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Research Article

Studies on variability and genetic components of yield and quality traits in turmeric (*Curcuma longa* L.)

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Abstract
A study was conducted to evaluate stable and heritable variations among 55 turmeric (*Curcuma longa* L) genotypes in relation to morphological, biochemical, yield and quality traits. High Genotypic (GCV) and Phenotypic Coefficient of Variations (PCV) were registered for most of the traits except number of leaves per plant. High heritability coupled with high genetic advance as per cent of mean was observed for the traits plant height, pseudostem girth, number of tillers, petiole length, leaf area, number of mother rhizomes, weight of mother rhizomes, length of mother rhizome, girth of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length of primary rhizomes, girth of primary rhizomes, number of secondary rhizomes, weight of secondary rhizomes, length of secondary rhizomes, girth of secondary rhizomes, fresh yield per plant, oleoresin content, curcumin content except core diameter and number of leaves per plant which exhibited moderate and low heritability.

Keywords
Turmeric, GCV, PCV, Heritability, Genetic Advance

Introduction

Turmeric, (Curcuma *longa* L.) is a rhizomatous perennial crop, belonging to the Zingiberaceae family that has its origin in tropical South East Asia. Turmeric also known as 'Indian saffron' is much valued for its colouring principle 'the curcumin'. Besides its use in cooking to add colour and as a preservative, turmeric is used in Indian Traditional Medicine to treat various ailments (Singh *et al.*, 2012), food industry, confectionery, pharmaceuticals and cosmetic industry. Awareness on the use of natural dyes for the culinary, medicinal and cosmetic use has put in demand for turmeric and its value added products. In the recent years, use of turmeric and its value added products has been increasing and thus increasing the demand for turmeric. To expand the area under turmeric, productivity and to increase the production it is essential to identify / develop genotypes with high curcumin and rhizome yield.

India has a rich collection of genotypes/ cultivars based on the vernacular names. Owing to its sterility, rare seed set and incompatibility to a certain extent, has made it difficult for hybridization in turmeric. Genetic variability is the prime concern for the breeder for exercising selection and isolation of superior types. A very good response to selection is possible only when divergent genotypes are pooled in the breeding stock. Hence, crop improvement programme in turmeric has been confined mainly to selection and to some extent, mutation breeding (Ravindran *et al.*, 2007).

Hence the knowledge on the genetic variation and heritable variation present in the turmeric germplasm is essential to increase the efficiency of selection in breeding programme. It also directs conservation strategies in germplasm for further crop improvement programme for high curcumin, oleoresin and essential oil content to meet the demand of turmeric for industrial and pharmaceutical uses.

Material and Methods

A set of 55 genotypes was evaluated to study variations among the genotypes. The experiment was laid at Horticultural College and Research Institute, College Orchard, TNAU, Coimbatore during 2017- 18, following augmented design with 2 checks *viz.*, BSR 2 and CO 2, planted at spacing 45 x 15 cm. Each germplasm comprised a row of 11 plants. Morphological observations were recorded in five randomly chosen plants in each germplasm at 180 DAP. The total leaf soluble protein was estimated using Lowry's method at 180 DAP. A single randomly selected clump was taken in each germplasm to study rhizome parameters. The harvested rhizomes were cured, powdered and the curcumin and oleoresin content were analysed (ASTA, 1968). Analyses of variance (ANOVA) and the estimates on genetic components on

growth, yield, yield attributing and quality characters were computed using the breeding tool TNAU STAT.

Result and Discussion

It is evident from the study, that the analysis of variance indicated significant differences in mean values for all the twentyfour traits observed among the genotypes (Table1). Estimates of PCV was greater than GCV for all the traits (Table 2) and the apparent variation is not only due to genotypes but also due to the influence of environment as normally expected (Salimath *et al*., 2016; Prajapathi *et al*., 2014; Hanchinamani *et al*., 2016). The co-efficient of variation is a measure to assess variability in a population (Phundan and Narayanan, 1993). The genotypic coefficient of variation alone is not sufficient for the determination of the amount of heritable variation. The genes cannot cause the character to develop unless they have the proper environment for expression. Nevertheless, it must be recognized that variability observed in some character is caused primarily by the difference in the genes and the variability in other character is due to primary difference in the environment to which individuals have been exposed. The importance of heritability in addition to the mean performance and variability was stressed by Panse, (1957).

Genetic advance is an improvement in the mean genotype value over the base population. Johnson *et al.* (1955) suggested the use of heritability coupled with genetic advance in formulating evaluation suitable for selection procedure. When the character is highly heritable, the phenotype reflects the genotype very strongly. Therefore, the combination of variability, heritability and genetic advance will be useful to make an efficient selection.

Considering the above ground characters number of tillers (30.98 and 31.17) showed highest GCV and PCV followed by petiole length (23.97 and 24.71), leaf area (23.39 and 23.60) and plant height (18.99 and 19.10) (Fig.1). The high GAM and very high heritability values indicated that the characters were result of additive gene effects and inherited over generations (Fig.2.). The findings were in accordance with the results of Rajyalakshmi *et al.* (2013); Salimath *et al*., 2016; Hanchinamani *et al*., 2016. The variations in these characters helps to breed plants with better architecture which ultimately reflects on yield.

The environmental impact was highly pronounced over the trait, number of leaves (6.56 and 18.95) which exhibited relatively very low GCV, PCV and heritability values (Fig.1&2). This finding was in congruence with the reports of Prajapathi *et al*. (2014) and Mishra *et al*. (2015) who reported low and moderate heritability values. Hence it is wise to setaside this character for indirect selection, as the selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effect. According to Ravinder *et al.,* 2007 the active compound, curcumin in turmeric is actively synthesized in the earlier 3 to 4 leaf stage of the crop. The number of leaves is an important trait in deciding quality compounds hence indirect selection can be employed to improve this character. However, the estimates on GAM (38.21%) signifies chances for selection in upcoming generations.

The characters *viz.*, weight of secondary rhizomes (60.81 and 61.47), weight of primary rhizomes (53.61 and 52.83) and weight of mother rhizomes (55.83 and 54.98) recorded high GCV and PCV respectively emphasizing those characters to be potentially variable (Fig.1). Although GCV and PCV reveal the extent of genetic variability present, the heritability decides the stability of the variation across generations and ensures the selection is effective and repeatable. The high heritability and genetic advance means signified, the characters weight, number, length and girth of mother, primary and secondary rhizomes are governed by additive gene effects and can be inherited across generations by simple selection (Fig 2). The findings are in corroboration with the earlier works of Prajapathi *et al*., 2014; A.K.Gupta *et al*., 2016; Salimath *et al*., 2016; Hazra *et al*. (2000).

In rhizome characters, the dimensions of rhizomes (*viz.*, length and girth of mother, primary and secondary rhizomes), registered relatively low genotypic and phenotypic variations than weight and number of primary, secondary and mother rhizomes (Table 2). But very high heritability coupled with high genetic advance mean denoted the variations were due to additive gene effects and can be improved by direct selection (Fig 2). Similar results were obtained by Salimath *et al*., 2016 for length and number of mother, primary and secondary rhizomes. The core diameter exerted the least GCV and PCV (12.70 and 15.02) in rhizome characters. The moderate heritability values indicated that the character was influenced by environment to some extent and high genetic advance mean signified additive gene action, the core diameter can be improved by indirect selection.

Considering the quality characters, oleoresin content (45.01 and 45.79) showed the highest GCV and PCV followed by curcumin (16.09 and 16.16) and curing percent (8.61 and 11.09). Moderate heritability but high genetic advance mean for curing percentage expressed, the phenotype represents genotype only to certain extent, hence indirect selection can be employed to improve curing percentage.

High heritability (>90 per cent) was registered for all the traits except number of leaves per plant (Fig.2) which indicated that selection of such characters is easy because of the close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype (Fig. 1 & Table 2). All the traits showed very high heritability values while, pseudostem girth, and soluble protein showed high heritability rate, moderate level of heritability for core diameter and the character number of leaves per plant exhibited very low heritability values (Table 2). High and very high heritability estimates implied the poor influence of environmental on expression of the characters plant height, pseudostem girth, number of tillers, petiole length, leaf area, number of mother rhizomes, weight of mother rhizomes, length of mother rhizome, girth of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length of primary rhizomes, girth of primary rhizomes, number of secondary rhizomes, weight of secondary rhizomes, length of secondary rhizomes, girth of secondary rhizomes, fresh yield per plant, oleoresin content, curcumin content (Fig.2). The broad sense heritability estimate is based on total genetic variance which includes fixable (additive) variance and non-fixable (dominance and epistatic) variance (Singh & Narayanan, 2013). High heritability coupled with genetic advance is governed by additive genes (Panse, 1957), hence the variance so obtained all are fixable. Thus, suggesting the predominance of additive gene effect in the expression of these traits and simple direct selection as the more reliable method in the crop improvement programme.

The results of the investigation revealed, that all the observed traits except number of number of leaves per plant and curing percentage possess high heritable variations with high genetic advance mean which can be improved and passed on through generations by simple selection procedures. The characters *viz.*, weight of mother rhizomes, weight of primary rhizomes and weight of secondary rhizomes exhibited very high genetic advance mean and genotypic variability suggesting, selection based on these traits can bring about elite genotypes for high yield and quality. The quality traits oleoresin and curcumin showed relatively poor genetic variations, with high heritability and genetic advance mean, signifying scope of improving the traits by simple selection.

Reference

American Spice Trade Association (ASTA). (1968). Official analytical Methods. 2nd ed. New York: American Spice Trade Association, p. 38.

Gupta, A. K., Mishra, R., & Lal, R. K. (2016). Genetic variability and character interrelationship among indigenous germplasm of Turmeric (*Curcuma longa*). *Journal of Herbs, Spices & Medicinal Plants*, ***22*(2)**, 190-201.

Hazra, P., Roy, A., & Bandopadhyay, A. (2000). Growth characters as rhizome yield components of turmeric (*Curcuma longa* L.). *Crop Research (Hisar)*, **19(2)**, 235-240.

Johnson, H. W., Robinson, H. F., & Comstock, R. (1955). Estimates of Genetic and Environmental Variability in Soybeans 1. *Agronomy journal*, **47(7)**, 314-318.

Mishra, R., Gupta, A. K., Lal, R. K., Jhang, T., & Banerjee, N. (2015). Genetic variability, analysis of genetic parameters, character associations and contribution for agronomical traits in turmeric (*Curcuma longa* L.). *Industrial Crops and Products*, ***76,*** 204-208.

Panse, V. G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet,* ***17*(2)**, 318-328.

Phundan, S., & Narayanan, S. (1993). *Biometrical techniques in plant breeding.* 5th edition, Kalyani Publishers, New Delhi. pp.153-163.

Prajapati, K. N., Patel, M. A., Patel, J. R., Joshi, N. R., & Patel, A. D. (2014). Research Note Genetic Variability, Character Association and Path Coefficient analysis in Turmeric (*Curcuma longa* L.). *Electronic Journal of Plant Breeding*, ***5*(1)**, 131-137

Rajyalakshmi, R., Naidu, L. N., Rajasekhar, M., & Sudhavani, V. (2013). Genetic variability, correlation and path coefficient analysis in turmeric (*Curcuma longa* L.). *Journal of Spices and Aromatic Crops*, ***22*(1)**, 104-107.

Ravinder, P. N., Babu, K. N., & Sivaraman, K. (2007). Tumeric :The Genus Curcuma, *CRC press*

Salimath, S., Venkatesha, J., Kotikal, Y. K., Sheety, R. R., & Kattimani, K. N. (2017). Genetic Variability Studies in Turmeric (*Curcuma longa* L.) under Southern Dry Zone of

Karnataka. *Int. J. Pure App. Biosci*, ***5*(4)**, 719-722.

Singh, S., Panda, M. K., & Nayak, S. (2012). Evaluation of genetic diversity in turmeric (*Curcuma longa* L.) using RAPD and ISSR markers. *Industrial Crops and Products*, ***37*(1)**, 284-291.

Veena, H., Shetty, G. R., & Agasimani, A. A. (2017). Correlation studies in turmeric (*Curcuma longa* L.) under hill zone of Karnataka. *HortFlora Research Spectrum*, ***6*(1)**, 51-54.

Table 1. Analysis of variance for growth, yield, yield attributing and quality parameters in turmeric genotypes

	DF	PH	PSG	NT	NL	PL	LA	NMR
Treatment	56	338.1138**	1.041**	3.0457**	3.7427**	29.6958**	14627.0024**	2.6537**
Checks	1	291.7716**	0.0013	44.3722**	66.6125**	0.1345*	191310.5026**	6.7512**
Test Genotypes	54	344.6298**	1.0444*	2.1365**	2.4199**	29.5993**	8647.6651**	1.9879**
Check vs Test	1	32.5953**	1.8979**	10.8119**	12.3037**	64.473**	160827.7161**	34.5089**
Error	18	4.0893	0.3857	0.0259	0.1248	1.767	151.1499	0.0656

	WMR	LMR	GMR	NPR	WPR	LPR	GPR	CD	NSR
Treatment	3613.6262**	1.0152**	1.5387**	13.9832**	8847.4771**	3.0885**	0.7836**	0.0538**	21.4562**
Checks	1174.007**	9.842**	4.077**	0.0442	1574.2475**	50.1178**	1.6474**	0.0238**	256.6861**
Test Genotypes	3221.0451**	0.7347**	1.4938**	11.9953**	9005.1293**	1.9265**	0.7644**	0.0488**	16.4357**
Check vs Test	27252.6229**	7.3302**	1.424**	135.268**	7607.4877**	18.8093**	0.9591**	0.3542**	57.333**
Error	97.6006	0.0517	0.0987	0.1397	258.4867	0.0689	0.0669	0.0139	0.0214

	WSR	LSR	GSR	Y/p	CP	Oleoresin content	Curcumin content	SP
Treatment	1956.3378**	2.3694**	2.4108**	23491.3701**	5.4153*	11.0569**	0.1197**	59.4998**
Checks	132.7155**	41.4144**	72.8474**	651.1687**	5.1511*	0.45 NS	0.2691**	233.7912**
Test Genotypes	1181.0842**	1.3707**	1.1436**	24348.2613**	5.4632*	7.6245**	0.1057**	56.409**
Check vs Test	45643.6584**	17.2544**	0.3982**	59.448**	3.0931	207.0107**	0.7276**	52.1089**
Error	25.3597	0.0258	0.0246	1178.5005	2.1738	0.1853	0.0010	12.51

*- Significance at 5% level, ** - Significant at 1% level.

Note: PH - Plant height (cm), PSG - Pseudo stem girth (cm), NT – No. of tillers per plant, NL – No. of leaves per plant, PL - Petiole length (cm), LL - Leaf length (cm), LW - Leaf width (cm), LA - Leaf area (cm^2), NMR - No. of mother rhizome, WMR - Weight of mother rhizome (g), LMR - Length of mother rhizome (cm), GMR - Girth of mother rhizome (cm), NPR - No. of primary rhizome, WPR - Weight of primary rhizome (g), LPR - Length of primary rhizome (cm), GPR - Girth of primary rhizome (cm), CD - Core diameter (cm), NSR - No. of secondary rhizome, WSR - Weight of secondary rhizome (g), LSR - Length of secondary rhizome (cm), GSR - Girth of secondary rhizome (cm), Y/p - Yield / plant (g) , CP – Curing percentage (%).SP – Soluble protein (mg/g).

Table 2. Estimates of variability and genetic components in turmeric genotypes

Traits	Grand Mean	Range	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability (Broadsense) (%)	Genetic Advance	Genetic Advance as per cent mean (%)
Plant height (cm)	96.79	46.00 - 136.7	19.10	18.99	98.81	36.33	37.54
Pseudo stem girth (cm)	7.16	4.88 - 9.56	14.09	11.19	63.07	2.00	27.95
No of tillers per plant	4.46	1.40 - 8.60	31.17	30.98	98.79	2.86	64.14
No of leaves per plant	7.97	3.20 -10.80	18.95	6.56	11.98	3.04	38.21
Petiole length (cm)	21.45	7.40 - 34.44	24.71	23.97	94.03	10.65	49.63
Leaf area (cm^2)	366.13	163.30 – 666.51	23.60	23.39	98.25	181.99	49.71
No. of mother rhizome	4.88	2.00 – 8.00	26.65	26.20	96.70	2.76	56.52
Weight of mother rhizome (g)	113.15	21.00 – 400.00	55.83	54.98	96.97	111.07	98.16
Length of mother rhizome (cm)	6.44	3.90 – 8.50	13.70	13.21	92.96	1.68	26.03
Girth of mother rhizome (cm)	9.47	4.90 – 11.90	13.01	12.58	93.39	2.39	25.25
No. of primary rhizome	10.68	3.00 – 19.00	30.14	29.96	98.84	6.78	63.46
Weight of primary rhizome (g)	187.09	30.00 – 473.00	53.61	52.83	97.13	185.71	99.26
Length of primary rhizome (cm)	8.10	3.40 – 11.00	17.81	17.49	96.42	2.72	33.55
Girth of primary rhizome (cm)	7.48	5.70 – 9.80	11.80	11.27	91.25	1.71	22.89
No. of secondary rhizome	10.04	2.00 – 19.00	38.38	38.35	99.87	7.93	79.05
Weight of secondary rhizome (g)	70.79	6.00 – 198.00	61.47	60.81	97.85	67.26	95.01
Length of secondary rhizome (cm)	4.11	2.00 – 6.80	30.68	30.39	98.12	2.29	55.81
Girth of secondary rhizome (cm)	5.60	3.80 – 7.50	18.94	18.73	97.85	2.09	37.35
Core diameter (cm)	1.43	1.00 – 2.20	15.02	12.70	71.52	0.43	30.24
Yield/plant (g)	334.59	90.00 – 798.00	46.56	45.42	95.16	305.37	91.27
Curing percentage (%)	20.95	14.67 – 27.50	11.09	8.61	60.21	4.57	21.84
Oleoresin (%)	5.76	2.00 – 10.60	45.79	45.01	96.61	4.58	79.42
Curcumin (%)	2.07	1.38 – 2.79	16.16	16.09	99.05	0.64	30.73
Soluble protein (mg/g)	20.90	10.90 – 41.81	35.09	30.95	77.82	14.70	70.32

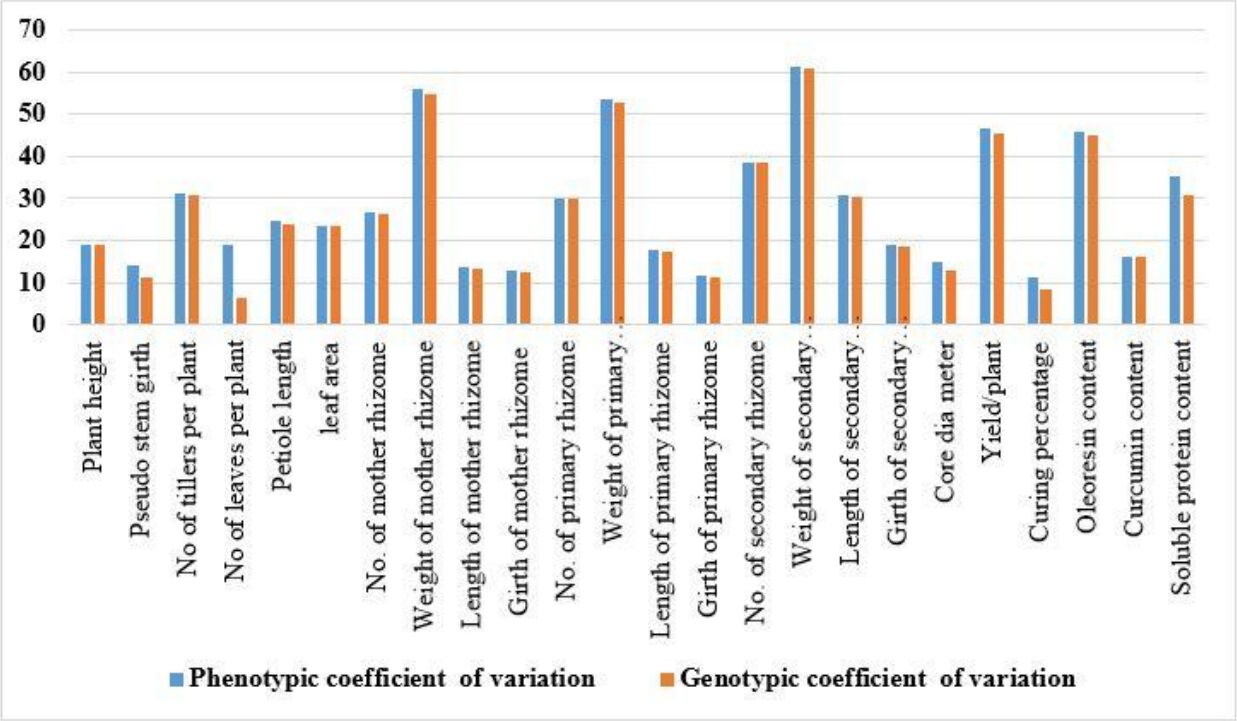

Fig. 1. Genotypic co-efficient of variation of observed prominent traits among the evaluated turmeric genotypes

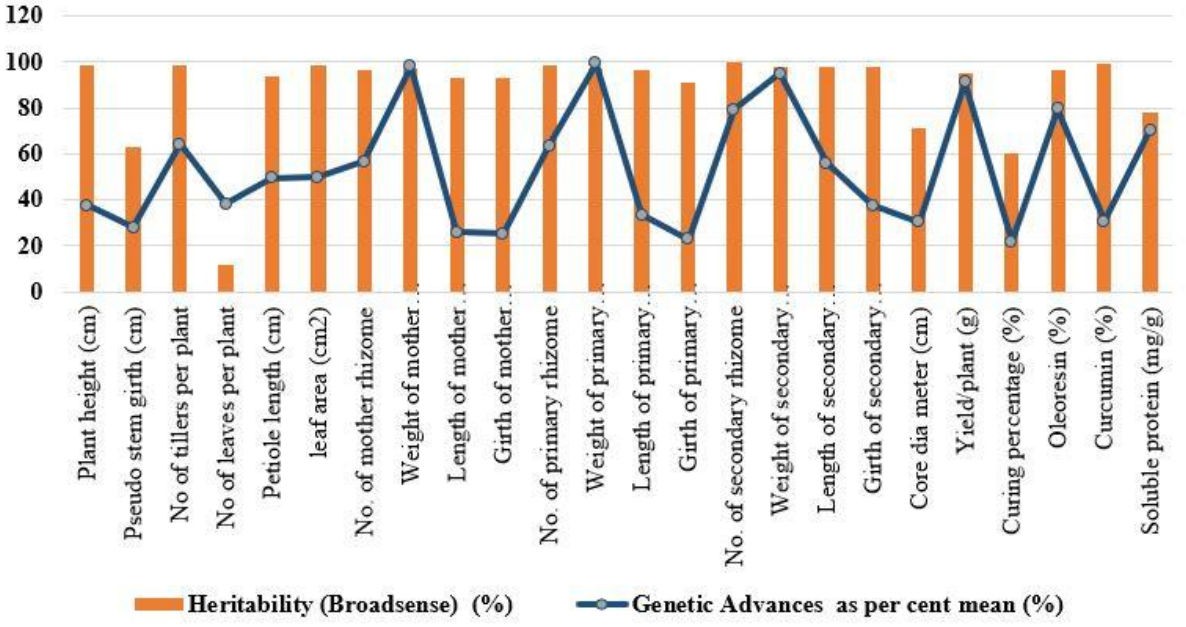

Fig. 2. Per cent heritability and genetic advance over mean for prominent characters in turmeric genotypes