

## International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693  
 ISSN Online: 2617-4707  
 IJABR 2024; SP-8(1): 129-134  
[www.biochemjournal.com](http://www.biochemjournal.com)  
 Received: 14-10-2023  
 Accepted: 18-12-2023

**Baseerat Afroza**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Razia Sultan**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Ummyiah H Masoodi**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Sabina Malik**  
 Dryland Agriculture Research  
 Station, SKUAST, Kashmir,  
 Jammu & Kashmir, India

**Asima Amin**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Bisma Bashir**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Rani Shamma**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Tamanna Khan**  
 Division of Vegetable Science,  
 SKUAST-Kashmir, Shalimar,  
 Srinagar, Jammu & Kashmir,  
 India

**Corresponding Author:**  
**Sabina Malik**  
 Dryland Agriculture Research  
 Station, SKUAST, Kashmir,  
 Jammu & Kashmir, India

## Divergence studies in knolkhol (*Brassica oleracea* var. *gongylodes* L.)

**Baseerat Afroza, Razia Sultan, Ummyiah H Masoodi, Sabina Malik, Asima Amin, Bisma Bashir, Rani Shamma and Tamanna Khan**

DOI: <https://doi.org/10.33545/26174693.2024.v8.i1Sb.292>

### Abstract

An investigation was carried out at the Experimental field, Division of Vegetable Science, SKUAST-K, Shalimar during Rabi season 2021-22. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications and plant spacing of 30 cm × 30 cm for thirty genotypes including three checks, Pusa Virat, Purple Vienna and White Vienna. Observations were recorded for various quantitative and quality traits. Based on Mahalanobis  $D^2$  statistics, 30 genotypes were grouped into eleven clusters. Maximum number of 6 genotypes were included in cluster II followed by cluster I with 5 genotypes. Highest intra cluster distance was observed in cluster V and inter cluster distance ( $D^2$ ) was recorded maximum between cluster XI and cluster IV, indicating that the genotypes in these clusters are genetically very diverse hence, can be used as parents in any breeding programme to get higher heterotic effects.

**Keywords:** Knolkhol, diversity analysis

### Introduction

Knol-khol (*Brassica oleracea* var. *gongylodes* L.) is an important crop grown particularly in Kashmir and northern parts of India. It is a highly cross-pollinated crop which requires cool climate for seed production. Genetic variability created either through natural processes or through crop breeding is essential for generating new gene complexes for realizing higher economic yield quality and resistance to biotic and abiotic stresses. Selection is perhaps the most important activity of all plant breeding programmes, the effectiveness of which in turn depends upon the range of genetic diversity existing already in the population in respect of economic characters. The presence of unique genetic characteristics distinguishes members of a given population from those of any other population. Genetic diversity is, therefore, a key component of conservation efforts associated with population management (Andayani *et al.*, 2001) [1]. Genetic diversity is critical for identifying the best genotypes for making rapid progress in desirable traits and for selecting the most diverse parents for future breeding efforts.

Keeping in view the importance of the crop, lack of sufficient information on genetic diversity Knol-khol under the climatic conditions of Kashmir and in other parts of India, it becomes imperative to evaluate Knol-khol germplasm for its utilization in breeding programme, to generate information on genetic diversity and to identify superior parents with desirable yield and quality traits.

### Material and Methods

The single factor experiment was laid out in Randomized Complete Block Design (RCBD) with three replications at the Experimental field, Division of Vegetable Science, SKUAST-K, Shalimar during Rabi season 2021-22 using thirty genotypes. Observations were recorded on thirty-four quantitative and quality traits. The data collected was subjected to standard statistical analysis.

### Results and Discussion

The perusal of Table 1 indicated that Mahalanobis  $D^2$  statistics clustered thirty genotypes of knolkhol into 11 clusters with cluster II had maximum number of genotypes (6); followed by cluster I (5), cluster III (5); cluster IV (4), cluster V (4); cluster VI (1), cluster VII (1), cluster

VIII (1), cluster IX (1), cluster X (1) and cluster XI (1). Using Mahalanobis  $D^2$  clustering Quamruzzaman *et al.* (2007) [14] grouped twenty genotypes of cauliflower into six clusters; Khan *et al.* (2009) [8] grouped forty genotypes of kale into four clusters; Santhosha *et al.* (2011) [15] reported fourteen clusters in fifty-one genotypes of cauliflower, Meena *et al.* (2013) [10] reported three clusters in thirty accessions of cabbage and Dolkar *et al.* (2020) [4] grouped thirty genotypes of knol-khol into six clusters; Pramila *et al.* (2021) [13] grouped fourteen genotypes of cauliflower into four clusters.

Maximum intra cluster distance was recorded for cluster V (475570.30) followed by cluster IV (283734.90), cluster III (221743.20), cluster II (180522.30) and cluster I (149931.00). The minimum intra-cluster was found in cluster I (149931.00). The maximum intra-cluster distance ( $D^2$ ) (cluster V) indicated high heterogeneity in genetic constitution of genotypes in that cluster while minimum intra-cluster distance ( $D^2$ ) (cluster I) indicated homogeneity in genetic constitution of genotypes in that cluster. The highest value of inter-cluster distance between cluster XI and IV (4849918.00) followed by cluster X and XI (4051389.00) and cluster IV and cluster VI (3824375.00) (Table 2) indicated more heterogeneous genetic constitution of genotypes included in both clusters. In contrast, minimum inter-cluster distance (cluster VIII and V) indicated closer relationship among the genotypes included. Parent selection from highly divergent cluster is expected to manifest high heterosis in hybridization. Genotypes belonging to clusters separated by maximum genetic distance may be used in hybridization programme to obtain a wide spectrum of variation among the segregants (Doddabhimappa *et al.*, 2010) [3]. Genotypically distant parents can exert high heterosis (Farhad *et al.*, 2010) [5] and (Dar *et al.*, 2010) [2]. It is also mentioned that crossing involving parents belonging to the medium divergent cluster may also exhibit significant and positive heterosis (Mian and Bahl, 1989) [11].

Genetic constellation means of different clusters helps to identify the clusters to be chosen for hybridization. Cluster means and co-efficient of variation present an interesting picture of the nature of diversity (Sardana *et al.*, 1997) [16]. Perusal of the results representing cluster means (Table-3 a-b) for different growth characters revealed that cluster V registered the maximum mean value for number of leaf whorls (7.44), internode length (1.23 cm), leaf length (36.97 cm), leaf width (24.63 cm), stem length (5.55 cm), stem breadth (8.04 cm), gross stem weight (583.76 g), net stem weight (478.09 g), number of leaves per plant (15.95), yield per hectare (246.04 q), cluster IV for silique length (106.23 cm), silique width (1.65 cm), number of seeds per silique (24.96), seed yield per plant (19.82 g) and seed yield per hectare (231.84 kg), cluster IX for 1000 seed weight (6.59 g), total chlorophyll content (200.63), carbohydrate content in leaf (6.93) and total carotenoid content in knob (4.97), cluster II for petiole length (23.46 cm), plant height (57.59 cm) and plant spread (67.14 cm); cluster VIII for vitamin C content in leaf (108.28), moisture content in knob (62.60) and vitamin C content in knob (74.71), cluster X for total carotenoids content in leaf (14.38), TSS content in leaf (6.38) and TSS content in knob (7.94), cluster III for days to 50% harvest (57.31 days) and days to seed maturity (210.83 days), cluster VI for days to 50% flowering (156.55 days) and carbohydrate content in knob (9.91), cluster VII for days to 50% stem swelling (38.84 days), cluster XI for

moisture content in leaf (77.53). Hence, crosses between genotypes selected from these clusters may be used to generate Knol-khol genotypes with good yield and quality traits. Similar comparison of clusters based on the range of mean value of each character had been done by Quamruzzaman *et al.* (2007) [14], Khan *et al.* (2009) [8], Santhosha *et al.* (2011) [15], Meena *et al.* (2013) [10], Dolkar *et al.* (2020) [4] and Pramila *et al.* (2021) [13].

The selection and choice of parents mainly depends on contribution of traits towards divergence. The results in Table 4 depicted that the traits contributing maximum (up to 90%) towards divergence were yield per hectare followed by gross knob weight, net knob weight, number of leaves per plant, stem breadth, stem length, leaf length, leaf width, plant height, plant spread, petiole length, seed yield per plant, seed yield per hectare, number of seeds per silique, 1000 seed weight, number of leaf whorls, internode length, silique width, silique length, days to 50% stem swelling, days to 50% harvest, days to 50% flowering, days to seed maturity, total chlorophyll content, vitamin C content in leaf and knob, total carotenoids in leaf and knob, carbohydrate content in leaf and knob, TSS content in leaf and knob and moisture content in leaf and knob. The traits contributing maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridization and the subsequent selection of the parents from the clusters be based on their *per se* performance. In Knol-khol, maximum contribution from traits towards divergence has been reported by Khan *et al.* (2009) [8], Dolkar *et al.* (2020) [4] in knol- khol.

Maximum per cent contribution of the traits towards total genetic divergence was observed from yield per hectare (q) (20.30%) followed by gross stem weight (g) (12.10%), net stem weight (g) (10.93%) and number of leaves per plant (8.69%) suggesting that selection of one or two elite genotypes from such divergent clusters based on the above characters and crossing would result in more heterosis.

While selecting genotypes from distant clusters, the mean values for different traits should be given importance to generate promising breeding material (Hazara *et al.*, 2002) [6]. The findings of the current investigation into genetic variability and genetic constellation suggested that there was a significant amount of genetic diversity and variability available to take advantage of the superior allelic resources present in the genotypes through deliberate breeding and selection techniques in order to recover high yielding segregants that also possessed high-quality traits. Given that the genotypes were divided up into several clusters in the current study, it was concluded that geographic distribution was not a necessary component for clustering the genotypes. The presence of factors other than geographic origin, such as genetic stock exchange, drift, and natural and artificial selection, may be the cause of genetic diversity. Therefore, selection of genotypes for hybridization should have genetic diversity rather than geographical diversity as reported by Quamruzzaman *et al.* (2007) [14] in cauliflower; Khan *et al.* (2009) [8] in kale, Santhosha *et al.* (2011) [15] and Meena *et al.* (2013) [10] in cabbage, Dolkar *et al.* (2020) [4] in Knolkhol and Pramila *et al.* (2021) [13] in cauliflower. Maurya and Singh (1977) [9] suggested that more diverse the parents within overall limits of fitness, the greater are the chances of obtaining higher magnitude of heterotic  $F_1$ 's and subsequently result in the release of broad spectrum of genetic variability in the segregating generations (Joshi and

Dawan, 1966; Panday and Ghorai, 1987) [7, 12]. Singh *et al.* (1996) [17] suggested, the selection of parents should be done from different clusters having wide inter cluster distance and

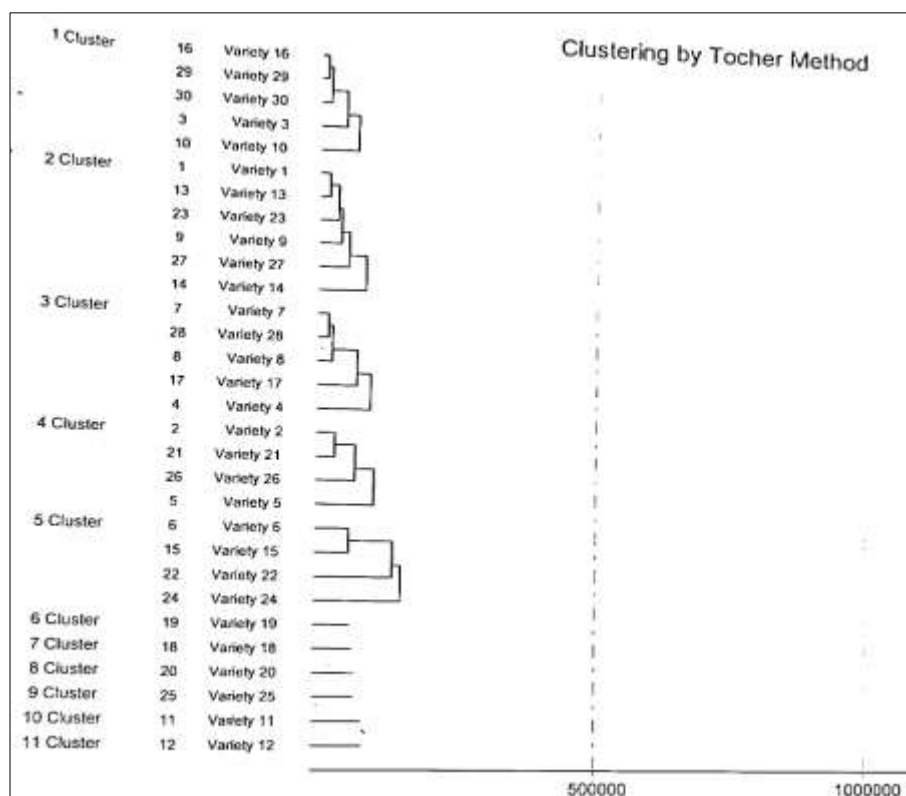
the parents should have high mean performance for traits that are contributing maximum towards divergence.

**Table 1:** Distribution of Knol-khol (*Brassica oleracea* var. *gongylodes* L.) genotypes into clusters based on D<sup>2</sup> Statistics

Cluster	No of genotypes in the cluster	Name of genotypes
I	5	SK-KK-3, SK-KK-38, SK-KK-72(B), Purple Vienna, Pusa Virat
II	6	SK-KK-1, SK-KK-32, SK-KK-64, SK-KK-65, SK-KK-180, SK-KK-175
III	5	SK-KK-9, SK-KK-22, SK-KK-23, SK-KK-80, White Vienna
IV	4	SK-KK-2, SK-KK-10, SK-KK-129, SK-KK-IC-6
V	4	SK-KK-14, SK-KK-72(A), SK-KK-154, SK-KK-197
VI	1	SK-KK-90
VII	1	SK-KK-88
VIII	1	SK-KK-123
IX	1	SK-KK- IC-2
X	1	SK-KK-45
XI	1	SK-KK-51

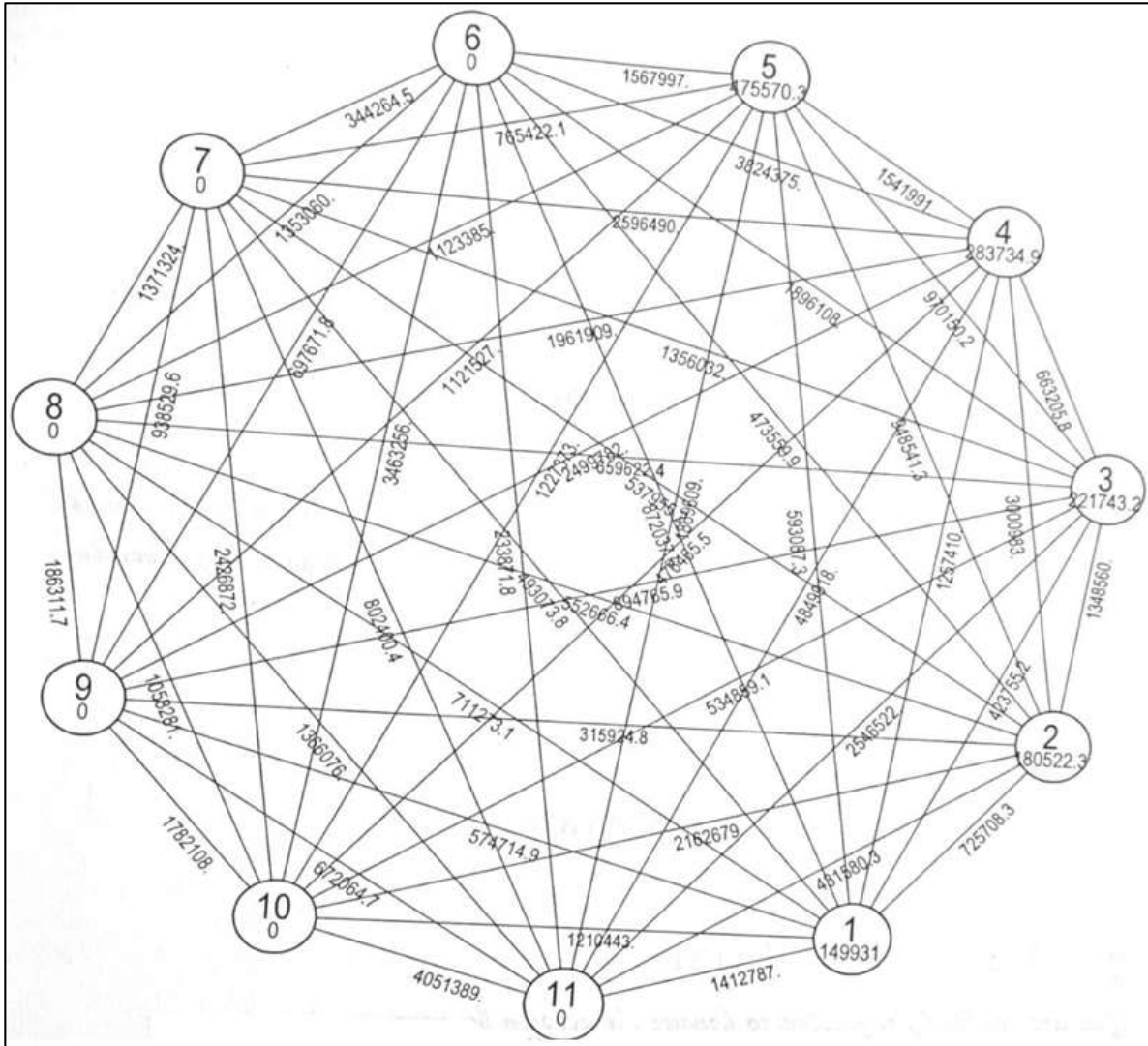
**Table 2:** Average intra-cluster (Diagonal) and inter-cluster (Above diagonal) distance values in Knol-khol

S. No.	Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1.	I	149931.00	725708.30	423755.20	257410.00	593087.30	872037.60	493073.80	711273.10	574714.90	1210443.00	412787.00
2.	II		180522.30	348560.00	3000983.00	948541.30	473559.90	537955.20	552666.40	315924.80	2162679.00	431580.30
3.	III			221743.20	663205.80	970150.20	1896108.00	356032.00	659622.40	894765.90	534859.00	2546522.00
4.	IV				283734.90	541991.00	3824375.00	2596490.00	1961909.00	499782.00	476465.50	4849918.00
5.	V					475570.30	1567997.00	765422.10	123385.00	1121527.00	227373.00	1869609.00
6.	VI						0.00	344264.50	353060.00	697671.80	3463256.00	233871.80
7.	VII							0.00	371324.00	938529.60	2426872.00	802400.40
8.	VIII								0.00	186311.70	1058281.00	366076.00
9.	IX									0.00	1782108.00	672064.70
10.	X										0.00	4051389.00
11.	XI											0.00



1= SK-KK-1	7= SK-KK-22	13= SK-KK-64	19= SK-KK-90	25= SK-KK-197
2= SK-KK-2	8= SK-KK-23	14= SK-KK-65	20= SK-KK-123	26= SK-KK-IC-2
3= SK-KK-3	9= SK-KK-32	15= SK-KK-72(A)	21= SK-KK-129	27= SK-KK-IC-6
4= SK-KK-9	10= SK-KK-38	16= SK-KK-72(B)	22= SK-KK-154	28= Purple Vienna
5= SK-KK-10	11= SK-KK-45	17= SK-KK-80	23= SK-KK-175	29= Pusa Virat
6= SK-KK-14	12= SK-KK-51	18= SK-KK-88	24= SK-KK-180	30= White Vienna

**Fig 1:** Clustering of genotypes by Tocher method (Dendrogram)



**Fig 2:** Mahalanobis Euclidean distance within and between clusters

**Table 3(a):** Cluster means for various quantitative traits in different clusters of Knol-khol genotypes (Tocher method)

S. No.	Parameters	Cluster										
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1.	Number of leaf whorls	6.17	5.93	5.36	5.73	7.44	6.73	6.48	5.21	4.72	5.92	6.61
2.	Internode length (cm)	0.99	0.74	0.89	1.08	1.23	0.52	0.80	0.52	0.46	0.82	0.93
3.	Leaf Length (cm)	28.00	25.84	23.61	34.97	36.97	22.70	24.71	15.52	17.75	28.84	21.13
4.	Leaf width (cm)	18.71	17.13	16.73	22.20	24.63	15.67	18.63	12.39	13.00	20.04	15.46
5.	Petiole length (cm)	17.34	23.46	15.68	20.13	21.32	16.55	18.63	17.71	13.22	20.66	15.36
6.	Days to 50% stem swelling	33.92	33.23	37.38	33.88	32.46	26.04	38.84	28.91	27.46	33.07	22.00
7.	Days to 50% harvest	53.53	49.73	57.31	48.62	49.21	49.33	49.47	48.36	44.64	52.61	50.74
8.	Stem length (cm)	4.53	4.55	4.21	5.01	5.55	4.63	4.79	4.06	3.60	4.63	3.62
9.	Stem breadth (cm)	7.45	6.18	6.42	7.33	8.04	6.26	7.34	5.86	5.40	7.48	6.38
10.	Net stem weight (g)	274.74	266.60	257.34	423.82	478.09	249.94	268.59	174.83	297.05	285.00	245.92
11.	Gross stem weight (g)	370.92	352.60	323.81	500.98	583.76	398.83	379.72	222.89	330.72	394.91	373.69
12.	Plant height (cm)	47.36	57.59	47.66	45.00	53.21	40.76	41.77	53.60	33.41	38.52	45.18
13.	Plant spread (cm)	58.19	67.14	49.30	51.16	63.74	49.17	54.15	40.52	41.16	58.67	48.82
14.	No. of leaves plant <sup>-1</sup>	13.12	11.23	11.16	15.12	15.95	11.14	11.86	8.84	9.58	12.71	10.98
15.	Yield per hectare (q)	197.22	162.82	152.42	202.43	246.04	143.20	206.10	116.13	190.87	178.07	134.27
16.	Days to 50% flowering	132.96	131.97	151.81	137.99	135.26	156.55	128.45	136.78	120.95	131.35	150.13
17.	Days seed maturity	195.62	183.70	210.83	192.19	188.19	195.57	207.04	206.41	179.71	181.32	187.74
18.	Siliqua length (mm)	75.17	74.80	82.49	106.23	66.24	80.58	87.01	86.31	68.40	64.92	51.60
19.	Siliqua width (mm)	0.82	0.86	0.80	1.65	0.71	0.88	0.88	0.86	0.64	0.54	0.96
20.	No. of seeds siliqua <sup>-1</sup>	13.70	14.29	16.27	24.96	10.60	15.14	17.22	16.83	11.81	10.66	6.11
21.	Seed yield plant <sup>-1</sup> (g)	13.18	16.35	17.10	19.82	10.68	14.71	18.09	15.52	10.26	8.41	7.12
22.	Seed yield hectare <sup>-1</sup> (kg)	181.16	193.08	205.20	231.84	136.20	186.24	226.68	196.20	128.48	100.92	71.40
23.	1000 seed weight (g)	4.48	5.10	5.66	4.02	5.84	5.26	5.78	5.26	6.59	5.02	4.98

**Table 3(b):** Cluster means for various quality traits in different clusters of Knol-khol genotypes (Tocher method)

S. No.	Parameters	Cluster										
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1.	Total Chlorophyll content (mg/100 g)	169.17	98.28	151.55	148.91	154.08	113.09	92.93	136.43	200.63	71.86	163.42
2.	Moisture content in leaf (%)	69.55	73.86	72.52	73.14	76.99	74.53	68.10	71.46	71.91	78.45	77.53
3.	Moisture content in knob (%)	55.11	55.21	53.85	59.76	58.37	49.53	57.56	62.60	59.06	56.52	47.96
4.	TSS in leaf (°B)	5.64	5.07	5.90	4.98	6.24	4.93	5.97	4.94	5.51	6.38	4.44
5.	TSS in knob (°B)	6.39	7.28	6.58	6.71	7.28	6.58	8.09	5.79	7.19	7.94	7.38
6.	Vitamin C content in leaf (mg/100 g)	107.23	93.93	94.45	104.85	94.51	90.47	86.78	108.28	103.29	89.04	87.53
7.	Vitamin C content in knob (mg/100 g)	58.49	58.30	55.36	59.15	50.81	63.98	73.52	74.71	61.47	65.87	57.64
8.	Carbohydrate content in leaf (%)	5.30	5.03	6.05	5.79	5.30	5.44	4.16	3.47	6.93	4.90	5.62
9.	Carbohydrate content in knob (%)	9.32	8.25	9.37	8.65	8.85	9.91	8.96	8.48	9.87	8.60	9.59
10.	Total carotenoids content in leaf (mg/100 g)	7.63	11.33	6.92	7.00	7.51	7.39	7.14	7.51	7.59	14.38	7.53
11.	Total carotenoids content in knob (mg/100 g)	3.30	2.78	3.40	3.65	4.89	2.23	3.48	5.59	4.97	2.45	2.48

**Table 4:** Percent contribution of thirty-four traits towards total genetic divergence in knol-khol (*Brassica oleracea* var. *gongylodes* L.)

S. No.	Traits	Percent contribution
1.	Yield per hectare (q)	20.30%
2.	Gross stem weight (g)	12.10%
3.	Net stem weight (g)	10.93%
4.	Number of leaves per plant	8.69%
5.	Stem breadth (cm)	7.78%
6.	Stem length (cm)	7.40%
7.	Leaf length (cm)	6.04%
8.	Leaf width (cm)	5.43%
9.	Plant height (cm)	4.40%
10.	Plant spread (cm)	2.84%
11.	Petiole length (cm)	2.20%
12.	Seed yield per plant (g)	1.34%
13.	Seed yield per hectare (kg)	1.15%
14.	Number of seeds per siliqua	1.14%
15.	1000 seed weight (g)	1.12%
16.	Number of leaf whorls	0.99%
17.	Internode length (cm)	0.90%
18.	Siliqua length (mm)	0.76%
19.	Siliqua width (mm)	0.52%
20.	Days to 50% stem swelling	0.51%
21.	Days to 50% harvest	0.47%
22.	Days to 50% flowering	0.46%
23.	Days to seed maturity	0.45%
24.	Total chlorophyll content (mg/100 g)	0.36%
25.	Vitamin C content in knob (mg/100 g)	0.35%
26.	Vitamin C content in leaf (mg/100 g)	0.25%
27.	Total carotenoids content in knob (mg/100 g)	0.20%
28.	Total carotenoids content in leaf (mg/100 g)	0.17%
29.	Carbohydrate content in knob (%)	0.15%
30.	Carbohydrate content in leaf (%)	0.14%
31.	TSS content in leaf (°B)	0.13%
32.	TSS content in knob (°B)	0.12%
33.	Moisture content in leaf (%)	0.11%
34.	Moisture content in knob (%)	0.10%
	Total	100.00

## Conclusion

Geographic distribution was not a necessary component for clustering the genotypes. The presence of factors other than geographic origin, such as genetic stock exchange, drift, and natural and artificial selection, may be the cause of genetic diversity. Therefore, selection of genotypes for hybridization should have genetic diversity rather than geographical diversity. Parent selection from highly divergent cluster is expected to manifest high heterosis in hybridization. Genotypes belonging to clusters separated by maximum genetic distance may be used in hybridization programme to obtain a wide spectrum of variation among the segregants

## References

- Andayani N, Morales JC, Forstner MR, Supriatna J, Melnick DJ. Genetic variability in mt DNA of the silvery gibbon implications for the conservation of a critically endangered species. *Conserv Biol.* 2001;15(3):770-775.
- Dar ZA, Wani SA, Zaffar G, Ishfaq A, Wani MA, Habib M, *et al.* Genetic divergence studies in brown sarson (*Brassica rapa* L.). *Res J Agric. Sci.* 2010;1(2):140-141.
- Doddabhimappa R, Gangapur B, Prakash G, Hiremath P. Genetic diversity analysis of Indian mustard (*Brassica juncea* L.). *Electron J Plant Breed.* 2010;1(4):407-413.

4. Dolkar R, Samnotra RK, Sharma SK. Clustering of knolkhol (*Brassica oleracea* var. *gongylodes* L.) genotypes for various quantitative and quality traits. *Vegetable*. 2020;47(1):69-73.
5. Farhad M, Hasanuzzaman M, Biswas BK, Arifuzzaman M, Islam MM. Genetic divergence in chilli (*Capsicum annuum* L.). *Bangladesh Res Publ J*. 2010;3(3):1045-1051.
6. Hazara P, Basu D, Sahu FK. Genetic divergence in okra. *Indian J Hort*. 2002;59(4):406-410.
7. Joshi AB, Dhawan NL. Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J Genet Plant Breed*. 1966;36:101-113.
8. Khan SH, Ahmed N, Jabben N, Mushtak F, Hussain K. Genetic divergence in kale (*Brassica oleracea* L. var. *acephala*). *Asian J Hort*. 2009;4(1):134-137.
9. Maurya DM, Singh DP. Adaptability in Rice. *Indian J Genet Plant Breed*. 1977;37:403-410.
10. Meena ML, Ram RB, Dwivedi DH, Bharti N. Estimation of biological divergence in cabbage (*Brassica oleracea* var. *capitata* L.). *Prog Hort*. 2013;45(2):351-354.
11. Mian MAK, Bahl PN. Genetic divergence and hybrid performance in chickpea. *Indian J Genet*. 1989;40(1):119-129.
12. Panday K, Ghorai. Genetic divergence in rice. *Oryza*. 1987;24:353-357.
13. Pramila, Kumar U, Ghosh S, Sinha B, Deepak AK. Genetic variability and genetic divergence study in Early Cauliflower (*Brassica oleracea* L. var. *botrytis* L.). *Int. J Curr Microbiol. Appl. Sci*. 2021;11:2715-2722.
14. Quamruzzaman AKM, Rahman MM, Uddin MN, Siddiky MA, Prodhan MDH. Genetic diversity in cauliflower (*Brassica oleracea* L. var. *botrytis* L.). *Indian J Hort*. 2007;64(1):50-52.
15. Santhosha HM, Varalakshmi B, Gowda NCN. Genetic diversity in early cauliflower (*Brassica oleracea* var. *botrytis* L.) germplasm. *J Hort. Sci*. 2011;6(1):21-24.
16. Sardana S, Borthakur DN, Lakhnopal TT. Genetic divergence in rice germplasm of Tripura. *Oryza*. 1997;34(3):201-208.
17. Singh AK, Singh SB, Singh SM. Genetic divergence in scented and fine genotypes of *Oryza sativa* L. *Ann Biol*. 1996;18(2):125-128.