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**GENETIC DIVERGENCE AND ITS IMPLICATION IN BREEDING OF  
DESIRED PLANT TYPE IN CORIANDER (*CORIANDRUM SATIVUM* L.)**

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Seventy germplasm lines of coriander (*Coriandrum sativum* L.) of diverse eco-geographical origin were undertaken in present investigation to determine the genetic divergence following multivariate and canonical analysis for seed yield and its 9 component traits. The 70 genotypes were grouped into 9 clusters depending upon the genetic architecture of genotypes and characters uniformity and confirmed by canonical analysis. Seventy percent of total genotypes (49/70) were grouped in 4 clusters (V, VI, VIII and IX), while apparent diversity was noticed for 30 percent genotypes (21/70) that diverged into 5 clusters (I, II, III, IV, and VII). The maximum inter cluster distance was between I and IV (96.20) followed by III and IV (91.13) and I and VII (87.15). The cluster VI was very unique having genotypes of high mean values for most of the component traits. The cluster VII had highest seeds/umbel ( $35.3 \pm 2.24$ ), and leaves/plant ( $12.93 \pm 0.55$ ), earliest flowering ( $65.05 \pm 1.30$ ) and moderately high mean values for other characters. Considering high mean and

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inter cluster distance breeding plan has been discussed to select desirable plant types.

*Key words:* *Coriandrum sativum* L., germplasm, multivariate analysis, Canonical vector, clusters

## INTRODUCTION

Coriander (*Coriandrum sativum* L.) is an important spice crop among spices with pleasant aroma. Its green foliage rich in vitamins, protein and other minerals is used in vegetables and salad and seeds are used as spice besides containing essential oil rich in linalool. The crop can grow well on sodic soil (SINGH *et al.*, 2000; 2003a) but the literature on the development of suitable high yielding variety for sodic soil is very meager. The availability of genetic variability among population is most important for judicious selection and breeding to desired plant genotypes. D<sup>2</sup> analysis following multivariate analysis plays an important role in screening germplasm lines for breeding purposes. Crosses between genetically diverse parents would manifest more heterosis than crosses of between closely related parents (SINGH, 1991; SHUKLA and SINGH, 2002). Such study has been made in coriander germplasms grown on normal soil (BHANDARI and GUPTA, 1993a; 1993b) but similar study to screen and select suitable genotypes for sodic soil is meager (SINGH *et al.*, 2000). Hence, the present study was undertaken on sodic soil with the objectives, i) to study the nature and magnitude of genetic divergence, ii) to identify characters which contribute maximum to genetic diversity and iii) to identify suitable genotypes for use in breeding program for broadening the genetic base in coriander.

## MATERIALS AND METHODS

In the present investigation seventy accessions of coriander obtained from different eco-geographical regions of India were sown in randomized block design with three replications in sodic soil of the Banthera Research Station (BRS) of National Botanical Research Institute (NBRI), Lucknow, India, during winter of 2000-2001. The BRS is situated at 26°40' N to 26°45' N latitude and 80°45' E to 80°53' E longitude at an elevation of 129 m above sea level. The soil at BRS is silty-clay loam non-saline sodic type having a pH value of 8.5-10 and electrical conductivity of 0.6 dsm<sup>-1</sup>. The soil is poor in organic carbon (0.43 %) with low availability of nitrogen (190 kg/ha). The porosity is low and is the reason for the low availability of the existing nutrients, which limit the growth and establishment of the plants. Each treatment was sown in two rows 3m long/replication. The row-to-row and plant-to-plant distance was kept 60cm and 15cm respectively. Normal cultural practices were followed through out crop season to harvest good crop. Ten plants/treatment/replication were selected before flowering to record the observations on days to flower, plant height (cm), branches/plant, leaves/plant, internodal distance (cm), umbels/plant, seeds/umbel, test weight (g.) and seed yield/plant (g).

**Statistical analysis:** Mean data of each treatment over replications was used for statistical analysis.  $D^2$  statistic was employed to determine the degree of differentiation among  $n(n-1)/2$  pairs of 'n' population (RAO, 1952). Grouping of genotypes was done according to Tochar, s method (RAO, 1952).

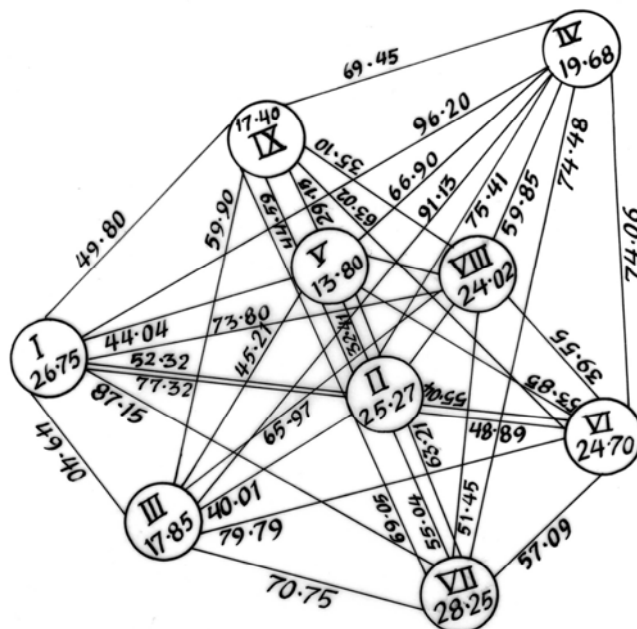


Fig. 1. Canonical analysis of inter-cluster relationships

## RESULTS AND DISCUSSION

The analysis of variance for individual character as well as the aggregate of 10 characters was found significant ( $\chi^2 760 \text{ df} = 360.89^{**}$ ) suggesting the need to estimate  $D^2$  for further study. Seventy germplasm lines were grouped in nine clusters, following Tochar's method (RAO, 1952) and were further confirmed by canonical analysis (Fig. 1). Among component traits plant height followed by umbels/plant, leaves/plant and seeds/umbel possessed maximum divergence towards seed yield. This showed that wide diversity in umbels/plant, seeds/umbel, plant height and leaves/plant could be utilized in improvement of seed yield by making crosses and selecting the recombinants combining above component traits. The canonical analysis also confirmed the above findings. In canonical analysis the internodal distance (0.744) contributed maximum divergence followed by plant height (0.595) and leaves/plant (0.165) in vector 'I' while in vector 'II' plant height (0.644) followed by seed yield/plant (0.375), test weight (0.253) and leaves/plant (0.207) contributed maximum towards divergence. Out of total diversity of uncor-

related 'Y' variate, 91 percent was accounted by first three canonical roots and of these 87 percent was contributed by first two vectors indicating that the differentiation for the traits was nearly completed in 3 phases (Table 1).

Table 1. Canonical vectors for different characters in coriander

Characters	Canonical vectors		
	I	II	III
Days to flower	0.033	0.105	0.375
Plant height	0.596	0.644	-0.309
Branches / plant	-0.087	-0.047	0.153
Leaves / plant	0.167	0.207	-0.115
Internodal distance	0.742	-0.557	0.227
Umbels / plant	0.116	-0.104	0.217
Seeds / plant	-0.185	0.024	0.122
Test weight	-0.076	0.253	0.201
Seed yield / plant	0.064	0.376	0.755
Percentage variation	59.80	24.60	9.08

Table 2. Grouping of germplasm lines in different clusters with their cluster composition in Coriander

Clusters	Varieties included	Name of varieties in each cluster
I	6	COR-12 (2), DH-52 (6), COR-14 (13), COR-8 (31), DH-1 (61), DH-30 (69)
II	5	GCO-327 (1), DH-84 (3), COR-18 (30), Pant Haritima (43), DH-13b (51)
III	4	COR-7 (7), COR-4 (40), DH-7 (52), Dh-48 (51)
IV	2	DH-38 (67), DH-33 (68)
V	10	COR-11 (12), DH-36 (44), COR-9 (46), R.Swati (49), DH-19M-11 (50), CH-695 (53), DH-2 (62), DH-4 (64), GC-30 (70)
VI	11	DH-19M-13 (9), COR-13 (16), DH-57 (22), DH-49 (23), RCR-41 (25), DH-19M-7 (27), UD-686 (29), PH-M-9 (42), DH-38 (48), DH-9 (65), DH-8 (66)
VII	4	DH-58 (8), COR-7 (11), DH-13 (20), UD-684 (39)
VIII	10	DH-53 (8), DH-54 (5), COR-17 (10), COR-6 (14), COR-7 (15), DH-19 (17), DH-27 (26), PH-M-4 (41), UP-447 (58), DH-28 (59)
IX	18	RD-120 (18), UD-685 (19), UD-2 (21), COR-3 (24) CS-335 (28), RD-23 (32), COR-2 (33) DH-19M-2 (34), DH-6 (35), COR-5 (36), DH-50 (37), UD-446 (38), DH-13 (45), PH-M-5 (47), UDH-435 (54), DH-19 (55), COR-10 (60), DH-40 (63).

Values in parentheses denote the serial number of accessions

On the basis of genetic constitution and components uniformity all the seventy genotypes of coriander were grouped in nine clusters (Table 2). The cluster 'IX' was very unique containing 18 genotypes followed by cluster 'VI' (11 genotypes) and clusters 'VIII' and V each having 10 genotypes. This indicates

that among 70 germplasm lines, majority of genotypes (49/70) were grouped in 4 clusters and apparent diversity was noticed only in 21 genotypes which diverged in 5 clusters. Clustering pattern was also confirmed by canonical analysis. The random distribution of cultivars was evident from different clusters. Grouping pattern did not show any relationship between genetic divergence and geographical diversity which has always been the point of discussion (SINGH, 1991; SINGH *et al.*, 2003b). Genetic drift and selection in different environments could cause greater genetic divergence than geographical distance.

Table 3. Intra and inter cluster distance ( $D^2$ ) in coriander

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	26.75	52.35	49.40	96.20	44.04	77.82	87.15	73.80	49.80
II		22.27	40.01	75.41	32.41	48.89	55.04	37.68	44.59
III			17.85	91.13	45.21	79.79	70.75	65.97	59.90
IV				19.68	66.90	74.90	74.48	59.85	69.45
V					13.80	53.85	63.21	43.25	29.15
VI						24.70	57.09	39.55	63.02
VII							28.25	51.45	69.05
VIII								24.02	35.10
IX									17.40

The intra- cluster  $D^2$  values ranged from 13.80 to 28.02, the maximum was in cluster VII followed by I (26.75), II (25.27), VI (24.70) and VIII (24.04). The inter cluster distance ranged from 29.15 to 96.20 (Table 3, Fig. 1). The maximum inter cluster distance was noticed between cluster 'I' X 'IV' (96.20) followed by 'III' X 'IV' (91.13) and 'I' X 'VII' (87.15) suggesting wide diversity between these groups. Hence inter-mating between cultivars included in these clusters may give high heterotic response and thereby better segregants. However, low inter cluster distance noticed between 'V' X 'IX' (29.15), 'II' X 'V' (32.41), 'VIII' X 'IX' (35.10) and 'II' X 'VIII' (37.68) indicates that genotypes involved in these clusters have low genetic diversity. Intensive selection for agronomically important characters and similarity in parentage might be cause of narrow genetic diversity and uniformity between these clusters (SINGH *et al.*, 2003b).

The cluster mean of all the characters is presented in Table 4. The clusters II, V, and IX are very close to each other due to their low inter- cluster distances. The cluster 'I' in general had low mean values for plant height (93.78 cm), branches/plant (8.22), leaves/plant (10.36) and umbels/plant (24.80), which separated this cluster from, rests of the clusters. The genotypes of cluster 'VI' (8, 11, 20 39) which had highest intra- cluster distance was separated from other clusters due to earliest flowering ( $65.05 \pm 1.30$ ), maximum leaves/plant ( $12.83 \pm 0.55$ ), umbels/plant ( $35.12 \pm 2.26$ ), seeds/umbel ( $35.33 \pm 2.24$ ) and next highest plant height ( $132.42 \pm 5.33$ ). This cluster also showed moderately high inter- cluster distance with all the clusters. Contrary to this, cluster 'V' which had lowest intra-cluster



distance, also exhibited low mean values of all the characters. The cluster 'VI' was very unique in comparison to all the characters having 11 genotypes with maximum seed yield/plant ( $32.03 \pm 1.58$ ), test weight ( $8.49 \pm 0.12$ ), late flowering ( $77.64 \pm 0.75$ ) and next to highest umbels/plant ( $32.71 \pm 1.17$ ) and branches/plant ( $12.03 \pm 0.43$ ). This cluster had moderately intra-cluster distance and also inter-clusters distance with other clusters. Similarly, the clusters 'IV' and 'VIII' were separated with each other and both with other clusters due to containing genotypes of tallest plant height ( $188.8 \pm 1.78$ ) in 'IV' and maximum branches/plant ( $12.13 \pm 0.19$ ) and leaves/plant ( $13.07 \pm 0.34$ ) in cluster 'VIII' respectively. Both these clusters had also moderately high yielding genotypes. The genotypes of above clusters (IV, VI, and VII) may be used in heterosis breeding and selection program to optimize the seed yield. In genetic improvement following conventional breeding program the choice of more correlated component traits should be taken into consideration for selecting genetically diverse parents. Component breeding among selected genotypes based on multivariate analysis would be advantageous in developing ideal plant types in coriander. On the basis cluster means of all the characters genotypes were categorized in 4 groups. i) Early flowering and poor yielder (I, IX), ii) early flowering and medium yielder (VII), iii) medium to late flowering and poor yielder (III, V) and iv) late flowering and high yielder (II, IV, VI, VIII).

In present study though highest inter cluster distance could be registered between cluster I and IV, I and VII, III and IV, III and VI and III and VII, the superior derivatives could not be expected from their crosses due to low mean performance of clusters I and III. However, genotypes of cluster VI can be utilized as donor parent for improving yield due to its high mean performance for seed yield/plant and most of the yield contributing characters with good amount of genetic divergence. Further moderately high inter cluster distance between IV and VI and IV and VII with high mean performance of one or more component characters contributing towards seed yield suggests that some sampled crosses between these clusters may be attempted to select the recombinants for high seed yield.

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**GENETIČKA DIVERGENTNOST I IMPLIKACIJE I OPLEMENJIVANJE  
NA DOBIJANJE ŽELJENE BILJKE KORIJANDERA (*CORIANDRUM  
SATIVUM* L.)**S.P. SINGH, R.S. KATIYAR, S.K. RAI, S.M. TRIPATHI<sup>1</sup> i J. SRIVASTAVA<sup>1</sup>

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## Izvod

Vršena su ispitivanja sedamnaest linija germplazme koriandera (*Coriandrum sativum* L.) različitog ekogeografskog porekla u cilju određivanja genetičke divergentnosti praćenjem analizom multivarijanse i konikalne analize prinosa semena i devet komponenata te osobine. Sedamdeset genotipova, su grupisani u devet klastera, analizom genetičke arhitekture genotipova i osobina uniformnosti što je potvrđeno konikalnom analizom. Sedamnaest procenata ukupno ispitivanih genotipova (49 od 70) su se grupisali u četiri klastera (V, VI, VIII i IX), dok je uočena vidljiva razlika za 30 procenata genotipova (21 od 70) koji su se grupisali u 5 klastera (I, II, III, IV i VII). Maksimalna inter-klaster distanca je bila između klastera I i IV (96.20), zatim III i IV (91.13) i I i VII (87.15). Klaster VI je unikatan i uključuje genotipove visokih srednjih vrednosti za većinu komponenata prinosa. Klaster VII ima najviše semena po cvasti ( $35.3 \pm 2.24$ ), listova po biljci ( $12.93 \pm 0.55$ ), ranije cvetanje ( $65.05 \pm 1.30$ ) i umereno visoku srednju vrednost za druge karakteristike. Polazeći od visoke srednje vrednosti i inter distance klastera diskutovan je program oplemenjivanja na selekciju poželjnih tipova biljke.

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