

Genetic Variability and Character Association Studies in Turmeric (*Curcuma longa* L.) Cultures

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ABSTRACT: A study was conducted in 22 turmeric cultures to evaluate the level of variability, associative relationship of yield and its contributing traits along with direct and indirect effects of 15 quantitative traits. All the turmeric cultures (22 nos.) for evaluation purpose were collected from various geographical regions of India to examine the variations among them and to study their performance and suitability for Coimbatore condition. The experiment was laid out in Randomized block design with three replications at the Department of Spices and Plantation Crops, TNAU, Coimbatore. Availability of high yielding varieties of turmeric for particular locality are limited and identification of contributing characters towards yield is needed for the selection of varieties with high yield. Owing to clonal propagation, self-incompatibility and self-sterility, availability of natural genetic variation in turmeric is reported to be narrow. Among the 15 quantitative traits studied, many of the characters recorded high GCV and PCV viz. plant height, number of tillers, petiole length, number of mother rhizomes, weight of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, number of secondary rhizomes, length of secondary rhizome and fresh rhizome yield per plant. All the biometrical traits recorded high heritability (74.88 % to 99.43 %) and high genetic advance as per cent of mean (23.09 % to 80.02 %) except number of leaves and leaf width. Fresh rhizome yield per plant was associated significantly and positively with all the biometrical traits at phenotypic and genotypic levels. Weight of mother rhizomes, length of secondary rhizome, length of mother rhizome and number of tillers exhibited high direct positive effects on yield. Quantitative traits with high genetic variability, heritability, GAM, positive association with yield can be exploited for selection of high yielding turmeric cultures with traits of major interest.

Keywords: Variability, association, heritability, direct effects and yield improvement.

INTRODUCTION

Turmeric (*Curcuma longa* L.) is an important rhizomatous, herbaceous perennial, indigenous (South Eastern parts of Asia) spice crop and it comes under the Zingiberaceae family. Turmeric is also known as 'Golden spice', 'Indian Saffron' and 'Sacred spice' (Ravindran *et al.*, 2007). Underground dried rhizomes of turmeric are the main parts of commercial value which has anti-inflammatory, antibacterial and antiviral properties. Turmeric is cultivated in India, China, Sri Lanka, Thailand, Indonesia, Taiwan and in more other tropical countries. Higher genetic variation in turmeric is available in India and Thailand (Jan *et al.*, 2011 & Velayudhan *et al.*, 2012). The genus *Curcuma* consists of more than 100 species, among which 40 species are reported to have originated in India

(Sasikumar, 2005). About ninety per cent of total turmeric production of India is utilized domestically and the remaining ten per cent is only exported to many countries such as USA, UK, Japan, Australia, Singapore, Malaysia and South Africa. India is the leading producer of turmeric with an area, production and productivity of 2,96,181 ha, 11,78,750 t and 3.98 t/ha respectively (Indiastat, 2019-20). Telangana, Maharashtra, Karnataka, Tamil Nadu and Andhra Pradesh are the major turmeric producing states of India. More usage of turmeric rhizomes for medical and pharmaceutical application increases the demand of turmeric rhizomes (Chattapadhyay *et al.*, 2004). India is the prominent producer of turmeric in the world, however yield and quality of the released varieties is not up to the point of acceptance (Shanmugasundaram

et al., 2001). Collection and evaluation of germplasm from various sources is considered as the base for enrichment of genetic variation and to promote crop improvement with trait of interest (Vimal *et al.*, 2018; Barik *et al.*, 2021). So, identification of superior turmeric cultures with high yield and quality is regarded as the major desirable trait for any crop improvement programmes in turmeric. In turmeric, genetic variation for morphological, yield and quality parameters are widespread which is a prerequisite for effective breeding programme and to avail productive results (Mishra and Singh, 2017). Yield parameter is associated with other yield attributing traits, so determination of traits with their contribution regard to yield is necessary. Correlation coefficient and path analysis is essential to target the traits which have a great sense of impact on yield enhancement by the effects of yield attributing traits (Vimal *et al.*, 2018). With this background, this study was mainly focused on evaluation of the performance of several turmeric cultures and to deduce the traits based on variability, association and path analysis for yield improvement in turmeric as well as selection of high yielding genotypes.

MATERIALS AND METHODS

Twenty two different turmeric cultures which included released varieties, local cultivars and germplasm lines collected from various geographical locations of India (Tamil Nadu, Kerala, Orissa, Bihar, Uttar Pradesh and North Eastern regions) were evaluated during 2019-2020 and 2020-2021 for their yield performance

(Table 1). The investigation was conducted at the experimental field, Department of Spices and Plantation Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. The experimental design was laid out in Randomized Block Design with three replications. The plot size maintained for the study was $3 \times 1 \text{ m}^2$ accommodating 15 plants per plot. Morphological characters were recorded at 150 days after planting from five randomly selected plants from each replication. Morphological and yield parameters were denoted as individual plant basis throughout this study. Major morphological and yield parameters recorded for this study were plant height, number of tillers, number of leaves, petiole length, leaf length, leaf width, number and weight of mother rhizomes, length of mother rhizome, number and weight of primary rhizomes, length of primary rhizome, number of secondary rhizomes, length of secondary rhizome and fresh rhizome yield per plant. Pooled data of two seasons were utilized and standard methods were followed for statistical analysis using GENRES software and R studio. The genotypic, phenotypic and environmental coefficients of variation were calculated based on the method given by Burton, (1952). Heritability and genetic advance was estimated as suggested by Johnson *et al.* (1955); Allard, (1960). Genotypic and phenotypic correlation coefficients were calculated using the formula suggested by Al-Jibouri *et al.* (1958). Path analysis was done using the formula given by Dewey and Lu, (1959).

Table 1: Source of collection of turmeric cultures.

Turmeric cultures	Source of collection
CO 2	TNAU, Coimbatore, Tamil Nadu
BSR 2	TNAU, Coimbatore, Tamil Nadu
IISR Pragati	IISR, Calicut, Kerala
Salem local	Salem, Tamil Nadu
IISR Prathibha	IISR, Calicut, Kerala
Salem Nariyappanur	Salem, Tamil Nadu
Lakadong	Meghalaya, India
Salem Eraiyur	Salem, Tamil Nadu
Erode local	Erode, Tamil Nadu
Megha turmeric	Shillong, Meghalaya
Rajendra Sonia	BAU, Dholi, Bihar
Suroma	Pottangi, Orissa
NDH 11	NDUAT, Kumarganj, Uttar Pradesh
Kanti	KAU, Vellanikkara, Kerala
NDH 128	NDUAT, Kumarganj, Uttar Pradesh
CL 272	Sathyamangalam, Erode, Tamil Nadu
CL 258	Nariyappanur, Salem, Tamil Nadu
CL 118	Bhavanisagar, Erode, Tamil Nadu
CL 123	KAU, Vellanikkara, Thrissur, Kerala
CL 197	Pottangi, Orissa
CL 225	Talavadi, Erode, Tamil Nadu
CL 95	Bhavanisagar, Erode, Tamil Nadu

RESULTS AND DISCUSSION

Study of genetic variability parameters is necessary for selection of better performing lines and to find out the parameters responsible for crop improvement (Dutta *et al.*, 2017). Analysis of genetic variability parameters in Vithya *et al.*,

22 turmeric cultures revealed that significant level of variation was observed for the 15 biometrical traits and results of this analysis are presented in Table 2. Both genotypic coefficient of variation and phenotypic coefficient of variation was high in weight of mother

rhizomes (39.34 % and 40.02 %) followed by fresh rhizome yield per plant (38.98 % and 39.12 %), weight of primary rhizomes (37.59 % and 37.70 %), number of secondary rhizomes (36.33 % and 36.88 %), number of primary rhizomes (24.87 % and 25.94 %), petiole

length (23.42 % and 23.97 %), number of tillers (22.22 % and 23.52 %), length of secondary rhizome (18.67 % and 20.00 %), number of mother rhizomes (18.06 % and 19.82 %) and plant height (17.92 % and 18.22 %) respectively (Fig. 1).

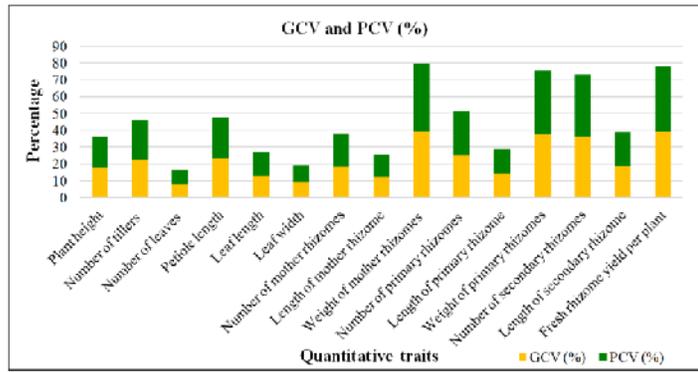


Fig. 1. Genotypic and phenotypic coefficient of variation of turmeric cultures.

Low GCV and PCV was recorded by length of primary rhizome, leaf length, length of mother rhizome, leaf width and number of leaves. Phenotypic coefficient of variation denotes the effects of climate (non-inherited) and genetic components whereas the genotypic coefficient of variation denotes the heritable part (Hamidou *et al.*, 2018). Minimum deviation between PCV and GCV was detected in weight of primary rhizomes followed by fresh rhizome yield per plant, plant height and number of secondary rhizomes. Genotypic coefficient of variation was lesser than phenotypic coefficient of variation and this indicated the extent of environmental influence on the traits. Traits with less deviation between PCV and GCV shows that, selection is effective for those traits because of minimal environmental effect. Therefore, traits with high GCV and PCV indicated high degree of variability and so selection of turmeric cultures based on those traits will be useful for crop improvement in turmeric. Bahadur *et al.*, (2016) proposed that, weight of primary rhizomes, weight of secondary rhizomes, number and diameter of secondary rhizome and length of primary and secondary rhizome exhibited high percentage of PCV and GCV. The finding is in accordance with Paw *et al.*, (2020) who evaluated the variability parameters of 78 germplasm lines and reported high per cent of

PCV and GCV by number of secondary rhizomes, rhizome yield per plant, number of primary and mother rhizomes. Characters with higher level of coefficient of variations are beneficial for crop improvement through selection (Bahadur *et al.*, 2016). Heritability analysis is used to determine the potentiality of individual character at phenotypic levels for selection (Sharma *et al.*, 2019). All the 15 quantitative traits showed high magnitude of heritability from 74.88 % to 99.43 %. High per cent of heritability was exhibited by weight of primary rhizomes (99.43 %) subsequently by fresh rhizome yield per plant (99.30 %), number of secondary rhizomes (97.00 %), weight of mother rhizomes (96.66 %) and plant height (96.70 %). High genetic advance as per cent of mean was noticed in all the quantitative traits except number of leaves and leaf width, which recorded moderate level of GAM. Fresh rhizome yield per plant recorded high genetic advance as per cent of mean (80.02 %) followed by weight of mother rhizomes (79.68 %), weight of primary rhizomes (77.22 %) and number of secondary rhizomes (73.70 %) (Fig. 2). High heritability together with high genetic advance as per cent of mean was due to additive gene action. Hence, selection of turmeric cultures based on those characters is found effective.

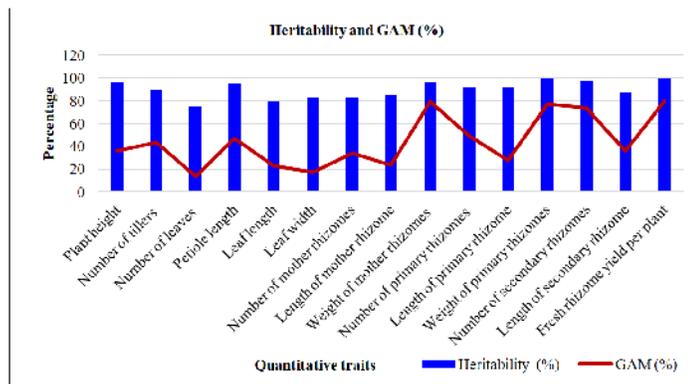


Fig. 2. Heritability and GAM analysis of turmeric cultures.

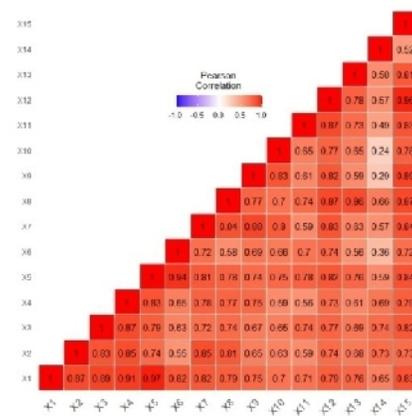
Table 2: Variability and genetic components analysis of turmeric cultures for 15 quantitative traits.

Traits/Genetic Parameters	GCV (%)	PCV (%)	H ² (%)	GAM (%)
Plant height (cm)	17.92	18.22	96.70	36.31
Number of tillers	22.22	23.52	89.28	43.25
Number of leaves	7.59	8.77	74.88	13.53
Petiole length (cm)	23.42	23.97	95.50	47.15
Leaf length (cm)	12.55	14.05	79.75	23.09
Leaf width (cm)	9.07	9.94	83.26	17.04
Number of mother rhizomes	18.06	19.82	83.07	33.91
Length of mother rhizome (cm)	12.39	13.39	85.70	23.63
Weight of mother rhizomes (g)	39.34	40.02	96.66	79.68
Number of primary rhizomes	24.87	25.94	91.93	49.13
Length of primary rhizome (cm)	14.00	14.63	91.60	27.60
Weight of primary rhizomes (g)	37.59	37.70	99.43	77.22
Number of secondary rhizomes	36.33	36.88	97.00	73.70
Length of secondary rhizome (cm)	18.67	20.00	87.18	35.92
Fresh rhizome yield per plant (g)	38.98	39.12	99.30	80.02

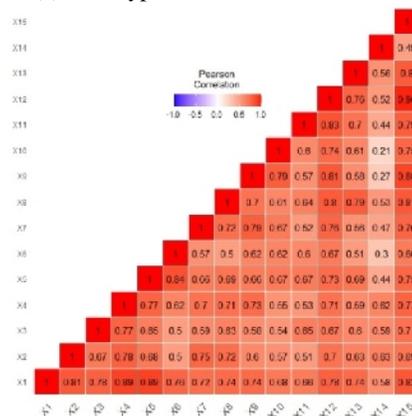
GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H²: Heritability; GAM: Genetic Advance as per cent of mean

Fresh rhizome yield per plant, weight of primary rhizomes, number of secondary rhizomes, weight of mother rhizomes, plant height, petiole length, number of primary rhizomes, length of primary rhizome, number of tillers, length of secondary rhizome, length of mother rhizome, number of mother rhizomes and leaf length exhibited high heritability coupled with high genetic advance as per cent of mean. Leaf width and number of leaves recorded high heritability with moderate genetic advance as per cent of mean. Choice of traits based on variability parameters is effective for selection of turmeric cultures. Paw *et al.* (2020) who reported that, high heritability and high GAM was observed in rhizome yield per plant in turmeric. In line with this, analysis of genetic parameters of turmeric was reported by Vinodhini *et al.* (2018) in 55 genotypes with 24 characters, Singh *et al.* (2018) in 25 genotypes using 19 characters, Sadanand *et al.* (2019) in ten genotypes using 12 characters, Singh *et al.* (2020) in 32 genotypes with 20 characters, Suresh *et al.* (2020) in 200 genotypes using 19 characters, Meenakshi *et al.* (2021) in 21 genotypes with 17 characters and Pathak *et al.* (2021) in 24 turmeric genotypes with 13 traits.

Correlation coefficients are useful to measure the degree of association of characters towards yield. Path analysis is used to calculate the direction of association of quantitative traits on dependent variable. The data on genotypic correlation coefficient and phenotypic correlation coefficient was measured and furnished in Table 3, 4 and Fig. 3. Linkage or pleiotropy is the main reason for genotypic association of yield and its contributing traits (Thakur *et al.*, 2018). Plant height, number of tillers, number of leaves, petiole length, leaf length, number of mother rhizomes, length of mother rhizome, weight of primary rhizomes, number of secondary rhizomes and fresh rhizome yield per plant recorded highly significant and positive genotypic correlation with 14 quantitative traits (plant height, number of tillers, number of leaves, petiole length, leaf length, leaf width, number of mother rhizomes, length of mother rhizome, weight of mother rhizomes, number and weight of primary rhizomes, length of primary rhizome, number of secondary rhizomes, length of secondary rhizome and fresh rhizome yield per plant) except with that of same trait.



(a) Genotypic correlation coefficient



(b) Phenotypic correlation coefficient

Fig. 3. Heat map of genotypic and phenotypic correlation coefficients of 15 quantitative traits in turmeric cultures.

Weight of mother rhizomes and number of primary rhizomes had highly significant and positive genotypic correlation with 13 quantitative traits except the trait length of secondary rhizome. Leaf width and length of primary rhizome was more significantly and positively correlated (genotypic level) with the 13 quantitative traits and it showed significant positive genotypic correlation with length of secondary rhizome. Fresh rhizome yield per plant recorded highly significant and

positive genotypic correlation with weight of primary rhizomes (0.961), weight of mother rhizomes (0.890), length of mother rhizome (0.874), leaf length (0.839), number of mother rhizomes (0.838), plant height (0.835), length of primary rhizome (0.827), number of leaves (0.818), number of secondary rhizomes (0.812), petiole length (0.787), number of primary rhizomes (0.784), number of tillers (0.730), leaf width (0.722) and length of secondary rhizome (0.522). Mamatha *et al.* (2020) studied the genotypic and phenotypic correlation of 83 turmeric germplasm lines with 21 characters, wherein the rhizome yield per plant showed

positive correlation with all the characters studied at phenotypic and genotypic levels. Character association studies in turmeric were carried out by Singh *et al.* (2018) in 30 turmeric genotypes with 14 traits, Singh *et al.* (2018) in 80 genotypes with 12 characters, Suresh *et al.* (2019) in 200 turmeric genotypes with 16 traits, Luiram *et al.* (2019) in 32 genotypes with 44 traits, Sivakumar *et al.* (2020) in 12 turmeric genotypes with seven traits, Paw *et al.* (2020) in 78 germplasm lines with ten traits and Man *et al.* (2021) in 22 genotypes of turmeric with ten traits.

Table 3: Genotypic correlation coefficient analysis of turmeric cultures.

Traits	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
X ₁	1	0.871**	0.886**	0.909**	0.972**	0.821**	0.816**	0.788**	0.749**	0.704**	0.707**	0.792**	0.757**	0.653**	0.835**
X ₂		1	0.831**	0.846**	0.743**	0.554**	0.847**	0.805**	0.645**	0.632**	0.586**	0.743**	0.681**	0.729**	0.730**
X ₃			1	0.873**	0.789**	0.626**	0.717**	0.742**	0.669**	0.645**	0.740**	0.772**	0.687**	0.737**	0.818**
X ₄				1	0.829**	0.650**	0.780**	0.765**	0.751**	0.589**	0.557**	0.727**	0.610**	0.695**	0.787**
X ₅					1	0.942**	0.813**	0.783**	0.743**	0.754**	0.779**	0.819**	0.757**	0.590**	0.839**
X ₆						1	0.716**	0.582**	0.690**	0.660**	0.700**	0.743**	0.564**	0.363**	0.722**
X ₇							1	0.842**	0.882**	0.799**	0.588**	0.835**	0.634**	0.567**	0.838**
X ₈								1	0.770**	0.698**	0.744**	0.869**	0.865**	0.656**	0.874**
X ₉									1	0.832**	0.607**	0.821**	0.591**	0.294	0.890**
X ₁₀										1	0.652**	0.767**	0.650**	0.237	0.784**
X ₁₁											1	0.872**	0.731**	0.487**	0.827**
X ₁₂												1	0.776**	0.567**	0.961**
X ₁₃													1	0.583**	0.812**
X ₁₄														1	0.522**
X ₁₅															1

**Correlation is significant at 1 per cent level & *Correlation is significant at 5 per cent level
X₁: Plant height; X₂: Number of tillers; X₃: Number of leaves; X₄: Petiole length; X₅: Leaf length;
X₆: Leaf width; X₇: Number of mother rhizomes; X₈: Length of mother rhizome; X₉: Weight of mother rhizomes;
X₁₀: Number of primary rhizomes; X₁₁: Length of primary rhizome; X₁₂: Weight of primary rhizomes;
X₁₃: Number of secondary rhizomes; X₁₄: Length of secondary rhizome; X₁₅: Fresh rhizome yield per plant

Table 4: Phenotypic correlation coefficient analysis of turmeric cultures.

Traits	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
X ₁	1	0.809**	0.775**	0.890**	0.892**	0.759**	0.718**	0.738**	0.737**	0.676**	0.658**	0.778**	0.737**	0.579**	0.822**
X ₂		1	0.673**	0.775**	0.681**	0.495**	0.753**	0.718**	0.595**	0.566**	0.511**	0.700**	0.631**	0.629**	0.686**
X ₃			1	0.768**	0.651**	0.495**	0.587**	0.628**	0.582**	0.538**	0.648**	0.668**	0.602**	0.592**	0.710**
X ₄				1	0.774**	0.615**	0.697**	0.710**	0.728**	0.548**	0.530**	0.709**	0.593**	0.622**	0.768**
X ₅					1	0.841**	0.659**	0.686**	0.655**	0.666**	0.671**	0.732**	0.687**	0.445**	0.748**
X ₆						1	0.570**	0.501**	0.623**	0.624**	0.599**	0.673**	0.514**	0.302	0.659**
X ₇							1	0.725**	0.788**	0.670**	0.517**	0.763**	0.559**	0.473**	0.763**
X ₈								1	0.702**	0.615**	0.644**	0.804**	0.788**	0.533**	0.807**
X ₉									1	0.792**	0.569**	0.808**	0.575**	0.273	0.884**
X ₁₀										1	0.597**	0.736**	0.611**	0.214	0.751**
X ₁₁											1	0.830**	0.696**	0.445**	0.787**
X ₁₂												1	0.760**	0.524**	0.959**
X ₁₃													1	0.556**	0.799**
X ₁₄														1	0.485**
X ₁₅															1

**Correlation is significant at 1 per cent level & *Correlation is significant at 5 per cent level
X₁: Plant height; X₂: Number of tillers; X₃: Number of leaves; X₄: Petiole length; X₅: Leaf length; X₆: Leaf width; X₇: Number of mother rhizomes;
X₈: Length of mother rhizome; X₉: Weight of mother rhizomes; X₁₀: Number of primary rhizomes; X₁₁: Length of primary rhizome;
X₁₂: Weight of primary rhizomes; X₁₃: Number of secondary rhizomes; X₁₄: Length of secondary rhizome; X₁₅: Fresh rhizome yield per plant

Table 5: Direct and indirect effects of 15 biometrical traits on fresh rhizome yield in turmeric cultures.

Traits	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
X ₁	0.464	0.524	-0.104	-0.767	-0.509	0.561	-1.536	0.485	1.120	0.236	-0.304	0.397	-0.227	0.496	0.835
X ₂	0.404	0.602	-0.097	-0.714	-0.389	0.378	-1.595	0.496	0.965	0.212	-0.252	0.372	-0.204	0.554	0.730
X ₃	0.411	0.500	-0.117	-0.737	-0.413	0.428	-1.350	0.457	1.000	0.216	-0.318	0.387	-0.206	0.560	0.818
X ₄	0.421	0.509	-0.102	-0.843	-0.434	0.445	-1.469	0.471	1.122	0.197	-0.240	0.364	-0.183	0.528	0.787
X ₅	0.451	0.447	-0.092	-0.699	-0.523	0.644	-1.530	0.482	1.111	0.253	-0.335	0.410	-0.227	0.448	0.839
X ₆	0.381	0.333	-0.073	-0.549	-0.493	0.683	-1.349	0.358	1.031	0.221	-0.301	0.372	-0.169	0.276	0.722
X ₇	0.378	0.510	-0.084	-0.658	-0.425	0.490	-1.883	0.518	1.319	0.268	-0.253	0.418	-0.190	0.431	0.838
X ₈	0.365	0.485	-0.087	-0.645	-0.410	0.398	-1.585	0.616	1.151	0.234	-0.320	0.435	-0.260	0.498	0.874
X ₉	0.347	0.388	-0.078	-0.633	-0.389	0.472	-1.661	0.474	1.495	0.279	-0.261	0.411	-0.178	0.223	0.890
X ₁₀	0.326	0.380	-0.076	-0.497	-0.395	0.451	-1.504	0.430	1.244	0.335	-0.280	0.384	-0.195	0.180	0.784
X ₁₁	0.328	0.352	-0.087	-0.470	-0.408	0.479	-1.108	0.458	0.907	0.218	-0.430	0.436	-0.220	0.370	0.827
X ₁₂	0.367	0.447	-0.090	-0.613	-0.428	0.508	-1.572	0.535	1.228	0.257	-0.375	0.501	-0.233	0.430	0.961
X ₁₃	0.351	0.410	-0.080	-0.515	-0.396	0.386	-1.194	0.532	0.884	0.218	-0.314	0.388	-0.300	0.443	0.812
X ₁₄	0.303	0.439	-0.086	-0.586	-0.309	0.248	-1.068	0.404	0.439	0.080	-0.210	0.284	-0.175	0.760	0.522

Residual Effect: 0.218

X₁: Plant height; X₂: Number of tillers; X₃: Number of leaves; X₄: Petiole length; X₅: Leaf length; X₆: Leaf width; X₇: Number of mother rhizomes;
X₈: Length of mother rhizome; X₉: Weight of mother rhizomes; X₁₀: Number of primary rhizomes; X₁₁: Length of primary rhizome;
X₁₂: Weight of primary rhizomes; X₁₃: Number of secondary rhizomes; X₁₄: Length of secondary rhizome; X₁₅: Fresh rhizome yield per plant

Analysis of genotypic and phenotypic correlation coefficients has key role to determine the component characters associated with yield which are governed by polygenes (Vimal *et al.*, 2018). Plant height, number of tillers, number of leaves, petiole length, length of mother rhizome, weight of primary rhizomes and number of secondary rhizomes had highly significant and positive phenotypic correlation with plant height, number of tillers, number of leaves, petiole length, leaf length, leaf width, number of mother rhizomes, weight of mother rhizomes, length of mother rhizome, number and weight of primary rhizomes, length of primary rhizome, number of secondary rhizomes, length of secondary rhizome and fresh rhizome yield per plant except with that of same character. Leaf length, number of mother rhizomes and length of primary rhizome were exhibited positive and highly significant association with 13 quantitative traits and had significant positive phenotypic correlation with length of secondary rhizome. Leaf width, weight of mother rhizomes and number of primary rhizomes recorded highly significant and positive phenotypic association with 13 biometrical traits only except the trait length of secondary rhizome. Fresh rhizome yield per plant was exhibited highly significant and positive phenotypic correlation with weight of primary rhizomes (0.959), weight of mother rhizomes (0.884), plant height (0.822), length of mother rhizome (0.807), number of secondary rhizomes (0.799), length of primary rhizome (0.787), petiole length (0.768), number of mother rhizomes (0.763), number of primary rhizomes (0.751), leaf length (0.748), number of leaves (0.710), number of tillers (0.686) and leaf width (0.659) and had only significant and positive phenotypic association with length of secondary rhizome (0.485). Singh *et al.*, (2018) reported that weight of fresh rhizome per plant had significant and positive correlation with plant height, weight of mother rhizome, number of primary and secondary rhizome and rhizome yield. Traits with positive and significant correlation with yield are vital to increase the yield by improving that traits (Bahadur *et al.*, 2016).

Correlation and path analysis is important to study the association and effects of yield contributing traits on the trait of yield and importance of traits in further breeding programme (Paw *et al.*, 2020). Selection of traits based on correlation studies alone is not enough and it may mislead. Hence, correlation coefficient is divided into direct and indirect effects, which is much supportive for selection of traits because those traits are linked with each other for contribution towards yield (Geethanjali *et al.*, 2014; Devi *et al.*, 2021). With regard to path analysis, fresh rhizome yield per plant was considered as a dependent variable and other traits as independent variables and to measure the effects of other variables on dependent variable. Among the 15 biometrical traits observed, weight of mother rhizomes exhibited very high direct positive effect (1.495) on fresh rhizome yield per plant. High positive direct effect was registered by length of secondary rhizome (0.760), leaf width (0.683), length of mother rhizome (0.616), number of tillers (0.602), weight of primary rhizomes

(0.501), plant height (0.464) and number of primary rhizomes (0.335). Number of mother rhizomes (1.319), number of primary rhizomes (1.244), weight of primary rhizomes (1.228), length of mother rhizome (1.151), plant height (1.120) and leaf length (1.111) had a very high indirect positive effect on fresh rhizome yield per plant through weight of mother rhizomes. Hence, the quantitative traits such as weight of mother rhizomes, weight of primary rhizomes, number of mother rhizomes, number of primary rhizomes, number of tillers and leaf width should be given more priority during selection for enhancement of yield in turmeric. In path analysis, residual effect recorded was 0.218, which indicates that the quantitative traits contribute 78 % of variability for fresh rhizome yield per plant. Suresh *et al.* (2019) suggested that, weight of mother rhizome per plant showed high positive direct effect on rhizome yield per plant. Man *et al.* (2021) observed that, plant height, number of mother rhizome, single rhizome weight revealed positive direct effect on yield. Choosing of characters with high and positive direct and indirect effects will have an impact on fresh rhizome yield of turmeric cultures. Direct and indirect effects of different quantitative characters on yield of turmeric was reported by Vimal *et al.*, (2018); Mamatha *et al.*, (2020); Man *et al.*, (2021).

CONCLUSION

Genetic components analysis and association studies is aided for knowledge on the significance of traits in further screening of turmeric cultures. In the present study, all the 15 biometrical traits showed variation based on GCV, PCV, heritability and GAM analysis, but traits like weight of mother rhizomes, fresh rhizome yield per plant, weight of primary rhizomes, number of secondary rhizomes and number of primary rhizomes exerted high genetic variability and genetic components than other quantitative traits. Weight of primary and mother rhizomes, length of mother rhizome, number of mother rhizomes, plant height and length of primary rhizome exhibited maximum positive and significant correlation with fresh rhizome yield per plant at genotypic and phenotypic levels. High positive direct effects on fresh rhizome yield per plant was recorded by weight of mother and primary rhizomes, length of secondary and mother rhizome, number of tillers and plant height. Selection of these characters will be much beneficial for crop improvement in turmeric cultures and to select turmeric cultures with high yield and quality.

FUTURE SCOPE

Characters with high variability and association with direct effects regards to yield were identified. Based on these results, turmeric cultures with better yield performance will be screened. Selected turmeric cultures can be exploited for their quality estimation and tolerance capacity against biotic and abiotic stress conditions.

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