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## Genetic variability studies in turmeric (*Curcuma longa* L.)

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### Abstract

The present study was conducted to determine the extent of genetic variability in turmeric genotype using 14 qualitative and quantitative characters. A total of 22 genotypes collected from four different regions were studied under field condition. A considerable level of variability for various characters was observed among different genotypes. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels were observed for number of tertiary rhizome per plant, number of secondary rhizome per plant, weight of primary rhizome per plant, number of primary rhizome per plant, number of leaves per shoot and number of tillers per clump. 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 presence of high heritability in broad sense was found for most of the character except oleoresin content. High heritability for different character indicated that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. High heritability coupled with high genetic advance as percent of mean was observed for all the character except dry matter percent and oleoresin content, which suggest a wide scope for improvement through selection of these traits.

**Keywords:** *Curcuma longa* L., genetic variability, GCV, PCV, heritability, genetic advance

### Introduction

The turmeric (*Curcuma longa* L.) is a perennial rhizomatous plant of tropical and subtropical regions belongs to family Zingiberaceae and native to South Asia, particularly India. India is the largest producer (93.3% of the total world production), consumer and exporter (approximately 90%) of turmeric (Sashikumar, 2005) [14]. It was valued mainly as a spice for food and a natural dye for clothing until recently, when it was discovered to be a potential source of new drugs for a variety of diseases (Corcolon and Dionisio-Sese, 2014) [2]. It is estimated that Indians consume between 80 and 200 mg turmeric extract per day and as a whole the total consumption is about 480,000 ton annually (Deb *et al.*, 2013) [4]. Indian turmeric is regarded as the best in the world market because of its high curcumin. Turmeric being a cross-pollinated triploid species ( $2n = 3x = 63$ ), vegetatively propagated by its underground rhizomes restricted to clonal selection, induced mutation and subsequent selection in the crop improvement programme. Rich morphological and genetic diversity is observed among the cultivated types of turmeric (*C. longa* L.); probably due to vegetative mutations accumulated over a period of time (Ghosh *et al.*, 2013) [5]. The viable seed sets obtained in certain cases enable recombination breeding through hybridization and open-pollinated progeny selection (Sasikumar, 2005) [14]. For genetic improvement of turmeric germplasm collections represents the main source of variability and efforts to characterize these collections, conducted specially in India because of the economic importance crop and most of the genetic diversity found here (Lynrah *et al.*, 1998 and Singh *et al.*, 2003) [9, 18]. The existing variability in germplasm collections need to be exploited to facilitate genotype selection. The availability of information on extent of variations, estimates of heritability and expected genetic advance in respect of yield and yield determining traits are the basic requirement for formulating the suitable breeding strategy on genetic improvement program in turmeric. The objective of the present study was to determine the patterns of distribution of morphological variation for 14 quantitative characters in 22 turmeric germplasm collected from wide geographical range.

## Materials and Methods

Twenty-two genotypes of turmeric were grown in randomized bloc design (RBD) with three replications at Main Experiment Station of the Department of Vegetable Science, Narendra Dev University of Agriculture and Technology (Narendra Nagar), Kumarganj, Faizabad during summer season 2016-17. Geographically the experimental site falls under humid subtropical climate and is located at 26.47°N latitude and 82.12°E longitude at an altitude of 113 m above mean sea level. The experimental field had sandy loam soil and slightly alkaline (pH 8.0) in nature. The climate of experimental site is semi-arid with hot summer and cool winter. Healthy and treated rhizomes having 2-3 buds were planted at 30 cm apart in rows keeping 25 cm plant to plant distance. All the recommended package of practices was followed to raise a good crop. Five plants in each replication of each genotypes were selected and tagged to record observations on ten quantitative characters *i.e.*, plant height (cm), number of tillers per clump, number of leaves per shoot, weight of fresh rhizomes per plant (g), weight of mother rhizomes (g), number of primary rhizomes per plant, weight of primary rhizomes per plant (g), number of secondary rhizomes per plant, number of tertiary rhizomes per plant, rhizomes yield (qha<sup>-1</sup>) and four qualitative characters namely dry matter(%), TSS(%), curcumin and oleoresin content. The mean values were subjected to statistical analysis of data for each character as per method given by Panse and Shukhatme (1985)<sup>[12]</sup>. PCV

and GCV for different characters was estimated as suggested by Burton and de Vane (1953)<sup>[1]</sup>. Heritability in broad sense ( $h^2$ ) was calculated by the following formula suggested by Hanson *et al.* (1956)<sup>[6]</sup> and Expected genetic advance was estimated by the method given by Johnson *et al.* (1955)<sup>[8]</sup>.

## Result and Discussion

The analysis of variance was conducted to test significance difference among genotypes studied. The analysis of variance showed that all the genotypes differed for all the characters under study. The range, general means, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance in percent of mean for different character of turmeric (*Curcuma longa* L.) germplasm statistically worked out to facilitate selection for various traits and has been presented in Table 1.

The character number of tertiary rhizome per plant, number of secondary rhizome per plant, weight of primary rhizome, number of primary rhizome per plant, weight of fresh rhizome per plant and number of tillers per clump showed comparatively high genotypic and phenotypic coefficient of variation. Genotypic coefficient of variation (GCV) for all the character varied from 7.38 to 51.64, while phenotypic coefficient of variation (PCV) ranged between 8.67 and 53.06. The phenotypic variability may be due to genetic constitution of the material as well as environment influences. Very little difference between genetic coefficient.

**Table 1:** Estimates of Range, general mean, coefficient of variation, heritability and genetic advance in per cent of mean for 14 characters

S. No	Characters	Range		General mean	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Heritability (%)	Genetic advance in per cent of mean
		Minimum	Maximum					
1.	Plant Height (cm)	54.83	120.70	83.29	21.87	22.39	95.47	44.03
2.	Number of tillers per clump	1.73	3.66	2.43	19.67	24.02	67.1	33.20
3.	Number of leaves per shoot	8.43	20.07	13.44	22.48	29.84	56.79	34.90
4.	Weight of fresh rhizome per plant (g)	121.33	252.21	193.16	16.82	17.02	97.68	34.24
5.	Weight of mother rhizome (g)	19.91	43.50	30.32	18.89	20.97	81.2	35.08
6.	Number of primary rhizomes per plant	2.96	9.43	5.96	31.03	33.44	86.09	59.31
7.	Weight of primary rhizome (g)	43.76	164.00	91.02	34.57	34.84	98.47	70.68
8.	Number of secondary rhizomes per plant	3.53	20.93	10.53	39.57	42.46	86.78	75.91
9.	Number of tertiary rhizomes per Plant	2.20	10.63	4.36	51.64	53.06	94.73	103.53
10.	Rhizome Yield (q/ha)	175.30	318.55	276.06	14.20	14.63	94.21	28.40
11.	Dry matter (%)	17.60	24.76	21.50	7.38	8.67	72.36	12.93
12.	TSS (%)	3.60	8.30	6.65	19.12	19.36	97.51	38.90
13.	Curcumine	3.16	5.80	3.93	17.53	17.73	97.76	35.71
14.	Oleoresin	6.45	11.45	8.39	18.24	18.25	18.25	37.55

of variation and phenotypic coefficient of variation observed for most of the character which indicates that there was little influence of environmental factor on their phenotypic expression thus there is possibility of obtaining very high selection response in respect of these traits. The above result show conformity with finding of Nirmal and Yamgar (1998)<sup>[10]</sup>, Pandey *et al.* (2002)<sup>[11]</sup>, Sinkar *et al.* (2005)<sup>[19]</sup>, Singh *et al.* (2007)<sup>[17]</sup> and Jan *et al.* (2012)<sup>[7]</sup>.

Heritability estimates the assessment of amount of transmissible genetic variability to the total variability and happens to most important basic factor that determines the genetic improvement or response to selection. The high heritability was found for most of the character under studied. High heritability was found for most of the character except oleoresin content. High heritability for different character indicated that large proportion of phenotypic variance has been attributed to genotypic variance and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. The findings of present study are in

agreement with Lynrah *et al.* (1998)<sup>[9]</sup>, Shanmugasundaram *et al.* (2000)<sup>[15]</sup>, Datta *et al.* (2006)<sup>[3]</sup> and Singh *et al.* (2012)<sup>[16]</sup>. Although high heritability estimates have been found to be helpful in making selection of superior genotype on the basis of phenotypic performance; Johnson *et al.* (1955)<sup>[8]</sup> suggested that heritability estimates along with genetic gain were more useful in predicting selection of the best individual. It is therefore, necessary to utilize heritability in conjunction with selection differential which would then indicate the expected genetic gain resulting from selection. Genetic advance as percent of mean was recorded from 12.93 to 103.53, it was found high for most of the character under study except dry matter percent. High heritability coupled with high genetic advance as percent of mean was observed for all the character except dry matter percent and oleoresin content, which suggest a wide scope for improvement through selection of these traits. The findings of present study are in agreement with findings of Rao *et al.* (2004)<sup>[13]</sup>, Datta *et al.* (2006)<sup>[3]</sup> and Singh *et al.* (2012)<sup>[16]</sup>.

### Conclusion

Analysis of variance revealed the presence of considerable amount of variability for yield and attributing traits. The genotypes expressed high genotypic and phenotypic coefficient of variation, heritability (broad sense) accompanied with high value of genetic advance for number of primary rhizome per plant, weight of primary rhizome and number of secondary and tertiary rhizomes per plant which revealed that these traits are under the control of additive gene action and lower influence of environmental factor in expression of these traits with possibility for further improvement through selection.

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