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PATTERN OF GENETIC VARIABILITY IN A COLLECTION OF TURMERIC (*CURCUMA* spp) GENOTYPES

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ABSTRACT

Twenty five genotypes of turmeric including one wild were evaluated for genetic variability for growth, yield and quality characters for two years. Curcumin content, tillers/clump and mother and finger rhizome yield components showed high genetic variation and broad sense heritability. Yield and curcumin content were negatively correlated. Metroglyph analysis showed wide genetic diversity among the genotypes. PCT-13 and VK-145 were superior genotypes for yield and curcumin content.

Key words: Turmeric, *Curcuma* spp., genetic variability, metroglyph analysis.

Turmeric is an important spice crop of India. In northeast India, a number of local varieties are grown. Often the yield of these genotypes is low and the curcumin content is generally not known. Very little crop improvement work has been done to breed high yielding, high curcumin varieties. As the crop is vegetatively propagated, assessment of genetic diversity of the genotypes for economically important metric traits and character correlations would provide useful information for improvement of this crop through clonal selection. There are few reports on the genetic variability and character association in some genotypes of India [1-4]. In this paper, the pattern of genetic variability is assessed through genetic parameters and metroglyph analysis in a set of turmeric genotypes including some collections of northeast India.

MATERIALS AND METHODS

The experiments were conducted in the Experimental Farm, Department of Horticulture, Assam Agricultural University, Jorhat during 1994 and 1995. The soil was sandy loam with a pH of 4.65. In each year, the trial was laid out in randomized complete block design with three replications. Twenty five genotypes of turmeric, collected from various places in Assam and the ICAR Research Complex for NE

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Hills Region, Shillong were used. Rhizomes weighing 20-30g were planted on raised beds of 1.5 m X 1.5 m plot size at a row-to-row and plant-to-plant spacing of 30 cm during the third week of April. Fertilizers were applied @ 200 : 100 :175 Kg/ha N:P_2 O_5 : K_2O in the form of urea, single super phosphate and muriate of potash.

Ten competitive plants were sampled for recording data on 16 characters related to growth, yield and quality. Growth characters were recorded at 165 days after planting. Rhizome yield and component characters were measured at the time of harvest. Leaf area was measured using leaf area meter and curcumin content was determined spectrophotometrically [5]. The plot mean values were subjected to analysis of variance. Genetic coefficient of variation (GCV), broad sense heritability and expected genetic advance at 5 per cent selection intensity were estimated following Allard [6]. Genotypic correlations between rhizome yield/clump and other characters and between curcumin content and other characters were calculated from the pooled ANOVA following A1- Jibouri *et al.* [7]. Metroglyph analysis was done according to Anderson [8].

RESULTS AND DISCUSSION

The pooled ANOVA indicated highly significant differences among the 25 genotypes for all the 16 characters. The GCV ranged from 6 per cent for girth of mother rhizome to 69.4 per cent for curcumin content (Table 1). Curcumin content showed amazingly large genetic variation, with genotype value ranging from 0.08 per cent to 8.6 per cent suggesting that the materials were very diverse for this important quality character. Other characters showing usefully significant genetic variation were finger rhizome yield/clump, number of finger rhizomes/clump, number of tillers/clump, volume of mother rhizomes and mother rhizome yield/clump. Characters exhibiting moderate GCV were fresh rhizome yield/clump, volume of finger rhizome and number of mother rhizomes/clump. Broad sense heritability was high (> 90%) for most of the characters except leaf area/clump. Expected genetic advance at 5% selection intensity was highest (142.7%) for curcumin content; it was high for finger rhizome yield (72.2%), number of finger rhizome (52.2%), tillers/clump, volume of mother rhizome, mother rhizome yield, fresh rhizome yield, volume of finger rhizomes, and volume of mother rhizomes (40%). Thus, there was appreciable genetic variation, high genetic determination and genetic advance for fresh rhizome yield/clump and its component characters, viz, tillers/clump, number, volume and yield individually of mother and finger rhizomes/clump. Immense genetic variation with strong genetic determination was also evident for curcumin content in the turmeric genotypes. This indicated the possibility of improvement of fresh turmeric yield through clonal selection for rhizome yield and its component characters. Clonal selection for curcumin content would be still more effective.

Table 1. Estimates of genetic parameters for growth, yield and quality characters in turmeric

Character	General Mean	Range	GCV (%)	Heritability (%)	Expected genetic advance	Genotypic correlations with	
						yield/ clump	curcumin content
Plant height (cm)	126.1	104-161	12.1	93.0	24.0	0.082	–0.369
Tillers/clump (No.)	2.6	1.6-5.1	26.3	94.1	52.5	0.325	–0.261
Leaves/clump(No)	25.3	20.1-39.3	16.2	96.2	32.7	0.340	–0.203
Leaf area/clump(cm^2)	6.9×10^3	3.6×10^3-14×10^3	8.3	76.9	23.8	0.088	–0.117
Mother rhizomes							
No./clump	3.7	2.4-5.2	19.7	96.4	40.1	0.520	–0.344
Yield/clump(g)	203.8	119.5-315.0	25.3	94.6	50.7	0.421	–0.777
Volume (cc)	57.2	42.9-112.5	25.4	97.5	51.6	–0.025	–0.538
Length (cm)	7.8	5.9-10.9	12.7	97.6	25.8	–0.085	–0.359
Central girth (cm)	12.2	10.8-14.3	6.2	90.5	12.1	–0.108	–0.476
Finger rhizomes							
No./clump	15.1	8.7-28.8	28.0	98.2	57.2	0.729	–0.071
Yield/clump(g)	251.1	111.9-418.1	35.5	97.3	72.2	0.846	0.085
Volume(cc)	16.8	11.6-28.2	20.3	95.1	40.9	0.523	0.231
Length(cm)	6.6	5.4-8.1	11.0	96.3	22.2	0.155	0.543
Central girth(cm)	6.9	5.8-8.5	9.4	95.5	18.9	0.312	–0.247
Rhizome yield/clump	454.8	328-708	20.9	93.0	41.6	1.000	–0.341
Curcumin content (%)	3.96	0.08-8.58	69.4	99.6	142.7	–0.341	1.000

*Significant at P=0.05 **Significant at P = 0.01

Pathania *et al.* [1] reported high genetic variation and heritability of curcumin content. High genetic variation and determination was also reported for fresh rhizome yield and its components [2]. The genetic variability of the collections of turmeric was thus enormous. There was great scope for improvement through clonal selection for individual yield characters.

Fresh rhizome yield/clump and curcumin content determine the economic value of a turmeric genotype. The genetic relationship between these two characters and their relationships, in turn, with the yield components are also important consideration in this context.

There was strong positive correlation between fresh rhizome yield/clump and yield and number of finger rhizomes/clump. Volume of finger rhizome was significantly correlated with fresh rhizome yield/clump (Table 1). Positive association was also observed between fresh rhizome yield/clump and mother rhizomes number and yield/clump (Table 1). Thus finger rhizome characters were more closely related to total yield/clump than the mother rhizome characters. Such correlations were also reported earlier [1, 9]. Tillers/clump was weakly correlated with yield/clump. The two economically important characters, i.e. fresh rhizome yield/clump and curcumin content were, however, weakly negatively correlated.

The negative correlation between yield and curcumin content (Table 1) was reflected in the negative correlation of curcumin content with most of the components traits of yield, although most of these correlations were very weak. Nevertheless the correlation between curcumin content and mother rhizome traits were appreciably negative. Negative correlation is generally observed between yield and quality traits, for example in dioscorea [10].

Thus, based on the genetic parameters including genotypic correlations, it can be inferred that tillers/clump, and number, yield and volume of mother and finger rhizomes, per clump, respectively, were important yield component characters in the present materials. Selection of plants based on these characters and on the basis of curcumin content would be most effective. The negative correlations of curcumin content implied that some compromise has to be made for optimising the selections. In the genotypes with strong negative relations between yield and curcumin content, probably, induction of mutation might be helpful for breaking the negative correlations.

Metroglyph analysis was done using the fresh rhizome yield/clump and curcumin content as the leading characters, as they showed high genetic variability and were economically important. Of the mother and finger rhizome characters, only yields of mother and finger rhizomes were included since these two characters showed high variation and directly accounted for the total fresh rhizome yield/clump. The mean values of the five chosen characters along with the index scores for low (=1), medium (=2), and high expression (=3) of the characters, are presented in Table 2. On the basis of these five characters, the genotypic performances are summarized in Table 3. Ouguri Nepali and Black Turmeric were overall high scores for all the yield components. However, their curcumin contents were very low and, therefore, would not be economically valuable. On the other hand, CL-24 VK-145, PCT-11 and Lakadong were superior quality genotypes for their high curcumin contents but where low yielding. The only genotype combining relatively high rhizome yield/clump and high curcumin content was 'PCT-13'. This genotype is distinct in the metroglyph scatter diagram (Fig. 1). VK-145 was another valuable genotype with high curcumin content and medium rhizome yield. Majority of the genotypes were low yielding. But some of these genotypes were superior in quality. The wide distribution of the

Table 2. Mean performance of 25 turmeric genotypes for five important characters pooled from two years (index score in parenthesis)

Sl. No.	Genotype	Total rhizome yield/ clump(g)	Curcumin content (%)	Tillers/ clump (no)	Mother rhizome yield/ clump (g)	Finger rhizome yield/ clump (g)	Total index score
1	Tall Clone	328 (1)	3.09 (2)	3.35 (2)	192 (2)	136 (1)	8
2	Lakadong	405 (1)	7.17 (3)	1.91 (1)	119 (1)	286 (2)	8
3	CL-24	394 (1)	8.58 (3)	3.42 (2)	164 (1)	230 (2)	9
4	Borpather 1	441 (1)	2.62 (1)	2.72 (1)	261 (3)	180 (1)	7
5	Borpather 2	372 (1)	2.31 (1)	2.15 (1)	229 (2)	141 (1)	6
6	Sel-3	446 (1)	2.33 (1)	2.73 (1)	235 (2)	211 (1)	6
7	Sel-12	473 (2)	0.45 (1)	2.42 (1)	241 (2)	231 (2)	8
8	Ca-69	351 (1)	1.61 (1)	2.20 (1)	239 (2)	112 (1)	6
9	Nagajanka	454 (1)	0.46 (1)	2.12 (1)	277 (3)	177 (1)	7
10	Kokilamukh	492 (2)	2.43 (1)	3.53 (2)	315 (3)	177 (1)	9
11	Sarupathar	471 (2)	0.35 (1)	2.46 (1)	203 (2)	268 (2)	8
12	Ouguri Nepali	708 (3)	0.38 (1)	2.92 (2)	296 (3)	412 (3)	12
13	Black Turmeric	701 (3)	0.08 (1)	5.05 (3)	284 (3)	418 (3)	13
14	PTS-9	402 (1)	2.58 (1)	2.40 (1)	182 (1)	220 (2)	6
15	PTS-10	389 (1)	6.73 (3)	1.83 (1)	189 (2)	201 (1)	8
16	PTS-11	465 (2)	2.92 (2)	2.45 (1)	182 (1)	283 (2)	8
17	PTS-38	509 (2)	5.81 (3)	2.46 (1)	188 (2)	324 (3)	11
18	PTS-43	474 (2)	3.54 (2)	2.93 (2)	183 (1)	291 (2)	9
19	PCT-11	415 (1)	7.99 (3)	2.03 (1)	124 (1)	291 (2)	8
20	PCT-13	617 (3)	6.61 (3)	1.60 (1)	150 (1)	466 (3)	11
21	VK-77	343 (1)	6.16 (3)	2.83 (2)	178 (1)	165 (1)	8
22	VK-145	463 (2)	8.17 (3)	2.91 (2)	183 (1)	279 (2)	10
23	GL Puram	338 (1)	6.19 (3)	2.56 (1)	143 (1)	195 (1)	7
24	Kasturi Tanaka	493 (2)	4.52 (2)	1.86 (1)	160 (1)	333 (3)	9
25	Sugandham	426 (1)	5.90 (3)	2.80 (2)	176 (1)	250 (2)	9
	C.D. (P = 0.05)	11		0.22	8	7	

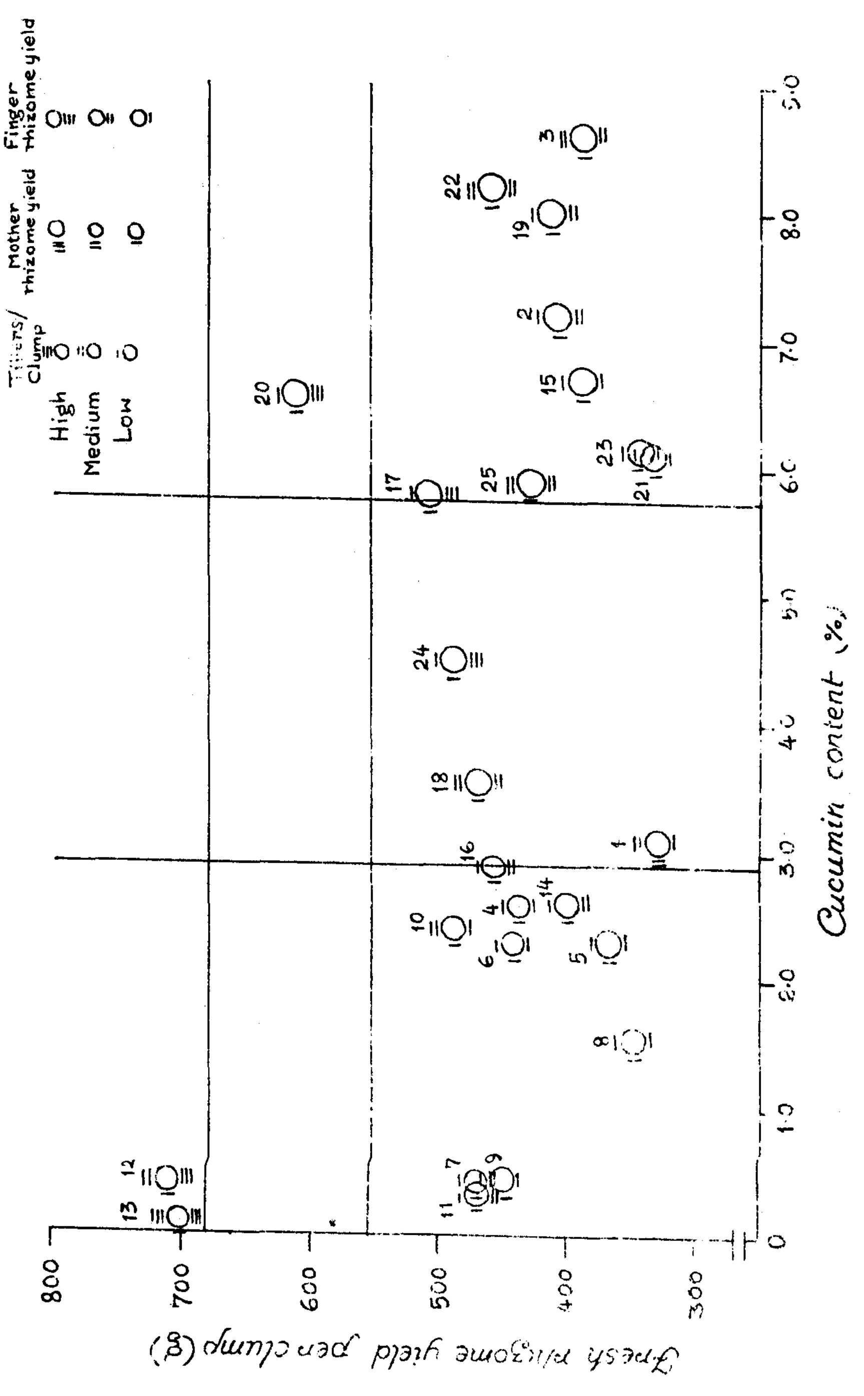

Fig. 1. Metroglyph scatter diagram

genotypes in the scatter diagram indicates their genetic diversity in the materials.

Table 3. Index score distribution of 25 turmeric genotypes

Range of index score	Category	No. of genotypes	Genotypes (serial numbers as in Table 2)
6-8	Low	(15)	1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 14, 15, 16, 19, 2, 1, 23
9-11	Medium	(8)	3, 10, 17, 18, 20, 24, 25
12-14	High	(2)	12, 13

The superior genotypes identified in the analysis could be further tested for general cultivation and the indicated yield and quality characters could be emphasized in crop improvement programme.

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