

Genetic Variability, Correlation, Path Coefficient Analysis and Diversity Assessment of Yield and Yield Related Components in Indian Mustard (*Brassica juncea* L.)

Amit Kumar, P. N. Verma, Vinod Kumar Pandey, Sajal Saha

Received 6 August 2024, Accepted 13 November 2024, Published on 16 December 2024

ABSTRACT

The present investigation was conducted during the *rabi* season December 2022 to April 2023 at Instructional Farm Unit 4 of the Integral Institute of Agricultural Science and Technology (IIAST), Integral University Lucknow. The objective was to assess the genetic variability, heritability, and genetic divergence among ten mustard genotypes (*Brassica juncea* L.) crossed in a half diallel mating design, resulting in 56 genotypes, including a standard check 'Kranti'. These genotypes were cultivated in a Randomized Complete Block Design with three replications. Key yield-affecting traits were observed, including days

to 50% flowering, days to maturity, plant height, number of primary and secondary branches, number of siliqua plant⁻¹, number of seeds siliqua⁻¹, length of siliqua, thousand seed weight, and seed yield plant⁻¹. The analysis revealed significant genetic variability for traits like the number of primary and secondary branches plant⁻¹, number of siliqua plant⁻¹, and thousand seed weight. High heritability was noted for plant height, days to maturity, number of secondary branches plant⁻¹, and number of siliqua plant⁻¹. Seed yield plant⁻¹ showed strong positive correlations with thousand seed weight, length of siliqua, and number of siliqua plant⁻¹. Path coefficient analysis indicated that thousand seed weights had the most substantial positive direct effect on yield. Cluster analysis demonstrated significant genetic diversity, with notable differences among clusters, which is beneficial for breeding programs. Thousand seed weight and oil content were the primary contributors to genetic divergence.

Amit Kumar¹, P. N. Verma^{2*}, Vinod Kumar Pandey³, Sajal Saha⁴

^{1,3,4}PhD Scholar, ²Assistant Professor

^{1,2,3}Department of Agriculture, Integral Institute of Agricultural Science and Technology (IIAST), Integral University, Lucknow 226026, India

Integral University MCN No – IU/R&D/2024-MCN0002907

⁴School of Agricultural Sciences, Nagaland University, Medziphema 797106, India

Email : prem.verma124@gmail.com

*Corresponding author

Keywords Variability, Genetic diversity, GCV, PCV, Heritability, Genetic advance.

INTRODUCTION

Mustard, a significant oilseed crop in India, is a member of the *Brassicaceae* family and holds the second rank in terms of production and cultivated area, following soybeans (FAOSTAT 2020). Historically, mustard is one of the earliest domesticated crops, with

evidence of its cultivation dating back to around 5000 BC. Traces of mustard seeds have been found from the Neolithic age and excavated from the ancient Indus Valley civilization, indicating their long-standing presence in the Indian subcontinent (IAS 2019). The *Brassicaceae* family comprises approximately 3,500 species and 350 genera, encompassing various crops cultivated for vegetables, fodder, oils and condiments (Gressel 2005). Among these, the *Brassica oleiferous* species, collectively known as rapeseed-mustard, hold significant global economic importance. Countries such as India, Canada, China and members of the European Union play pivotal roles in rapeseed-mustard cultivation³. Globally, rapeseed-mustard cultivation spans 53 nations, with notable producers including India, Canada, China, the European Union, Pakistan, Poland, Bangladesh and Sweden. During the 2019-20 season, the global rapeseed-mustard cultivation area covered 36.59 million hectares, yielding 72.37 million tonnes with an average productivity of 1980 kg/ha. India ranked fourth in terms of cultivation area (17.19%) and production (8.54%), contributing 19.8% and 9.8% to the total global area and production, respectively (Allaby *et al.* 2015, Kumar *et al.* 2020). In Uttar Pradesh, rapeseed-mustard is cultivated over an area of 1.225 million hectares, producing 1.71 million tonnes with a productivity of 11.85 quintals per hectare. This crop thrives in regions such as Agra, Mathura, Aligarh, Kanpur, Auraiya, Unnao, and Hathras, with Mathura emerging as the leading district in terms of area, production and productivity (Song *et al.* 2020, Sharma *et al.* 2018). Understanding genetic variability, heritability and genetic advance is crucial for improving economic yield. This involves assessing the association of different quantitative traits and their contributions to seed yield (FAOSTAT 2020). Developing new and improved varieties, along with efficient production and seed supply systems, is essential for sustained increases in agricultural production and productivity. The objectives of such studies include identifying genetic variability, determining heritability and genetic advance, assessing trait associations, and understanding their roles in defining seed yield.

MATERIALS AND METHODS

The current investigation was executed during the

rabi season, spanning from December 2022 to April 2023 at Instructional Farm Unit 4 of the Integral Institute of Agricultural Science and Technology (II-AST), Integral University Lucknow. The research was conducted in experimental plots exhibiting uniform topography and fertility, with average temperatures ranging from 18°C to 36°C and minimal rainfall throughout the study period. The experimental design incorporated ten genetically diverse mustard genotypes: Azad, Mahak, Varuna, Pitambri, Maya, Rohini, Urwashi, RH749, PM31, NDR 8501, and NDYR-8. These genotypes were crossed in a diallel mating design, excluding reciprocals, during the *rabi* season of 2021-2022. The resulting 56 genotypes, including 45 crosses, 10 parents, and a standard check 'Kranti', were cultivated in a Randomized Complete Block Design with three replications during the *rabi* season of 2022-2023. Standard agronomic practices were adhered to, ensuring optimal crop growth. Each genotype was grown in three rows, each row measuring 5 meters in length and 1.35 meters in width. The rows were spaced 45 cm apart, with a 15 cm gap between plants within rows. A 45 cm gap was maintained between entries within the block, and a 1 meter space was provided between blocks to facilitate access and data collection. Observations were recorded for various yield-affecting traits, including days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant⁻¹, number of secondary branches plant⁻¹, number of siliqua plant⁻¹, number of seeds siliquae⁻¹, length of siliquae (cm), 1000 seed weight (g), and seed yield plant⁻¹ (g). Measurements were taken from five plants entry⁻¹, and mean values for all traits were calculated for each treatment.

Analysis of variance (ANOVA) was performed using the model proposed by Federer and Meredith (1992). Genotypic and phenotypic coefficients of variation (GCV and PCV) were assessed using Burton's formula (1952). Broad-sense heritability (h^2 (bs)) was calculated according to the formula developed by (Hanson *et al.* 1956), and genetic advance as a percentage of the mean (GAM) was determined using the equation by Johnson *et al.* (1955). Genetic diversity among the genotypes was evaluated using Mahalanobis' D² statistic.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance (ANOVA) results, as shown in Table 1, demonstrated significant differences among the treatments for all evaluated traits, indicating a considerable degree of genetic variation among the treatments for the traits analyzed. This finding aligns with previous research that reported significant genetic variation among treatments for wheat traits.

Variability parameters

The results for minimum, maximum, mean, CV, GCV, PCV, h^2 (bs), GA, and GAM are placed in the Table 2.

Genotypic and phenotypic coefficient of variation

The analysis demonstrated that certain traits exhibited high Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), indicating significant genetic variability (Singh *et al.* 2020). Traits such as the number of primary branches per plant, number of secondary branches per plant, number of siliquae plant⁻¹, and thousand seed weight fall into this category (Kumar *et al.* 2018). Specifically, the number of primary branches plant⁻¹ shows a GCV of 17.620 and a PCV of 18.761, while the number of secondary branches plant⁻¹ has a GCV of 18.909 and a PCV of 19.240 (Singh *et al.* 2021). Similarly, the number of siliquae plant⁻¹ (GCV: 18.724, PCV:

19.017) and thousand seed weights (GCV: 19.262, PCV: 19.671) also demonstrated high variability (Rout *et al.* 2019). This significant genetic diversity indicated a strong potential for improvement through selective breeding, as these traits can be effectively manipulated to enhance crop performance and yield (Pradhan *et al.* 2021).

Heritability and genetic advance over per cent mean

Heritability (bs) is a measure of the extent of phenotypic variation caused by action of the genes (Johnson *et al.* 1955). It is a good index for transmission of the characters from parents to their offspring (Allard 1960). The estimate of heritability helps plant breeder in selection of elite genotypes from diverse genetic population (Falconer and Mackay 1996). The estimate of heritability is more advantageous when expressed in terms of genetic advance (Yashpal *et al.* 2020, Gupta *et al.* 2019). Traits such as plant height (0.991), days to maturity (0.955), number of secondary branches plant⁻¹ (0.966), and number of siliqua plant⁻¹ (0.969) exhibit higher heritability, indicating that the majority of their phenotypic variation is attributable to genetic differences among individuals (Gupta *et al.* 2019, Awasthi *et al.* 2020). The genetic advance as a percentage of the mean is a critical metric in understanding the potential for selection and improvement of various traits in plant breeding (Lakra *et al.* 2019). High genetic advance indicates a greater potential for genetic

Table 1. Analysis of variance. Df: Degree of freedom, DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height, NPB: Number of primary branches per plant, NSB: Number of secondary branches per plant, NSP: Number of siliqua per plant, NSS: Number of seeds per siliqua, LS: Length of siliqua, TSW: 1000-seed weight, OC: Oil content, SYP: Seed yield per plant.

Source	Df	DTF	DTM	PH	NPB	NSB
Replications	2	2.2296	0.141	18.96	0.088	0.088
Genotypes	44	27.07***	70.4***	550.3**	2.862***	2.862***
Error	88	0.9872	1.095	1.75	0.12224	0.12224

Table 1. Continued.

Source	Df	NSP	NSS	LS	TSW	OC	SYP
Replications	2	81.8	1.038	0.0165	1.202	1.192	0.641
Genotypes	44	740.9***	2.301***	0.215***	3.96***	4.73***	1.501***
Error	88	77.1	0.14125	0.033356	0.056	0.5148	0.12701

Table 2. Estimation of genetic variability. GM: Grand mean, SEM: Standard error of mean, GV: Genotypic variance, PV: Phenotypic variance, GCV: Genotypic coefficient of variance, PCV: Phenotypic coefficient of variance, GA: Genetic advance, GA% m: Genetic advance per cent of mean.

Source	Maximum	Minimum	GM	Sem	GV	PV	GCV	PCV	Heritability		GA % m
									bs	GA	
DTF	56.000	41.000	47.696	0.574	8.695	9.683	6.182	6.524	0.898	5.757	12.069
DTM	142.000	119.000	128.970	0.604	23.114	24.209	3.728	3.815	0.955	9.677	7.503
PH	208.800	148.200	182.532	0.764	182.855	184.605	7.408	7.444	0.991	27.724	15.188
NPB	7.000	2.800	5.424	0.202	0.914	1.036	17.620	18.761	0.882	1.849	34.088
NSB	13.600	5.800	10.787	0.221	4.161	4.308	18.909	19.240	0.966	4.130	38.283
NSP	357.000	155.200	264.041	5.070	2444.260	2521.387	18.724	19.017	0.969	100.276	37.977
NSS	15.400	11.000	12.924	0.217	0.720	0.861	6.566	7.181	0.836	1.598	12.367
LS	5.300	4.000	4.555	0.105	0.061	0.094	5.414	6.739	0.645	0.408	8.960
SW	8.900	3.800	5.928	0.137	1.304	1.360	19.262	19.671	0.959	2.303	38.854
OC	38.600	31.400	34.985	0.414	1.406	1.920	3.389	3.961	0.732	2.089	5.972
SYP	15.500	11.600	13.427	0.206	0.458	0.585	5.042	5.698	0.783	1.234	9.191

improvement through selection (Singh *et al.* 2019). Based on the genetic advance as a percentage of the mean enumerated in the given table, the values range from 5.97% to 38.85%. The traits with high genetic advance percentages include thousand seeds weight (38.85%), number of secondary branches per plant (38.28%), number of siliquae plant⁻¹ (37.97%), and number of primary branches plant⁻¹ (34.08%). Traits such as thousand seeds weight, number of secondary branches plant⁻¹, number of siliqua plant⁻¹, and num-

ber of primary branches plant⁻¹ show high genetic advance percentages, suggesting that these traits are strongly influenced by additive genetic factors and can be effectively improved through selection (Singh *et al.* 2019).

Estimation of correlation coefficient

Seed yield per plant exhibited several notable correlations with other traits presented in Table 3. At

Table 3. Estimation of correlation coefficient.

Traits	SYP	DFP	DM	PH	NPB	NSB	NSP	NSS	LS	TSW	OC	
SYP	G	1**										
	P	1**										
DFP	G	-0.439**	1**									
	P	-0.380**	1**									
DM	G	-0.415**	0.845**	1**								
	P	-0.358**	0.795**	1**								
PH	G	-0.340**	0.612**	0.782**	1**							
	P	-0.295**	0.587**	0.765**	1**							
NPB	G	0.054	0.229**	0.337**	0.593**	1**						
	P	0.048	0.211**	0.310**	0.568**	1**						
NSB	G	0.098	0.231**	0.356**	0.575**	0.924**	1**					
	P	0.078	0.214**	0.347**	0.564**	0.886**	1**					
NSP	G	0.411**	0.029	0.152*	0.219**	0.535**	0.647**	1**				
	P	0.369**	0.022	0.143	0.214**	0.506**	0.633**	1**				
NSS	G	0.153*	-0.174*	-0.232**	-0.405**	-0.704**	-0.690**	0.007	1**			
	P	0.11	-0.162*	-0.227**	-0.396**	-0.659**	-0.667**	0.004	1**			
LS	G	0.654**	-0.444**	-0.377**	-0.357**	-0.09	0.052	0.261**	0.071	1**		
	P	0.490**	-0.339**	0.286**	-0.297**	-0.042	0.034	0.224**	0.06	1**		
TSW	G	0.857**	-0.619**	-0.647**	-0.525**	-0.258**	-0.225**	0.115	0.251**	0.608**	1**	
	P	0.707**	-0.578**	-0.619**	-0.513**	-0.245**	-0.220**	0.107	0.241**	0.507**	1**	
OC	G	0.227**	0.068	0.175*	-0.021	0.046	0.026	0.326**	0.245**	0.199**	-0.042	1**
	P	0.196*	0.056	0.174*	-0.024	0.039	0.024	0.316**	0.230**	0.176*	-0.05	1**

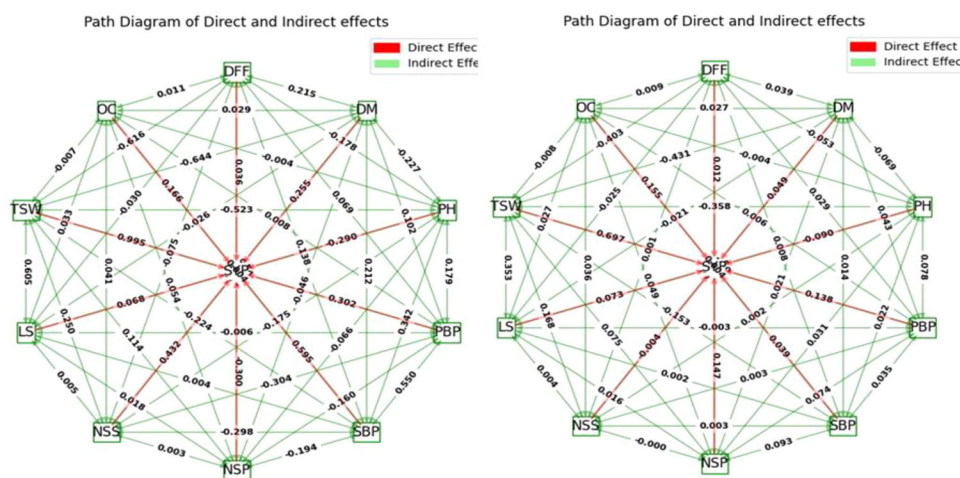


Fig. 1. Path diagram at genotypic and phenotypic level.

the genotypic level, Seed yield plant⁻¹ was highly significantly and positively correlated with thousand seed weight (0.857**), length of siliqua (0.654**), and number of siliqua plant⁻¹ (0.411**) (Ompal *et al.* 2018, Kumar *et al.* 2019). These relationships suggest that plants with higher seed yields tend to have heavier seeds, larger siliqua, and more seeds silique⁻¹ (Parvin and Haque 2020, Singh *et al.* 2020). However, seed yield plant⁻¹ also showed highly significant

negative correlations with days to 50% flowering (-0.439**), days to maturity (-0.415**), and plant height (-0.340**) (Chaturvedi *et al.* 2021, Ompal *et al.* 2018). This indicates that plants yielding more seeds flower and mature earlier and are generally shorter. At the phenotypic level, the positive correlations with thousand seed weight (0.707**), length of siliqua (0.490**), and number of siliqua plant⁻¹ (0.369**) were maintained, while the significant and

Table 4. Estimation of path analysis.

		DFE	DM	PH	NPB	NSB	NSP	NSS	LS	TSW	OC	SYP
DFE	G	0.036	0.215	-0.178	0.069	0.138	-0.009	-0.075	-0.03	-0.616	0.011	-0.439**
	P	0.012	0.039	-0.053	0.029	0.008	0.003	0.001	-0.025	-0.403	0.009	-0.380**
DM	G	0.03	0.255	-0.227	0.102	0.212	-0.046	-0.1	-0.026	-0.644	0.029	-0.415**
	P	0.01	0.049	-0.069	0.043	0.014	0.021	0.001	-0.021	-0.431	0.027	-0.358**
PH	G	0.022	0.199	-0.29	0.179	0.342	-0.066	-0.175	-0.024	-0.523	-0.004	-0.340**
	P	0.007	0.037	-0.09	0.078	0.022	0.031	0.002	-0.022	-0.358	-0.004	-0.295**
NPB	G	0.008	0.086	-0.172	0.302	0.55	-0.16	-0.304	-0.006	-0.257	0.008	0.054
	P	0.003	0.015	-0.051	0.138	0.035	0.074	0.003	-0.003	-0.17	0.006	0.048
NSB	G	0.008	0.091	-0.167	0.279	0.595	-0.194	-0.298	0.004	-0.224	0.004	0.098
	P	0.003	0.017	-0.051	0.122	0.039	0.093	0.003	0.002	-0.153	0.004	0.078
NSP	G	0.001	0.039	-0.064	0.161	0.385	-0.3	0.003	0.018	0.114	0.054	0.411**
	P	0	0.007	-0.019	0.07	0.025	0.147	0	0.016	0.075	0.049	0.369**
NSS	G	-0.006	-0.059	0.118	-0.212	-0.411	-0.002	0.432	0.005	0.25	0.041	0.153*
	P	-0.002	-0.011	0.036	-0.091	-0.026	0.001	-0.004	0.004	0.168	0.036	0.11
LS	G	-0.016	-0.096	0.104	-0.027	0.031	-0.078	0.031	0.068	0.605	0.033	0.654**
	P	-0.004	-0.014	0.027	-0.006	0.001	0.033	0	0.073	0.353	0.027	0.490**
TSW	G	-0.022	-0.165	0.153	-0.078	-0.134	-0.034	0.108	0.041	0.995	-0.007	0.857**
	P	-0.007	-0.03	0.046	-0.034	-0.009	0.016	-0.001	0.037	0.697	-0.008	0.707**
OC	G	0.002	0.044	0.006	0.014	0.015	-0.098	0.106	0.014	-0.042	0.166	0.227**
	P	0.001	0.008	0.002	0.005	0.001	0.046	-0.001	0.013	-0.035	0.155	0.196*

Table 5. Mean performance of all clusters.

	DFF	DM	PH	NPB	NSB	NSP	NSS	LS	TSW	SYP	OC
Cluster i	48.62	131.08	189.11	5.72	11.52	279.90	12.78	4.48	5.48	13.30	34.96
Cluster ii	46.20	124.08	164.82	3.96	7.35	181.71	13.80	4.58	6.77	13.48	34.85
Cluster iii	45.80	125.13	169.90	5.55	11.39	294.76	12.56	4.90	7.22	14.18	36.01
Cluster iv	47.93	130.33	177.86	5.64	11.51	291.99	13.49	4.70	4.97	13.62	41.04
Cluster v	47.33	133.83	206.33	5.95	10.98	256.68	13.86	4.61	5.00	13.07	40.16
Cluster vi	46.33	127.66	181.10	6.76	13.76	359.00	12.86	4.86	8.50	15.18	41.66
Cluster vii	43.00	120.66	151.10	3.20	6.33	359.00	21.76	4.96	8.40	14.74	42.00
Cluster viii	30.00	82.66	113.26	4.10	8.03	236.33	8.63	3.50	5.70	10.53	27.00

Table 6. Number of genotypes in different cluster.

	Total number of genotypes	Genotypes
Cluster i	23	45, 56, 44, 54, 49, 46, 51, 55, 50, 52, 53, 42, 37, 23, 43, 47, 48, 22, 17, 24, 18, 8, 41, 27, 26, 15, 16, 36, 38, 25, 40, 28, 39
Cluster ii	8	31, 32, 35, 33, 34, 30, 29, 21
Cluster iii	5	19, 20, 12, 14, 13
Cluster iv	5	9, 10, 11, 5, 4
Cluster v	2	7, 6
Cluster vi	1	2
Cluster vii	1	3
Cluster viii	1	1

negative correlations with days to 50% flowering (-0.380**), days to maturity (-0.358**), and plant height (-0.295**) were also observed (Parvin and Haque 2020, Singh *et al.* 2020).

Direct and indirect effects of ten characters on grain yield per plant in mustard genotypes at genotypic and phenotypic level

Direct and indirect effects of ten characters on grain yield plant⁻¹ in mustard genotypes presented in Table 4 & Fig. 1. Thousand seed weight (0.995) contributed maximum positive direct effect on yield at the genotypic level, followed by number of secondary branches plant⁻¹ (0.595), days to maturity (0.255), length of siliqua (0.432), and number of primary branches (0.302). High order negative direct effect on yield at the genotypic level was contributed by the number of siliqua plant⁻¹ (-0.3), followed by plant height (-0.29). At the phenotypic level, thousand seed weight (0.697) contributed maximum positive direct effect on yield, followed by oil content (0.155), length of siliqua (0.073), number of siliqua plant⁻¹ (0.147),

and days to maturity (0.049). High order negative direct effect on yield at the phenotypic level was contributed by the number of primary branches (-0.09) and plant height (-0.09). Similar result reported by (Gupta *et al.* 2019, Devi *et al.* 2017).

Genetic Diversity

Cluster means of all the characters

From the results of cluster mean generated by Tocher

Table 7. Contribution of various traits to divergence.

Traits	Contribution %
Days to 50% flowering	1.493
Days to maturity	8.441
Plant height	6.428
Number of primary branches per plant	3.961
Number of secondary branches per plant	1.948
Number of siliqua per plant	14.675
Number of seeds per siliqua	3.116
Length of siliqua	7.662
Thousand seed weight	32.792
Seed yield per plant	1.363
Oil content	18.116

Table 8. Average intra and inter cluster distance.

	Cluster i	Cluster ii	Cluster iii	Cluster iv	Cluster v	Cluster vi	Cluster vii	Cluster viii
Cluster i	17.32	40.50	33.17	45.22	77.16	68.04	27.21	71.14
Cluster ii		14.74	37.26	65.35	35.62	77.75	51.73	97.99
Cluster iii			14.00	76.82	49.39	75.95	33.39	87.47
Cluster iv				19.93	64.57	41.28	42.47	128.99
Cluster v					12.52	81.14	51.45	37.21
Cluster vi						0	54.99	30.32
Cluster vii							0	61.32
Cluster viii								0

method (Table 5), it can be concluded that considerable differences existed for all the studied traits among the clusters. Clusters means can be selected to use in crossing program to create desirable variations in the breeding material for yield improvement.

Number of genotypes in different cluster

The clustering analysis of mustard genotypes reveals significant genetic diversity and distribution among the genotypes, presented in Table 6. Cluster i contains the highest number of genotypes (23), followed by cluster ii, iii, iv and v, while cluster vi-viii contains only one genotype, indicating substantial genetic similarity, likely attributable to shared ancestry or similar selective pressures. This genotype distribution provides critical insights for breeding programs, with larger clusters offering a broad genetic base for selecting desirable traits and single-genotype clusters presenting unique genetic resources with potential rare or valuable traits for breeding purposes (Singh *et al.* 2020, Devi *et al.* 2017).

Contribution of various traits to divergence

The analysis of the contribution of various traits to genetic divergence in mustard genotypes presented in Table 7. It revealed that thousand seed weight is the most significant contributor, accounting for 32.792% of the divergence. Oil content follows with 18.116%, indicating its crucial role in genotype differentiation (Gupta *et al.* 2019, Meena *et al.* 2020). The number of siliquae plant⁻¹ also plays a substantial role, contributing 14.675%. This analysis highlights the key traits for breeding programs, suggesting that focusing on the most influential characteristics, such as thousand seed weight and oil content, can significantly

enhance genetic improvement efforts in mustard (Singh *et al.* 2018).

Average intra and inter cluster distance

The analysis of intra-cluster distances among mustard genotype clusters reveals varying levels of genetic similarity within each group, presented in Table 8. Cluster-v exhibits the lowest intra-cluster distance of 12.52, indicating a high degree of genetic cohesion among its members. In contrast, Clusters-iv and ii have higher intra-cluster distances of 19.93 and 14.74, respectively, suggesting a moderate level of genetic relatedness within these clusters. Clusters-vi, vii, and viii demonstrate perfect cohesion with intra-cluster distances of 0, indicating identical or highly similar genotypes within each cluster.

In terms of inter-cluster distances, significant genetic divergence was observed between clusters. The highest inter-cluster distances were recorded between Cluster-iv and others, particularly Cluster-viii, with a 128.99 distance, indicating significant genetic differentiation. Conversely, Cluster v shows relatively lower divergence from other clusters, with inter-cluster distances ranging from 37.21 to 81.14 (Meena *et al.* 2020).

Therefore, these findings provided valuable information into the genetic structure of mustard genotypes, which is crucial for breeding programs to enhance genetic diversity and improve desired traits. By understanding the genetic similarity and divergence among clusters, we can make informed decisions to select genotypes for cross-breeding and ultimately develop improved mustard varieties with desirable agronomic traits.

CONCLUSION

The investigation into mustard genotypes unveiled a substantial degree of genetic variability, with traits including the number of primary and secondary branches plant⁻¹, number of siliqua plant⁻¹, and thousand seed weights exhibiting notable genetic and phenotypic variations. Traits such as plant height, days to maturity, number of secondary branches, and number of siliqua plant⁻¹ demonstrated high heritability. There was a positive correlation observed between seed yield plant⁻¹ and other traits like thousand seed weight, length of siliqua, and number of siliqua plant⁻¹. Thousand seed weight exerted the most significant positive direct impact on yield, whereas the number of siliqua plant⁻¹ and plant height had a detrimental effect. Clustering analysis highlighted considerable genetic diversity across the genotypes, with some clusters housing a multitude of genotypes and others containing just a single one. Key contributors to genetic divergence were traits like thousand seed weight and oil content, underscoring their significance in breeding programs. Prioritizing traits like thousand seed weight and oil content may greatly expedite the advancement of mustard breeding programs. The observed genetic diversity provides a solid foundation for selecting desirable traits and augmenting crop yields.

ACKNOWLEDGMENT

I would like to express my sincere gratitude to Integral University in Lucknow for providing me with the resources and support necessary to complete this research. Special thanks to Dr PN Varma for his invaluable guidance, encouragement, feedback throughout the research. His expertise and mentorship have been instrumental in shaping this work. I am deeply grateful for the opportunity to learn under his supervision.

REFERENCES

- Allaby RG, Kistler L, Gutaker RM, Ware R, Kitchen JL, Smith O, Clarke AC (2015) Archaeogenomic insights into the adaptation of plants to the human environment: Pushing plant–hominin co-evolution back to the pliocene. *Journal of Human Evolution* 79 : 150–157.
- Allard RW (1960) Principles of plant breeding. John Wiley & Sons, pp 485.
<https://doi.org/10.2134/agronj1962.00021962005400040037x>
- Awasthi D, Tewari VK, Kandalkar VS (2020) Evolution of heritability and genetic advance for morphological traits of Indian mustard germplasms. *Current Journal of Applied Science and Technology* 39 (21) : 39–47.
- Burton GW (1952) Quantitative inheritance in grasses. *Proceedings of Sixth International Grassland Congress* 1: 277–283.
- Chaturvedi VD, Maurya KN, Upadhyay DK, Singh PK, Chaubey S (2021) Genetic diversity for yield and its contributing components in Indian mustard (*Brassica juncea* (L.) Czern & Coss.). *Journal of Pharma Innovation* 10 : 748–754.
- Devi TR, Devi ND, Vivekananda Y, Sharma PR (2017) Falconer DS, Mackay TF (1996) Introduction to quantitative genetics (4th edn). Longman.
- FAOSTAT (2020) FAOSTAT Database on agriculture. Food and agriculture organization of the united nations.
- Federer WT, Meredith MP (1992) Covariance analysis for split-plot and split-block designs. *The American Statistician* 46 (2) : 155–162.
- Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern and Coss) genotypes using agro-morphological parameters. *Electronic Journal of Plant Breeding* 8 (3) : 749–753.
- Gressel J (2005) Crop ferality and volunteerism, 1st edn. CRC Press.
<https://doi.org/10.1201/9781420037999>
- Gupta MC, Roy HS, Bhadauria SS (2019) Genetic variability analysis in F2/F3 population derived through inter-specific hybridization in oilseed *Brassica*. *Electronic Journal Plant Breeding* 10 (3) : 1275–1282.
- Hanson CH, Robinson HF, Comstock RE (1956) Biometrical studies of yield in segregating populations of Korean lespe-deza. *Agronomy Journal* 48 (6) : 268–272.
- Indian Agricultural Statistics (2019) Agricultural statistics at a glance. Ministry of agriculture & farmers welfare, Government of India.
- Johnson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47 (7) : 314–318.
- Kumar R, Kaur S, Bala K, Kaur S, Sharma L (2019) Assessment of genetic variability, correlation and path analysis for yield traits in fl hybrids of Indian mustard. *Agriways* 7 (2) : 1–7.
- Kumar R, Saini DK, Kumar M, Priyanka V, Akhatar J, Kaushik D, Kaushik P (2018) Revealing the genetic architec of yield-related and quality traits in Indian mustard (*Brassica juncea* (L.) Czern. and Coss.) using Meta-QTL analysis. *Agronomy* 1210 : 2442.
- Kumar S, Seepaul R, Mulvaney MJ, Colvin B, George S, Marois JJ, Small IM (2020) *Brassica carinata* genotypes demonstrate potential as a winter biofuel crop in South East United States. *Industrial Crops and Products* 150 (3) : 112–117.
- Lakra A, Tantuway G, Aditi Eliza Tirkey, Kartikeya Srivastava (2019) Genetic variability and trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss). *International Journal of Current Microbiology and Applied Science* 9 (1) : 2556–2563.
- Meena HO, Meena PKP, Singh K, Meena HP, Meena D (2020)

- Genetic divergence analysis in Indian mustard (*Brassica juncea* L.). *International Journal Current Microbiology Applied Science* 9 (10) : 2185—2192.
- Ompal Kerkhi SA, Chand P, Singh SK, Yadav SK (2018) Study of correlation and path coefficient analysis in Indian mustard (*B. juncea* L.) Czern & Coss). *Journal Pharmacognosy and Phytochemistry* 7 (6) : 890—894.
- Parvin F, Haque MM (2020) Heritability, genetic advance, correlation and path coefficient analysis in advanced generation of *Brassica napus* L. *American-Eurasian Journal Agricultural & Environment Sciences* 20 (2) : 116—212.
- Pradhan AM, Choudhury MR, Sawarkar A, Das S (2021) Genetic analysis of some genotypes of Indian mustard (*Brassica juncea* L.) for yield and yield attributing traits. *Current Journal of Applied Science and Technology* 40 (34) : 51—60.
- Rout S, Sur B, Sadhu S, Ghimiray TS, Mondal HA, Hijam L, Roy SK (2019) Trait's association, cause and effect analyses in Indian mustard (*Brassica juncea* L.) Czern & Coss). *Electronic Journal of Plant Breeding* 10 (4) : 1482—1494.
- Sharma S, Raghuvanshi JS, Srivastava SC (2018) An economic analysis of costs and returns of rapeseed and mustard production in Morena district of Madhya Pradesh. *Journal of Community Mobilization and Sustainable Development* 13 (3) : 475—482.
- Singh H, Kumar R, Kaur S, Singh I, Kaur R (2019) Genetic analysis of Indian mustard for yield by calculating heterosis and combining ability. *Journal of Agricultural Science* 10 (1-2) : 1—12.
- Singh M, Avtar R, Lakra N, Hooda E, Singh VK, Bishnoi M, Choudhary RR (2021) Genetic and proteomic basis of sclerotinia stem rot resistance in Indian mustard (*Brassica juncea* L.) czern & coss.E). *Genes* 12 (11) : 1784.
- Singh S, Dwivedi AK, Ashutosh Kumar, Kumar K (2018) Genetic divergence analysis in Indian mustard (*Brassica juncea* L.) *International Journal Current Microbiology Applied Science* 7 (6) : 2496—2503.
- Singh VK, Avtar R, Mahavir NK, Manjeet RK, Rathore V (2020) Assessment of genetic relationship among diverse Indian mustard (*Brassica juncea* L.) genotypes using XL STAT. *Electronic Journal of Plant Breeding* 11 (02) : 674—680.
- Song JM, Guan Z, Hu J, Guo C, Yang Z, Wang S, Guo L (2020) Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of *Brassica napus*. *Nature plants* 6 (1): 34—45.
- Yashpal Saini N, Singh N, Chaudhary R, Yadav S, Singh R, Yadava DK (2020) Genetic improvement of oil quality using molecular techniques in *Brassica juncea*. *Brassica improvement: Molecular, Genetics and Genomic Perspectives*. *Nature Genetics* 7 (4) : 109—125.