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# A STUDY ON THE GENETIC CONTROL OF THE KEY AGRONOMIC CHARACTERS OF *ZINGIBER ZERUMBET* (L.) ROSCOE EX SM.

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**ABSTRACT** *Zingiber zerumbet* (L.) Roscoe ex Sm., widely known as shampoo ginger and pinecone ginger is a medicinal and ecologically important Zingiberaceous plant. The pharmaceutical and cosmetic industries are interested in this plant because of its bioactive components like zerumbone, which are anti-inflammatory, antioxidant, antibacterial, and anticancer. Physicochemical and pharmacological investigations of *Zingiber zerumbet* have been described, but no efforts have been made to study its genetic diversity geographically and comprehend its genetic control of agronomic traits. Thus, an experiment was carried out to analyze the genetic control of the major agronomic characters in *Zingiber zerumbet.* Seven growth characters and eleven yield characters were studied. All the growth characters, plant height, stem circumference, number of tillers, number of leaves per tiller, leaf length, leaf breadth and leaf area exhibited continuous frequency distribution with skewness toward the proximal end indicating that their gene pools have more recessive alleles. Eight of the eleven yield parameters studied such as fresh yield per plant, dry yield per plant, length of primary finger, number of secondary fingers, length of secondary finger, circumference of secondary finger, length of mother rhizome and circumference showed skewness toward the proximal side. This indicated the presence of more recessive alleles. The number and diameter of primary fingers revealed a balanced genotype distribution almost evenly towards the proximal and distal sides indicating that recessive and dominant alleles contributing to these traits occur at the same frequency. Therefore, fifteen of the 18 agronomic characters had a continuous frequency distribution with proximal skewness showing a predominance of recessive alleles in the gene pool suggesting limited expression of dominant traits and the need for selection to develop superior genotypes.

**KEYWORDS :** *Zingiber Zerumbet*, agronomic traits, genetic control, frequency distribution, skewness, proximal side, distal side, recessive alleles and dominant alleles.

## INTRODUCTION

*Zingiber zerumbet* (L.) Roscoe ex Sm., popularly known as shampoo ginger or pinecone ginger is a perennial herbaceous plant with tuberous roots that grows naturally in thickets on hill slopes or in moist, shaded lowland environments (Yob *et al.*, 2011). *Zingiber zerumbet* has a varied phytochemical profile with a range of bioactive compounds present in its rhizomes, leaves and flowers. These include phenolic compounds, gingerols, terpenoids, flavonoids and paradols. The rhizomes are particularly rich in the bioactive substances that give the plant its medicinal properties (Pradhan and Sarkar, 2023). In many parts of the world *Z. zerumbet* has long been used in traditional medicine to treat a wide range of ailments. The plant is said to have anti-inflammatory, antibacterial, antioxidant, analgesic, and antidiabetic properties. It has also been used to treat cardiovascular diseases, cancer, diabetes, arthritis, respiratory disorders, digestive problems and skin concerns. Additionally, shampoo ginger has antibacterial qualities that protect against a variety of diseases such as viruses, fungi and bacteria. Because of its powerful scent, shampoo ginger is utilized in the perfume industry. In floral arrangements, the perennial pinecone-like blossoms are employed. There may be unidentified industrial, medical, and phytochemical applications for *Z. zerumbet* (Sahu *et al.,* 2018). Therefore, it is necessary to properly harvest, cultivate and conserve this plant. Pharmacological properties of *Zingiber zerumbet* continue to draw scientific attention and its therapeutic efficacy is still unclear, highlighting the need for more research to confirm its potential uses.

Plant breeding frequently requires genetic diversity to enhance crop genetic output potential and use variance for development. Plant breeding combines genetic diversity and selection methods to improve quantitative and qualitative traits. Morphological characterization is essential for the description and classification of plant germplasm in any crop since the degree of genetic variability is a fundamental determinant in the formulation of a targeted breeding program (Smith and Smith, 1989). Therefore, research was conducted at the Genetics and Plant Breeding Division of the Department of Botany, University of Calicut, India, during 2023-2024 to assess the genetic control of agro-morphometric characters of the germplasm collected from diverse places throughout Kerala State, India.

## MATERIALS AND METHODS

Seventy two *Z. zerumbet* accessions with nine plants each that were collected from various parts of Kerala State, India comprised the study material (Figure1). Fresh, healthy rhizomes weighing between 25 and 30g and measuring between 4 and 7 cm were used as planting material. The rhizomes were planted in 38 cm × 35 cm grow bags filled with soil, potting mixture and cow dung in a 3:1:1 ratio during the first week of February 2023. Irrigation was carried out once a day on all non-rainy days and weeding was done as and when required. 10g of vermicompost was applied to each plant at monthly intervals starting from the 30th day of growth up to the 6th month of growth. Growth parameters were recorded and analyzed after the sixth month of growth and yield characters in the 9th month after harvesting. Field observations of agronomic characters were conducted at the time of maturity like plant height, stem circumference, number of tillers, number of leaves per tiller, leaf length and leaf breadth. Leaf area was calculated using a conversion factor (leaf length x leaf breadth x conversion factor). The conversion factor was determined using the graphical method by measuring the areas of five randomly selected leaves and calculating their mean. The conversion factor in the case of *Zingiber zerumbet* has been calculated as 0.62. Fresh yield per plant, dry yield per plant, number of primary fingers, length of primary finger, circumference of primary finger, number of secondary fingers, length of secondary finger, circumference of secondary finger, length of mother rhizome, circumference of mother rhizome and moisture content were recorded after the harvest of rhizomes. In order to investigate the genetic control of the characters and ascertain the pattern of distribution of dominant and recessive alleles in the gene pool, data were combined and subjected to frequency distribution analysis.

**Figure 1: *Zingiber Zerumbet* in the Experimental Field**

## RESULTS AND DISCUSSION

An experiment was carried out to assess the genetic control of seven growth characters and eleven yield characters namely plant height, stem circumference, number of tillers, number of leaves per tiller, leaf length, leaf breadth, leaf area, fresh yield per plant, dry yield per plant, number of primary fingers, length of primary finger, circumference of primary finger, number of secondary fingers, length of secondary finger, circumference of secondary finger, length of mother rhizome, circumference of mother rhizome and moisture content of a population of 648 plants.

All the seven growth characters such as plant height, stem circumference, number of tillers, number of leaves per tiller, leaf length, leaf breadth and leaf area showed continuous frequency distribution as evidenced by their frequency curves (Figure 2). Continuous frequency distribution with all possible intermediates indicates polygenic control of these characters. Skewness towards the proximal end of the distribution with accumulation of a higher number of recessive alleles indicating that the gene pools of these characters exhibit skewness towards the proximal side of the distribution curve. This suggested that the population being studied has a higher accumulation of recessive contributing alleles.

Among the eleven yield characters studied, the eight characters namely fresh yield per plant, dry yield per plant, length of primary finger, number of secondary fingers, length of secondary finger, circumference of secondary finger, length of mother rhizome and circumference of mother rhizome showed skewness towards the proximal side of the distribution. This indicates that a higher number of recessive contributing alleles are accumulated in the population studied. So, choosing better genotypes and phenotypes with more dominant contributing alleles is necessary to develop superior varieties.

The number of primary fingers and circumference of the primary finger showed a comparatively balanced distribution of genotypes almost equally towards the proximal and distal sides of the distributions indicating the occurrence of equal frequency of the recessive and dominant alleles contributing to these characters. Balanced frequency distribution can be regarded as an ideal situation in the case of a non-selected natural population. Moisture content showed continuous distribution with skewness towards the distal side of the distribution. This distribution indicates that the gene pool of this character shows accumulation of a higher number of dominant alleles even when maintaining a fairly good genetic base ranging from comparatively lower to higher values.

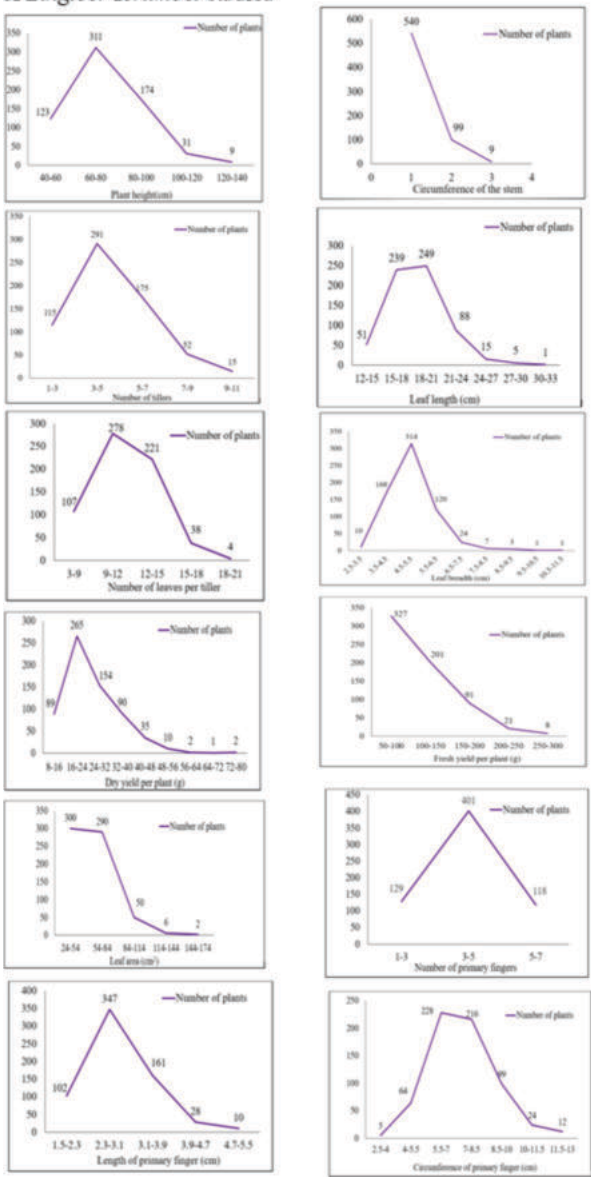
Quantitative characters that are regulated by a number of genes typically show continuous and frequently normal distributions, particularly when allele frequencies are balanced and gene effects are minimal (Falconer and Mackay,1996). When the frequencies of the dominant and recessive alleles are equal, quantitative features with polygenic control have a normal frequency distribution (Chahal and Gosal, 2002). When the frequency of dominant or recessive alleles varies within the distribution, the bell-shaped normal frequency distribution curve exhibits skewness (Senthil *et al.,* 2020). All the morphometric traits studied showed a continuous frequency distribution as seen in Figure 2. A continuous pattern with many intermediate values showed that these traits are controlled by several genes.

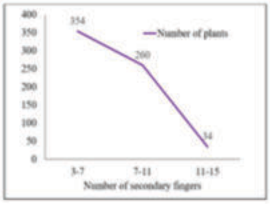
In a number of crops, frequency-distribution analysis has been extensively documented as a means of comprehending genetic behaviour. The significance of class distribution in root crops has been highlighted by studies in sweet potatoes and cassava that have also used phenotypic distribution patterns to investigate tuber yield, dry matter, and starch content (Woolfe, 1992). Class distribution curves and skewness patterns have been used to assess grain yield and morphometric parameters in rice in order to deduce polygenic control and allele frequency correlations (Rashmi *et al.,* 2017). *Curcuma amada* had more dominant alleles in terms of primary finger length and secondary finger diameter (Jayasree, 2009). Radhakrishnan (2003) discovered that in cardamom, features such as leaf breadth, seeds per capsule, and recovery percentage were more common in dominant alleles. The frequency distributions of phenotypes for genetic analysis in a range of crops, such as soybean (Nayana and Fakrudin, 2020), tomato (Reddy *et al.,* 2023), *Curcuma aeruginosa* (Soorya *et al.,* 2016), Western Indian arrowroot (Sintu *et al.,* 2016), *Cassia tora* (Chandramohanan and Mohanan, 2005), brinjal (Tripathy *et al.,* 2025) and vanilla (Umamaheswari, and Mohanan, 2011) were also done. Similar approaches were applied in maize, where frequency curves helped identify transgressive segregants and understand the distribution of favourable alleles (Hallauer *et al.,* 2010). In bananas, morphological and yield traits have been analysed using frequency classes to assess diversity and guide selection strategies (Robinson and Sauco, 2010). Studies in green gram have demonstrated the usefulness of skewness and kurtosis in interpreting variability in seed yield and plant architecture (Kanavi *et al.,* 2020). Studies like these have become key to evaluating genetic diversity and initiating future breeding programmes.

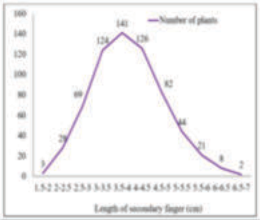
## CONCLUSION

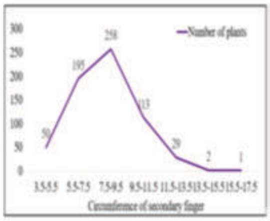
*Zingiber zerumbet* is a promising plant rich in health-enhancing compounds. Preserving the existing genetic diversity of this species in its natural habitats and homestead cultivation systems is crucial for sustaining its genetic potential. The continuous frequency distribution of the eighteen agronomic traits, with most of them showing skewness towards the proximal side indicates a greater accumulation of recessive contributing genes in the genetic pool. At the same time, identifying and selecting genotypes that accumulate favourable dominant traits governing key agronomic characters is necessary for developing improved varieties. Such improvement would benefit both homestead growers and commercial cultivators by enhancing yield and promoting wider acceptance of the crop for nutraceutical and economic purposes.

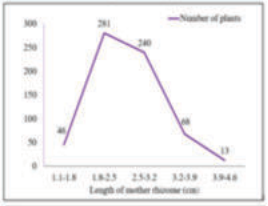
Figure 2: Frequency curves of agronomic characters of *Zingiber zerumbet* studied

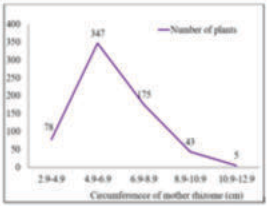


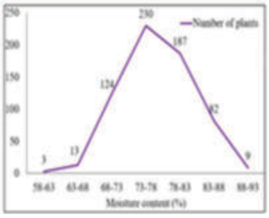












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