The Pharma Innovation Journal 2017; 6(8): 40-46

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating 2017: 5.03
TPI 2017; 6(8): 40-46

www.thepharmajournal.com
Received: 29-06-2017
Accepted: 30-07-2017

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Genetic diversity and heritability analysis in coriander

Ranjeet Singh Dhakad, SK Sengupta, Narayan Lal and Govind Shiurkar

Abstract
The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for plant height at 60 DAS (26.3-72.75cm) followed by plant height at 90 DAS (82.99-162.75cm), seed yield per hectare (3.61-22.49q), number of leaves per plant at 90 DAS (22.2-53.07), days to first flowering (45.67-67.00), days to 50% flowering (57.00-76.00), number of umbel per plant (17.2-37.00), number of primary branches per plant (4.8-10.40), plant height at 30 DAS (4.49-11.27cm), number of leaves per plant at 30 DAS (5.33-13.27), number of seeds per umbel (17.6-32.6), number of secondary branches per plant (8.13-15.47), number of leaves per plant at 60 DAS (10.07-19.33), days to germination (11.33-19.33), test weight (10.23-17.13g), number of umbellets per umbel (5.00-8.73) and days to maturity (103-118). While it was low for while number of seeds per plot (0.21-1.35kg) and seed yield per plant (5.13-9.53g) was found to be lowest. The values of heritability in broad sense was found to be estimates were observed very high for Plant height (cm) at 90DAS, followed by Plant height (cm) at 60DAS, Plant height (cm) at 30DAS. Genetic advance as percentage of mean ranged between 5.84% for Days to maturity to 58.38% for Seed yield/ ha (q). The highest estimate of genetic advance as percentage of mean was recorded for Seed yield/ ha (q), Seed yield/ plot (kg), No. of leaves / plant at 30DAS, No. of leaves / plant at 90DAS, plant height at 60DAS and plant height at 90DAS. In the present findings phenotypic coefficient of variations were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however, the differences were narrow which implied their relative resistance to environmental variation.

Keywords: Genotypes, Variability, Heritability, Genetic advances, Phenotypic

1. Introduction
India is well known as "land of spices" across the world since long back. The seed spices have emerged as one of the important group of spice crop of our country. India is the largest producer, consumer and exporter of seed spices in the world. Coriander plays a major role in the group of seed spices. Coriander *(Coriandrum sativum* L.) also called cilantro or dhania is an annual herb, belong to the family Apiaceae, and is a native of Mediterranean region. The genus *Coriandrum* comprised of two species. Among them, C. *sativum* is cultivated. The basic chromosome number of this genus is x=11 and *Coriandrum sativum* is diploid with 2n=22.Coriander is an aromatic member of the Apiaceae with a wide diversity (Diederichsen, 1996)[8]. Three subspecies and 10 botanical varieties of coriander been proposed at the intra specific level (Diederichsen and Hammer, 2003) [7] based on phenotypic character. However; molecular evidence does not support classification based on phenotypic and/or biochemical characteristics (Lopez, 2006) [13]. In India, coriander is cultivated in the state of Madhya Pradesh, Rajasthan, Gujarat and Tamil Nadu. The productivity of this crop is very low. In India, it occupies an area of 516.00 MH with a production of 496.00 MT with an average productivity of 0.7 million tones/ha. The crop is also cultivated in Tamil Nadu, Karnataka, Orissa and Haryana**.** Madhya Pradesh is the producing coriander Area 160.00 MH, production 75.00 MT and productivity 0.47 T/h of coriander (Anonymous, 2015) [2]. However, the crop is also cultivated in considerable acreage in Kymore plateau &satpura hills region of Madhya Pradesh. The cultivation of local varieties, are very low yielder and susceptible to diseases and pest. This crop is exported to other countries like Malaysia, Singapore, USA, Australia and Europe etc. It alarms for breeding of improved high yielding varieties of coriander through systematic breeding programmes.
Genetic variability is a prerequisite for any improvement in a crop. The success of any crop improvement programme depends on the magnitude of genetic variability and extent to which the desirable characters are heritable. The ultimate goal of breeding programme aims to improve the characteristic of plants so that they become more desirable. The survey of genetic variability with the help of suitable genetic parameters like genotypic and phenotypic

coefficients of variations, heritability estimates and genetic advance as percentage of mean are indispensable in breeding programmes aimed at improvement of seed yield. The heritability measures the contribution of genetic variability to the total variability i.e. phenotypic variability observed for any quantitative trait The estimated heritability can be utilized for the estimation of genetic gain expected for the selection of top 5 percent individuals; such studied enable the breeders to have a maximum selection response of the variance exhibited by the population which is largely due to additive genetic effects. Seed yield being a complex polygenic trait composed of several components some of which affect yield directly while; others were contributing towards it indirectly. The knowledge of the magnitude and direction of inter-relationship between yield and its component characters has great importance in breeding programmes for the selection of desirable types, when correlation studies involve, many characters then it becomes difficult to determine the importance of each of the factors.

2. Material and Methods

The present investigation was conducted at Vegetable Research Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during the year 2015-16. Jabalpur is situated in "Kymore Plateau and Satpura Hills" agro climatic region of M.P. It falls on 23.9° N latitude and 79.58°E longitudes with an altitude of 411.8 m above the mean sea level. Jabalpur is situated in the semi-arid region having sub-tropical climate with hot dry summer, and cold winter. The maximum and minimum temperature ranges between 34.5°C and 4.2°C. The average annual relative humidity is 85%. The experiment was laid out in randomized block design with three replications and thirty different genotypes were selected.

2.1 Treatment detail

Table 1: The following thirty genotypes of coriander were included in trial

Treatments	Genotypes	Source
T1	COR 95	IISR, Marikunnu, Kerala
T2	COR 96	IISR, Marikunnu, Kerala
T3	COR 97	IISR, Marikunnu, Kerala
T4	COR 98	IISR, Marikunnu, Kerala
T5	COR 99	IISR, Marikunnu, Kerala
T6	COR 100	IISR, Marikunnu,Kerala
T7	COR 101	IISR, Marikunnu, Kerala
T8	COR 102	IISR, Marikunnu, Kerala
T9	COR 103	IISR, Marikunnu, Kerala
T10	COR 104	IISR, Marikunnu, Kerala
T11	COR 105	IISR, Marikunnu, Kerala
T12	COR 106	IISR, Marikunnu, Kerala
T13	COR 107	IISR, Marikunnu, Kerala
T14	COR 108	IISR, Marikunnu, Kerala
T15	COR 109	IISR, Marikunnu, Kerala
T16	COR 110	IISR, Marikunnu, Kerala
T17	COR 111	IISR, Marikunnu, Kerala
T18	COR 112	IISR, Marikunnu, Kerala
T19	COR 113	IISR, Marikunnu, Kerala
T20	COR 114	IISR, Marikunnu, Kerala
T21	COR 115	IISR, Marikunnu, Kerala
T22	COR 116	IISR, Marikunnu, Kerala
T23	COR 117	IISR, Marikunnu, Kerala
T24	COR 118	IISR, Marikunnu, Kerala
T25	COR 119	IISR, Marikunnu, Kerala
T26	COR 120	IISR, Marikunnu, Kerala
T27	COR 121	IISR, Marikunnu, Kerala
T28	CIMPO S 33	Bangalore
T29	Local	Jabalpur
T30	RCr 728	IISR, Marikunnu, Kerala

2.2 Estimation of mean, components of variance, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean:

The mean of different characters were calculated by conventional method:- Mean $= \frac{\Sigma xi}{n}$

Where,

Σx_i = The sum of all the observations for i^{th} character.

N = Number of observations.

Range was recorded by observing the lowest and the highest mean values for each character.

The component of variance was calculated as follows:

S. No.	Source	M.S.S.	Expected M.S.S.
1.	Replications	-	-
2.	Genotypes	M_i	$\sigma^2_{e\,i} + r.\ \sigma^2_{g\,i}$
3.	Error	E_i	$\sigma^2_{e\,i}$

$$\sigma^2_{g\,i} = M_I - E_i$$

$$\sigma^2_{e\,i} = E_i$$

$$\sigma^2_{p\,i} = \sigma^2_{g\,i} + \sigma^2_{e\,i}$$

Where,

$\sigma^2_{g\,i}$ = Genotypic variance for i^{th} character.

$\sigma^2_{e\,i}$ = Environmental variance for i^{th} character.

$\sigma^2_{p\,i}$ = Phenotypic variance for i^{th} character.

Phenotypic and genotypic coefficient of variation (expressed in %) were calculated by using the formula given by Burton (1952) [5]. Genotypic coefficient of variation (GCV) was calculated as below:

Phenotypic $$GCV\ \% = \frac{\sqrt{\sigma^2 g_i}}{\overline{X}_i} X 100$$

coefficient of variation (PCV)

$$PCV\% = \frac{\sqrt{\sigma^2 P_i}}{\overline{X}_i} X 100$$

Where,

$\overline{X}_i$ = General mean of the i^{th}character under consideration.

$\sigma^2_{g\,i}$ and $\sigma^2_{p\,I}$ = Genotypic and phenotypic variances of the i^{th} character respectively.

2.3 Heritability and genetic advance

Heritability (broad sence) which is ratio of genotypic variance to the total phenotypic variance is symbolized as h^2 (BS) and expressed in percentage. Estimation of heritability was done as per the formula given by Hanson *et al*. (1956) [10].

$$h^2\ (BS) = \frac{\sigma^2_{g\,i}}{\sigma^2_{p\,i}} \times 100$$

Or

$$= \frac{\text{Genotypic varianceof the } i^{th}\text{character}}{\text{Phenotypic varianceof the } i^{th}\text{character}}$$

Expected genetic advance was calculated by using the method suggested by Johnson *et al.* (1955) [12] at 5% selection intensity.

Genetic advance (GA) = K. P_i. h^2_i

Genetic advance as percentage of mean wascalculated as follows:

$$\frac{\text{Genetic advance}}{\overline{X}}$$

Where,

K= Selection intensity its value at 5% selection level is 2.06.

P_i = Phenotypic standard deviation of the i^{th}character.

h^2_i = Broad sense heritability (fraction) of the i^{th}character.

$\overline{X}_i$ = General mean of the i^{th} character under consideration.

2.4 Correlation coefficients

Correlation coefficients were calculated in all possible combinations taking all the characters in to consideration at genotypic, phenotypic and environmental levels by using the formula as proposed by Miller *et al.* (1958) [16].

$$r = \frac{\sum xy - \frac{\sum x \sum y}{n}}{\sqrt{\left(\sum x^2 - \frac{(\sum x)^2}{n}\right)\left(\sum y^2 - \frac{(\sum y)^2}{n}\right)}}$$

Where,

R = Correlation coefficient

N = Number of treatments

X and Y = Character under study

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the above formula,

e.g.

$$rG(Xi\ Xj) = \frac{G\ Cov\ (Xi\ Xj)}{\sqrt{VG\ (Xi).\ VG\ (Xj)}}$$

$$rP(Xi\ Xj) = \frac{P\ Cov\ (Xi\ Xj)}{\sqrt{VP\ (Xi).\ VP\ (Xj)}}$$

Where,

VG (Xi) = Genotypic variance of character xi

VP (yi) = phenotypic variance of character yi

Results and Discussion

3.1 Genetic Variability

The mean performance of the genotypes (Table 2) revealed a wide range of variability for all the traits. The variation was highest for plant height at 60 DAS (26.3-72.75cm) followed by plant height at 90 DAS (82.99-162.75cm), seed yield per hectare (3.61-22.49q), number of leaves per plant at 90 DAS (22.2-53.07), days to first flowering (45.67-67.00), days to 50% flowering (57.00-76.00), number of umbel per plant (17.2-37.00), number of primary branches per plant (4.8-10.40), plant height at 30 DAS (4.49-11.27cm), number of leaves per plant at 30 DAS (5.33-13.27), number of seeds per umbel (17.6-32.6), number of secondary branches per plant (8.13-15.47), number of leaves per plant at 60 DAS (10.07-19.33), days to germination (11.33-19.33), test weight (10.23-17.13g), number of umbel lets per umbel (5.00-8.73) and days to maturity (103-118). While it was low for while number of seeds per plot (0.21-1.35kg) and seed yield per plant (5.13-9.53g) was found to be lowest.

All the genotypes were provided similar experimental conditions variation in plant height was due to the inherent genetic makeup of the genotypes, which in some way influenced this morphological expression through the activity of endogenous growth regulators. The early germination was recorded under the genotypes COR-108 respectively. However, the genotypes COR-113 was found to be late with respect of germination. The variation for plant height was also observed by Shrivastava *et al.* (2000) [20], Choudhary and Ramkrishna (2003) [6], Sharma *et al.* (2004) [19], Beemnet and Getinet (2010) [3] and Bertini *et al.* (2010) [4].

Maximum leaves per plant were recorded in genotype COR 108, while it was lowest in genotype COR 105. Number of leaves per plant has been primarily found to be relating with endogenous hormonal leaves and apical dominance. The findings were quite similar to as reported by Megiji and Korla (2002) [15]. The maximum number of primary and secondary branches per plant recorded under the genotypes COR 118 respectively, while the genotypes COR-98 exhibited minimum number of primary branches and secondary branches per plant genotypes COR-111 recorded, probable reasons for enhanced more number of primary and secondary branches per plant, might be due to endogenous hormonal level and apical dominanace. This finding is also in agreement with the findings of Shrivastava *et al.* (2000) [20], Rajput and singh (2003) [18], Singh *et al.* (2005) [23], Singh *et al.* (2011) [22] and Dyulgerov and Dyulgerova (2013) [9].

The early first flowering and 50% flowering was recorded under the genotypes COR-117 respectively. However, the genotypes COR-113 was found to be late with respect of days taken to first and 50% flowering. Early flowering might be due to minimum branches per plant resulted in low quantity of florigen (a flowering hormone) which might have been responsible for period of reproductive phase. These genotypes can introduce diversity in crop improvement programme because the early and late type can easily fetch the market demand and give better economic returns. The result have been reported by Shrivastava *et al.* (2000) [20], Singh *et al.* (2005) [23], Singh *et al.* (2006) [24], Patel and Agalodiya (2007) [17], Bertini *et al.* (2010) [4] and Meena *et al.* (2014) [14]. The maximum number of umbels per plant were recorded in the genotypes COR-118. However, the genotypes COR-102 was recorded the minimum umbels per plant. These finding are in agreement with the findings of Shrivastava *et al.* (2000) [20], Jain *et al*. (2002) [11], Rajput and Singh (2003) [18], Singh *et al.* (2006) [24], and Meena *et al.* (2014) [14]. The maximum number of umbellets per umbe was recorded in the genotypes COR-102 while lowest umbellets per umbel were noted in COR-111. The results are in confirmation with the findings of Shrivastava *et al.* (2000) [20], Tripathi *et al.* (2000) [25], Rajput and Singh (2003) [18], Singh *et al.* (2005) [23], Singh *et al.* (2006) [24] and Bertini *et al.* (2010) [4].

The maximum seeds per umbel were recorded in genotype COR-118, COR-112, COR-121 while it was lowest in COR-111. Variation observed in these factors may be due to genetic makeup of the genotype. These results are in agreement with the finding of Shrivastava *et al.* (2000) [20], Choudhary and Ramkrishna (2003) [6], Rajput and Singh (2003) [18], Singh *et al*. (2006) [24]. Genotypes COR-118, COR-121, COR-114 and COR-113 were recorded in maximum test weight (g). However, the lowest test weight (g) was obtained in COR-111. Variation observed in these factors may be due to genetic makeup of the genotypes. These results are in agreement with the finding of Shrivastava *et al.* (2000) [20] and Sharma *et al.* (2004) [19].

The early days to maturity was recorded under the genotypes COR-98 respectively. However, the genotypes COR-104 was

found to be late with respect of germination. The results are in confirmation with the findings of Bertini *et al.* (2010) [4]. Maximum seed yield per plant, seed yield per plot (kg) and per hectare was noted in COR-118, while it observed in lowest in COR-111. The findings are in close conformity with Shrivastava *et al.* (2000) [20], Jain *et al.* (2002) [11], Rajput and Singh(2003) [18], Vijayalatha and Chezhiyan (2005) [26].

3.2 Heritability

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as high (above 90%), medium (70-90%) and low (less than 70%).

The values of heritability in broad sense was found to be estimates were observed very high for Plant height (cm) at 90DAS, followed by Plant height (cm) at 60DAS, Plant height (cm) at 30DAS. The findings are in close harmony with the result of Rajput and Singh (2003) [18], Sharma *et al*. (2004) [19] and Ali *et al*. (2005) [1]. However it was recorded to be medium for No. of leaves / plant at 30 DAS, Number of secondary branches/ plant, Seed yield/ plant (g), No. of leaves / plant at 90 DAS, No. of leaves / plant at 60 DAS, No. of umbels/ plant, No. of seeds/ umbel, No. of primary branches / plant, No. of umbellate/ umbel, Test weight (g), Seed yield/ plant (g). The findings are in close harmony with the result of Megeji and Korla (2002) [15], Jain *et al*. (2002) [11], Singh and Shah (2003) [21] and Singh *et al*. (2005) [23]. Low estimation of heritability was Days to 50% flowering, Days to germination, Days to 1st flowering and Days to maturity. The findings are in close harmony with the result of Sharma *et al*. (2004) [19] and Ali *et al*. (2005) [1].

3.3 Genetic advance

Heritability however, indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson *et al.*, 1955) [12]. The estimated values of genetic advance as percent of mean were classified as high (more than 40%), moderate (15-40%) and low (less than 15%). Genetic advance as percentage of mean ranged between 5.84% for Days to maturity to 58.38% for Seed yield/ ha (q). The highest estimate of genetic advance as percentage of mean was recorded for Seed yield/ ha (q), Seed yield/ plot (kg), No. of leaves / plant at 30DAS, No. of leaves / plant at 90DAS, plant height at 60DAS and plant height at 90DAS. The results were in consonance with Rajput and Singh (2003) [18], Sharma *et al*. (2004) [19] and Singh *et al*. (2005) [23]. However, it was found to be medium for Plant height at 30DAS, No. of leaves / plant at 60DAS, No. of primary branches / plant, No. of umbels/ plant, No. of secondary branches/ plant, Seed yield/ plant (g), No. of umbellate/ umbel, Test weight (g), No. of seeds/ umbel, Days to germination and Days to 1st flowering. The results were in close proximate to that of Megeji and Korla (2002) [15], Jain *et al*. (2002) [11], Rajput and Singh (2003) [18] and Singh *et al*. (2005) [23]. Whereas, low estimates were observed for Days to maturity and Days to 50% flowering. The results were in close proximate to that of Ali *et al*. (2005) [1], Singh *et al*. (2005) [23] and Meena *et al*. (2014) [14].

Table 2: Genetic parameters in coriander

Characters		Grand Mean	Range		Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean
			Min.	Max.	Phenotypic	Genotypic			
Days to germination		15.71	11.33	19.33	13.93	11.24	65.12	2.94	18.69
Plant height (cm) at	30DAS	8.63	4.49	11.27	17.83	16.91	90.02	2.85	33.05
	60DAS	52.13	26.30	72.75	22.23	21.21	90.97	21.72	41.67
	90DAS	114.66	82.99	162.75	20.62	19.99	94.00	45.79	39.93
No. of leaves / plant at	30DAS	7.86	5.33	13.27	25.23	23.63	87.69	3.58	45.57
	60DAS	14.44	10.07	19.33	17.89	16.46	84.62	4.51	31.20
	90DAS	35.39	22.20	53.07	24.49	22.56	84.86	15.15	42.81
No. of primary branches / plant		6.82	4.80	10.40	19.59	16.93	74.67	2.05	30.13
No. of secondary branches/ plant		11.07	8.13	15.47	16.17	15.07	86.86	3.20	28.94
Days to 1st flowering		54.57	45.67	67.00	11.02	8.99	66.62	8.25	15.12
Days to 50% flowering		66.03	57.00	76.00	7.73	5.97	59.64	6.27	9.50
No. of umbels/ plant		26.22	17.20	37.00	18.19	16.17	78.98	7.76	29.60
No. of umbellate/ umbel		6.37	5.00	8.73	14.53	12.44	73.26	1.40	21.92
No. of seeds/ umbel		27.97	17.60	32.60	12.22	10.81	78.26	5.51	19.70
Test weight (g)		14.09	10.23	17.13	14.05	11.98	72.70	2.96	21.04
Days to maturity		112.68	103.00	118.00	4.10	3.41	69.10	6.58	5.84
Seed yield/ plant (g)		6.96	5.13	9.53	15.67	13.24	71.38	1.60	23.03
Seed yield/ plot (kg)		0.95	0.22	1.35	33.31	30.73	85.08	0.55	58.31
Seed yield/ ha (q)		15.81	3.61	22.49	33.31	30.73	85.08	9.23	58.38

3.4 Coefficient of Variation

In the present findings phenotypic coefficient of variation (Table 3) were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however, the differences were narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The finding of Tripathi *et al.* (2000) [25], Mageji and Korla (2002) [15] and Rajput and Singh (2003) [18] were similar to that of the present findings.

3.5 Phenotypic coefficient of variations

The phenotypic coefficient of variation ranged from 4.10% for days maturity to 33.31% for Seed yield/ plot (kg). The phenotypic coefficient of variations was highest for characters viz Seed yield/ plot (kg), Seed yield/ ha (q), No. of leaves / plant at 30DAS, No. of leaves / plant at 90DAS, plant height at 60 DAS. The findings are in close harmony with the result of Shrivastava *et al.* (2000) [20], Tripathi *et al.* (2000) [25], Jain *et al.* (2002) [11] and Beemnet and Getinet (2010) [3].

However, it was exhibited in low for characters like days to maturity, Days to 50% flowering, Days to 1st flowering, No. of seeds/ umbel, Days to germination, Test weight (g) and No. of umbellate/ umbel. The findings are in close harmony with the result of Shrivastava *et al.* (2000) [20], Tripathi *et al.* (2000) [25], Sharma *et al.* (2004) [19], Singh *et al.* (2006) [24], Bertini *et al.* (2010) [4]. The remaining of the characters such as Plant height (cm) at 90, No. of primary branches / plant, No. of umbels/ plant, No. of leaves / plant at 60DAS, Plant height (cm) at 30DAS, No. of secondary branches/ plant and Seed yield/ plant (g) exhibited moderate phenotypic coefficient of variation.

3.6 Genotypic coefficient of variation

It is revealed from the Table 3 that genotypic coefficient of variation varied from 3.41% for Days to maturity to 30.73% for Seed yield/ plot (kg). High genotypic coefficient of variation was noted for Seed yield/ plot (kg), followed by Seed yield/ ha (q), No. of leaves / plant at 30DAS, No. of leaves / plant at 90DAS, Plant height (cm) at 60DAS and Plant height (cm) at 90DAS. The findings are in close harmony with the result of Shrivastava *et al.* (2000) [20], Beemnet and Getinet (2010) [3]. However, it was found to be low for characters like Days to maturity, Days to 50% flowering, Days to 1st flowering, No. of seeds/ umbel, Days to germination, Test weight (g), No. of umbellate/ umbel and Seed yield/ plant (g). The findings are in close harmony with the result of Shrivastava *et al.* (2000)[20], Sharma *et al.* (2004)[19] and Meena *et al.* (2014)[14].

A wide range of variation in quantitative characters provides the basis for selection in plant breeding programme. The knowledge of association among the characters is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. Correlation coefficient provides a clear picture of the extent of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component characters help in improving the efficiency of selection for yield by making proper choice and balancing one component with another. A positive correlation between desirable character is helpful to the plant breeder because it helps in simultaneous improvement of both characters. It helps in simultaneous improvement of both characters. A negative correlation on the other hand shall find the simultaneous expression of both the characters with high values. In such situation some economic compromises has to be made, for crop improvement. The magnitude of genotypic correlation was higher than the phenotypic correlation for all the traits that indicated inherent association between various characters. The results of phenotypic correlation coefficient have been discussed only as the mostly influenced by the environmental conditions, hence phenotypic correlation will give the correct idea about the association between two variables.

Table 3: Estimates of genotypic and phenotypic correlation coefficients among seed yield and its attributing traits in coriander

Characters		Plant height (cm) 90 DAS	No. of leaves / plant 90 DAS	No. of primary branches / plant	No. of secondary branches / plant	Days to 1st flowering	Days to 50% flowering	No. of umbels/ plant	No. of umbellate/ umbel	No. of seeds/ umbel	Test weight (g)	Days to maturity	Seed yield/ plant (g)
Days to germination	G	-0.087	-0.323	-0.157	0.129	0.391	0.405	-0.157	0.120	0.187	-0.104	0.126	-0.383
	P	-0.089	-0.188	-0.130	0.087	0.260*	0.238*	-0.152	0.096	0.105	0.012	-0.007	-0.306**
Plant height (cm) 90 DAS	G		-0.038	-0.168	0.172	-0.081	-0.121	0.161	-0.360	0.099	-0.195	-0.262	0.028
	P		-0.042	-0.145	0.151	-0.080	-0.114	0.142	-0.273**	0.067	-0.154	-0.222*	0.019
No. of leaves / plant 90 DAS	G			0.218	0.261	0.086	0.207	0.033	0.215	-0.147	-0.121	0.111	0.246
	P			0.212*	0.242*	0.167	0.263*	-0.003	0.210*	-0.082	-0.107	0.113	0.228*
No. of primary branches / plant	G				-0.115	-0.081	-0.246	0.157	0.350	0.102	-0.018	0.243	-0.186
	P				-0.101	-0.096	-0.202	0.112	0.223*	0.058	0.009	0.241*	-0.080
No. of secondary branches / plant	G					-0.169	-0.098	-0.109	-0.174	-0.128	-0.004	-0.348	-0.053
	P					-0.141	-0.085	-0.062	-0.140	-0.075	0.003	-0.250*	-0.022
Days to 1st flowering	G						0.841	-0.157	-0.041	0.167	-0.324	0.201	0.096
	P						0.857**	-0.241*	-0.069	0.135	-0.214*	0.226*	-0.080
Days to 50% flowering	G							-0.102	0.050	-0.002	-0.276	0.037	0.314
	P							-0.198	-0.009	0.027	-0.208*	0.163	-0.235*
No. of umbels/ plant	G								0.073	0.023	0.034	0.192	0.246
	P								0.109	-0.053	0.005	0.149	0.224*
No. of umbellate/ umbel	G									0.264	0.041	0.348	-0.337
	P									0.154	0.052	0.139	-0.272**
No. of seeds/ umbel	G										0.014	-0.059	0.364
	P										0.001	-0.035	0.268*
Test weight (g)	G											-0.022	0.279
	P											-0.048	0.233*
Days to maturity	G												-0.089
	P												-0.058

Significant at 5% level = * Significant at 1% level = **

Conclusion

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for plant height at 60 DAS followed by plant height at 90 DAS, seed yield per hectare, number of leaves per plant at 90 DAS, days to first flowering and days to 50% flowering. The association studies indicated that the advantages of upgrading coriander genotypes were through simultaneous selection for number of seeds per plant and number of umbel lets per umbel.

Acknowledgement

Authors are thankful to Department of Horticulture, JNKVV for providing all the facility and chemicals to complete the study.

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