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Studies on genetic divergence in coriander [*Coriandrum sativum* L.]

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Abstract

An investigation was undertaken to study the genetic divergence of 122 coriander genotypes subjected to non-hierarchical Euclidean cluster analysis for 11 characters. Based on analysis 122 genotypes were grouped into 12 distinct non-overlapping clusters. Cluster-VIII was the largest comprising 22 genotypes, followed by Clusters-IX (14). Cluster V, VI, II, XII, IV, III, VII and X having 13, 13, 11, 10, 9, 8, 7 and 7 entries, respectively. Maximum intra-cluster distance was observed for cluster VI (165.37) followed by cluster V (142.19), cluster IV (95.10), cluster VII (91.45), cluster II (73.00) and cluster I (65.01). The maximum inter cluster distance was observed between cluster VII with XI (2752.43), followed by cluster VII with cluster VIII (2415.95). Whereas, the minimum inter-cluster distance was found between clusters I and III (108.23), followed by cluster III and IV (110.56). As regards cluster means, Clusters-XI, XII, II and VIII, VI and Clusters-XI performed better in most of the biometric characters studied. The high per cent contribution towards genetic divergence was exhibited by the plant height (59.25%), followed by umbels per plant (36.05%).

Highlights

- Vast inter-cluster distance was found between cluster VII with XI and cluster VII with VIII.
- Cluster XI recoded highest cluster mean value for yield per plant, umbels per plant and branches per plant. Whereas, Cluster XII recorded the highest value for umbellets per umbel, umbels per plant and branches per plant.
- The plant height and umbels per plants contributed maximum towards genetic divergence.

Keywords: Coriander, germplasm, genetic divergence, cluster analysis

Introduction

Coriander [*Coriandrum sativum* L.], is an herbaceous dicot spices crop belonging to family *Apiaceae*. It is cultivated mainly for its green leaves and dry seeds, which is richest source of vitamin C. The nature and degree of genetic divergence available in the coriander germplasm is very important for success of its hybridization programme leading to development of high yielding varieties. Knowledge on genetic divergence is, therefore, important to identify and organize the available genetic resources aiming at the production of promising cultivars (Palomino *et al.*, 2005) [7]. Genetic diversity is the key to improvement and development of effective conservation strategies (Hodgkin, 1997. Khan *et al.* 2016) [4, 5]. Keeping all the view, present study was conducted with the objective of assessment of genetic divergence in coriander germplasm.

Materials and methods

The investigation was carried out at Main Experimental Station of Vegetable Science, Narendra Nagar (Kumarganj), Faizabad (U.P.) during *Rabi* season 2014-15. The experimental materials comprised 122 genotypes (NDCor-1, NDCor-2...to...NDCor-122) of coriander including two check variety *viz.*, NDCor-2 and Hissar Anand collected from different places of India and maintained at main experimental station of the Department of Vegetable Science, N.D. University of Agriculture & Technology, Narendra Nagar, (Kumarganj), Faizabad (U.P.). Each genotype was planted on in the well prepared field at 30 cm × 15 cm spacing. Observations were recorded on five randomly taken plants from each block for eleven quantitative characters *viz.*, Days to 50% flowering, branches per plant, fruiting nodes per plant, umbels per plant, umbellets per umbel, fruits per umbellate, fruits per umbel, umbel diameter (cm), plant height (cm), test weight (g) and yield per plant (g). Non-hierarchical Euclidean cluster (Spark, 1973 and Beale, 1969) [11, 1] was used for assessing the genetic divergence among the populations. All the $n(n-1)/2$ D^2 values were clustered using Tocher's method as described by Rao (1952) [8].

The intra, inter cluster distance and the character contribution towards diversity were calculated by the formulae given by Singh and Chaudhary (1977)^[10].

Result and discussion

Using non-hierarchical Euclidean cluster analysis, the 122 germplasm of sweet potato were grouped into twelve distinct non-overlapping clusters. These indicated the large genetic diversity (Table-1). Cluster-VIII was the largest comprising 22 genotypes, followed by Clusters-IX (14) cluster V, VI, II, XII, IV, III, VII and X having 13, 13, 11, 10, 9, 8, 7 and 7 entries, respectively. From the clustering pattern, it was found that the genotypes from different region were independent of their genetic origin. Hence, the genotypes studied were reliable enough for hybridisation and selection. Similar opinions were also exhibited by Dash *et al.* (2013) in sweet potato, Sattar *et al.* (2011) in potato.

Although the genotypes collected from same geographic location were also grouped together in same cluster, the intense of grouping of genotypes from different geographic region in the same cluster were observed in case of all the twelve clusters. This shows that lack of parallelism between genetic and geographic diversity (Patel *et al.*, 2000). Thus, the selection of parental materials based on geographic diversity may not be a successful exercise for hybridization programme and it would be more rewarding to select suitable diverse parents based on genetic divergence analysis than geographical diversity.

An investigation on the assessments of intra and inter-cluster genetic diversity, it was found that the genotypes of same cluster had little genetic divergence from each other with respect to aggregate effect of 13 characters studied. Therefore, the chances of obtaining good segregates by crossing the members belong to same cluster are very low.

It would be logical to attempt crosses between the genotypes belonging to clusters separated by large inter-cluster distances. In this context, the highest intra-cluster distance was recorded cluster VI (165.40) followed by cluster V

(142.20), cluster IV (95.10), cluster VII (91.45), cluster II (73.00) and cluster I (65.00). Intra-cluster distance of clusters such as VIII, IX, X, XI and XII showed nil value which suggested numbers of these five clusters are genetically very low diverse to each other. The maximum inter-cluster distance was found by cluster VII with XI (2752.23) followed by cluster VII with VIII (2415.95), cluster IV with VII (1682.64), cluster V with XI (1678.26), cluster X with XI (1645.68), cluster V with VIII (1618.57) and cluster VI with VII (1565.40). The minimum inter-cluster distance was observed between clusters I with IX (105.60), clusters I with III (108.23) cluster III with IV (110.60) cluster II with X (134.20) and cluster III with IX (151.22), this indicated that these groups were less divergence.

Cluster mean of 122 genotypes (Table-3) showed that mean values of clusters varied in magnitude for all the 12 characters studied. Maximum cluster mean for yield per plant was observed in cluster XI (12.87g) followed by cluster I (11.9 g), cluster X (11.72 g), cluster II (11.67g), cluster XII (11.55g), cluster VII (11.51g) and cluster VI (11.45g), while the lowest was found in cluster IX (9.52 g). Cluster II recorded highest cluster mean for test weight (11.27g) followed by cluster XI (10.62g), cluster V (10.56g), cluster IX (10.48g) and cluster VIII (10.23g), while the clusters X, VII and I have low value cluster mean for test weight. Cluster VI recorded highest fruits per umbel (39.60g) followed by cluster II (38.60g), cluster I (38.40) and cluster IX (38.20). Cluster XI recorded highest branch per plant (7.32) followed by cluster V (7.27), cluster XII (6.60) and cluster III (6.51). In case of umbels per plant cluster XI recorded highest cluster mean (96.52) followed by cluster XII (90.09), cluster X (85.27) and cluster VIII (76.45).

In the contribution of each character to divergence presented in table-4, which showed by plant height (59.25%) toward total genetic divergence followed by umbels per plant (36.05%) contributed maximum. Similar results were also reported by Meena *et al.* (2014)^[16] and Beemnet *et al.* (2011)^[2]. Whereas, remaining all characters contributes least.

Table 1: Estimates of average intra- and inter-cluster distances for 11 clusters in coriander

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster	VIII Cluster	IX Cluster	X Cluster	XI Cluster	XII Cluster
I Cluster	65.01	208.51	108.23	164.04	758.98	452.65	1035.00	407.52	105.57	310.50	767.74	1004.36
II Cluster		73.00	359.22	526.61	322.17	568.42	456.94	902.42	174.51	134.20	1203.18	715.51
III Cluster			0.00	110.56	1129.86	748.95	1288.66	486.65	151.22	434.44	1026.33	1511.11
IV Cluster				95.10	1323.49	612.04	1682.64	262.31	265.00	659.36	697.15	1483.99
V Cluster					142.19	793.00	334.95	1618.57	717.72	437.64	1678.26	412.79
VI Cluster						165.37	1565.39	369.60	668.46	911.03	306.69	429.78
VII Cluster							91.45	2415.95	807.62	358.03	2752.43	1166.37
VIII Cluster								0.00	668.49	1217.83	158.58	1253.51
IX Cluster									0.00	129.15	1097.43	1214.82
X Cluster										0.00	1645.68	1123.28
XI Cluster											0.00	978.63
XII Cluster												0.00

Table 2: Clustering pattern of 122 coriander genotypes on the basis of Non-hierarchical Euclidean cluster analysis for 11 characters

Cluster Number	Number of genotypes	Genotypes
I	3	NDCor-1, NDCor-8, NDCor-8
II	11	NDCor-22, NDCor-23, NDCor-110, NDCor-34, NDCor-109, NDCor-71, NDCor-108, NDCor-13, NDCor-111, NDCor-120, NDCor-116
III	8	NDCor-112, NDCor-113, NDCor-114, NDCor-115, NDCor-107, NDCor-117, NDCor-118, NDCor-106
IV	9	NDcor-53, NDcor-60, NDcor-54, NDcor-119, NDcor-43, NDcor-56, NDCor- 65, NDcor-66, NDcor-64
V	13	NDcor-5, NDCor-6, NDCor-11, NDCor-15, NDCor-59, NDCor-4, NDCor-38, NDCor-97, NDcor-12, NDcor-61, NDcor-14, NDcor-9, NDcor-10

VI	13	NDCor-18, NDCor-105, NDCor-29, NDCor-31, NDCor-92, NDcor-35, NDcor-87, NDcor-77, NDcor-83, NDcor-36, NDcor-49, NDcor-93, NDcor-104
VII	7	NDCor-21, NDCor-46, NDCor-79, NDcor-16, NDcor-67, NDcor-98, NDcor-78
VIII	22	NDCor-26, NDCor-27, NDCor-33, NDCor-89, NDCor-17, NDcor-88, NDCor-99, NDCor-95, NDCor-96, NDCor-90, NDCor-91, NDCor-28, NDCor-62, NDCor-42, NDCor-30, NDCor-32, NDCor-41, NDcor-94, NDcor-101, NDcor-121, NDcor-45, NDcor-51
IX	14	NDCor-24, NDCor-84, NDCor-37, NDCor-75, NDCor-102, NDCor-103, NDCor-100, NDCor-57, NDCor-76, NDCor-58, NDCor-81, NDCor-80, NDcor-82, NDcor-20
X	7	NDCor-25, NDCor-50, NDCor-19, NDCor-47, NDCor-20, NDCor-48, NDCor-3
XI	5	NDCor-40, NDcor-74, NDcor-44, NDCor-52, NDCor-39
XII	10	NDCor-55, NDCor-85, Hisar Anand ©, NDCor-63, NDCor-86, NDCor-68, NDCor-73, NDCor-70, NDCor-72, NDCor-69

Table 3: Clusters means for 11 characters in coriander

	Days to 50% flowering	Plant height (cm)	Branches per plant	Fruiting nodes per plant	Umbels per plant	Umbellates per umbel	Fruits per Umbellates	Fruits per umbel	Umbel diameter (cm)	Test weight (g)	Yield per plant (g)
I Cluster	85.543	126.640	5.683	12.896	69.138	5.176	6.819	38.399	5.724	8.838	11.901
II Cluster	89.922	117.975	6.304	13.442	75.713	5.786	6.115	38.575	4.752	11.269	11.674
III Cluster	90.396	126.099	6.509	13.384	73.239	5.813	5.445	36.804	4.473	9.515	10.666
IV Cluster	90.034	110.874	6.258	15.009	74.079	5.763	7.939	37.312	6.033	10.189	10.913
V Cluster	87.765	136.359	7.264	12.840	74.179	6.061	7.681	36.136	6.022	10.558	10.766
VI Cluster	90.292	130.671	5.994	13.268	72.405	6.130	8.362	39.598	4.426	9.902	11.444
VII Cluster	90.190	140.873	5.954	12.384	72.658	6.561	8.655	37.199	5.398	8.977	11.505
VIII Cluster	90.323	133.832	6.289	13.231	76.447	6.533	8.330	36.835	4.072	10.289	11.536
IX Cluster	89.933	137.497	5.971	13.929	75.682	6.671	8.584	38.112	5.752	10.484	9.517
X Cluster	88.779	135.012	6.327	14.985	85.271	6.056	8.812	34.919	4.696	8.993	11.726
XI Cluster	89.069	136.131	7.321	14.230	96.522	6.440	8.579	37.681	5.423	10.618	12.875
XII Cluster	92.071	122.560	6.604	13.477	90.082	6.694	8.201	37.461	6.217	10.021	11.546

Table 4: Per cent Contribution in genetic divergence in coriander

S. No.	Source	Contribution (%)
1.	Days to 50% flowering	1.49
2.	Plant height (cm)	59.25
3.	Branches per plant	0.07
4.	Fruiting nodes per plant	0.24
5.	Umbels per plant	36.05
6.	Umbellates per umbel	0.05
7.	Fruits per umbellate	0.51
8.	Fruits per umbel	1.75
9.	Umbel diameter (cm)	0.16
10.	Test weight (g)	0.01
11.	Yield per plant (g)	0.41

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