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Genetic resources, diversity, characterization and utilization of agronomical traits in turmeric (*Curcuma longa* L.)

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ABSTRACT

The nature and magnitude of genetic divergence were estimated among sixty-five turmeric (*Curcuma longa* L.) genotypes using Mahalanobis D^2-statistics on thirteen agro-morphological quantitative traits. Mahalanobis's D^2 analysis revealed considerable amount of diversity among the *Curcuma* genotypes. The genotypes were grouped into seven clusters. Cluster I had maximum number of genotypes (37) followed by cluster II and III (9 genotypes each), IV (4), V (3), VI (2) and VII (1) in order. The genotypes falling under cluster I had the maximum divergence (430.90), which was closely followed by cluster II (332.99) and cluster IV (325.72). The highest inter-cluster distances were observed between cluster VI (959.96) and cluster VII (1020.64), suggesting that the genotypes included in these clusters may be used for future breeding programme. Traits like plant height, fresh weight of rhizome were the major contributors to genetic divergence.

1. Introduction

Turmeric (*Curcuma longa* L.) is a perennial rhizomatous plant of tropical and subtropical regions belonging to family Zingiberaceae. It was originally valued mainly as a spice for food and natural dye for clothing until recently it was discovered as a potential source of new drugs for variety of diseases (Elvira Corcolon and Maribel Dionisio-Sese, 2014). India is the world's largest producer (93.3%), consumer and exporter (approximately 90%) of turmeric and its cultivation is done in 150,000 hectares (Sasikumar, 2005). It is reckoned that Indians consume on an average about 80–100 mg turmeric extract every day and total consumption in India is around 480,000 tons annually (Deb et al., 2013). Because of high curcumin content, the Indian turmeric is considered best in the world (Muthusamy, 2013). It was reported by Sasikumar (2005) that the total curcumin may vary from 2 to 7% with turmeric cultivars classified either as high or low curcumin varieties. Turmeric is basically a triploid, sterile and cross pollinated species, which is clonally propagated using its underground rhizomes. Although vegetative propagation is the usual means of reproduction, several studies have shown the existence of genetic variation in the species.

Turmeric has worldwide importance to cure variety of ailments, as the genus contains curcumin and its derivatives e.g. demethoxycurcumin and bisdemethoxycurcumin (Tiyaboonchai et al., 2007) have vivid yellow natural phenols used in the treatment of inflammatory disorder (Villages et al., 2008), anorexia, cough, diabetic wounds (Mohamed et al., 2009), tumors, hepatic disorders, cardiovascular diseases, rheumatism, sinusitis, multiple sclerosis (Valsala and Peter, 2007), antimicrobial activity and health problems (Morshed et al., 2011). It has been also known to modulate lipid metabolism and therefore; it is used to treat obesity (Alappat and Awad, 2010). Besides these, curcumin is also used in clinical trials of Alzheimer's treatment (Hamaguchi et al., 2010). The extracts of turmeric roots have traditionally been used as an insect repellent and antimicrobial. Evaluation of germplasm is of immense important in genetic improvement of crop. Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm. The antioxidant activity of *C. longa* L. has their importance as a food additive to prevent rancidity of oils and fats due to oxidation (Khanna, 1999). Recently curcumin has been found to be anti-depressive and hypolipidimic (Bhutani et al., 2009). Low seed set is a major hindrance to the crop improvement programmes in turmeric. Therefore, modern technologies e.g. clonal selection, polyploidy induction, mutation breeding and molecular assisted breeding methods is generally used for the genetic improvement of this crop (Ravindran et al., 2007). Occurrence of rich morphological genetic diversity among the cultivars of turmeric (*C. longa*) is most likely because of accumulation of vegetative mutations over

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Table 1
Origin/places of collection of sixty-five accessions of turmeric (*Curcuma longa*).

S.No.	Accessions	Rhizome color	Places of collection/origin	S.No.	Accessions	Rhizome color	Places of collection/origin
1.	CH56	Yellow	CIMAP (Lucknow), India	34.	Namchai	Orange	Arunachal Pradesh, India
2.	CH55	Orange	CIMAP (Lucknow) India	35.	Baghjan	Yellow	Nagaon, Assam, India
3.	CH39	Orange	CIMAP (Lucknow), India	36.	Hijuguri-1	Orange	Tinsukia, Assam, India
4.	CH25	Orange	CIMAP (Lucknow), India	37.	Khetri	Orange	Kamrup, Assam, India
5.	CH23	Red	CIMAP(Lucknow), India	38.	Gohpur	Orange	Sonitpur, Assam, India
6.	CH92	Yellow	CIMAP (Lucknow), India	39.	Moran	Orange	Dibrugarh, Assam, India
7.	CH10	Orange	CIMAP (Lucknow), India	40.	Jagun	Orange	Tinsukia, Assam, India
8.	CH8	Orange	CIMAP (Lucknow), India	41.	Champathar	Orange	Tetalia, Assam, India
9.	CH21	Orange	CIMAP (Lucknow), India	42.	Latapuri	Orange	Kamrup, Assam, India
10.	CH104	Yellow	CIMAP (Lucknow), India	43.	Boraikhuwa	Orange	Golaghat, Assam, India
11.	CH71	Orange	CIMAP (Lucknow), India	44.	Bhalukpong	Orange	AP-Assam border, India
12.	CH2	Green	CIMAP (Lucknow), India	45.	Amjong	Orange	Marigaon, Assam, India
13.	CH60	Orange	CIMAP (Lucknow), India	46.	Hijuguri-2	Orange	Tinsukia, Assam, India
14.	CH43	Red	CIMAP (Lucknow), India	47.	KH	Orange	Tinsukia, Assam, India
15.	CH59	Yellow	CIMAP (Lucknow), India	48.	Captan-chuk (G)	Blue	Tinsukia, Assam, India
16.	CH72	Red	CIMAP (Lucknow), India	49.	Borali gaon	Orange	Nagaon, Assam, India
17.	CH7	Orange	CIMAP (Lucknow), India	50.	Riya bari	Orange	Golaghat, Assam, India
18.	CH65	Orange	CIMAP (Lucknow), India	51.	Captan chuk	Orange	Tinsukia, Assam, India
19.	CH17	Orange	CIMAP (Lucknow), India	52.	Chariduwar	Orange	Sonitpur, Assam, India
20.	CH30	Orange	CIMAP (Lucknow) India	53.	Barlaipuli	Orange	Tinsukia, Assam, India
21.	CH73	Yellow	CIMAP (Lucknow), India	54.	Dethopahar	Orange	Bihora bazaar, Assam, India
22.	CH15	Orange	CIMAP (Lucknow), India	55.	Turuya barigaon	Orange	Golaghat, Assam, India
23.	CH3	Orange	CIMAP (Lucknow), India	56.	Milanpur	Orange	Bokakhat, Assam, India
24.	CH31	Orange	CIMAP (Lucknow), India	57.	Rupahimukh (L)	Orange	Sivasagar, Assam, India
25.	CH76	Orange	CIMAP (Lucknow), India	58.	Dhekiajuli	Orange	Sonitpur, Assam, India
26.	CH12	Orange	CIMAP (Lucknow), India	59.	Chinakan	Orange	Golaghat, Assam, India
27.	60	Orange	CIMAP (Lucknow), India	60.	Missa	Orange	Borali gaon, Assam, India
28.	FFDC	Orange	Kannauj, U.P., India	61.	Barampur	Orange	Gumutha gaon, Assam, India
29.	CH67	Orange	CIMAP (Lucknow), India	62.	Rupahimukh (R)	Yellow	Sivasagar, Assam, India
30.	Rangamati	Orange	Golaghat, Assam, India	63.	Neli	Orange	Morigaon, Assam, India
31.	Laipuli	Orange	Dibrugarh, Assam, India	64.	Poya	Yellow	Dudhwa (TRF) U.P., India
32.	KH(W)	Blue	Tejpur, Assam, India	65.	Prithvi	Orange	Niwari, Madhya Pradesh, India
33.	Moharachapari	Orange	Golaghat-Jorhat border,Assam, India				

a period of time (Ghosh et al., 2013). Demand of Turmeric is continuously increasing in both food and pharmaceutical industries and therefore, turmeric growing techniques have been the focus of several studies (May et al., 2005).

The characterization of germplasm is an important link between conservation and plant genetic resource utilization. In any breeding programme, genetic diversity is a raw material to the breeder because spectrum of available genetic variation determines the potential for selection and is useful in resolving phylogenetic relationships. For genetic improvement of *C. longa* L. especially in India, germplasm collections represent the main source of variability. Rhizome yield in turmeric is a complex trait and its ultimate expression is determined by number of yield component and their interactions. Due to its economic importance and availability of the genetic diversity, efforts have been made to collect and characterize the germplasm collection and the present investigation has been undertaken to assess the amount of genetic divergence among the genotypes and selection of desirable genotypes for further experimentation in turmeric crop.

2. Materials and methods

Sixty-five germplasm of turmeric (*C. longa* L.) were collected from various wild/cultivated sources and places of India like Assam (34), Uttar Pradesh (29) and one each from Arunachal Pradesh and Madhya Pradesh (Table 1). The genotypes were grown in a completely randomized block design, replicated thrice at the experimental research farm of the CSIR—Central Institute of Medicinal and Aromatic Plants, Lucknow India, in two consecutive years (2012–2013 and 2013–2014) under normal fertility condition with plot size of single row of 3 m each planted at 50 cm apart. Plants were harvested 10 months after planting. The experimental farm located at 26.5° N latitude and longitude of 80.50° E with above mean sea level of 120 m. The climate was semiarid to subtropical in nature. Agro-morphological observations were recorded on five plants per replications for thirteen economic traits, namely days to sprout = DS; petiole length = PL (cm); fresh weight of rhizome = FWR (g/plant); dry weight of rhizome = DWR (g/plant); days to leaves emergence = DLE; Leaves length = LL (cm); number of leaves = NL; length of stipulated tuber = LST (cm); leaves width = LW (cm); plant height = PH (cm); rhizome length = RL (cm); thickness of rhizome = TR (cm); thickness of stipulated tuber = TST (cm).

2.1. Statistical analysis

Statistical analysis of collected data was done by using statistical software version 0.3 available at CSIR—CIMAP, Lucknow India in the division of genetics and plant breeding for genetic diversity following D^2- statistics. Mahalanobis (1936) D^2- analysis was used for estimating the genetic divergence among the germplasm accessions involving quantitative characters. All $n(n-1)/2 = 2080$ pairs D^2 values was clustered using Tocher's method described by Rao (1952) based on Singh and Chaudhury (1979).

3. Results and discussion

The analysis of variance revealed the presence of highly significant differences among the genotypes for the all thirteen characters, clearly indicating that high degree of genetic variability were present in the material of *C. longa* genetic stocks/genotypes. Based on D^2 statistics sixty five genotypes were grouped into seven different clusters (Table 2). The clustering pattern showed appreciable amount of divergence among the clones/genotypes of *C. longa*. This was also confirmed by canonical analysis (Fig. 1). Among the clusters, the maximum number of genotypes were included in Cluster I (37) and considered to be largest cluster followed by clus-