

Original Research Paper

Multivariate analysis for various agro-morphological traits of turmeric (*Curcuma longa* L.)

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ABSTRACT

Turmeric is one of the potential spice crops having importance in culinary, colouring in textiles and therapeutic in pharmaceutical industries. The present investigation was carried out to estimate the genetic diversity of 21 turmeric genotypes representing different geographical locations of India. The principal component (PC) analysis indicated that the most of the variation among the genotypes was contributed by the first two principal components (61.38%), which were largely governed by plant height, number of leaves per plant, leaf lamina length, leaf area, total leaf area, collar girth and weight of the mother rhizomes per clump. These traits showed high positive correlation with first two PCs and influenced significantly for grouping. Based on PC correlation analysis, it is evident that morphological and yield attributing traits of PC1 and PC2 are influenced and contributed for most of the variation among the genotypes. The cluster analysis revealed that the 21 genotypes fall into five clusters, and among them most divergent with distinct genotypes were cluster I, III and cluster IV. However, IISR Pragati, Rajendra Sonali and NDH 8 were found superior for fresh rhizome yield and Acc. 849 was found unique with robust mother rhizome. The present study contributes to the knowledge of genetic diversity and defining strategies for yield improvement in turmeric.

Keywords: Clustering, multivariate analysis, principal component analysis, turmeric

INTRODUCTION

Turmeric (*Curcuma longa* L.) is one of the most important species which is used as a spice, colouring agent, medicinal purposes and vital part of Asian culinary. It is a rhizomatous perennial herb from the ginger family, Zingiberaceae originated from South East Asia and distributed almost all Asian countries. India ranks first in terms of production, consumption, and export (Spices Board, 2022). Turmeric possess multiple pharmacological properties including antimicrobial, antioxidant, chemopreventive, antimutagenic, bioprotectant, anticancer, hepatoprotective, anti inflammatory, antithrombotic, hypo glycaemic properties and immune modulatory potential (Iweala et al., 2023; Jyotirmayee & Mahalik, 2022; Razavi et al., 2021).

Turmeric is mainly regarded as triploid ($2n = 63$) which have speculated origins by dibasic amphiploidy or secondary polyploidy. Although, turmeric is mainly propagated through rhizomes, seed set and germination was also reported (Nair & Sasikumar, 2009). The crop improvement efforts in turmeric mainly depended on

identifying superior genotypes through selection, polyploidy, and mutation breeding. The genetic variability and diversity in turmeric is largely depended on collection of germplasm from different geographical locations (Chandra et al., 1997). Wide genetic diversity has been reported in turmeric (Gupta et al., 2015; Mishra et al., 2015; Prasath et al., 2016 and Aarthi et al., 2022). The turmeric yield was the most complex trait influenced by multiple factors such as genetic and environment (Prasath et al., 2014). Utilisation of conventional breeding in turmeric is seldom because the variability is mostly based on selection of germplasm and exploitation of variability. The objective of the present study was to estimate genetic diversity of traits and clustering of genotypes through multivariate analysis in turmeric.

MATERIALS AND METHODS

A total of 21 turmeric genotypes *viz.*, IISR Pragati, IISR Prathiba, IISR Alleppey Supreme, Rajendra Sonali, Megha Turmeric 1, Waigon Turmeric, Roma, CIM Pitambar, Uttar Rangini, Chhattisgarh Haldi 2, NDH 8, Co 3, Acc. 1545, Erode Local, Mydukur



Local, Acc. 849, Acc. 379, Acc. 14, Acc. 179, Acc. 214 and Acc. 69/5/22/I₃ were collected from different geographical locations across India were used for the present study. The experiment was conducted at the ICAR-Indian Institute of Spices Research, Experimental Farm, Peruvannamuzhi (11° 36' 34" N and 75° 49' 12" E), Kozhikode, Kerala, over two seasons (2021-2022 and 2022-2023) using a randomised block design (RBD) with two replicates. Standard cultural practises were followed to grow the crop (Prasath *et al.*, 2022). Morphological and yield characters were recorded as per distinctness, uniformity and stability (DUS) guidelines of Protection of Plant Variety & Farmers Rights Authority, 2009 (PPV & FRA 2009). The observations recorded on plant height, number of leaves and tillers per plant, petiole length, leaf lamina length, leaf lamina width,

leaf area, total leaf area, collar girth, number of primaries per clump, weight of primaries rhizomes per clump, number of mother rhizomes per clump, weight of mother rhizomes per clump, and fresh rhizome yield per plant (g). The data was standardised using mean and standard deviation and subjected to principal component analysis (PCA), Eigen values, biplot between PC1 and PC2, and clustering was done based on 'K means' by using R 4.3.0 software (R Core Team, 2023).

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference for all the traits except number of tillers per plant. The principal component analysis indicated first four components contributed over 85% of variation for traits under study (Table 1). The PC1, PC2, PC3 and PC4 displayed 41.46%, 19.92%, 16.03% and 8.23%,

Table 1 : Loading Eigen values and variation of turmeric genotypes for different principal components

Source	Loading Eigen values				Correlation coefficients of PCs with traits		
	PC1	PC2	PC3	PC4	PC1	PC2	PC3
PH	0.326	0.189	-0.280	-0.139	0.785	0.317	-0.419
NL	0.328	0.001	0.300	-0.059	0.791	0.002	0.448
NT	-0.108	0.317	-0.240	0.422	-0.260	0.529	-0.361
PL	0.049	0.513	-0.112	0.084	0.120	0.857	-0.167
LLL	0.360	0.123	-0.169	0.079	0.868	0.206	-0.253
LLW	0.310	-0.072	-0.012	0.398	0.747	-0.120	-0.018
LA	0.388	0.040	-0.084	0.259	0.935	0.067	-0.126
TLA	0.402	0.017	0.101	0.102	0.969	0.028	0.151
CG	0.336	-0.094	0.244	-0.146	0.811	-0.158	0.366
PN	-0.050	0.365	-0.236	-0.538	-0.121	0.611	-0.353
PW	-0.117	0.303	0.518	0.096	-0.283	0.504	0.776
MN	-0.048	0.498	-0.031	0.085	-0.116	0.832	-0.045
MW	0.313	0.100	0.104	-0.469	0.753	0.166	0.156
FRY	-0.067	0.293	0.566	0.051	-0.160	0.487	0.849
Eigen values	5.81	2.79	2.24	1.15	-	-	-
S ² - test P value	3.33e-16	2.11e-05	9.04e-04	2.83e-01	-	-	-
Variation (%)	41.46	19.92	16.03	8.23	-	-	-
Cumulative variation (%)	41.46	61.38	77.41	85.64	-	-	-

PH=plant height, NL=number of leaves, NT=number of tillers, PL=petiole length, LLL=leaf lamina length, LLW=leaf lamina width, LA=leaf area, TLA=total leaf area, CG=collar girth, PN=number of primaries clump⁻¹, PW=weight of primaries rhizomes clump⁻¹, MN=number of mother rhizomes clump⁻¹, MW=weight of mother rhizomes clump⁻¹, FRY=fresh rhizome yield plant⁻¹, PC=principal component

Table 2 : Rotated matrix results of agro-morphological traits of turmeric

PC1	PC2	PC3	PC4
Plant height	Petiole length	Weight of primary rhizomes per clump	Number of tillers per plant
Number of leaves per plant	Number of primary rhizomes per clump	Fresh rhizome yield	Leaf lamina width
Leaf lamina length	Number of mother rhizomes per clump		
Leaf area			
Total leaf area			
Collar girth			
Weight of mother rhizomes per clump			

respectively. In the present study, PCA described by the first two axes suggested that the observed traits inside the axes had a significant impact among the genotypes. The first principal component accounts the most variability of 41.46% with substantial loadings which was contributed positively by plant height, number of leaves per plant, leaf lamina length, leaf area, total leaf area, collar girth and weight of the mother rhizomes per clump. It was clear that most of the morphological traits along with weight of mother rhizome per clump influenced the PC1. The PC2 was dominated by petiole length, number of primary rhizomes and mother rhizomes per clump (Table 1 & 2).

Correlation analysis was also performed to understand the relationship of each trait with principal components (Table 1). Total leaf area followed by leaf area, leaf lamina length, collar girth, number of leaf, plant height, weight of the mother rhizomes, and leaf lamina width showed highest positive correlation with the PC1. On the other hand, PC2 showed maximum positive correlation with petiole length, number of mother rhizomes, number of primary rhizomes, number of tillers, weight of primary rhizomes and fresh rhizome yield per plant. While Fresh rhizome yield and weight of primary rhizomes per clump was positively correlated with PC3. Based on PC analysis, it is evident that morphological and yield attributing traits of PC1 and PC2 are influenced and contributed for most of the variation among the genotypes. Roy et al. (2011) also found that PC1 and PC2 had the most diverse components with highest share of traits.

Contribution of PC scores for all the 21 turmeric genotypes are represented in the Table 3. The maximum positive PC score was observed for the Acc. 849, followed by Roma, Acc. 1545, Waigon turmeric, Mydukur Local, CIM Pitambar and IISR

Prathiba in the PC1, whereas, in PC2 it was observed maximum for genotypes Uttar Rangini followed by Acc. 69/5/22/I₃, Acc. 14, Acc. 179, Chhattisgarh Haldi 2, Acc. 379 and NDH 8. The genotypes, Megha turmeric 1, Erode Local, Co 3 and IISR Alleppey supreme recorded maximum scores for PC3. IISR Pragati and Acc. 214 recorded maximum PC score in PC4. Estimation of principal component score helps to identifying genotypes which are most influenced by a particular trait. The emphasis on these traits will pave way for precise selection of genotypes from pool of turmeric germplasm for future breeding programs.

The extent of variation correlated with each principal component is presented through Scree plot (Fig. 1), which visualizes the relation between Eigen values and principal components, amount of variation contributed by the principal components. As presented in the scree plot, the first three principal components exhibited maximum variation. The elbow curve explained the Eigen values for PC1, PC2, PC3 and PC4 which gradually decreased (5.81, 2.79, 2.24 and 1.15, respectively). Apparently, the PC1 recorded the highest variance, followed by others, as also reported in principal component analysis studies (Roy et al., 2011; Bahadur et al., 2016; Bahadur & Meena, 2016). Promising genotypes were categorized based on the highest PC scores respectively under first four principal components are presented in Table 4.

The Eigen vectors exhibits influence of each trait on the principal component axes. The length of the vector indicates the impact of each trait on the other traits, and the angle between the vectors indicates their relationship. An obtuse angle between vectors means that there is a positive relationship between the traits, while a perpendicular angle indicates a negative or no relationship. It was evident from the Fig. 2, that all the traits were divided into two

Table 3 : PCA scores of 21 turmeric genotypes

Genotype	PC1	PC2	PC3	PC4
IISR Pragati	-3.384	-1.722	-2.454	0.893
IISR Prathiba	0.248	-2.007	-0.124	-0.099
IISR Alleppey Supreme	-0.099	-0.774	1.609	0.547
Rajendra Sonali	-4.797	-1.040	-1.106	-0.510
Megha Turmeric 1	-1.795	0.009	2.350	-2.535
Waigon Turmeric	1.677	1.643	-3.296	-0.319
Roma	3.220	-2.327	0.969	1.607
CIM Pitambar	0.347	-2.506	-1.083	0.105
Uttar Rangini	0.242	2.066	1.124	1.329
Chhattisgarh Haldi 2	-0.085	1.342	0.953	0.888
NDH 8	-4.101	0.408	-1.361	-0.678
Co 3	-1.432	0.979	1.694	-0.999
Acc. 1545	1.715	-2.915	0.081	-0.331
Erode local	1.736	-0.758	1.881	-1.413
Mydukur Local	1.454	-1.400	0.165	0.271
Acc. 849	5.986	1.447	-2.169	-1.775
Acc. 379	-0.421	1.309	0.345	0.324
Acc. 14	-0.782	1.953	0.782	1.077
Acc. 179	-0.483	1.361	0.206	0.454
Acc. 214	1.049	0.893	0.192	1.312
Acc. 69/5/22/I3	-0.294	2.041	-0.758	-0.148

Table 4 : Selected genotypes based on highest positive PC scores in each of 4 components

PC1	PC2	PC3	PC4
IISR Prathiba	Uttar Rangini	IISR Alleppey Supreme	IISR Pragati
Waigon Turmeric	Chhattisgarh Haldi 2	Megha Turmeric 1	Acc. 214
Roma	NDH 8	Co 3	
CIM Pitambar	Acc. 379	Erode local	
Acc. 1545	Acc. 14		
Mydukur Local	Acc. 179		
Acc. 849	Acc. 69/5/22/I ₃		

groups where total leaf area, leaf area, leaf lamina length, number of leaves per plant, mother weight, plant height and collar girth had significant effect on first two principal components. According to the loading plot (Table 1), total leaf area showed a significant level of variance, followed by leaf area on positive side, whereas on negative side weight

of primary rhizomes per clump followed by number of tillers per plant for PC1. The present results are in line with the reports of Roy et al. (2011) and Bahadur et al. (2016). The results suggest that the focus on traits which positively influence fresh rhizome yield will be a key factor for future crop improvement in turmeric.

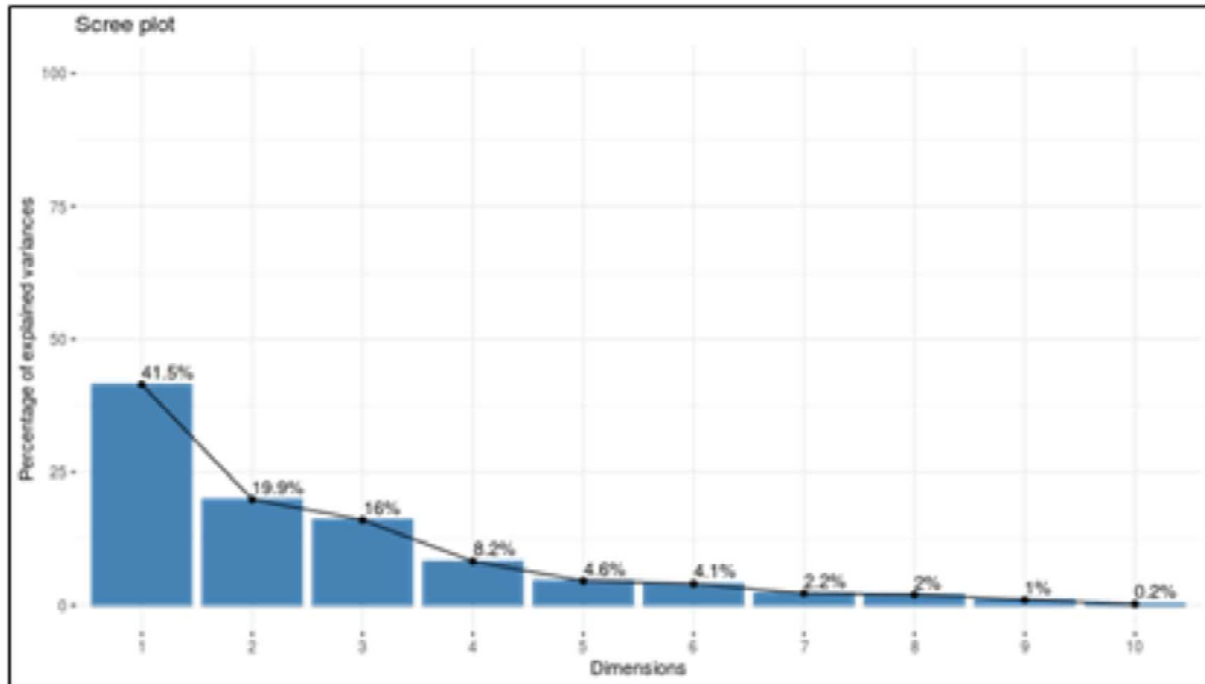
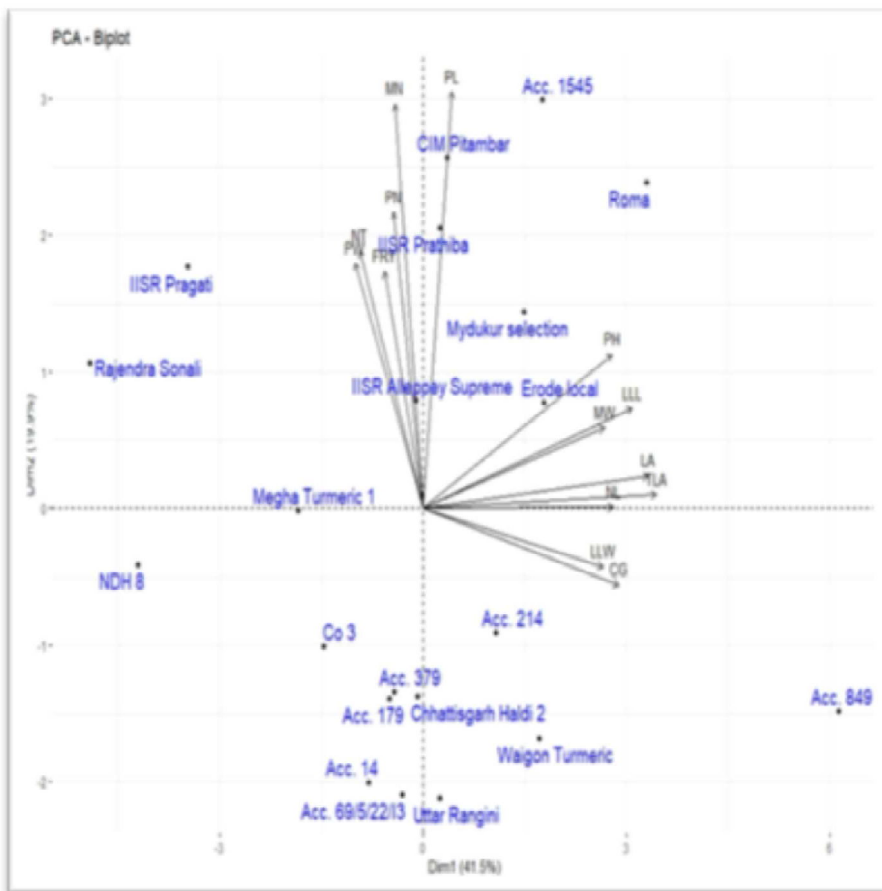


Fig. 1 : Scree plot and threshold Eigen values for agro-morphological traits 21 turmeric genotypes in principal component analysis



PH=plant height, NL=number of leaves, NT=number of tillers, PL=petiole length, LLL=leaf lamina length, LLW=leaf lamina width, LA=leaf area, TLA=total leaf area, CG=collar girth, PN=number of primaries clump⁻¹, PW=weight of primaries rhizomes clump⁻¹, MN=number of mother rhizomes clump⁻¹, MW=weight of mother rhizomes clump⁻¹, FRY=fresh rhizome yield plant⁻¹

Fig. 2 : Distribution and grouping of genotypes and variables across first two principal components

The clustering of genotypes was done based on k means and 21 genotypes were grouped into five clusters (Fig. 3) based on the similarity of genotypes for morphological and yield traits. The following are the details of the five clusters:

Cluster I: Acc 849

Cluster II: Waigon turmeric, Uttar Rangini, Chhattisgarh Haldi-2, Acc. 379, Acc. 14 Acc. 179, Acc. 214 and Acc. 69/5/22/I₃

Cluster III: IISR Pragati, Rajendra Sonali and NDH 8

Cluster IV: Megha Turmeric 1, IISR Alleppey Supreme and Co 3

Cluster V: IISR Prathiba, Roma, CIM Pitambar, Acc 1545, Erode local and Mydukur Local.

The cluster analysis results showed that the genotypes in cluster I was primarily categorised by the weight of mother rhizome per clump, while, cluster II was characterized by leaf lamina length. Cluster III was mainly contributed by fresh rhizome yield, however, cluster IV distinguished by the number of tillers, collar girth, and leaf lamina width and cluster V by the number of primaries and weight of mother rhizomes. Our morphological data also supports the clustering well. The most divergent clusters are, Cluster I, III and IV, whereas, cluster I have only one genotype and other two clusters having three genotypes each that differing significantly for morphological and yield

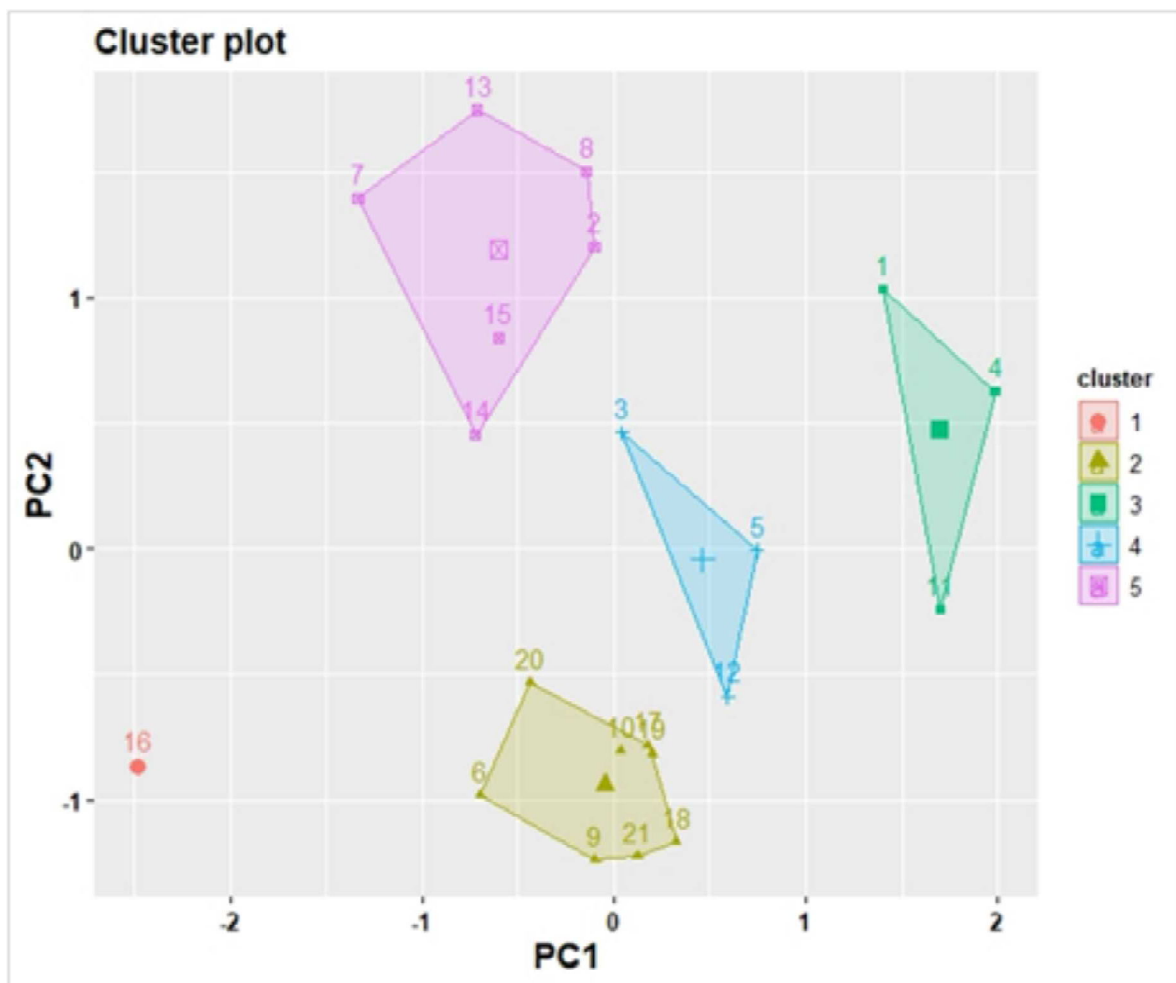


Fig. 3 : Grouping of 21 turmeric accessions using clustering based on K means

Each number 1-21 denotes respective genotype viz., 1-IISR Pragati, 2-IISR Prathiba, 3-IISR Alleppey Supreme, 4-Rajendra Sonali, 5-Megha Turmeric 1, 6-Waigon Turmeric, 7-Roma, 8-CIM Pitambar, 9-Uttar Rangini, 10-Chhattisgarh Haldi 2, 11-NDH 8, 12-Co 3, 13-Acc. 1545, 14-Erode Local, 15-Mydukur Local, 16-Acc. 849, 17-Acc. 379, 18-Acc. 14, 19-Acc.179, 20-Acc. 214 and 21-Acc.69/5/22/I₃.

traits compared to the other clusters. The present findings are consistent with previous studies (Bahadur et al., 2016; Bahadur & Meena, 2016; Aswathi et al., 2022; Vithya et al., 2022), where, similarly by homogeneity of genotypes based on similarity of traits.

CONCLUSION

Considerable amount of genetic diversity is present among the turmeric genotypes which will be useful for future crop improvement programs in turmeric. Principal component analysis and cluster analysis suggests that most of the variation is contributed from the first two principal components. Traits such as total leaf area, leaf area, number of mother rhizomes and petiole length had significant effect on first principal component. Among the five clusters, most divergent clusters with distinct genotypes such as IISR Pragati, Rajendra Sonali and NDH 8 which are yielding superior fresh rhizome yield and Acc. 849, later was unique one with distinct and robust mother rhizomes. The genotypes from the diverse clusters having superior performance for desirable traits could be selected for as parents in hybridization.

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