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Genetic divergence in turmeric (*Curcuma longa* L.) genotypes

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Abstract
The genetic divergence among 200 turmeric genotypes was evaluated based on twenty five agro morphological traits. The experiment was conducted during 2017 - 2018 at the Department of spices and plantation crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. 200 turmeric genotypes were grouped into three clusters by using euclidean distance with wards method. Cluster III showed 91 genotypes, cluster II recorded 55 genotypes and Cluster I registered 54 genotypes. Based on principle component analysis, seven principle components PC1, PC2, PC3, PC4, PC5, PC6 and PC7 with an eigen values 8.43, 3.99, 1.99, 1.57, 1.22, 1.09 and 0.98 respectively, have accounted for 77.16 percentage of the total cumulative variability with 200 turmeric genotypes. The first two principle components PC1 and PC2 showed eigen values are more than one and percentage of cumulative variability 49.72 %. This is would be the essential steps to research facilitate and utilization of the genetic resources within the genotypes studied.

Keywords: Turmeric, genetic divergence, euclidean distance and principle component analysis

Introduction
Turmeric (*Curcuma longa* L.) is a rhizomatous perennial crop, belonging to the Zingiberaceae family that has its origin in tropical South East Asia. Turmeric also known as 'Indian saffron' is much valued for its colouring principle the curcumin. Besides its use in cooking to add colour and as a preservative, turmeric is used in Indian Traditional Medicine to treat various ailments (Singh *et al.*, 2012) [10], food industry, confectionery, pharmaceuticals and cosmetic industry. Awareness on use of natural dyes for the culinary, medicinal and cosmetic use has put in demand for turmeric and its value added products.

Collection, maintenance, characterization and evaluation of germplasm are the important primary steps in any crop improvement programme. Association between conservation and utilization of plant genetic materials is necessary for formulating a successful breeding programme. In any breeding programme, genetic variability or genetic diversity is very important for selection and it's used to identify the relationship between phylogenetic traits. Genetic variability is the occurrence of difference among the individuals of plant population. Genetic variability or diversity results due to the difference in genetic constitution of the individuals of a population.

Selection is very effective when there is high degree of genetic diversity present among the individuals of a population. High magnitude of genetic diversity present in a population is very useful for a plant breeder to initiate the breeding programme. High degree of diversity available in the genotypes would be the better chance for selecting greater genotypes (Simmonds, 1962) [9].

Materials and Methods
The present study was conducted during 2017-18 at Department of Spices and Plantation crops, Horticultural College & Research Institute, TNAU, Coimbatore, Tamil Nadu, India. Two hundred turmeric genotypes were collected from various sources in different places of India *viz.*, Tamil Nadu, Kerala, Orissa and North East region. The turmeric genotypes were grown in Augmented Randomized Complete Block Design (Federrer, 1956) [3]. The design consisting of 20 augmented blocks with two checks and ten entries were planted per block. The twenty plants were accommodating each row and ten plants were selected and tagged from each genotype for collection of data. Twenty five profitable quantitative and qualitative traits were recorded namely plant height (cm), pseudo stem girth (cm), number of tillers, number of leaves, petiole length (cm), lamina length (cm), lamina width (cm), leaf area (cm^2), soluble protein (mg/100g), number of mother rhizome, weight of mother rhizome (g), length of mother rhizome (cm), number of primary rhizome, weight of primary rhizome (g),

length of primary rhizome (cm), girth of primary rhizome (cm), number of secondary rhizome, weight of secondary rhizome (g), length of secondary rhizome (cm), girth of secondary rhizome (cm), dry recovery (%), curcumin content (%), oleoresin content (%) and essential oil content (%) and rhizome yield per plant (g).

The statistical analyses as done based on the standard methods as cluster analysis technique was done by agglomerative hierarchical clustering technique by Anderberg (1993) [1]. Principle component analysis or canonical analysis is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, are derived (Rao, 1952) [5]. The analysis was done by using STAR 2.0 statistical package.

Result and Discussion

Quantification of genetic diversity is very vital in a breeding programme as it is expose the genetic structure of the population particularly in clonally propagate crop (Sharma and Devi, 2013) [7]. 200 turmeric genotypes were grouped into three clusters by using euclidean distance with wards method. Cluster III showed more number of genotypes (91 genotypes), cluster II recorded 55 genotypes and Cluster I registered 54 genotypes these are presented in table 1.

The dendrogram obtained from the cluster analysis formed by Euclidean's distance method grouped the 200 turmeric genotypes into two main-clusters (Fig. 1). The first major cluster had 138 genotypes, while the second major cluster consisted of 62 genotypes.

The first major cluster was divided into two sub clusters. The first sub-cluster had 67 genotypes while, the second sub-cluster had 71 genotypes. The first sub cluster was divided into two sub clusters. The first sub cluster showed 14 genotypes and second sub cluster registered 53 genotypes. The second sub – sub cluster also divided into two sub cluster. The first sub cluster had 17 genotypes and second sub cluster recorded 36 genotypes.

The second sub-cluster of first major cluster was further divided into two sub clusters. The first sub consisted of 22 genotypes, while second sub cluster had 49 genotypes. Second sub cluster divided into two sub cluster, one sub cluster had 19 genotypes another sub cluster showed 30 genotypes.

The second major cluster was divided into two sub clusters. The first sub-cluster had 16 genotypes while, the second sub-cluster had 46 genotypes. The second sub cluster divided into two sub cluster, one sub cluster had registered 10 genotypes another sub cluster had showed 36 genotypes, these cluster also divided into two sub cluster. The first sub cluster had 21 genotypes and second sub cluster recorded 15 genotypes. The clustering of the genotypes indicated no parallelism between genetic diversity and geographical diversity. In line with this Cintra *et at*., (2005) [2] grouped 21 turmeric genotypes into five clusters. Jan *et al.*, (2012) [4] evaluate 20 turmeric genotypes by euclidian dissimilarity coefficients. Similarly, Verma *et al*., (2014) [11] clustered 83 turmeric genotypes into ten clusters using Mahalanobis distance.

The purpose of principal component analysis is to obtain a small number of independent linear combinations of a set of variables that capture as much of the variability in the original variables as possible. The principle component analysis of the correlation matrix represents seven components. The principle component analysis showing eigen values less than one was considered as non significant. The component loadings and the percent variability for each principle component are presented in table 2.

In the present study principle component analysis conclude that, seven principle components PC1, PC2, PC3, PC4, PC5, PC6 and PC7 with an eigen values 8.43, 3.99, 1.99, 1.57, 1.22, 1.09 and 0.98 respectively, have accounted for 77.16 percentage of the total cumulative variability with turmeric genotypes (Fig. 2). The first two principle components PC1 and PC2 showed eigen values are more than one and percentage of cumulative variability 49.72 % (Fig. 2).

PC 1 recorded highest variability (33.70 %), the results showed yield per plant (0.308), weight of primary rhizome per plant (0.287), weight of secondary rhizome per plant (0.270), girth of primary rhizome (0.269), girth of secondary rhizome (0.266), weight of mother rhizome per plant (0.259), plant height (0.240), length of primary rhizome (0.224), length of mother rhizome (0.213), number of leaves (0.212), leaf area (0.208) and number of secondary rhizome per plant (0.208) in decreasing order of element and explained the variability. Number of tillers (-0.056), dry recovery (-0.072), soluble protein (-0.091) and essential oil (-0.098) contributed negatively towards the genetic diversity (Table 2).

In PC 2 recorded 15.996 % total variability and showed high loadings for leaf length (0.358) followed by leaf area (0.357), pseudo stem girth (0.322), length (0.295), leaf width (0.282), plant height (0.279) and number of leaves (0.229) in decreasing order of element and explained the variability while curcumin (-0.113), weight of mother rhizome per plant (-0.114), weight of secondary rhizome per plant (-0.163), weight of primary rhizome per plant (-0.166), yield per plant (-0.168), number of tillers (-0.197), number of secondary rhizome per plant (-0.207), number of primary rhizome per plant (-0.208), number of mother rhizome per plant (-0.222) recorded negatively genetic divergence.

Traits which contributed highest values in PC 3 were curcumin (0.561) followed by length of primary rhizome (0.196) and oleoresin (0.155) in decreasing order of element and explained the variability in this vector. In PC 4 showed 6.279 % variability and highest loadings for number of mother rhizome per plant (0.394) followed by curcumin (0.367), number of primary rhizome per plant (0.256) and weight of mother rhizome per plant (0.229).

In PC 5, relatively attributed a total variability 4.884 per cent with a high load for number of tillers (0.578), oleoresin (0.453), leaf width (0.324), essential oil (0.138), leaf area (0.135), number of mother rhizome per plant (0.124), length of mother rhizome (0.107) and weight of mother rhizome per plant (0.101) being positive and negative correlation noted length of secondary rhizome (-0.048), girth of primary rhizome (-0.049), leaf length (-0.053), yield per plant (-0.072), plant height (-0.086), number of primary rhizome per plant (-0.092), number of leaves (-0.107), petiole length (-0.109), weight of secondary rhizome per plant (-0.113), number of secondary rhizome per plant (-0.116), curcumin (-0.138), weight of primary rhizome per plant (-0.145), dry recovery (-0.246), soluble protein (-0.309).

PC 6 registered a total variance 4.361 % and characterized by soluble protein (0.618), length of mother rhizome (0.381), girth of primary rhizome (0.207), number of leaves (0.201), length of primary rhizome (0.151), girth of secondary rhizome (0.143), number of tillers (0.128), pseudo stem girth (0.079), plant height (0.058), weight of mother rhizome per plant (0.055), curcumin (0.041) and leaf width (0.008) being positive correlation. Leaf area (-0.015), leaf length (-0.028), yield per plant (-0.03), oleoresin (-0.047), essential oil (-

0.048), weight of secondary rhizome per plant (-0.053), weight of primary rhizome per plant (-0.065), dry recovery (-0.098), number of mother rhizome per plant (-0.123), length of secondary rhizome (-0.157), number of secondary rhizome per plant (-0.205), number of primary rhizome per plant (-0.296) and petiole length (-0.351) noted negatively divergence.

The seventh PC 7 accorded 3.954 % total variability, showing high positive loadings for dry recovery (0.835) followed by oleoresin (0.267), leaf width (0.205), length of secondary rhizome (0.201), soluble protein, (0.195), leaf area (0.111), number of secondary rhizome per plant (0.108) and number of tillers (0.105) while negative correlation noted for girth of primary rhizome (-0.009), length of primary rhizome (-0.018), number of primary rhizome per plant (-0.023), weight of mother rhizome per plant (-0.024), girth of secondary rhizome (-0.024), weight of primary rhizome per plant (-0.025), leaf length (-0.032), length of mother rhizome (-0.069), essential oil (-0.07), plant height (-0.089), number of leaves (-0.098) and petiole length (-0.184). The results indicate that there is sufficient variation for the twenty five traits observed in the in the first two principle components in the turmeric genotypes collection that could be used to improve turmeric cultivars for these traits. Similar result was also reported by Sigrist *et al*., (2011) [8]. One variable is selected from these identified groups depending on respective loadings. Consequently, for the first group rhizome yield per plant was the best choice, which had the largest loading from PC1, leaf length for PC 2, curcumin for PC 3 and dry recovery for seventh group PC 7. These findings are similar to the observations by Sanni *et al*., (2008) [6].

Table 1: Distribution of 200 turmeric genotypes in different clusters

Cluster No.	Number of genotypes	Name of the genotypes
I	67	CL 1, CL 7, CL 26, CL 37, CL 59, CL 61, CL 62, CL 68, CL 69, CL 70, CL 76, CL 77, CL 80, CL 83, CL 84, CL 86, CL 87, CL 90, CL 94, CL 95, CL 96, CL 97, CL 98, CL 99, CL 103, CL 107, CL 109, CL 110, CL 111, CL 112, CL 113, CL 117, CL 127, CL 128, CL 136, CL 137, CL 139, CL 181, CL 191, CL 206, CL 208, CL 210, CL 211, CL 214, CL 218, CL 219, CL 220, CL 224, CL 226, CL 227, CL 229, CL 231, CL 232, CL 233, CL 234, CL 235, CL 236, CL 247, CL 248, CL 249, CL 250, CL 252, CL 253, CL 254, CL 256, CL 258, CL 261
II	62	CL 3, CL 4, CL 5, CL 6, CL 8, CL 9, CL 10, CL 12, CL 13, CL 14, CL 16, CL 17, CL 18, CL 19, CL 20, CL 21, CL 23, CL 24, CL 25, CL 27, CL 28, CL 29, CL 30, CL 32, CL 33, CL 34, CL 36, CL 38, CL 39, CL 40, CL 44, CL 45, CL 46, CL 47, CL 48, CL 50, CL 51, CL 54, CL 55, CL 56, CL 57, CL 58, CL 60, CL 63, CL 66, CL 67, CL 71, CL 73, CL 79, CL 91, CL 92, CL 93, CL 165, CL 193, CL 203, CL 204, CL 205, CL 223, CL 241, CL 243, CL 251, CL 266
III	71	CL 53, CL 82, CL 101, CL 102, CL 104, CL 105, CL 106, CL 115, CL 116, CL 118, CL 119, CL 123, CL 124, CL 125, CL 126, CL 129, CL 138, CL 140, CL 141, CL 143, CL 145, CL 153, CL 154, CL 155, CL 157, CL 159, CL 161, CL 162, CL 163, CL 164, CL 166, CL 167, CL 168, CL 171, CL 176, CL 177, CL 178, CL 179, CL 180, CL 182, CL 183, CL 186, CL 188, CL 196, CL 197, CL 202, CL 207, CL 215, CL 216, CL 217, CL 221, CL 222, CL 225, CL 237, CL 238, CL 239, CL 240, CL 242, CL 244, CL 245, CL 246, CL 257, CL 265, CL 267, CL 268, CL 270, CL 271, CL 272, CL 273, CL 274, CL 275

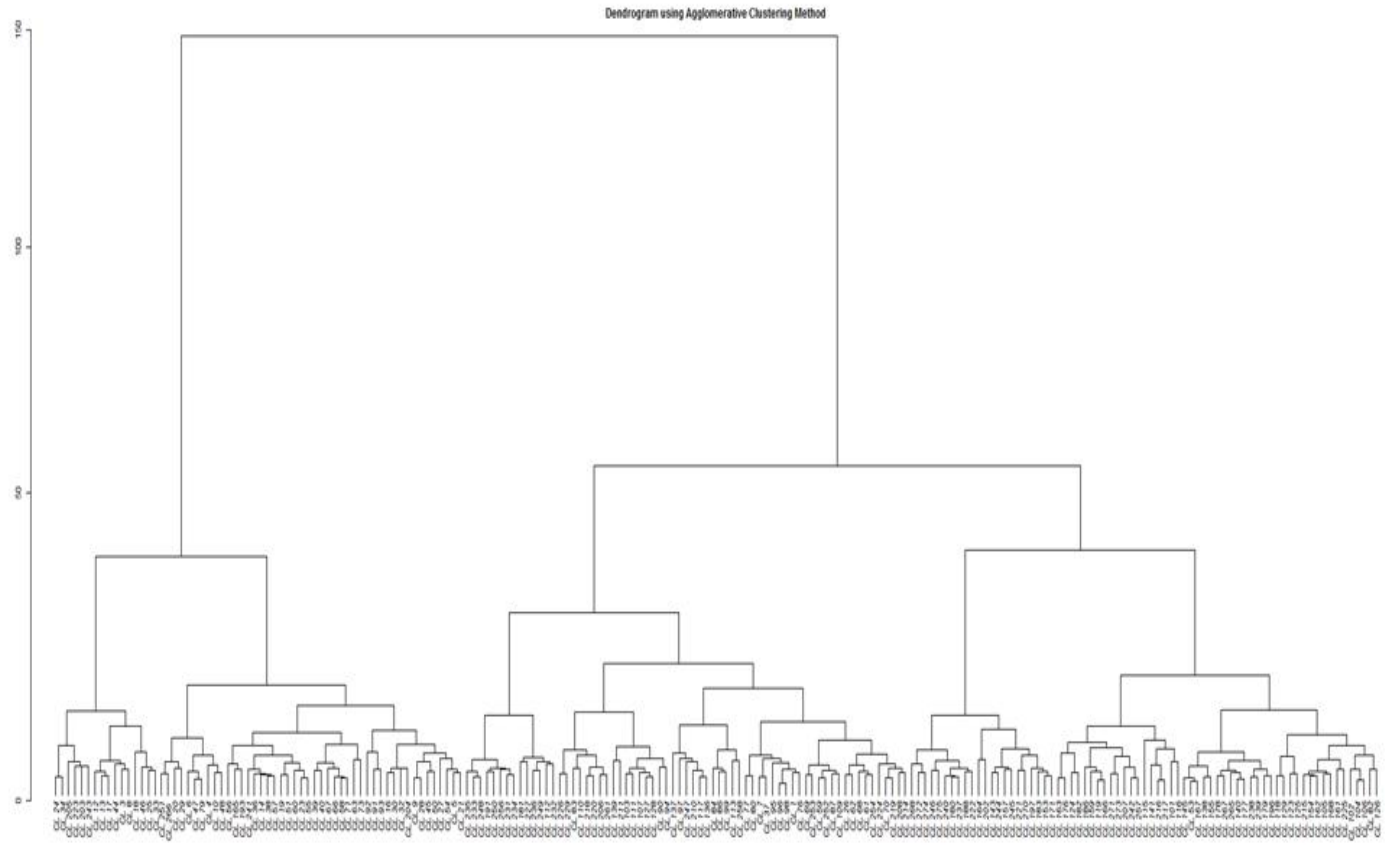

Fig 1: Dendrogram based on quantitative characters for turmeric genotypes

Table 2: Variation among turmeric genotypes accounted for first seven principal components

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Plant height (cm)	0.240	0.279	-0.018	0.074	-0.086	0.058	-0.089
Pseudo stem girth (cm)	0.169	0.322	0.026	0.052	0.064	0.079	0.067
Number of Tillers	-0.056	-0.197	0.076	0.021	0.578	0.128	0.105
Number of leaves	0.212	0.229	-0.109	0.087	-0.107	0.201	-0.098
Petiole length (cm)	0.116	0.295	0.081	-0.019	-0.109	-0.351	-0.184
Leaf length (cm)	0.195	0.358	0.019	0.010	-0.053	-0.028	-0.032
Leaf width (cm)	0.175	0.282	0.014	0.142	0.324	0.008	0.205
Leaf area (cm2)	0.208	0.357	0.009	0.073	0.135	-0.015	0.111
Soluble Protein	-0.091	-0.039	-0.146	0.075	-0.309	0.618	0.195
Number of mother Rhizome per plant	0.146	-0.222	-0.299	0.394	0.124	-0.123	0.041
Weight of mother rhizome per plant (g)	0.259	-0.114	-0.276	0.229	0.101	0.055	-0.024
Length of Mother Rhizome (cm)	0.213	-0.083	-0.136	0.071	0.107	0.381	-0.069
Number of primary rhizome per plant	0.190	-0.208	-0.192	0.256	-0.092	-0.296	-0.023
Weight of primary rhizome per plant (g)	0.287	-0.166	-0.104	0.056	-0.145	-0.065	-0.025
Length of primary Rhizome (cm)	0.224	-0.097	0.196	-0.281	0.025	0.151	-0.018
Girth of primary Rhizome (cm)	0.269	-0.066	0.083	-0.200	-0.049	0.207	-0.009
Number of secondary rhizome per plant	0.208	-0.207	0.060	-0.167	-0.116	-0.205	0.108
Weight of secondary rhizome per plant	0.270	-0.163	0.033	-0.188	-0.113	-0.053	0.072
Length of secondary Rhizome (cm)	0.198	-0.099	0.039	-0.360	-0.048	-0.157	0.201
Girth of secondary Rhizome (cm)	0.266	-0.057	0.099	-0.281	0.049	0.143	-0.024
Dry recovery (%)	-0.072	0.102	-0.106	0.030	-0.246	-0.098	0.835
Curcumin (%)	0.083	-0.113	0.561	0.367	-0.138	0.041	0.012
Oleoresin (%)	0.123	-0.040	0.155	-0.035	0.453	-0.047	0.267
Essential oil (%)	-0.098	0.118	-0.540	-0.374	0.138	-0.048	-0.070
Yield per plant (g)	0.308	-0.168	-0.134	0.048	-0.072	-0.030	0.001
Eigen value	8.432	3.999	1.990	1.570	1.221	1.090	0.988
Total Variability (%)	33.730	15.996	7.958	6.279	4.884	4.361	3.954
Total Cumulative (%)	33.730	49.726	57.684	63.963	68.847	73.207	77.161

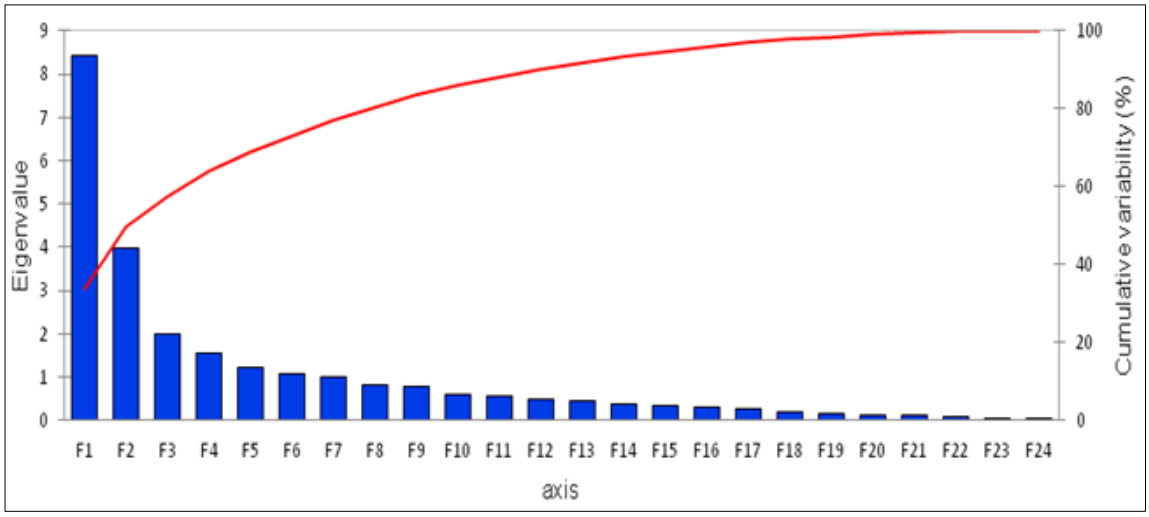

Fig 2: Scree plot of principal components analysis among 200 turmeric genotypes

Conclusion

The present study concluded that, the huge and individual range in the twenty five traits among 200 genotypes studied in this research. Cluster analysis has proved to be effective method in grouping of turmeric genotypes that may make possible their very useful to utilization in crop improvement programme through direct selection. Each genotype could be distinguished individually. This would be the important first steps to research facilitate and utilization of the genetic resources within the genotypes studied. Selection of varied parents from different cluster is considered to be an acceptable procedure in further breeding programme.

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