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GENETIC DIVERSITY ANALYSIS OF CORIANDER (*CORIANDRUM SATIVUM* L.) GENOTYPES FOR SEED YIELD AND ITS ATTRIBUTING CHARACTERS

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ABSTRACT

The objective of the current study was to examine genetic differences in coriander (*Coriandrum sativum* L.) seed yield and its associated characteristics among forty genotypes. At the C.P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, the field experiment was conducted during the *rabi* season. Three replications of a randomized block design were used to assess all coriander genotypes. Forty genotypes tested for seed yield were grouped into eight clusters by the genetic divergence as determined by the Mahalanobis D^2 statistic. Clusters II and VIII were found to have the greatest inter cluster distance, followed by clusters II and V. The traits, including seed yield per plant, test weight, harvest index, number of seeds per umbellate, volatile oil, days to flowering and number of branches per plant, would be useful for producing transgressive segregants if commercially feasible as these seven traits contributed the most to total genetic divergence.
Keywords: Coriander, genetic divergence, Mahalanobis D^2 statistic

Introduction

The annual spice herb coriander (*Coriandrum sativum* L.) is a diploid, having chromosome number 2n=22 Ameta *et al.* (2016) Coriander is a cross pollinated crop belongs to Apiaceae family. According to Awas *et al.* (2015), it is a native of the Mediterranean and Western Asian regions. The unripe fruits smell of bed bugs and thus character is responsible for determination of the name coriander from the Greek world "*Koris*" meaning bed bug (Sandhu *et al.* (2018). The spice coriander is a key component of the seed spice family. India, Morocco, Romania, France, Spain, Italy, Holland, Myanmar, Pakistan, Turkey, Mexico, and Argentina are some of the nations that grow coriander. India is the largest producer, consumer, and exporter of coriander in the world. In the Indian states of Madhya Pradesh, Rajasthan, Gujarat, Tamil Nadu, Karnataka, Orissa, and Haryana, coriander is grown. The crop grows in tropics and requires a cool but comparatively dry frost-free climate, particularly at flowering and seed formation stages (Nagappa *et. al.* (2018). Coriander is grown mostly in Rajasthan and Gujarat, which have become known as the "Seed Spices Bowl" and contribute 80% of the country's coriander production. According to strain, the oil content of the seed's ranges from 8.8 to 19%, with an average of 18%. The percentage of essential oils in seeds ranges from 0.3-2.06 percent. Dry, mature coriander seeds contain 6.3–8.0% moisture, 11.5-21.3% crude protein, 17.8–19.15% crude fat, 28.4–29.1% crude fiber, and 4.9–6.0% ash. The quantity of genetic variety found in the experimental material is the fundamental criterion for a successful breeding effort. D^2 statistics, which are based on measurements of morphological characteristics, are frequently employed by plant breeders as a technique to evaluate genetic divergence (Mahalonobis, 1936; Rao, 1952). For an appropriate approach to increase yield, the capacity of a plant to yield is its most important feature. The relationship

between the various yield components should require precise data.

Material and Methods

Forty genotypes were used in the coriander experiment to examine genetic diversity. Using a randomized block design (RBD), the experiment was set up with three replications. The experiment was place during *rabi* season at the agronomy instructional farm of the Sardarkrushinagar Dantiwada Agricultural University, Dantiwada (Gujarat).

The Seed Spices Research Station, SDAU, Jagudhan (Gujarat) provided the experimental materials. All genotypes were spaced 45 cm apart from one another in rows and 10 cm apart from one another in plants. From each row in each replication, five competitive plants were chosen at random. Phenotypic data were recorded for twelve characters, including days to flowering, days to maturity, plant height, number of branches per plant, number of seeds per umbellate, number of umbellates per umbel, number of umbels per plant, test weight, harvest index, biological yield per plant, volatile oil, and seed yield per plant. Data was analysed for different parameters by method suggested by Mahalanobis, 1936 and first suggested by Rao, 1912 for the assessment of genetic diversity in plant breeding.

Results and Discussion

All the accessions were grouped into 8 clusters according Tocher method Rao, 1952. Cluster I contained maximum number of genotypes (25 genotypes) followed by cluster II (6 genotypes), cluster III (4 genotypes) and rest of the clusters *i.e.* cluster IV, V, VI, VII, VIII there was only one genotype in each cluster (Table 1). The distribution pattern revealed that genotypes from different geographic regions were grouped in same cluster. Similarly, the genotypes from same geographic regions were scattered in different clusters.

In all the combinations, each character was ranked on the basis of di values. The analysis on contribution of individual character toward the expression of genetic divergence present in Table 2, indicated that among the traits studied, seed yield per plant contributed maximum divergence (27.56%) followed by test weight (18.85%), harvest index (12.44%), number of seeds per umbellate (8.85%), volatile oil (8.33%), days to flowering (7.31%), number of branches per plant (7.18%), days to maturity (3.84%), number of umbels per plant (2.31%), biological yield per plant (1.28), number of umbellates per umbel (1.15) and plant height (0.90%), similar results found by Singh *et al*.(2018), Mengesha *et al.* (2011) and Singh *et al*. (2002).

Based on D^2 values, forty genotypes of various geographical origins were grouped into eight clusters. Maximum diversity was observed due to these characters *viz.* seed yield per plant, test weight, harvest index, number of seeds per umbellate, volatile oil, days to flowering, and number of branches per plant. Genotypes of cluster II showed the maximum genetic diversity between the genotypes of cluster V and cluster VIII. Based upon these studies, crosses may attempt between the genotypes of cluster II and cluster VIII followed by cluster II and cluster V (Table 3), similar results found by Mengesha *et al.* (2011), Gauhar *et al.* (2018) and Natwaria *et al.* (2020).

Cluster II showed the maximum mean value for volatile oil, cluster III showed maximum mean value for plant height and test weight, cluster V showed maximum mean value for days to flowering and number of branches per plant, cluster VI showed maximum mean value for number of umbellates per umbel, umbels per plant and seed yield per plant, cluster VII showed maximum mean value for days to maturity and harvest index and cluster VIII showed maximum mean value for number of seeds per umbellates and biological yield per plant (Table 4), similar result found for higher cluster mean value for days to maturity by Awas *et al*. (2015) and for lowest cluster mean value for plant height by Mengesha *et al.* (2011).

The result revealed wide genetic divergence and substantial genetic diversity in the experimental material for majority of the characters. Bhandari and Gupta (1993), Patel *et al.* (2000), Singh *et al.* (2005), Mengesha *et al*. (2011), Awas *et al*. (2016), Singh *et al.* (2018), Gauhar *et al.* (2018) and Natwaria *et al.* (2020) also found significant genetic diversity in this crop. The comparison of clusters III, V, VI and VIII had better cluster means for most of the characters therefore, these clusters might be considered better for selecting genotypes. Thus, the genotypes of these cluster may be selected for hybridization for generating genetic variability.

Conclusion

Based on D^2 values, forty genotypes of various geographical origins were grouped into eight clusters. Maximum diversity was observed due to these characters viz. seed yield per plant, test weight, harvest index, number of seeds per umbellate, volatile oil, days to flowering, and number of branches per plant. Genotypes of cluster II showed the maximum genetic diversity between the genotypes of cluster V and

cluster VIII. Based upon these studies, crosses may attempt between the genotypes of cluster II and cluster VIII followed by cluster II and cluster V. The comparison of clusters III, V, VI and VIII had better cluster means for most of the characters therefore, these clusters might be considered better for selecting genotypes. Thus, the genotypes of these cluster may be selected for hybridization for generating genetic variability.

Table 1: Distribution of genotypes evaluated for seed yield into different clusters of coriander

Cluster	Number of genotypes	Name of genotypes
I	25	Lam 6, Lam 73, JCr-375, JCr-398, JCr 2013-1, JCr 2013-7, JCr 16-03, JCr-403, COR 183, UD-357, JCr-360, JCr-340, JCr-383, JCr-402, JCr 16-01, JCr 16-09, COR 181, COR 182, JCr-390, JCr 2013-2, JCr 2013-24, Lam-16, JCr-394, JCr 2013-4, G Cor 1
II	6	JCr-329, JCr-372, JCr-330, Lam 43, Lam 5, JCr 2013-3
III	4	G Cor 3, G Cor 2, COR 192, COR 180
IV	1	JCr-401,
V	1	JCr-399,
VI	1	Dhana-98,
VII	1	JCr-327
VIII	1	JCr-395

Table 2: Contribution of various traits towards total genetic divergence

Sn. No.	Characters	Number of times ranked first	% Contribution towards divergence
1	Days to flowering	57	7.31
2	Days to maturity	30	3.85
3	Plant height	7	0.90
4	Number of branches per plant	56	7.18
5	Number of seeds per umbellate	69	8.85
6	Number of umbellates per umbel	9	1.15
7	Number of umbels per plant	18	2.31
8	Test weight	147	18.85
9	Harvest index	97	12.44
10	Biological yield per plant	10	1.28
11	Volatile oil	65	8.33
12	Seed yield per plant	215	27.56

Table 3 : Average intra and inter clusters D^2 value of 40 genotypes of coriander

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**10.44**	15.15	17.57	15.56	22.35	17.90	14.46	19.90
II		**12.43**	23.42	29.90	35.71	30.88	23.58	40.17
III			**15.39**	23.46	26.85	21.78	25.93	24.07
IV				**0.00**	7.80	19.41	8.35	11.86
V					**0.00**	29.46	25.78	17.00
VI						**0.00**	21.21	13.05
VII							**0.00**	22.86
VIII								**0.00**

Table 4: Cluster mean for 12 different characters in 40 genotypes of coriander

Cluster	DF	DM	PH	NBP	SPU	UPU	UPP	TW	HI	BY	VO	YP
I	58.80	113.87	81.20	5.61	7.76	6.75	17.45	11.61	46.02	14.18	0.45	6.42
II	59.39	115.61	86.27	5.68	6.88	6.04	18.08	11.89	48.45	13.40	0.55	6.40
III	59.17	114.25	94.53	6.16	8.88	6.93	19.67	13.18	49.09	14.85	0.38	7.33
IV	64.33	116.67	75.33	5.73	7.30	5.60	20.33	10.23	41.71	15.46	0.31	6.45
V	68.67	116.00	81.93	7.43	8.47	6.97	21.13	10.37	40.86	15.98	0.37	6.53
VI	53.67	104.00	72.13	5.63	8.20	7.83	22.93	12.66	52.11	15.41	0.34	8.03
VII	61.67	121.67	70.93	4.70	6.87	5.50	17.63	11.00	52.25	12.36	0.35	6.46
VIII	59.33	104.67	74.93	5.30	11.13	7.50	18.40	11.10	41.49	16.70	0.35	6.93

Whereas, DF= Days to flowering, DM= Days to maturity, PH= Plant height, NBP= Number of branches per plant, SPU= Number seeds per umbellate, UPU= Number of umbellates per umbel, UPP= Number of umbels per plant, TW= Test weight, BY= Biological yield per plant, HI= Harvest index, VO= Volatile oil and YP= Seed yield per plant

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