

Study of genetic divergence in coriander (*Coriandrum sativum* L.)

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Abstract

Genetic diversity was studied in 85 coriander genotypes for fifteen yield and yield contributing traits. Based on euclidean distance, genotypes were grouped in to seven clusters. Cluster II consisted of maximum genotype (37) with maximum intra cluster distance of 40.84. Cluster I, III, IV and VI had 4, 11, 17 and 14 genotypes, respectively. While cluster V and cluster VII had only one genotype. The maximum inter cluster distance was observed between clusters V & VII (109.74), I & VII (102.59). Cluster VII, Cluster VI and Cluster II showed highest mean value for the traits studied.

Key words : *Coriandrum sativum* L., cluster analysis, genetic diversity.

Introduction

Coriander (*Coriandrum sativum* L., 2n = 22) is a cross pollinated Apiaceae family plant of Mediterranean origin and an important crop of India as well as of Rajasthan State, India. Coriander is cultivated both for seed as well as for leaves. Fresh coriander leaves are more commonly known as cilantro. The seeds are extensively employed as a condiment in the preparation of curry powder, pickling, spices, sausages, seasoning and are also used to flavor pastry, biscuits, buns, cakes and liquors, particularly gin. Genetic improvement for yield and essential oil is the major breeding objective. Genetic diversity is also very important for any crop improvement programme as it helps in the development of superior recombinants. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981). Population improvement is generally followed in coriander for genetic improvement by using mass or recurrent selection. Information on genetic divergence in coriander is very helpful in identifying diverse population; which can be recombined together for creating new population for enhancement of genetic variability and thus performing selection in these diverse populations for identifying better plant types. The present study was conducted in 85 coriander genotypes to know the extent of genetic diversity existing in the crop which can be utilized for genetic improvement.

Material and methods

Eighty five coriander genotypes including five checks varieties i.e., RCr-435, RCr-684, Hisar Anand, APHU-D-1 and ACr-2 were grown in Augmented Block Design. All

recommended agronomic practices and plant protection measures were timely followed. Each entry was sown in single row of 2m length with row to row spacing of 50 cm and plant to plant spacing 10 cm. Five plants were randomly selected and tagged from each plot before flowering to record the data on plant height (cm), primary branches plant⁻¹, secondary branches plant⁻¹, umbels plant⁻¹, umbellate umbel⁻¹, seeds umbel⁻¹, 1000-seed weight (g), seed yield plant⁻¹ (g), while data on days to 50% flowering was recorded on whole plot basis. Based up on observation of fifteen characters the calculated weighted mean values obtained from Augmented Design were subjected to diversity analysis using NTSYS-pc ver. 2.02e software, Euclidean distance (ED) coefficients were estimated among each pair of 85 genotypes to assess the extent of diversity.

Results and discussion

All the 85 genotypes were grouped in to seven clusters (Table 1). The maximum numbers of genotype i.e., 37 were found in cluster II. Whereas, cluster I, cluster III, cluster IV and cluster VI had 4, 11, 17 and 14 genotypes, respectively. While cluster V and cluster VII had one genotype.

Inter and intra cluster distances between seven clusters were computed (Table 2). The maximum intra cluster distance was recorded for cluster II (40.84), which had maximum genotypes. The maximum inter cluster distance was observed between clusters V & VII (109.74), I & VII (102.59) followed by clusters II & VII, III & VII (89.03) and IV & VII (84.74). Similarly studies done by Singh *et al.*, 2002, Singh *et al.*, 2005, Mengesha *et al.*, 2011, Fufa,

Table 1. Distribution of coriander germplasm lines in seven clusters.

Clusters	Number of genotypes	Name of Genotypes
I	4	RKC-MLT-1, RKC-MLT-2, RKC-MLT-3, RKC-MLT-4
II	37	RKC-MLT-5, LCC-250, LLC-230, RKC-MLT-6, LCC-226, CS-150, LCC-229, CS-196, CS-131, CS-161, LCC-234, LCC-241, LCC-244, CS-142, JCr-2013-18, LCC-233, CS-104, CS-273, RSR-RSM-7, RKC-MLT-10, RSR-RSM-8, RSR-RSM-9, CS-141, APHU-D-1, NDCor-106, CS-198, RCr-435, RSR-RSM-1, NDCor-102, LCC-247, RSR-RSM-2, RSR-RSM-10, LCC-231, RD-388, NDCor-109, NDCor-110, RCr-684
III	11	RSR-RSM-3, RSR-RSM-11, RKC-MLT-7, RSR-RSM-4, RKC-MLT-9, RSR-RSM-12, RD-154, RD-365, RD-377, CS-170, Hissar-Anand
IV	17	JCr-2013-6, GCr-2, JCr-2013-15, NDCor-118, RD-417, DH-276, RD-401, NDCor-120, RD-397, RD-385, ACr-2, JCr-2013-23, RD-416, JCr-2013-17, DH-283, NDCor-111, DH-277
V	1	RSR-RSM-8
VI	14	JCr-2013-7, JCr-2013-9, JCr-2013-12, JCr-2013-14, NDCor-94, NDCor-119, RD-393, DH-261
VII	1	DH-268, DH-275, DH-278, DH-279, DH-280, DH-281 NDCor-90

2013, Awas *et al.*, 2016 have also shown that genetic diversity is high in coriander.

A comparison of the mean values for fifteen characters of different clusters is given in Table 3. Cluster VII comprising single genotype NDCor-90 showed highest mean values for seed yield plant⁻¹ (19.57), umbel plant⁻¹ (70.85), secondary branches plant⁻¹ (18.70), primary branches plant⁻¹ (8.57), plant height up to top of the plant (119.55), plant height up to main umbel (81.60) and longest basal leaf (9.55). Cluster VI was having the highest mean value for the characters, seeds umbel⁻¹ (43.43), umbellate umbel⁻¹ (5.41), days to 50% flowering (71.19), days to stem initiation (52.04), number of leaflets (2.88) and

number of basal leaf (6.54). Cluster III had the highest mean value for days to germination (11.41). However, cluster II had the highest mean value for test weight (13.78). Similar studies have also been done by Patel *et al.*, 2000, Singh *et al.*, 2002, Dyulgerov and Dyulgerov 2013, Arif *et al.*, 2014, Tomar *et al.*, 2014 to know the extent of cluster mean differences in coriander

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

Table 2. Inter and intra cluster distance between clusters.

Cluster	I	II	III	IV	V	VI	VII
I	13.72	58.79	58.79	54.27	79.50	77.60	102.59
II	58.79	40.84	11.90	19.52	60.22	61.17	89.03
III	58.79	11.90	37.14	19.52	60.22	61.17	89.03
IV	54.27	19.52	19.52	7.50	55.94	56.89	84.74
V	79.50	60.22	60.22	55.94	0	81.88	109.74
VI	77.80	61.17	61.17	56.81	81.88	38.67	43.56
VII	102.59	89.03	89.03	84.74	109.74	43.56	0

Table 3. Cluster mean value for different characters in coriander germplasm

Clusters No.	Days to germination	Longest basal leaf	No. of basal leaf	No. of leaflets	Days to stem initiation	Days to 50% flowering	Plant height 1(main umbel)	Plant height 2(top of the plant)	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Umbel plant ⁻¹	Umbellate umbel ⁻¹	Seeds umbel ⁻¹	Test weight (g)	Seed yield plant ⁻¹
I	11.20	4.54	2.89	1.38	41.65	56.65	29.63	63.09	3.36	9.71	18.32	4.31	31.85	11.94	4.90
II	11.39	5.84	3.21	1.44	42.52	61.40	39.60	84.34	5.78	12.58	39.64	4.58	36.34	13.78	10.04
III	11.41	5.96	3.57	2.06	45.77	62.04	39.70	82.20	6.21	13.20	52.74	4.79	40.24	11.68	11.58
IV	11.36	7.15	4.58	2.74	49.26	67.52	59.23	98.18	6.84	14.50	50.49	5.32	39.15	11.39	12.76
V	10.45	5.87	2.89	1.38	36.40	55.15	41.48	80.99	5.61	10.46	31.97	4.71	34.80	13.85	10.33
VI	11.16	9.40	6.54	2.88	52.04	71.19	80.79	107.88	7.77	15.22	42.50	5.41	43.43	10.17	8.82
VII	10.65	9.55	4.13	1.98	46.20	64.15	81.60	119.55	8.57	18.70	70.85	5.11	40.64	12.34	19.57

breeding; genetic diversity analysis helps in identifying diverse genotypes and also to group genotypes showing genotyping similarity for target traits. Thus, it can be suggested that for selection in cluster II which had maximum genotypes and recombination strategies between genotypes of cluster II and VI or cluster II and VII may generate highly variable combination, probability for getting transgressive segregates is also high in these kind of recombination between diverse parents.

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