Int J Seed Spice, 15(1), June, 2025: 82-91 DOI: https://doi.org/10.56093/IJSS.v15i1.7

Analysis of Variability Parameters and Genetic Divergence in Cumin (*Cuminum cyminum* L.)

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Received: 20 December 2025
Revision: 29 December 2025
Accepted: 27 January 2026

Citation

Yadav, Suman., Ramesh., Namrata., Dhoot, Rupal., Yadav, Suresh., Kumar, Manish., Singh, Netajit L., Bhanwariya, Yudhisthir 2025. Analysis of Variability Parameters and Genetic Divergence in Cumin (*Cuminum cyminum* L.). *Int J Seed Spice*.15 (1): 82-91

DOI

https://doi.org/10.56093/IJSS.v15i1.7

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Abstract

The Experiment was conducted on 60 diverse cumin genotypes and observations were recorded on thirteen characters at Dr. B. R. Choudhary Agricultural Research Station, Mandor-Jodhpur (Rajasthan) during Rabi season, 2024-25 in Randomized Block Design (RBD) with three replications. The mean sum of squares (analysis of variance) due to blocks were highly significant for all the thirteen characters under study represent variability among the genotypes. The higher value of phenotypic and genotypic coefficient of variation was observed for biological yield per plant. However, high heritability with high genetic advance as a percentage of the mean was recorded for the number of umbellate per umbel, the number of umbels per plant, the biological yield per plant, the seed yield per plant and the essential oil content, indicating the influence of additive gene action. Genetic diversity analysis grouped the sixty diverse cumin genotypes into sixteen clusters, with maximum intra-cluster distance observed in cluster-VI, followed by cluster-III. The maximum inter-cluster distance was recorded between cluster-X and XII, followed by cluster-XII, and cluster-XIII, indicating the presence of wide diversity between the cumin genotypes of the clusters.

Key words: *Cuminum cyminum*, Heritability, Variability, Genetic divergence

Introduction

Seed spices such as coriander, cumin, fennel, nigella, ajwain, and fenugreek play significant roles in both traditional medicine and modern culinary practices (Mahatma *et al*., 2024). Cumin (*Cuminum cyminum* L.) is an annual herbaceous spice cum medicinal plant belongs to family Apiaceae, having the basic chromosome number of 2n=2x=14. The Latin name *Cuminum* is derived from the Greek *Kuminon*, originated probably from the old Babyleniun name for cumin *Ka-ma-nu* (Lal *et al*., 2014). Cumin, sometimes referred to as "*Jeera*" or "*Zeera*" is a prominent seed spice in Indian homes and traditional medicine because of its many uses, including as an anti-inflating and antioxidant and for flavoring a variety of foods (Gohari and Saeidnia, 2011). It is the second most popular spice in the world after black pepper (Ghanbari *et al.*, 2014). The center of origin of cumin is Egypt and being grown mostly in Indian sub-continent. India is the largest producer of spices and seed spices in the world and leads in production of major seed spices including their export. Cumin, primarily is a seed spice, commands a substantial presence, covering 51.79% of the total area and accounting for 19.06% of production in India (Kumar *et al.* 2021). India occupies an area of 10.94 lakh ha with a production of 7.23 lakh tonnes and a productivity of 647 kg ha^{-1} in 2024-25 (Anonymous, 2024). It is mostly adapted to dry cool sunny areas with low humidity and sandy loam soils in semiarid and arid climate. Cumin is highly susceptible to various environmental factors, including temperature fluctuations, cloudy weather at maturity, and irrigation water quality (Kumhar *et al.*, 2020). Cumin productivity is frequently constrained by biotic stresses, particularly diseases and insect pests (Prajapati, B., & Patel, N. 2024).

Genetic variability is the basis for crop improvement. Selection and hybridization approaches are easily followed in bringing about the quantitative improvement in order to bring about the desired improvement (Singh *et al.*, 2024). The survey of genetic variability with the help of suitable genetic parameters like genotypic and phenotypic coefficients of variation, heritability estimates and genetic advance as per cent of mean are indispensable in breeding programmes aimed at improvement of seed yield. The heritability measures the contribution of genetic variability to the total variability, *i.e.* phenotypic variability observed for any quantitative traits.

The estimation of heritability can be utilized for the estimation of genetic gain expected for the selection of the top 5 % of individuals. Such studies enable the breeders to have a maximum selection response of the variance exhibited by the population, which is largely due to additive gene effects (Antiya *et al.*, 2024). The availability of natural diversity in cumin is very limited, although for yield and related traits, diversity can be generated through selection, sib matting and mutation. Genetic diversity studies are useful for identifying traits for crop improvement and for estimating their associations, which are suitable for breeders to improve crop yield through directional plant breeding approaches. Low exploitation of genetic diversity, narrow genetic base and limited breeding work and the understanding for breeding behavior is very limited in cumin (Kumhar *et al.*, 2020).

In the present study, Mahalanobis D^2 analysis was applied to assess the genetic divergence among the genotypes, to identify promising genotypes with more divergence to initiate crossing program and, to assess the contribution of different characters to genetic diversity.

Material and Methods

The experimental material comprised 60 genotypes of cumin collected and developed at Dr. B. R. Choudhary Agricultural Research Station, Mandor-Jodhpur and SDAU, Dantiwada (Gujarat). This experiment was laid out in Randomized Block Design along with three replications during *Rabi,* 2024–25. The genotypes were grown in two-row plots of 4 m length, following a crop geometry of 30 cm × 7 cm. The soil of the experimental field was loamy sand in texture, slightly alkaline in pH reaction (8.12), poor in organic carbon (0.22%), low in available nitrogen (175 kg/ha), medium in available phosphorus (19.91 kg/ha) but high in available potassium (373 kg/ha). Geographically, the experimental site is situated between 26°15' N and 26°45' North latitude and 73°00' E and 73°29' E longitude at an altitude of 231 meters above mean sea level. This region falls under agro-climatic zone Ia, (Arid Western Plains) of Rajasthan, India.

The observations were recorded on five randomly selected plants taken from each replication for plant height (cm), number of branches per plant, number of umbels per plant, number of umbellate per umbel, number of seeds per umbel, 1000 seed weight, biological yield per plant (g), seed yield per plant (g), harvest index (%) and essential oil content (%), total fat/crude oil content (%) were estimated through Fourier Transform Near-Infrared spectroscopy (FT-NIR). Days to 50% flowering and days to maturity were measured across the population.

The data were subjected to analysis of variance as suggested by Panse and Sukhatme (1985) and GCV and PCV were calculated according to the formula given by Lush (1940). Genotypic and phenotypic coefficients of variance were estimated as per suggested by Burton (1952). Heritability (broad sense) and genetic advance (GA) as a percentage of the mean at 5% selection intensity were estimated as per Johnson *et al.* (1955). Clusters and diversity analysis was worked out by using Mahalanobis D^2 statistic as suggested by P. C. Mahalanobis (1936).

Results and Discussion

The analysis of variance for different characters demonstrated that mean sum of square estimates attributable to genotypes were significant for all the characters under study, suggesting a sufficient amount of genetic variability in the existing materials. It was generally noted that the phenotypic variances were consistently greater than corresponding genotypic variances. The research conducted recently indicated a trend comparable to that of earlier studies by Bahraminejad *et al.* (2011), Bairwa *et al.* (2015), Jat and Singh (2016), Kumhar *et al.* (2020), Saroj *et al.* (2021) and Singh *et al.* (2024) for nearly all the characteristics of the study.

The seed yield varied from 1.86 g (MMCU-13-24) to 3.93 g (MMCU-45-24) with general mean of 2.87 g. Genotype (GC-2) was the earliest to flower (50 DAS) and (MMCU-20-24) matured first (110 days). Plant height varied from 36.34 cm (MCU-2) to 52.44 cm (MMCU-10-24) with general mean of 44.08 cm. While for the primary branches per plant, MCU-105 had maximum numbers (9.16) and GC-2 recorded the lowest (4.43). MCU-511, MMCU-4-24 and MCU-105 were the best for umbellate per umbel, umbels per plant and seeds per umbel, respectively.

1000 seed weight varied from MMCU-41-24 (3.76 g) to MCU-511 (5.87 g) with general mean of 5.06 g. The Biological yield per plant varied from 6.20 g (MMCU-26-24) to 15.60 g (MMCU-16-24), harvest index from 22.52% (MMCU-41-24) to 35.88% (MMCU-35-24), essential oil content from 2.84% (MMCU-35-24) to 5.08% (MMCU-39-24) and total fat/crude oil content from 8.73% (MMCU-7-24) to 9.50% (MMCU-6-24) with general mean of 9.17%. High range of variability was also reported by Singh *et al.* (2004), Bairwa *et al.* (2015), Meena *et al.* (2015), Jat and Singh (2016), Kumhar *et al.* (2020) and Khan *et al.* (2022).

The high magnitudes of phenotypic as well as genotypic coefficient of variation for biological yield per plant depicted the presence of a vast amount of variation, as presented in Table 2. High heritability (72%-90%) coupled with high genetic advance was observed for number of umbellate per umbel, followed by number of umbels per plant, biological yield per plant, seed yield per plant and essential oil content, indicating the influence of additive gene action, as such simple selection would be effective for improvement of

Table 1: Analysis of Variance (ANOVA) for different characters

Source of variation	Replication	Treatment	Error
degree of freedom	**2**	**59**	**118**
Days to 50 % flowering	9.61	68.91**	3.96
Days to maturity	0.05	41.60**	9.01
Plant height	12.13	49.21**	4.61
Number of branches per plant	0.16	1.37**	0.15
Number of umbels per plant	30.44	278.26**	12.46
Number of umbellate per umbel	0.05	1.50**	0.05
Number of seeds per umbel	5.48	18.68**	4.48
1000 seed weight	0.08	0.83**	0.02
Biological yield per plant	0.53	14.25**	0.87
Harvest index	7.32	34.03**	6.74
Essential oil content	0.12	0.69**	0.06
Total fat/crude oil content	0.03	0.06**	0.01
Seed yield per plant	0.05	0.65**	0.04

*, ** Significant at 5% and 1% probability level of significance respectively.

Table 2: Mean, range, variability, heritability (broad sense) and genetic advance as per cent of mean of the characters.

Characters	Mean	Range	Coefficient of variation (%)		Heritability Broad sense (%)	Genetic Advance (as per cent of mean)
			Genotypic	Phenotypic		
Days to 50% Flowering	61.16	50.33-71.00	7.60	8.27	84.50	14.40
Days to maturity	118.85	110.66-131.00	2.77	3.75	54.60	4.22
Plant height (cm)	44.08	36.34-52.44	8.74	10.01	76.30	15.73
Number of branches per plant	7.16	4.43-9.16	8.86	10.43	72.10	15.50
Number of umbels per plant	54.03	36.23-82.01	17.42	18.60	87.70	33.60
Number of umbellate per umbels	5.27	3.86-6.66	13.15	13.85	$90.20^{\#\#}$	25.73
Number of seeds per umbel	30.91	21.26-36.83	7.03	9.81	$51.30^{\#}$	10.38
1000 seed weight	5.06	3.76-5.93	10.18	10.72	$90.20^{\#\#}$	19.93
Biological yield per plant (g)	10.06	6.20-15.60	$20.97^{\#\#}$	$22.93^{\#\#}$	83.60	$39.50^{\#\#}$
Harvest index (%)	28.80	22.52-35.88	10.47	13.81	57.40	16.34
Essential oil content (%)	4.09	2.84-5.08	11.11	12.67	76.90	20.08
Total fat/crude oil content (%)	9.17	8.73-9.50	$1.35^{\#}$	$1.81^{\#}$	55.80	$2.08^{\#}$
Seed yield per plant (g)	2.84	1.86-3.93	15.79	17.45	81.80	29.42

#, ## Represents minimum and maximum values, respectively.

these traits. These results are in close agreement with reported by earlier workers Bairwa *et al.* (2015), Meena *et al.* (2015), Kumhar *et al.* (2020), Seet *et al.* (2020), Antiya *et al.* (2024) and Singh *et al.* (2024).

A study of genetic diversity categorized all the sixty genotypes of cumin into sixteen clusters (Table 3 and Fig.1), based on D^2 values using Tocher's method (Rao, 1952). Cluster-Ⅲ was the largest comprising of 15 genotypes followed by cluster-Ⅱ with 14 genotypes, cluster- I with 11 genotypes, cluster-Ⅵ with 8 genotypes, clusters-Ⅳ, Ⅴ, Ⅶ, VIII, IX, X, XI, XII, XIII, XIV, XV and XVI were the clusters having single genotype. The findings are confirmed by earlier reports of Bairwa *et al.* (2015), Kumhar *et al.* (2020), Lemma *et al.* (2020), Khan *et al.* (2023), Palanikumar *et al.* (2024), Ejigu *et al.* (2025) and Selvi *et al.* (2025).

The maximum intra-cluster distance was observed in cluster-Ⅵ (24.54), followed by cluster-Ⅲ (20.95), indicating that some genetic divergence still existed among the genotypes within the clusters. The maximum inter cluster distance was recorded between cluster-X and XII (205.08) followed by cluster-XII and XIII (199.14) and cluster-VIII and XII (193.75) indicating the presence of wide diversity between the genotypes of the clusters (Table 4 and Fig.2). Selection of parents from these groups may be useful to obtain greater

Table 3: Clustering pattern among 60 genotypes of cumin (Tocher's method)

Cluster	Number of genotypes	Name of genotypes
I	11	MMCU-17-24, MMCU-30-24, MMCU-12-24, MMCU-18-24, MMCU-11-24, MMCU-28-24, MCU-504, MMCU-22-24, MMCU-24-24, MMCU-33-24, MMCU-47-24
II	14	MMCU-2-24, MMCU -5-24, MMCU -10-24, MMCU -9-24, MMCU -19-24, MCU-73, MMCU -3-24, MMCU -8-24, MMCU -1-24, MMCU -14-24, MMCU -38-24, MMCU-15-24, MMCU-29-24, MMCU-31-24
III	15	MMCU-32-24, MMCU -46-24, MMCU -7-24, MCU -117, MCU -501, MMCU -27-24, MMCU -48-24, MMCU -43-24, MCU -2, MCU -121, MMCU -42-24, MMCU-41-24, GC-4, MMCU-36-24, MMCU-35-24
IV	1	MMCU-34-24
V	1	MMCU-20-24
VI	8	MMCU-44-24, MCU -502, MMCU -37-24, MMCU -39-24, MMCU -26-24, MMCU-13-24, MMCU-40-24, MMCU-25-24
VII	1	MMCU-21-24
VIII	1	MMCU-16-24
IX	1	MMCU-45-24
X	1	MCU-511
XI	1	MMCU-23-24
XII	1	GC-2
XIII	1	MCU-105
XIV	1	MMCU-6-24
XV	1	MMCU-4-24
XVI	1	MCU-507

variability in segregating generations. The wide range of D^2 values revealed that enormous diversity could be created through inter-cluster hybridization. Similar findings were reported by Meena *et al*. (2015), Gauhar *et al*. (2018), Acharya *et al*. (2020), Gebremedin *et al*. (2024) and Sharangi *et al*. (2024) for the cluster analysis.

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 5). The genotypes grouped in cluster means 50% flowering was highest in cluster XI (70.00) and the lowest in cluster-XII (50.33). Days to maturity exhibited the highest means in cluster-XIII (131.00) and lowest in cluster-V (110.67). Cluster-XIII exhibited the highest plant height (48.90), while the lowest height was observed in cluster-XII (36.76). Numbers of branches per plant were found highest and lowest for clusters-XIII (9.17) and cluster-XII (4.43), respectively. Cluster-XV recorded the highest number of umbels per plant (82.02) and lowest was recorded in cluster-XII (36.23). The number of umbellate per umbel was highest in cluster-X (6.67) and lowest was recorded in cluster-XII (3.87). The number of seeds per umbel was highest in cluster-XIII (36.83) and lowest in cluster-XII (21.27). Cluster-XVI exhibited the highest 1000-seed weight (5.93), while in cluster-XII (3.83), it was the lowest. The biological yield per plant was highest in cluster-VIII (15.60) while lowest in cluster-VI (7.86). Cluster-XI exhibited the highest harvest index (35.27) the lowest was recorded in cluster-VIII (23.99). The highest essential oil content was recorded in cluster-XI (4.93) and the lowest was recorded in cluster-XVI (3.15). The highest total fat/crude oil content was recorded in cluster- XIV (9.50) and the lowest was recorded in cluster- XI (8.91). Cluster-IX exhibited the highest seed yield per plant (3.93) and the lowest was recorded in cluster- XII (2.26). These results showed that different cluster genotypes were superior for different characters, and genotypes with these characters offer a good scope for improving cumin through selection. Among the traits studied, the maximum genetic divergence was contributed by 1000

Table 4: Average intra (bold values) and inter cluster distances of D^2 values of 60 genotypes of cumin.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**17.32**	24.94	33.62	33.56	28.63	32.39	24.76	44.54	43.13	52.93	36.55	98.59	42.78	43.06	45.86	31.81
II		**20.38**	53.81	25.11	40.14	46.32	25.42	33.94	42.26	35.89	25.03	127.82	30.48	71.70	35.26	31.10
III			**20.95**	72.60	30.64	37.67	47.20	94.80	60.78	106.17	62.88	48.38	86.98	44.89	83.41	75.63
IV				0.00	51.37	80.29	36.82	12.92	17.38	18.90	25.16	154.63	30.83	99.18	40.97	27.80
V					0.00	33.90	43.53	74.74	48.38	68.16	53.76	70.58	78.72	66.42	80.92	59.75
VI						**24.54**	39.51	88.01	87.57	94.59	61.25	85.00	76.68	40.66	78.05	60.96
VII							0.00	56.23	55.80	67.62	16.04	121.91	35.00	40.93	59.52	56.72
VIII								0.00	31.20	14.24	38.84	193.75	28.03	118.57	43.84	21.24
IX									0.00	37.09	32.55	123.61	40.90	118.84	49.95	55.44
X										0.00	45.84	205.08	28.51	149.65	30.93	20.43
XI											0.00	146.94	19.65	88.68	46.50	56.53
XII												0.00	199.14	92.77	165.65	164.04
XIII													0.00	112.39	27.47	41.40
XIV														0.00	115.28	87.17
XV															0.00	28.95
XVI																0.00

Table 5: Cluster means of different characters in cumin genotypes

Characters	DF	DM	PH	BR	UMP	UML	SUM	TW	BY	HI	EO	TO	SY
Cluster 1	61.79	119.00	44.31	7.53	6.26	5.40	30.52	5.15	10.28	28.47	3.77	9.24	2.90
Cluster 2	63.50	118.62	47.96	7.16	58.38	5.70	31.63	5.37	11.43	27.53	4.25	9.15	3.09
Cluster 3	59.44	118.11	40.87	6.83	47.72	4.88	30.63	4.43	8.74	29.54	4.07	9.14	2.53
Cluster 4	64.33	120.00	47.40	7.20	61.85	6.60	28.57	5.17	13.97	28.54	3.52	9.18	3.90
Cluster 5	56.67	110.67*	41.96	6.87	38.96	5.70	30.73	5.17	9.17	32.12	3.82	9.25	2.94
Cluster 6	59.08	118.08	42.98	7.22	47.43	4.43	30.82	5.48	7.86*	30.49	4.35	9.19	2.37
Cluster 7	69.67	129.00	48.15	7.07	47.90	5.73	30.10	5.27	8.73	31.97	4.40	9.33	2.79
Cluster 8	62.00	117.33	43.68	8.13	68.99	6.07	28.62	5.63	15.60#	23.99*	3.93	9.15	3.75
Cluster 9	60.00	118.67	40.11	7.60	61.43	6.47	29.57	4.43	13.07	30.08	4.32	9.14	3.93#
Cluster 10	55.67	118.33	43.84	7.67	70.36	6.67#	34.37	5.87	14.27	26.24	4.03	9.17	3.72
Cluster 11	70.00#	128.00	48.41	7.33	54.00	6.07	33.23	5.13	9.90	35.27#	4.93#	8.91*	3.48
Cluster 12	50.33*	112.67	36.76*	4.43*	36.23*	3.87*	21.27*	3.83*	8.50	26.71	4.48	9.16	2.26*
Cluster 13	65.33	131.00#	48.90#	9.17#	69.60	6.23	36.83#	5.23	11.80	28.43	4.85	9.17	3.34
Cluster 14	68.67	121.33	44.19	7.00	47.18	4.13	28.33	5.03	8.10	29.95	3.21	9.50#	2.43
Cluster 15	58.00	119.67	43.53	7.00	82.02#	5.83	35.84	5.27	10.92	24.65	4.65	9.03	3.02
Cluster 16	56.00	118.33	42.67	7.40	71.82	5.63	32.99	5.93#	13.07	24.50	3.15*	9.06	3.19

*, # Represents minimum and maximum values, respectively

DF : Days to 50% Flowering PH : Plant height (cm) UMP : Number of umbels per plant
DM : Days to maturity TW : 1000 seed weight UML : Number of umbellate per umbels
BY : Biological yield per plant (g) EO : Essential oil content (%) HI : Harvest index (%)
TO : Total fat/crude oil content (%) SY : Seed yield per plant (g) BR : Number of branches per plant
SUM : Number of seeds per umbel

Table 6: Contribution of various characters towards genetic divergence in cumin genotypes.

S. No.	Characters	Per cent contribution	No. of times ranked first
1	Days to 50% Flowering	10.51	186
2	Days to maturity	1.07	19
3	Plant height (cm)	3.73	66
4	Number of branches per plant	1.86	33
5	Number of umbels per plant	10.79	191
6	Number of umbellate per umbels	14.92	264
7	Number of seeds per umbel	0.45	8
8	1000 seed weight	26.33	466
9	Biological yield per plant (g)	14.52	257
10	Harvest index (%)	0.51	9
11	Essential oil content (%)	11.81	209
12	Total fat/crude oil content (%)	2.49	44
13	Seed yield per plant (g)	1.02	18

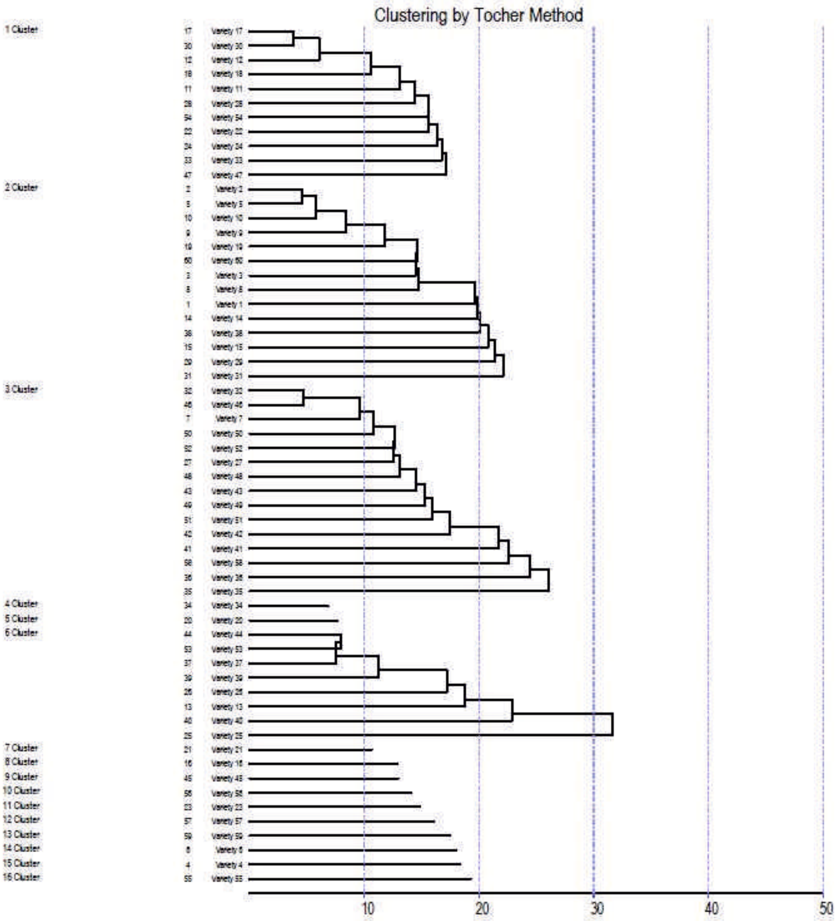

Fig. 1. Dendrogram of 60 genotypes of cumin based on thirteen traits

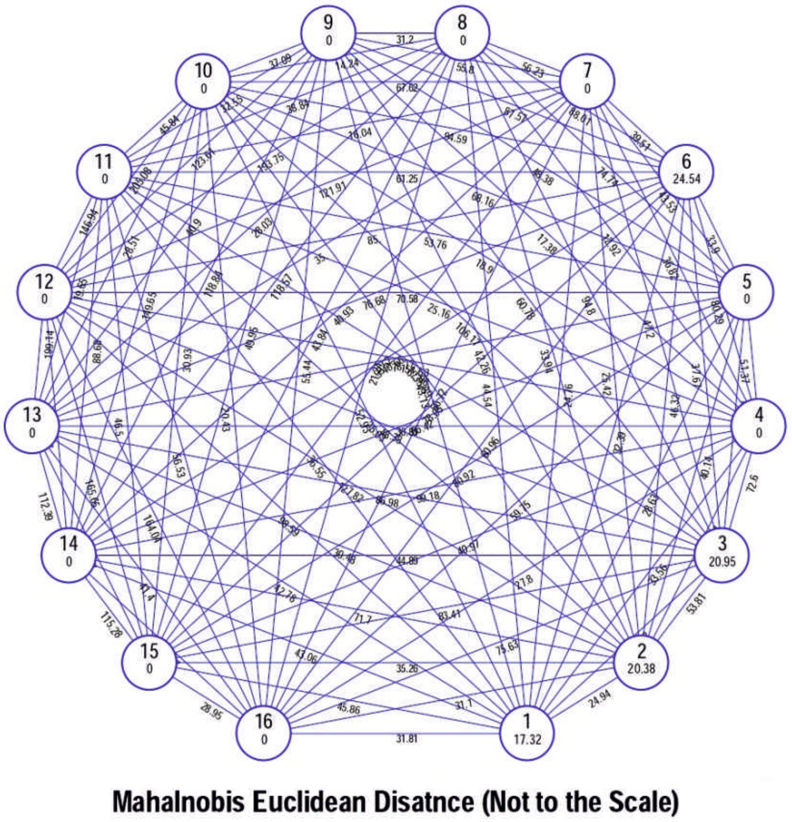

Fig. 2. Cluster diagram of 60 genotypes of cumin based on Mahalanobis D^2 Statistic

seed weight (26.33%) followed by number of umbellate per umbel (14.92%), biological yield per plant (14.52%), essential oil content (11.81%), number of umbels per plant (10.79%) and days to 50% flowering (10.51%) indicated that attributes could offer ample scope for selecting desired genotypes (Table 6). Similar findings were reported by Kumhar *et al.* (2020) and Moharana *et al.* (2023).

Conclusion

The investigated cumin genotypes possess immense variability and genetic diversity. Biological yield per plant, umbels per plant, umbellate per umbel, test weight, days to 50% flowering and essential oil content can be suitably considered for selection indices targeting enhanced seed yield of the crop. Crossing between genotypes of cluster-X and XII (most distant clusters) is likely to create superior progenies upon which selection can be exercised.

Acknowledgement

The authors acknowledge the facilities provided by Zonal Director Research, Dr. BRC ARS, Mandor. We are grateful to the Director Research, Agriculture University, Jodhpur (Rajasthan) for providing necessary support and facilities to conduct this experiment successfully.

Conflict of Interest

The authors declare that they have no conflict of interest.

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