



## Genetic divergence among genotypes of cumin (*Cuminum cyminum*)

R S MEENA<sup>1</sup>, R K SOLANKI<sup>2</sup>, R K KAKANI<sup>3</sup>, BALRAJ SINGH<sup>4</sup> and ALKA PANWER<sup>5</sup>

National Research Centre on Seed Spices, Tabiji, Ajmer, Rajasthan 305 206

Received: 12 December 2014; Accepted: 16 September 2016

### ABSTRACT

Cumin (*Cuminum cyminum* L.) is an important seed spice crop having high cash value. The genetic improvement for yield and biotic stress resistance is the major challenge in the crop. The extent of genetic diversity observed in the genus is low, even though it is essential to evaluate the extent of diversity available in the germplasm. Hence a set of 19 genotypes were tested for the diversity index using  $D^2$  technique over yield and nine morphological traits which were observed during 2009–10 and 2010–11. All the genotypes grouped into only two clusters, showing narrow genetic base. Primary branches contributed maximum to the genetic divergence, followed by yield/plot.

**Key words:** *Cuminum cyminum*, Genetic divergence,  $D^2$

Cumin (*Cuminum cyminum* L.) is an important seed spice crop belonging to *Apiaceae* family. It is consumed as raw and do have value added market, cumin aldehyde is a major constituent of essential oil in cumin and it constitutes nearly 63% of the total essential oil (Guenther 1975). Cumin aldehyde has a powerful odour and is used only in traces in compounding synthetic floral perfumes such as cassia (Agarwal *et al.* 2010). Cumin is grown in India, Bulgaria, Egypt, Argentina, Turkey, Bangladesh, China, Italy, Pakistan and Syria etc. In India cumin is mainly grown in Rajasthan and Gujarat in arid and semi-arid climate during *rabi* season.

Most of the studies carried on cumin were mainly on its essential oil, medicinal properties and aspects of agronomy (Kafie *et al.* 2002), tissue culture and cytogenetic studies

(Nadernejad *et al.* 2001). Limited efforts have been placed to understand the genetic for genetic improvement of target traits. In cumin, conventional methods based on selection of desirable genotypes have responded well for yield enhancement, study of the extent of diversity is necessary for performing selection cycles in a population (Avatar *et al.* 1991).

Initial evaluation of the germplasm has shown that the variability is limited in this crop. Geographical and genetic diversity play a significant role in crop characteristics. Keeping the above facts in mind, the present study was conducted to assess the genetic diversity available in the germplasm which is collected from different geographical areas and is being maintained at Indian Council of

Agriculture Research-National Research Centre on Seed Spices, Ajmer, India.

### MATERIALS AND METHODS

Nineteen genotypes were sown in a randomized block design with three replications during 2009–10 and 2010–11 at National Research Center on Seed Spices, Ajmer (26° 27' 0" N, 74° 38' -1" E and 486 meter above sea level). During growing season minimum and maximum temperature was recorded to be 5° and 25° C, respectively (October to March). Each genotypes were sown in six rows, each 2 m long, with 50 cm row-to-row and 15 cm plant-to-plant spacing. Five plants were randomly selected in each plot and tagged for recording observations such as plant height, primary branches, secondary branches, umbels per plant, umbellate per umbel, seed per umbellates, test weight and seeds yield. Genetic diversity was estimated as per Mahalanobis  $D^2$  statistics (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). Statistical analysis was done using statistical programme Windostat version 8.5 software.

### RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters used in the study. All the nineteen genotypes were grouped into only two clusters (Table 1). Cluster I was the largest with 18 genotypes. The cluster II had only one genotype, no correlation between geographical diversity and genetic diversity was observed.

Relative contributions of each character for cluster differences are given in Table 3. It indicate that primary branches (17.34%) contributed maximum to the genetic divergence, followed by yield/plot (16.37%). Test weight

<sup>1</sup>Senior Scientist (email: rsm.nrscs@gmail.com), <sup>2</sup>Scientist SS (e mail: rksolanki.ars@gmail.com), <sup>3</sup>Principal Scientist (e mail: rkkankani.nrscs@rediffmail.com), <sup>4</sup>Director (e mail: nrscs.director@gmail.com), <sup>5</sup>Senior Research Fellow (e mail: simiran.saini@rediffmail.com).

Table 1 Cluster composition in cumin

Cluster no.	No. of lines	Lines
I	18	EC-279081, EC-2443375, EC-637344, UC-243, UC-341, UC-346, JC-2002-8, JC-2002-14, JC-2002-17, JC-2002-23, JC-2002-28, JC-2002-32, C.Cumin-09-S-1, C.Cumin-09-I-2, C.Cumin-09-E-3, C.Cumin-09-Y-4, AC-167, RZ-19
II	1	GC-4 (Sel)

Table 2 Cluster means of nine characters in cumin

Characters	Cluster-I	Cluster-II
Primary branches	4.99	6.10
Secondary branches	11.84	21.67
Plant height	37.90	35.60
Umbels/plant	28.84	26.23
Umbellates/umbel	5.04	4.20
Seeds/umbellate	7.33	7.10
Seeds/umbel	36.70	35.20
Test west	3.27	3.66
Yield/plot	128.64	272.17

Table 3 Contribution of different characters towards genetic divergence in cumin

Characters	Contribution (%)
Primary branches	17.34
Secondary branches	1.17
Plant height	15.79
Umbels/plant	10.53
Umbellates/umbel	7.60
Seeds/umbellate	14.62
Seeds/umbel	15.79
Test west	0.58
Yield/plot	16.37

contributed minimum to the total divergence, followed by secondary branches. Similar results were reported by Avatar *et al.* (1991). Arunachalam and Sharma (1967) with the view that those characters which are important to fitness and natural selection provide a good choice for classification of genotypes. The inter and intra-cluster  $D^2$  values (Table 4) show that cluster I and II have lower intra-cluster distances, suggesting that the genotypes grouped in these clusters are related.

The dendrogram of the evaluated cumin genotypes

Table 4 Average inter and intra cluster  $D^2$  values in cumin

Cluster	I	II
I	2.19	4.24
II	4.24	0.00

is presented in Fig 1. Genotypes were grouped into two clusters. Cluster means of each character are given in Table 2. Comparison of means for various traits in different clusters revealed that cluster I recorded the highest value for yield/plot (128.6) followed by plant height (37.9) and seeds per umbel (36.7) and similar trend was observed in cluster mean II. It has been a well established fact that recombination between the more genetically diverse parents results in high vigour. Even, chances of obtaining broad spectrum variability in segregating generations (Arunachalam 1981) is also high. It has also been reported that the most productive hybrids may come for high yielding parents with high genetic diversity (Marker and Krupakar 2009, Meena *et al.* 2010).

The variation studied through Principal Component Analysis revealed three principal components, of which variance reflected on PCA 1 (35.73) with eigen value 19.91, followed by PCA-II showing variance contribution 22.09 with eigen value 12.29, whereas, PCA-III had 20.91 variance proportion with eigen value 11.65 (Table 5). In PCA-I seed yield per plot contributes positively and maximum (0.62) followed by seeds/umbel (0.44), in PCA-II,

Table 5 Principal Component analysis of 19 cumin genotypes

Characters	PCAI	PCA II	PCA III
Eigene value	19.91	12.29	11.65
Proportion of variance	35.73	22.06	20.91
Cumulative variance	35.73	57.80	88.68
<i>Factor loadings</i>			
Primary branches	0.08302	0.31947	0.71251
Secondary branches	0.23937	0.24082	0.28422
Plant height	-0.30322	-0.40160	0.35476
Umbel/plant	-0.24031	0.37758	0.32690
Umbellate/umbel	-0.38736	-0.09536	0.14287
Seeds/umbellate	-0.09967	-0.44506	0.31793
Seeds/umbel	0.44565	-0.54205	0.22974
Test west	0.18877	-0.14693	0.02961
Yield/plot	0.62602	0.11629	0.06069

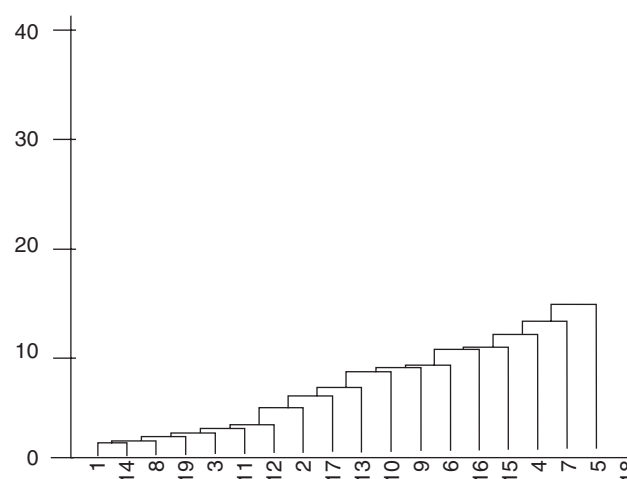


Fig 1 Dendrogram base on 9 traits of cumin by Tocher method

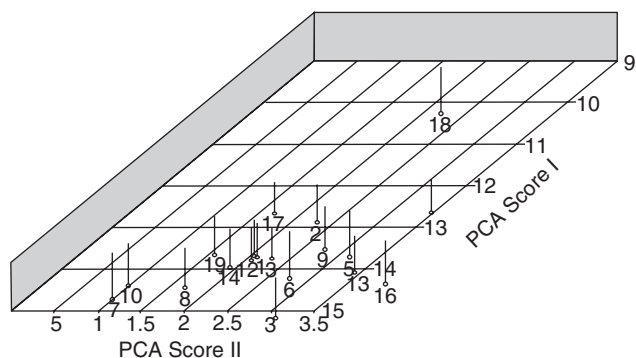


Fig 2 3D plot diagram for PC-I and PC-II in 19 cumin genotypes

maximum positive contribution of umbel per plant (0.37) was observed. Whereas, in PCA-III, all traits contributed positively of which primary branches contribution was high (0.71) followed by plant height (0.35), similar results were reported by Singh *et al.* (2005).

3D plot shows in Fig 2 depicts the dimension of the first and second PCs and delineation of the 19 genotypes on coordinates. The genotype GC-4 (sel) stood differently from rest of the eighteen genotypes which grouped closed in the plotting. Close grouping of maximum genotypes reflected narrow genetic base and the genotype GC-4 (sel) can be effectively utilized for genetic enhancement in cumin yield.

CONCLUSION

The studied on genetic diversity in cumin performed on nineteen germplasm lines and for nine traits exhibited narrow genetic base based on formation if two major clusters. The cluster-II comprised of sole genotype GC-4 (sel) depicting significant genetic difference from rest of the genotypes. The character contribution to total diversity was observed to be high for plant height and seed yield. The genotypes significantly varied for all the traits, which in turn showed mean differences between the two clusters. Traits, viz. seed yield, seeds/umbel, primary branches/plant, umbels/

plant contributed high to the principal component analysis, these traits shows high variation in the germplasm set, the association of these traits with yield is high hence the same can be exploited for performing effective selection for yield enhancement in cumin. Recombination between diverse genotypes may also deliver better segregants for genetic improvement in cumin for yield and other desirable traits.

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