The Pharma Innovation Journal 2022; 11(12): 141-143

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(12): 141-143

www.thepharmajournal.com
Received: 16-10-2022
Accepted: 19-11-2022

Vishnu Choudhary
M.Sc. Research scholar, Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Kota, Rajasthan, India

Preeti Verma
Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Kota, Rajasthan, India

SC Sharma
Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Kota, Rajasthan, India

DL Yadav
Assistant Professor, Department of Plant Pathology, College of Agriculture, Agriculture University, Kota, Rajasthan, India

RS Narolia
Associate Professor, Department of Agronomy, College of Agriculture, Agriculture University, Kota, Rajasthan, India

Corresponding Author:
Vishnu Choudhary
M.Sc. Research scholar, Department of Genetics and Plant Breeding, College of Agriculture, Agriculture University, Kota, Rajasthan, India

Genetic divergence studies in coriander (*Coriandrum sativum* L.) genotypes

Vishnu Choudhary, Preeti Verma, SC Sharma, DL Yadav and RS Narolia

Abstract
Genetic diversity was studied in 65 coriander genotypes for ten yield and yield contributing traits. The cluster analysis grouped 65 coriander genotypes in to 13 clusters. Cluster I consisted of maximum genotype (47) followed by cluster II (4 genotypes) and clusters III, IV, V (2 genotypes each) while rest of the clusters had a single genotype in each. The maximum intra-cluster distance was observed in cluster V, followed by cluster II and IV, cluster I and cluster III. Highest inter-cluster distance was found in cluster VII and IX followed by cluster IX and XIII, cluster XI and XIII and cluster VI and IX. Cluster III and VI has smallest inter-cluster distance. The clusters VII, VIII and XI comprising a single genotype in each *viz.*, NDCor 110, LCC 229 and RKCF 24, respectively were the best clusters for yield and other important yield contributing characters.

Keywords: *Coriandrum sativum* L., cluster analysis, genetic diversity

Introduction
A spice is a dried seed, fruit, root, bark or vegetative substance used in flavouring, seasoning and imparting aroma in food items and beverages. Seed spices are annual herbs, whose dried seed of fruits are used as spices. India is well known as "land of spices" across the world and wide varieties of spices are grown in different parts of country. India is the largest producer, consumer and exporter of seed spices in the world.

Coriander (*Coriandrum sativum* L.) is an annual herbaceous plant of family Apiaceae (Umbelliferae) with chromosome number 2n=22. It is a cross pollinated (25 to 50 % cross pollination) entomophilous crop, honey bees as the major pollinating agent. In India, coriander is cultivated for seed as well as for leaves. It is a tropical crop and sown in the winter season for seed production. Coriander is used as a spice, in culinary, medicine and in perfumery, pharmaceuticals and food industries. The dried ground fruit is the major ingredient in the preparation of curry powder. The whole fruit is also used to flavor foods like sauces, pickles, pastry, cakes, biscuits, liquors and confectionary. The young plants and leaves are used in the preparation of chutney and seasoning in curries, sauces and soups. The essential oil from fully ripe and dried coriander seeds is a colourless or pale-yellow liquid with, characteristic odour and mild, sweet, warm and aromatic flavor, and linalool is its major constituent (Burdock and Carabin, 2009) [3]. The essential oil content of ripe and dried coriander fruits varies between 0.03 to 2.6% and linalool constitutes 67.7% of total essential oil (Diederichsen, 1996) [4]. In India, coriander is cultivated in an area of 529 thousand hectare yielding a production of 701 thousand metric tonnes with the productivity of 1325 kg/ha (Anonymous, 2019-20) [1]. The major coriander growing states are Madhya Pradesh, Rajasthan, Gujarat, Assam, Odisha and West Bengal. Rajasthan produces 89605 tons coriander from 60216 ha. area thus, contributing 11.38 and 12.78 percent, respectively to the total area and production of the country.

Genetic diversity is very important for any crop improvement programme as it helps in the development of superior recombinants. Information on genetic divergence in coriander is very helpful in identifying diverse genotypes and population; which can be recombined together for enhancement of genetic variability for exercising effective selection to identify better plant types. Therefore, the present study was conducted in 65 (60 accessions + 5 checks) coriander genotypes to know the extent of genetic diversity existing in the crop which can be utilized for genetic improvement.

Materials and Methods

The field experiment for present investigation was conducted at experimental field, Agricultural Research Station, Ummedganj, Agriculture University, Kota (Raj.) during *Rabi*, 2020-21. The experiment was laid out in an Augmented Block Design in two rows of 3 m length and spaced 30 cm apart. Thus, 12 genotypes and 5 checks were sown in each block. The checks were common in the blocks but were randomized among themselves. Five plants were randomly selected from each plot to record the observations on plant height (cm), number of umbels per plant, number of umbellate per umbel, number of seeds per umbellet, biological yield per plant (g), test weight (g) and harvest index (%) while observations on days to 50 % flowering, days to maturity and seed yield per plot (g) were recorded on whole plot basis. The data collected on 65 genotypes was subjected to analysis of genetic divergence using Mahalanobis D^2 statistics, (1936) following Rao (1952) [8]. Inter and intra cluster distances were calculated by method as suggested by Rao (1952) [8].

Results and Discussion

The 65 genotypes under study were categorized into 13 different clusters (Table 1). The highest number of genotypes (47) were found in cluster I followed by cluster II (4 genotypes), cluster III, IV, V (2 genotypes each) and cluster VI, VII, VIII, IX, X, XI, XII and XIII (only one genotype each). Maximum number of intra-cluster crossings (1081) was reported in cluster I which indicated the intra-cluster crossing among the 47 genotypes in cluster I may give higher number of transgressive segregants. In addition to this, the single genotypes present in last eight clusters indicated that they could be more diverse from other genotypes and the inter-cluster crossing with them may show heterosis for some of the most essential traits.

Inter-cluster and intra-cluster distance in all the 13 clusters was computed (table 2). It was observed that the inter-cluster distance was greater in magnitude than the intra-cluster distance which suggested a significant level of genetic diversity among the 65 genotypes. The maximum intra-cluster distance was observed in cluster V (0.52), followed by cluster II and IV (0.51), cluster I (0.49) and cluster III (0.46). It may be suggested that the genotypes present in these clusters have wide range of genetic diversity. Rest of the clusters have 0.00 intra-cluster distances. Highest inter-cluster distance was found between cluster VII and IX (1.01), followed by cluster IX and XIII (0.94), cluster XI and XIII (0.90) and cluster VI and IX (0.88). Therefore, the genotypes within these clusters may be used as parents in hybridization programme to unfold greater genetic diversity for further selection for yield and yield contributing traits. Cluster III and VI had smallest inter-cluster distance (0.52), followed by cluster III and XII (0.56), cluster IV and I (0.56), cluster I and X (0.57) and cluster I and XII (0.57); indicating close association among the genotypes of these clusters. Therefore, these genotypes can be exploited in the breeding programmes for creating biparental crosses between the most diverse and the closest groups in order to disrupt the unfavourable correlations between yield and its related characteristics. Similar studies reported by Singh *et al.* (2005) [9], Mengesha *et al.* (2011) [7] and Gauhar *et al*. (2018) [5].

A comparison of the mean values for ten characters of thirteen different clusters is shown in Table 3. It should be noted that the character which contributes to maximum divergence should be given more weightage when determining clusters for selecting parents in hybridization programme. The perusal of data showed that cluster XI comprising of a single genotype i.e., RKCF 24 had lowest mean values for days to 50% flowering (55) and days to maturity (100). The highest mean value for number of umbels per plant and number of umbellate per umbel were exhibited by cluster V (34.40) and cluster XI (7.68), respectively. Cluster VIII had highest mean values for number of seeds per umbellet (9.24) and biological yield per plant (25.87). Similarly, cluster VII had highest mean values for characters *viz*., harvest index (39.24), test weight (15.92) and seed yield per plot (365.40). Similar studies reported by Awas *et al.* (2016) [2] and Gauhar *et al.* (2018) [5].

Table 1: Distribution of coriander genotypes in thirteen clusters

Clusters	Number of Genotypes	Genotypes included in the clusters
I	47	COR 174, COR 175, COR 176, COR 177, COR 181, COR 182, COR 183, COR 185, COR 187, COR 188, COR 189, COR 190, COR 191, COR 192, WFGS 16-7, LCC-219, ND COR-120, CS-142, RKC-20, NDCOR-90, NDCOR-119, RKCF-43, NDCOR-10, UD-663, PD-21, JCr-379, JCr-404, LCC-226, RKC-54, RD-416, LCC-234, CS-104, CS-131, PFPS 16-13, LCC-224, LCC-242, CS-150, RCC 12-6, RD-397, LCC-250, RD-417, RD-401, RKCF-45, RKCF-36, PFPS 16-17, ACr-2, RCr-436
II	4	COR 178, COR 179, COR 180, WFGS 16-15
III	2	RKD-39, Hisar Anand
IV	2	COR 184, JCr 13-7
V	2	COR 186, RD-377
VI	1	CS-141
VII	1	NDCOR-110
VIII	1	LCC-229
IX	1	RD-388
X	1	RKCF-28
XI	1	RKCF-24
XII	1	RKD-18
XIII	1	ACr-1

Table 2: Estimates of average intra and inter-cluster distances for thirteen clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	0.49	0.58	0.59	0.56	0.61	0.63	0.67	0.60	0.76	0.57	0.64	0.57	0.75
II		0.51	0.67	0.66	0.67	0.64	0.66	0.59	0.77	0.68	0.68	0.75	0.71
III			0.46	0.58	0.69	0.52	0.72	0.58	0.82	0.59	0.68	0.56	0.61
IV				0.51	0.70	0.67	0.76	0.69	0.62	0.59	0.67	0.64	0.73
V					0.52	0.75	0.73	0.63	0.80	0.73	0.70	0.67	0.81
VI						0	0.58	0.58	0.88	0.69	0.63	0.72	0.84
VII							0	0.69	1.01	0.75	0.72	0.66	0.83
VIII								0	0.59	0.60	0.64	0.70	0.84
IX									0	0.84	0.71	0.89	0.94
X										0	0.70	0.72	0.82
XI											0	0.70	0.90
XII												0	0.82
XIII													0

Table 3: Cluster mean value for different traits in coriander genotypes

Cluster	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of umbels per plant	Number of umbellate per umbel	Number of seeds per umbellet	Biological yield per plant (g)	Harvest index (%)	Test weight (g)	Seed yield per plot (g)
I	57.96	108.03	87.66	22.46	5.98	6.7	14.98	30.5	12.46	237.64
II	61.5	107.25	100.26	20.4	6.1	7.12	18.76	28.18	11.07	225.85
III	63.7	115.3	83.97	28.56	6.25	7.3	20.35	30.8	13.23	283.88
IV	60	109.5	83.07	23	6.72	6.48	12.88 (L)	27.46 (L)	13.47	201.78
V	59	105	102.6	34.4 (H)	5.78	7.24	21.11	32.45	14.9	303.93
VI	59	112	92.7	28.2	6.44	6.72	25.2	31.47	12.1	289.98
VII	57	103	88.02	21.6	6.24	6.32	22.88	39.24 (H)	15.92(H)	365.4 (H)
VIII	57	104	107.1	31.4	6.6	9.24 (H)	25.87 (H)	34.13	13.6	363.96
IX	59	103	108 (H)	31.2	7.68 (H)	8.84	16.64	28.19	11.56	249.48
X	55	107	80.64	19.8	5.76 (L)	7.64	15.52	32.09	14.8	203.04
XI	55 (L)	100 (L)	86.51	29.2	6.64	7.28	17.94	35.62	10.43 (L)	192.78 (L)
XII	57	105.4	69.88 (L)	26.52	5.99	6.29 (L)	16.41	32.33	14.52	342.49
XIII	74.6 (H)	122.4 (H)	92.27	19.64 (L)	6.18	6.8	13.73	30.83	12.02	207.64

Conclusion

Coriander being a cross pollinated crop is subjected to population improvement strategies following mass selection or recurrent selection in general. Genetic improvement for yield is the basic objective of coriander breeding like all other crops. Genetic diversity analysis helps in identifying diverse genotypes and also to group genotypes showing genotyping similarity for target traits. In the present study, the maximum inter-cluster distance was found between cluster VII and IX followed by cluster IX and XIII. It can be suggested that recombination strategies between genotypes of these clusters may generate highly variable combinations. Besides these, the clusters VII, VIII and XI comprising a single genotype in each *viz.*, NDCor 110, LCC 229 and RKCF 24, respectively were the best clusters for yield and other important yield contributing characters *viz*., days to flowering and maturity, number of umbels per plant, umbellate per umbel and seeds per umbellet, test weight, biological yield and harvest index. Therefore, these genotypes should be used as parents in hybridization and/or recombination breeding programme to develop promising breeding material and high yielding varieties of coriander.

References

1. Anonymous. Directorate of Economics & Statistics, Department of Agriculture, Cooperation & Farmers Welfare, Ministry of Agriculture & Farmers Welfare, Government of India; c2020.
2. Awas G, Mekbib F, Ayana A. Genetic diversity analysis of Ethiopian coriander (*Coriandrum sativum* L.) genotypes for seed yield and oil content. J Experimental Agric. International. 2016;14(6):1-8.
3. Burdock GA, Carabin IG. Safety assessment of coriander (*Coriandrum sativum* L.) essential oil as a food ingredient. Food and Chemical Toxicology. 2009;47:22-34.
4. Diederichsen A. Coriander (*Coriandrum sativum* L.) promoting the conservation and use of underutilized and neglected crops 3. International Plant Genetics Resources Institute, Rome, Italy; c1996. p. 22-23.
5. Gauhar T, Solanki RK, Choudhary M. Study of genetic divergence in coriander (*Coriandrum sativum* L.). International J. Seed Spices. 2018;8(1):56-59.
6. Mahalanobis PC. On the generalized distance in statistics. Proceedings of the National Academy of Science (India). 1936;2:49-55.
7. Mengesha B, Alemaw G, Tesfaye B. Genetic divergence in Ethiopian coriander accessions and its implication in breeding of desired plant types. African Crop Sci. J. 2011;19(1):39-47.
8. Rao CR. Advanced statistical methods in biometrical research. 1st Edition. John Wiley and Sons. Inc., New York; c1952.
9. Singh SP, Katiyar RS, Rai SK, Tripathi SM, Srivastva JP. Genetic divergence and its implication in breeding of desired plant type in coriander (*Coriandrum sativum* L.). Genetika. 2005;37(2):155-163.