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Estimates of genetic diversity for morphological and yield contributing traits in coriander genotypes

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ABSTRACT

Genetic variability, divergence, correlation and path coefficient were estimated in twenty eight genotypes of coriander during *Rabi* 2014-15 and 2015-16. Highest genetic advance was observed for seed yield per plot followed by plant height. Highest heritability was estimated for number of primary branches followed by plant height. Genotypes were grouped into 12 clusters. Minimum inter-cluster D^2 value (2.57) was estimated between clusters II and V whereas, maximum inter-cluster D^2 value (9.54) was estimated between clusters III and VI. The seed yield was found significantly and positively correlated with plant height, test weight and seed yield per plot. Path coefficient analysis indicated the highest positive direct effect of number of umbels per plant on 5 plants seed yield followed by number of primary branches and test weight.

Keywords: *Coriandrum sativum*, variability, divergence, path coefficient.

INTRODUCTION

Coriander (*Coriandrum sativum* L.) is an annual herb in the family Apiaceae and is known to be originated in the Mediterranean region. It is a diploid cross pollinated crop and possess 2n=22 chromosomes with cross-pollination as mode of reproduction. It is grown for both green leaves and dried seeds. In India, it is grown on an about 3,457 thousand hectares area with 69,01,780 tonnes production and 2.0 tonnes per hectare productivity (Anonymous, 2). Coriander is a good melliferous plant and studies indicated that one hectare of coriander allows honey bees to collect about 500 kg of honey.

Discovery of genetic resources in line with the rapid development of genetics and its application in plant breeding stimulated widespread interest in the study of variability and improvements in different crop species. When initiating a breeding programme with any crop having genetic variation, it is important to gather information on the traits of agronomic importance in order to select and breed better varieties. The development of high yielding-cultivars is the main objective of any breeding program.

The extent of genetic diversity available in the crop decides the success of any crop improvement program with manifested objectives. To make the crossing programme effective, parents should belong to different genetic cluster. The more distant the parents with in over all limits of fitness are the greater the chances of obtaining higher amount of heterotic expression in F_1 and broad spectrum of variability in segregating populations.

Correlation and path analysis have been used in breeding studies in different aromatic plants (Gurubuz, 6). The exact picture of the relative importance of direct and indirect influences of the component characters towards seed yield is determined by path analysis (Bhatt, 4).

MATERIALS AND METHODS

The present study was carried out to assess the variability, divergence, correlation and path coefficient in 28 genotypes of coriander. The genotypes under study were grown in Randomised Block Design (RBD) with three replications at the research farm of ICAR-NRCSS, Ajmer (Rajasthan) during *Rabi* 2014-15 and 2015-16. The study location is lying between 74˚ 35'39” to 74˚ 36' 01”E longitude and 26˚ 22'12” to 26˚ 22' 31” N latitude with an altitude of 486 MSL. The soil of the site was sandy loam in texture, poor in fertility and water holding capacity, having pH 8.0 to 8.3, EC 0.07 to 0.12 and 0.15 to 0.23% organic carbon, available N 178.5 kg/ha (low) and P_2O_5 12 kg/ha (medium), K_2O 5 kg/ha (low). Climate of the Ajmer area characterized as semi-arid. All the recommended package of practices were followed to raise a good crop. Observations were recorded on five randomly selected plants from each plot per replications for plant height, number of primary branches, number of secondary branches, number of umbels per plant, number of umbellates per umbel, number of seeds per umbellate and 5 plants seed yield while for test weight and seed yield per plot, the data recorded on whole plot basis. Analysis of variance was done by the method suggested by Panse and Sukhatme (11).

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All the genotypes used were clustered into different groups based on D^2 statistics following Tocher's Methods and used Windostate software. Mean data from each of the replications were used to estimate phenotypic and genotypic coefficients of variations heritability (broad sense) and genetic advance were determine by following the methodology of Johnson *et al.* (8). The phenotypic and genotypic correlation coefficients were calculated as per the methods. The path coefficients were obtained by following the method of Dewey and Lu (5) and data analysis was done with the help of Windostate software.

RESULTS AND DISCUSSION

Analysis of variance was estimated and found significant for all characters studied indicating presence of significant variability in the material. Range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance and genetic advance as % of mean is given in Table 1. The range of variation was high for seed yield/plot (1348.33-2448.67) followed by plant height (101.00-136.60) and 5 plants seed yield (16.93-14.17. Phenotypic coefficient of variability (PCV) values ranged from 8.94% for the plant height to 28.02% for the 5 plants seed yield, whereas the genotypic coefficient of variability (GCV) ranged from 8.38% for plant height to 24.89% for 5 plants seed yield (Table 1). PCV and GCV values roughly more than 20% are regarded as high, whereas, values less than 10% are considered to be low and values between 10 and 20% to be medium. Based on this delineation, PCV value was low for plant height; medium for number of primary branches, number of secondary branches, number of umbel/plant, and seed yield/plot; high for number of umbellates/umbel, number of seeds/umbellate, test weight and 5 plants seed yield. Similar variation among the genotypes of coriander were reported by earlier workers (Ali *et al.*, 1; Rajput and Singh, 12; Singh *et al.*, 15)

Estimates of heritability in broad sense ranged from 45% for test weight to 88% for number of primary branches. According to Singh *et.al.* (16), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. Although, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical. Considering this benchmark, heritability estimate was high (>80%) for plant height, number of primary branches, number of secondary branches, number of seeds/umbellate and seed yield/plot. It was moderate (45 to 78.9%) for the remaining quantitative characters (Table 1).

In the present investigation, expected genetic advance was recorded maximum with seed yield/plot followed by plant height and 5 plants seed yield whereas, expected genetic advance expressed as percentage of mean was high for number of seeds/umbellate followed by 5 plants seed yield and number of umbellates/umbel (Table 1). 5 plants seed yield and seed yield/plot can be improved by selection, as these characters exhibited moderate genotypic and phenotypic coefficient of variations along with both medium to high heritability and genetic advance. These results are similar with the results obtained by earlier workers (Singh *et al*., 17).

The D^2 value ranged from 3.18 (between Cor-122 and Cor-129) to 123.28 (between Cor-141 and ACr-1). The multivariate analysis based on D^2 values among 28 genotypes revealed that all genotypes can be grouped into 12 clusters. Among these, cluster-I consisted of 8 genotypes, cluster-III consisted of 9 genotypes, cluster-XII consisted of 2 genotypes and remaining all clusters (II, IV, V, VI, VII, VIII, IX, × and XI) were consisted of single genotype (Table 3).

The inter-cluster distances were greater than intra-cluster distances, revealing considerable amount

Table 1. Range, mean, genotypic and phenotypic coefficient of variation (GCV&PCV), heritability and genetic advance.

Character	Range	Mean	GCV	PCV	Heritability (%)	Genetic advance (%)
Plant height (cm)	101.0 - 136.6	116.1	8.3	8.9	87.7	16.16
No. of primary branches	4.3 - 8.0	6.5	15.2	16.2	88	29.50
No. of secondary branches	6.8 - 13.6	10.8	14.1	15.5	83.3	26.59
No. of umbel/ Plant	14.9 - 25.2	19.6	15.4	17.4	78.2	28.12
No. of umbellates/umbel	4.4 - 8.6	6.3	18.2	21.8	69.4	31.24
No. of seeds/umbellate	4.2 - 10.2	7.4	24.7	26.5	87	47.52
Test weight (g)	11.4 - 20.2	15.2	13.9	20.8	45	19.33
5 plant's seed yield (g)	16.9 - 41.1	26.9	24.8	28.0	78.9	45.55
Seed yield/plot (g)	1348.3 - 2448.6	1980.7	14.6	15.8	86.3	28.11

Table 3. Inter and intra cluster distance between clusters.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	3.36	3.85	6.64	5.96	3.93	4.39	4.26	4.32	4.88	5.31	4.72	5.21
II		0.00	7.46	7.77	2.57	4.51	2.93	5.52	4.86	7.31	4.25	5.68
III			0.00	4.40	6.20	9.54	7.74	6.05	9.53	4.96	5.72	6.25
IV				0.00	6.10	8.08	8.31	4.76	8.87	3.71	6.30	4.91
V					0.00	5.12	4.26	5.35	6.37	6.49	3.63	4.43
VI						0.0	5.03	6.08	4.21	7.93	6.22	6.24
VII							0.00	6.57	5.39	7.36	3.60	6.67
VIII								0.00	4.92	4.49	6.18	4.12
IX									0.00	7.92	7.18	6.56
X										0.00	6.57	6.27
XI											0.00	5.20
XII												3.79

of genetic diversity among the genotypes. The intra-cluster distance is lower than the inter-cluster distances, which suggested heterogeneous and homogenous nature between and within groups, respectively. Cluster XII showed maximum intra-cluster distance. Intra-cluster distance is the main criterion for selection of genotypes using D^2 analysis. Inter-cluster distance varied from 2.57 to 9.54. Minimum inter-cluster D^2 value was observed between clusters II and V (2.57) indicating the close relationship among the genotypes included in these clusters (Table 4). Maximum inter-cluster value was observed between clusters III and VI (9.54) indicating maximum divergence between the genotypes of these clusters. The inter-cluster D^2 values were also higher between the clusters III and VI (9.54), clusters III and IX (9.53), clusters IV and IX (8.87) and clusters IV and VII (8.31). Hence, it is suggested that inter-mating between the genotypes included in these diverse clusters may give high heterotic response and thus better segregants. The intra-cluster distance in this study is similar tointra-cluster distance (2.81 to 5.59) recorded by Mengesha *et al.* (10), but relatively lower than the values between 13.8 and 28.25 reported by Singh *et al.* (17). The contribution of individual character to the divergence was worked out in terms of number of times it appeared first. Plant height contributed maximum towards genetic divergence, followed by number of primary branches, number of seeds per umbellates, seed yield per plot and 5 plants' seed yield.

A comparison of the mean value of thirteen characters of different clusters has been presented in Table 4. Considerable differences in cluster mean values were evident for all the characters. Cluster means for different characters revealed that genotypes included in cluster × showed maximum number of seeds per umbellates and seed yield per plot (Table 4). Genotypes in cluster III had maximum number of umbels per plant and test weight. Genotypes in cluster IV had maximum number of primary branches and number of secondary branches. Genotypes in clusters V, VIII and XI had the highest plant height, number of umbellates per umbel and 5 plants seed yield, respectively. It can, therefore, be concluded from the present study that hybridization among genotypes of these cluster combinations is expected to enhanced variability in fenugreek for the targeted traits.

The seed yield showed positive and significant correlations with plant height and test weight at both genotypic and phenotypic levels whereas showed positive and significant correlation with seed yield/plot at genotypic level (Table 2). The results obtained in present study were in agreement with the findings of Gurbuz, 6; Sanker and Khader, 14; Singh *et al.* 17. Plant height showed positive and significant correlations with number of primary branches, number of secondary branches, number of umbels per plant, test weight and seed yield/plot at both genotypic and phenotypic levels whereas showed positive and significant correlation with number of umbellates per umbel and number of seeds per umbel at genotypic level. These findings are in agreement with Bhandari and Gupta (3). Number of primary branches showed positive and significant correlation with plant height, number of secondary branches, number of umbels per plant, number of umbellates per umbel and number of seeds per umbel. Number of secondary branches showed positive and significant correlation with number of primary branches, plant height, number of umbels per plant, number of umbellates per umbel, number of

Table 2. Genotypic and phenotypic correlation coefficient among 9 characters in coriander.

Character	Reg.	Plant height	No. of primary branches	No. of secondary branches	No. of umbels/ plant	No. of umbellates/ umbel	No. of seeds/ umbellate	Test weight	Seed yield/ plot	5 plants seed yield
Plant height	r_g	**1.00**	0.48**	0.48**	0.45**	0.40*	0.33*	0.95**	0.44**	0.64**
	r_p	**1.00**	0.41*	0.42*	0.36*	0.28	0.29	0.61**	0.40*	0.57**
No. of primary branches	r_g		1.00	0.83**	0.64**	0.68**	0.65**	0.48**	0.50**	0.12
	r_p		**1.00**	0.72**	0.51**	0.50**	0.55**	0.24	0.41*	0.09
No. of secondary branches	r_g			**1.00**	0.63**	0.48**	0.45**	0.52**	0.57**	0.05
	r_p			**1.00**	0.54**	0.37*	0.39*	0.39*	0.50**	0.07
No. of umbels/ plant	r_g				1.00	0.90**	0.75**	0.42*	0.73**	0.16
	r_p				**1.00**	0.74**	0.64**	0.31	0.63**	0.15
No. of umbellates/ umbel	r_g					**1.00**	0.86**	0.41*	0.66**	0.05
	r_p					**1.00**	0.66**	0.24	0.46**	0.05
No. of seeds / umbellate	r_g						**1.00**	0.29	0.66**	-0.06
	r_p						**1.00**	0.16	0.63**	-0.02
Test weight	r_g							1.00	0.48**	0.60**
	r_p							**1.00**	0.27	0.41*
Seed yield/plot	r_g								1.00	0.33*
	r_p								**1.00**	0.27

*and ** Significant at 5 and 1% levels; r g= genotypic correlation, r p= phenotypic correlation

Table 4. Cluster mean values for 9 characters in coriander germplasm.

Cluster No.	Plant height	No. of primary branches	No. of secondary branches	No. of umbels/ plant	No. of umbellates/ umbel	No. of seed/ umbellate	Test weight	5 plant's seed yield	Seed yield / plot
I	109.11	5.89	10.09	18.48	5.53	6.49	13.51	23.82	1935.92
II	120.93	5.00	9.60	17.00	5.87	4.53	16.60	29.27	1850.00
III	124.36	7.48	12.22	23.28	7.72	9.10	17.57	30.39	2266.82
IV	112.47	8.07	12.67	20.13	6.87	8.93	13.87	16.93	1923.33
V	126.40	5.93	11.33	16.13	4.93	5.13	16.83	25.60	1886.67
VI	101.00	5.47	10.13	14.93	4.40	4.20	13.17	20.97	1451.33
VII	115.20	5.53	9.87	17.47	5.13	5.20	12.67	40.77	1986.67
VIII	109.67	6.07	8.53	19.40	7.93	8.67	13.70	18.53	1718.67
IX	103.00	4.33	6.87	18.73	5.93	7.00	13.93	26.03	1585.00
X	104.53	7.07	11.00	18.40	6.87	10.27	12.10	19.10	2356.67
XI	120.73	7.20	11.33	17.67	5.33	5.27	17.13	41.17	1800.00
XII	123.03	6.77	10.60	16.50	5.67	7.77	15.62	25.60	1507.50

seeds per umbel and seed yield/plot. These findings are similar with Meena *et al.,* 9 and Sanker and Khader, 14. Number of umbels per plant showed positive and significant correlations with plant height, number of primary branches, number of secondary branches, number of umbellates per umbel, number of seeds per umbel and seed yield/plot at both genotypic and phenotypic levels. Similar findings were also noted by Singh *et al.,*17 and Vedamuthu 18. Number of seeds per umbel showed positive and significant correlations with plant height, number of primary branches, number of secondary branches, number of umbels per plant, number of umbellates per umbel and seed yield/plot. Test weight showed positive and significant correlation with plant height, number of primary branches, number of secondary branches, number of umbels per plant, number of umbellates per umbel and seed yield/plot. Similar result also reported by Sanjeev *et al.* (13).

The result of the present investigation on path coefficient analysis as presented in Table 4 revealed that number of umbels per plant (1.981) had highest direct effect on 5 plants seed yield followed by number of primary branches per plant (1.758) and test weight (1.30). These indicate that seed yield could be improved by making selection on the basis these characters. These findings are in agreement with that Jain *et al.*, (7) for number of umbel per plant. It was concluded from the study that, highest heritability was estimated for number of primary branches, this shows these character goes to parents to progeny, which is highly heritable. Genotypes were grouped into 12 diverse clusters, it means among the genotypes, a wide genetic variability was existed. The seed yield was found significantly and positively correlated with plant height, test weight and seed yield per plot. It shows, these characters should be given more emphasized for improvement in coriander.

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