Vegetable Science (2024) 51(1): 86-95

doi: 10.61180/vegsci.2024.v51.i1.12

ISSN- 0970-6585 (Print), ISSN- 2455-7552 (Online)

www.isvsvegsci.in

RESEARCH ARTICLE

Genetic diversity for horticultural traits in vegetable mustard (*Brassica juncea*)

Dharminder Kumar[1], Praveen Kumar[2], Jagmeet Singh[2], Balbir Singh Dogra[3], Sandeep Kumar[4]*, VGS Chandel[5] and Renu Kapoor[1]

Abstract

This research was conducted to study the extent of genetic variability and character association for yield and other horticultural traits along with the estimation of genetic divergence among 101 diverse genotypes of vegetable mustard. Analysis of variance indicated significant differences among all the genotypes for all the characters studied. PCV and GCV were high for various traits, i.e., total anthocyanin content (89.07, 85.91%), number of secondary branches per plant (30.39, 29.85%), total phenol content (28.93, 25.78%) and number of primary branches per plant (24.02, 22.92%), respectively. High heritability estimates were recorded for ascorbic acid content (98.44%) followed by number of leaves per plant (97.65%), number of secondary branches per plant (96.48%) anthocyanin content (93.01%), number of primary branches per plant (91.00%), yield per plant (88.44%), leaf length (88.36%), plant height (85.73%) and total phenol content (79.41%). The correlation studies revealed that yield per plot had a positive and significant correlation with yield per plant and plant height at both genotypic and phenotypic levels (0.512, 0.207 and 0.414, 0.187, respectively). The path coefficient analysis revealed the maximum positive direct effect towards yield per plot by leaf length (0.591) followed by yield per plant (0.538). The first six principal components resulted in 64.925% of the total variance for all the characteristics. On the basis of genetic divergence studies, 101 genotypes were grouped into six clusters and the highest inter-cluster distance was recorded between cluster VI and cluster III (7.755).

Keywords: Clusters, Genetic divergence, Heritability, Vegetable mustard.

[1]Regional Horticultural Research & Training Station, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Jacch, Kangra, Himachal Pradesh, India.

[2]Department of Vegetable Science, College of Horticulture, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India.

[3]Department of Vegetable Science, College of Horticulture and Forestry, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Neri, Hamirpur, Himachal Pradesh, India.

[4]ICAR-Indian Agricultural Research Institute Regional Station, Katrain, Kullu, Himachal Pradesh, India.

[5]Department of Entomology, College of Horticulture, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India.

*__Corresponding author;__ Email: sandeepkdhatwalia@gmail.com

Citation: Kumar, D., Kumar, P., Singh, J., Dogra, B.S., Kumar, S., Chandel, V.G.S. and Kapoor, R. (2024). Genetic diversity for horticultural traits in vegetable mustard (*Brassica juncea*). Vegetable Science, 51(1), 86-95.

Source of support: Nil

Conflict of interest: None.

Received: 12/03/2024 **Revised:** 27/05/2024 **Accepted:** 27/05/2024

Introduction

Vegetables are an important part of a well-balanced diet because they contain important protective nutrients such as proteins, minerals, dietary fibers, micronutrients, and antioxidants, in addition to providing energy. Among *Brassica* crops, vegetable mustard is the choice of farmers and consumers over rapeseed because of its better production and relative resilience to a variety of biotic and abiotic challenges (Singh et al., 2021). Vegetable mustard (*Brassica juncea)* belongs to the family *Brassicaceae* (Syn. *Cruciferae*). The family currently includes 3709 species and 338 genera (Warwick et al., 2006) and is one of the ten most economically important plant families (Rich, 1991). The crop can be raised well under both irrigated and rainfed conditions. In Punjab, Haryana, U.P., Himachal Pradesh, and Madhya Pradesh, it is grown mainly as a catch crop. Every crop development initiative must start with an understanding of genetic variability (Kumar et al., 2015). Furthermore, the variability should be highly heritable as selection progress depends on heritability, selection intensity, and genetic advancement of the character. A quantitative measure of genetic variability would be very helpful in quantitative and qualitative breeding. Genetic diversity is one of the most

Table 1: List of vegetable mustard genotypes

S. No.	*Genotype*	*Source*	*S. No.*	*Genotype*	*Source*
1.	Aravali	ICAR-DRMR	52.	IC597867	West Siang
2.	Ashirwad	ICAR-DRMR	53.	IC597868	West Siang
3.	Bhagirathi	ICAR-DRMR	54.	IC597869	West Siang
4.	BR-40	ICAR-DRMR	55.	IC597870	West Siang
5.	CS-52	ICAR-DRMR	56.	IC597872	West Siang
6.	CS-54	ICAR-DRMR	57.	IC597873	West Siang
7.	CS-56	ICAR-DRMR	58.	IC597876	West Siang
8.	CS-58	ICAR-DRMR	59.	IC597878	West Siang
9.	CS-60	ICAR-DRMR	60.	IC597879	West Siang
10.	DRMR-150-35	ICAR-DRMR	61.	IC597880	West Siang
11.	IJ-31	ICAR-DRMR	62.	IC597881	West Siang
12.	Durgamani	ICAR-DRMR	63.	IC597882	West Siang
13.	GDM-4	ICAR-DRMR	64.	IC597883	West Siang
14.	GM-1	ICAR-DRMR	65.	IC597884	West Siang
15.	GM-2	ICAR-DRMR	66.	IC597885	West Siang
16.	GM-3	ICAR-DRMR	67.	IC597887	West Siang
17.	Jagannath	ICAR-DRMR	68.	IC597888	West Siang
18.	JM-1	ICAR-DRMR	69.	IC597889	West Siang
19.	JM-2	ICAR-DRMR	70.	IC597892	West Siang
20.	JD-6	ICAR-DRMR	71.	IC597893	East Siang
21.	Kanti	ICAR-DRMR	72.	IC597894	East Siang
22.	Kranti	ICAR-DRMR	73.	IC597895	East Siang
23.	Krishna	ICAR-DRMR	74.	IC597903	East Siang
24.	Laxmi	ICAR-DRMR	75.	IC597904	East Siang
25.	LES-43	ICAR-DRMR	76.	IC597905	East Siang
26.	LET-36	ICAR-DRMR	77.	IC597907	East Siang
27.	Maya	ICAR-DRMR	78.	IC597910	East Siang
28.	Narendra Rai	ICAR-DRMR	79.	IC597914	East Siang
29.	NDRE-4	ICAR-DRMR	80.	IC597917	East Siang
30.	NDYR-8	ICAR-DRMR	81.	IC597921	East Siang
31.	NRCDR-2	ICAR-DRMR	82.	IC597922	East Siang
32.	NRCDR-601	ICAR-DRMR	83.	IC597932	East Siang
33.	NRCHB-101	ICAR-DRMR	84.	IC597924	West Siang
34.	Pant Rai-18	ICAR-DRMR	85.	IC597925	West Siang
35.	Pant Rai-20	ICAR-DRMR	86.	IC597929	West Siang
36.	Pant Rai-21	ICAR-DRMR	87.	IC597931	L Subansiri
37.	Pant Mustard-67	ICAR-DRMR	88.	IC597934	L Subansiri
38.	PBR-210	ICAR-DRMR	89.	IC597936	L Subansiri
39.	PBR-357	ICAR-DRMR	90.	IC597939	Papum Pare
40.	PBR-91	ICAR-DRMR	91.	IC597943	Papum Pare

41.	PBR-97	ICAR-DRMR	92.	IC597944	Papum Pare
42.	Vaibhav	ICAR-DRMR	93.	IC597947	Papum Pare
43.	Pant Rai-19	ICAR-DRMR	94.	IC597948	Papum Pare
44.	Pusa Tarak	ICAR-DRMR	95.	IC597886	West Siang
45.	Pusa Agrani	ICAR-DRMR	96.	IC597901	East Siang
46.	Pusa Bahar	ICAR-DRMR	97.	IC597911	East Siang
47.	Pusa Bold	ICAR-DRMR	98.	IC597919	East Siang
48.	Pusa Jai Kisan	ICAR-DRMR	99.	IC597920	East Siang
49.	RGN-487	ICAR-DRMR	100.	IC597942	Papum Pare
50.	Pusa Mahak	ICAR-DRMR	101.	Pusa Sag-1	ICAR-IARI
51.	IC597866	West Siang			

Table 2: Estimates of phenotypic and genotypic coefficients of variation, heritability (%) and genetic advance as % of mean for various traits in vegetable mustard

Character	*Mean*	*Range*		*Coefficient of variation (%)*		*Heritability (%)*	*Genetic advance as % mean*
		Min.	*Max.*	*Phenotypic*	*Genotypic*		
Number of leaves/plant	12.22	7.40	16.42	15.33	15.15	97.65	30.84
Leaf length (cm)	19.02	12.04	22.36	9.52	8.94	88.36	17.32
Leaf Width (cm)	14.35	11.95	16.49	8.07	6.97	74.44	12.38
Leaf area index (cm^2)	0.54	0.34	0.73	18.73	14.24	57.78	22.30
No. of primary branches per plant	4.20	2.30	6.89	24.02	22.92	91.00	45.04
Number of secondary branches per plant	9.05	5.19	16.52	30.39	29.85	96.48	60.41
Plant height (cm)	122.44	76.29	160.66	13.95	12.91	85.73	24.64
Days to harvest	75.73	67.32	83.43	4.50	3.91	75.50	7.00
Total plant weight (g)	140.86	120.72	161.53	9.91	7.25	53.44	10.92
Yield per plant (g)	46.33	30.29	75.88	14.91	14.02	88.44	27.17
Total phenol content (mg/g)	4.00	1.54	6.37	28.93	25.78	79.41	47.34
Anthocyanin content (mg/100g)	1.51	0.08	7.13	89.07	85.91	93.01	170.68
Ascorbic acid content (mg/100g)	20.51	13.45	27.15	16.15	16.02	98.44	32.75
Chlorophyll content (mg/100g)	0.46	0.31	0.61	19.03	15.36	65.16	25.55
Yield per plot (kg)	2.65	2.25	3.18	11.84	5.00	17.81	4.34

important techniques for assessing genetic variety in both cross- and self-pollinated crops (Sharma and Prasad, 2010). The correlation analysis will help identify characteristics that closely resemble yield. Since path coefficient analysis divides the correlation coefficient into the factors' direct and indirect effects, it provides a more accurate picture of how the variables interact. It also makes it easier to assess the degree of correlation between yield and the attributes that contribute to it (Singh et al., 2023). Thus, character association and path analysis give information on the traits that contribute to yield, and breeders may utilize this knowledge to apply selection in order to isolate better genotypes that can be employed in subsequent improvement projects (Lakra et al., 2020).

Table 3: Genotypic and phenotypic correlation coefficients between yield per plot and its component characters in vegetable mustard (*B. juncea*)

Traits		*X 1*	*X2*	*X3*	*X4*	*X5*	*X6*	*X7*	*X8*	*X9*	*X10*	*X11*	*X12*	*X13*	*X14*	*X15*
X1	G	1.000														
	P	1.000														
X2	G	-0.017	1.000													
	P	-0.017	1.000													
X3	G	0.021	-0.026	1.000												
	P	0.019	-0.015	1.000												
X4	G	-0.092	0.725**	0.419**	1.000											
	P	-0.083	0.499**	0.328**	1.000											
X5	G	0.027	0.489**	0.110	0.630**	1.000										
	P	0.022	0.434**	0.118*	0.472**	1.000										
X6	G	-0.019	0.361**	-0.094	0.411**	0.539**	1.000									
	P	-0.020	0.337**	-0.094	0.311**	0.500**	1.000									
X7	G	0.284**	0.018	0.098	0.043	0.226**	0.039	1.000								
	P	0.266**	0.004	0.107	0.036	0.200**	0.011	1.000								
X8	G	-0.116*	0.101	-0.016	-0.050	-0.083	-0.083	-0.043	1.000							
	P	-0.114*	0.095	-0.020	-0.027	-0.072	-0.040	-0.045	1.000							
X9	G	0.203**	0.109	-0.081	0.024	0.124*	0.294**	0.104	0.081	1.000						
	P	0.141*	0.078	-0.154**	-0.006	0.085	0.274**	-0.009	0.090	1.000						
X10	G	0.329**	0.159**	0.062	0.275**	0.386**	0.374**	0.307**	-0.112*	0.068	1.000					
	P	0.299**	0.147*	0.077	0.236**	0.351**	0.328**	0.295**	-0.093	-0.042	1.000					
X11	G	-0.028	0.037	0.013	0.052	-0.012	-0.000	0.080	0.099	0.071	0.054	1.000				
	P	-0.024	0.017	0.004	0.024	-0.011	-0.002	0.060	0.065	0.041	0.039	1.000				
X12	G	-0.019	-0.179**	-0.145*	-0.345**	-0.212**	-0.261**	0.002	0.006	-0.049	-0.117*	0.180**	1.000			
	P	-0.017	-0.164**	-0.131*	-0.261**	-0.196**	-0.247**	-0.005	-0.008	-0.030	-0.123*	0.150**	1.000			
X13	G	0.073	-0.245**	0.039	-0.228**	-0.013	0.005	-0.050	-0.040	0.031	0.120*	0.049	0.156**	1.000		
	P	0.073	-0.226**	0.046	-0.169**	-0.011	-0.005	-0.035	-0.070	0.001	0.120*	0.043	0.146*	1.000		
X14	G	0.096	0.241**	0.018	0.132*	0.090	0.194**	0.014	-0.044	0.058	0.272**	0.061	-0.084	-0.143*	1.000	
	P	0.066	0.193**	0.072	0.090	0.080	0.172**	0.010	0.137*	-0.003	0.227**	0.050	-0.108	-0.135*	1.000	
X15	G	0.249**	0.069	0.222**	0.082	0.056	0.174**	0.414**	-0.408**	0.054	0.512**	-0.018	0.051	0.156**	0.019	1.000
	P	0.109	-0.004	0.100	0.065	0.041	0.058	0.187**	-0.155**	-0.025	0.207**	-0.006	0.026	0.064	-0.016	1.000

* Significant at 5% level of significance and ** significant at 1% level of significance
X1= No. of leaves per plant; X2= Leaf Length(cm); X3=Leaf Width (cm); X4 = Leaf area index(cm^2); X5 = No. of primary branches per plant; X6= No. of secondary branches per plant; X7= Plant height(cm); X8 = Days to harvest; X9= Total plant weight(g); X10= Yield per plant(g); X11= Total phenol content(mg/g); X12 = Total Anthocyanin content (mg/g); X13 = Ascorbic acid content (mg/100g); X14 =Chlorophyll content(mg/100g); X15 = Yield per plot(kg).

Table 4: Genotypic path coefficient analysis for direct and indirect effects of component characters on yield in vegetable mustard (*B. juncea*)

Traits	*X1*	*X2*	*X3*	*X4*	*X5*	*X6*	*X7*	*X8*	*X9*	*X10*	*X11*	*X12*	*X13*	*X14*	*X15*
X1	-0.087	-0.01	0.01	0.05	-0.009	-0.004	0.084	0.051	0.005	0.177	0.001	-0.001	0.004	-0.021	0.249**
X2	0.002	0.591	-0.012	-0.397	-0.161	0.075	0.005	-0.044	0.002	0.086	-0.001	-0.012	-0.013	-0.053	0.069
X3	-0.002	-0.015	0.469	-0.229	-0.036	-0.020	0.029	0.007	-0.002	0.033	0.000	-0.009	0.002	-0.004	0.222**
X4	0.008	0.428	0.197	-0.547	-0.208	0.086	0.013	0.022	0.001	0.148	-0.002	-0.022	-0.012	-0.029	0.082
X5	-0.002	0.289	0.051	-0.345	-0.330	0.113	0.066	0.037	0.003	0.208	0.000	-0.014	-0.001	-0.020	0.056
X6	0.002	0.213	-0.044	-0.225	-0.178	0.209	0.012	0.036	0.007	0.201	0.000	-0.017	0.000	-0.042	0.174**
X7	-0.025	0.010	0.046	-0.024	-0.074	0.008	0.295	0.019	0.002	0.165	-0.003	0.000	-0.003	-0.003	0.414**
X8	0.010	0.060	-0.008	0.028	0.027	-0.017	-0.013	-0.441	0.002	-0.060	-0.004	0.000	-0.002	0.010	-0.408**
X9	-0.018	0.064	-0.038	-0.013	-0.041	0.061	0.031	-0.036	0.023	0.037	-0.003	-0.003	0.002	-0.013	0.054
X10	-0.029	0.094	0.029	-0.150	-0.127	0.078	0.090	0.050	0.002	0.538	-0.002	-0.008	0.006	-0.059	0.512**
X11	0.002	0.022	0.006	-0.028	0.004	0.000	0.023	-0.043	0.002	0.029	-0.036	0.012	0.002	-0.013	-0.018
X12	0.002	-0.106	-0.068	0.189	0.070	-0.055	0.001	-0.003	-0.001	-0.063	-0.006	0.065	0.008	0.018	0.051
X13	-0.006	-0.145	0.018	0.124	0.004	0.001	-0.015	0.018	0.001	0.064	-0.002	0.010	0.051	0.031	0.156**
X14	-0.008	0.142	0.008	-0.072	-0.030	0.041	0.004	0.019	0.001	0.146	-0.002	-0.005	-0.007	-0.218	0.019

Residual are 0.31764** Significance at 1% level of significance

X1= No. of leaves per plant; X2= Leaf Length(cm); X3=Leaf Width; X4 = Leaf area index(cm^2); X5 = No. of primary branches per plant; X6= No. of secondary branches per plant; X7= Plant height(cm); X8 = Days to harvest; X9= Total plant weight(g); X10= Yield per plant(g); X11= Total phenol content(mg/g); X12 = Total Anthocyanin content; X13 = Ascorbic acid content (mg/100g); X14 =Chlorophyll content(mg/100g); X15 = Yield per plot(kg).

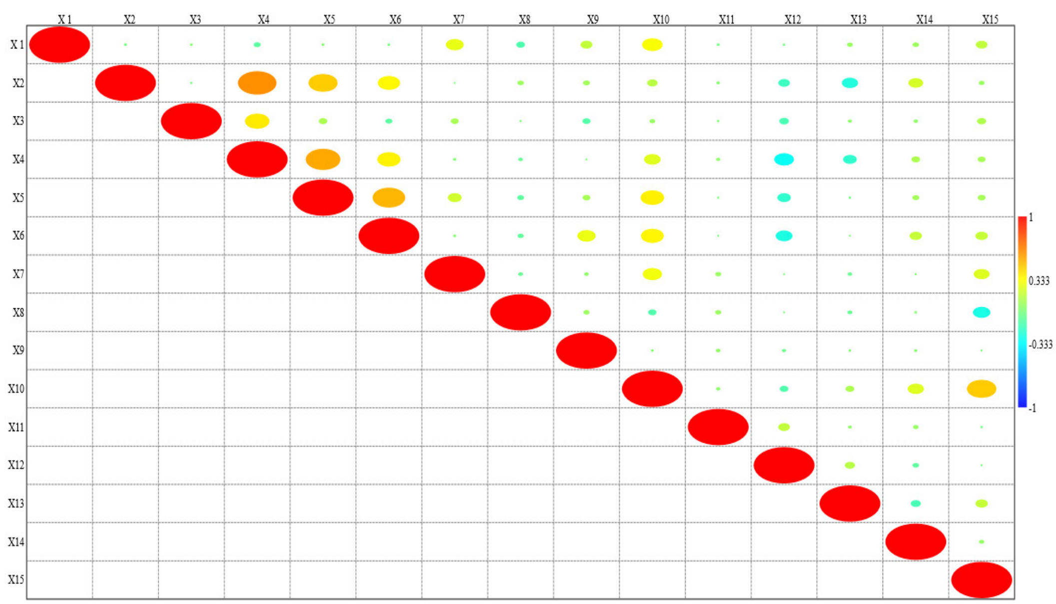

Figure 1: Graphical representation of genotypic correlation coefficient studies among different traits

Materials and Methods

The present investigation was carried out at The Experimental Research Farm of Regional Horticultural Research Station, Department of Vegetable Science RHR&TS, Jachh (H.P.), which is located at an altitude of 428 m above mean sea level, lying between 32⁰16′54.02″ N latitude and 75⁰51′4.38″ E longitude. The experimental material comprised of 101 genotypes (Table 1) of vegetable mustard were transplanted in Randomized Complete Block Design with three replications during the main season (Nov-Mar) of 2021-22 to study the extent of genetic variation and their related components in the existing germplasm. Observations were recorded on various growth, yield and qualitative traits including number of leaves per plant, Leaf length (cm), Leaf width

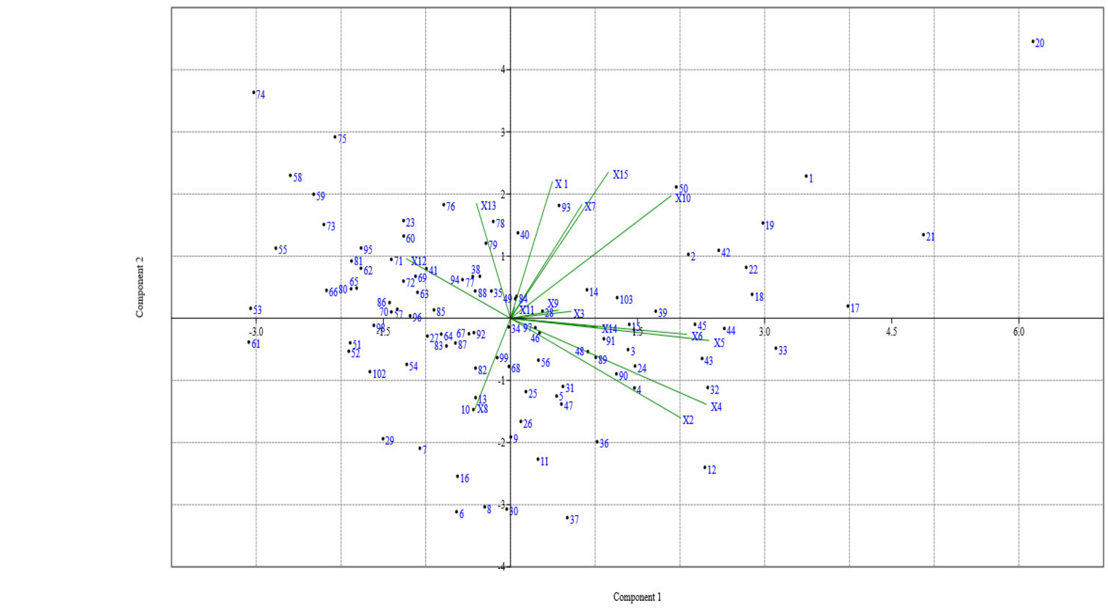

Figure 2: Biplot between PC I and PC II depicting contribution of different traits causing variability between vegetable mustard (*B. juncea*) genotypes

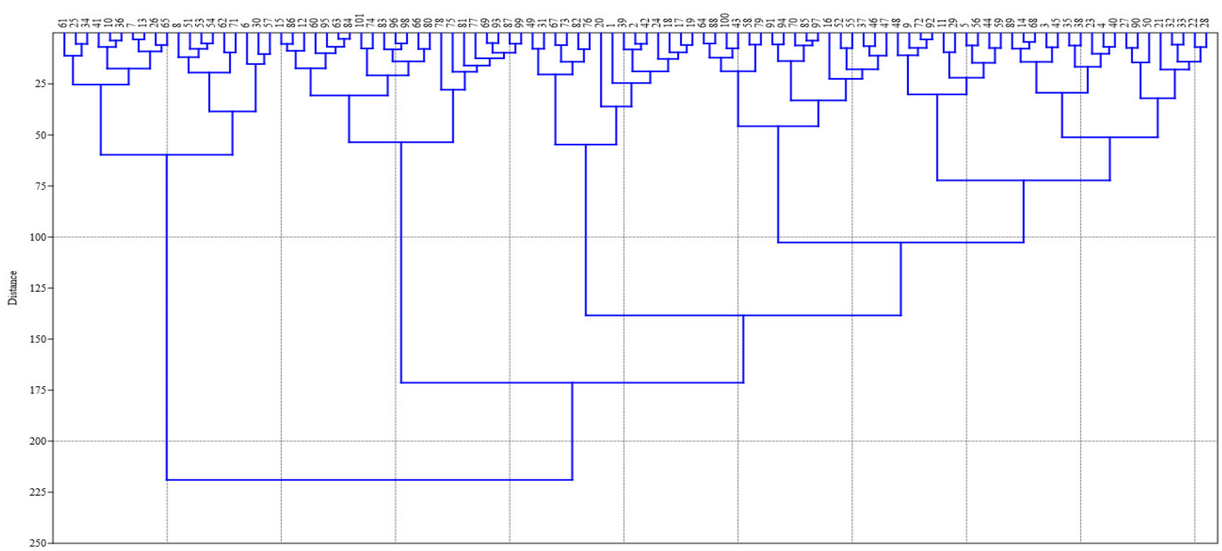

Figure 3: Dendrogram depicting genetic relationship between various vegetable mustard (*B. juncea*) genotypes (Ward's Method)

(cm), Leaf area index (cm^2), Number of Primary Branches per plant, Number of Secondary Branches per plant, Plant height (cm), Days to harvest, Yield per plant (g), Total leaf weight per plant (g), Total plant weight (g), yield per plot (kg), Leaf color, Total phenol content (mg/g), Anthocyanin content (mg/100g), Ascorbic acid (mg/100 g), Chlorophyll content (mg/100 g) and Incidence of insect-pest and disease (if any). Parameters of variability were calculated as per suggested by Burton and De Vane (1953). Heritability, in a broad sense, was studied as per the formula given by Burton and De Vane (1953) and Allard (1960). Genetic advance as a percentage of the mean was calculated as per the formula given by Johnson et al. (1955). The correlation coefficient among all important quantitative character combinations at phenotypic and genotypic levels will be estimated by employing the formula given by Al-Jibouri et al. (1958). The path coefficient was studied as per the procedure suggested by Wright (1921) and was elaborated by Dewey and Lu (1959). Mahalanobis D^2 statistics were used to estimate the genetic divergence, as indicated by Rao (1952).

Table 5: PC scores, Eigen value and the amount of variance described by the first five main components

Trait	*PC1*	*PC2*	*PC3*	*PC4*	*PC5*	*PC6*	*PC7*	*PC8*	*PC9*	*PC10*	*PC11*	*PC12*	*PC13*	*PC14*	*PC15*
X 1	-0.092	0.410	-0.164	0.146	-0.422	-0.149	0.038	0.188	0.342	-0.472	-0.257	0.101	0.318	-0.065	0.128
X2	-0.374	-0.299	-0.088	0.103	0.053	0.125	-0.168	-0.053	0.403	-0.024	-0.294	-0.429	0.026	0.165	-0.492
X3	-0.133	0.021	0.591	0.235	0.023	-0.353	0.316	0.277	0.122	0.164	0.208	0.176	0.170	0.025	-0.361
X4	-0.431	-0.258	0.264	0.063	0.121	-0.094	-0.068	0.131	0.156	-0.023	-0.110	0.037	-0.162	0.280	0.697
X5	-0.436	-0.066	-0.016	-0.092	0.167	-0.153	-0.204	-0.151	0.041	-0.275	0.342	0.064	-0.071	-0.690	-0.027
X6	-0.388	-0.048	-0.311	-0.286	0.166	0.029	0.067	-0.024	-0.225	0.063	0.155	0.265	0.620	0.316	-0.047
X7	-0.157	0.341	0.030	0.337	-0.233	-0.253	-0.405	-0.268	-0.254	0.147	0.324	-0.365	0.054	0.244	0.051
X8	0.078	-0.271	-0.208	0.371	0.001	-0.325	0.363	-0.621	0.099	0.145	-0.170	0.117	0.126	-0.110	0.124
X9	-0.105	0.025	-0.573	-0.048	-0.050	-0.427	0.084	0.430	0.109	0.393	0.080	-0.023	-0.327	-0.031	-0.017
X10	-0.353	0.367	-0.030	0.054	0.007	0.145	0.157	-0.270	-0.085	-0.098	-0.116	0.429	-0.536	0.244	-0.240
X11	-0.009	0.032	-0.149	0.573	0.483	0.017	-0.053	0.315	-0.438	-0.192	-0.267	-0.013	0.054	-0.098	-0.034
X12	0.229	0.178	-0.124	0.262	0.393	0.200	-0.302	-0.034	0.569	0.136	0.311	0.295	0.071	0.106	0.051
X13	0.075	0.344	-0.003	-0.251	0.499	-0.222	0.395	-0.120	0.132	-0.271	0.099	-0.462	-0.040	0.155	0.071
X14	-0.191	-0.026	-0.135	0.306	-0.199	0.553	0.491	0.109	0.023	0.031	0.408	-0.237	-0.008	-0.090	0.139
X15	-0.215	0.438	0.146	-0.095	0.124	0.189	0.022	-0.055	0.044	0.578	-0.391	-0.106	0.175	-0.357	0.136
Eigen value	3.074	1.910	1.372	1.207	1.139	1.038	0.953	0.830	0.751	0.694	0.659	0.497	0.372	0.306	0.199
% variance	20.491	12.731	9.143	8.047	7.594	6.919	6.353	5.532	5.007	4.628	4.396	3.310	2.480	2.042	1.327
Cum-ulative variance	20.491	33.222	42.365	50.412	58.006	64.925	71.278	76.81	81.817	86.445	90.841	94.151	96.631	98.673	100.000

X1= No. of leaves per plant; X2= Leaf Length(cm); X3=Leaf Width (cm); X4 = Leaf area index(cm^2); X5 = No. of primary branches per plant; X6= No. of secondary branches per plant; X7= Plant height(cm); X8 = Days to harvest; X9= Total plant weight(g); X10= Yield per plant(g); X11= Total phenol content(mg/g); X12 = Total Anthocyanin content (mg/g); X13 = Ascorbic acid content (mg/100g); X14 =Chlorophyll content(mg/100g); X15 = Yield per plot(kg).

Results and Discussion

The perusal of Table 2 showed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied, which indicated that environment played a greater role in creating variation among the various genotypes. High magnitude of genotypic and phenotypic coefficients of variation were seen in traits like number of primary branches per plant (PCV- 24.02% and GCV- 22.92%), number of secondary branches per plant (PCV- 30.39% and GCV- 29.85%), total phenol content (PCV- 28.93% and GCV- 25.78%) and total anthocyanin content (PCV-89.07 and GCV- 85.91%). However, moderate values of PCV and GCV were observed in traits like number of leaves per plant (PCV- 15.33% and GCV-15.15%), leaf area index (PCV- 18.73% and GCV- 14.24%), plant height (PCV- 13.95% and GCV- 12.91%), yield per plant (PCV- 14.91% and GCV-14.02%), ascorbic acid content (PCV- 16.15% and GCV- 16.02%) chlorophyll content (PCV- 19.03% and GCV- 15.36%) and yield per plot (PCV- 11.84%). Whereas the low values for PCV and GCV were exhibited in leaf length (PCV- 9.52% and GCV- 8.94%), leaf width (PCV- 8.07% and GCV- 6.97%), days to harvest (PCV- 4.50% and GCV- 3.91%) and total plant weight (PCV-9.91% and GCV- 7.25%). The highest value of heritability, along with a high genetic advance %mean was observed for a number of secondary branches per plant (96.48% and 60.41), followed by a number of leaves per plant (97.65 and 30.84%), anthocyanin content (93.01 and 170.68%), number of primary branches per plant (91.00 and 45%), yield per plant (88.44% and 27.17%) and total phenol content (79.41 and 47.34%), high heritability coupled with moderate genetic advance was recorded in leaf length (88.36 and 17.32%) and leaf width (74.44 and 12.38%) which may be attributed to additive and non-additive gene effects. Character association plays a major role in any plant breeding program which aims at improving the quality and yield traits. Correlation determines the relationship among different characters and thus, helps in making selection more effective. Further, the knowledge pertaining to the magnitude of association between different characters of the crop enhances the precision of genetic improvement. A perusal of Table 3 and Figure 1 showed that the genotypic correlations were greater in magnitude as compared to the phenotypic correlations for most of the characters, which meant that the environment

Table 6: Vegetable mustard genotypes clustering pattern on the basis of genetic divergence

Clusters	*Genotypes*
I	PBR-357, IC597889, IC597904, IC597907, IC597910, IC597921, IC597931, IC597947 and IC597920 (9 genotypes).
II	ASHIRWAD, BHAGIRATHI, JAGANNATH, JM-1, JM-2, KRISHNA, LAXMI, NRCDR-2, NRCDR-601, PANT RAI-20, PBR-210, VAIBHAV, PANT RAI-19, RGN-487, IC597876, IC597883, IC597887, IC597895, IC597905, IC597914 and IC597922 (21 genotypes).
III	ARAVALI and JD-6 (2 genotypes).
IV	BR-40, CS-56, GDM-4, GM-3, KANTI, KRANTI, LES-43, LET-36, NARENDRA-RAI(NDR-8501), NRCHB-101, PANT RAI-18, PANT MUSTARD-67, PBR-91, PUSA BAHAR, PUSA BOLD, IC597867, IC597870, IC597880, IC597884, IC597892, IC597925, IC597934, IC597943, IC597948, IC597911 and IC597942 (26 genotypes).
V	CS-52, CS-60, IJ-31, DURGAMANI, GM-1, GM-2, MAYA, NDRE-4, PUSA TARAK, PUSA AGRANI, PUSA JAI KISAN, PUSA MAHAK, IC597872, IC597878, IC597879, IC597882, IC597885, IC597888, IC597893, IC597894, IC597903, IC597917, IC597932, IC597924, IC597929, IC597936, IC597939, IC597944, IC597886, IC597901, IC597919 and PUSA SAG-1 (32 genotypes).
VI	CS-54, CS-58, DRMR-150-35, NDYR-8, PANT RAI-21, PBR-97, IC597866, IC597868, IC597869, IC597873 and IC597881 (11 genotypes).

Table 7: Clustering pattern of 101 genotypes of vegetable mustard based on genetic divergence

Cluster	*I*	*II*	*III*	*IV*	*V*	*VI*
I	5.221					
II	4.937	4.586				
III	5.691	5.145	6.185			
IV	6.105	4.742	6.366	4.731		
V	4.542	4.995	6.153	4.740	4.302	
VI	7.208	6.933	7.755	5.314	5.603	6.887

played a lesser role in governing the phenotype of the vegetable mustard genotypes studied. The phenotypic and genotypic correlation coefficients across several characters revealed a positive and significant association of yield per plot as presented in Table 3 and Figure 1. The positive and significant correlation coefficient was observed for plant height (0.414**, 0.187**) and yield per plant (0.512**, 0.207**), whereas it was negative and significant for days to harvest (-0.408**, -0.155**) at both phenotypic (P) and genotypic (G) levels. Additionally, it was positive and significant for the number of leaves per plant (0.249**), leaf width (0.222**), number of secondary branches per plant (0.174**) and ascorbic acid content (0.156**) at only genotypic (G) level. This reflects the strong genetic association between these traits and yield per plot. Hence, selection on the basis of these traits might lead to a higher yield per plot. The results were familiar with the findings of Tiwari et al. (2017). The results of path coefficient analysis at the genotypic level, indicating the direct and indirect effects of different traits on yield per plot, are shown in Table 4. The path coefficient analysis at the genotypic level indicated that the maximum positive direct effect on yield per plot by leaf length followed by yield per plant, leaf width, plant height, number of secondary branches per plant, total anthocyanin content, ascorbic acid content and total plant weight. Similar findings were found by Verma et al. (2008). The residual effect reported at the genotypic level was noted low, that is, 0.31764 for fruit yield, which revealed that characters in the current analysis contributed in the higher part of the variation.

The principal component analysis (PCA) is used to show the significance of the major contribution to the overall variance (Table 5). From the variable loadings of PC I; it was found that leaf length, leaf area index, number of primary branches per plant, number of secondary branches per plant, yield per plant and total anthocyanin content were the dominant features that contributed to 20.491% of the total variation. In PC II; the number of leaves per plant, leaf length, leaf area index, plant height, days to harvest, yield per plant, ascorbic acid content and yield per plot had the most impact, i.e., 12.731% of the total variation. In PCA III; leaf width, number of secondary branches per plant and total plant weight were the predominant traits i.e. 9.143 % of the observed total variation, while in PC IV; the number of secondary branches per plant, plant height, days to harvest, total phenol content and chlorophyll content had the most impact, i.e., 8.047 of the observed total variation. In PCA V; the number of leaves per plant, total phenol content, total anthocyanin content and ascorbic acid content were the predominant traits, i.e., 7.594 % of the observed total variation, while in PC VI; leaf width, days to harvest, total plant weight and chlorophyll content had the most impact i.e. 6.919 of the observed total variation. Saikrishna et al. (2021) also observed high genetic diversity using PCA. Using the values of PC I and PC II, a biplot was produced (Figure 2). When compared on certain qualities, genotypes that are close together are seen as similar, but genotypes that are further away exhibit more variation.

The clustering pattern of 101 distinct vegetable mustard genotypes has been described in Table 6 and Figure 3. Based on the performance of different traits, all genotypes were grouped into six clusters. The cluster V (32) has the highest number of genotypes**.** Rabbani et al. (1998) also placed 52 *B. juncea* accessions into six clusters, while Gupta et al. (1991) grouped 48 lines of *B. juncea* into five clusters. Rout et al. (2019) grouped 71 genotypes of vegetable mustard in seven clusters. The genotypes from one source of origin clustered with the genotypes of other source of origin. This indicated that there was no parallelism between geographical distribution and genetic diversity. Verma and Sachan (2000),

Table 8: Cluster means for various traits among 101 genotypes of vegetable mustard

Traits	*Cluster I*	*Cluster II*	*Cluster III*	*Cluster IV*	*Cluster V*	*Cluster VI*
Number of leaves per plant	12.55	12.81	14.03	12.24	11.98	11.19
Leaf length (cm)	17.92	19.24	20.80	19.06	19.03	19.01
Leaf width (cm)	14.98	14.06	14.24	14.38	14.47	14.01
Leaf area index (cm^2)	0.52	0.55	0.64	0.54	0.54	0.54
Number of primary branches per plant	4.12	4.45	6.05	4.16	4.10	3.83
Number of secondary branches per plant	7.24	10.06	14.39	9.81	8.15	8.55
Plant height (cm)	143.00	136.72	142.95	114.49	122.78	91.72
Days to harvest (cm)	76.35	75.99	69.66	76.29	75.32	75.46
Yield per plant (g)	48.05	47.50	71.34	44.33	45.89	44.22
Total plant weight (g)	127.92	151.24	147.52	151.45	130.73	134.85
Yield per plot (kg)	2.66	2.67	3.17	2.60	2.69	2.57
Total phenol content	4.21	4.21	4.50	4.04	3.78	4.00
Anthocyanin content	1.55	1.65	1.93	1.30	1.49	1.72
Ascorbic acid	20.54	20.28	23.99	20.72	20.22	20.67
Chlorophyll content	0.43	0.46	0.54	0.47	0.48	0.44

and Chaubey and Katiyar (1979) also found a similar trend. Average values for inter-cluster and intra-cluster divergence (D^2) are presented in Table 7. The distance for the intra-cluster was the highest in cluster VI (6.887) and the highest inter-cluster distance was reported between cluster VI and cluster III (7.755). Similar results were also observed by Rout et al. (2019). Table 8 shows the cluster means for various attributes among 101 genotypes of vegetable mustard. It would be desirable to employ genotypes from various clusters, depending on the distances between them, to create desired segregants since there is little chance of distinct populations arising via hybridization between parents within a cluster.

Conclusion

In the present studies, high heritability along with high genetic advance was observed for a number of secondary branches per plant followed by the number of leaves per plant, anthocyanin content, number of primary branches per plant, yield per plant and total phenol content, indicating that most likely the heritability for these characters is due to additive gene effects. Thus, improvement can be brought about by phenotypic selection for these characters. A positive and significant correlation coefficient was observed for plant height and yield per plant, reflecting the selection on the basis of these traits to get a higher yield. The path coefficient analysis indicated that the maximum positive direct effect on yield per plot by leaf length followed by yield per plant. On the basis of genetic divergence studies, all the genotypes were grouped into six clusters. The highest inter-cluster distance was reported between cluster VI and cluster III. Hence, hybridization between the genotypes of these clusters is expected to yield superior hybrids or transgressive sergeants in later generations.

References

Al-Jibouri, H.A., Miller, P.A., & Robinson, H.F. (1958). Genotypic and environmental variance and co-variance in upland cotton crops of inter-specific origin. Agronomy Journal, 50, 633-636.

Allard, R.W .(1960). Principles of Plant Breeding. John Wiley and Sons, New York p 485.

Burton, G.M., & De Vane, E.H. (1953). Estimating heritability in tall Fescue (Festuca arundinacea) from replicated colonal material. Agronomy Journal, 45, 310-314.

Chaubey, C.N., & Katiyar, R.P. (1979). Genetic divergence for yield component and some developmental traits related tofitness in *Brassica campestris* var. *Toria*. Indian Journal of Genetics, 27, 289-292.

Dewey, D.R., & Lu, K.H. (1959). A correlation and path analysis of components of crested wheat grass seed production. Agronomic Journal, 15, 515-518.

Gupta, V.P., Sekhon, M.S., & Satija, D.R. (1991). Studies on genetic diversity, heterosis and combining ability in Indian mustard [*Brassica juncea* (L.) (Czern and Coss)]. The Indian Journal of Genetics and Plant Breeding, 51(4), 448-453.

Johnson, H.W., Robinson, H.F., & Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47, 310-314.

Kumar, R., Babu, S.G., Kumar, S., & Sandhya. (2015). Genetic variability and divergence studies in elite rice genotypes for biometrical traits. The Ecoscan, 9, 209-212.

Lakra, A., Tantuway, G., Tirkey, A.E., & Srivastava, K. (2020). Genetic variability and Trait association studies in Indian mustard (*Brassica juncea* L. Czern & Coss). International Journal Current Microbiological Applied Science, 9(1), 2556-2563.

Rabbani, M.A., Aki, I., Yoshie, M., Tohru, S., & Kenji, T. (1998). Phenotypic variation and the relationships among mustard (*Brassica juncea* L.) germplasm from Pakistan. Euphytica, 101, 357-366.

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc. New York Edn. 1.

Rich. (1991). Crucifers of Great Britain and Ireland. Botanical Society of the British Isles, London, p 336.

Rout, S., Kerkhi, S.A., & Gupta, A. (2019). Estimation of genetic variability, heritability and genetic advance in relation to seed yield and its attributing traits in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Journal of Pharmacognosy and Phytochemistry, 8(3), 4119-4123.

Saikrishna, A., Arunkumar, B., Khan, H., Kuchanur, P.H., & Patil, A. (2021). Genetic diversity studies in Indian mustard [*Brassica juncea* (L.) Czern&Coss.] for yield and its component traits. The Pharma Innovation Journal, 10(10), 534-538.

Sharma, R.K., & Prasad, K. (2010). Classification of promising okra (*Abelmoschus esculentus* (L.) Moench) genotypes based on principal component analysis. Journal of Tropical Agriculture and Food Science 38, 161-169.

Singh, J., Sharma, A., Sharma, P., & Kumar, N. (2023). Genetic Variability and Association Studies in Mid-late and Late Group of Cauliflower (*Brassica oleracea* L. var. *botrytis*). Indian Journal of Plant Genetic Resources, 36(1), 45-51.

Singh, S., Yadav, R., Rramawat, N., Rana, J.C., Raiger, H.L., Bhardwaj, R., and & Meena, B.L. (2021). Revealing genetic diversity of Indian mustard (*Brassica juncea*) for yield improvement. Indian Journal of Agricultural Sciences 91(1), 170–1715.

Tiwari, A.K., Singh, S.K., Tomar, A., & Singh, M. (2017). Heritability, genetic advance and correlation coefficient analysis in Indian mustard (*Brassica Juncea* (L.) Czern&Coss). Journal of Pharmacognosy and Phytochemistry, 6(1), 356-359.

Verma, R., Sharma, R., & Sharma, S.K. (2008). Association studies among yield and its component characters in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. Indian Journal of Genetics and Plant Breeding, 68(1), 87–89.

Verma, S.K., and Sachan, J.N. (2000). Genetic divergence in Indian mustard (*Brassica juncea* (L.) Czern&Coss.). Crop Research (Hisar), 19(2), 271-276.

Warwick, S.I., Francis, A., & Shehbaz, I.A. (2006). Brassicaceae: Species checklist and database on CD-Rom. Plant System Evolution, 259, 249-258.

Wright, S. (1921). Correlation and causation. Journal of Agricultural Research, 20(7), 557-585.

सारांश

यह अनुसन्धान कार्य सरसों साग के 101 विविध जीन प्ररूपों के बीच आनुवंशिक विचलन के अनुमान के साथ-साथ उपज और अन्य बागवानी लक्षणों के लिए आनुवंशिक परिवर्तनशीलता और चरित्र संघ की सीमा का अध्ययन करने के लिए आयोजित किया गया । विचरण के विश्लेषण से अध्ययन किए गए सभी लक्षणों के सभी जीनोटाइप के बीच महत्वपूर्ण अंतर का संकेत मिला। पी.सी.वी. और जी.सी.वी. विभिन्न लक्षणों के लिए उच्च थे, जैसे कि कुल एंथोसायनिन सामग्री (89.07%, 85.91%), प्रति पौधे की माध्यमिक शाखाओं की संख्या (30.39%, 29.85%), कुल फिनोल सामग्री (28.93%, 25.78%) और प्रति पौधे की प्राथमिक शाखाओं की संख्या (24.02%, 22.92%)। एस्कॉर्बिक एसिड सामग्री (98.44%) के बाद प्रति पौधे पत्तियों की संख्या (97.65%), प्रति पौधे माध्यमिक शाखाओं की संख्या (96.48%) एंथोसायनिन सामग्री (93.01%), प्रति पौधे प्राथमिक शाखाओं की संख्या (91.00 %), प्रति पौधा उपज (88.44%), पत्ती की लंबाई (88.36%), पौधे की ऊंचाई (85.73%) और कुल फिनोल सामग्री (79.41%) के लिए उच्च आनुवंशिकता अनुमान दर्ज किए गए । सहसंबंध अध्ययनों से पता चला कि प्रति प्लॉट उपज का जीनोटाइपिक और फेनोटाइपिक दोनों स्तरों (क्रमशः 0.512, 0.207 और 0.414, 0.187) पर प्रति पौधा उपज और पौधे की ऊंचाई के साथ सकारात्मक और महत्वपूर्ण सहसंबंध था। पथ गुणांक विश्लेषण के आधार पर प्रति प्लॉट उपज पर पत्ती की लंबाई (0.591) और प्रति पौधा उपज (0.538) का अधिकतम सकारात्मक प्रत्यक्ष प्रभाव पड़ा । पहले छह प्रमुख घटकों के परिणामस्वरूप सभी विशेषताओं के लिए कुल भिन्नता 64.925% थी। आनुवंशिक विचलन अध्ययनों के आधार पर, 101 जीनोटाइप को छह समूहों में समूहीकृत किया गया और क्लस्टर VI और क्लस्टर III (7.755) के बीच उच्चतम अंतर-क्लस्टर दूरी दर्ज की गई।