



A STUDY OF THE GENETIC VARIABILITY OF WILD TURMERIC (*CURCUMA AROMATICA* SALISB.) IN KERALA STATE OF INDIA

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ABSTRACT

Curcuma aromatica Salisb., commonly known as wild turmeric, belonging to the family Zingiberaceae is an important medicinal herb that face acute narrowing of natural populations due to human activities. A study was carried out to assess the genetic variability of wild turmeric in Kerala State of India in relation to growth and yield characters. Sixty two accessions of wild turmeric collected from different locations 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. Wide range of 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 the case of yield per plant (74.59%) followed by length of secondary finger (52.19%). Heritability was maximum for plant height (83.71%) followed by yield per plant (78.16%) and length of primary finger (76.95%). Most of the agronomic characters showed heritability above 50% while only one character *i.e.*, number of tillers showed heritability below 50%. Heritability of the characters ranged from 30% to 83.71% and genetic advance varied from 15.06 to 74.59. The results indicate the occurrence of broad genetic base in the study area in the case of the wild turmeric populations studied and also the feasibility of selection of superior genotypes based on the characters that show broad range of variation.

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INTRODUCTION

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). Evaluation and characterization of germplasm is beneficial to find out the qualitative and quantitative characters useful for breeding programmes and also to assess the genetic variability of the germplasm and confirm the presence of genetic variability accountable to yield, an essential character in a breeding programme (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). A comparison of plant morphology is the simplest approach for the detection of mislabelled accessions and the assessment of genetic diversity. This type of genetic diversity assessment 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).

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 all major and most 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

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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). *Curcuma aromatica* Salisb. (wild turmeric) is a valuable aromatic medicinal herb belonging to the family Zingiberaceae (Sabu, 2006). Studies on its genetic diversity and the stability of its genetic base are limited. The cosmetic use of the plant is highly exploited, providing protection to skin from pollution, bacteria and allergies. The paste made from the rhizome is commonly used in skin care to treat pimples, acne, blackheads and also it helps to reduce the superfluous hair (Zawar, 2011). This plant requires special attention because it is an important drug in ayurveda possessing a wide range of beneficial advantages such as anticancerous activity, antidiabetic activity, antimicrobial activity, antifungal activity, anti-inflammatory activity as well as mosquito repellent activity (Kim *et al.*, 2002; Madhu *et al.*, 2010; Saleem *et al.*, 2011; Zawar, 2011; Srividya *et al.*, 2012; Pant *et al.*, 2013; Liu *et al.*, 2014;). 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 different parts of Kerala State, India.

MATERIALS AND METHODS

Curcuma aromatica is a perennial erect herb native to southern India, widely cultivated for its aromatic rhizome (Sabu, 2006; Pant *et al.*, 2013). The plant grows best in different soils from light black sandy loam and red soils to clay loams (Krishnamurthy, 1993). 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 garden is located at 75°46' E longitude and 11°15' N latitude at an elevation of 50m from MSL. Annual rainfall is about 290cm and average temperature varies from 21.9°C-32.2°C. The experimental area has got a tropical monsoon climate with southwest 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). The experiments were laid out in randomized block design (RBD) with three replications.

Sixty two accessions of *Curcuma aromatica* collected from different locations of Kerala State of India were used for the study (Table 1). Healthy rhizomes were planted in the experimental plot in the first week of May 2016. 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 regularly and optimum soil moisture was maintained. 2g of NPK (18:18:18) was applied per plant at monthly intervals starting from the 30th 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 (Fisher and Yates, 1963).

Table 1 Details of *Curcuma aromatica* accessions studied

Accession Number	Source	District
CUK 1	Nellikunnu	Thrissur
CUK 2	Kottakkal	Malappuram
CUK 3	Peruvannamuzhi	Kozhikode
CUK 4	Puliyilapara	Thrissur
CUK 5	Kumali	Idukki
CUK 6	Pokalapara	Thrissur
CUK 7	Muthanga	Wayanad
CUK 8	Kurishupara	Idukki
CUK 9	Villunniyal	Malappuram
CUK 10	Audit 1	Idukki
CUK 11	Kundalamtheru	Kozhikode
CUK 12	Mukkam	Kozhikode
CUK 13	Thoppipala	Idukki
CUK 14	West Manasserri	Kozhikode
CUK 15	Meenkunnam	Ernakulam
CUK 16	Dhottapankulam	Wayanad
CUK 17	Vetilapara	Thrissur
CUK 18	Cheruthoni dam top	Idukki
CUK 19	Maradi	Ernakulam
CUK 20	Anakkayam	Thrissur
CUK 21	Odakkali	Ernakulam
CUK 22	Thankamani	Idukki
CUK 23	Vazhara Waterfalls	Idukki
CUK 24	SholayarUpperdam	Thrissur
CUK 25	Vazhachal	Thrissur
CUK 26	Narakakkanam	Idukki
CUK 27	Mariyapuram	Idukki
CUK 28	Kalkkandi	Palakkad
CUK 29	Palakkal	Kozhikode
CUK 30	Pambala	Idukki
CUK 31	Mukkali	Palakkad
CUK 32	3 rd Mile, Kumali	Idukki
CUK 33	Vazhikadavu	Malappuram
CUK 34	Kunduthod	Malappuram
CUK 35	Imangalam	Wayanad
CUK 36	Kukupadi	Palakkad
CUK 37	Nadukanichuram	Malappuram
CUK 38	Kuppadi	Wayanad
CUK 39	Koravankandi	Palakkad
CUK 40	Thavalam	Palakkad
CUK 41	Mannuthi	Thrissur
CUK 42	Kangazha	Kottayam
CUK 43	Tholpetti	Wayanad
CUK 44	Kalpetta	Wayanad
CUK 45	Thookupara	Idukki
CUK 46	Chambakkara	Kottayam
CUK 47	Mailamood	Kollam
CUK 48	Palaruvi	Kottayam
CUK 49	Chippanchira	Thiruvananthapuram
CUK 50	Kulathupuzha	Kollam
CUK 51	Madakkathara	Thiruvananthapuram
CUK 52	West Maradi	Ernakulam
CUK 53	Mannur	Ernakulam
CUK 54	Poothankuti	Ernakulam
CUK 55	Manjikadu	Ernakulam
CUK 56	Matnampadi	Kottayam
CUK 57	Poovakulath	Kottayam
CUK 58	Mangalasseri	Kannur
CUK 59	Edathua	Alappuzha
CUK 60	Thuruthikkad	Pathanamthitta
CUK 61	Vazhoor	Kottayam
CUK 62	Pallikathod	Kottayam

Phenotypic and genotypic variations of fifteen characters were estimated as per Singh and Choudhary (1985). Heritability (broad sense), the fraction of the total variance that is heritable was estimated as the percentage of genotypic variance over phenotypic variance as per Chahal and Gosal (2002) and genetic advance as per Singh and Choudhary (1985).

RESULTS AND DISCUSSION

Mean, range, standard deviation and phenotypic and genotypic coefficients of variation with respect to characters of *Curcuma*

aromatica studied are presented in Table 2. Analysis of variance showed that the sixty two accessions differed significantly for all the fifteen characters showing differences between them at genotypic level.

The lowest heritability was recorded for number of tillers (30%). High heritability of characters indicates that they are influenced by environmental factors to a very low extent.

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

Character	Range	Mean	Standard deviation	Genotypic Coefficient of Variation	Phenotypic Coefficient of Variation	Heritability (Broad Sense) (%)	Genetic Advance (%)
Plant height (cm)**	62.18- 130	102.02	15.57	14.79	16.16	83.71	27.87
Number of tillers**	1-1.99	1.25	0.22	13.6	25.6	30	15.82
Number of leaves per tiller**	7.22- 11.88	9.50	1.12	10.21	14.32	51.08	15.06
Leaf length (cm)**	32.95- 65.73	50.92	6.88	12.86	14.69	76.63	23.19
Leaf breadth (cm)**	10.98- 17.81	14.12	1.50	9.77	12.18	64.41	16.16
Leaf area (sq.cm)**	226.33- 694.56	442.48	98.14	21.05	24.28	75.12	37.58
Yield per plant (g)**	86.11- 491.67	205.96	87.48	40.95	46.32	78.16	74.59
Number of primary fingers**	4.55- 7.33	6.17	0.68	10.21	12.64	65.57	17.08
Length of primary finger (cm)**	7.09- 13.21	9.09	1.47	15.40	17.61	76.95	27.90
Circumference of primary finger (cm)**	1.65- 2.81	2.23	0.25	9.87	13.45	55.56	15.40
Number of secondary fingers**	30.66- 60.66	41.73	6.06	13.08	17.04	58.99	20.70
Length of secondary finger (cm)**	2.24- 8.40	4.66	1.43	29.18	33.69	75.20	52.19
Circumference of secondary finger (cm)**	0.84- 2.24	1.59	0.32	18.87	23.27	64.29	30.82
Length of mother rhizome (cm)**	4.26- 8.42	6.20	0.85	12.90	15.16	71.91	22.46
Circumference mother rhizome (cm)**	2.09- 4.17	2.98	0.47	14.77	17.79	67.86	24.86

Plant height showed a mean value of 102.02cm and the range varied from 62.18cm to 130cm. Number of tillers per plant ranged from 1 to 1.99 and it showed a mean value of 1.25. Number of leaves per tiller ranged from 7.2 to 11.88 and the mean value was 9.50. Leaf length varied from 32.95cm to 65.73cm with a mean value of 50.92. Leaf breadth showed a mean value of 14.12 and it ranged from 10.98cm to 17.81cm. Leaf area ranged from 226.33cm² to 694.56cm² and the mean value was 442.48cm². Yield per plant varied from 86.11 g to 491.66 g with a mean value of 205.96. Number of primary fingers showed a mean value of 6.17 and the range varied from 4.55 to 7.33. Length of primary finger ranged from 7.09cm to 13.21cm and the mean value was 9.09. Circumference of primary finger ranged from 1.65cm to 2.81cm with a mean value of 2.23. Number of secondary fingers ranged from 30.66 to 60.66 and the mean value was 41.73. The mean value of length of secondary finger was 4.66 with a range varied from 2.24cm to 8.40cm. Circumference of secondary finger varied from 0.84cm to 2.24cm with a mean value of 1.59. Length of mother rhizome ranged from 4.26cm to 8.42cm and the mean value was 6.20. Circumference of mother rhizome varied from 2.09cm to 4.17cm with a mean value of 2.98. Differential variability of quantitative characters in the case of cultivated plants and its application in crop improvement has been discussed by different workers in crops like coffee (Nikhila *et al.*, 2002; Raghu *et al.*, 2003), ashwagandha (Misra *et al.*, 1998), cardamom (Radhakrishnan *et al.*, 2006a; Radhakrishnan *et al.*, 2006b), cassia (Chandramohan and Mohanan, 2005), and vanilla (Umamaheswari and Mohanan, 2004).

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and heritability (broad sense) of characters can provide an idea of the extent of environmental impact on them, providing an estimate of inheritance of characters that can be expected from parent to progeny which is very necessary in identifying superior genotypes and plant types for agronomic purposes. In the present study PCV was higher than GCV in all the agronomic characters. Broad sense heritability of the agronomic characters ranged from 30% to 83.71%. The maximum heritability was observed for plant height (83.71%) followed by yield per plant (78.16%), length of primary finger (76.95%) and leaf length (76.63%).

Similar experiments have been done in coffee (Nikhila *et al.*, 2008) and coriander (Tripathi *et al.*, 2000).

Highest genetic advance was observed in yield per plant (74.59%) followed by length of secondary finger (52.19%) and leaf area (37.58%). Genetic advance was minimum in the case of number of leaves per tiller (15.06%), circumference of primary finger (15.40%) and number of tillers (15.82%). These results show that superior genotypes of *Curcuma aromatica* can be selected based on the agronomic characters like yield per plant, length of secondary finger and leaf area.

All the agronomic characters of *Curcuma aromatica* 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 utilization of agricultural land for other purposes and changes in cropping pattern.

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