International J. Seed Spices 7(2), July 2017:8-13

Variability for qualitative and quantitative characters in coriander (*Coriandrum sativum* L.) genotypes

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Abstract

Coriander (*Coriandrum sativum* L.) is an annual dual purpose herb belonging to the family Apiaceae. Coriander which is native of Mediterranean region enjoys the status of a commercial crop in many countries like India, Morocco, USSR, Hungary, Poland, Rumania, Guatemala, Mexico and USA. In India, coriander occupies the pride place among the seed spices. It is valued for its tender leaves and grains. Variability for qualitative and quantitative traits were investigated in 70 coriander genotypes received from different AICRP on spices centres. These genotypes were subjected to diversity analysis based on minimal descriptor developed by NRCSS, Ajmer. Twelve qualitative and ten quantitative characters of coriander were evaluated to assess the morphological variations among the collected genotypes. Genetic diversity analysis on 70 genotypes involving twelve qualitative traits resulted in grouping the genotypes into three different clusters. The genetic similarity coefficients for 70 coriander genotypes ranged from 38.00 per cent to 68.00 per cent. In the ten quantitative traits observed, seed yield per plant showed the highest variation ranging from 2.00 g (GDH 252) to 7.5 g (RD-410). These easily observable morphological traits are useful tool for preliminary evaluation, because they offer a fast and useful approach for assessing the extent of diversity in coriander genotypes.

Key words : Cluster analysis, *coriandrum sativum*, descriptors, morphological markers, seed yield.

Introduction

Coriander (*Coriandrum sativum*) is an annual aromatic herb that belongs to the umbel family (Apiaceae) with a wide variety of uses. Its short duration allows it to fit into different growing seasons, making it possible to grow the crop under a wide range of conditions (Diederichsen, 1996). Coriander has long been cultivated in the Mediterranean region, Southern Europe, Asia and the Caucasus. The major coriander producers includes members of the former Soviet Union, Hungary, Poland, Romania, Czech Republic, Slovakia, Morocco, Canada, India, Pakistan, Iran, Turkey, Guatemala, Mexico and Argentina (Lopez *et al.*, 2009; Qureshi *et al.*, 2009). The fresh green herb and a dry spice are the two main products obtained from coriander plants besides steam distillated oil and solvent extracted oleoresin for the aroma and flavor industry (Islam *et al.*, 2009; Msaada *et al.*, 2009).

It is used to spice the food, as an important ingredient in perfumery, food, beverage and pharmaceutical industry; it is also used as a medicine, such as antioxidant, treatment of nervous disorder, gut modulator, for lowering blood pressure and for diuretic properties; also used as anti diabetic and antimicrobial agent (Isabelle *et al.*, 2010; Qaiser *et al.*, 2009; Ylmaz, 2008). Although coriander has got diverse uses the knowledge on the extent and magnitude of genetic variability of agronomic and quality traits is limited. The existence of sufficient level of genetic variability is a prerequisite for variety development and therefore detailed evaluation of the accessions for different morphological, agronomic and quality traits is necessary in order to identify accessions with useful traits for improvement programs. Genetic diversity in coriander has long been based on morphological traits which often have notable advantages such as straightforward detection and measurement and relevance to characters of importance to germplasm users (Tomar *et al.*, 2014). This study was designed to assess the variation that exists in coriander accessions for morphological markers and yield components.

Material and methods

The preliminary characterization and evaluation of 70 genotypes was carried out at the Horticulture College and Research Institute, Tamil Nadu Agricultural University (11^{o}N, 77^{o}E, 426.72 m MSL), Coimbatore, Tamil Nadu during 2012 - 2014. The accessions received from different AICRP centres of various states mainly from Gujarat, Rajasthan, Haryana, Bihar, Uttar Pradesh, Andhra Pradesh

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Table 1. Genotype details of *Coriandrum sativum*

CSSR Jagudan (Gujrat)	Hisar, Haryana	Kumarganj, Uttar Pradesh	Dholi, Bihar	Jobner, Rajasthan	Coimbatore, Tamil Nadu	Guntur, Andhra Pradesh
JCr-405	DH-258	ND-1	RD-414	GL-15	CS-66	LCC -197
JC r-380	DH-238	ND-38	RD-422	GL-20	CS-65	LCC-144
JCr-407	DH-240	ND-14	RD-410	GL-26	CS-64	LCC-167
JCr -404	DH-252	ND-10	RD-391	GL-49	CS-63	LCC-193
JCr-406	DH-246	ND-4	RD-120	GL-40	CS-62	LCC-168
JCr-379	DH-339	ND-3	RD-409	GL-103	CS-61	LCC-164
JCr-389	DH-36	ND-31	RD-400	GL-37	CS-70	LCC-170
JCr-390	DH-344	ND-82	RD-387	GL-129	CS-69	LCC-166
JCr-391	DH-242	ND-68	RD-424	GL-74	CS-60	LCC-191
JCr-401	DH-254	ND-80	RD-394	GL-117	CS-67	LCC-174
				Check 1	CO-3	
				Check 2	CO-4	
				Check 3	Hisar Anand	
				Check 4	RCr-436	

and Tamil Nadu (Table 1). From this collection, random samples of 70 lines were evaluated in augmented block design with three blocks. The checks namely Co-3, CO-4, Hisar Anand, and RCr-436, repeated in every block. The checks and entries within a block were randomized to reduce bias (3 m longness). Each genotype was sown in a single row with spacing of 30 cm and 3 m long. The interplant spacing within a row was maintained at 10 cm when the crop was 27 days old. A random sample of 5 plants was chosen for making observations. These plants were tied and observed on daily basis for various morphological traits. Observations were taken on five randomly selected plants from each plot for qualitative characters as per minimal descriptor developed by NRCSS, Ajmer (Malhotra and Vashishtha, 2006).

Qualitative traits that depict an array of characters were converted into binary characters (Sneath and Sokal, 1973) based on the variations present in each trait. The data matrix was read by NTSYS-pc version 2.2 (Numerical Taxonomy and Multivariate Analysis System for Personal Computers, Exeter Software) developed by Rohlf (1998) and analyzed by the SIMQUAL (similarity for qualitative data) program with Jaccard's similarity coefficient. SIMQUAL is a program for computing a variety of similarity and dissimilarity coefficients for qualitative data. The similarity matrix was entered into SAHN (sequential, agglomerative, hierarchical and nested clustering method) clustering program, a tree matrix was produced and a dendrogram constructed using UPGMA (unweighted pair-group method with arithmetic averages). The assumption underlying the use of UPGMA clustering is the equal rate of evolution along all dendrogram branches. Dendrogram of publication quality were produced from the output tree file of SAHN by TREE (tree display) program in graphics mode (Mantel, 1967).

At maturity, ten plants were randomly selected from each plot and data were collected for quantitative characters *viz.*, plant height, number of branches per plant, days to 50% flowering, number of umbels per plant, number of seeds per umbellate, seed yield per plant, 1000 seed weight and Powdery mildew incidence. Accession means were used to calculate the mean, minimum, maximum, range and coefficient of variation (CV) for each trait.

Results and discussion

Observations for twelve qualitative traits taken from five randomly selected plants of 70 different coriander genotypes indicated that four traits did not show any difference between genotypes. Among the traits that were showing variations *viz.*, growth habit, leaf size, stem colour, Inflorescence colour, type of umbel, fruit shape, fruit size and incidence of powdery mildew (PDI) revealed that most of the genotypes possessed a particular variant phenotype (Table 2). Cluster analysis was performed on Jaccard's similarity coefficient matrices calculated from morphological markers to generate a dendrogram of 70 Coriander genotypes. The genetic similarity coefficients for 70 coriander genotypes ranged from 38.00 per cent to

68.00 per cent. The dendrogram separated the 70 genotypes into three major clusters namely A, B and C. Cluster A was further divided into two sub clusters, A1 and A2. Cluster A1 was again divided into two sub clusters, A3 and A4. Cluster A1 comprised of 19 genotypes (ND 1, ND 31, JCr 391, GL 28P, LCC 193, LCC 191, ND 82, DH 339, DH 242, RD 400, DH 240, JCr 401, CS 65, CO 4, ND 80, CO 3, JCr 407, RD 414 and RD 409) and cluster A2 contained 10 genotypes (ND 38, ND 68, RD 391, RD 424, DH 36, JCr 406, DH 254, RD 394, JCr 380 and DH 258). Cluster B was further divided into two sub clusters namely B1 and B2. Cluster B1 comprised of the genotypes *viz*., DH 344 and LCC 168. Cluster B2 was further divided into two sub groups namely B3 and B4. Cluster B3 consisted of one genotype LCC 197and cluster B4 consisted of LCC 144 genotype.

Cluster C was further divided into two sub clusters namely C1 and C2. Cluster C1 was again divided into two sub clusters, C3 and C4. Cluster C3 comprised of 14 genotypes *viz*., ND 4, LCC 166, CS 60, GL 49P, GL 40P, JCr 389, GL 37P, LCC 170, GL 103P, CS 62, CS 68, CS 70, LCC 174 and CS 63. Cluster C4 contained seven genotypes *viz*., ND 3, GL 117P, RD 422, GL 129P, RD 387, DH 252 and DH 238. Cluster C2 consisted of 13 genotypes *viz*., DH 5, LCC 167, CS 67, JCr 405, DH 246, JCr 390, CS 69, GL 15P, CS 54, LCC 164, CS 61 and GL 20P (Fig 1).

The maximum number of genotypes was found in cluster A1 having 19 genotypes with high degree of similarity (68-100 %). This clearly indicated that there was less variation existed between genotypes with respect to morphological observation. Morphological description can provide unique identification of genotypes, however their ability to provide reliably discriminating identification being at best cumbersome (Patterson and Weatherup, 1984). Morphological descriptions reflect not only the genetic constitution of the cultivar, but also the interaction of the genotypes with the environment (G x E), within which, it is expressed (Patterson and Weatherup, 1984). G x E interaction effects have been found to cause aberrant means for traits such that morphological data collected in field plots can provide, at best, only an initial screening of genotype identity or distinctiveness. Morphological variations have been eliminated with the consequence that most of the genotypes outwardly appear similar due to their unknown genetic control. It is known that multiple genotypes can give phenotypes of similar outward appearance (Ravi, 2000).

Table 2. Phenotype variants observed for various qualitative traits across 70 coriander genotypes

Character	Score	No of genotypes
Growth Habit	3	6
	5	60
	7	4
Plant type	1	—
	2	70
	3	—
Leaf Margin	1	—
	2	—
	3	70
Leaf size	1	34
	5	34
	7	2
Stem Colour	1	20
	2	22
	3	28
Inflorescence pubescence	0	70
	1	-
Stem shape	1	70
	2	-
Inflorescence colour	1	41
	2	29
	3	-
Type of umbel	1	44
	2	-
	3	26
Fruit shape	1	49
	2	21
Fruit size	3	50
	7	20
Biotic stress susceptibility	1	6
(Powdery mildew)	3	52
	5	12
	7	-
	9	-

Apart from qualitative characters, the quantitative characters were also evaluated to assist diversity comparisons (Table 3). Wide range of variability was recorded in those characters. In the ten traits observed, seed yield per plant showed the highest variation ranging from 2.00 g (GDH 252) to 7.5 g (RD-410). Days to 50% flowering, days taken for maturity and 1000 seed weight also showed considerable variation. A minimum of 10.33 and a maximum of 40.00 number of seeds per umbellate were observed in GL 74 and GL 15, respectively. The

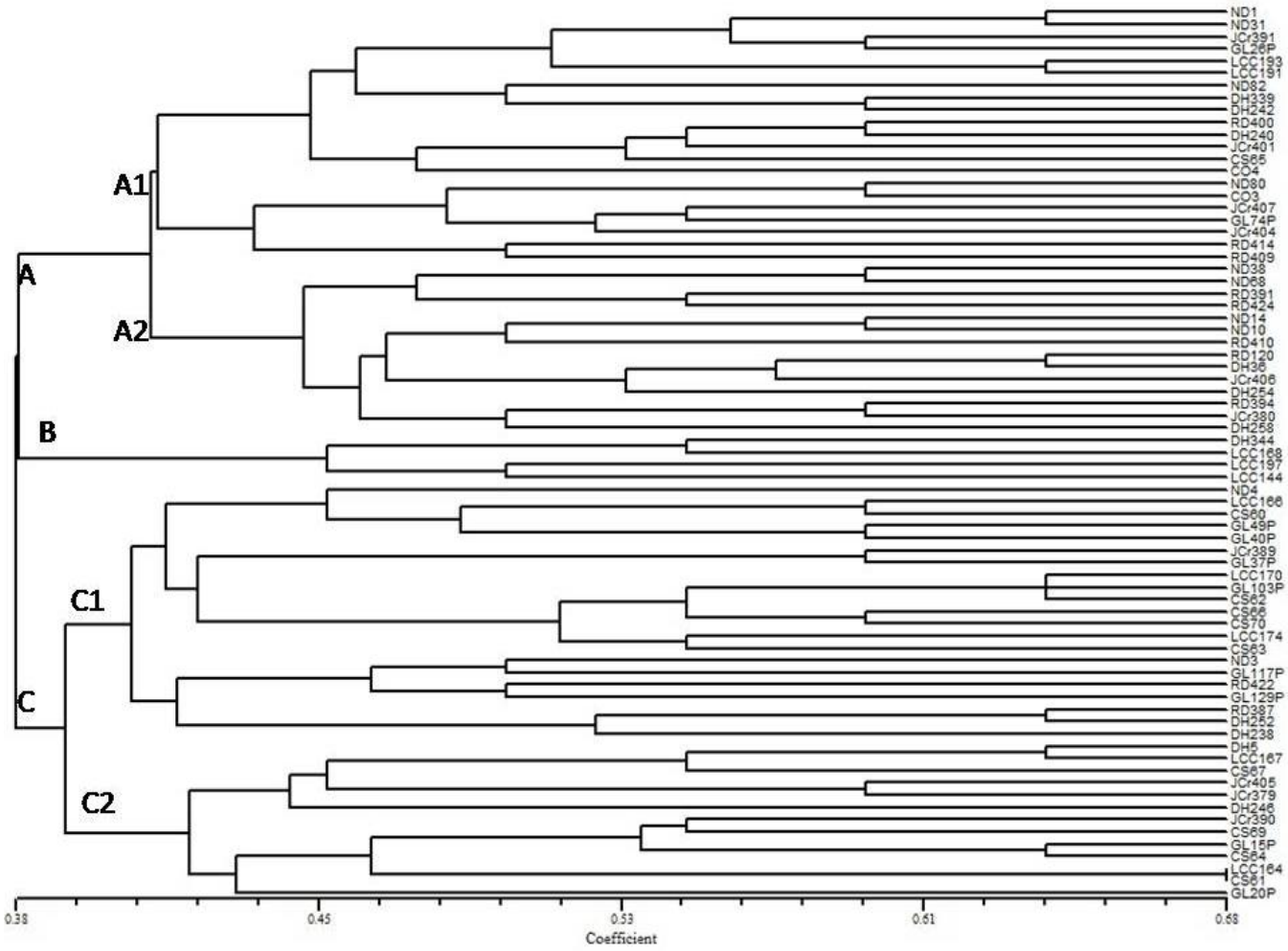

Fig 1. Dendrogram of coriander genotypes for qualitative traits using UPGMA based on Jaccard's coefficient

Table 3. Mean and variation of yield components in 70 coriander accessions

Characters	Mean	Range	SD	CV %
Plant height (cm)	58.94	34.57 - 74.63	7.53	12.77
No. of branches	5.19	2.00 ï 10.00	1.44	27.73
Days to 50% flowering	43.88	40.00 ï 55.00	3.47	7.90
Umbel diameter (cm)	5.29	3.10 - 7.50	0.88	16.59
No. of umbels/plant	17.91	7.00 ï 37.00	5.58	31.18
No. of seeds/ umbellate	19.90	10.33 ï 40.00	5.77	29.02
Days taken for maturity	73.88	70.00 ï 85.00	3.50	4.74
Seed yield/plant (g)	3.83	2.00 - 7.50	1.28	33.31
1000 seed weight (g)	20.22	20.00 ï 21.00	0.19	0.92
BSS (Powdery Mildew)	13.88	10.00 ï 20.00	2.67	19.22

number of umbels per plant was maximum in Jcr 405 (37.00) and minimum in LCC 170 (7.00). The powdery mildew incident was 10 per cent in DH 240, Jcr 405 and 20.00 per cent in ND 4. Similarly, Tomar Rukam *et al*. (2014) reported the germplasm of coriander had marked variability for yield and morphological characters. The means observed in this study were comparable to the reports of Diederichsen (1996). The wider ranges of some traits observed by the same author could be due to the larger sample size of 237 world coriander collections. Sastry *et al.,* (2016) observed the variation in flowering and maturity durations and their relation with other morphological traits which may influence seed yield of coriander. Coriander is very sensitive to of the environmental variation and its yield shows high fluctuations over environments. Knowledge of the nature and magnitude of genotype x environmental interactions is very important for design strategy leading for progressive coriander breeding program (Dyulgerov and Dyulgerova, 2013). In the present study, variation in the mean performance of the genotypes may be due to interaction between environment and genotype as reported by Chandran (1987). These easily observable morphological traits are useful tool for preliminary evaluation, because they offer a fast and useful approach for assessing the extent of diversity in coriander genotypes.

Acknowledgement

The author is gratefull to the ICAR and the Project Co-ordinator, AICRP on Spices, Calicut, Kerala for providing the seed materials.

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Received : February 2017; Revised : June 2017; Accepted : June 2017.