The Pharma Innovation Journal 2021; 10(12): 2723-2728

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(12): 2723-2728

www.thepharmajournal.com
Received: 11-09-2021
Accepted: 06-11-2021

Hardik R Patel
Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

VL Parmar
Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

RK Patel
Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

GD Vadodariya
Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

Corresponding Author:
Hardik R Patel
Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat, India

Genetic variability and divergence analysis for seed yield and its attributes in coriander

Hardik R Patel, VL Parmar, RK Patel and GD Vadodariya

Abstract
Genetic variability forms the basis for crop improvement, hence detailed appraisal of the accessions for different traits is necessary in order to identify useful traits in improvement programs. The present experiment was carried out to assess genetic diversity using 40 genotypes of coriander at Navsari Agricultural University, Navsari in *Rabi* 2018-19. There was sufficient amount of variability present among studied genotypes of coriander. High heritability coupled with high genetic advance were found in total oil content, yield per plant, secondary branches per plant, seed yield per plot, umbels per plant, test weight, seeds per umbel, primary branches per plant and days to 50% flowering. The D^2 analysis grouped into eleven clusters through Mahalanobis D^2 statistics among genotype studied. The maximum inter cluster distance was observed between cluster VI and XI (482.66). The maximum intra-cluster distance was observed within cluster IV (D = 36.48) which included five genotypes.

Keywords: Coriander, variability, diversity, seed yield, cluster analysis

Introduction
Coriander (*Coriandrum sativum* L.) is an annual aromatic spice herb. It is commonly known as dhania or dhana belongs to family Apiaceae (Umbelliferae) and having a somatic chromosome number 2n = 22. According to the climatic conditions, it is mainly cultivated as a winter annual crop. Western Europe and Asia is considered as the centre of origin for coriander. It is probably one of the earliest seed spice known to mankind (Pruthi, 1976) [18]. The genus *Coriandrum* comprised of two species *viz*., *Coriandrum sativum* and *Coriandrum tordylium*. Among them, *C. sativum* is the cultivated one (Dhakad *et al*., 2017) [10].
It is a cross pollinated crop, possessing average 1-3 feet height (Tomar *et al*., 2014) [22]. It is having epigeal seed germination and tap root system. The leaves are alternate, decompound and petiolate with a pair of stipules. The leaves are green or light green and their underside is often shiny waxy. The aromatic odour and taste of coriander fruits is due to the presence of an essential oil containing linalool. The entire plant is used in preparing chutney, whereas the leaves are used for its flavouring the curries, sauce and soups. The leaves are also used for garnishing dishes.
Coriander has compound umbel types of inflorescence. The flowers are protandrous and having an inferior ovary. Flowers are small whitish or pinkish purple in colour born on compound terminal umbels. Fruit is a schizocarp and white to light brown in colour. Coriander is dicot type of seed. It is also known as the Cilantro, Chinese parsley, Dizzy corn and Japanese parsley. The crop grows in tropical condition and requires a cool environment, but at flowering and seed formation stages it requires dry frost-free climate. The coriander seeds are utilized as spices in the preparation of pickling spice and curry powder. They are used for flavouring pastry, cookies-cakes, bakery product, meat, fish, soda, candy and syrups.
The total area under coriander cultivation in India is 532 thousand hectares with an annual production of 710 thousand tones during the year 2017-18. Similarly, in Gujarat, the area and production of coriander during 2017-18 were 74.9 thousand hectares and 116.81 thousand metric tons, respectively with an average productivity 1.56 tones/ha.
Genetic variability is a prerequisite for any improvement in a crop. The success of any crop improvement programme depends on the quantum of genetic variability and extent to which the desirable characters are heritable. The ultimate goal of breeding programme aims to improve the characteristic of plants so that they become more desirable. Heritability is estimated either performing analysis of variance or regressing the value of the offspring on the mean value of the parents. Heritability has been used as an index of transmissibility of a character from the parent to its offspring and thus an aid to predict the improvement that can be made in a crop by selection for various characters.

Genetic divergence can be judged by multivariate analysis, a procedure that is widely used in different crops for parent selection. Multivariate analysis by means of Mahalanobis (1936) D^2 cluster analysis has been proved to be useful in selecting accessions for hybridization in several crops. It is powerful tool in identifying the degree of genetic divergence among parents.

Materials and Methods

The present study was carried out during *Rabi* 2018-19 at the Research Farm, Dept. of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari agricultural University, Navsari using forty different genotypes of coriander. The soil of experimental plot was medium black having medium to poor drainage and good water holding capacity with pH 7.5 to 7.8. Navsari is situated at the coastal region of western part of India, geographically with an altitude of 11.98 meter above mean sea level. It situated at 20^0 55' North latitude and 72^0 53' East longitudes. The weather during the growing season was normal and favourable. The forty different genotypes were grown in randomized block design in three replications. In experiment, each plot consisted of 120 plants at 30 x 10 cm^2 inter and intra row spacing. For raising a successful and healthy crop all the recommended package of practices were adopted.

Five plants are randomly selected, excluding the border ones, from each plot of all the three replications were tagged and used for recording the observations at harvesting stage. The average value of data from these plants were computed and used for statistical analysis. Observation were recorded for thirteen characters *viz.*, days to 50% flowering, plant height (cm), primary branches per plant, secondary branches per plant, umbels per plant, umbellate per umbel, seeds per umbel, days to maturity, yield per plant (g), test weight (g), seed yield per plot (kg), harvest index (%), total oil content (%). The calculation of data by analysis of variance with formula suggested by Panse and Sukhatme (1978) [16].

Genotypic and phenotypic co-efficient of variation were calculated by using the following formula suggested by Cockerham (1963) [7]. Heritability has been estimated as per the formula stated by Allard (1960) [2] and genetic advance as percentage over mean was also worked out using formula as specified by Johanson *et al.* (1955). The genetic divergence in 40 genotypes for 13 characters was analysed through Mahalanobis's D^2 statistic technique. Grouping of the genotypes into different clusters was done by using Ward's minimum variance method as described by Rao (1952) [19].

Results and discussion

Analysis of variance

The mean sums of square of all the thirteen characters are summarized in Table 1. The genotypic differences were found significant for thirteen characters under study indicating considerable amount of genetic variability among the studied genotypes for various characters (Patel *et al.,* 2018). This shows that there is vast scope to generate high yielding varieties and also the existence of possibility of improvement of different key traits simultaneously by exposing the materials to judicious selection pressure.

Genotypic coefficient of variation and phenotypic coefficient of variation

The higher magnitude of genotypic and phenotypic coefficient of variation was exhibited by total oil content followed by yield per plant, secondary branches per plant, seed yield per plot, umbels per plant, test weight, seeds per umbel and primary branches per plant. Similar higher magnitude of GCV and PCV was reported for total oil content by Desai *et al.* (2018) [8]; for yield per plant and secondary branches per plant by Ameta *et al.* (2016) [3] and Farooq *et al.* (2017) [11]; for seed yield per plot by Dhakad *et al*. (2017) [10]; for umbels per plant and seeds per umbel by Singh *et al.* (2006) [21] and Sharma *et al.* (2016) [20]; for test weight by Acharya *et al.* (2020) [1] and for primary branches per plant by Desai *et al.* (2018) [8] and Devi *et al.* (2019) [9].

Moderate magnitude of genotypic and phenotypic coefficient of variation was exhibited by harvest index, plant height, days to 50% flowering and umbellets per umbel. Similarly, moderate estimate of GCV and PCV was found for harvest index by Desai *et al.* (2018) [8]. For plant height, days to 50% flowering and umbellate per umbel, similar results had also been exhibited by Singh *et al.* (2006) [21]. However, low magnitude of genotypic and phenotypic coefficient of variation were depicted for days to maturity. Similar results had also been reported by Mayura and Devi (2016) [14], Anilkumar *et al.* (2018) [4] and Acharya *et al.* (2020) [1] for days to maturity.

Heritability and genetic advance

Heritability and genetic advance are important parameters. Heritability estimates along with genetic advance are normally more useful in predicting the genetic gain under selection than heritability estimates alone. The broad sense heritability for all the thirteen characters under study are presented in Table 3. Table indicated that high estimate of heritability was found for total oil content (98.37%) followed by test weight (91.79%), days to maturity (88.01%), days to 50% flowering (85.16%), secondary branches per plant (70.33%), yield per plant (68.47%), plant height (67.05%), seed yield per plot (66.94%), umbels per plant (64.81%) and seeds per umbel (63.00%); which indicated that these characters are less influenced by environmental fluctuations and largely governed by additive genes, so selection might be effective for improvement of such attributes. Similar results of high heritability for total oil content, test weight and days to maturity by Desai *et al.* (2018) [8]. For yield per plant, plant height, umbels per plant, seeds per umbel, secondary branches per plant and days to 50% flowering by Farooq *et al.* (2017) [11] and Devi *et al.* (2019) [9]. However, moderate estimates of heritability were recorded for umbellets per umbel (59.31%) followed by primary branches per plant (57.49%) and harvest index (46.93%) revealing higher environmental influence. These results were akin with Acharya *et al.* (2020) [1] for umbellets per umbel and harvest index.

The genetic advance is that the improvement within characters of selected population over the base population. Heritability is efficient with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more useful and valid in predicting the improvement through selection. The ranged of genetic advance from 0.37 (seed yield per plot) to 23.60 (umbels per plant). The high genetic advance expressed as percentage of mean was observed for total oil content (73.24%) followed by yield per plant (47.14%), secondary branches per plant (46.49%), seed yield per plot (44.59%), umbels per plant (42.79%), test weight (42.72%), seeds per umbel (32.08%), primary branches per plant (26.26%), plant height (23.30%), days to

50% flowering (20.48%) (Singh *et al.*, 2006, Dhakad *et al*., 2017) [21, 10]. The moderate genetic advance expressed as percentage of mean was obtained for harvest index (19.78%) followed by umbellets per umbel (16.53%) and days to maturity (10.01%).

In the present study, high heritability including high genetic advance as per cent of mean was observed for total oil content, yield per plant, seed yield per plot, umbels per plant, secondary branches per plant, seeds per umbel, test weight, plant height and days to 50% flowering revealing the importance of additive gene action in the inheritance of those characters. High heritability with high genetic advance as per cent of mean was reported for umbels per plant, seed yield per plant, seeds per umbel and plant height by Singh *et al.* (2006) [21], Dhakad *et al*. (2017) [10] and Mishra and Balaji (2017) [15]; for secondary branches per plant, days to 50% flowering and test weight by Mishra and Balaji (2017) [15] and for total oil content by Desai *et al.* (2018) [8]. High heritability along with moderate genetic advance was recorded for days to maturity. The result was in agreement with the finding of Patel *et al.* (2018) [17] and Acharya *et al.* (2020) [1].

Diversity analysis

Grouping of genotypes into clusters

Plant breeders are always interested to assess and utilize the genetic diversity among the germplasm in direct breeding programme because genetically diverse parents are likely to produce high heterotic effects and the distantly related parents within the same species when utilized in cross breeding programme are likely to produce wider spectrum of variability. Forty genotypes of coriander were grouped into eleven clusters by Tocher's method and the distribution of genotypes into eleven clusters shown in Table 4 as well as presented in fig. 1. The results indicated that a maximum number of diverse genotypes (11 genotypes) appeared in cluster I and II followed by cluster III (6 genotypes), cluster IV (5 genotypes) and remaining cluster like V, VI, VII, VIII, XI, X, XI had only 1 genotype.

Cluster distances among eleven clusters

The average inter and intra-cluster Euclidean distance were estimated based on Ward's minimum variance and are presented in the Table 5 and fig. 1. Inter cluster distance ranged from 17.95 to 482.66 and intra cluster distance ranged from 0.00 to 36.48. The maximum inter cluster distance was observed between cluster VI and XI (D^2 = 482.66). Whereas, the minimum inter cluster distance was observed between cluster V and cluster VI (D^2 = 17.95). The maximum intra-cluster distance was observed within cluster IV (D = 36.48) which included 5 genotypes followed by cluster II (D = 26.63) which included 11 genotypes. The minimum intra-cluster distance was observed within cluster I (D = 19.23) which include 11 genotypes followed by cluster III (D =23.40) which include 6 genotypes. The cluster V, VI, VII, VIII, IX, X and XI contained single genotype therefore; its intra-cluster distance was zero.

Average cluster mean for 14 different morphological traits

Average Cluster mean for different morphological traits in 40 coriander genotypes were presented in Table 6. Days to 50% flowering ranged from 48 days (cluster IV) to 68 days (cluster VIII), plant height ranged from 68 cm (cluster VIII) to 122.3 cm (cluster VII), primary branches per plant ranged from 5.75 (cluster IV) to 9.4 (cluster VIII), secondary branches per plant ranged from 21.61 (cluster IV) to 39.67 (cluster VI), umbels per plant ranged from 39.38 (cluster VII) to 92 (cluster V), umbellets per umbel ranged from 6.05 (cluster IV) to 8 (cluster V & VI), seeds per umbel ranged from 45 (cluster I) to 77.53 (cluster VIII), days to maturity ranged from 101.67 days (cluster VI) to 124.33 days (cluster XI), yield per plant ranged from 4.6 g (cluster V) to 10.59 g (cluster VI), seed yield per plot ranged from 0.63 kg (cluster V) to 1.4 kg (cluster VIII), test weight (100 seed weight) ranged from 0.76 g (cluster V) to 1.5 g (cluster III), harvest index ranged from 30.24% (cluster V) to 49.47% (cluster VIII) and total oil content ranged from 5.59% (cluster VIII) to 23.51% (cluster XI).

Conclusion

The analysis of variance for all the characters revealed highly significant differences among the genotypes studied indicated sufficient amount of variability present among forty genotypes of coriander under study. High heritability was also coupled with high genetic advance as per cent of mean for these traits, which indicated the predominance of additive gene effects, thus more emphasis should be given to mass selection and progeny selection for further improvement of these characters. Based on above findings, it could be concluded that more weightage should be given to seed yield per plant, umbels per plant, seeds per umbel and test weight to improve seed yield per plot in coriander.

D^2 analysis indicated wider genetic diversity among the forty genotypes, which were grouped in eleven different clusters. cluster I and cluster II include 11 genotypes, cluster III include 6 genotypes, cluster IV include 5 genotypes. While, remaining V to XI cluster were solitary. The maximum inter cluster distance was observed between cluster VI and cluster XI. From the results, it will be stated that inter-crossing from cluster VI and cluster XI genotypes might result in wide array of variability for exercising effective selection.

Acknowledgement

We are heartily grateful to Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari for providing research materials and facility to carry out this research.

Table 1: Analysis of variance (Mean sum of squares) for different characters of coriander

Source of variation	D. F.	Days to 50% Flowering	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Umbels per plant	Umbellets per umbel	Seeds per umbel
Replication	2	14.06	81.96	1.98	62.28	80.56	0.60	103.41
Genotypes	39	108.92**	561.23**	4.92**	187.68**	717.47**	1.71**	347.02**
Error	78	5.98	78.98	0.97	23.14	109.97	0.32	56.81
S. Em ±		1.41	5.13	0.57	2.77	6.05	0.33	4.35
C.D at 5%		3.98	14.45	1.60	7.82	17.05	0.92	12.25
C.V%		4.50	9.68	14.45	17.47	19.01	8.63	15.03

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

Source of variation	d. f.	Days to maturity	Yield per plant (g)	Seed yield per plot(kg)	Test weight(g)	Harvest index (%)	Total oil content (%)
Replication	2	17.56*	4.06	0.04	0.01	86.21	1.03*
Genotypes	39	99.58**	12.58**	0.17**	0.20**	127.49**	59.02**
Error	78	4.33	1.67	0.02	0.01	34.90	0.32
S. Em ±		1.20	0.75	0.09	0.04	3.41	0.33
C.D at 5%		3.38	2.10	0.25	0.12	9.60	0.93
C.V%		1.91	18.77	18.59	6.47	14.90	4.62

Table 2: Range, mean and component of variance of thirteen different characters of coriander

Sr. No	Character	Range	Mean	Component of variance		
				Genotypic	Phenotypic	Environmental
1	Days to 50% flowering	41.67-68.00	54.38	34.31	40.29	5.98
2	Plant height (cm)	57.93-122.30	91.78	160.75	239.73	78.98
3	Primary branches per plant	5.00-9.40	6.83	1.32	2.29	0.97
4	Secondary branches per plant	11.53-48.36	27.52	54.85	77.98	23.14
5	Umbels per plant	26.20-92.60	55.15	202.50	312.47	109.97
6	Umbellets per umbel	5.20-8.00	6.54	0.46	0.78	0.32
7	Seeds per umbel	24.75-77.53	50.13	96.74	153.55	56.81
8	Days to maturity	101.33-124.33	108.78	31.75	36.08	4.33
9	Yield per plant (g)	3.35-11.93	6.89	3.63	5.31	1.67
10	Seed yield per plot(kg)	0.42-1.40	0.84	0.05	0.07	0.02
11	Test weight (g)	0.76-1.66	1.17	0.06	0.07	0.01
12	Harvest index (%)	25.97-51.51	39.65	30.86	65.77	34.90
13	Total oil content (%)	5.59-23.51	12.34	19.56	19.89	0.32

Table 3: Genotypic and phenotypic coefficients of variations, heritability, and genetic advance as per cent of mean for thirteen different characters of coriander

Sr. No	Character	GCV%	PCV%	$h^2_{bs\%}$	Genetic advance	Genetic advance (% of mean)
1	Days to 50% flowering	10.77	11.67	85.16	11.13	20.48
2	Plant height (cm)	13.81	16.87	67.05	21.39	23.30
3	Primary branches per plant	16.81	22.17	57.49	1.79	26.26
4	Secondary branches per plant	26.91	32.08	70.33	12.79	46.49
5	Umbels per plant	25.80	32.05	64.81	23.60	42.79
6	Umbellets per umbel	10.42	13.53	59.31	1.08	16.53
7	Seeds per umbel	19.62	24.72	63.00	16.08	32.08
8	Days to maturity	5.18	5.52	88.01	10.89	10.01
9	Yield per plant (g)	27.66	33.42	68.47	3.25	47.14
10	Seed yield per plot (kg)	26.45	32.33	66.94	0.37	44.59
11	Test weight (g)	21.65	22.59	91.79	0.50	42.72
12	Harvest index (%)	14.01	20.45	46.93	7.84	19.78
13	Total oil content (%)	35.85	36.14	98.37	9.04	73.24

Table 4: The distribution of 40 genotypes of coriander into eleven different clusters on the basis of Mahalanobis D^2 Statistic

Cluster	Number of genotypes	Name of genotypes
I	11	NC- 42, NC- 47, NC- 48, NC-49, NC- 51, NC- 52, NC- 53, NC- 54, NC- 63, NC- 69, NC- 78
II	11	NC- 41, NC- 44, NC- 46, NC- 50, NC- 55, NC- 58, NC- 67, NC- 68, NC- 77, NC- 79, NC- 80
III	6	NC- 56, NC- 60, NC- 61, NC- 62, NC- 65, NC- 71
IV	5	NC- 57, NC- 59, NC- 64, NC- 66, NC- 73
V	1	NC- 45
VI	1	NC- 43
VII	1	NC- 70
VIII	1	NC- 75
IX	1	NC- 74
X	1	NC- 72
XI	1	NC- 76

Table 5: Average Inter and Intra – cluster (D^2) value for 40 genotypes of coriander

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	19.23	48.29	39.27	179.90	36.68	33.09	115.40	46.22	89.28	193.02	349.82
II		26.63	57.14	106.89	74.23	85.44	49.48	90.36	48.42	92.14	208.38
III			23.40	117.02	89.96	75.06	98.95	68.12	67.88	158.37	275.53
IV				36.48	276.52	275.39	70.23	252.60	56.04	54.68	79.54
V					0.00	17.95	173.83	61.65	161.85	269.08	460.37
VI						0.00	185.17	42.27	160.02	286.39	482.66
VII							0.00	147.08	21.40	22.19	100.04
VIII								0.00	127.99	240.43	408.04

IX									0.00	43.12	116.16
X										0.00	34.77
XI											0.00

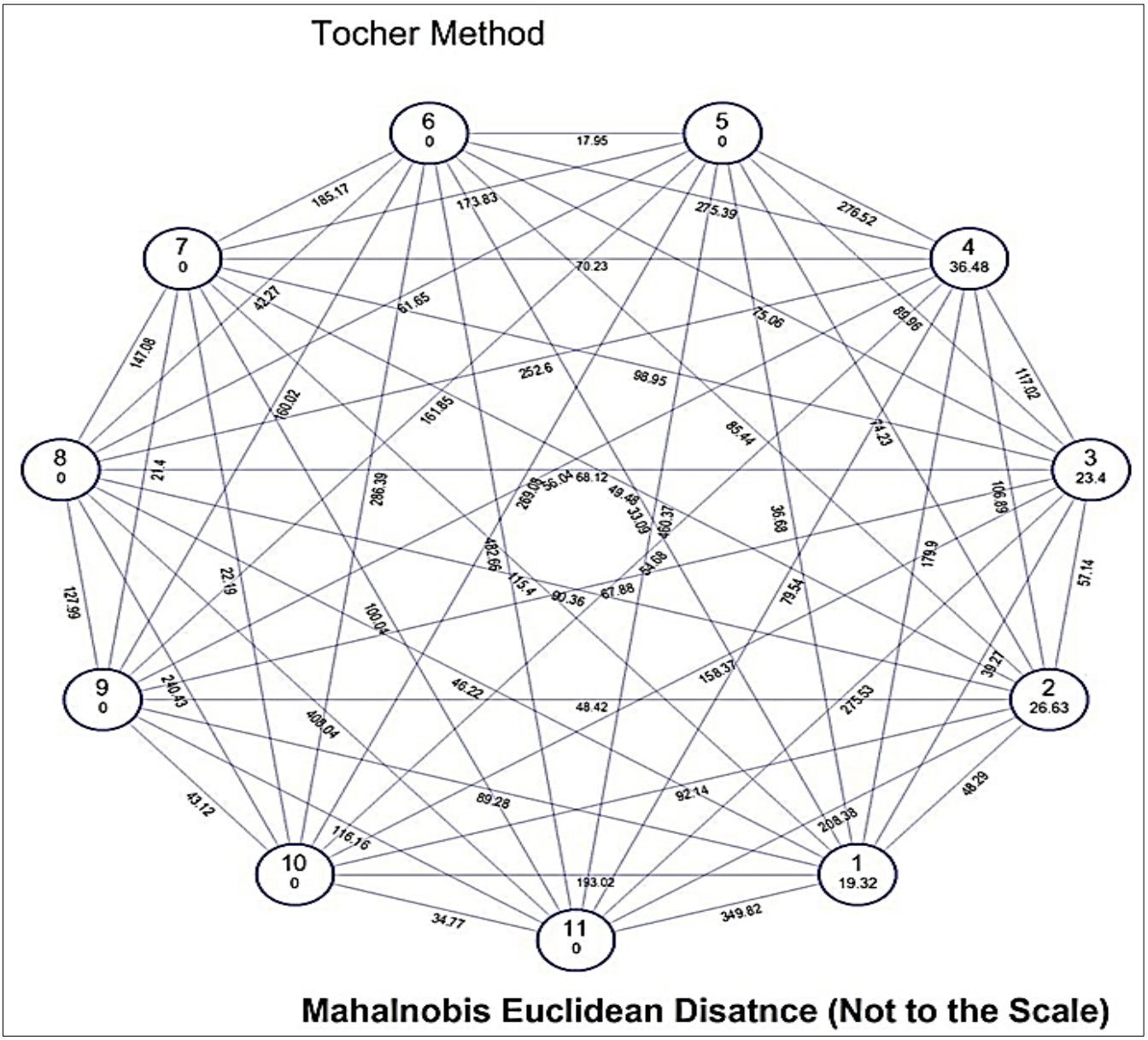

Fig 1: Clustering pattern in coriander genotypes based on morphological characters

Table 6: Cluster means for thirteen characters in forty genotypes of coriander

Cluster	DF	PH	PB	SB	UPP	UPU	SPU	DM	YPP	SYPP	TW	HI	TOC
I	54.27	85.02	6.43	25.98	52.02	6.51	45.00	105.73	5.81	0.72	1.18	39.46	8.95
II	55.70	96.45	7.57	30.55	60.71	6.46	51.04	107.24	6.25	0.77	0.93	35.45	13.06
III	48.50	87.77	6.07	23.67	49.41	6.14	48.84	110.56	7.88	0.94	1.50	43.85	10.50
IV	48.00	93.14	5.75	21.61	45.67	6.05	47.79	109.80	8.37	0.99	1.44	44.13	19.15
V	53.67	110.53	8.80	35.40	92.00	8.00	58.05	103.67	4.60	0.63	0.76	30.24	7.27
VI	53.67	105.17	6.73	39.67	80.07	8.00	57.64	101.67	10.59	1.14	1.07	37.34	6.24
VII	66.00	122.30	6.80	25.13	39.38	6.40	49.95	116.67	6.84	0.89	0.92	39.72	15.46
VIII	68.00	68.00	9.40	38.92	62.01	7.07	77.53	118.67	10.32	1.40	1.19	49.47	5.59
IX	66.67	99.23	7.33	28.67	57.11	7.67	49.41	112.67	6.23	0.71	1.38	40.26	15.38
X	64.00	97.90	6.40	25.53	45.27	7.27	55.66	118.67	8.29	1.02	0.87	42.89	19.26
XI	62.67	79.47	8.40	35.68	65.28	7.40	68.66	124.33	7.00	0.89	1.11	38.28	23.51

DF = Days to 50% flowering UPP = Umbels per plant YPP = Yield per plant (g) HI = Harvest index (%)
PH = Plant height (cm) UPU = Umbellets per umbel TW = Test weight (g) TOC = Total oil content (%)
PB = Primary branches per plant SPU = Seeds per umbel SYPP = Seed yield per plot (kg)
SB = Secondary branches per plant DM = Days to maturity

References

1. Acharya VR, Singh M, Patel RK, Goyal L. Genetic diversity of coriander for yield and its attributing characters. International Journal of Current Microbiology and Applied Science. 2020;9(2):222-228.
2. Allard RW. Principles of Plant Breeding. John Wiley and sons, New York. 1960, 485.
3. Ameta HK, Ranjan JK, Kakani RK, Mehta RS, Solanki RK, Panwar A, *et al*. Genetic variability studies in coriander (*Coriandrum sativum* L.). International Journal Seed Spices. 2016;6(2):103-105.
4. Anilkumar GS, Umesha K, Shivapriya M, Halesh GK, Nithin Kumar VC. Genetic Variability, Heritability and Genetic Advance Studies in Coriander (*Coriandrum sativum* L.). International Journal of Pure Applied Bioscience. 2018;6(3):426-430.
5. Anonymous. NHB Database 2017-18. http://nhb.gov.in/statistics/State_Level/2017-18-(Final).pdf
6. Anonymous. Directorate of Horticulture 2017-2018. https://doh.guja-rat.gov.in/Images/directorofhorticulture/pdf/statistics/Area-Production horticulture-2017-18-191118.pdf
7. Cockerham CC. Estimation of genetic variance in statistical Genetics and Plant breeding. *National research council*, Washington, DC. 1963, 53.
8. Desai PK, Asati J, Patel RK. Genetic Variability Analysis in Coriander (*Coriandrum sativum* Linn.). International Journal of Pure and Applied Bioscience. 2018;6(6):93-96.
9. Devi AR, Sharangi AB, Haokip MC. Genetic variability studies of coriander (*Coriandrum sativum* L.) genotypes. Journal of Pharmacognosy and Phytochemistry. 2019;8(4):419-421.
10. Dhakad SR, Sengupta SK, Narayanlal, Shiurkar G. Genetic diversity and heritability analysis in coriander. The Pharma Innovation Journal. 2017;6(8):40-46.
11. Farooq M, Hegde RV, Imamsaheb SJ. Variability, heritability and genetic advance in coriander genotypes. Plant Archive. 2017;17(1):519-522.
12. Johnson HW, Robinson HR, Comstock RE. Estimation of genetic and environmental variability in soybean (*Glycine max* L.). Agron. J. 1955;47:314-318.
13. Mahalanobis PC. On generalize distance in statistics. Proceedings of the National Institute of science of India. 1936;2:49-55.
14. Mayura KR, Devi B. Genetic variability analysis in coriander (*Coriandrum sativum* L.) in agroclimatic condition of Jhansi, India. International Journal of Current Research. 2016;8(9):37769-37771.
15. Mishra TD, Balaji Vikram. Genetic variability, heritability and character association in coriander genotypes (*Coriandrum sativum* L.) under Allahabad agro-climatic condition. International Journal of Pure Applied Bioscience. 2017;5(3):151-158.
16. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR, New Delhi. 1978, 103-108.
17. Patel DG, Patel PR, Patel HB, Patel AM. Assessment of Genetic Variability in Coriander (*Coriandrum sativum* L.). International Journal of Science and Research. 2018;8(3):629-632.
18. Pruthi JS. Spices and condiments: chemistry, microbiology and technology. New York, Academic Press. 1976, 1-6.
19. Rao CR. Advanced statistical methods in biometric research. Jhon Wiley and Sons, Newyork 1952, 357-369.
20. Sharma D, Naruka IS, Shaktawat RPS, Ajnave SR. Genetic variability studies in coriander (*Coriandrum sativum* L.). The Bioscan. 2016;11(2):1033-1036.
21. Singh D, Jain UK, Rajput SS, Khandelwal V, Shiva KN. Genetic variation for seed yield and its components and their association in coriander (*Coriandrum sativum* L.) germplasm. Journal of Spices and Aromatic Crops. 2006;15(1):25-29.
22. Tomar RS, Kulkarni GU, Parakhia MV, Thakkar JR, Rathod VM, Solanki RK, *et al*. Genetic diversity analysis in coriander (*Coriandrum sativum* L.) genotypes through morphological and molecular characterization. Research Journal of Biotechnology. 2014, 9(3).