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Short Communication

Cluster Analysis to Assess the Genetic Diversity in Peacock Ginger (*Kaempferia rotunda* L.)

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Kaempferia rotunda L. is a highly valued medicinal plant belonging to the family Zingiberaceae. *Kaempferia rotunda* is commonly called peacock ginger or Indian crocus. It is a handsome aromatic herb with very fragrant sub globose yellow-white tuberous rhizome used in traditional medicine of Kerala. The rhizomes and root tubers of the plant have a bitter, camphoraceous taste and has been widely used as vegetable and a food flavouring spice in India and south east Asia. The plant is widely distributed in the tropics and sub-tropics of Asia and Africa. It is distributed throughout the Indian subcontinent from eastern Himalayas to Sri Lanka and the Malay Peninsula to Malay Island. It is seen naturally growing in the Western Ghat region of Kerala State of India. To enhance the production and productivity, large scale planting of high yielding varieties is imperative. An understanding of the extent of genetic diversity among different accessions is essential for the selection of parents in breeding programmes and hence the study was undertaken. Induction of genetic variability in *K. galanga* was attempted by Kanakamany [1]. Jayasree [2] analyzed the genetic variability, character association and genetic divergence in *Curcuma amada* and *Kaempferia galanga* to identify the superior genotypes from them. The efforts to study the genetic diversity *K. rotunda* in Kerala State are scanty. Being a plant species, which is very marginally cultivated in spite of its medicinal and commercial importance, the present study has been designed to evaluate the genetic diversity of the same. It is also essential to identify superior genotypes from the germplasm which is essential for the selection of parents in breeding programmes. Moreover, genetic diversity analysis using clustering method has been used for grouping the germplasm accessions in many other crops [3-7].

The experiment was conducted in the experimental plot of the Genetics and Plant Breeding Division of the Department of Botany, University of Calicut, Kerala, India during 2017-2020. The experiments were laid out in randomized block design (RBD) with three replications in open field condition. The experimental plot is located at 75°46' E longitude and11°15' N latitude at an elevation of 50 m from MSL. Average temperature of the study area ranges from 17.83°C to 36.83°C with an annual rainfall of 247cms. *K. rotunda* accessions collected from different locations across the length and breadth of Kerala State of India have been used for the present study. The morphometric observations recorded for three consecutive years were pooled and the resultant data were used for the analysis. The data consist of measurements on 15 growth and yield attributes such as plant height (cm), number of tillers, number of leaves per tiller. leaf length (cm), leaf breadth (cm), leaf area (cm^2), number of primary fingers, number of secondary fingers, length of primary fingers, diameter of primary fingers, length of secondary fingers, diameter of secondary fingers, length of mother rhizome (cm), diameter of mother rhizome (cm) and yield per plant (g). In order to assess the genetic diversity, statistical analysis was carried out using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) agglomerative hierarchical clustering as given by Sokal and Michener [8] and the accessions were grouped into different clusters.

The success of any breeding programme depends on the availability and extent of genetic diversity in the base population. The main aim of using cluster analysis in plant breeding trials is to group the accessions into several homogeneous groups such that those accessions within a group have a similar response pattern across the locations. The sixty-eight accessions of *K. rotunda* have been subjected to cluster analysis using UPGMA which is a simple agglomerative hierarchical clustering method to identify the closeness and distance that pertain between the accessions on the basis of fifteen agronomic characters.

Cluster analysis grouped the entire accessions into three clusters at a linkage distance of 0.998 (Fig 1). The first cluster is occupied by sixty-six accessions, showing maximum

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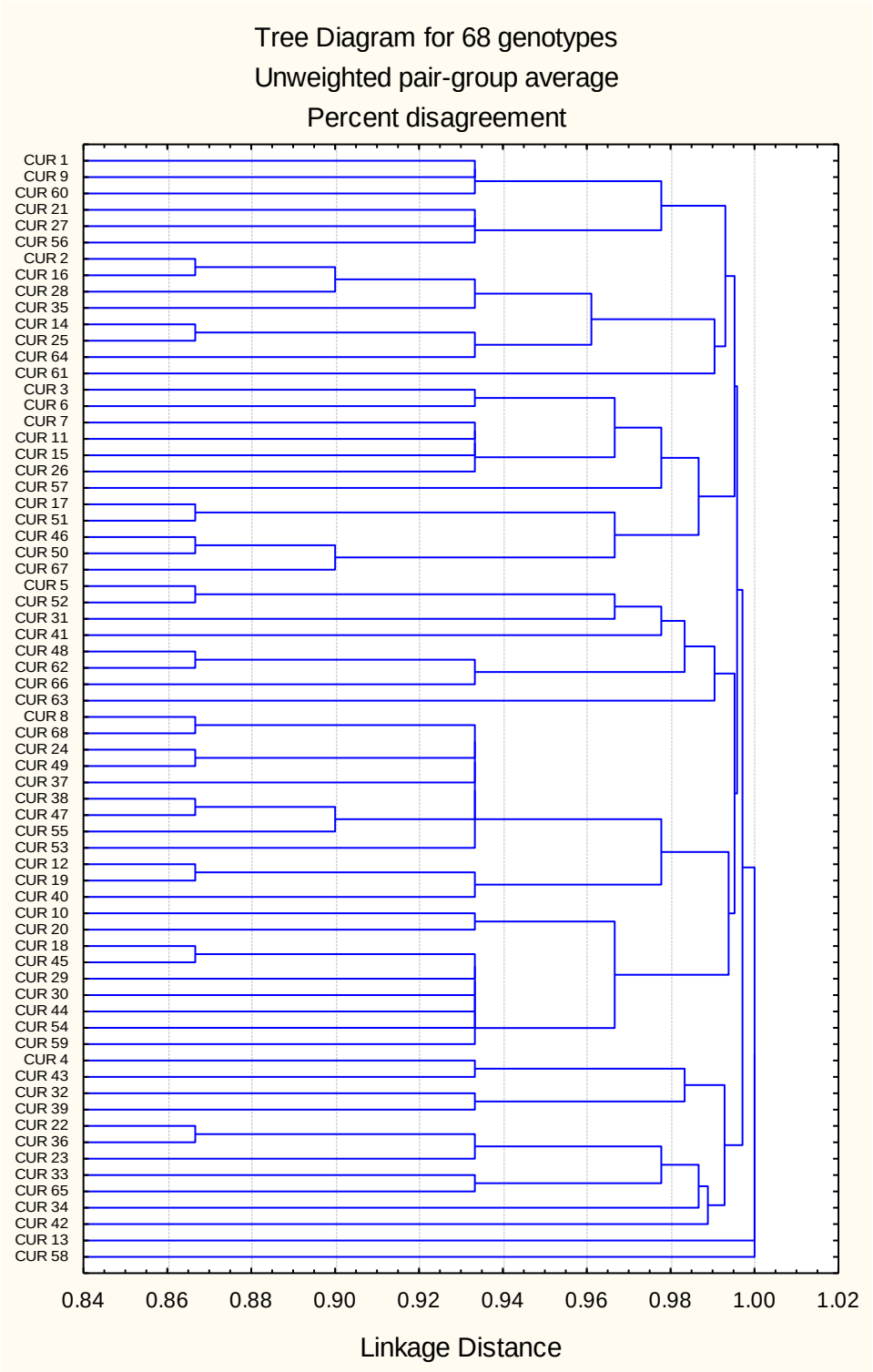
accommodation of genotypes which are related. The second cluster is occupied by one accession namely CUR 13 collected from Kottayam District and third cluster occupied by CUR 58 collected from Wayanad District. The first cluster at a linkage distance of 0.996 is bifurcated again into two sub clusters, the first consisting of 55 genotypes and the second consisting of 11 genotypes. These sub clusters got again divided repeatedly into different groups with maximum genetic closeness [9].



The genotypes CUR 2 and CUR 16; CUR 14 and CUR 25; CUR 17 and 51; CUR 46 and CUR 50; CUR 5 and CUR 52; CUR 48 and CUR 62; CUR 8 and CUR 68; CUR 24 and CUR 49; CUR 38 and CUR 47; CUR 12 and CUR 19; CUR 18 and CUR 45; and CUR 22 and CUR 36 were found to be more genetically related with regard to the characters subjected to the study. All these twelve groups come under the first cluster and they bifurcate at a linkage distance of 0.865. Cluster I have got genotypes from all the thirteen districts. Hence, each cluster is a mixture of genotypes collected from different geographical areas and it indicates that geographical separation is not a major criterion for genetic closeness and distance between the accessions studied. Difference in genetic constitution and the influence of environmental factors may be responsible for this type of clustering [10]. Genotypes belonging to same clusters show higher levels of similarity and it is generally presumed that they exhibit genetic proximity and those belonging to different clusters are genetically distant from each other thus showing higher levels of divergence in genetic makeup. Distantly related genotypes can be considered as genetically

diverse (Table 1). The diverse accessions of *Kaempferia rotunda* could be selected for further improvement programmes based on further assessment of performance so that exploitation of genetic variability and production of high yielding varieties will be possible.

Table 1 Clustering of the genotypes studied in *Kaempferia rotunda*

Cluster number	Sub cluster number	Accessions
I	1A	CUR 1, CUR 9, CUR 60, CUR 21, CUR 27, CUR 56, CUR 2, CUR 16, CUR 28, CUR 35, CUR 14, CUR 25, CUR 64, CUR 61, CUR 3, CUR 6, CUR 7, CUR 11, CUR 15, CUR 26, CUR 57, CUR 17, CUR 51, CUR 46, CUR 50, CUR 67, CUR 5, CUR 52, CUR 31, CUR 41, CUR 48, CUR 62, CUR 66, CUR 63, CUR 8, CUR 68, CUR 24, CUR 49, CUR 37, CUR 38, CUR 47, CUR 55, CUR 53, CUR 12, CUR19, CUR 40, CUR 10, CUR 20, CUR 18, CUR 45, CUR 29, CUR 30, CUR 44, CUR 54, CUR 59
	1B	CUR 4, CUR 43, CUR 32, CUR 39, CUR 22, CUR 36, CUR 23, CUR 33, CUR 65, CUR 34, CUR 42
II		CUR 13
III		CUR 58

SUMMARY

Sixty-eight accessions of peacock ginger were subjected to UPGMA simple agglomerative hierarchical clustering method in order to identify the closeness and distance that pertain between the accessions on the basis of fifteen agronomic characters. The accessions were grouped into three clusters. Based on the inter cluster distance, the accessions belonging to the most distant clusters could be identified and used for hybridization programmes to produce better and promising hybrids. UPGMA clustering method provides an efficient tool to identify the genetic diversity present in the population. This technique helps in the selection of genetically divergent parents and can be exploited in the crop improvement programmes.

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