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Genetic Variability Studies of Turmeric (*Curcuma longa* L.) Genotypes of North Eastern Region of India

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Thirty two (32) genotypes of turmeric from all the north eastern state of India along with Duggirala Red as check variety were evaluated to study the genetic parameters in respect of yield and yield attributing characters. Fifty three (53) traits were analyzed for phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and expected genetic advance at 5 per cent selection intensity. The study revealed the presence of significant genetic variability, moderate to high heritability along with good genetic advance as percent of mean. The genotypes giving higher values of these characters indicated that the individual plant selection based on these characters may be given more emphasis and hence better selection process for further crop improvement programme. Thus, the result of the present study demonstrated that there exists variability among different turmeric genotypes of north eastern region of India indicating high potential for effective crop improvement and/or for further manipulation of the genetic resources through breeding as the genotypes in this region are good sources of genes for many desirable traits.

Introduction

Creation of genetic variability, heritable variation and the expected genetic gain forms the basis for plant breeding. The availability of genetic variability among population is most important for judicious selection and breeding to desired plant genotypes in any future crop improvement programme. In order to conserve the genetic resources and get consistent variability, genetic studies of morphological characterization among turmeric genotypes are essential. The objective of the present study was to determine the patterns of distribution of morphological variations and genetic parameters for rhizome yield and yield determining characters in thirty two (32) turmeric genotypes collected from wide geographical range of north eastern region of India.

Materials and Methods

The experiment was conducted at Horticulture Experimental Farm, AAU, Jorhat, Assam during 2016. The experimental materials were collected from the farmer's field from all the eight (8) north eastern state of India. The treatments comprises of 33 genotypes which were replicated thrice under Randomized Block Design (RBD). Plot size of 1.5 m x 1.5 m (2.25 sq. m) was laid out with plant to plant spacing of 30 cm x 30 cm accommodating 25 plants per plot. The analysis of variance was worked out according to the method suggested by Panse and Sukhatme (1989). The GCV and PCV were worked out according to Burton and Devane (1953). Subsequently, the heritability in broad sense and genetic advance as per cent of mean at 5 % selection intensity were worked out respectively.

Results and Discussion

The nature and magnitude of genetic variations were studied for fifty three (53) traits of turmeric genotypes using genetical parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance (GA) as per cent of mean. The study revealed that the GCV varied from 4.73 % for numbers of leaves per main shoot at 165 DAP to 55.98 % for numbers of leaves per tiller at 105 DAP. Among the 53 traits of turmeric genotypes evaluated, twenty five (25) traits exhibited relatively high GCV, twenty one (21) characters are medium and the rest seven (7) characters have low genetic coefficient of variation (GCV). The high GCV exhibited were also reflected in a wide range of their mean values. In general, the GCV estimates is lower than the PCV estimates which was also found in the present study indicating the influence of environment.

Genetic variability parameters studied for 53 traits of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h_{bs}^2) and genetic advance as per cent of mean showed high GCV and PCV for weight of mother, primary and secondary rhizome per plant, fresh rhizome yield per plant, number of leaves per hill, number of tillers per hill, number of primary rhizome and curcumin contents indicating presence of variability in these traits. Whereas plant height, leaf length and width, number of leaves per main shoot, number of days to maturity, length and girth of mother, primary and secondary rhizome, harvest index, dry recovery, oleoresin content and dry rhizome yield per plant showed low GCV and PCV indicating presence of low genetic variability for these parameters. Similar results have also been reported by Prajapati *et al.,* (2014), Jalata *et al.,* (2011), Yudhvir *et al.,* (2003) and Jalgaonkar *et al.,* (1990). Generally, the differences between phenotypic and genotypic coefficient of variability for all the corresponding characters was small indicating that these characters were less influenced by the environment. Several workers indicated that genetic variability of important agronomic traits is predominantly additive genetic variance, while the non-additive genetic variance is generally smaller than the additive genetic variance (Moll and Stuber, 1974). Genotypic coefficient of variability estimate gives good implication for genetic potential in crop improvement through selection (Johnson *et al.,* 1955). High values of GCV suggest better scope of improvement for these traits by selection. Burton (1952) suggested that the genetic coefficient of variation together with heritability estimates gave the better picture of heritable variations.

The broad sense heritability estimates of the character provide a measure of the effectiveness of selection on phenotypic basis for that particular character. In the present study most of the characters showed high heritability (> 80 %) for 39 characters, medium (60-80%) for 9 characters and low heritability (< 60 %) for the rest five (5) characters respectively. This showed that genetic determination for most characters were high with less environmental influence on the expression of characters. Panse (1957) reported that the genetic variations, heritability and genetic advance were high in the weight and number of finger rhizome per clump, tillers number per clump which indicated the effect of additive genes. Lynrah *et al.,* (1998) reported tillers/clump and mother rhizome and finger rhizome yield components showed high genetic variation and high broad-sense heritability.

Table.1 Genetic variability estimation of different turmeric genotypes

Sl. No.	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GA% Mean
1	Plant height (cm) 75 DAP	89.14	43.62-114.58	16.94	16.22	0.95	44.00
2	Plant height (cm) 105 DAP	105.77	71.48-132.61	14.06	13.50	0.95	36.87
3	Plant height (cm) 135 DAP	112.64	82.42-144.02	13.74	13.30	0.96	38.25
4	Plant height (cm) 165 DAP	116.24	89.73-158.85	14.21	13.88	0.98	40.41
5	Leaf length (cm) 75 DAP	45.06	26.59-56.96	16.11	13.01	0.84	39.14
6	Leaf length (cm) 105 DAP	51.20	35.91-64.90	14.90	13.53	0.83	35.21
7	Leaf length (cm) 135 DAP	53.49	41.44-68.68	15.86	14.45	0.83	31.51
8	Leaf length (cm) 165 DAP	56.34	41.69-82.23	15.86	14.45	0.86	31.93
9	Leaf width (cm) 75 DAP	13.95	9.06-18.24	14.55	9.30	0.88	49.10
10	Leaf width (cm) 105 DAP	14.72	11.05-18.42	18.41	15.23	0.69	26.22
11	Leaf width (cm) 135 DAP	15.21	11.48-18.56	14.60	10.09	0.74	28.66
12	Leaf width (cm) 165 DAP	15.90	12.75-18.56	13.66	9.79	0.73	26.54
13	Leaves/main shoot 75 DAP	6.39	4.22-8.39	18.04	7.46	0.60	31.29
14	Leaves/main shoot 105 DAP	7.77	5.46-9.34	21.10	7.82	0.49	25.48
15	Leaves/main shoot 135 DAP	8.54	6.48-10.38	16.43	8.24	0.52	22.13
16	Leaves/main shoot 165 DAP	9.13	7.46-11.09	17.25	4.73	0.23	9.20
17	Leaves/tiller 105 DAP	6.20	0.60-9.60	59.17	55.98	0.92	96.45
18	Leaves/tiller 135 DAP	8.83	0.76-13.76	49.40	46.48	0.95	94.00
19	Leaves/tiller 165 DAP	10.17	3.36-18.88	47.10	45.03	0.95	98.23
20	Leaves/hill 75 DAP	7.65	5.05-16.33	30.13	25.05	0.89	76.20
21	Leaves/hill 105 DAP	12.38	7.51-17.34	24.78	20.25	0.79	50.32
22	Leaves/hill 135 DAP	14.81	8.55-23.48	25.21	21.90	0.87	60.76
23	Leaves/hill 165 DAP	17.19	11.82-28.34	26.65	24.71	0.93	67.07
24	Tillers/hill 105 DAP	1.79	0.54-2.79	50.73	50.08	0.98	87.00
25	Tillers/hill 135 DAP	2.35	0.77-3.44	46.79	45.98	0.96	86.00
26	Tillers/hill 165 DAP	2.17	1.12-3.48	38.85	38.51	0.97	90.32
27	Days to maturity	242	218.66-265.33	5.33	4.93	0.85	9.49
28	Leaf area index at 135 DAP	2.49	1.17-4.94	36.29	34.51	0.91	67.46
29	Leaf area index at165 DAP	2.57	1.52-4.34	28.93	26.80	0.85	51.75
30	Leaf area duration at165 DAP	79.95	52.70-135.16	27.75	26.72	0.92	50.13
31	Chlorophyll content (mg/g)	0.07	0.046-0.123	30.16	29.74	0.97	65.71
32	Photosynthesis (µmole $(CO_2)m^{-2} s^{-1}$)	10.54	6.28-15.39	24.62	23.43	0.90	45.35

Contd:

Sl. No.	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	GA% Mean
33	Transpiration (mmol (H_2O)m $^{-2}$ s $^{-1}$)	4.48	1.26-9.70	52.90	51.44	0.93	89.00
34	Stomatal conductance (mole (H_2O)m^{-2} s$^{-1)}$	0.179	0.09-0.33	52.77	52.42	0.17	2.23
35	Internal CO^2 (µmol mol^{-1})	240.78	85.81-322.26	23.77	23.41	0.97	47.00
36	Harvest index	49.50	51.33-83.67	17.25	11.78	0.21	7.23
37	Length of mother rhizome (cm)	6.32	4.52-8.48	17.03	14.42	0.85	39.87
38	Length of primary rhizome (cm)	7.50	5.56-9.78	17.89	15.16	0.86	41.86
39	Length of secondary rhizome (g)	7.50	5.7-9.78	27.64	19.71	0.79	26.00
40	Girth of mother rhizome (cm)	3.26	2.56-4.91	17.09	10.69	0.65	27.60
41	Girth of primary rhizome (cm)	1.51	1.22-2.52	22.13	13.29	0.71	35.76
42	Girth of secondary rhizome (cm)	1.10	0.84-1.48	17.38	12.69	0.80	32.72
43	Primary rhizome/ plant	7.99	4.73-14.93	30.51	28.84	0.94	78.09
44	Wt. of mother rhizome/plant (g)	68.39	35.42-109.29	27.84	26.08	0.92	56.66
45	Wt. of primary rhizome/plant (g)	128.89	75.74-202.53	27.70	27.10	0.97	83.77
46	Wt. of secondary rhizome/pl. (g)	68.33	35.07-97.25	30.20	28.16	0.92	73.39
47	Fresh rhizome yield / plant (g)	251.93	150.7-374.47	25.52	24.77	0.97	70.96
48	Fresh rhizome yield / ha (qtls)	279.92	166.67-413.89	24.77	24.56	0.96	71.24
49	Dry rhizome yield / plant (g)	49.30	30.02-68.38	22.75	19.89	0.91	59.49
50	Dry rhizome yield / ha (qtls)	39.77	24.02-55.35	24.08	19.71	0.90	60.29
51	Dry recovery (%)	19.76	14.16-24.50	14.96	12.54	0.69	21.25
52	Curcumin content (%)	4.36	1.72-6.51	34.60	34.21	0.97	69.03
53	Oleoresin content (%)	12.63	7.63-17.52	20.53	19.69	0.92	38.87

Pathania *et al.*, (1988) reported that curcumin content exhibited wide range, maximum genotypic coefficient of variation, heritability and genetic advance. Reddy and Rao (1988) observe high GCV, heritability and genetic advance for rhizome yield and number of primary fingers indicating high degree of genetic variability for these characters. Sasikumar and Sardana (1989) also observe maximum genetic advance for weight of fingers. Ramanujam and Thirumalachar (1967) indicated the limitations of estimating heritability in narrow sense as it includes both additive and epistatic gene effects and suggested that heritability estimates in broad sense will be reliable if accompanied by a high genetic advance. In the present study, the genetic advance as percent of mean at 5 % selection intensity varied from 2.23% for stomatal conductance to 98.23 for number of leaves per tiller at 165 DAP. Subsequently, twenty four (24) traits have high genetic advance as per cent of mean, seventeen (17) traits have medium genetic advance as per cent of mean while the remaining twelve (12) traits showed low genetic advance as per cent of mean (Table 1).

High heritability along with high genetic advance as per cent of mean found in this study suggested the role of additive genes in the expression of the character which would effectively be improved upon selection. Thus, there is ample scope for improving these characters based on direct selection. These results are in agreement with the earlier findings of Rajalakhsmi *et al.,* (2013), Hikmat *et al.,* (2012), Jalata *et al.,* (2011), Lynrah *et al.,* (1998), Pathania *et al.,* (1988) and Philips and Nair (1986). High heritability with appreciable genetic advance was reported for turmeric rhizome yield, crop duration, number of leaves, number of primary fingers, yield of secondary fingers and plant height (Yadav and Singh, 1996).Therefore selection for the above characters are expected to be effective for crop improvement programme.

In conclusion, the result of the present study demonstrated that there exists wide variability among different turmeric genotypes of north eastern region of India indicating high potential for effective crop improvement and/or for further manipulation of the genetic resources through breeding as the genotypes in this region are good sources of genes for many desirable traits. Summarizing the PCV, GCV, Heritability and Genetic advance characters, it can be concluded that the genotypes giving higher values of these characters may be given more emphasis and hence better selection process for further crop improvement programme.

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