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## Genetic divergence in coriander (*Coriandrum sativum* L.)

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### Abstract

Ninety genotypes and three checks were classified into six non-overlapping clusters on the basis of non-hierarchical Euclidean cluster analysis for yield and growth traits. The maximum (2.997) intra cluster distance was seen in cluster III and minimum (0.000) was observed in VI and V. The maximum inter cluster distance 13.414 was found in between clusters VI and V, followed by 10.279 between clusters I and VI than 10.047 between clusters II and VI. Whereas, minimum inter cluster distance 2.694 was observed between clusters IV and II, followed by 2.890 between clusters III and I and 3.085 between clusters II and I. Cluster I have the maximum number of genotypes (25) followed by cluster II and III have 23 genotypes in each cluster. The minimum numbers of genotypes have cluster V and VI only one genotype in each cluster. The grouping of genotypes in clusters reflects the relative divergence of clusters and allows a convenient selection group of genotypes with their overall phenotypic similarity for hybridization programme facilitating better exploitation of germplasm. Thus it may be suggested that crosses between accessions of clusters VI & V, I & VI and II & VI may result in substantial segregates and further selection for overall improvement of species may be possible.

**Keywords:** Genetic, coriander, Euclidean, *Coriandrum sativum* L.

### Introduction

Coriander (*Coriandrum sativum* L.), is an annual herb that belongs to the umbel family (Apiaceae). It displays broad adaptation as a crop around the world, growing well under many different types of soil and weather conditions (spice board of India 2029); Coriander is one of the major seed spice crops in India (Raghavan 2000). It is used in spices and its seeds are used for extracting essential oil for its linalool content. India is a major seed spices producer in the world because of its favorable climatic and soil conditions for growing spices and other tropical herbs therefore it is known as the “Home of Spices”

The major seed spices growing area is concentrated in semi-arid to arid areas of Gujarat and Rajasthan, together contributing more than 80% of the total seed spices produced in the country. Therefore both the states are esteemed as “Seed Spice Bowl of India”. Out of 20 seed spices crops cumin, coriander, fennel, fenugreek, dill and ajowain contributed more than 95% towards area and production.

Germplasm is a vital source in generating new plant types having desirable traits that help in increasing crop production with quality and thus improve the level of human nutrition. In order to maintain, evaluate and utilize germplasm efficiently and effectively, it is important to investigate the extent of genetic diversity, it contains (Smith and Smith, (1989). Most of these studies were related to yield contributing characters and estimation of variability existing in them. The present study aimed at grouping diverse germplasm lines in to different clusters based on diversity/similarity and thus exploiting the diversity in genetic improvement programme.

### Materials and Methods

Field research was conducted at Vegetable Research Centre (VRC), G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The healthy seeds of ninety germplasm lines and three checks of *Coriandrum sativum* L. Were sown directly in field at row to row distance of 45 cm and plant to plant distance of 10 cm in the second week of November 2009-10 and 2010-11. Observation on metric traits such as, days to 50% flowering, plant height up to main umbel (cm), plant height including main umbel (cm), number of primary branches / plant, number of secondary branches / plant, umbel / plant, umbellets / umbel, number of fruits/umbel, number of fruits/umbellate, yield /plot (gm), yield/plant (gm), yield kg/ha, 1000 seed weight (gm), was recorded at different stages of crop. The observation was recorded on 5 plants, selected at random.

The data were analyzed statistically using Principal Component Analysis based Euclidean distances. The computation was done using the computer software

## Result and Discussion

### Non-hierarchical Euclidean cluster analysis

Non-hierarchical Euclidean cluster analysis was done to study divergence on 90 genotypes and three checks of coriander in respect of various morphological economic traits. The genotypes were grouped into 6 non over-lapping clusters. Appropriate cluster arrangement was determined by using 'F' test. It was determined that cluster combination with 5 and 6 were most appropriate for the material, because the "F" value was significant at 5 per cent level of significance than the expected "F" values. Sequential F-ratio tests for comparison of cluster solutions have been presented in table 1.

**Table 1:** Sequential F-ratio tests for comparison of cluster solutions

Cluster number	Degree of freedom (df <sup>1</sup> )	Degree of freedom (df <sup>2</sup> )	'F' value
5 and 6	11	957	3.78*

\* Significance at 5 per cent level of probability

The Inter and Intra cluster distances were presented in Table 2. The intra cluster distance was ranged from 0.000 to 2.997. The maximum intra cluster distance was found in cluster III (2.997) and minimum in cluster V and VI (0.000). The clustering pattern does not correspond to their pedigree in general. The maximum inter cluster distance 10.294 was found in between clusters IV and VI, followed by 10.279 between clusters I and VI and 10.047 between cluster II and VI. Whereas, inter cluster distance 10.022 between cluster III and VI and 9.288 between cluster II and V.

The clustering of genotype based on growth and yield characters of corianders were presented in table 3 on the basis of clustering of genotype cluster I had maximum number 25 genotypes followed by cluster number clusters II which had 23 and cluster III contains 23 genotypes in each cluster and cluster IV had 20 genotype and cluster V and VI had one genotype in each cluster namely respectively.

The cluster mean and standard deviation of 13 growth and yield characters of coriander in six clusters have been presented in Table 4. Cluster means indicate significant variation as it is indicated from Table 4. The days to 50 per cent flowering has the maximum value (97.36 days) in cluster VI followed by cluster III (94.36 days) and minimum value has in cluster V (80.36 days). Plant height upto main umbel had maximum value in cluster IV (108.44 cm) followed by cluster II (99.22 cm) and minimum value in cluster VI (79.85 cm). Plant height including main umbel had maximum value in cluster IV (124.15 cm) followed by cluster II (114.4 cm) and minimum value have cluster VI (96.08 cm). Number of primary branch per plant had maximum value in cluster II

(5.91) followed by cluster I (5.90) and minimum value in cluster VI (3.0090). Number of secondary branches per plant had maximum value in cluster I (14.08) than cluster V (12.97) and minimum value had in cluster 0. (9.67).

Number of umbels per plant had maximum value in cluster VI (37.44) than cluster I (25.59) and minimum value had in cluster V (14.19). Number of umbellates per umbel had maximum in cluster V (5.94) than cluster VI (5.89) and minimum value had in cluster I (4.89). Number of fruits per umbel had maximum value in cluster I(37.05) than cluster IV (35.20) and minimum value had in cluster I (24.17). Number of fruits per umbellate had maximum value in cluster IV (7.05) than cluster III (6.92) and minimum value had in cluster (3.574). Seed yield per plot had maximum value in cluster II (271.10 g) than cluster VI (241.44 g) and minimum value in cluster. (106.28 g).

Seed yield per plant had maximum value in three clusters V, VI and II (0.03 g) and minimum value had in cluster. I (0.01 g). Seed yield kg per ha maximum value in cluster II (1869.46 kg/ha) than in cluster VI (1828.17 kg/ha) and minimum value had in cluster I (250.83 kg/ha). 1000 -seed weight had maximum value in cluster II (11.4 g) than cluster I (11.34 g) and minimum value in cluster VI (16.83 g).

Cluster. I had maximum of genotypes 25. It had maximum value of number of secondary branches per plant (14.08). Similarly, i.e. cluster II had maximum value for number of primary branches per plant (5.91), seed yield per plot (271.10 g), seed yield per ha (1869 kg\ ha) and weight of 1000 seed (11.45 g). Cluster III had the maximum value for days to 50 flowering (94.36 days). Cluster IV had the maximum value for the plant height up to main umbel (108.44 cm), plant height including main umbel (124.15 cm) and number of fruits per umbellate. Cluster V had maximum value for number of umbellates per umbel (5.94) and seed yield per plant (0.03 g). Cluster. IV had maximum value for number of umbels per plant (37.44) and number of fruits per umbel (37.05).

Similarly minimum value for number of umbellates perumbel (4.89), number of fruits per umbel (24.17), seed yield per plant (0.01 g) and seed yield (750.83 kg/ha) in cluster I. Cluster III had minimum value for number of secondary branches per plant (9.67). Cluster V had minimum value for days to 50 per cent flowering (80.36 days), number of umbel per plant (14.19), number of fruits per umbellate (3.574) and yield per plot (106.26). Cluster VI had minimum value for plant height up to main umbel (79.85), plant height including main umbel (79.85 cm) and number of primary branches per plant (3.090) and weight of 1000- seed (6.83 g).

The similar approach earmarking distant genotypes have been emphasized by several workers in clustering for coriander germplasm Ali *et al.* (2000) <sup>[1]</sup>; Srivastava *et al.* (2000) <sup>[10]</sup>; Ravi *et al.* (2007) <sup>[5]</sup>; Beemnet *et al.* (2011) <sup>[2]</sup> and Singh *et al.* (2005) <sup>[6]</sup>.

**Table 2:** Average intra and inter cluster distances between six clusters coriander germplasm.

Cluster.	I.	II.	III.	IV.	V.	VI.
I.	2.431					
II.	3.085	2.643				
III.	2.890	3.720	2.997			
IV.	3.516	2.694	3.261	2.430		
V.	9.138	9.288	8.833	9.161	0.000	
VI.	10.279	10.047	10.022	10.294	13.414	0.000

The intra cluster distances are shown in bold

**Table3:** Clustering of genotypes based on growth and yield characters of coriander

Cluster No.	No. of Genotypes	Per centage of Total Collection (%)	
I.	25	27.78	ACr-4, ACr-20, ACr-25, MKSM-1084, UD-594, UD-607, UD-609, UD-610, UD-615, UD-618, UD-620, UD-684, UD-699, UD-704, UD-715, UD-716, UD-717, UD-719, UD-742, UD-746, UD-748, UD-752, UD-753, UD-784 Hisar Aanand
II.	23	25.56	ACr-10, ACr-18, ACr-19, ACr-23, ACr-24 SC-13 UD-601, UD-610, UD-622, UD-623, UD-634, UD-635, UD-643, UD-689, UD-720, UD-722, UD-730, UD-743, UD-744, UD-745, UD-747, UD-750, UD-787, UD-789.
III.	23	25.56	ACr-13, MKSM-1052, MKSM-1055, MKSM-1056, MKSM-1059, MKSM-1065, MKSM-1059, MKSM-1072, MKSM-1079, MKSM-1101, MKSM-1104, MKSM-1111, MKSM-1119, MKSM-1122, MKSM-1125, SC-1, SC-6, SC-8, SC-10, SC-11, SC-12, UD-718,
IV.	20	22.22	ACr-1, MKSM-1088, MKSM-1091, MKSM-1117, SC-4, SC-9 UD-325, UD-326, UD-373, UD-590, UD-603, UD-605, UD-711, UD-721, UD-725, UD-728, UD-772, UD-788 Pant Haritama, ACr-728
V.	1	1.11	UD-727
VI.	1	1.11	MKSM-1110

**Table 4:** Mean and standard deviation of 13 growth and yield characters of coriander in six clusters

Cluster No.	Days to 50 per cent flowering.	Plant height upto main umbel (cm).	Plant height including main umbel (cm).	Number of primary branches per plant	Number of secondary branches per plant	Number of umbels per plant	Number of umbellates per umbel.	Number of fruits per umbel.	Number of fruits per umbellate	Seed yield per plot (g).	Seed yield per plant (g).	Seed yield (kg/ha)	Weight of 1000 seeds (g).
I	85.76±7.64	91.65±9.31	158.2±7.69	5.90±0.83	14.08±1.90	25.59±8.20	4.89±0.55	24.17±7.18	6.32±1.26	113.71±40.53	0.01±0.00	750.83±376.53	11.34±1.87
II	89.63±6.36	99.22±8.22	114.04±7.45	5.91±0.66	13.21±2.67	25.34±5.97	5.01±0.66	27.32±8.95	6.84±1.63	271.10±66.47	0.03±0.01	1869.46±512.63	11.45±1.46
III	94.36±18.05	87.25±7.05	98.73±9.14	5.80±0.81	9.67±1.48	23.00±3.65	5.29±0.52	31.16±8.38	6.92±2.02	109.02±49.36	0.02±0.02	976.59±382.90	7.19±2.13
IV	97.75±6.37	108.44±8.76	124.15±8.47	5.82±0.74	11.61±2.32	24.72±6.03	5.73±0.65	35.20±7.69	7.05±1.67	179.00±59.01	0.02±0.01	1348.46±280.80	8.95±1.98
V	80.36±0.00	90.76±0.00	98.57±0.00	6.25±0.00	12.97±0.00	14.19±0.00	5.94±0.00	34.19±0.00	3.574±0.00	106.28±0.00	0.03±0.00	944.00±0.00	9.75±0.00
VI	82.86±0.00	79.85±0.00	96.08±0.00	3.09±0.00	12.92±0.00	37.44±0.00	5.89±0.00	37.05±0.00	5.77±0.00	241.44±0.00	0.03±0.00	1828.17±0.00	6.83±0.00

Different traits. These genotypes may effectively used as donor for various characters in yield improvement programme.

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