2	12.3	114	5.10	39.51	20.25
20	QM 16-3	56	154.2	5.7	10.35	46.45	36.4	11.2	111	3.56	36.44	18.65
C3	Vardan	56	147.6	6.75	11	54.6	50.55	13.5	113	3.5	40.42	19.65
C2	Kranti	57	146	6.5	10.5	51.25	39.5	12.3	112	4.25	39.73	18.56
C1	Narendra Rai	65	144.6	5.9	10	48.8	36.75	13.2	113	4.95	39.34	18.75
21	QM 16-4	65	170	5.3	10.45	56.25	42.5	11.5	114	3.61	40.66	19.20
22	QM 16-5	68	111	9.2	10.5	59	45.25	16.60	114	3.7	41.16	19.75
23	MCN16-7	69	171	6.8	10.2	48.75	37.4	13.7	112	4.3	40.21	19.56
24	MCN16-8	54	145.5	5.1	10.4	43.75	31.75	13.3	115	3.3	38.11	19.54
25	MCN16-9	56	137.5	5.7	10.8	50.2	41	12.5	116	3.64	40.59	20.21
26	MCN16-10	50	142	9.8	10.6	69.81	33.45	16.9	113	4.84	40.43	20.55
27	MCN16-11	51	146.5	9.5	11.05	52.57	42.4	16.5	113	3.51	40.79	19.50

28	MCN16-12	52	151	9.5	10.4	51	41.2	14.5	114	2.45	40.77	18.50
29	QM 16-21	54	148	9.4	10.45	53	42	12.5	110	3.84	42.08	19.90
30	QM 16-22	56	139.5	9.1	10.25	43.8	34.6	12.4	117	5.36	40.15	20.20
C1	Narendra Rai	64	141.5	5	10.2	42	40	13.5	111	4.95	39.34	18.90
C2	Kranti	63	144	5.6	10.9	42.45	42.25	12.4	112	4.42	39.61	17.25
C3	Vardan	61	146.8	6	12	43.8	41	11.5	114	3.75	40.42	18.25
31	QM 16-23	64	173	5.4	11.25	50.05	37.8	13.6	113	4.51	40.32	19.45
32	QM 16-24	64	111	5.3	10.4	51.5	42.4	12.7	113	3.81	40.21	20.23
33	QM 16-25	56	137.5	5.4	11	51.3	43	12.6	112	3.43	40.79	20.98
34	MLN(E)1421	54	138.8	4.6	11.5	45.56	36.4	13.5	112	3.95	40.72	19.78
35	MLN(E)1422	53	140	4.6	10.55	42.5	37	12.8	110	3.87	40.71	16.90
36	V3MCN(E)1425	53	143.6	5.4	10.4	45.2	38.5	12.9	119	4.62	39.63	17.10
37	V5MCN(E)1424	56	142.5	5.5	9.95	44.4	32.2	12.5	117	3.7	40.35	17.14
38	V5MCN(E)1425	57	145	5.4	10.65	46.65	33.8	13.8	110	4.5	40.01	17.76
39	V5MCN(E)1426	64	137.5	5.8	10.75	52.44	42	12.7	111	3.77	41.21	18.67
40	V7MCN(E)1430	66	142.6	5.5	10.35	53	41.2	14.3	112	4.64	39.93	19.45
C2	Kranti	61	142	5.75	11	43.7	41	13.6	112	3.06	39.6	20.22
C3	Vardan	62	141.5	5.8	11.56	42.8	39.75	11.7	111	3.56	40.42	21.00
C1	Narendra Rai	61	146	6	11.5	45	40.75	12.5	110	4.9	39.35	19.99
41	V7MCN(E)1431	52	146	5.3	10.9	56.65	43	15.6	119	3.06	40.72	20.00
42	V7MCN(E)1432	55	142.5	5.6	10.4	43.25	39.6	12.6	118	2.86	39.95	17.90
43	V8MCN(E)1430	66	143	5.4	10.8	47.25	40	11.5	114	2.89	40.95	18.50
44	NDRY8	64	144.2	4.6	10	48.55	35.6	13.6	123	3.94	40.51	17.60
45	NDRY20	63	142	5	10.55	43.2	38	12.6	121	3.66	40.81	18.56
46	PR2012-9	52	144	5.1	10.5	45.54	39.8	11.6	124	2.92	40.16	19.56
47	RRW871	63	142	5.25	10.3	47.75	34.6	12.7	123	4.46	39.32	19.99
48	RH749(F)	67	134.6	5.35	10.7	49.2	23.82	12.8	123	4.24	40.97	20.22
49	NDRS2007-1	63	138.8	5.75	10.2	52.7	41.25	13.6	124	3.44	40.87	21.00
50	NDRS2008-1	53	145	5.4	10.88	68.71	37	13.7	126	3.78	41.29	18.95
C2	Kranti	63	139	6	12	41	39.75	11.6	113	3.75	39.61	21.10
C1	Narendra Rai	57	141.7	5.5	10	42.5	40	13.9	123	4.42	39.34	20.00
C3	Vardan	53	150	5.8	11.5	47.7	34	12.7	118	5	40.4	20.86
51	NDRE 16-17	68	133.6	5.75	10.35	42.25	36.4	12.8	118	2.45	40.42	19.45
52	NDRE 16-18	63	144.8	5.9	10	43	33.7	11.7	118	3.02	41.61	17.99
53	NDRS2009-1	68	139	5.45	10.25	42.1	35.4	12.8	116	3.76	39.96	18.97
54	RGN 385	64	138.4	5.6	10.5	43	32.75	13.6	116	4.32	40.39	19.56
55	RGN73(LR)	64	142	5.2	10.2	60	23.82	13.7	117	4.14	40.84	20.22
56	V8MCN(E)1430	62	143	5.4	10.8	47.25	40	11.8	117	2.89	40.95	21.00
57	NDRY8	67	173	4.6	10	44.4	35.6	13.7	119	3.94	40.51	19.05
58	NDRY20	51	166	5	10.55	43.2	38	12.8	114	3.66	40.81	19.00
59	PR2012-9	55	116	5.1	10.5	45.54	39.8	11.9	113	2.92	40.16	20.00
60	RRW871	50	123	5.25	10.3	47.75	34.6	12.7	112	4.46	39.32	19.65
C3	Vardan	52	139	6	12	41	39.75	11.7	126	3.75	39.61	19.55
C1	Narendra Rai	53	141.7	5.5	10	42.5	40	13.8	125	4.42	39.34	17.85
C2	Kranti	52	150	5.8	11.5	47.7	34	12.9	121	5	40.4	16.90
61	RH749(F)	54	134.6	5.35	10.7	49.2	35	12.7	112	4.24	40.97	21.00
62	NDRS2007-1	56	138.8	5.75	10.2	52.7	41.25	13.8	112	3.44	40.87	20.25
63	NDRS2008-1	64	145	5.4	10.9	42.65	37	13.9	122	3.78	41.29	19.55
64	NDRE 16-17	56	133.6	5.75	10.35	42.25	36.4	12.8	121	2.45	40.42	18.95
65	NDRE 16-18	67	144.8	5.9	10	43	33.7	11.7	112	3.02	41.61	17.00
66	NDRS2009-1	65	139	5.45	10.25	42.1	35.4	12.6	120	3.76	39.96	16.85
67	RGN 385	63	138.4	5.6	10.5	43	32.75	13.8	113	4.32	40.39	18.78
68	RGN73(LR)	61	142	5.2	10.2	60	31.5	13.6	118	4.14	40.84	17.76
69	CSCN 15-1	62	132.8	5.45	10.6	47.8	34.6	14.7	114	3.88	40.73	18.75
70	CSCN15-2	51	144.8	5.75	10.25	53.24	41	15.7	114	3.17	40.37	20.5
C3	Vardan	53	141.2	5.5	10.2	39	41	12.6	114	3.7	40.42	19.45
C2	Kranti	52	144.8	5.8	11	44	39	11.7	112	4.42	39.61	18.50
C1	Narendra Rai	62	146	5.5	10.5	45.52	38.75	14.5	112	4.99	39.34	17.25

Table 2: Estimates of genotypic correlation coefficients between different characters in seventy three germplasm of mustard

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plant	Number of secondary branches/plant	Length of main raceme	No. of siliquae on main raceme	No. of seed per siliqua	Test weight	Oil content %	Seed yield/plant (g)
Days to 50% flowering	1.0000	-0.0876	-0.4577	4.0447	0.1506	0.0323	-0.0566	0.4097	0.2051	0.2754	-0.2735
Days to maturity		1.0000	-0.0581	0.7087	0.0801	-0.3288	0.0992	-0.5229	-0.1183	-0.1554	0.1239
Plant height (cm)			1.0000	2.9180	0.3337	-0.2718	0.1709	-0.3129	-0.4005	-0.0725	0.1675
Number of primary branches				1.0000	-6.6755	0.8325	-1.7450	-0.8883	1.8244	-2.5137	2.0683
Number of secondary branches					1.0000	0.2232	-0.0975	-0.3974	0.1210	-0.2898	0.2076
Length of main raceme						1.0000	0.9580	-0.2761	-0.2435	0.5029	0.3162
No. of siliquae on main raceme							1.0000	0.8371	0.0040	0.4599	0.0335
No. of seed per siliqua								1.0000	-1.1670	0.1566	0.1145
Test weight									1.0000	0.2916	0.8519
Oil content %										1.0000	-0.2504

Table 3: Estimates of phenotypic correlation coefficients between different characters in seventy three genotypes of mustard

Characters	Days to 50% flowering	Plant height (cm)	Days to maturity	Primary branch/plant	Secondary branch/plant	Length of main raceme (cm)	No. of siliqua on main raceme	Seeds/siliqua	Test weight (gm)	Oil content %	Yield/plant
Days to 50% flowering	1.0000	-0.2878*	0.0859**	0.1301	0.0032	0.0586	-0.0932	0.0941	0.1654	0.1695**	0.0062
Plant height (cm)		1.0000	0.1093**	0.0042	0.0802	-0.0220	0.1588	0.0836	-0.1126	-0.0435**	-0.0043
Days to maturity			1.0000	0.1904	0.0723	0.1278	0.0830	0.0446	-0.0349	0.0840	0.0913**
Primary branch/plant				1.0000	0.0916	0.1060	0.0928	0.0439	-0.0051	0.0291	-0.0255
Secondary branch/plant					1.0000	0.5412**	0.3099**	-0.1343	-0.0116	0.2794**	0.0955**
Length of main raceme						1.0000	0.0171	0.0116	-0.0214	0.2365**	0.1191**
No. of siliqua on main raceme							1.0000	-0.0397	-0.1284	-0.0599**	-0.1237**
Seeds/siliqua								1.0000	0.0345	-0.1723**	0.0003
Test weight (gm)									1.0000	-0.0782**	0.0408
Oil content %										1.0000	0.0544

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

Table 4: Direct and indirect effect phenotypic of different characters on seed yield per plant in mustard

Characters	Days to 50% flowering	Plant height	Days to maturity	Primary branch/plant	Secondary branch/plant	Length of main raceme	No. of siliquae on main raceme	Seeds/siliqua	Test weight	Oil content %	Yield/plant (g)
Days to 50% flowering	0.1805	-0.0024	-0.007	0.0011	0.0000	0.0005	-0.0008	-0.0008	0.0014	0.0014	0.0062
Plant height	-0.0085	0.0297	-0.0032	0.0001	0.0024	-0.0007	0.0047	0.0025	-0.0033	-0.0013	-0.0043
Days to maturity	-0.0090	-0.0114	0.1047	0.0199	0.0076	0.0134	0.0087	-0.0047	-0.0037	0.0088	0.0913
Primary branch/plant	-0.0062	-0.0002	-0.0091	-0.0479	-0.0044	-0.0051	-0.0044	-0.0021	0.0002	-0.0014	-0.0255
Secondary branch/plant	0.0004	0.0093	0.0084	0.0106	0.1155	0.0625	0.0358	-0.0155	-0.0012	0.0323	0.0955
Length of main raceme	0.0031	-0.0012	0.0067	0.0056	0.0284	0.3838	0.0009	0.0006	-0.0011	0.0124	0.1191
No. of siliquae on main raceme	0.0154	0.0308	-0.0137	-0.0153	-0.0511	-0.0028	0.2203	0.0065	0.0212	0.0099	-0.1237
Seeds/siliqua	-0.0012	0.0010	-0.0005	0.0005	-0.0016	0.0001	-0.0005	0.1590	0.0004	-0.0021	0.0003
Test weight	0.0044	-0.0030	-0.0009	-0.0001	-0.0003	-0.0006	-0.0034	0.0009	0.7525	-0.0021	0.0408
Oil content %	-0.0006	0.0002	-0.0003	-0.0001	-0.0010	-0.0008	0.0002	0.0006	0.0003	-0.0035	0.0544

Residual effect = 0.0493, Bold figures indicate direct effects.

Table 5: Direct and indirect effect genotypic of different characters on seed yield per plant in mustard

Characters	Days to 50% flowering	Plant height	Days to maturity	Primary branch/plant	Secondary branch/plant	Length of main raceme	No. of siliquae on main raceme	Seeds/siliqua	Test weight	Oil content %	Yield/plant (g)
Days to 50% flowering	0.0940	-0.0430	0.3803	0.0142	0.0030	-0.0053	0.0385	-0.0082	0.0193	0.0259	-0.2733
Plant height	-0.0076	0.0165	0.0483	0.0055	-0.0045	0.0028	-0.0052	-0.0010	-0.0066	-0.0012	0.1675
Days to maturity	-0.0376	-0.0271	-0.0093	0.0620	-0.0077	0.0162	0.0083	-0.0066	-0.0169	0.0233	2.0683
Primary branch/plant	-0.0166	-0.0367	0.7341	-0.1100	-0.0275	0.0107	0.0437	-0.0088	-0.0133	0.0319	0.2076
Secondary branch/plant	-0.0112	0.0943	-0.2889	-0.0774	-0.3471	-0.3325	0.0958	0.1141	0.0845	-0.1745	0.3162
Length of main raceme	-0.0595	0.1796	-1.8338	-0.1025	1.0067	1.0509	0.8796	0.1043	0.0042	0.4833	0.0335
No. of siliquae on main raceme	-0.1558	0.1190	0.3377	0.1511	0.1050	-0.3182	-0.3802	0.1988	0.4437	-0.0595	0.1145
Seeds/siliqua	0.0287	0.0191	-0.2326	-0.0263	0.1079	-0.0326	0.1716	-0.3282	0.0388	0.0510	0.1239
Test weight	0.1081	-0.2110	0.9613	0.0638	-0.1283	0.0021	-0.6149	-0.0623	0.5269	0.1536	0.8519
Oil content %	-0.2159	0.0568	1.9711	0.2272	0.2272	-0.3607	-0.1228	0.1219	-0.2286	-0.7842	-0.2504

Residual effect = 0.7606, Bold figures indicate direct effects

Table 6: Clustering pattern of seventy three mustard genotypes on the basis of non-hierarchical Euclidean cluster analysis

Cluster number	Number of genotypes	Genotypes
I	8	MCNWR-16-1, MCNWR-16-4, MCNWR-16-3, IVT TS MCN-16-1, MCNWR-16-6, MCNWR16-2, MCNWR16-5, IVTSMCN-16-2
II	7	MCNWR-16-8, MCNWR-16-9, MCNWR-16-7, C2 KRANTI, C3 VARDAN, C1 NARENDRA RAI, IVTQM 16-2
III	9	MCNWR-16-11, NDRY 20, IVT TS MCN 16-6, NDRY 8, IVT TS MCN-16-4, IVT TS MCN 16-5, IVT QM 16-1, IVT QM 16-3, IVT TS MCN 16-3
IV	3	V8 MCN(E)1430, PR2012-9, V7 MCN(E)1432
V	12	MCNWR 16-10, MLN(E)1421, RGN73(LR), AVT QM 16-21, NDRS2008-1, MLN(E)1422, NDRS 2009-1, RGN 385, IVT TS MCN 16-10, NDRE 16-18, NDRE 16-17, CSCN15-1
VI	8	AVT QM 16-22, AVT QM 16-23, AVT QM 16-24, NDRE 7, NDRE 16-13, NDRE 16-14, NDRE 16-15, NDRE 16-16
VII	4	AVT QM 16-25, RH 7499F), V5 MCN(E)1426, IVT TS MCN 16-7
VIII	10	IVT TS MCN 16-8, NDI 196, V3 MCN (E)1425, V5 MCN (E) 1425, V7 MCN(E)1430, V5 MCN (E) 1424, NDRE 16-11, NDRE 16-12, RIJEB 52, RRW 871
IX	12	IVT QM 16-4, IVT QM 16-5, IVT TS MCN 16-9, NDRS 2007-1, NDRE 4, IVT TS MCN 16-11, RH 1202, CSCN 15-2, CSCN 15-10, IVT TS MCN 16-12, V7MCN(E) 1431, CSCN 15-11

Table 7: Estimates of average intra and inter-cluster distances for the nine clusters in mustard

Clusters	I	II	III	VI	V	VI	VII	VIII	IX
I	16.940	20.425	23.497	26.310	25.363	29.890	36.332	26.240	38.024
II		10.509	16.261	18.112	18.441	21.622	23.473	20.376	20.898
III			11.909	17.432	21.079	25.144	30.735	23.793	24.555
IV				6.070	21.184	24.395	25.225	20.036	18.784
V					12.400	18.275	19.301	21.777	18.571
VI						12.422	19.585	21.438	25.813
VII							14.464	24.485	19.613
VIII								15.313	25.140
IX									13.492

Bold figure represents intra cluster distance

Results and Discussion

The mean performance of 73 mustard genotypes along with three checks for 11 characters is presented in Table 1. Very wide range of variation in mean performance of genotypes was observed for all the characters under study. The comparison of mean performance of 73 mustard entries for 11 quantitative traits using least significant differences revealed existence of very high level of variability in germplasm collections. Among the genotypes, QM 16-1 (21.55g), QM 16-2 (21.50g), IVT QM 16-3 and QM 16-5 were produced highest seed yield per plant with first, second, third and fourth ranks. Seed yield per plant ranged from 16.75 g WR 4 to 21.55 g QM 16-1 with general mean 19.15 g. 34 genotypes showed significantly higher seed yield per plant than the

general mean performance. In addition some other genotypes showing very high mean performance for other characters that may be utilized as donors for improving those characters in a component breeding approach even if they had medium or low seed yield per plant. Similar findings for yield and yield related traits has been discussed in many studies (Upadhyay and Kumar, 2011, Bhogal *et al.*, 2013, Sharma *et al.*, 2015, Akabari and Niranjana, 2015, Priyamedha *et al.*, 2015) [1, 3, 18, 24, 29].

The seed yield or economic yield in almost all the crops is referred to multiplicative interaction of several other characters with yield traits. Thus the genetic architecture of seed yield in mustard is directly or indirectly by interacting with one another. Therefore, identification of yield

components and information about their association with yield and also with each other is very useful for developing efficient breeding strategy for evolving high yielding varieties. In this respect, the correlation coefficient, which provides symmetrical measurement and degree of association between two variable or other characters, helps in understanding the nature and magnitude of association among yield and yield components (Mondal and Khajuria, 2009, Shalini *et al.*, 2000) [16, 23]. Direct and indirect correlation of different characters is given in table 2 & 3. The seed yield per plant exhibited non-significant but positive correlation with primary branches per plant, secondary branches per plant and days to maturity. Many reports available in agreements of this results (Sirohi *et al.*, 2015, Kumar and Pandey, 2017) [27]. Number of siliqua per plant exhibited highly significant and positive correlation with primary branches per plant, and non-significant and positive correlation with secondary branches per plant, days to maturity, and plant height. Correlation coefficient into direct and indirect effects of independent variable on dependent variable has been studied in Indian mustard for many agri-horticultural traits from yield and its components (Lal *et al.*, 2011, Sirohi *et al.*, 2015, Gangapur *et al.*, 2009, Kumar and Pandey, 2017, Lodhi *et al.*, 2017) [7, 13, 14, 27].

Sewall Wright (1921) [31] developed the concept of Path coefficient analysis as a tool to partition the observed correlation coefficient into direct and indirect effects of independent variable on dependent variable. Path analysis differs from simple correlation in that it points out the causes and their relative importance, whereas, the later measures simply the mutual association ignoring the causation. Path analysis has emerged as powerful and widely used technique for understanding the direct and indirect contribution of different characters to economic yield in crop plants so that the relative importance of various yield contributing characters can be assessed (Rathod *et al.*, 2015, Kumar *et al.*, 2016) [12, 20]. In the present study, the path coefficient analysis was carried out using simple correlation coefficient (Table 4&5). The high positive direct contribution towards seed yield per plant. The highest positive direct effect on seed yield per plant was exerted by number of siliqua on main raceme followed by primary branch per plant whereas plant height, number of siliqua per plant, oil content and secondary branches per plant showed positive direct effect. Remaining characters seed per siliqua, 1000 seed weight, days to maturity and days to 50% flowering contributed negative direct effect. Earlier, many researchers has been reported about path coefficient analysis in their study they observed that the yield traits were significantly affected by other yield components and exhibited positive direct and indirect effects (Shalini *et al.*, 2000 and Kumar *et al.*, 2017) [23].

The germplasm is the reservoir of genetic diversity, which is exploited to meet the changing needs for developing improved varieties of a crop. It is also important that considerable variability for economic traits must exist in the germplasm for profitable exploitation following recombination breeding or selection. However, the genetic diversity of selected parents is not always based on factors such as geographic diversity of release or ploidy level. Thus, the characterization of germplasm for genetic divergence and selection of suitable and diverse genotypes should be based on second statistical procedures, such as D² statistics and non-hierarchical Euclidean cluster analysis (Verma and Sachan, 2009, Goswami and Behl, 2010, Pandey *et al.*, 2013,

Shekhawat *et al.*, 2014, Singh *et al.*, 2016) [8, 17, 25, 26, 30]. The genetic divergence existing in 73 mustard germplasm collections was studied by employing non-hierarchical Euclidean cluster analysis for 11 quantitative characters. The 73 genotypes were grouped into 1 to 9 different cluster arrangements. Therefore, the 73 genotypes were accepted to be grouped into 9 different non-overlapping clusters. The distribution of 73 mustard genotypes in 9 clusters is given in Table 6. The highest number of genotypes appeared in cluster V and cluster IX which contained 12 entries each followed by cluster VIII having 10 entries. Cluster III possess 9 entries. Cluster VI and I contains 8 entries each. Cluster II possessed 7 lines. Cluster VII having 4 lines. The estimates of intra and inter cluster distance for 11 characters are presented in Table-7. The highest intra-cluster distance was observed in case of cluster I (16.940), followed by cluster VIII (15.313). The maximum inter cluster distance was observed between cluster I and IX (38.024) followed by cluster I and VII (36.332). The minimum inter-cluster distance was observed between cluster II and III (16.261) followed by cluster III and IV (17.432). The genotypes of cluster VII were responsible for highest cluster mean for days to 50% flowering (50.23 days) followed by entries of cluster VI (48.81 days). Previously, many related literatures on diversity analysis in Indian mustard has been published from various workers (Singh *et al.*, 2010, Doddabhimappa *et al.*, 2010, Goyal *et al.*, 2012, Mohan *et al.*, 2017) [5, 9, 15]. The associations between the yield related attributes reveal the mutual relationship between two or more characters; therefore, it is an important parameter for taking a decision regarding the selection and its further utilization in improvement in the crop.

References

1. Akabari VR, Niranjana M. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). International J Agril. Sci 2015;11(1):35-39.
2. Beale EML. Euclidean cluster analysis. A paper contributed to 37th session of the International Statistical Institute 1969.
3. Bhogal NS, Chauhan JS, Singh M, Singh KH, Meena ML, Meena DR. Genetic variability for micro and macro-nutrients in Indian mustard (*Brassica juncea* L.) under two environments. Indian J Genet and Plant Breed 2013;73(2):177-181.
4. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J 1959;51:515-51.
5. Doddabhimappa R, Gangapur B, Prakash G, Hiremath CP. Genetic diversity analysis of Indian mustard (*Brassica juncea* L.). Electronic J Plant Breed 2010;1(4):407-413.
6. Federer WT. Augmented (or Hoonuiaku) design. Hwaaiian Planters Record 1956;55:191-208.
7. Gangapur BG, Doddabhimappa R, Prakash P, Salimath M, Ravikumar RL, Rao MSL. Correlation and path analysis in Indian mustard (*Brassica juncea* L. Czern and Coss). Karnataka J Agric. Sci 2009;22(5):971-977.
8. Goswami PK, Behl RK. Genetic divergence in Indian mustard. Ann. Agric. Res 2010;27(2):187-190.
9. Goyal B, Singh D, Avtar R, Singh A. Genetic divergence in elite gene pool of Indian mustard (*Brassica juncea* L. Czern & Coss.). Res. on Crops 2012;13(3):1102-1104.
10. Jan SA, Shinwari ZK, Rabbani MA. Morphobiochemical evaluation of *B. rapa* sub-species for salt tolerance.

- Genetika 2016;8:323-338.
11. Kumar B, Pandey A. Association analysis of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). Environment and Ecology 2014;32(4B):1778-1783.
 12. Kumar R, Gaurav SS, Jayasudha S, Kumar H. Study of correlation and path coefficient analysis in germplasm lines of Indian mustard (*Brassica juncea* (L). Agric. Sci, digest 2016;36(2):92-96.
 13. Lal M, Singh DP, Begadi DL. Genetic variability, heritability, genetic advance and character association in Indian mustard [*Brassica juncea* (L.) Czern and Coss.] grown in semi-reclaimed alkali soils. J of Farming Systems Research & Development 2011;13(2):284-287.
 14. Lodhi B, Thakral NK, Singh D, Avtar R, Bahadur R. Genetic diversity analysis in Indian mustard (*Brassica juncea* L.). J Oilseed Brassica 2017;4(2):57-60.
 15. Mohan S, Yadav RK, Tomar A, Singh M. Genetic divergence analysis in Indian mustard (*Brassica juncea* (L) Czern & Coss). J Pharmacology and Phytochemistry 2017;6(1):350-351.
 16. Mondal SK, Khajuria. Genetic analysis for yield attributes in mustard. Environ. and Ecology 2009;18(1):1-5.
 17. Pandey R, Kumar B, Kumar M. Genetic divergence for quantitative traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). American-Eurasian J Agric. & Environmental Sci 2013;13(3):348-351.
 18. Priyamedha, Singh VV, Chauhan JS, Meena ML, Mishra DC. Correlation and path coefficient analysis for yield and yield components in early generation lines of Indian mustard (*Brassica juncea* L.). Current Advances in Agri. Sci 2015;5(1):37-40.
 19. Rao P, Avtar R, Kumari N, Jattan M, Rani B, Manmohan, Sheoran RK. Multivariate analysis in Indian mustard genotypes for morphological and quality traits. Elect. J Plant Breed 2017;8:450-458.
 20. Rathod VB, Mehta DR, Solanki HV. Correlation and path coefficient analysis in Indian mustard (*Brassica juncea* (L) Czern & Coss) AGRES - An Int. e-journal 2015;2(4):514-519.
 21. Saleem N, Jan SA, Atif MJ, Khurshid H, Khan SA, Abdullah M *et al.* Multivariate based variability within diverse Indian mustard (*B. juncea* L.) genotypes. Open J Genet 2017;7:69-83.
 22. Searle SR. Phenotypic genotypic and environmental correlations. Biometrics 1961;17:474-480.
 23. Shalini TS, Sheriff RA, Kulkarni RS, Venkataravana P. Genetic divergence in Indian mustard (*Brassica juncea* L. Czern and Coss.). Mysore J of Agri. Sci 2000;34(3):251-256.
 24. Sharma RM, Kumar B, Kumar K, Chauhan MP. Variability analysis for yield and its component of Indian mustard (*Brassica juncea* L. Czern and Coss.). Trends in Bio. Sci 2015;7(17):2539-2543.
 25. Shekhawat N, Jadeja GC, Singh J, Ramesh. Genetic diversity analysis in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss). The Bioscan 2014;9(2):713-717.
 26. Singh SK, Singh AK, Kumar K. Genetic variability for yield and its components in Indian mustard (*Brassica juncea* L. Czern & Coss.). New Botanist 2016;34(1/4):147-150.
 27. Sirohi SPS, Malik S, Kumar A. Correlation and path analysis of Indian mustard (*Brassica juncea* L. Czern and Coss.). Ann. Agri. Res 2015;25(4):491-494.
 28. Spark DN. Euclidean cluster analysis. Algorithm As. 58. Applied statistics 1973;22:126-130.
 29. Upadhyay DK, Kumar K. Analysis of heritability and genetic advance in relation to yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss.) under normal and late sown conditions. International J Plant Sci 2011;4(1):12-14.
 30. Verma SK, Sachan JN. Genetic divergence in Indian mustard (*Brassica juncea* L. Czern & Coss.). Crop Res. (Hisar) 2009;19(2):271-276.
 31. Wright S. Systems of mating I. The biometric relations between parent and offspring. Genetics 1921a;6:111-123.