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Genetic variability, heritability and genetic advance as per cent mean in turmeric (*Curcuma longa* L.) genotypes

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Abstract

The investigation was undertaken on nineteen genotypes of turmeric (*Curcuma longa* L.) with a view to assess the genetic parameters in respect of yield and yield determining characters. The highest percentage of phenotypic and genotypic coefficient of variation was observed in number of tillers, leaf area, number of secondary rhizomes, length of mother rhizome, fresh weight of rhizome per plant, dry weight of rhizome per plant, yield per plot, estimated yield per ha, curcumin content, and oleoresin content. High heritability was observed for plant height (92), number of tillers (63), leaf length (89), leaf width (63), leaf area (99), number of secondary rhizomes (91), length of mother rhizome (88), fresh weight of rhizome per plant (97), dry weight of rhizome per plant (87), duration of the crop (95), dry recovery of rhizome (89), curcumin content (91), oleoresin content (92) indicating that these characters are important in crop improvement. Highest estimates of heritability observed for Leaf area (99) and Fresh weight of rhizome per plant (97), could be utilized for the improvement of fresh turmeric yield through clonal selection.

Keywords: Genetic variability, genetic advance, *Curcuma longa* L.

Introduction

Turmeric (*Curcuma longa* L.) is a herbaceous plant belonging to the family Zingiberaceae and order Sacitaminae. It’s chromosome number is 2n = 32. The karyomorphological studies concluded that the species seems to be allotetraploid with basic number of X = 8 (Sato, 1960) [13]. India is known as the land of spices and they are popular for their flavour and medicinal properties both domestic and international market. Turmeric believed to be originated in South-East Asia and some species are naturalized in north eastern regions of India and Java. Turmeric is either grown as a pure crop or inter/mixed crop in coconut, areca nut and coffee plantations. In India it is being cultivated in more than 20 states in an area of 2.37 lakh ha with an annual production of 11.63 MT and earning 1241.89 crores by exporting 1.16 MT to other countries. In India, it is mainly grown in Telangana, Andhra Pradesh, Odisha, West Bengal, Tamil Nadu, Assam, Maharashtra, Karnataka, Bihar and Kerala. Among these, Telangana occupies 50,000 ha of total area and 2.55 MT of total production of the country. The national productivity of crop is 5 tonnes per hectare. (NHB, 2017-18).

An information on extent of variation, estimates of heritability and expected genetic advance in respect of yield and yield determining traits constitutes the basic requirement for a crop improvement programme. Hence, the present investigation was undertaken with a view to estimate the genetic parameters for rhizome yield and yield determining characters in turmeric.

Materials and Methods

The experimental site was located in the Horticulture Research Station, Chinthapalli, Andhra Pradesh. The location falls under Agro-climatic zone of High Altitude and Tribal Zone with an average annual rainfall from South-west monsoon of more than 1200 mm, maximum temperature range 17 to 35 ºC, minimum temperature range from 3 to 24ºC and is located at an altitude of 933 m MSL. The geographical situation is 17^0.13’ N latitude and 84^0.33’ E longitudes. The experiment was laid out in a Randomised Block Design with 19 treatments and 3 replications. The planting was done on raised beds spaced row to row 30 cm with plant to plant distance of 25 cm and the net plot size was 3 x 1 m^2. The soil of the experimental field was alluvial and it was endowed with good drainage. Recommended package of practices and plant protection measures were followed to raise a healthy crop.

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The analysis of variance for all characters was carried out as per the procedure suggested by Verma *et al.* (1987) [19]. Genotypic variance and phenotypic variance was calculated using the method suggested by Johnson *et al.* (1955) [8] and Al-Jibouri *et al.* (1958) [1] for the data. Heritability in broad sense, which is the ratio of genotypic variance to the phenotypic variance, was calculated by the method given by Burton and De Vane (1953) [3], Johnson *et al.* (1955) [8] and Hanson *et al.* (1956) [5] using the formula. Genetic advance is the genetic improvement of the progeny possible through selection over the original population. Genetic advance as per cent mean was worked out for each character adopting the formula given by Johnson *et al*. (1955) [8]

Results and Discussion

The estimates of variability *viz.* coefficients of variability (phenotypic and genotypic), heritability (in broad sense**)** and genetic advance as percent of mean were worked out for selection of various characters. The results are presented in Table 1.

The observed variations in the characters among the genotypes were due to the effect of genotype and environment. Environmental variations are not fixable. For determining the magnitude of genotypic and phenotypic variability, the genotypic and phenotypic coefficients of variability were calculated (Table 1).

For all the characters studied, phenotypic coefficients of variability were higher in magnitude than genotypic coefficients of variability, though differences were very less in majority of cases. Thus, it is showing that these traits are less influenced by environmental factors. Coefficients of variability varied in magnitude from character to character, either low or moderate or high. Therefore, it indicated that there is always a great diversity.

The phenotypic coefficients of variability (PCV) was high (>20%) for number of tillers (29.00), leaf area (26.71), number of secondary rhizomes (24.65), length of mother rhizome (24.48), fresh weight of rhizome per plant (30.09), dry weight of rhizome per plant (26.20), yield per plot (23.08), estimated yield per ha (23.09), curcumin content (26.82) and oleoresin content (27.11), whereas the moderate phenotypic coefficients of variability (PCV) were recorded (10-20%) for plant height (18.54), number of leaves (13.49), leaf length (17.28), leaf width (13.43), number of mother rhizomes (18.34), number of primary rhizomes (19.31**),** length of secondary rhizome (13.81), dry recovery of rhizome (18.16), whereas for length of primary rhizome (9.89) and duration of the crop (6.91) phenotypic coefficients of variability (PCV) were low (0-10%) in magnitude (Table 1).

The results are in line with the findings of Sinkar *et al*. (2005) [18] reported high PCV for curcumin content, Babu *et al.* (1993) [2] found high PCV for number of tillers, secondary rhizomes per plant and yield per plot and Singh *et al.* (2003) [17] found high PCV for number of secondary rhizomes per plant and moderate PCV for plant height and number of leaves per plant.

The genotypic coefficients of variability (GCV) were high (>20%) for number of tillers (22.95), leaf area (26.63), number of secondary rhizomes (23.57), length of mother rhizome (22.97), fresh weight of rhizome per plant (29.59), dry weight of rhizome per plant (24.42), curcumin content (25.60) and oleoresin content (26.00), whereas moderate (10-20%) genotypic coefficients of variability (GCV) were recorded for plant height (17.26), leaf length (16.29), leaf width (10.63), number of mother rhizomes (13.07), number of primary rhizomes (13.62), length of secondary rhizome (10.43), yield per plot (16.89), estimated yield per ha (16.90) and dry recovery of rhizome (17.13). For number of leaves (8.94), length of primary rhizome (5.92), duration of the crop (6.72) genotypic coefficients of variability (GCV) were low (0-10%) (Table 1).

Similar results were reported by Yadav and Singh (1996) [20] as moderate GCV for width and length of rhizome. High GCV for curcumin content similar to present study was reported by Sinkar *et al*. (2005) [18], while Babu *et al.* (1993) [2] found high GCV for number of secondary rhizomes per plant, Singh *et al.* (2003) [17] found high GCV for length of secondary rhizomes and moderate GCV for plant height and leaves per plant. This might be due to the presence of genotypic variation among the genotypes studied.

The estimates of heritability (broad sense) varied from 36 to 99 % for different characters under the study (Table 1). It was found that high heritability (> 60%) for plant height (92), number of tillers (63), leaf length (89), leaf width (63), leaf area (99), number of secondary rhizomes (91), length of mother rhizome (88), fresh weight of rhizome per plant (97), dry weight of rhizome per plant (87), duration of the crop (95), dry recovery of rhizome (89), curcumin content (91), oleoresin content (92). Moderate heritability (30-60%) was recoeded for number of leaves (44), number of mother rhizomes (51), number of primary rhizomes (50), length of primary rhizome (36), length of secondary rhizome (57), yield per plot (54) and estimated fresh yield per ha (54).

The results of present findings are in line with the findings of Shanmugasundaram *et al.* (2001) [14], Jana *et al.* (2001) [7], Singh *et al.* (2003) [17] while Chattopadhyay *et al.* (2004) revealed that the high heritability estimates for length of mother rhizome, fresh weight of mother, primary and secondary rhizomes and Babu *et al.* (1993) [2] reported high heritability for weight of secondary rhizome and moderate heritability for number of leaves and number of primary rhizomes. Indiresh *et al.* (1992) [6] revealed high heritability for fresh rhizome yield, Yadav and Singh (1996) [20] reported that length of rhizomes showed high heritability, whereas Rao *et al.* (2004) [12] reported that weight of the mother rhizome and number of secondary rhizomes had moderate to high heritability. Singh *et al.* (2012) [15] reported high heritability estimates for weight of mother, fresh and secondary rhizomes per plant, length and width of mother rhizome, rhizome girth and dry recovery.

The results obtained in the present studies, it was concluded that selection can be performed at phenotypic performance for highly heritable characters *viz.* length and weight of mother, primary, secondary rhizomes, yield per plot, yield per hectare and dry recovery.

Heritability along with genetic advance is more helpful in predicting the gains under selection than heritability estimated alone (Johanson *et al*. 1955) [5]. In the present study, genetic advance as percentage mean ranged from 7.29 (length of primary rhizome) to 59.94 (fresh weight of rhizome per plant) (Table 1).

High heritability along with high genetic advance was observed for plant height (35.04), number of tillers (37.42), leaf length (31.62), leaf area (54.68), number of secondary rhizomes (46.42), length of mother rhizome (44.41), fresh weight of rhizome per plant (59.94), dry weight of rhizome per plant (46.87), yield per plot (25.47), estimated yield per ha (25.48), dry recovery of rhizome (33.28), curcumin content (50.35), oleoresin content (51.39) indicating the predominance of additive genes and pave the way for improvement of those characters in individual plant selection. Similar findings were reported by Lynrah *et al*. (1998) [9] and Singh and Ramakrishna (2013) [16]. Heritability and genetic advance were observed to be high for rhizome yield and number of tillers per plant. According to Manohar *et al*. (2004), there was moderate to high heritability and genetic advance for dry recovery of rhizome, fresh weight of mother rhizomes and number of secondary rhizomes.

High heritability coupled with high genetic advance was observed for plant height, number of tillers per plant, leaf area, fresh weight of rhizome per plant, dry weight of rhizome per plant, dry recovery, curcumin content and oleoresin content, therefore these characters shall be given prime importance for future improvement in rhizome yield for varietal development programme.

Table 1: Estimates of variability and genetic parameters for yield and yield attributes in turmeric

S. No.	Character	Mean	Range	PCV	GCV	h^2	GAM
1	Plant height (cm)	126.40	91.17- 169.2	18.54	17.26	92	35.04
2	Number of tillers	2.32	1.00- 3.33	29.00	22.95	63	37.42
3	Number of leaves	16.36	12.46-19.00	13.49	8.94	44	12.21
4	Leaf length(cm)	54.94	39.17-70.53	17.28	16.29	89	31.62
5	Leaf width(cm)	15.32	12.20-17.89	13.43	10.63	63	17.35
6	Leaf area (cm^2)	10023.97	5362.86-13703.96	26.71	26.63	99	54.68
7	Number of mother rhizomes	1.55	1.00-1.93	18.34	13.07	51	19.20
8	Number of primary rhizomes	5.67	4.47-7.93	19.31	13.62	50	19.78
9	Number of secondary rhizomes	14.18	7.80-23.73	24.65	23.57	91	46.42
10	Length of mother rhizome (cm)	6.66	4.80-12.07	24.48	22.97	88	44.41
11	Length of primary rhizome (cm)	8.63	7.60-9.47	9.89	5.92	36	7.29
12	Length of secondary rhizome (cm)	3.18	2.73-4.20	13.81	10.43	57	16.23
13	Fresh weight of rhizome per plant	360.41	183.63-658.32	30.09	29.59	97	59.94
14	Dry weight of rhizome per plant	78.13	41.38-123.14	26.20	24.42	87	46.87
15	Yield per plot (g)	10.13	8.04-15.10	23.08	16.89	54	25.47
16	Estimated yield (t per ha)	34.16	26.80-50.35	23.09	16.90	54	25.48
17	Duration of The Crop (days)	230.33	196.00-256.60	6.91	6.72	95	13.48
18	Dry recovery of rhizome (%)	21.70	15.63-27.86	18.16	17.13	89	33.28
19	Curcumin content (%)	3.88	1.55-5.35	26.82	25.60	91	50.35
20	Oleoresin content (%)	6.34	3.83-10.13	27.11	26.00	92	51.39

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2= Heritability, GAM = Genetic Advance as per cent Mean (%)

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