



RESEARCH ARTICLE

GENETIC DIVERGENCE IN *CURCUMA AERUGINOSA* ROXB. - A PROMISING UNDERUTILIZED STARCH YIELDING CROP

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ABSTRACT

Genetic divergence analysis of sixty-eight genotypes of *Curcuma aeruginosa* Roxb. (pink and blue ginger) was laid out presently through cluster analysis following UPGMA on the basis of various growth and yield characters. The entire accessions fell in to three clusters at a linkage distance of 0.998. The first cluster consisted of sixty-two accessions showing maximum accommodation of genotypes which were related, the second cluster consisted of two accessions and the third cluster consisted of four accessions. Genotypes belonging to same clusters show higher levels of similarity and it is generally presumed that they show genetic proximity and those belonging to different clusters are genetically distant from each other thus exhibiting higher levels of divergence in genetic makeup. Distantly related genotypes can be considered as genetically diverse. Being a clonally propagated crop, diverse accessions of *Curcuma aeruginosa* could be selected for further breeding programs based on further assessment of performance so that exploitation of genetic variability and production of high yielding varieties could be possible.

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INTRODUCTION

Asia Pacific region is blessed with rich plant genetic resources and diverse agricultural practices and is a venue of domestication and diversification of various food crops. A vast majority of people in this region depends directly on this plant diversity for their dietary and medicinal needs. The region also harbours tremendous diversity of unexploited and underutilized crops and many of them are yet to be exploited. Underutilized crops are important from the economic point of view since they provide food security, health benefits, income and several environmental services (Arora, 2014). Wild plants have sustained human population in each of the inhabited continents and the use of them has been documented from antiquity to the current era (Khyade *et al.*, 2009). The use of wild edible plants is an age old practice and the diversity in them provides variety in family diet and also accounts for household food security (Radha *et al.*, 2013). Popularizing the use of wild edible plants not only strengthens multifunctional agricultural policies for food and livelihood security and environmental sustainability in rural areas but also helps in maintaining rural landscapes, biodiversity and cultural heritage. Assuring adequate food supply in rural areas is a major problem associated with the developing countries but the use of wild edible plants of such regions still remains an important but ignored aspect of food supply (Saha *et al.*, 2014). The Zingiberaceae member *Curcuma aeruginosa* Roxb. is such an underutilized wild tuber crop credited with various food values and immense medicinal properties. The plant popularly known as pink and blue ginger (Anonymous, 2011) is a native of Myanmar and is widely cultivated in Malaysia (Sabu, 2006). Common occurrence is found throughout South East Asia and in India it grows in West Bengal, Bihar, Coromandal coast and South Karnataka and, is fairly common in Kerala (Srivastava *et al.*, 2006).

The plant grows wild in South India and is very common throughout the coastal areas and riverine alluvial soils extending up to the midlands in Kerala and South Karnataka. The plant is seen as common undergrowth in coconut and arecanut groves and as a weed in waste lands in monsoon (Sabu, 2006). *Curcuma aeruginosa* is a perennial, semi erect rhizomatous herb. The whole plant is about 70-100cm tall and has weak aromatic odour. Rhizome is large, strongly aromatic, 5-10cm in size, has pink tips and greyish blue or blue centres. The rhizome possesses camphoraceous aroma and bitter taste. In South India, the rhizomes are widely used for the extraction of East Indian arrowroot or Travancore starch (Sabu, 2006) and therefore the plant gains the name Travancore starch plant, arrowroot wild and East Indian arrowroot. 100g of the rhizome showed a coloric value of 86cal, 76.8g moisture, 2.4 g protein, 0.4g fat, 18.3g of carbohydrate, 1.1g fibre, 1g ash, 0.02mg thiamine, 0.09mg riboflavin and 4.22mg ascorbic acid (Zanariah *et al.*, 1997). Approximately 125g of pure starch can be extracted from 1kg of rhizome (Sabu and Skornickova, 2003). Starch extracted from the rhizome is used as a substitute for arrowroot (Ranjini and Vijayan, 2006; Sabu, 2006). The starch extracted is an efficacious remedy for infantile diarrhoea and is also recommended for children and invalids (Ranjini and Vijayan, 2005) and is used as an alternative food source to replace cassava and corn (Anonymous, 2012). Starch from *Curcuma aeruginosa* is a highly amylose starch with lesser amount of amylopectin (Ranjini and Vijayan, 2006) and it is believed that the medicinal value of the starch increases, as the powder becomes aged (Sabu and Skornickova, 2003). *Curcuma aeruginosa* is one of the most eminently used medicinal plant in Bangladesh, India, Myanmar, Indonesia, Malaysia and Thailand (Hossain *et al.*, 2015). The rhizome is used to treat asthma and cough, scurvy and mental derangements and it is added in a beverage given to women in confinement to accelerate lochia and

decrease pain and inflammation of uterus (Pongbunrod, 1979; Perry, 1980; Ibrahim and Abd. Rahman, 1988). The rhizome is also used traditionally to treat rheumatism, contusions and irregular menstruation (Hembing, 2007), used as gastrointestinal remedy and spice in east and southern Asia and as medicine in child birth because of its purgative action (Sukari *et al.*, 2007). Evaluation of germplasm is pre-requisite to identify the desirable genotypes to feed the breeding programmes. Further, the value of germplasm collection depends not only on the number of accessions it possesses, but also up on the genetic diversity present in those accessions for yield and yield components. Genetic diversity is an important factor for any heritable improvement and the divergence analysis generates valuable information on the nature and degree of genetic diversity, which is useful for selecting desirable lines from germplasm for successful breeding programme (Reddy *et al.*, 2012). Being a vegetatively propagated crop, the farmer's homesteads have narrow genetic base of *Curcuma aeruginosa* Roxb. Therefore, the full genetic potential of this species has to be explored through genetic divergence analysis using the available germplasm collections. This could be a crucial step for isolating genetically divergent parents with promising yield attributes for successful crop improvement programs. The present study was there for undertaken to assess the genetic divergence available in the selected germplasm of pink and blue ginger through cluster analysis following UPGMA on the basis of various growth and yield characters.

MATERIALS AND METHODS

The present experiment was conducted in the experimental plot of the Genetics and Plant Breeding Division of the Department of Botany, University of Calicut, Kerala (Figure 1.). University of Calicut is located at 11° 25' - 11° 45' N latitude and 75° 45' - 75° 50' E longitude in the Malappuram district of Kerala and enjoys humid tropical climate and good annual rainfall (Umamaheswari and Mohanan, 2011).



Fig. 1. *Curcuma aeruginosa* Roxb. in the experimental plot

The district has got more or less the same climatic conditions prevalent in other parts of the state viz., dry season from December to February, hot season from March to May, the south west monsoon from June to September and the north east monsoon from October to November. The south west monsoon is usually very heavy which contributes nearly 75% of the annual rainfall. The climate is generally hot and humid with an average rainfall of 2900 mm (Anonymous, 2016a; Anonymous, 2016b). March and April form the hottest and January and February constitute the coldest months. Maximum temperature varies from 30°C to 36°C, minimum temperature from 17°C to 23°C and relative humidity from 84% to 94% during the morning hours (Sreenath, 2013). Sixty-eight genotypes of *Curcuma aeruginosa* Roxb. collected from different locations of northern districts of Kerala viz. Kasaragod, Kannur, Wayanad, Kozhikode,

Table 1. Accessions of *Curcuma aeruginosa* Roxb. studied for genetic divergence

Sl. No.	Accession No.	Source	District
1	CUA 1	Kuniyil	Malappuram
2	CUA 2	Pathiriyal	Malappuram
3	CUA 3	Kavanoor	Malappuram
4	CUA 4	Kondotty	Malappuram
5	CUA 5	Vazhayur	Malappuram
6	CUA 6	Cherukode	Malappuram
7	CUA 7	Mundakkulam	Malappuram
8	CUA 8	Irumbhuzhi	Malappuram
9	CUA 9	Alinchode	Malappuram
10	CUA 10	Pananthara	Thrissur
11	CUA 11	Edappal	Malappuram
12	CUA 12	Karipur	Malappuram
13	CUA 13	Panakkad	Malappuram
14	CUA 14	Kooriyad	Malappuram
15	CUA 15	Venniyur	Malappuram
16	CUA 16	Valiyora	Malappuram
17	CUA 17	Kainod	Malappuram
18	CUA 18	Cheruvannur	Kozhikode
19	CUA 19	Kunnamangalam	Kozhikode
20	CUA 20	Manassery	Kozhikode
21	CUA 21	Karassery	Kozhikode
22	CUA 22	Feroke	Kozhikode
23	CUA 23	Valluvambram	Malappuram
24	CUA 24	Alungal	Malappuram
25	CUA 25	Pallikkal	Malappuram
26	CUA 26	Karikkad	Malappuram
27	CUA 27	Pallippadi	Malappuram
28	CUA 28	Vythiri	Wayanad
29	CUA 29	Lakkidi	Wayanad
30	CUA 30	Ramanattukara	Kozhikode
31	CUA 31	Arappuzha	Kozhikode
32	CUA 32	Mampuzha	Kozhikode
33	CUA 33	Chevarambalam	Kozhikode
34	CUA 34	Muzhikkal	Kozhikode
35	CUA 35	Pantheerpadam	Kozhikode
36	CUA 36	Koduvalli	Kozhikode
37	CUA 37	Puthur	Kozhikode
38	CUA 38	Kakkayam	Kozhikode
39	CUA 39	Thalayad	Kozhikode
40	CUA 40	Kariyathumpara	Kozhikode
41	CUA 41	Puthukkode	Malappuram
42	CUA 42	Mannarkkad	Palakkad
43	CUA 43	Thachampara	Palakkad
44	CUA 44	Kalladikkode	Palakkad
45	CUA 45	Kallekkad	Palakkad
46	CUA 46	Mankkara	Palakkad
47	CUA 47	Kallidukku	Thrissur
48	CUA 48	Kandanassery	Thrissur
49	CUA 49	Agastyamuzhi	Kozhikode
50	CUA 50	Pulppally	Wayanad
51	CUA 51	Chakkunthara	Thrissur
52	CUA 52	Chittannur	Thrissur
53	CUA 53	Guruvayur	Thrissur
54	CUA 54	Arthat	Thrissur
55	CUA 55	Pathakkara	Thrissur
56	CUA 56	Muzhappilangadi	Kannur
57	CUA 57	Nadal	Kannur
58	CUA 58	Bakkalam	Kannur
59	CUA 59	Thalangara	Kasaragod
60	CUA 60	R.D Nagar	Kasaragod
61	CUA 61	Anangur	Kasaragod
62	CUA 62	Nayammarmoola	Kasaragod
63	CUA 63	Chemnad	Kasaragod
64	CUA 64	Perumbala	Kasaragod
65	CUA 65	Thazhe Cherur	Kasaragod
66	CUA 66	Thekkil	Kasaragod
67	CUA 67	Mangad	Kannur
68	CUA 68	Valapattanam	Kannur

Malappuram, Palakkad and Thrissur, during November - December 2012 formed the experimental material. The details of source of genotypes are given in Table 1. Fresh and healthy rhizomes of different genotypes of *Curcuma aeruginosa* procured from different

regions as mentioned above were planted for preliminary screening and multiplication of the planting material in the experimental field. The evaluational trials and other experiments were started in the first cropping season of 2013 in the first week of May before the onset of south west monsoon. Fresh and disease free seed rhizome fingers each of approximately 3cm - 5cm length and 25g - 30g weight were used as the planting material in the case of all the experiments. The rhizomes were sown in 38cm x 35cm polybags filled with garden soil, sand and cow dung in 3:1:1 ratio. Irrigation was carried out once a day on all non-rainy days and weeding was done as and when required. 2g of N:P:K (18:18:18) was applied to each plant at monthly intervals starting from the 30th day of planting up to the 5th month of growth and the plants were harvested simultaneously after six months of growth. The study used fifteen agronomic characters which included six growth characters such as plant height, number of tillers, number of leaves per tiller, leaf length, leaf breadth and leaf area; and nine yield characters such as 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, diameter of mother rhizome and yield per plant. Observation on growth characters were made in the field at the time of maturity of six months of growth and those of yield characters after harvest of the rhizome. The data were pooled and subjected to genetic divergence analysis. The Sixty eight genotypes mentioned above have been subjected to divergence analysis through cluster analysis using the software STATISTICA, following UPGMA (Unweighted Pair Group Method with Arithmetic mean) method as suggested by Sneath and Sokal (1973) to find out the closeness and distance that pertain between them on the basis of fifteen agromorphometric characters.

RESULTS AND DISCUSSION

Different genotypes of a plant species exhibit varying degrees of genetic divergence due to the similarities and variations of their genetic constitution.

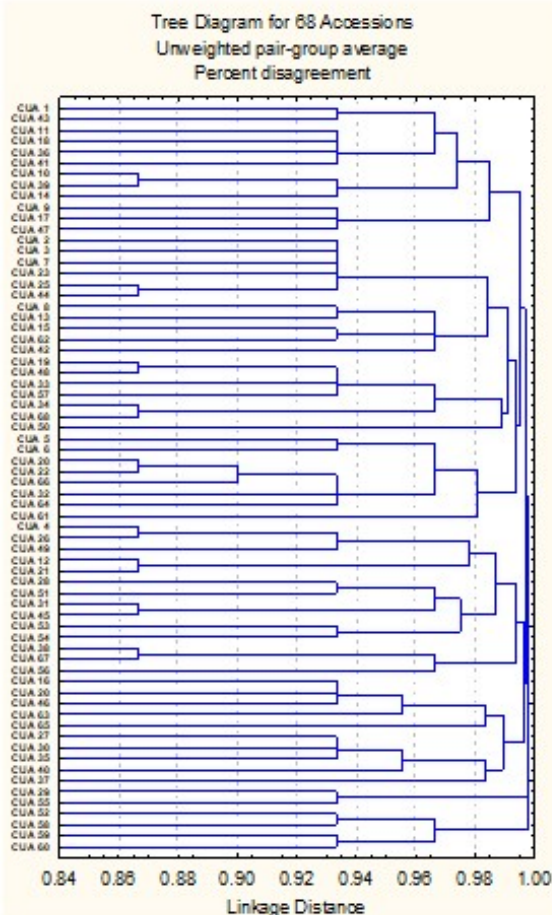


Fig. 2. Dendrogram showing the diversity of the sixty-eight accessions of *Curcuma aeruginosa* studied

Analysis of genetic divergence measures the extent of genetic diversity prevailing in the selected genotypes which further fastens the process of selection of diverse genotypes as parents for further breeding programmes. Cluster analysis is an efficient and widely used statistical tool which enables the understanding of the genetic behavior of genotypes under consideration and there by the genetic divergence. Sixty-eight genotypes of *Curcuma aeruginosa* have been subjected to divergence analysis through cluster analysis using the software STATISTICA, following UPGMA (Unweighted Pair Group Method with Arithmetic mean) method as suggested by Sneath and Sokal (1973) to find out the closeness and distance that pertain between them on the basis of fifteen agromorphometric characters.

Table 2. Clustering of the genotypes studied in *Curcuma aeruginosa* Roxb

Cluster No.	Sub cluster No.	Accessions
I	IA	CUA 1, CUA 43, CUA 11, CUA 18, CUA 36, CUA 41, CUA 10, CUA 39, CUA 14, CUA 9, CUA 17, CUA 47, CUA 2, CUA 3, CUA 7, CUA 23, CUA 25, CUA 44, CUA 8, CUA 13, CUA 15, CUA 62, CUA 42, CUA 19, CUA 48, CUA 33, CUA 57, CUA 34, CUA 68, CUA 50, CUA 5, CUA 6, CUA 20, CUA 22, CUA 66, CUA 32, CUA 64, CUA 61
	IB	CUA 4, CUA 26, CUA 49, CUA 12, CUA 21, CUA 28, CUA 51, CUA 31, CUA 45, CUA 53, CUA 54, CUA 38, CUA 67, CUA 56, CUA 16, CUA 20, CUA 46, CUA 63, CUA 65, CUA 27, CUA 30, CUA 35, CUA 40, CUA 37
II		CUA 29, CUA 55
III	III A	CUA 52, CUA 58
	III B	CUA 59, CUA 60

Cluster analysis grouped the entire accessions into three clusters at a linkage distance of 0.998 (Fig.2). The first cluster consisted of sixty-two accessions, showing maximum accommodation of genotypes which are related. The second cluster consisted of two accessions namely CUA 29 and CUA 55. And the third cluster consisted of four accessions namely CUA 52, CUA 58, CUA 59, CUA 60. The first cluster at a linkage distance of 0.997 bifurcated again into two sub-clusters, the first constituting 38 genotypes and the second consisting of 24 genotypes. These sub-clusters got again divided repeatedly in to different groups with maximum genetic closeness. The genotypes of the second cluster bifurcated at a linkage distance of 0.933. The third cluster got divided into two sub-clusters at a linkage distance of 0.967, both having two genotypes. The first is occupied by the accessions CUA 52 and CUA 58 collected from dissimilar geographic regions and the second sub-cluster by CUA 59 and CUA 60 collected from almost similar agro-climatic regions (Table 2.). The genotypes CUA 10 and CUA 39; CUA 25 and CUA 44; CUA 19 and CUA 48; CUA 34 and CUA 68; CUA 20 and CUA 22; CUA 4 and CUA 26; CUA 12 and CUA 21; CUA 31 and CUA 45; CUA 38 and CUA 67 were found to be more genetically related with regard to the characters subjected to the study. All these nine groups come under the first cluster and they bifurcate at a linkage distance of 0.867. Cluster I has got genotypes from all the seven districts, cluster II has got genotypes from two different districts and cluster III has got genotypes from three different districts selected. Hence each cluster is a mixture of genotypes collected from different geographical areas and it indicates that geographical separation is not a major criterion for genetic closeness and distance between the accessions studied. Genotypes belonging to same clusters show higher levels of similarity and it is generally presumed that they show genetic proximity and those belonging to different clusters are genetically distant from each other thus exhibiting higher levels of divergence in genetic makeup. Since there is scope to think that accessions showing closeness might have evolved from similar parental lines, there is lesser scope for the

selection of genetically divergent parents for crosses from the same cluster. Distantly related genotypes can be considered as genetically diverse. However, selection within groups for promising genotypes for use in selection and clonal propagation programmes will lead to the development of promising and improved planting material. Being a clonally propagated crop, diverse accessions of *Curcuma aeruginosa* could be selected for further breeding programmes based on further assessment of performance so that exploitation of genetic variability and production of high yielding varieties could be possible. Cluster analysis has been used to study genetic divergence by earlier workers like Hrideek *et al.* (2011) and Radhakrishnan *et al.* (2006) in cardamom; Thayumanavan *et al.* (2009) in rice; Punitha *et al.* (2010) in sunflower; Reddy *et al.* (2013) in tomato; Verma *et al.* (2014) in turmeric and Janaki *et al.* (2016) in chilli. Such studies have proved their usefulness in finding out the genetic distance and affinities of different genotypes of such crops and the present study has thrown light to the extent of genetic distance between different accessions of *Curcuma aeruginosa* Roxb. subjected for the study.

CONCLUSION

The present study indicates that majority of the genotypes collected belong to the same cluster and their genetic variability is only limited. This shows that the situation is a little alarming and the drain of genetic diversity will prove critical if proper attention is not paid for the conservation of the existing diversity and for the augmentation of diversity in the species.

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