Genetic variability, character association and diversity analysis in turmeric

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ABSTRACT

The experimental material comprised of 83 turmeric genotypes were evaluated at Faizabad (U.P.), India during 2011-12. The highest magnitude for coefficient of variation at genotypic (GCV) and phenotypic levels (PCV) was observed for number of tertiary rhizomes per plant followed by number of tillers per clump and number of secondary rhizomes per plant. High heritability coupled with high genetic advance was expressed for number of leaves per shoot followed by number of tertiary rhizomes per plant. The rhizome yield per plant exhibited highly significant and positive correlation with weight of fresh rhizome per plant followed by weight of mother rhizome and number of primary rhizomes per plant. The highest positive direct effect on rhizome yield was exerted by weight of fresh rhizomes per plant followed by number of leaves per shoot. Among 83 turmeric genotypes in 10 clusters, the highest number of genotypes was grouped in cluster V (18 genotypes) followed by cluster III (14 genotypes), clusters VIII, IV, VII, I, X, VI IX, and II possessed 11, 10, 9, 7, 6, 4, 2 and 2 genotypes, respectively. The maximum intra- and inter-cluster distance was observed for the cluster II followed by cluster IX and cluster I. The highest percent contribution of genetic divergence was noticed with rhizome yield followed by weight of primary rhizomes and plant height. These cluster based analysis have proved to be effective methods in grouping turmeric accessions that may facilitate their effective utilization in crop improvement programmes through direct selection.

Key words: Turmeric, genotype, correlation, path analysis, cluster analysis.

INTRODUCTION

Turmeric (*Curcuma longa* L.) is one the best known among various taxa of economic, medicinal, ornamental and cultural importance of the genus *Curcuma*. India and Thailand with at least 40 species in each area (Leong-Skorniekova *et al.*, 10) have the highest diversity. Turmeric is a triploid (2n = 3*x* = 63) vegetatively 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 spice is obtained from the underground rhizomes, which after drying and processing results in a bright yellow powder used as a natural food dye. In addition, the presence of various compounds like curcumin, the yellow coloured pigment, with pharmacological activities has broadened the commercial value of this crop. Conventional breeding is difficult in turmeric and hence its genetic improvement is limited to germplasm selection and to eventual sports arising during vegetative propagation. India has a high degree of variability of turmeric. Though some efforts have been made to identify the genetic potential of turmeric germplasms from India, very few studies have been conducted to characterize and evaluate the indigenous material from northern India. The existing variability in germplasm collections need to be exploited to facilitate genotype selection. The objective of the present study was to determine the patterns of distribution of morphological variation for ten quantitative characters in 83 turmeric germplasm collected from wide geographical range.

MATERIALS AND METHODS

The experimental material comprised of 83 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. Geographically the experimental site falls under humid sub-tropical climate and is located at 26.47°N latitude and 82.12°E longitude at an altitude of 113 m above the mean sea level. The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorous, potash and slightly alkaline (pH 8.0) in nature. The mechanical mixture of soil was 60.9% sand, 27.8% silt and 11.3% clay. 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.

The observations were recorded on 20 selected plants as per the recommended guidelines of ABD

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and replicated data of checks (Narendra Haldi-1, Narendra Haldi-14 and Rajendra Sonia) for twelve quantitative and qualitative 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. Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Feeder (5). GCV and PCV were calculated by the formula given by Burton and de Vane (2), heritability in broad sense (h²b) by Hanson *et al.* (6) and genetic advance, *i.e.* the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (8). Correlation coefficients were computed according to the method suggested by Singh and Chaudhary (14) and path analysis was analysed with the help of formula suggested by Dewey and Lu (4). The Genetic divergence among 83 genotypes including checks planted in ABD was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1; Spark, 15).

RESULTS AND DISCUSSION

The variation due to the blocks was highly significant for plant height, number of tillers per clump, number of leaves per shoot and rhizome yield (Table 1). The variation due to block was significant for weight of fresh rhizomes per plant, however, it was non-significant for remaining seven characters.

The differences among the three check varieties (Narendra Haldi-1, Narendra Haldi-14 and Rajendra Sonia) were found highly significant for weight of fresh rhizome per plant, primary rhizomes per plant and dry matter, significant for number of primary rhizomes per plant, while, rest of the traits were non-significant.

The highest magnitude coefficient of variation (Table 2) at genotypic level (GCV) as well as phenotypic level (PCV) was observed for number of tertiary rhizomes per plant (PCV = 57.47) followed by number of tillers per clump (PCV = 41.81) and number of secondary rhizomes per plant (PCV = 36.31). In general, the phenotypic coefficient of variability was higher than genotypic coefficient of variation, which indicates possibility of obtaining very high selection response in respect of these traits. The high estimates of GCV and PCV for these traits was reported by Jan *et al.* (7). The high broad sense heritability (h²b) was expressed for dry matter (98.33%), weight of fresh rhizomes per plant (97.52%), number of leaves per shoot (95.66%), number of tertiary rhizomes per plant (87.61%). Genetic advance in percent of mean was highest in case of number of tertiary rhizomes per plant (103.72%) followed by number of leaves per shoot (68.70%), number of tillers per clump (67.32%). The high heritability coupled with high genetic advance for weight of mother rhizome was observed. The findings of present study are in agreement with Datta *et al.* (3).

The rhizome yield per plant exhibited highly significant and positive correlation (Table 3) with weight of fresh rhizomes per plant (0.951), weight of mother rhizome (0.391), number of primary rhizomes per

Table 1. Analysis of variance of Augmented Block Design for 12 characters in turmeric genotypes.

*,** Significant at 5 and 1%, respectively.

plant (0.296), weight of primary rhizomes (0.548) and dry matter content (0.391). However, the TSS content showed significant and positive correlation only with number of tillers per clump (0.234) and remaining characters were non-significant. Dry matter exhibited highly significant and positive correlation with weight of fresh rhizomes per plant (0.360) number of secondary rhizomes per plant (0.378) and number of tertiary rhizomes per plant (0.331) along with significant and positive correlation with weight of primary rhizomes (0.267).The rest of the traits were non-significant with dry matter. The rhizome yield was negative and nonsignificantly correlated with TSS (Sharon *et al.*, 13).

The highest positive direct effect (Table 4) on rhizome yield (q/ha) was exerted by weight of fresh rhizomes per plant (0.985) followed by number of leaves per shoot (0.167). The very low amount of direct effect observed for remaining four traits indicated that there direct contribution to rhizome yield was too low to be considered on any consequences. The characterization of germplasm for genetic divergence, suitable and diverse genotypes should be based on sound statistical procedure, such as D $^{\rm 2}$ statistics and non-hierarchical Euclidean analysis (Beale, 1; Spark, 15). These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. Among all 83 turmeric genotypes in 10 clusters (Table 5), the highest number of genotypes were in cluster V (18 genotypes) followed by cluster III (14 genotypes), clusters VIII, IV, VII, I, X, VI IX, and II possessed 11, 10, 9, 7, 6, 4, 2 and 2 genotypes, respectively. The maximum intra-cluster distance (Table 6) observed in case of cluster II (26.58) followed by cluster IX (18.54), cluster I (14.3), cluster VIII (14.02), cluster X (12.08), cluster III (12.02), cluster VII (11.78) and cluster VI (10.42), while the minimum intra-cluster distance was showed by cluster IV (8.35) followed by cluster V (8.40). The maximum inter-cluster distance was found between II and IX (61.68), followed by cluster I and IX exhibiting very high inter-cluster distance from remaining 8 clusters. The minimum inter-cluster distance was found between IV and V (13.52), followed by cluster V and VI (17.21).

Cluster mean for different characters had considerable difference between the clusters for all the characters under study (Table 7). The cluster II showed maximum mean value for plant height (119.57) and number of tillers per clump (5.45). Cluster X showed the maximum value for number of leaves per shoot (17.23). Clusters VII, VIII, VII, VII, IX, IX, VII, X and VI showed maximum value for weight of fresh rhizomes per plant (254.42), weight of mother rhizome per plant (49.85), number of primary rhizomes per plant (6.89), weight

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Table 3. Estimates of correlation coefficients between 12 characters in turmeric. **Table 3.** Estimates of correlation coefficients between 12 characters in turmeric.

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Cluster No. of	Genotypes					
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\mathbf{L}	7	NDH-1, NDH-51, NDH-45, NDH-22, NDH-36, NDH-40, NDH-59.				
\mathbf{H}	2	NDH-44. NDH-67.				
Ш	14	NDH-46, NDH-20, NDH-23, NDH-29, NDH-66, NDH-68, NDH-73, NDH-125, NDH-70, NDH-71, NDH-16, NDH-31, NDH-72, NDH-92.				
IV	10	NDH-77, NDH-94, NDH-52, NDH-84, NDH-89, NDH-62, NDH-93, NDH-126, NDH-19, NDH-102.				
V	18	NDH-83, NDH-100, NDH-12, NDH-13, NDH-91, NDH-2, NDH-15, NDH-96, NDH-6, NDH-95, NDH-5, NDH-11, NDH-81, NDH-63, NDH-57, NDH-60, NDH-58, NDH-56.				
VI	4	NDH-54, NDH-55, NDH-88, NDH-86.				
VII	9	NDH-74, NDH-8, Narendra Haldi-1, Narendra Haldi-14, Rajendra Sonia, NDH-69, NDH-14, NDH-18, NDH-65.				
VIII	11	NDH-79, NDH-9, NDH-97, NDH-3, NDH-4, NDH-10, NDH-7, NDH-64, NDH-75, NDH-76, NDH-80.				
IX	2	NDH-99, NDH-17.				
\times	6	NDH-21, NDH-26, NDH-24, NDH-25, NDH-27, NDH-28.				

Table 5. Non-hierarchical Euclidean Cluster analysis for 12 characters in 83 turmeric genotypes.

Table 6. Estimates of average intra- and inter-cluster distances for 10 clusters in turmeric.

Cluster		Ш	Ш	IV	v	VI	VII	VIII	IX	X
	14.3	29.41	19.05	17.23	18.93	25.33	30.18	30.02	60.91	35.79
Ш		26.58	35.34	48.30	43.89	54.36	34.40	41.56	61.68	30.56
Ш			12.62	17.51	17.27	22.39	25.58	29.68	37.87	24.77
IV				8.35	13.52	18.91	33.77	29.30	54.053	40.60
V					8.40	17.21	25.04	20.59	39.09	36.14
VI						10.42	32.74	28.44	46.27	43.82
VII							11.78	19.62	46.12	22.89
VIII								14.02	45.80	27.83
IX									18.54	37.36
X										12.08

of primary rhizomes (134.19), number of secondary rhizomes per plant (24.69), number of tertiary rhizomes per plant (15.18), rhizome yield (380.54), dry matter content (22.74%) and TSS (11.12%), respectively (Roy *et al*., 12; Ravishanker *et al.*, 11; Kumar *et al.*, 9).

The highest percentage contribution of genetic divergence (Table 7) in turmeric by rhizome yield (64.68) followed by weight of primary rhizome (19.37) and plant height (10.84). The other five contributions were by weight of fresh rhizome (3.41), weight of mother rhizome (1.44), number of secondary rhizomes per plant (0.24) and the TSS (0.03). Based on estimates, number of tillers per clump, number of leaves per plant, number of primary rhizomes per plant, number of tertiary rhizomes per plant and dry matter per cent was found to contribute negligible (Kumar *et al.*, 9).

In conclusion, cluster analysis has proved to be effective methods in grouping turmeric accessions that may facilitate their effective utilization in crop improvement programmes through clonal selection, as conventional breeding is difficult in this crop. Moreover, correlation and path analysis of morphological traits indicated importance of desirable traits for strengthening the turmeric breeding programme for higher rhizome yield.

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