Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2018; SP1: 1097-1101

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Principal component analysis in Turmeric (Curcuma *longa* .L)

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Abstract
Turmeric is one of most important and common spice crop all over the world. It is a cross-pollinated, triploid species, which can be propagated through vegetative mean using its underground rhizomes. Since hybridization is ineffective in most cases, genetic improvement is often limited to germplasm selection and mutation breeding. Principal component analysis (PCA) is a useful tool in analyzing genetic variation among the accessions and determining the most important variables contributing to this variation in diversity analysis. This is an important step in evaluating the materials as genetic resources for breeding programs. In the current study, Eighty three geonotypes of turmaric collected from different areas were analyzed for phenotypic traits using PCA, and then they were grouped by cluster analysis based on principal components from PCA. The total genotypes were grouped into 10 different clusters on the basis of principle component analysis. Among the different clusters, cluster III consists the maximum number of genotypes followed by cluster IV. The highest intra–cluster distance was recorded for cluster 7 (8941.217) followed by cluster IV (6392.287), while highest inter cluster distance is found between cluster IX and VII. The genotypes of the distant cluster could be used as potential source for obtaining wide range of variation among the segregates and crop improvement programmes to produce populations with wider variability with transgressive segregates possessing high yielding.

Keywords: Turmeric, cluster, principal component analysis

Introduction
Turmeric is a triploid (2n = 3x =63) vegetative propagated rhizomatous crop which cultivated in South East Asia with India being the largest producer and exporter. In India, it is one of the important spice crops and plays a vital role in the national economy. Turmeric is one of most important and common spice crop all over the world with a long and distinguished human use particularly in the Eastern civilization (Ravindran, 2007). This spice has a subtle flavour which is obtained from dried and grounded rhizomes of the plant. The rhizomes are orange to white tuberous juicy stems that are formed below the ground at the base of the plant consist mother rhizomes with primary, secondary and tertiary fingers. Apart from being used as major ingredient in culinary purpose, turmeric powder is used as food-colouring agent and also as a natural dye. Since the time of Ayurveda (1900 Bc) numerous therapeutic activities have been assigned to turmeric for a wide variety of diseases and conditions, including those of the skin, pulmonary, and gastrointestinal systems, aches, pains, wounds, sprains, and liver disorders (Aggarwal *et al*., 2007). Its bright yellow color is due to the presence of curcumin pigment, which is also a powerful antioxidant, anti-parasitic, antispasmodic, anti-inflammatory and anticarcinogenic compound (Sasikumar 2005, Ravindran *et al*. 2007). Turmeric contains a wide variety of phytochemicals, including but not limited to curcumin, demethoxycurcumin, bisdemethoxycurcumin, zingiberene, curcumenol, curcumol, eugenol, tetrahydrocurcumin, triethylcurcumin, turmerin, turmerones, and turmeronols (Chattopadhyay *et al*., 2004). The presence of various metabolites such as curcuminoid, oil content, flavonoids, phenolics, some important amino acids, protein and high alkaloid content reveals that co-relation with its medicinal uses (Sarangthem and Haokip, 2010). Since hybridization is ineffective in most cases, genetic improvement is often limited to germplasm selection and mutation breeding (Ravindran *et al*., 2007). Turmeric is found throughout South and Southeast Asia with a few species extending to China, Australia and the South Pacific. The highest diversity is concentrated in India and Thailand, Recently, other alternatives have been successfully employed such as somaclonal variations, mutation breeding, and induction of polyploidy and genetic engineering (Shirgurkar *et al*. 2006). Principal component analysis (PCA) is useful in analyzing genetic variation among plant accessions and determining the most important variables contributing to this variation in diversity analysis.

Materials and methods

Plant Materials and Site of Study

In the present study 83 diverse turmeric genotypes (80 with three checks, viz., Narendra Haldi-1, Narendra Haldi-14 and Rajendra Sonia) were grown in Augmented Block Design (ABD) at Main Experiment Station of Department of Vegetable Science, Narendra Deva University of Agriculture and Technology, Faizabad during 2011-12. Healthy and treated long size rhizomes having 2-3 buds were planted in flat beds at 30 cm apart in the rows keeping 20 cm plant to plant distance.

Quantitative traits

The observations were recorded on 20 selected plants as per the recommended guidelines of ABD and replicated data of checks (Narendra Haldi-1, Narendra Haldi-14 and Rajendra Sonia) for twelve quantitative traits, viz., plant height (cm), number of tillers per clump, number of leaves per shoot, weight of fresh rhizomes per plant (g), weight of mother rhizome (g), number of primary rhizomes per plant, weight of primary rhizomes (g), number of secondary rhizomes per plant, number of tertiary rhizomes per plant, rhizome yield (q/ha), dry matter (%) and total soluble solids content (%) were recorded.

Statistical Analysis

The experiment data for various characters, recorded in course of this investigation were subjected to statistic analysis using suitable technique for different characters. Principal component analysis of eighty three turmeric genotypes based on yield and its attributing traits was performed by using statistical software SPSS 15.0.

Result and discussion

Principal component analysis reordered genotypes into ten broad groups that had within cluster similarities and inter-cluster morphological variation. The germplasm of turmeric appeared to have narrow genetic base which underwent high level of genetic erosion and selection pressure. This is perhaps due to the use of same ancestors and similar seed source by the farmers for cultivation of crop in selected areas of country. The given method of analysis may be helpful in selecting diverse parents and broadening local germplasm base which of turmeric for future breeding programme Table 1. Represents composition of clusters based on principal component analysis. On the basis of analysis, all the genotypes were grouped into different clusters. Information on genetic diversity was also used to identify the promising diverse genotype, which may be used in future breeding programme. Genotype from the same origin were placed in separate clusters, indicating wide genetic diversity among them. This may be due to frequent exchange of germplasm between different geographical region. In the present studies among the total 83 genotypes, 40 genotypes of turmeric showed high quantum of genetic divergence. Figure 1 shows composition of clusters based on principal component analysis. All the genotypes were grouped in to 10 clusters and maximum number of genotypes were accommodated in cluster III. The resultant clusters showed genetic diversity. Similar result were also obtained by Jan *et al.* (2012).

Intra and inter – cluster distance is the index of genetic diversity among clusters. Average of intra (diagonal) and inter cluster distance based on D^2 analysis is represented in Table 2. Inter- cluster distances were found higher than intra-cluster distances, revealing a considerable amount of genetic diversity among the genotypes studied. Figure 2 also Showing intra and inter cluster distances between turmeric genotypes. The highest intra – cluster distance was recorded for cluster 7 (8941.217) followed by cluster IV (6392.287). Genotypes from these clusters could be used as parental line for hybrid breeding programme owing to their higher mean performance within group. Lowest intra – cluster distance was observed for cluster V, VI, VIII, IX and X (0.0000), which was mainly due to the single genotype present in these clusters, and the highest inter-cluster distance was observed between cluster IX and cluster VII (142874.469) followed by between clusters X and VII (92044.727). Data clearly indicated that the genotypes did not cluster according to their geographical distribution. In general, the pattern of distribution of genotypes from various regions into different cluster was seen to be random. The genotypes of the distant cluster could be used as potential source for obtaining wide range of variation among the segregates and crop improvement programmes to produce populations with wide variability with transgressive segregates possessing high yielding (Singh *et al.*, 2014.). Table 3 representing the cluster means of different clusters based on different trait under study. Cluster 3 having maximum clusters value for trait like plant height (cm), tiller/ clum and leave/ plant, while cluster 8 has maximum cluster mean for weight of primary rhizomes/ plant and secondary rhizomes per plant.

Principal component analysis was used to identify the most significant variables in the data set (Table 4). The results indicated that vector 1 explain about 29.932 % and vector 2 has 19.063 % of the total variability observed whereby vector 3 accounted for 13.507 %. Variables with higher scores on PC1 are related to rhizome yield (q/ha), weight of fresh rhizome/ plant (g) and dry matter (%). The highest contribution on PC 2 corresponded to variables related to leaves/ plant, plant height (cm) and tillers/ clump. Canonical variable analysis suggested that some descriptors were more important to discriminate accessions and also that one of the descriptors could be discarded. The result provided useful insights for better management of the germplasm collection, optimizing conservational and breeding efforts similar result was also reported by Sigrist *et al*. (2011). Figure 3. Showing graphical representation of percentage contribution of studied major trait (in parentheses value) toward genetic divergence in which rhizome yield (q/ha) was found maximum (65%) contribution towards genetic diversity follow by weight of primary rhizome (19%). The result of this study showed genotypes from distant cluster could be used as potential source for obtaining wide range of variation among the segregates and crop improvement programmes to produce populations with wide variability with transgressive segregants possessing high yielding. The vast and distinctive range in the morphological and biochemical traits across genotypes studied in this research meant that each genotype could be distinguished individually. This would be the important first steps to research enabling utilization of the genetic resources within the genotypes studied. Selection of diverse parents from various clusters is considered to be an acceptable procedure in harnessing the heterosis.

Table 1: Composition of clusters based on principal component analysis

Cluster	Genotypes
Cluster I	NDH-1, NDH-51, NDH-22, NDH-70, NDH-16, NDH-71, NDH-102, NDH-10,NDH-17, NDH-66, NDH-68, NDH-4, NDH-45, NDH-29
Cluster II	NDH-8, NDH-14, NDH-1, NDH-74, NDH-7, R-SONIA, NDH-11, NDH-9
Cluster III	NDH-36, NDH-5, NDH-59, NDH-56, NDH-57, NDH-6, NDH-60, NDH-58, NDH-100, NDH-93, NDH-77, NDH-96, NDH-19, NDH-20, NDH-126, NDH-13, NDH-12, NDH-31, NDH-99, NDH-92, NDH- 46, NDH-84, NDH- 52, NDH-55, NDH-94, NDH-54, NDH- 2, NDH-72, NDH-95, NDH-91
Cluster IV	NDH-25, NDH-26, NDH-21, NDH-28, NDH-27, NDH-3, NDH-24, NDH-97, NDH-79, NDH-76, NDH-81, NDH-63, NDH-62, NDH-86, NDH-89, NDH-40, NDH-88, NDH-75, NDH-67, NDH-64
Cluster V	NDH-83
Cluster VI	NDH-23
Cluster VII	NDH-14, NDH-18, NDH-65, NDH-80, NDH-69, NDH-44
Cluster VIII	NDH-125
Cluster IX	NDH-15
Cluster X	NDH-73

Table 2: Inter & Intra Cluster Distances

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster
1 Cluster	1206.34	8725.343	5820.986	10323.229	3967.239	3479.891	53050.715	9086.744	25397.213	13645.359
2 Cluster		1891.201	19376.096	5182.029	9050.677	7339.967	29125.795	7787.152	50856.074	20736.545
3 Cluster			3101.28	22381.223	5481.374	7119.258	81381.172	9779.565	11122.171	8537.504
4 Cluster				6392.287	11120.119	12420.382	27264.248	14056.408	56004.625	29307.441
5 Cluster					0	6544.045	55218.125	4278.273	23110.869	12317.967
6 Cluster						0	57280.051	4887.411	25075.225	6110.172
7 Cluster							8941.217	58440.453	142874.469	92044.727
8 Cluster								0	26730.922	5795.531
9 Cluster									0	13485.128
10 Cluster										0

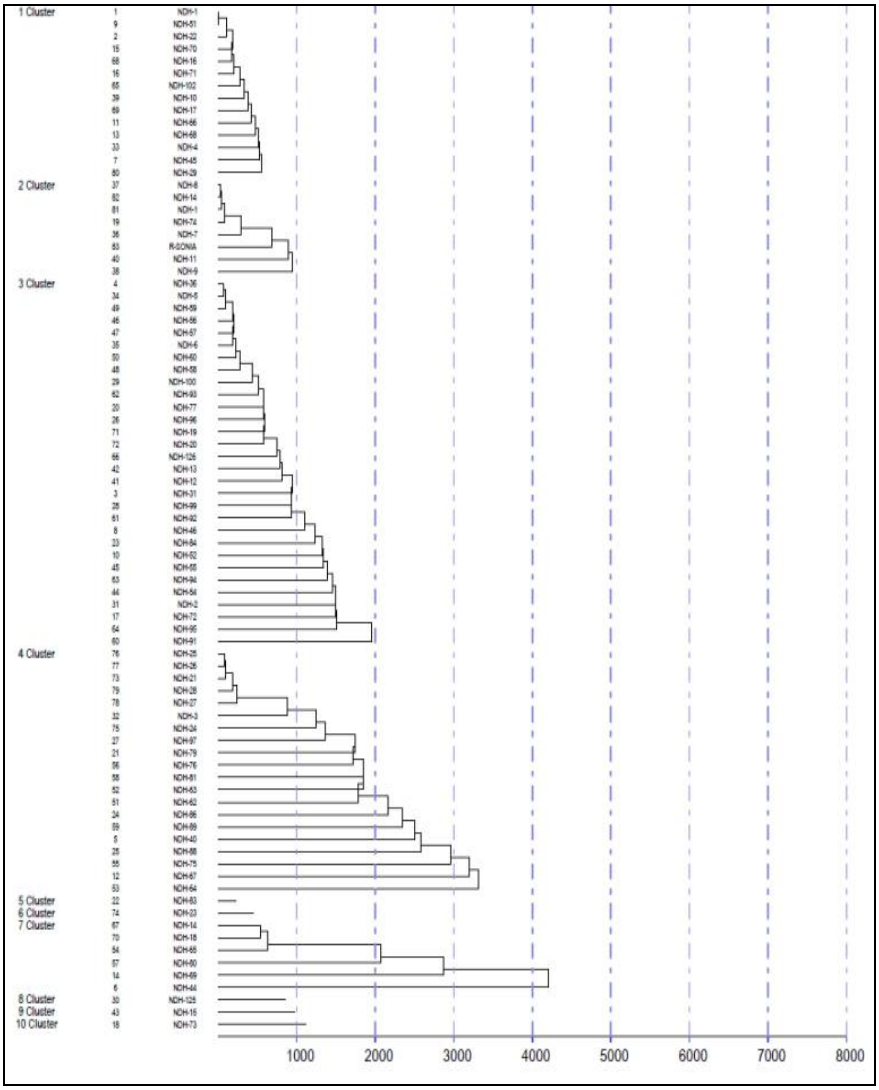

Fig 1: Composition of clusters based on principal component analysis

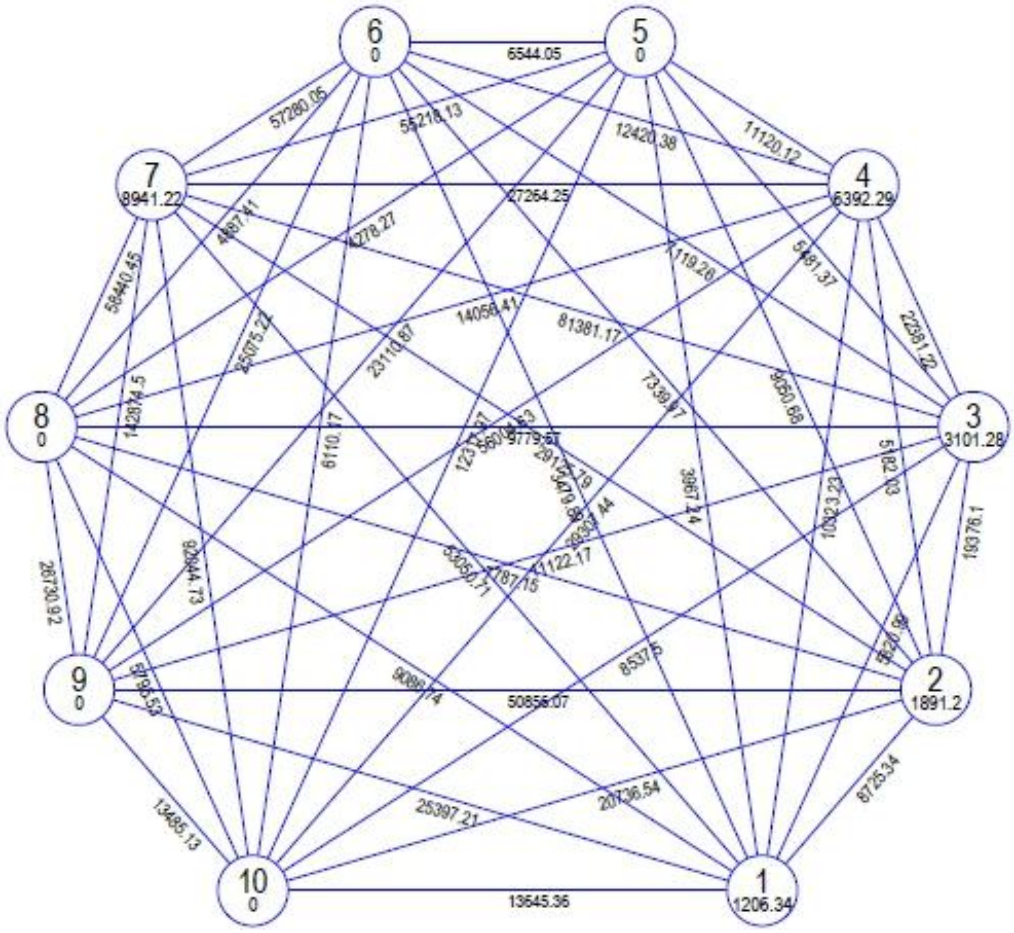

Fig 2: Showing intra and inter cluster distances between turmeric genotypes.

Table 3: Cluster Means

	Plant Height (cm)	Tillers/ Clump	Leaves/ Plant	Weight of Fresh Rhizome/ Plant (g)	Weight of Mother Rhizome (g)	Primary Rhizomes/ Plant	Weight of Primary Rhizome (g)	Secondry Rhizomes/ Plant	Tertairy Rhizomes/ Plant	Rhizome Yield (q/ha)	Dry Matter (%)	TSS (%)
1 Cluster	103.732	2.972	11.743	186.415	31.604	5.338	60.675	9.926	4.405	270.955	19.109	8.056
2 Cluster	97.339	2.021	7.325	218.613	32.747	7.008	123.05	11.437	6.813	319.217	21.479	6.554
3 Cluster	81.915	1.829	8.56	153.321	28.292	5.329	63.611	8.906	4.034	224.505	18.908	7.14
4 Cluster	89.003	2.562	10.96	215.373	37.069	6.364	94.052	10.519	5.547	338.186	21.079	8.089
5 Cluster	49.573	1.779	7.067	183.296	27.125	5.738	80.415	9.454	3.646	266.276	16.356	7.148
6 Cluster	124.46	4.713	17.267	178.316	21.912	6.604	106.995	8.854	3.679	258.806	19.183	7.255
7 Cluster	93.97	2.768	11.789	294.494	36.902	6.176	113.348	10.81	4.896	455.839	20.292	6.87
8 Cluster	65.613	1.979	6.467	177.776	21.065	5.537	142.255	15.454	5.646	257.996	20.106	9.708
9 Cluster	71.193	1.712	6.733	100.529	35.112	5.637	56.955	8.654	5.546	143.126	18.9	5.661
10 Cluster	103.28	2.846	11.933	141.256	23.712	6.004	140.482	14.654	5.213	203.216	19.556	9.461

Table 4: Vector analysis for 12 important traits of turmeric genotypes.

Canonical variable analysis						
	1 Vector	**2 Vector**	**3 Vector**	**4 Vector**	**5 Vector**	**6 Vector**
Eigene Value (Root)	3.592	2.288	1.621	1.097	0.988	0.792
% Var. Exp.	29.931	19.063	13.507	9.140	8.233	6.602
Plant Height (cm)	0.029	0.555	-0.001	-0.057	0.110	0.150
Tillers/ Clump	-0.032	0.546	-0.018	-0.043	-0.158	-0.077
Leaves/ Plant	0.067	0.576	0.074	0.124	0.036	-0.046
Weight of Fresh Rhizome/ Plant (g)	0.566	0.084	-0.020	-0.043	0.016	-0.075
Weight of Mother Rhizome (g)	0.213	-0.073	0.080	0.084	0.017	-0.849
Primary Rhizomes/ Plant	-0.100	-0.063	0.151	-0.745	-0.059	-0.104
Weight of Primary Rhizome (g)	0.217	0.035	-0.114	-0.612	0.069	0.147
Secondry Rhizomes/ Plant	-0.049	-0.035	0.683	-0.054	-0.025	-0.038
Tertairy Rhizomes/ Plant	-0.010	0.090	0.650	0.020	0.032	0.022
Rhizome Yield (q/ha)	0.602	0.003	-0.068	-0.052	-0.026	-0.050
Dry Matter (%)	0.454	-0.189	0.241	0.189	-0.018	0.453
TSS (%)	0.021	0.009	-0.009	0.007	-0.975	0.023

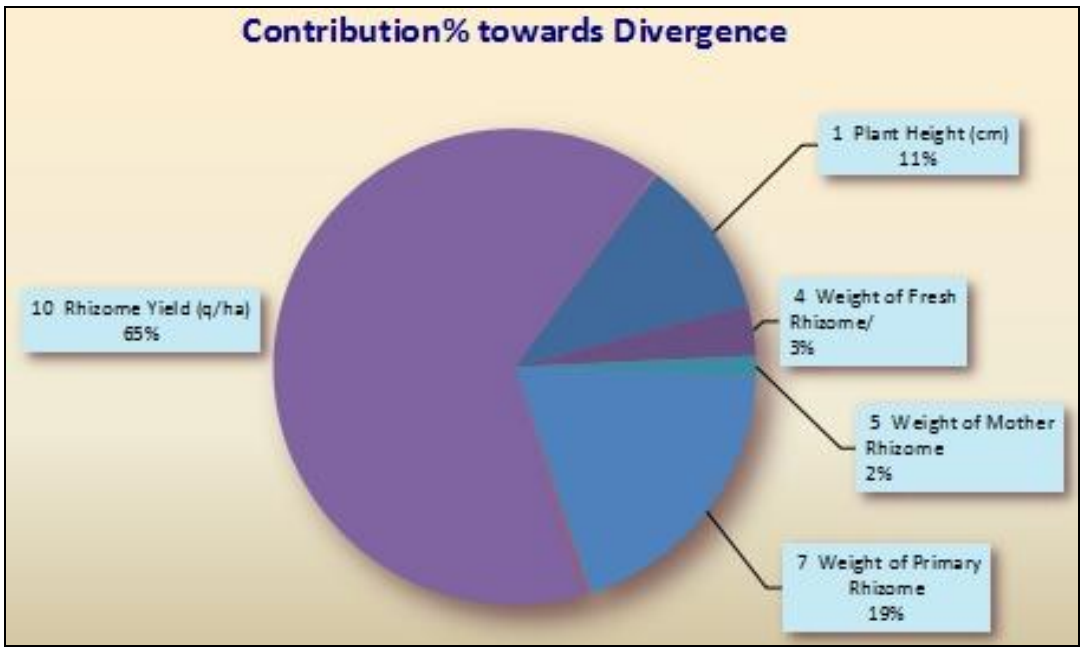

Fig 3: Showing graphical representation of percentage contribution of studied major trait (in parentheses value) toward genetic divergence

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