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Short Communication

Genetic Diversity Analysis Using D^2 Clustering in Small Cardamom (*Elettaria cardamomum* Maton)

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Cardamom is a perennial, herbaceous rhizomatous monocot belonging to the family Zingiberaceae. It is a native of the moist evergreen forests of the western Ghats of South India. This is often referred to as the 'Queen of Spices' because of its very pleasant aroma and taste and is highly valued from ancient times. Cardamom production in India during 2019-20 was 20,650 MT obtained from an area of 69,330 ha covering the southern states of Kerala, Karnataka and Tamil Nadu. To enhance the production and productivity, large scale planting of high yielding varieties is imperitive. Existence of wide variability in yield components and yield in cardamom is diversity well known [1-2]. An understanding of the extent of genetic diversity among different cardamom accessions is essential for the selection of parents in breeding programmes and hence the study was undertaken. Moreover, genetic diversity analysis using D^2 clustering method has also been used for clustering the hybrids in other crops [3-4].

Ninety accessions of cardamom were selected at random from a well-managed plantation in Udumbanchola taluk of Idukki district wherein cultural practices for intensive management were followed. The farm is situated at 9°53' N latitude, 77° 09' E longitude and 1068 m above mean sea level. Data on biometrical characters were recorded from ninety selected plants for 3 consecutive years from 2017 to 2020. The data for the 3 years were pooled and the resultant data was used for the analysis. The data consist of measurements on 11 growth and yield attributes such as leaf breadth, bearing tillers per clump, total tillers per clump, capsules per raceme, racemes per panicle, yield per clump, panicles per clump, internodal length, seeds per capsule, recovery percentage and capsules per kilogram. In order to assess the genetic diversity, analysis was carried out using Mahalanobis [5] generalized distance D^2 and the accessions were grouped into different clusters following Tocher's method as given by Rao [6].

The 90 accessions were grouped into eight clusters based on minimum generalized distance. Clusters I, II, III, IV, V, VI, VII and VIII comprised of 29, 29, 8, 22, 1, 1 and 1 accessions, respectively (Table 1). The clustering pattern revealed that the accessions collected from the same source were distributed in different clusters.

Table 1 Distribution of 90 accessions of cardamom in different clusters

Cluster No.	No. of accessions	Accessions
I	28	MCC-131, MCC-139, MCC-145, MCC-151, MCC-155, MCC-159, MCC-163, MCC-169, MCC-177, MCC-178, MCC-180, MCC-182, MCC-191, MCC-193, MCC-201, MCC-248 MCC-253, MCC-264, MCC-266, MCC-278, MCC-279, MCC-282, MCC-288, MCC-300, MCC-312, MCC-331, MCC-344, MCC-345
II	28	MCC-129, MCC-146, MCC-154, MCC-156, MCC-157, MCC-161, MCC-167, MCC-171, MCC-172, MCC-174, MCC-176, MCC-181, MCC-184, MCC-185, MCC-194, MCC-245, MCC-262, MCC-267, MCC-272, MCC-283, MCC-284, MCC-286, MCC-292, MCC-310, MCC-311, MCC-314, MCC-316, MCC-319, MCC-170, MCC-173, MCC-242, MCC-243, MCC-244, MCC-271, MCC-281, MCC-319
III	8	MCC-170, MCC-173, MCC-242, MCC-243, MCC-244, MCC-271, MCC-281, MCC-309
IV	22	MCC-130, MCC-140, MCC-160, MCC-162, MCC-168, MCC-175, MCC-179, MCC-183, MCC-186, MCC-187, MCC-188, MCC-189, MCC-192, MCC-247, MCC-250, MCC-255, MCC-268, MCC-273, MCC-274, MCC-276, MCC-299, MCC-334
V	1	MCC-241
VI	1	MCC-254
VII	1	MCC-152
VIII	1	MCC-246

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Difference in genetic constitution and the influence of environmental factors may be responsible for this type of clustering [7]. Though geographic diversity is considered as one of the criteria for selection, it may not necessarily be the only factor that determines the genetic diversity in the accessions. Accessions from different geographic regions were grouped in the same cluster. This may be due to the free exchange of propagating materials among locations.

Table 2 Average intra and inter cluster distances in cardamom

Cluster	I	II	III	IV	V	VI	VII	VIII
I	8.15							
II	21.15	8.63						
III	31.78	15.02	10.11					
IV	13.69	15.62	24.86	10.30				
V	26.64	11.66	12.88	21.97	0.00			
VI	10.97	27.65	37.63	17.40	33.46	0.00		
VII	22.44	12.48	17.91	19.97	9.83	29.55	0.00	
VIII	42.55	24.80	14.69	35.79	19.41	48.58	24.84	0.00

Intra and inter cluster D^2 values of the eight clusters are presented in (Table 2). The intra cluster distance was 8.15 in cluster I,8.63 in cluster II, 10.11 in cluster III and 10.30 in cluster IV. The maximum intra cluster distance was among accessions in cluster IV while it was the minimum in cluster I. The distance between clusters was found to be maximum between clusters VI and VIII (48.58) indicating the highest genetic distance between them. It was followed by clusters I and VIII (42.55) and clusters III and VI (37.63). The minimum distance was recorded between clusters V and VII (9.38) indicating the lowest genetic divergence between them. The character means of the accessions are given in (Table 5). Cluster VIII with only one accession, MCC-246, was found to be distinct since it has the maximum mean values for majority of the characters studied. This observation further indicates the genetic uniqueness of MCC-246 which can be exploited further in the breeding programmes. Accessions belonging to the most distant clusters can be utilized for hybridization programmes so as to generate recombinants with superior alleles belonging to distant gene pools since such combinations may result in the production of better and promising hybrids.

SUMMARY

Ninety cardamom accessions (*Elettaria cardamomum* Maton) were subjected to Tocher's clustering, in order to assess the genetic diversity available in the accessions. The analysis showed wide diversity for growth and yield attributes among the accessions. The accessions were grouped into eight clusters. Based on the inter cluster distance, the accessions belonging to the most distance clusters can be used for hybridization programmes to produce better and promising hybrids. Mahalanobis D^2 method provides an efficient technique to identify the genetic divergence present in the population. This technique helps in the selection of genetically divergent parents and can be exploited in the hybridization programme.

LITERATURE CITED

1. George KV, Dandin SB, Madhusoodanan KJ, John K. 1981. Natural variations in the yield parameters of cardamom (*Elettaria cardamomum Maton*). *In*: *Proceedings of the IV symposium on Plantation Crops (PLACROSYM-IV)* (Eds) Visveshwara, S. ISPC. Kasaragod, India. pp 216-223.
2. Korikanthimath VS, Mulge R, Hosmane MM. 1997. Preliminary evaluation of elite clones of cardamom (*Elettaria cardamomum Maton*) for yield and yield parameter in clonal nursery. *Jr. Spices and Aroniatic Crops* 6(1): 57-61.
3. Bhaganna H, Salimath PM, Aghora TS, Nagarajappa A, Ganga PS. 2017. Genetic diversity analysis by D^2 clustering of yield and yield attributing traits in French bean. *Journal of Pharmacognosy and Phytochemistry* 6(6): 1331-1335.
4. Kumari A, Mankar A, Kumari P, Kumari J, Ahmad F. 2018. D^2 Statistic techniques used for analysis of genetic divergence among litchi hybrids. *Int. Jr. Curr. Microbiol. App. Sciences* 7(5): 960-969.
5. Mahalonobis PC. 1936. On the generalized distance in Statistics. *Proc. Natl. Acad. Sci*. 2: 55-79.
6. Rao CR. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York. pp 328.
7. Murthy BR, Arunachalam V. 1966. The genetic divergence in relation to breeding system in crop plants. *Indian Jr. Genetics* 26: 188-198.