A study on the genetic variability of false turmeric (*Curcuma zanthorrhiza* Roxb.) in Central Kerala of India

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ABSTRACT *Curcuma zanthorrhiza Roxb., commonly known as false turmeric, belonging to the family Zingiberaceae is an important underutilized medicinal herb that faces acute narrowing of natural populations due to various anthropogenic activities. It is necessary to conserve the plant in order to meet pharmaceutical needs and also to prevent the species from becoming endangered and extinct. A study was carried out to assess the genetic variability of Curcuma zanthorrhiza accessions of Central Kerala, India in relation to growth and yield characters. Eighty four accessions of Curcuma zanthorrhiza collected from the central part of Kerala were grown in RBD and assessed for variability in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2) and genetic advance (GA). High estimates of PCV, GCV, heritability and genetic advance in the case of the characters studied indicated the presence of considerable variability in the genetic resources of this important crop in the study area and also the scope for selection for crop improvement and release of promising varieties. High value of range shown by the characters indicates the involvement of higher number of contributing alleles and higher involvement of environmental factors in the expression of characters. The highest genetic advance was found in number of secondary fingers (73.92 %) followed by yield per plant (67.90 %). Heritability was the maximum for yield per plant (53.87 %) followed by plant height (53.09 %) and number of secondary finger (51.78 %). Number of secondary fingers, plant height, yield per plant and length of primary finger showed heritability above 50 % where as all other characters showed below 50 % heritability. Heritability of the characters ranged from 13.99 % to 53.87 %. All the agronomic characters of Curcuma zanthorrhiza presently studied showed significant variation between the accessions indicating the presence of strong and diverse genetic base for the crop in the study area.*

Keywords: *False turmeric, Curcuma zanthorrhiza, Genetic variability*

Introduction

Genetic variability is a measure of tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity which is the amount of variation seen in a particular population. The study of genetic variability is the crucial step towards the understanding of genetic diversity of a plant species at a particular geographical area. It gives the basic foundation for the genetic improvement of the species (Hughes *et al*., 2008). A detailed knowledge of genetic variability of various quantitative and qualitative characters and their distribution to yield is important for crop improvement. Evaluation and characterization of germplasm is beneficial to assess the genetic variability of the germplasm and confirm the presence of genetic variability accountable to yield (Virmany *et al*., 1983; Hakim, 2013). Genetic variability, heritability along with genetic advance of traits, their association and direct and indirect influence on yield are important for crop improvement in order to estimate the heritable and non-heritable variance which will give clues on possible improvement for the characters under study (Rohman *et al.,* 2003; Tabasum *et al*., 2010; Hallauer *et al.,* 1981).

Morphological characters have been used to evaluate distinctness uniformity and stability and to establish a description of a genotype. This method is thought to be often influenced by environmental conditions, as well as labour intensive (Russel *et al.,* 1997). A comparison of plant morphology is the simplest approach for the detection of mislabeled accessions and the assessment of genetic diversity, and it does not require exorbitant technologies, rather require large area of land to conduct the field experiments. These means of morphological assessments are still having superiority and they are mandatory for identifying adult plants from genetic contamination in the field (Gilbert *et al*., 1999).

Plant genetic resources are the fundamental source for crop improvement which is being conserved *in situ* and *ex situ*. *Ex situ* conservation is designed to maintain genetic diversity available in and genetic integrity of the collected material to avoid loss or degradation. *Ex situ* conservation of landraces and wild relatives provides vital insurance against excessive erosion of a crop's genetic base. Based on this fact, gene bank collections have been established for major and minor crops. These repositories typically contain hundreds or even thousands of accessions originating from several geographic regions and representing a range of

genetic backgrounds. Their efficacy for breeding purposes rest largely on the accuracy of evaluation and passport data, and also on the genetic fidelity of the material held. In the course of time, there is significant scope for the accumulation of documentation errors that lead to wasteful duplication of stocks and also for genetic erosion to occur within accessions. Such events can be extremely difficult to detect but they dramatically reduce the practical value of collections. There is a need, therefore, for a simple system to test the genetic identity and diversity of individuals within accessions and also to compare all accessions held within a collection (Gilbert *et al*., 1999). Enhancement in any crop relies on the magnitude of genetic variability and the amount of transmission of characters from one generation to the next (Sujatha and Renuga, 2013). The low productivity can considerably be increased through the use of diverse donor genotypes for various qualitative and quantitative traits. The development of better cultivar by conventional method is slow but identification of superior clones based on phenotype, which are generally highly heritable, equally expressed in all environments may shorten breeding cycle. While geneticists and plant breeders are particularly interested with diversity at the molecular level (Dempsey, 1996), farmers are more concerned with visible morphological and agronomic variation, which helps them to identify cultivars that are productive and do well in their location specific environment.

Curcuma zanthorrhiza is a perennial rhizomatous herb with lots of medicinal properties. It belongs to the family Zingiberaceae. *Curcuma zanthorrhiza* rhizome is used to treat stomach diseases, liver disorders, constipation, bloody diarrhea, dysentery, children's fever, hemorrhoids and skin eruptions. It has antimicrobial, antimetastatic, anticancer, antioxidant and hypolipidemic activities (Yasni *et al.,* 1993 and Hwang *et al.,* 2000), and it has lot of medicinal and cosmetic properties. Low level productivity of *Curcuma zanthorrhiza* on marginal land is caused by the unavailability of superior varieties that are tolerant to marginal land. Breeding activities of *Curcuma zanthorrhiza* which include characterization of diversity, stability and the estimation of selection criteria need to be done as a basis from assembling superior varieties of *Curcuma zanthorrhiza* (Devy *et al.,* 2009, Pujismanto and Samanhudi, 2011). The demand for this crop is increasing due to its easy availability in herbal markets without adulteration in contrary to many other *Curcuma* species. In order to meet pharmaceutical needs and also to prevent the plant from becoming endangered or extinct, it is necessary to conserve and improve *Curcuma zanthorrhiza* for the benefit of the society (Wardiyati *et al.,* 2011). Hence, the present study has been designed to investigate the genetic variability, heritability and genetic advance of the morphological characters of the species using accessions collected from central part of Kerala State, India.

Materials and Methods

Curcuma zanthorrhiza an important member of the family Zingiberaceae with lots of medicinal and pharmacognostic properties form the experimental material. The plant grows well in well drained loamy soils. The present study was carried out in an experimental plot of the Genetics and Plant Breeding Division, Department of Botany, University of Calicut, Kerala, India. Experiments were laid out in a randomized block design (RBD) with three replications in open field condition. The experimental garden is located at $75^{0}46'$ E longitude and $11^{0}15'$ N latitude at an elevation of 50 m from MSL. Average temperature ranges from 21.9°C - 32.2°C and the annual rainfall is about 290 cm. The experimental area has got a tropical monsoon climate with south-west monsoon rains from June to August, north-east monsoon rains in October-November and dry spell from December to May with summer showers in March, April and May (Anonymous, 2011).

Eighty four accessions of *Curcuma zanthorrhiza* were collected from central part of Kerala State of India comprising Thrissur, Malappuram, Ernakulam, Idukki and Palakkad Districts (Table 1). Fresh, healthy and disease free rhizomes with uniform sized fingers having a weight of approximately 25 g with well developed buds were planted in the first week of April 2016. The rhizomes were planted in polythene bags of size 38 cm x 35 cm. The polythene bags were filled with garden soil, cow dung and sand in 3:1:1 ratio. Planting was done before the start of south west monsoon during the first week of May 2016. Weeding was carried out regularly and optimum soil moisture was maintained. 2 g of NPK (18:18:18) was applied per plant at monthly intervals starting from the 30^{th} day of planting. Growth and yield characters were observed and recorded by destructive sampling at maturity and the data were subjected to analysis of variance (ANOVA) to test the significance of variability. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance were estimated as per Singh and Choudhary (1985). Heritability (broad sense), the fraction of total variance that is heritable was estimated as the percentage of genotypic variance over phenotypic variance as per Chahal and Gosal (2002).

Table 1. Details of *Curcuma zanthorrhiza* accessions studied

Sl. Number	Accession Number	Location	District
1	CUZ 1	Kottekkad	Thrissur
2	CUZ 2	Mapranam	Thrissur
3	CUZ 3	Kuthiran	Thrissur
4	CUZ 4	Chemmanda	Thrissur
5	CUZ 5	Anandapuram	Thrissur
6	CUZ 6	Perinjanam	Thrissur
7	CUZ 7	Puthankurisu	Ernakulam
8	CUZ 8	Koovapally	Ernakulam
9	CUZ 9	Nellayi	Thrissur
10	CUZ 10	Athirapally	Thrissur
11	CUZ 11	Vaalkulambu	Palakkad
12	CUZ 12	Chovoor	Thrissur
13	CUZ 13	Perinthalmanna	Malappuram
14	CUZ 14	Kumbalangi	Ernakulam
15	CUZ 15	Thenjipalam	Malappuram
16	CUZ 16	Thechery	Thrissur
17	CUZ 17	Cherakkara	Thrissur
18	CUZ 18	Karuvannoor	Thrissur
19	CUZ 19	Kodali	Thrissur
20	CUZ 20	Ponnani	Malappuram
21	CUZ 21	Vangarapadi	Ernakulam
22	CUZ 22	Valakam	Ernakulam
23	CUZ 23	Chulliyod	Malappuram
24	CUZ 24	Elakkallu	Malappuram
25	CUZ 25	Erumbanam	Ernakulam
26	CUZ 26	Amalapuram	Ernakulam
27	CUZ 27	Edappal	Malappuram
28	CUZ 28	Kottanelloor	Thrissur
29	CUZ 29	Karimpuzha bridge	Palakkad
30	CUZ 30	Pattakarimbu	Palakkad
31	CUZ 31	Panagad	Thrissur
32	CUZ 32	Kottamkulam	Thrissur
33	CUZ 33	Vellimukku	Malappuram
34	CUZ 34	Thattanthodi	Palakkad
35	CUZ 35	Edakochi	Ernakulam
36	CUZ 36	Edakunnam	Ernakulam
37	CUZ 37	Valakkavu	Thrissur
38	CUZ 38	Edathala north	Ernakulam
39	CUZ 39	Thoikkavu	Thrissur
40	CUZ 40	East koratty	Thrissur
41	CUZ 41	Ezhumuttam	Idukki
42	CUZ 42	Mulappuram	Idukki
43	CUZ 43	Vaniyampara	Thrissur
44	CUZ 44	Kizhuthani	Thrissur
45	CUZ 45	Thekkumoola	Thrissur
46	CUZ 46	Chendrapinni	Thrissur
47	CUZ 47	Thommankuthu	Idukki
48	CUZ 48	Marottichal	Thrissur
49	CUZ 49	Peramangalam	Thrissur
50	CUZ 50	Kannambathoor	Thrissur
51	CUZ 51	Moovattupuzha	Ernakulam

52	CUZ 52	Nilambur	Malappuram
53	CUZ 53	Paingothur	Ernakulam
54	CUZ 54	Alathoor	Palakkad
55	CUZ 55	Karumbil	Malappuram
56	CUZ 56	Chittanda	Thrissur
57	CUZ 57	Kalloor	Thrissur
58	CUZ 58	Kallayi	Thrissur
59	CUZ 59	Potharikkad	Ernakulam
60	CUZ 60	Thuvanoor	Thrissur
61	CUZ 61	Kalambur	Ernakulam
62	CUZ 62	Changaramkulam	Malappuram
63	CUZ 63	Maranchery	Malappuram
64	CUZ 64	Neriyamangalam	Ernakulam
65	CUZ 65	Chovannor	Thrissur
66	CUZ 66	Kechery	Thrissur
67	CUZ 67	Elappara	Idukki
68	CUZ 68	Nandipulam	Thrissur
69	CUZ 69	Kothamangalam	Ernakulam
70	CUZ 70	Koratty	Thrissur
71	CUZ 71	Edarikkodu	Malappuram
72	CUZ 72	Chittissery	Thrissur
73	CUZ 73	Kannikkal	Idukki
74	CUZ 74	Puthanathani	Malappuram
75	CUZ 75	Pullikkanam	Idukki
76	CUZ 76	Puthukadu	Thrissur
77	CUZ 77	Komaramchira	Thrissur
78	CUZ 78	Muttom	Idukki
79	CUZ 79	Aduparambu	Ernakulam
80	CUZ 80	Kaduppasseri	Thrissur
81	CUZ 81	Iruttukkanam	Idukki
82	CUZ 82	Koprakalam	Thrissur
83	CUZ 83	Kozhikkada	Thrissur
84	CUZ 84	North Chalakudy	Thrissur

Results and Discussion

Mean, range, standard deviation and phenotypic and genotypic coefficients of variation with respect to the characters of *Curcuma zanthorrhiza* studied are presented in Table 2. Analysis of variance showed that the eighty four accessions differed significantly for all the fifteen characters showing differences between them at genotypic level.

Table 2. Estimates of the genetic parameters of agronomic characters in *Curcuma zanthorrhiza.*

Character	Range	Mean	Standard Deviation	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability (Broad sense) (%)	Genetic Advance (%)
Plant height (cm)**	59-194	139.04	14.46	9.14	12.54	53.09	13.71
Number of tillers**	1-6	1.90	0.44	17.07	31.93	28.56	11.45
Number of leaves per tiller *	2.33-12	7.71	0.34	6.28	16.80	13.99	4.84
Leaf Length (cm)**	27.30-90.97	56.94	4.62	6.09	11.11	30.08	6.88
Leaf breadth (cm)**	6.77-18.23	13.46	1.66	7.54	18.57	16.49	6.31

Leaf area (cm^2)**	134.60-995.13	531.04	81.32	12.02	20.35	34.88	14.63
Yield per plant (g)**	40-660	160.39	56.12	30.85	42.04	53.87	67.90
Number of primary fingers**	8-18	12.99	1.95	12.54	19.07	43.26	17.00
Length of primary finger (cm)**	1.1-14.6	6.93	1.48	18.68	26.10	51.23	27.55
Diameter of Primary finger (cm)**	0.1-4.17	1.88	0.40	17.48	27.77	39.62	22.67
Number of secondary fingers**	2-70	24.56	6.76	24.04	33.40	51.78	73.92
Length of secondary finger (cm)**	0.3-7.9	2.15	0.74	28.12	44.65	39.65	36.48
Diameter of secondary finger (cm)**	0.22-6.1	1.06	0.24	18.44	30.40	36.81	23.05
Length of mother rhizome (cm)**	2.9-10.6	4.13	0.31	9.02	15.80	32.62	10.62
Diameter of mother rhizome (cm)**	1.08-5.79	6.41	0.75	5.69	10.60	28.83	6.29

Plant height showed a mean value of 139.04 cm and the range varied from 59 cm to 194 cm. Number of tillers ranged from 1 to 6 with a mean value of 1.90. Number of leaves per tiller showed a mean value of 7.71, and the range varied from 2.33 to 12. Leaf length varied from 27.30 cm to 90.97 cm with a mean value of 56.94 cm. Leaf breadth ranged from 6.77cm to 18.23 cm and showed a mean value of 13.46 cm. Leaf area ranged from 134.60 cm^2 to 995.13 cm^2 and the mean value was 531.04 cm^2. Yield per plant showed a mean value of 160.39 g and the range varied from 40 g to 660 g. Number of primary fingers showed a mean value of 12.99 and the range varied from 8 cm to 18 cm. Length of primary finger ranged from 1.1 cm to 14.6 cm and the mean value was 6.93 cm. Diameter of primary finger showed a mean value of 1.88 cm and the range was from 0.1 cm to 4.17 cm. Number of secondary fingers ranged from 2 to 70 and the mean value was 24.56. The mean value of length of secondary fingers was 2.15 with a range varying from 0.3 cm to 7.9 cm. Diameter of secondary finger showed a mean value of 1.06 and the range varied from 0.22 cm to 6.1 cm. Length of mother rhizome ranged from 2.9 cm to 10.6 cm with a mean value of 4.13 cm. Diameter of mother rhizome showed a mean value of 6.41 cm and it varied from 1.08 cm to 5.79 cm. Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available germplasm. Heritability and genetic advance help in determining the influence of environment in the expression of characters and the extent to which improvement is possible after selection (Robinson *et al.,* 1949). In the present study PCV was higher than GCV in all the agronomic characters. All the characters studied showed higher values of PCV when compared to corresponding values of GCV symbolizing the additive nature, polygenic control and differential degrees of environmental influence on the characters under study. The PCV of the observed characters varied between 10.6% for diameter of mother rhizome and 44.65% for length of secondary fingers, while the GCV ranged between 5.69% for diameter of mother rhizome and 30.85% for yield per plant. Among the growth characters highest PCV (31.93%) and GCV (17.07%) were observed for number of tillers. Among the yield characters highest PCV (44.65%) was observed for length of secondary finger and highest GCV (30.85%) was observed for yield per plant. In the case of yield characters both the values of PCV and GCV were comparatively higher. The differences between PCV and the corresponding GCV were higher in the case of length of secondary finger, number of tillers and diameter of secondary fingers indicating comparatively higher influence of environment on the phenotypic expression of these characters compared to the remaining characters.

Broad sense heritability of the agronomic characters ranged from 13.99% to 53.87%. The maximum heritability was observed for yield per plant (53.87%) followed by plant height (53.09%), number of secondary fingers (51.78%), length of primary finger (51.23%) and length of secondary finger (39.65%). The lowest heritability was recorded for number of leaves per tiller (13.99%). High heritability of characters indicates that they are influenced by environmental factors to a very low extent. The above analysis indicates the occurrence of comparatively higher heritability in the case of yield characters as compared to growth characters. Among the growth characters plant height showed the highest and number of tillers showed the lowest heritability. Among the yield characters, yield per plant showed the highest heritability and diameter of mother rhizome showed the lowest heritability. Characters showing high heritability indicate the occurrence of minimal influence of environment on the expression of such characters in a population establishing the scope of effective selection based on such characters for improvement. Highest genetic advance was observed in number of secondary fingers (73.92%), yield per plant (67.90%) and length of secondary finger (36.48%). Genetic advance was the minimum in the case of number of leaves per tiller (4.84%). These results show that superior genotypes of *Curcuma zanthorrhiza* can be selected based on agronomic characters like yield per plant, number of secondary fingers and length of secondary finger. A good amount of variability and appreciably high magnitudes of heritability and expected genetic advance in respect of yield determining characters offer scope for identifying elite genotypes in this crop on the basis of their performance. Improvement in any crop depends on the magnitude of genetic variability and the extent of transmission of characters from one generation to the next.

According to Devi *et al.* (2009), among the fourteen characters of *Curcuma zanthorrhiza*, high heritability and wide genetic variability were shown by leaf length, plant height and leaf length and leaf width ratio. Tiller number could be used as a selection criterion for fresh rhizome weight in dry land under full sunlight while leaf width could be used in shaded area. Differential variability of quantitative characters in the case of cultivated plants and its application in crop improvement have been discussed by different workers in crops like coffee (Nikhila *et al.,* 2002; Raghu *et al*., 2003; Nikhila *et al*., 2008), ashwagandha (Misra *et al.,* 1998), cardamom (Radhakrishnan *et al.,* 2006a; Radhakrishnan *et al.,* 2006b), *Cassia* (Chandramohanan and Mohanan, 2005), *Curcuma amada* (Jayasree and Mohanan 2006), coriander (Tripathi *et al*., 2000), chickpea (Upadhyaya *et al.,* 2008), cotton **(**Alkuddsi *et al*., 2003) and vanilla (Umamaheswari and Mohanan, 2004). Panse and Sukhatme (1978) have shown that if a character is governed by additive gene action, both heritability and genetic advance would be high. High estimates of heritability along with high genetic advance provide ample scope for improvement of the crop for future requirements.

Conclusion

All the agronomic characters of *Curcuma zanthorrhiza* presently studied show significant variation between the accessions indicating the presence of a strong and diverse genetic base for the crop in the study area. However, utilization of this variability both for conservation and improvement of the species is very important since the crop is being marginalized due to the utilization of agricultural land for other purposes and changes in cropping pattern. Strategies for conservation and breeding can only be designed only based on the extent of genetic variability available in any crop. The present study indicates the nature of the genetic base of the species in the study area and this information will invariably provide the raw material for future conservation and improvement programmes.

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