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Genetic variability, heritability and genetic advance studies in turmeric (*Curcuma longa* L.)

S. Praneetha*, P. Vinoth and V.K.I. Sri Subalakshmi

Tamil Nadu Agricultural University, Coimbatore, TamilNadu

Abstract

The present investigation was carried out at Agricultural Research Station, Bhavanisagar, using 148 turmeric accessions along with two varieties. The genotypes were evaluated in Randomized Complete Block Design with two replications to ascertain extent of variability, heritability and genetic advance for yield and other horticultural traits among the genotypes. Analysis of variance showed significant differences among all the genotypes for all the characters under study. Eight genotypes *viz.,* BS 9, BS 50, BS 100, BS 122, CL101, B 2, B 3, CL 101, CL 206, and two varieties BSR 1and BSR 2 were found to be high yielding. They could be the promising parents for utilization in further breeding programmes. Moderate PCV and GCV were observed for yield of rounds plot^{-1}. High heritability estimates were observed for all the characters viz., plant height, no. of leaves plant^{-1}, no of tillers, rhizome yield plot^{-1}, finger rhizome yield and mother rhizome yield with projected yield (t ha^{-1}) studied.

Keywords: Genotypes, genetic variability, heritability, genetic advance, genetic advance as percent of mean, Turmeric.

Introduction

The most valued medicinal and spicy underground rhizomatous turmeric (*Curcuma longa* L.) belongs to family zingiberaceae. It is considered as native of South Asia, particularly India. India meets out 93.3% of the world production due to its high quality and high curcumin content. Turmeric is distributed in India, south-East Asian countries like Cambodia, China, Indonesia, Madagascar, Malaysia, Philippines and Vietnam and North Australia (Amzad H. *et al*., 2005). UAE is the major importer of turmeric from India followed by US, Japan, UK, France, Singapore, Srilanka and South Africa (Ravindran *et al*., 2007). In our country it is widely cultivated in the states of Andhra Pradesh, Tamil Nadu, Orissa, Karnataka, Kerala, Maharastra and West Bengal.

Genetic variability helps to assess the level of variation in different quantitative and qualitative parameters. For an effective and successful breeding programme genetic variability is essential. It is the important character to be considered for selecting the best genotypes with desirable characters and high yield as well as to select the most superior genotypes for further improvement. Effectiveness of selection depends upon the magnitude of genetic variability present in the germplasm and Knowledge of germplasm diversity has a significant impact on genetic improvement of crop plants. Thus, it becomes imperative to study the level of genetic variability.

The variation in the genetic make-up, interaction with environment, depicts the pattern of diversity shown. Development of varieties with high yield levels coupled with desired quality attributes requires information on the nature and extent of variability available in the germplasm collections. India is having a high degree of variability of turmeric. Though India enjoys the monopoly in turmeric production and export, because of its ever increasing demand in both food and pharmaceutical industries, there is a need to further increase the productivity of turmeric. However to increase the productivity, information regarding the crop genetic diversity is essential. Hence, the information regarding variability, heritability and crops genetic diversity are essential in turmeric to make further improvement on desirable character. The study was initiated to collect and preserve the genetic variability in turmeric germplasm to make it available to present and future generations. Genetic variation in turmeric for many economic traits has been reported by earlier workers (Babu *et al.,* 1993, Lynrah *et al.,* 1998, Hazra *et al.,* 2000, Sinker *et al.,* 2005, Singh *et al.,* 2012, Jan *et al.,* 2012, Rajyalakshmi *et al.,* 2013, Singh and Ramakrishna, 2014, Prajapati *et al.,* 2014 and Verma *et al.,* 2015).

Materials and Methods

An experiment was conducted at Agricultural Research station, Bhavanisagar, Tamilnadu to find out the genetic divergence in 150 turmeric accessions. The research farm is falls under Western Zone of Tamil Nadu which situated at 11° 29' N latitude and longitude of 77° 80' E at 256 m above MSL. The mean annual rainfall is 717 mm,

*Corresponding author email: prejan27@gmail.com

maximum temperature is 33.9° C and that of the minimum temperature is 21.6° C. The average wind velocity is 3.2 KMPH. The sunshine hours range from 3.7 to 7 per day with an average evaporation of 4.3 mm per day. The soils of this location considered to characterize the major soil types which are found in the Lower Bhavani Project ayacut area. Soil is sandy loam in nature belongs to Irugur series and Sathyamangalam series of Tamil Nadu. A total number of one hundred and forty eight turmeric genotypes were collected from various parts of the country for evaluating their performance for yield and quality along with BSR 1 and BSR 2 as check varieties under Western zone of Tamil Nadu. The experiment was conducted for three years consecutive years to assess the performance of collected genotypes. The collected seed rhizomes were graded in to 25-30 gram weight and treated with phosalone 35 EC 0.2 per cent plus 0.3 per cent copper oxychloride for 30 minutes to control seed born pest and diseases. The experimental plot was designed and laid out as per Randomized Block design (RBD) with two replications. The recommended fertilizer dose of 160: 60: 108 Kg N, P_2O_5 and K_2O were applied uniformly to all the experiment plots as per the TNAU recommendations.

The important traits like plant height, no. of leaves per plant, no of tillers, rhizome yield plot^{-1}, finger rhizome yield and mother rhizome yield with projected yield (t ha^{-1}). Mean of three year data were statistically analyzed as suggested by Panse and Sukhatme (1985).

Genotypic and phenotypic coefficients of variation were computed according to Burton (1952). Heritability in broad sense refers to the proportion of genetic variance to the total observed variance in the population. It has been estimated as per the formula given by Lush (1940). Genetic advance as per cent mean was worked out for each character adopting the formula given by Johnson *et al.,* (1955)

The mean data after computing for each character was subjected to standard methods of analyses of variance following Panse and Sukatme (1957). Phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (broad sense) and genetic advance as percentage of mean were estimated by the formulae suggested by Burton (1952) and Johnson *et al.* (1955).

Results and Discussion

The genetic parameters, *viz.,* phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as per cent mean were estimated for all the characters under study (Table 1). The genotypes exhibited a wide range of variability for all the characters. Analysis of variance revealed high level of variability for all the characters taken for study indicated the existence of highly significant differences among genotypes. It was found that the PCV estimates were higher than the GCV estimates indicating the influence of environment on the expression of these characters and possibility of obtaining very high selection response in respect of characters studied and it may differ with the genetic

Table 1. Range, mean, genotypic and phenotypic variance components, coefficient of variability, heritability and genetic advance for different traits in turmeric germplasm.

S. No.	Character	Range	Mean	Variance components		Coefficient of variability		Heritability (%)	Genetic advance	Genetic advance as % of mean
				Genotypic	Phenotypic	Genotypic	Pheno typic			
1	Plant height(cm)	38.63-77.11	65.10	34.03	36.64	8.96	9.30	92.88	11.58	17.79
2	No. of leaves	5.85 -8.65	7.27	0.20	0.23	6.18	6.67	85.80	0.86	11.80
3	No. of tillers	1.55 - 2.63	2.04	0.02	0.02	7.29	7.78	87.78	0.29	14.06
4	Yield of fingers plot^{-1} (Kg/6m2)	12.86 -24.36	17.95	0.98	1.20	5.52	6.10	81.98	1.85	10.30
5	Yield of rounds plot^{-1} (Kg/6m2)	3.49 - 5.65	3.89	0.16	0.16	10.15	10.44	94.57	0.79	20.33
6	Total Yield plot^{-1} (Kg/6m2)	18.41 -30.01	21.84	1.27	1.63	5.17	5.85	78.12	2.05	9.41
7	Yield ha^{-1} (t ha^{-1})	30.56-49.82	36.25	3.54	4.43	5.19	5.80	79.95	3.47	9.56

PCV, GCV and Genetic Advance as per cent Mean: Low = 0-10%; Medium = 10-20%; High = 20% above

Heritability: Low = Less than 30%; Medium = 30-60%; High = More than 60%

makeup of the genotype. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The percentage of genotypic and phenotypic coefficient of variation were medium for yield of rounds plot^{-1} (10.15 and 10.44 respectively). For rest of the characters *viz.,* plant height (8.96 and 9.30 respectively), no. of leaves plant^{-1} (6.18 and 6.67 respectively), no of tillers (7.29 and 7.78 respectively), finger rhizome yield (5.52 and 6.10 respectively) and total rhizome yield plot^{-1} (5.17 and 5.85 respectively) and projected yield (5.19 and 5.80 respectively) it was low, indicating that these characters are important in crop improvement as major part of the phenotypic variability in these characters was contributed by additive gene effects and hence improvement can be made by simple selection. Similar findings on low level of genotypic and phenotypic coefficient of variation estimates was reported by Pathania *et al.,* (1988), Indiresh *et al*.(1992), Babu *et al.,* (1993), Lynarah *et al.*(1998), Singh *et al.,* (2003), Sinker *et al.,* (2005) Rao *et al.,* (2004), Jan *et al*., (2011), Jan *et al.,* (2012), Rajyalakshmi *et al*., (2013), Singh *et al.,* (2013), Jayasree *et al.,* (2014), Prajapati *et al.,* (2014), Singh and Ramakrishna (2014) Verma *et al.,* (2015) and Mamatha *et al.,* (2020).

The heritability estimates help the breeders in selection based on the phenotypic performance. The practical implications in breeding programmes are based on magnitude of heritable variation of the character concerned. Although PCV and GCV reveal the extent of genetic variability present, they do not indicate the extent of heritable variation to make the selection effectively. The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character.

All the seven characters studied were exhibited high heritability which ranged from 78.12 to 94.57%. The high heritability measures for plant height (92.88%), number of leaves (85.80%), no.of tillers (87.78%), yield of fingers plot^{-1} (81.98%), yield of fingers plot^{-1} (81.98%), yield of rounds plot^{-1} (94.57%), total rhizome yield plot^{-1} (78.12%) and estimated yield/ ha (79.95%) declaring the possibility of improvement of fresh turmeric yield through selection for rhizome yield and its component characters and suggesting that emphasis should be given for all the studied characters while going for selection. High heritability was reported by Pathania *et al.,* (1988), Babu *et al.,* (1993), Lynarah *et al.,* (1998) Singh *et al.,* (2003), Singh *et al.,* (2012), Rajyalakshmi *et al.,* (2013), Jayasree *et al.,* (2014) and Verma *et al.,* (2015).

Heritability along with genetic advance is more helpful in predicting the gains under selection than heritability estimated alone (Johnson *et al*., 1955). In the present study, genetic advance as percentage mean ranged from 9.41 (Total yield plot^{-1}) to 20.33 (Yield of rounds plot^{-1}).

Low to medium level of genetic advance (as low as 0.29 for no. of tillers and medium of 11.58 for plant height) and genetic advance as percentage mean (low for Total yield plot^{-1} (9.41) and yield ha^{-1} (9.56) and medium for rest of the characters) were noticed for the characters studied indicating the large influence of environment for the expression of this character. According to Manohar *et al.,* (2004) and Singh and Ramakrishna (2014) there was high heritability and moderate to genetic advance for cured yield, Fresh weight of mother rhizomes and number of secondary rhizomes. Devraj *et al.,* (2020) recorded high heritability along with low genetic advance for plant girth, length of mother rhizome, width of mother rhizome, number secondary rhizomes plant^{-1}, number of tertiary rhizomes plant^{-1}, weight of tertiary rhizome plant^{-1}.

Based on variability and heritability estimates, it could be concluded that improvement by direct selection in turmeric is possible for traits studied. In general, the character that shows high heritability with high genetic advance are controlled by additive gene action (Panse and Sukatme, 1957) and can be improved through simple or progeny selection methods.

The traits showing high heritability along with low or moderate genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding (Samadia, 2005).

In the present study, out of 148 genotypes, eight superior genotypes *viz.,* BS 9, BS 50, BS 100, BS 122, CL101, B 2, B 3, CL 101, CL 206, and two varieties BSR 1and BSR 2 were found to be potential enough to be used as parents in heterosis breeding. These genotypes recorded highest values for one or the other yield contributing traits and hence their utilization in combination breeding may help in generating high yielding varieties/ hybrids for commercial cultivation.

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