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Exploiting Genetic Divergence for Crop Improvement in Coriander (*Coriandrum sativum* L.): A Neglected and Underutilized Crop

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Coriander (*Coriandrum sativum* L.) cultivars suitable for rainfed farming situation are needed for sustainable production. Understanding the genetic divergence of the crop facilitates the manipulation of desired traits through plant breeding. One hundred and eighty three germplasm lines of coriander of diverse geographical origin were screened under rainfed conditions to determine genetic divergence following multivariate and canonical analysis. Thirteen traits including grain yield were considered for studying the divergence. Utilizing cluster analysis, the germplasm were grouped into eight clusters. The four PCA components explained 77.8% of the total variability among thirteen quantitative traits. Some 84% of the total genotypes (154/183) were grouped in two clusters (1 and 8). Remaining clusters (2, 3, 4, 5, 6 and 7) contained 16% genotypes (29/183) representing wide diversity. The genotypes of similarity were identified. Apparent diversity was noticed in 69 genotypes which diverged in seven clusters. The cluster association revealed the relationship between genetic divergence and geographical diversity. Genotypes of clusters 2, 4 and 7 can be utilized for improving yield due to its high mean performance for grain yield/plant with good amount of genetic divergence in most of the yield contributing characters. The high inter-cluster distances and the high mean performance of the clusters 2, 4 and 7 suggest that successful recombinants for high grain yield may be obtained from the crosses among the genotypes from these clusters. Similarly, members of cluster 3 can be utilized for improving the essential oil content. For breeding bolder types, genotypes from clusters 6 and 7 can be utilized. Rational strategies for effective utilization of germplasm for crop improvement are also discussed.

Key Words: *Coriandrum sativum*, Genetic diversity, Germplasm

Introduction

The species *Coriandrum sativum* L., is grown for '*grain* or *seed*' spice and green leaf. It is widely cultivated throughout the world. However, production of coriander for '*grain*' is limited to some Mediterranean, African and Asian countries. The crop is grown mainly in Bulgaria, India, Morocco, Mexico, Romania, Argentina, Iran and Pakistan (Diederichsen, 1996). It is grown mainly in two farming situations – irrigated light soils and rainfed vertisols. Most crop improvement programmes mainly aim at developing long duration varieties suitable for irrigated light soils (Bhandari and Gupta, 1993a; 1993b), sodic wastelands (Singh *et al.*, 2005) and special uses (Lopez *et al.*, 2007). Large-scale production and the development of better varieties suitable for rainfed vertisols are restricted by the lack of information about their genetic diversity, intra-specific variability and genetic relationships among this species. Due to paucity of genetic diversity, crop improvement of coriander for rainfed vertisols has become a challenge in India. In this context it is very crucial to analyze, understand and exploit the untapped genetic diversity for effective crop improvement. Multivariate (Anderberg, 1973, Smith, 1984; Cox *et al.*, 1986) and principal component (PCA) analyses (Wiley, 1981; Johnson, 1998a) help in understanding the diversity and are extremely useful

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for crop improvement programmes. Mohammadi and Prasanna (2003) opined that concerted and planned utilization of germplasm utilizing the knowledge accrued from studies on genetic diversity is needed for effective crop improvement programmes. In this context, the present study was initiated to study the genetic diversity, possible classification and ordination, and utility of the germplasm diversity in developing rational strategies for effective utilization of germplasm for improvement of coriander.

Materials and Methods

The present investigation was conducted at the field of the "All India Coordinated Research Project on Spices (AICRPS)" project, Sub-center, Horticultural Research Station, Lam, Guntur of Dr YSR Horticultural University, Tadepalligudem, Andhra Pradesh, India. The experiment was conducted during the winter seasons of 2008 and 2009. The experimental station is located at 16°18' N latitude, 80°29' N longitude and at an elevation of 31.5 m above mean sea level (MSL). The experimental soil is vertisols (black clay loam to black clay) with a pH of 7.6, Electrical Conductivity of 0.47 dS/m and Cation Exchange Capacity of 0.5 me/g. Bulk density is 1.22 g/cm and hydraulic conductivity is 1.4 cm/hour. Water holding capacity of the soil is 47%. The available Nitrogen is 282 kg/ha, Phosphorous is 40.2 kg/ha and Potassium is 717 kg/ha. The field experiment was laid out in the Augmented Block Design (ABD) with 183 entries which included four checks in ten blocks with 4 × 1.2 m plot for each entry. The design contained ten randomized blocks in each of which four standard coriander varieties and eighteen entries to be evaluated were grown. The plot was fertilized with 45 kg N/ha, 40 kg P/ha and 20 kg/ha. Data were recorded from ten plants randomly selected from the plot on plant height (cm), number of primary branches, number of secondary branches, number of umbels/plant, number of umbellets/ umbel, number of fruits/umbel, days to 50% flowering, days to maturity, yield/plant (g), bio mass (g), test weight (g) and essential oil (%).

The data set, composed of 13 variables for 183 accessions collected from important coriander growing areas of Andhra Pradesh, Maharashtra and Rajasthan and were analyzed by multivariate statistical techniques. Principal Component Analysis (PCA) was utilized for description of spatial relationships among the germplasm lines. Standard version of the computer software SPSS 10.0.1 was used for the analysis. Cluster analysis was carried out to examine whether the genotypes could be regarded as consisting of number of partially dissociated groups or clusters. Clustering of germplasm was carried out as per the degree of similarity among the germplasm lines (Peeters and Martinell, 1989; Johnson, 1998b). The coordinates of the position of each accession were determined from the value of each variable. The accessions with similar values for each variable were closer to each other and, therefore, showed a similar pattern over the variables. Cluster analysis was performed by means of incremental sum of squares (ISS) and complete, single, and average linkage strategies (Johnson, 1998b). Dendrogram was generated using the average linkage strategy using the free statistics software housed on the website www.wessa.net. (Wessa 2010).

Results

For understanding the diversity, each germplasm accession is represented by a point in a three-dimensional space, the coordinates of which provide an indication of the scores for each character (Fig. 1). Accessions with similar responses among these characters are grouped in proximity in the three-dimensional space. The first four principal components gave eigen values greater than 1, and cumulatively accounted for 77.8% of the total variance. The principal components with eigenvalue > 1.0 are considered as inherently more informative than any single original variable alone (Iezzoni and Pritts, 1991), hence these were used in this study. The perusal of correlation matrix revealed significant correlations among majority of the traits (Table 1). The matrix revealed the fitness of the dataset in PCA analysis for classification and ordination of the genotypes. The magnitude of the eigen vectors indicates the importance of the variable to one particular component axis (Tables 2 and 3). The first PCA component was positively and strongly correlated with yield per plant and plant height in decreasing order of importance; and was negatively correlated with umbellets per umbel, days to 50% flowering, fruits/ umbel and days to maturity. The second component was positively and strongly correlated with number of primary branches, biomass, number of secondary branches, umbels/plant, fruits/umbel and days to maturity in decreasing importance. The third component was positively and strongly correlated with fruits/plant and negatively correlated with test weight. The fourth component was positively and strongly correlated with

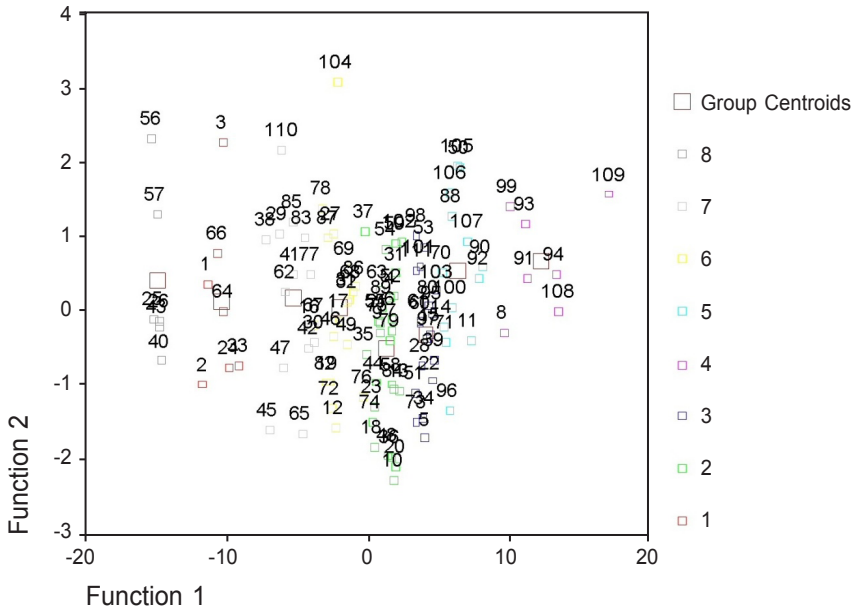

Fig. 1. Canonical discrimination of germplasm lines (accessions in ordinal numbers)

Table 1. Correlation matrix among different traits

	†PH	PBR	SBR	UPP	UPU	FPU	DF	DM	BM	YPP	OP	FPP
PBR	-0.306**											
SBR	0.103	0.625**										
UPP	0.152*	0.529**	0.871**									
UPU	-0.339**	0.313**	-0.212**	-0.284**								
FPU	-0.334**	0.465**	-0.028	-0.061	0.890**							
DF	-0.411**	0.422**	-0.102	-0.181*	0.621**	0.564**						
DM	-0.262**	0.463**	0.041	-0.037	0.608**	0.574**	0.650**					
BM	0.137	0.734**	0.863**	0.931**	0.004	0.206**	0.031	0.180*				
YPP	0.339**	0.169*	0.581**	0.652**	-0.470**	-0.284**	-0.464**	-0.373**	0.535**			
OIL	-0.017	-0.068	-0.164*	-0.112	-0.056	-0.087	0.150*	0.023	-0.124	0.021		
FPP	0.317**	-0.137	0.226**	0.268**	-0.339**	-0.278**	-0.301**	-0.328**	0.160**	0.337**	0.023	
TW	-0.087	-0.021	0.047	0.035	-0.110	-0.115	-0.100	-0.095	-0.022	0.071	-0.053	-0.322**

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels/ plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (g); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

Table 2. Eigen values of the correlation matrix of principal components and proportion of variance

Principal Components	Eigenvalues	Variance (%)	Cumulative (%)
I	4.101	31.543	31.543
II	3.623	27.867	59.410
III	1.335	10.269	69.679
IV	1.055	8.117	77.796

essential oil percentage.

The canonical analysis revealed that yield/plant (0.801) contributed maximum divergence followed by umbellets/ umbel (-0.784), days to 50% flowering (-0.704), fruits/ umbel (-0.636), days to maturity (-0.598) and plant height (0.517) in PC I. Number of primary branches (0.908) followed by biomass (0.859), number of secondary branches (0.724), umbels per plant (0.679), fruits/

Table 3. Eigen vectors and the principal components of thirteen traits in coriander

	Principal components			
	I	II	III	IV
PH†	0.517	-0.214	0.298	-0.179
PBR	-0.045	0.908	-0.07	0.103
SBR	0.595	0.724	-0.072	0.006
UPP	0.674	0.679	-0.042	0.038
UPU	-0.784	0.395	0.14	-0.19
FPU	-0.636	0.565	0.135	-0.195
DF	-0.704	0.424	0.117	0.23
DM	-0.598	0.539	0.095	0.057
BM	0.463	0.859	0.028	-0.008
YPP	0.801	0.239	-0.032	0.107
OP	-0.074	-0.133	0.217	0.926
FPP	0.535	-0.081	0.608	-0.052
TW	0.056	-0.043	-0.869	0.096

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels/plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (g); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

umbel (0.565) and days to maturity (0.539) contributed maximum divergence in PC II. Test weight (-0.869) and fruits/plant (0.608) contributed maximum divergence in PC III. The divergence contribution to fourth principal component was from essential oil percentage (0.926).

The PCA analysis was used to study the interrelationships in thirteen quantitative traits and to detect groupings based on similarities in trait interrelationship and to identify direct and indirect effects of characters on coriander crop improvement. The 183 coriander genotypes were grouped in eight clusters based on the genetic diversity studied (Table 4). The cluster means of the traits considered for the study of diversity are presented in Table 5. The canonical variables determined by canonical discriminant analysis were used to aggregate the accessions into groups that were similar in consequential ways by cluster analysis. The objective was to attain clusters of accessions that display small intra-cluster variation relative to the inter-cluster variation. The clusters 2, 3, 4, 5, 6 and 7 were unique containing 29 genotypes. Among the 183 genotypes, 154 accessions were grouped in 2 clusters (cluster 1 and cluster 8) representing 84.1% accessions. Apparent diversity was noticed only in 69 genotypes which diverged in 7 clusters. The cluster association revealed moderate relationship between genetic divergence and geographical diversity. Genetic drift and selection in different environments could cause greater genetic divergence. Similarly, geographical origin of the genotypes which is an embodiment of specific environment assisted by natural and human selection cause greater divergence though many similarities are found in the genotypes of similar geographical background. Further, genotypes of distant geographical origin show similarities if macro environments of the geographical origin are similar. Unless the macro environments differ, it is quite possible to see much similarity in the genotypes from different geographical regions.

The intra-cluster distances (D^2) values (Table 6) ranged from 14.4 to 279.5, the maximum was in cluster 6 followed by 1 (279.5), 5 (128.6) and 8 (60.9). The inter-cluster distance ranged from 28.2 to 289.8. The maximum inter-cluster distance was noticed between cluster '4' and '7' (289.8) followed by '1' and '7' (255.7), '3' and '7' (249.1), '2' and '7' (242.3), '6' and '7' (242.0) and '5' and '6' (221.4). Inter cluster distances between cluster 5 and clusters 1 to 6 are also considerably wide. Low inter cluster distance was found only in '2' X '4' (28.2). Such wide distances between clusters are indicative of wide diversity between these clusters and low genetic diversity was only observed between clusters '2 and '4' only. The composition of the clusters revealed that the accessions collected from nearby locations joined the similar or same cluster(s), those from geographically different locations fell in the different clusters showing that there is a relation between geographical location and diversity. Intensive selection for agronomically important characters and similarity in parentage might be the cause of narrow genetic diversity and uniformity between these clusters (Singh *et al.*, 2003). The important cluster traits

Table 4. Clusters of germplasm accessions with their cluster composition

Cluster	Number of accessions	Cluster members
1	114	LCC-121, LCC-122, LCC-123, LCC-124, LCC-125, LCC-126, LCC-128, LCC-130, LCC-131, LCC-132, LCC-133, LCC-134, LCC-135, LCC-136, LCC-137, LCC-138, LCC-139, LCC-139, LCC-140, LCC-141, LCC-142, LCC-143, LCC-144, LCC-145, LCC-146, LCC-148, LCC-149, LCC-150, LCC-151, LCC-152, LCC-153, LCC-154, LCC-155, LCC-156, LCC-157, LCC-158, LCC-159, LCC-160, LCC-161, LCC-162, LCC-163, LCC-164, LCC-165, LCC-166, LCC-167, LCC-168, LCC-169, LCC-170, LCC-171, LCC-172, LCC-173, LCC-174, LCC-175, LCC-178, LCC-179, LCC-181, LCC-182, LCC-183, LCC-184, LCC-187, LCC-188, LCC-189, LCC-190, LCC-191, LCC-192, LCC-196, LCC-197, LCC-198, LCC-199, LCC-201, LCC-203, LCC-204, LCC-205, LCC-206, LCC-207, LCC-208, LCC-211, LCC-212, LCC-213, LCC-215, LCC-216, LCC-218, LCC-219, LCC-220, LCC-222, LCC-223, LCC-224, LCC-225, LCC-226, LCC-227, LCC-228, LCC-229, LCC-230, LCC-235, LCC-236, LCC-238, LCC-240, LCC-241, LCC-242, LCC-243, LCC-244, LCC-247, LCC-248, LCC-249, LCC-250, LCC-251, LCC-252, LCC-253, LCC-254, LCC-255, Sindhu, Sadhana, Swathi, Sudha
2	12	LCC-127, LCC-147, LCC-176, LCC-185, LCC-186, LCC-193, LCC-194, LCC-195, LCC-231, LCC-233, LCC-234, LCC-246
3	4	LCC-129, LCC-200, LCC-202, LCC-221
4	1	LCC-177
5	7	LCC-180, LCC-209, LCC-210, LCC-214, LCC-237, LCC-239, LCC-245
6	4	LCC-217, LCC-256, LCC-286, LCC-297
7	1	LCC-232
8	40	LCC-257, LCC-258, LCC-259, LCC-260, LCC-261, LCC-262, LCC-263, LCC-264, LCC-265, LCC-266, LCC-267, LCC-268, LCC-269, LCC-270, LCC-271, LCC-272, LCC-273, LCC-274, LCC-275, LCC-276, LCC-277, LCC-278, LCC-279, LCC-280, LCC-281, LCC-282, LCC-283, LCC-284, LCC-285, LCC-287, LCC-288, LCC-289, LCC-290, LCC-291, LCC-292, LCC-293, LCC-294, LCC-295, LCC-296, LCC-298

Table 5. Cluster means of coriander germplasm for 13 traits

Cluster	PH†	PBR	SBR	UPP	UPU	FPU	DF	DM	BM	YPP	OIL	FPP	TW
1	69.7	5.0	12.9	18.5	5.9	31.4	52.9	91.6	45.7	4.7	0.31	319.9	15.9
2	71.1	8.2	20.4	31.0	5.2	35.8	52.1	93.3	71.8	8.0	0.31	430.6	13.9
3	64.3	5.5	11.2	12.7	5.6	22.1	55.3	91.8	36.0	5.5	0.53	160.5	18.4
4	73.4	8.3	19.1	28.6	11.0	75.9	52.0	95.2	74.0	7.2	0.18	199.8	16.2
5	65.9	5.5	13.8	18.4	5.6	29.8	51.3	90.3	45.2	4.5	0.14	206.1	22.3
6	59.6	6.5	12.5	17.5	8.3	44.3	56.3	91.7	46.2	4.7	0.33	99.8	48.8
7	66.8	8.7	21.3	36.1	4.3	30.7	53.0	95.2	78.4	7.5	0.28	149.3	30.9
8	60.8	7.3	11.9	15.1	12.0	60.3	61.1	100.2	48.0	2.4	0.31	185.6	13.5

†PH = plant height (cm); PBR = number of primary branches; SBR = number of secondary branches; UPP = number of umbels per plant; UPU = number of umbellets/umbel; FPU = number of fruits/umbel; DF = days to 50% flowering; DM = days to maturity; BM = biomass (g); YPP = yield/plant (gm); OP = oil percentage; FPP = number of fruits/plant; and TW = test weight (g).

Table 6. Intra- and inter-cluster distance (D^2) in coriander among 8 clusters formed by 183 germplasm accessions based on 13 traits

Cluster	I	II	III	IV	V	VI	VII	VIII
1	14.4	36.6	54.3	37.1	152.1	59.3	255.7	68.1
2		28.5	48.1	28.2	142.4	51.3	242.3	60.3
3			47.8	31.1	148.8	46.3	249.1	59.2
4				45.8	180.3	39.9	289.8	83.0
5					128.6	72.8	221.4	61.6
6						50.2	242.0	58.1
7							279.5	77.2
8								60.9

Table 7. Important traits of clusters of coriander germplasm

Cluster	Important traits
1	Moderate plant growth with average yield.
2	More primary and secondary branches, higher number of umbels per plant with high biomass and higher yield. Moderate essential oil content.
3	Moderate plant growth with lower number of umbels per plant with low biomass with slightly high yields with higher oil percentage. Low fruit number with slightly higher test weights. High essential oil content.
4	More primary and secondary branches, higher number of umbels per plant, higher number of umbellets per umbel with high biomass and higher yield. Low essential oil content.
5	Moderate plant growth with average yield. Low essential oil content. Slightly higher test weights.
6	Moderate plant growth, higher fruits per umbel, low number of fruits per plant with average yield. Very high test weight.
7	More primary and secondary branches, higher number of umbels/plant, low number of umbellets/umbel with high biomass and higher yield. Slightly lower essential oil content. High test weights.
8	Moderate plant growth with highest number of fruits/umbel, late maturing with low biomass and yield.

are presented in Table 7. The cluster traits revealed that the germplasm variability is scant in entries with high test weights (bold types), high number of fruits per umbel, high number of umbellets per umbel, high essential oil content, low or absence of essential oil content and high yield. Most genotypes were having low biomass (92.3 %) showing their adaptability to rainfed farming situation. The entries in the cluster 8 were having long duration, thus were unable to withstand the terminal moisture stress that prevailed in rainfed cultivation thus making them low yielders. However, the members of cluster 8 were having very high number of fruits per umbel which is a very important trait in view of crop improvement. Dendrogram clustering revealed that the genotypes grouped in eight major clusters (Fig. 2). Classification methods in conjunction with ordination techniques are very accurate in discriminating the accessions and proved useful in selecting the germplasm lines for crop improvement programmes. The cluster membership when viewed in the context of geographical origin of the accessions, certain clusters formed graciously coincided with the geographical origin. Thus, similarities in the accessions from similar geographical origin are clearly depicted in the dendrogram.

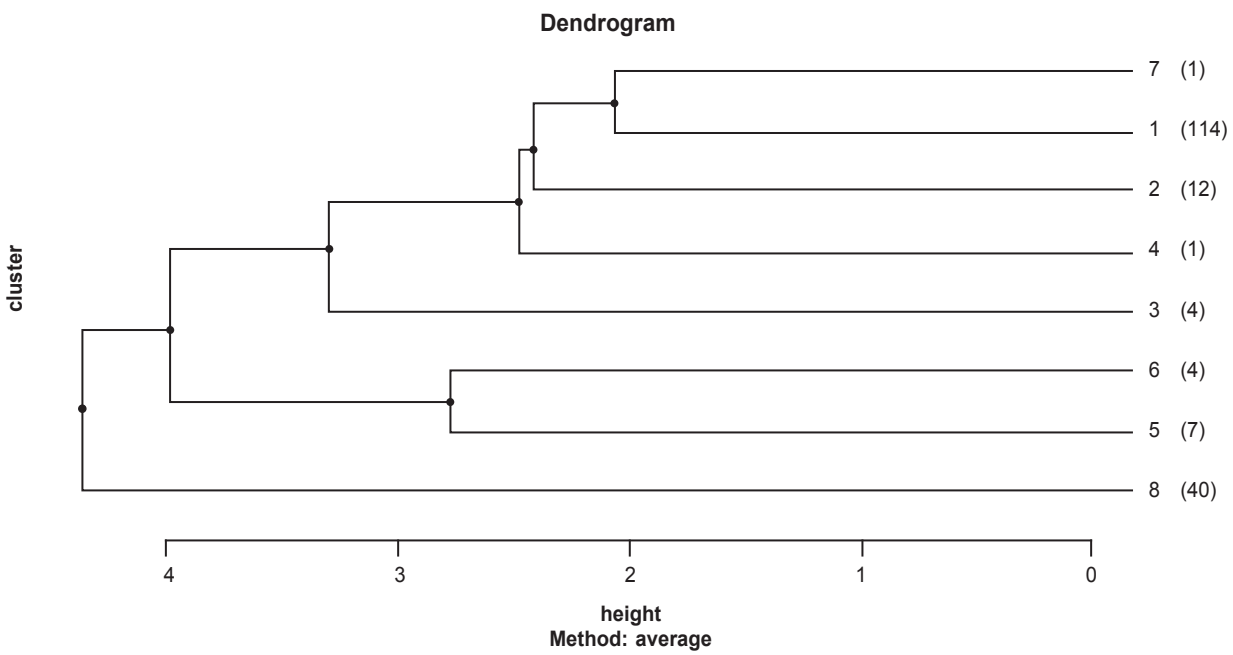

Fig. 2. Dendrogram depicting different clusters of germplasm accessions with number of accessions in parenthesis

Discussion

Crop improvement programmes using the inter-mating between diverse cluster members may generate high heterotic response and better segregants. Exploitation of such explained diversity through breeding programmes paves the way for successful crop improvement programmes. In the present study, cluster I represents the typical types grown in rainfed environments, thus having low diversity as indicated by intra-cluster distance (14.1). The members of cluster 6 are bolder types suitable for vertisols. The clusters 2, 4 and 7 are high yielders. However, members of cluster 4 and 5 are having low essential oil content. The members of cluster 3 are having high essential oil content. The members of cluster 8 are longer duration types with high number of fruits/umbel. On the basis of duration the clusters form two groups. (*i*) Medium duration (clusters 1 to 7) and (*ii*) Longer duration (cluster 8). On the basis of oil content the clusters form three major groups (*i*) Low oil content (cluster 5 and 6), (*ii*) Medium oil content (cluster 1, 2, 4, 7 and 8), (*iii*) High oil content (cluster 3). On the basis of boldness the clusters form two groups. (*i*) Medium bold types (clusters 1, 2, 3, 4, 5 and 8) *ii*) Bold types (cluster 6 and 7). On the basis of yield the clusters form three groups (*i*) Moderate yielders (clusters 1, 3, 5 and 6), (*ii*) High yielders (clusters 2, 4 and 7), (*iii*) Low yielders (cluster 8). Coriander crop improvement has several objectives such as high yield coupled with high essential oil content, bolder types, green types with higher essential oil content, green types with low essential oil content, high yielding with short duration/medium duration types and many more apart from tolerance to biotic and abiotic stresses. The present study envisages some of these objectives like high yield with high essential oil content and high yield with short duration can be met using genotypes from all the clusters using different combinations. Genotypes of clusters 2, 4 and 7 can be utilized for improving yield due to its high mean performance for grain yield/plant and most of the yield contributing characters with good amount of genetic divergence. Similarly, members of cluster 3 can be utilized for improving the essential oil content. For breeding bolder types, genotypes from cluster 6 and 7 can be utilized. The high inter-cluster distances and the high mean performance of the clusters 2, 4 and 7 suggests successful recombinants for high grain yield may be obtained from the crosses among the genotypes from these clusters.

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