

Factor Analysis in Peacock Ginger (*Kaempferia rotunda* L)

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ABSTRACT

A pooled factor analysis of fifteen morphometric variables representing growth and yield characters of sixty eight accessions of peacock ginger (*Kaempferia rotunda* L.) was carried out to determine character association and for identifying marker characters which accommodate the inheritance of associated characters. Among the fifteen variables subjected to factor analysis, three factors were identified as having maximum influence on growth and yield characters of peacock ginger. Out of the three factors identified, two factors controlled yield characters and the other factor controlled growth characters. The characters identified with maximum factor loadings in each group include diameter of primary finger, diameter of secondary finger and diameter of mother rhizome which can be regarded as the lead characters among the fifteen characters under study in *K. rotunda*. The three factors accounted for 76.12% of the total variance.

INTRODUCTION

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. One of the constraints in the successful utilization of germplasm in breeding programmes is the delay in its characterization, evaluation

and cataloguing. In the genetic evaluation of germplasm, observations on a large number of growth characters and yield characters are to be recorded for estimation of correlation among the characters. The recording of data on such large number of characters is time consuming when large number of genotypes is evaluated. In the present study, a factor analysis by means of principal component analysis was carried out to identify such underlined factors. The factor analysis is a useful statistical tool to reduce the total number of variables to be studied by identifying marker variables, which will accommodate the inheritance of a set of variables associated with it. Factor analysis has been utilized for data reduction and grouping of variables by earlier investigators like Tadesse et al in grass pea [1], Hrideek et al. in chilli [2], Radhakrishnan et al. and Hrideek et al. in small cardamom [3,4], Nikhila et al in robusta coffee [5], Filipovic et al. in maize [6], Yol et al. in sesame [7], Khan et al. in linseed [8], Shintu in West Indian arrowroot [9], Denton and Nwangburuka in *Solanum anguivi* and Umamaheswari and Mohanan in *Vanilla planifolia* [10]. The present study is the first of its kind to be undertaken in this underutilized crop.

MATERIALS AND METHODS

The experiment was conducted in the experimental plot of the Genetics and Plant Breeding Division of the Department of Botany, University of Calicut and 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 and 11° 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 247 cm. *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 (cm²), 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). Factor analysis was done using the principal component analysis method as described by Harman (1976) [11].

RESULTS AND DISCUSSION

The study of association of characters in different crops is an important approach in determining the relationship between quantitative morphometric characters of agronomically important plant species since such studies could provide genetic foundation for further breeding and improvement in such species. Analysis of 15 morphological, growth and yield characters enabled to get a set of reduced number of variables. From the analysis, three factors were identified, which accounted for 76.12% variability in these 15 variables. The percentage of variance contributed by the characters of the first factor was 45.87%, that contributed by the characters of the second factor was 19.99%, that contributed by the characters of the third factor was 10.26% (Table 1). All the variables were grouped with respect to various factors identified and marker variables were identified based on factor loadings for each character (Tables 2 and 3).

Table 1. Eigen values and percentage of total variance

Fact ors	Eigen value	Percentage of total variance	Cumulative Eigen value	Cumulative percentage of variance
1	6.880730	45.87154	6.88073	45.87154
2	2.998695	19.99130	9.87942	65.86283
3	1.538332	10.25555	11.41776	76.11838

Table 2. Factor loadings

Characters	Factor 1	Factor 2	Factor 3
Plant height	-0.391931	-0.829121	0.121279
Number of tillers	-0.561726	0.359516	0.063133
Number of leaves per tiller	0.078180	-0.747636	-0.527882
Leaf length	-0.513012	-0.769417	0.284222
Leaf breadth	-0.701499	-0.123744	0.326282
Leaf area	-0.688183	-0.560532	0.368340
Number of primary fingers	-0.488531	0.122187	-0.587466
Number of secondary fingers	-0.697642	0.225920	-0.553630
Length of primary finger	-0.815597	0.051847	-0.068903
Diameter of primary finger	-0.908291	0.220105	0.038651
Length of secondary finger	-0.848075	0.065925	-0.119067
Diameter of secondary finger	-0.886737	0.178536	-0.070793
Length of mother rhizome	-0.815030	0.227604	0.117072
Diameter of mother rhizome	-0.866097	0.238975	0.119813
Yield per plant	-0.202747	-0.662790	-0.461463
*Figures in bold represent maximum factor loadings of the characters			

Table 3. Characters showing association as per factor analysis

Factor	Characters associated
1	Length of primary finger, diameter of primary finger, length of secondary finger, diameter of secondary finger, length of mother rhizome, diameter of mother rhizome
2	Plant height, number of leaves per tiller, leaf length
3	Number of primary fingers

In the study, the first factor was associated with length of primary finger, diameter of primary finger, length of secondary finger, diameter of secondary finger, length of mother rhizome, diameter of mother rhizome. All these variables can be expected to behave alike in their inheritance as a single factor and it is believed to control the inheritance of these variables. The first factor was associated with the yield characters. Here diameter of primary fingers, diameter of secondary fingers and diameter of mother rhizome could be identified as the marker characters as they possess maximum factor loadings. The second factor was found to be associated with growth characters like plant height, number of leaves per tiller, leaf length. Here the maximum factor loading was for the character plant height which could be identified as the marker character. The third factor was also found to be associated with yield characters like number of primary fingers and number of secondary fingers. The characters number of primary fingers and number of secondary fingers were found to have maximum factor loadings and they could be considered as the marker characters. The characters with maximum factor loadings identified under each factor could be identified as marker characters. Therefore, diameter of primary finger, diameter of secondary finger, diameter of mother rhizome, plant height, number of primary fingers and number of secondary fingers could be regarded as the marker characters among the fifteen characters under study in *K. rotunda*. Thus, the dimension of the data could be reduced to six variables controlled by 3 factors, which can very well present the structure of the whole data from the complete set of variables.

Factor analysis provides an efficient tool to identify the marker characters which could very well present the structure of the whole data, thereby reducing the dimension of the data. This assumes importance in the context of

evaluating large number of germplasm accessions. While practising selection and further crop improvement of this valuable medicinal plant, the marker characters identified shall be given preference for selection.

CONCLUSION

Analysis of 15 morphological, growth and yield characters enabled to get a set of reduced number of variables. From the analysis, three factors were identified, In the study, the first factor was associated with length of primary finger, diameter of primary finger, length of secondary finger, diameter of secondary finger, length of mother rhizome, diameter of mother rhizome. All these variables can be expected to behave alike in their inheritance as a single factor and it is believed to control the inheritance of these variables.

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