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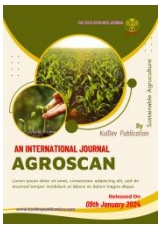

Research Article

Using Cluster Analysis to Evaluate Peacock Ginger's Genetic Diversity (*Kaempferia rotunda* L.)

*[1]Sonal Mukesh Sharma and [2]Dipti Sukesh Zawar

[1, 2]Department of Agricultural Biotechnology, Government College of Science, Kishore, Maharashtra, India

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ABSTRACT

One of the most prized medicinal plants in the Zingiberaceae family is Kaempferia rotunda L. Common names for Kaempferia rotunda include Indian crocus and peacock ginger. Keralan traditional medicine uses this attractive, aromatic plant with a highly fragrant subglobose yellow-white tuberous rhizome. The plant's rhizomes and root tubers are used extensively in India and Southeast Asia as a vegetable and culinary flavoring spice due to their bitter, camphoraceous taste. The plant is extensively found in Asia and Africa's tropical and subtropical regions. It is found all throughout the Indian subcontinent, from the Malay Peninsula to Malay Island, and from the eastern Himalayas to Sri Lanka. In Kerala State, India's Western Ghat area, it grows naturally. It is essential to plant high yielding types on a big scale in order to increase productivity and output. The research was conducted because it is crucial to know how much genetic variation exists between various accessions when choosing parents for breeding programs. Kanakamany tried to induce genetic diversity in K. galanga.

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Introduction

An analysis of *Curcuma amada* and *Kaempferia galangal* were to determine which genotypes were better by looking at genetic diversity, character association, and genetic divergence. There have been few attempts to investigate the genetic diversity of K. rotunda in Kerala State. This research aims to assess the genetic diversity of a plant species that is grown to a relatively little extent despite its medicinal and economic significance. Finding better genotypes in the germplasm is also crucial as it helps with parent selection in breeding initiatives. Furthermore, a variety of different crops' germplasm accessions have been grouped using genetic diversity analysis and the clustering approach [3–7]. The study was carried out from 2017 to 2020 on the experimental plot of the Department of Botany, Genetics and Plant Breeding Division, University of Calicut, Kerala, India. The trials were set up in three replications in an open field setting using randomized block design (RBD). Situated 50 meters above mean sea level, the experimental plot is situated at 75°46' E longitude and 11°15' N latitude.

* Corresponding author.
E-mail address: sharmasonalm143@gmail.com (Sonal Mukesh Sharma)

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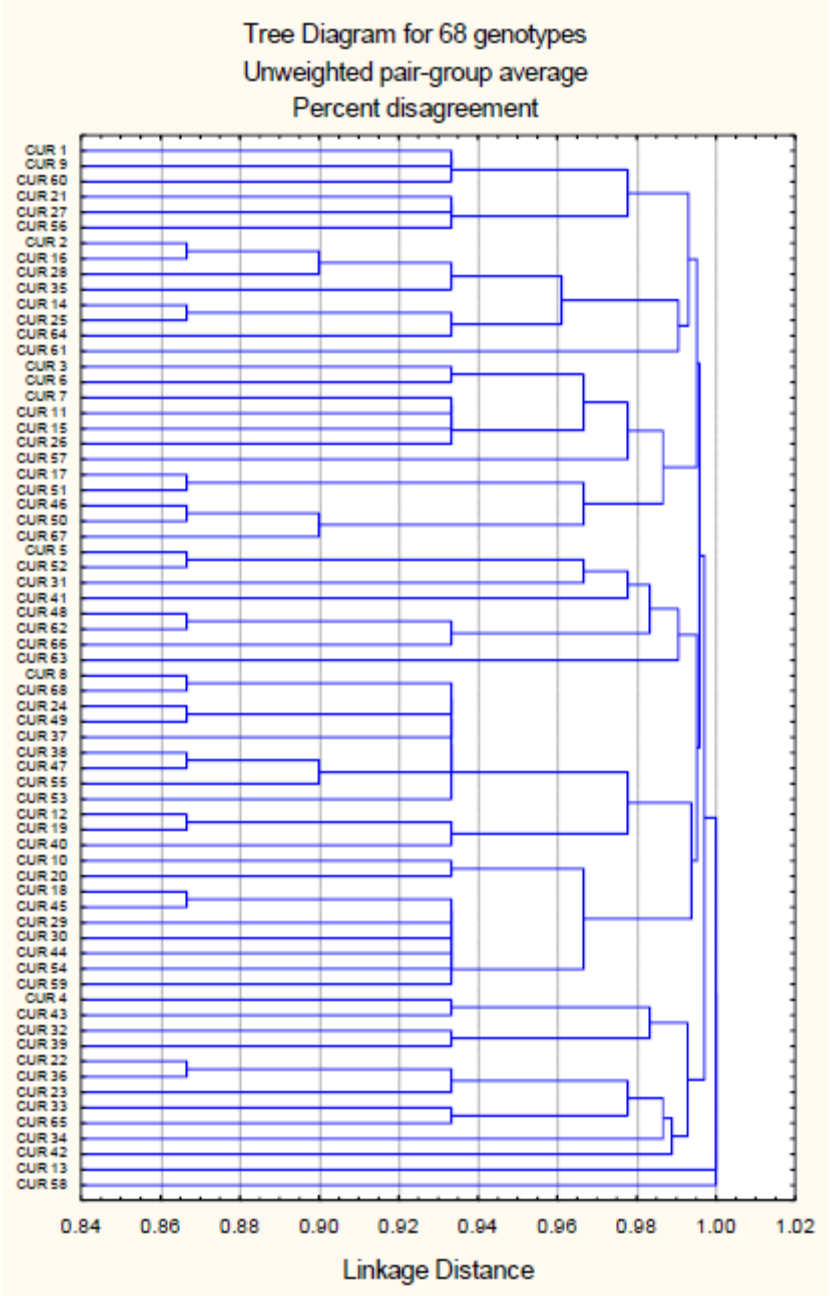
The research region has an average temperature between 17.83°C and 36.83°C and receives 247 cm of rainfall annually. For this research, K. rotunda accessions that were gathered from several sites around Kerala State, India, were used. Three years' worth of morphometric observations were combined, and the resulting data were used for the study. Measurements on fifteen growth and yield characteristics, including plant height (cm), the number of tillers, and the number of leaves per tiller, are included in the data. Leaf measurements include length (cm), width (cm), area (cm2), number of primary and secondary fingers, length (cm), diameter (dm), length (cm) of the mother rhizome, length of the secondary fingers, diameter of the mother rhizome, and yield per plant (g). The accessions were sorted into several groups using Sokal and Michener's [8] UPGMA (Unweighted Pair Group Method with Arithmetic Mean) agglomerative hierarchical clustering technique, which was used for statistical analysis in order to evaluate the genetic diversity.

Any breeding program's capacity to succeed relies on the base population's level of genetic variety and availability. Cluster analysis is mostly used in plant breeding experiments to divide accessions into many homogenous groups so that accessions within a group respond to stimuli similarly across sites. Using UPGMA, a straightforward agglomerative hierarchical clustering technique, sixty-eight K. rotunda accessions were analyzed to determine the proximity and separation between them based on fifteen agronomic characteristics. The whole set of accessions was sorted using cluster analysis into three clusters with a linkage distance of 0.998 (Fig 1). Sixty-six accessions make form the first cluster, indicating maximal accommodations for related genotypes. One accession, CUR 13, was obtained from Kottayam District and is occupied in the second cluster; CUR 58 was acquired from Wayanad District and is occupied in the third cluster. Once again, at a linkage distance of 0.996, the first cluster splits into two subclusters: the first has 55 genotypes, while the second has 11 genotypes. These subclusters were periodically split into distinct groups based on their highest level of genetic similarity [9].



In relation to the characters under investigation, it was discovered that 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 more genetically related. The first cluster includes all twelve of these groupings, and at a linkage distance of 0.865, they split apart. All thirteen districts' genotypes are present in Cluster I. As a result, each cluster has a combination of genotypes that were obtained from various geographic locations, showing that physical distance is not a significant factor in determining the genetic distance and proximity between the accessions under study. This kind of grouping might be caused by genetic differences in makeup as well as environmental influences [10]. Genotypes that are part of the same clusters are thought to have greater genetic closeness due to their higher levels of similarity, whereas genotypes that are part of separate clusters are thought to be genetically distant from one another and have higher degrees of genetic divergence.

Genetic diversity may be defined as genotypes that are distantly related (Table 1). Based on further performance evaluations, the various Kaempferia rotunda accessions may be chosen for enhanced programs in order to maximize genetic diversity and produce high-yielding cultivars.

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

Conclusion

The UPGMA simple agglomerative hierarchical clustering algorithm was used to sixty-eight peacock ginger accessions in order to determine the proximity and separation between the accessions based on fifteen agronomic characteristics. Three clusters were formed from the accessions. The accessions from the farthest-flung clusters may be discovered and employed in hybridization programs to create more promising and superior hybrids, based on the inter-cluster distance. The UPGMA clustering approach is a useful tool for determining the genetic diversity found in a population. This method may be used in crop development initiatives to aid in the selection of genetically distinct parents.

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