



A STUDY ON THE GENETIC VARIABILITY OF *CURCUMA ZEDOARIA* ROSC. ACCESSIONS OF KERALA

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ABSTRACT

Curcuma zedoaria Rosc., an important member of the family Zingiberaceae possesses antioxidant and anti-inflammatory curcuminoids in it and has wide applications in the treatment of various diseases like diarrhoea, stomach ache, ulcer, cancer etc. This medicinal herb faces acute narrowing of natural populations due to overexploitation and human activities. The production of promising genotypes of the species has immense scope in the field of medicine. The present study was conducted to assess the genetic variability of *C. zedoaria* in Kerala state of India with regard to its 15 agronomic characters. Fifty seven accessions of the species were collected from different locations across the state and grown in RBD. The variability studies were performed in terms of GCV, PCV, heritability and genetic advance. All the characters showed statistically significant variation as revealed by ANOVA. The characters with higher values of GCV, PCV, heritability and genetic advance show considerable variability in the study area. The results can be used for the selection of parental plants in crop improvement practices to develop promising genotypes. The presence of high range of variation in the case of the characters studied indicates high influence of the environment on their phenotypic expression. The heritability of characters ranged from 4.76% to 92.65%. The maximum heritability was observed for plant height (92.65%) followed by leaf length (92.18%). Genetic advance varied from 5.71% to 98.79%. The highest genetic advance was recorded for leaf area (98.79%) followed by yield per plant (80.36%). The experiment reveals the presence of a broad genetic base for *C. zedoaria* in the study area.

Keywords: *Curcuma zedoaria*, white turmeric, genetic variability, genetic advance, heritability.

1. INTRODUCTION

Genetic variability analysis of a species deals with the study of the measures of variation present between individual genotypes of a population. A thorough knowledge on genetic variability is important for a better understanding of genetic diversity of the species and ultimately for the genetic improvement practices [1]. Formulation of suitable breeding strategies on genetic improvement programmes requires the availability of information on the extent of genetic variations, heritability and genetic advance with respect to yield and yield determining traits in the crop [2]. Study of association of agronomic traits with yield also has a vital role in crop improvement programmes. It helps to estimate the heritable and nonheritable traits of crops and for the possible improvement of the characters under

study [3]. Improvement of a crop strictly depends upon the magnitude of genetic variability and the extent of transmission of characters over generations [4]. Heritability estimates of the crop help the breeder to perform better selection based on phenotypic performances [5].

About 60% of the world's population depends upon the traditional medicinal systems [6]. The one and only source of traditional medicine is green plants. Indian forests serve as rich reservoirs of thousands of medicinal plants from which the herbal drugs are prepared [7].

The genus *Curcuma* is having immense importance among medicinal plants. *Curcuma* belongs to the family Zingiberaceae and comprises of about 80 species [8]. Members of the genus have great economic value and many of them are commercially cultivated. Some

members possess beautiful inflorescences and luxurious foliage making them ornamentally important [9].

Among the members of the genus *Curcuma*, *C. zedoaria* is an important member because of its immense medicinal value. The species is commonly known as white turmeric and is a perennial aromatic herbaceous plant. The plant is variously used as vegetable, spice, perfuming agent, medicine, etc. [10- 12]. Various parts of the plant are used in Ayurveda and other folk and traditional medicinal systems. It is an inevitable constituent of several ayurvedic preparations like *valiya rasnadi kashayam*, *bractiyadi kwatha*, *dashamularishtam*, etc. [13]. Known as white turmeric and zedoary, it is being cultivated throughout India, and it grows wild in Eastern Himalayas and in the moist deciduous forests of the central regions of Kerala and Karnataka. The plant has several vernacular names like *kachooram* (Malayalam), *krachura* (Sanskrit), *sutha* (Bengali) and *gandamatsi* (Hindi) [14]. Zedoary is reported to have antiarthritic, analgesic, antiulcer, antiasthmatic, antipyretic, antidiabetic and diuretic activities along with cytotoxic effects against human ovarian cancer cells [15-18]. In spite of its varied commercial values *C. zedoaria* is a less studied crop with respect to its genetic variability and improvement. Also, the continued exploitation of the species will result in the gradual decline of its population size. In the light of these factors, it is necessary to initiate priority actions for the conservation and improvement of the available genetic resources of *C. zedoaria*. Hence, the present study aims to investigate the genetic variability, heritability and genetic advance of the morphological characters of the collected accessions of *C. zedoaria* across Kerala State, India.

2. MATERIAL AND METHODS

Fifty seven accessions of *Curcuma zedoaria* collected from various locations of Kerala State, India upon extensive field exploration formed the experimental material (Table 1). The present study was carried out in the experimental plot of the Genetics and Plant Breeding Division of Department of Botany, University of Calicut, Kerala, India. The experimental field is located at 75°46' E longitude and 11°15' N latitude at an elevation of 50m from MSL. Preliminary screening of the germplasm was carried out in 2018-19 and the field experiment was done in 2019-20. The experiment was laid out in randomized block design (RBD) with three replications. Healthy rhizomes collected from the germplasm developed in the previous year were planted in the experimental plot during the first week of May 2019.

Table 1: Accessions of *Curcuma zedoaria* collected

Sl. No.	Accession No.	Source	District
1	CUW1	Kolothupadi	Thrissur
2	CUW2	Nadavarambu	Thrissur
3	CUW3	Vellangallur	Thrissur
4	CUW4	Konathukunnu	Thrissur
5	CUW5	Narayanamangalam	Thrissur
6	CUW6	Moothakunnam	Ernakulam
7	CUW7	Vadakkemkara	Ernakulam
8	CUW8	Kalluchira	Ernakulam
9	CUW9	Maliankara	Ernakulam
10	CUW10	Kottuvallikkad	Ernakulam
11	CUW11	Kodungallur	Thrissur
12	CUW12	Santhipuram	Thrissur
13	CUW13	Mathilakam	Thrissur
14	CUW14	Edamuttam	Thrissur
15	CUW15	Thriprayar	Thrissur
16	CUW16	Ramavarnapuram	Thrissur
17	CUW17	Vellanikkara	Thrissur
18	CUW18	Velloor	Kottayam
19	CUW19	Koyilandy	Kozhikode
20	CUW20	Mukkam	Kozhikode
21	CUW21	Chevayoor	Kozhikode
22	CUW22	Thenhipalam	Malappuram
23	CUW23	Olipramkadavu	Malappuram
24	CUW24	Arakkapparambu	Ernakulam
25	CUW25	Pithrukunnam	Kottayam
26	CUW26	Muravanthuruthu	Ernakulam
27	CUW27	Murinjapuzha	Kottayam
28	CUW28	Kattikkunnu	Kottayam
29	CUW29	Kundannoor	Thrissur
30	CUW30	Arukkutti	Alappuzha
31	CUW31	Kumbalam	Ernakulam
32	CUW32	Kalathezath	Alappuzha
33	CUW33	Pallipuram	Alappuzha
34	CUW34	Vazhathara	Alappuzha
35	CUW35	Thirunalloor	Alappuzha
36	CUW36	Vattassery	Alappuzha
37	CUW37	Arthunkal	Alappuzha
38	CUW38	Pottikavala	Alappuzha
39	CUW39	Muttathiparambu	Alappuzha
40	CUW40	Karikkad	Alappuzha
41	CUW41	Kattachira	Kottayam
42	CUW42	Kudavechoor	Kottayam
43	CUW43	Arippanthara	Kottayam
44	CUW44	Vechoor	Kottayam
45	CUW45	Kadanad	Kottayam
46	CUW46	Pizhaku	Kottayam
47	CUW47	Chazhoor	Thrissur
48	CUW48	Ammadam	Thrissur
49	CUW49	Peringottukara	Thrissur
50	CUW50	Chemmapilly	Thrissur
51	CUW51	Vadakkumuri	Thrissur
52	CUW52	Padiyam	Thrissur
53	CUW53	Kattoor	Thrissur
54	CUW54	Manavalassery	Thrissur
55	CUW55	Konathukunnu	Thrissur
56	CUW56	Kodakkepparambu	Thrissur
57	CUW57	Karooppadanna	Thrissur

The rhizomes were separated and each rhizome was planted in 38cm x 35cm polybag filled with garden soil, sand and enriched compost in 3:1:1 ratio. Weeding was carried out systematically and optimum soil moisture was maintained. Starting from the 30th day of planting, 2g of NPK (18:18:18) was applied per plant at monthly intervals. The data on growth and yield characters were recorded by destructive sampling at maturity and the data were subjected to analysis of variance (ANOVA) to test the significance of variation [19]. Phenotypic variance, genotypic variance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance were analysed to study the extent of variation in the case of each character. Phenotypic and genotypic variations of

the fifteen characters were estimated using standard methods of analysis [20]. Heritability (broad sense) and genetic advance were calculated as suggested by earlier workers [20, 21].

3. RESULTS AND DISCUSSION

Table 2 represents the values of range, mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance with respect to all the 15 agronomic characters of *C. zedoaria* under study. Analysis of variance revealed statistically significant differences between the accessions at 1% level for all the 15 characters studied.

Table 2: Range, mean, genotypic variance, phenotypic variance, GCV, PCV, heritability (broad sense) and genetic advance of the characters studied in *Curcuma zedoaria*

Sl. No.	Characters	Range	Mean	Genotypic variance	Phenotypic variance	GCV (%)	PCV (%)	Heritability	Genetic advance
Growth characters									
1	Plant height (cm)**	13-113	66.86	484.32	5522.76	32.92	34.19	92.65	65.26
2	Number of tillers**	1-3	1.20	0.003	0.25	4.17	20.83	4.76	2.04
3	Number of leaves per tiller**	2.5-11	6.79	0.19	1.00	6.48	14.80	18.81	5.71
4	Leaf length (cm)**	8.3-75.3	44.06	179.55	194.78	30.41	31.68	92.18	60.17
5	Leaf breadth (cm)**	1.83-11.16	6.50	4.24	4.64	31.69	33.08	91.38	62.26
6	Leaf area (cm ²)**	9.25-422.05	189.14	9120.56	10111.95	50.49	53.17	90.20	98.79
Yield characters									
1	Yield per plant (g)**	20-635	156.44	4875.91	6383.67	44.64	51.07	76.38	80.36
2	Number of primary fingers**	1-8	3.01	0.25	0.65	16.61	26.91	38.46	21.32
3	Length of primary finger (cm)**	2.1-28.7	12.74	8.66	13.03	23.08	28.34	66.46	38.79
4	Circumference of primary finger (cm)**	1.6-9	4.84	0.96	1.32	20.25	23.76	72.73	35.60
5	Number of secondary fingers**	3-43	16.77	28.77	47.42	31.96	41.09	60.67	51.35
6	Length of secondary finger (cm)**	1-18.7	6.71	5.63	8.01	35.32	42.18	70.29	61.07
7	Circumference of secondary finger (cm)**	0.8-8.1	3.79	0.73	1.12	22.43	27.97	65.18	37.55
8	Length of mother rhizome (cm)**	2-8.6	4.46	0.70	0.94	18.83	21.75	74.47	33.36
9	Circumference of mother rhizome (cm)**	2.8-16.4	7.73	5.69	6.52	30.92	32.99	87.27	59.31

Plant height showed a mean value of 66.86 cm and its range varied from 13cm to 113cm. The range of number of tillers varied from 1 to 3 and the mean value was 1.20. The mean value of number of leaves per tiller was 6.79 with the range varying from 2.5 cm to 11cm. Leaf length had a mean value of 44.06 cm with its range varying from 8.3 cm to 75.3 cm. The range of leaf breadth varied from 1.83 cm to 11.16 cm with a mean value of 6.50. Leaf area had the mean value of 189.14 cm² and the range varied from 9.25 cm² to 422.05 cm². Yield per plant varied from 20 g to 635 g with a mean value of 156.44. Number of primary fingers showed a mean value of 3.01 and the range varied from 1 to 8. Length of primary finger varied from 2.1 cm to 28.7 cm with the mean value of 12.74 cm. The mean value of circumference of primary finger was 4.84 cm with the range varying from 1.6cm to 9 cm. Number of

secondary fingers ranged from 3 to 43 and the mean value was 16.77. The length of secondary finger had the mean value of 6.71 cm with its range varying from 1cm to 18.7 cm. The mean value of circumference of secondary finger was 3.79 and its range varied from 0.8cm to 8.1 cm. Length of mother rhizome varied from 2cm to 8.6 cm with the mean value of 4.46 cm. The circumference of mother rhizome ranged from 2.8 cm to 16.4 cm with the mean value of 7.73 cm.

The amount of variability present in a germplasm can be detected using its genotypic coefficient of variation and phenotypic coefficient of variation. Likewise, the influence of environment on the expression of a character can be measured by looking at the broad sense heritability and genetic advance of the characters being studied [22].

All the 15 agronomic characters studied have their PCV values higher than the corresponding GCV values. This symbolizes the additive nature, polygenic control and differential degrees of environmental influence on the characters under study.

Among the agronomic characters observed for the study, the PCV value varied between 14.80 for the number of leaves per tiller and 53.17 for the leaf area. The range of GCV was between 4.17 for the number of tillers and 50.49 for leaf area. Leaf area showed the highest PCV and GCV values among the growth characters while yield per plant possessed highest values of PCV and GCV among the yield characters. The difference between PCV and corresponding GCV values gives an idea on the influence of environment on the phenotypic expression of a character. The difference between PCV and corresponding GCV was higher for the characters such as number of tillers, number of primary fingers and number of secondary fingers. This higher difference indicates that these characters are having higher environmental influence on their phenotypic expression, over the remaining characters under study.

The value of broad sense heritability of a character also indicates the extent to which it gets influenced by the environmental factors. Higher value of heritability indicates very low environmental influence on the character. The heritability values of the characters studied ranged from 4.76% to 92.65%. Plant height was the character with the highest heritability (92.65%), followed by leaf length (92.18%) and leaf breadth (91.38%). Heritability was the lowest for number of tillers (4.76%). For the yield characters, diameter of mother rhizome possessed the highest heritability (87.27%) and the lowest value was observed for the number of primary fingers (38.46%). Genetic advance, the next parameter studied is the measure of the amount variation present in a particular population. The highest value for genetic advance was recorded for leaf area (98.79) followed by yield per plant (80.36) and plant height (65.26) while the lowest value was for number of tillers (2.04).

Various workers have used the same pattern of analysis to assess the quantum of variability of quantitative characters in the case of different crop plants like cassia [23], cardamom [24,25], vanilla [26], wild turmeric [27], false turmeric [28], coffee [29], etc. The findings have been used to develop crop improvement protocols both via selection and hybridization. It is expected that

the variability explored presently will also provide the material base for such improvement programmes in white turmeric.

4. CONCLUSION

The present study has shown that the agronomic characters like plant height, yield per plant and leaf area can be used for the selection of superior genotypes of *C. zedoaria*. Significant variation is observed between all the 57 accessions of *C. zedoaria* in the study area, which is an indication of the strong and diverse genetic base of the crop under study. Since the crop faces acute marginalization due to human activities and exploitation, conservation strategies and improvement studies should to be initiated making use of this variability.

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