



## Genetic diversity studies of cumin (*Cuminum cyminum* L.) genotypes in western plains of Rajasthan

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### Abstract

Genetic diversity was studied in fifty-four genotypes of cumin, *Cuminum cyminum* L. at “Agricultural Research Station, Mandor, Jodhpur” during *rabi* season 2017–18. The mean squares were found significantly different for all the characters under study, depicting the variability among the study materials. The high magnitude of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) for seed yield, primary branches per plant and number of umbels per plant depicted the presence of vast amount of variation for the character along with high heritability (68–97%) combined with higher genetic advances as percentage of means for seed yield. The highest intra-cluster distance was recorded in cluster VI (11.8) along with cluster VII (11.33) and cluster VIII (8.29) depicting large genetic variability among the genotypes of these three clusters. The highest inter-cluster distance was reported among cluster III and VIII (51.97) followed by cluster III and VII (40.07) and cluster IV and cluster VIII (34.77), suggesting wide range of diversity between genotypes of the clusters. Amongst the characters, seed yield contributed the highest towards genetic divergence (47.80%) followed by number of umbels plant<sup>-1</sup> (25.65%), branches per plant (8.60%) and 1000 seed weight (6.64%).

**Keywords:** cumin, genetic advance, genetic variability, heritability

Seed spices are important crops to fetch foreign exchange through international trade. Among these seed spice crops, cumin is major one and it is grown in Rajasthan and Gujarat. The center of origin of cumin is Egypt and being grown mostly in Indian sub-continent. India is the largest grower, consumer and exporter of

cumin in the world with 9.88 lakh hectare area and 5.88 lakh tonnes production (Anonymous 2019). Apart from this, China, North Africa, Syria, Egypt, Iran and Turkey also cultivate this crop. It is mostly adapted to dry cool sunny areas with low humidity and sandy loam soils in semiarid and arid climate. Cumin is highly

susceptible to different environmental factors such as temperature deviations, cloudy weather at maturity and irrigation water quality.

The availability of natural diversity in cumin is limited, although, for yield and related traits, diversity can be generated through selection, sib matting and mutation. Genetic diversity studies are helpful for identification of traits for crop improvement and association between them, which is suitable for breeder to improve crop yield through directional plant breeding approaches. Low exploitation of genetic diversity, narrow genetic base and limited breeding work and the understanding for breeding behavior is very limited in cumin. Quantitative assessment of the available variability will provide the base for improvement of agronomical characters of crop. Keeping in view of the above facts, this study was conducted for character association and genetic diversity in cumin for yield and related attributes.

The experiment materials of current study comprised of 54 genotypes of cumin collected and developed at Agricultural Research Station, Mandor, Jodhpur (Rajasthan). This experiment was conducted in Random Block Design with three replications during *rabi* 2017–18. The genotypes were grown in two row plots of 4 m length following crop geometry of 30 × 15 cm. The data were recorded on five competitive plants taken from each replication for plant height (cm), number of primary branches plant<sup>-1</sup>, number of umbels plant<sup>-1</sup>, number of umbellate umbel<sup>-1</sup>, seeds umbel<sup>-1</sup>, 1000 seed weight (g), seed yield (kg ha<sup>-1</sup>), and days to 50% flowering and maturity. The data were subjected to ANOVA as suggested by Panse & Sukhatme (1985). GCV and PCV were calculated according to the formulae given by Lush (1949). Genotypic and phenotypic coefficients of variance were estimated as per Burton (1952). Heritability (broad sense) and genetic advance (GA) as per cent of mean at 5% selection intensity were estimated as per Johnson *et al.* (1955). Clusters

were drawn by method of Ward's minimum variance (Ward, 1963).

The analysis of variance revealed highly significant mean squares indicating sufficient variability was present in study material. The yield varied from 104 kg ha<sup>-1</sup> (IC-054355) to 572 kg ha<sup>-1</sup> (MCU 22) with general mean of 299 kg ha<sup>-1</sup>. Genotype IC-595357 was the earliest to flower (69 DAS) and MCU 6 matured first (110 days). Plant height varied from 20.8 cm (IC-595339) to 39.0 cm (MCU 25) with general mean of 29.9 cm. With respect to primary branches plant<sup>-1</sup>, MCU 5 had maximum numbers (7.0) and IC-595339 recorded the lowest (2.4). MCU 14, MCU 15 and MCU 27 were the best for umbellates umbel<sup>-1</sup>, umbels plant<sup>-1</sup> and seeds umbel<sup>-1</sup>, respectively. 1000 seed weight varied from 3.6 g (MCU 34) to 6.8 g (IC-595337) with general mean of 5.1 g. Similar findings were also reported by Bairwa *et al.* (2015) and Meena *et al.* (2015).

The high magnitudes of phenotypic as well as genotypic coefficient of variation for seed yield, primary branches plant<sup>-1</sup> and number of umbels plant<sup>-1</sup> depicted the presence of vast amount of variation (Table 1). The high heritability (68–97%) combined with high genetic advance as per cent of mean for seed yield, plant height, number of primary branches plant<sup>-1</sup>, umbels plant<sup>-1</sup> and 1000 seed weight revealed that these characters were controlled by additive gene action, suggesting that selection for these traits would be effective for crop improvement. These results were in agreement with those reported by earlier workers (Singh *et al.* 2001; Bairwa *et al.* 2015; Meena *et al.* 2015).

A hierarchical cluster analysis of Ward's minimum variance method produced a dendrogram showing successive fusion of individuals which clearly partitioned the genotypes into eight clusters. The cluster-I contains maximum (20) genotypes, while cluster-III had the least (1) genotypes (Table 2). Intra and inter-cluster

**Table 1.** Estimates of genetic parameters of seed yield and its component traits in cumin

Character	Mean	Range		Coefficient of variation (%)		Heritability (%)	Genetic advance as per cent of mean (5%)
		Min.	Max.	GCV	PCV		
Seed yield (kg ha <sup>-1</sup> )	299	104	572	52.48	53.26	97.1	106.53
Days to 50 % flowering	77	69	82	4.52	4.88	86.0	8.63
Days to maturity	114	110	119	1.80	2.18	68.7	3.08
Plant height (cm)	29.9	20.8	39.0	14.53	15.78	84.8	27.55
Primary branches plant <sup>-1</sup>	4.4	2.4	7.0	24.19	25.21	92.1	47.82
No. of umbels plant <sup>-1</sup>	32	18	52	25.89	26.46	95.8	52.20
No. of umbellets umbel <sup>-1</sup>	4.8	3.0	5.6	8.93	10.78	68.7	15.25
No. of seeds umbel <sup>-1</sup>	5.2	4.0	6.4	10.17	12.59	65.2	16.92
1000 seed weight (g)	5.1	3.6	6.8	11.16	12.38	81.3	20.73

**Table 2.** Intra (diagonal) and inter Euclidean cluster distance among eight clusters in cumin

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	4.680	20.141	23.259	16.722	12.520	14.674	23.611	24.038
Cluster II		3.795	23.574	20.248	20.824	17.838	21.275	28.419
Cluster III			0.000	21.298	27.579	30.611	40.066	51.975
Cluster IV				7.729	15.753	17.096	28.750	34.766
Cluster V					7.974	15.513	23.935	23.729
Cluster VI						11.800	30.757	17.857
Cluster VII							11.326	28.724
Cluster VIII								8.287

Cluster I= MCU-1, MCU-18, MCU-12, MCU-24, MCU-23, MCU-11, MCU-4, MCU-13, MCU-22, MCU-9, MCU-19, MCU-28, MCU-31, MCU-21, MCU-7, GC 4, MCU-3, MCU-26, MCU-30, MCU-10

Cluster II= MCU-2, IC-595336

Cluster III= MCU-5

Cluster IV= MCU-8, MCU-17, IC-595353, MCU-14, MCU-25, MCU-15

Cluster V= MCU-16, MCU-32, MCU-6, IC-574092, IC-574099

Cluster VI= MCU-29, IC-595335, MCU-27, MCU-35, RZ 223, IC-054366, IC-595355

Cluster VII= MCU-20, MCU-33, MCU-34

Cluster VIII= IC-054355, IC-574093, IC-574094, IC-595357, IC-595359, IC-595339, IC-595337, IC-595338, IC-574097, IC-595334

**Table 3.** Cluster means for different characters & per cent contribution

Cluster	Seed yield (kg ha <sup>-1</sup> )	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches plant <sup>-1</sup>	No. of umbels plant <sup>-1</sup>	No. of umbellets umbel <sup>-1</sup>	Seeds umbel <sup>-1</sup>	1000 seed weight (g)
Cluster I	478.31	78.6	113.0	29.5	5.1	29.1	4.8	5.3	5.1
Cluster II	151.17	81.5	118.5	27.2	4.4	46.0	4.5	5.4	4.6
Cluster III	343.67	80.0	119.0	37.6	7.0	32.7	5.6	6.0	4.2
Cluster IV	269.17	76.2	113.5	36.8	5.0	48.4	5.3	5.3	5.0
Cluster V	221.60	78.2	112.4	31.0	3.7	30.9	5.3	5.1	4.4
Cluster VI	175.71	75.7	114.6	29.1	4.0	34.9	5.0	5.6	5.6
Cluster VII	201.44	77.7	115.0	33.1	4.8	33.3	3.8	4.1	4.1
Cluster VII	139.67	71.2	115.8	25.1	3.1	23.2	4.6	4.6	5.6
<b>Mean</b>	<b>299.38</b>	<b>76.6</b>	<b>114.1</b>	<b>29.9</b>	<b>4.4</b>	<b>32.0</b>	<b>4.8</b>	<b>5.1</b>	<b>5.1</b>
Contribution to Diversity (%)	47.80	3.63	1.47	2.87	8.60	25.65	1.89	1.47	6.64

average Euclidean distances are shown in Table 2. The highest intra-cluster deviations were observed in cluster-VI (11.8) followed by cluster-VII (11.33) and cluster-VIII (8.29) indicating wide genetic variability within the genotypes of these three clusters. The highest inter-cluster distance was observed between cluster-III and VIII (51.97) followed by cluster-III and VII (40.07) and cluster-IV and cluster-VIII (34.77), suggesting wide diversity between genotypes of these clusters (Table 2). Therefore, genotype belonging to these clusters may be used in hybridization programme for improvement, which might yield better segregants. The least inter-cluster distance was observed between clusters-I and V (12.52) indicating close relationship between the genotypes of these two clusters. The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 3). These results showed that different cluster genotypes were superior for different characters and genotypes having these characters would offer a good scope of improvement of cumin through selection. Amongst the characters, seed yield contributed maximum towards genetic divergence (47.80%) followed by number of umbels plant<sup>-1</sup> (25.65%), no. of primary branches plant<sup>-1</sup> (8.60%) and 1000 seed weight (6.64%), while other characters contributed low to genetic divergence (Table 3). These results are in conformity with those reported by Bairwa *et al.* (2015) and Meena *et al.* (2015).

Since varieties with narrow genetic base are more vulnerable to diseases and adverse climatic conditions, availability of genetically diverse genotypes for hybridization programme and selection becomes more important. Since quantitative characters *viz*, seed yield, number of primary branches plant<sup>-1</sup>, number of umbels plant<sup>-1</sup> and 1000 seed weight contributed maximum towards the divergence, direct selection for these traits helps in crop improvement.

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