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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR GROWTH AND RHIZOME YIELD TRAITS IN *CURCUMA CAESIA* ROXB

Mohan Kumar A.B.[1], Rajath H.P.[1]*, Yogesh G.S.[2], Pampangouda B.[1] and Shruthi M.K.[1]
[1]I.C.A.R., K.V.K. Chamarajanagar, Karnataka, India.
[2]University of Agricultural Sciences, Mandya, Karnataka, India.
*Corresponding author E-mail: rajathkempa@gmail.com

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ABSTRACT

Curcuma caesia Roxb. is a critically endangered medicinal herb, conservation is the need of the hour. Analysis of variance revealed significant differences due to the genotypes for all the forty-five characters studied. PCV is higher than the GCV for all the traits. Relatively narrow difference between phenotypic & genotypic coefficient of variation was evident in majority of the characters, indicated low environmental effect on expression of these traits.

Leaf lamina width (cm) @ 150DAS & 180DAS, petiole length (cm) @ 150DAS & 180 DAS, fresh rhizome yield (g/plant), weight of root tubers (g/plant), weight of roots (g/plant), weight of leaves & pseudo stem (g/plant), fresh biomass (g/plant), length and weight of the mother rhizomes, primary rhizome length (cm), girth & weight per plant, secondary rhizome numbers, primary rhizome internode pattern, fresh rhizome yield per plot (kg), cured rhizome yield (g/plant) and fresh rhizome projected yield (t/ha) had higher magnitude of phenotypic and genotypic coefficient of variation, evident that these characters were under the influence of genetic control. Hence, these characters can be used for crop improvement by simple selection.

High heritability along with high GAM was recorded for leaf area of the plant (at 150 & 180 DAS), leaf lamina length (at 150 & 180 DAS), leaf lamina width (at 150 & 180 DAS), petiole length (at 150 & 180 DAS), plant diameter (at 150 & 180 DAS), fresh weight of leaves & pseudo stem (g/plant), fresh biomass (g/plant), length and girth of the mother & primary rhizomes, number of secondary rhizomes, fresh rhizome yield per plot and fresh rhizome projected yield per ha. This is an indication of more additive gene action, shows the amount of progress expected from the selection of individual traits.

High magnitude of variance, high broad sense heritability along with high GAM was observed in leaf lamina width (at 150 & 180 DAS), petiole length (at 150 & 180 DAS), weight of leaves & pseudo stem (g/plant), fresh biomass per plant, length of the primary rhizomes, number of secondary rhizomes, fresh rhizome yield per plot and fresh rhizome projected yield per ha. Represents that these characters are under the influence of genetic control and highest amount of progress can be expect from the selection of individual traits, showing usefulness of these characters in selection programmes.

Keywords: Black turmeric, Phenotypic coefficient of variation, Genotypic coefficient of variation, Heritability, Genetic advance mean. Curing percentage.

Introduction

Curcuma caesia Roxb., is an important, lesser known, non-conventional medicinal plant belongs to Zingiberaceae family. Native to North-East and central India. All parts of the plant *viz.,* leaves, roots, bulbs and rhizomes used in Ayurvedic, Unani and Siddhha herbal medicine system (Pandey and chowdhary, 2003). Traditionally rhizomes are used as home remedy for several ailments by tribal communities. Pharmacologically blood purifying activity (Arulmozhi *et al.,* 2006), bronchodilating activity (Paliwal *et al.,* 2011), antioxidant activity (Mangla *et al.,* 2010), anxiolytic and CNS depressant activity, locomotor depressant, anticonvulsant (Karmakar *et al.,* 2011), anthelmintic activity (Gill *et al.,* 2011), anti-bacterial activity (Rajamma *et al.,* 2012), anti-ulcer activity (Das *et al.,* 2012) were reported by several workers.

Black turmeric is sterile triploid (2n=3x=42), mainly propagated through underground rhizomes. Presently this herb is considered as critically endangered (threatened) species, due to wide destruction of natural habitat through several anthropogenic activities *viz.,* over exploitation for traditional medicine purposes, destructive harvesting, industrialization, urbanization etc. By looking in to the present status and pharmacological importance urgent need is there to conserve this rare and unconventional medicinally important plant.

Genetic variation has implications for the conservation at the species level. Systematic and detailed characterization of available genotypes is required for better conservation. Since the plant has reproductive sterility, creation of variability by conventional hybridization technique is difficult. The best option is exploitation of available natural variability through collection and evaluation of different genotypes. Even though germplasm collection represents the main source of variability for black turmeric genetic improvement, presently studies on characterizing germplasm collections are scarce or nil in this species.

It is necessary to understand the genetic architecture and morphological characters and interrelationship among them for improvement of both quantitative and qualitative traits. The inheritance as well as varying climatic conditions of different regions resulted in different economic yield which is considered as very complex trait of the crop (Prajapati *et al.,* 2014). Different variability parameters such as GCV, PCV and heritability should be thoroughly studied for the selection of the superior lines for high yielding genotypes (Dutta, 2015). Importance should be given to development of identification criteria's for selection of high yielding genotypes.

Morphological characterization is an important tool even in the era of molecular characterization because of its reliability and easy identification with less resources for certain stable characters unaltered with environmental interactions. The important link between the conservation and utilization of plant genetic resources is collection and characterization of germplasm. Studies on the genetic variability and the genetics of various agronomic characters of black turmeric are very sparse, and no improved high yielding varieties have been developed so far and no scientific publications on its cultivation practices have been released. Therefore, the present study was undertaken to characterize a set of thirty-three black turmeric genotypes collected from provenance of the country as a conservation measure of the species.

Material and Methods

Thirty-three black turmeric genotypes were collected from the provenance of the country (Table1). The genotypes were characterized at ICAR-KVK Chamarajanagar, Karnataka. Crop was grown during two consecutive seasons of 2018-19 and 2019-20 in a randomized block design (RBD) with three replications. 54 rhizomes were planted in each plot (3m X 2m) at spacing of 30cm X 30cm. The field was maintained under uniform recommended cultural practices. Five plants of uniform size and vigour was selected for recording observations.

Genotypes were evaluated for 45 morphological traits at different stages of crop growth. On the basis of individual plant observations, the mean for each character in all the populations was computed as follows.

$$Y = \frac{1}{n}\sum_{i=0}^{n} Yi$$

Where,

Y = Population mean
Yi = Individual value
n = Number of observations

The minimum and maximum value on the basis of individual plant observations was used to indicate the range for a given character.

In all the populations, variance was computed for all the characters as follows.

$$\text{Variance} = \frac{1}{n-1}\left[\sum (Yi - Y)^2\right]$$

Where,

Yi = Individual value
Y = Population mean
n = Number of observations

$$\text{Standard error (Se)} \quad Se = \frac{SD}{\sqrt{n}}$$

Where,

SD = Deviation of individual value from population mean
n = Number of observations

Analysis of variance (ANOVA) done as per the below mentioned formulae;

Source	**d.f.**	**Expected values of M.S.S.**	**MSS**	**Calculated Value of (F)**
Replication	r-1	MSSr (M1)	-	-
Genotype	g-1	MSSg (M2)	M2/(g-1)	(M2/M3)
Error	(r-1) (g-1)	MSSe (M3)	M3/ (r-1) (g-1)	-
Total	(rg-1)	M1+ M2 M3	M1 + (M2/M3)	-

Where, r = Number of replications
g = Number of genotypes
MSSr = Mean sum of squares due to replication
MSSg = Mean sum of squares due to genotypes
MSSe = Mean sum of squares due to error
$\sigma^2 e$ = Error variance
$\sigma^2 g$ = Genotypic variance

Critical difference

In order to compare the means of entries, critical difference (CD) was calculated by the following formula.

CD = SE X ‘t’ value at error degrees of freedom

Where

$$S.E(d) = \sqrt{2}(MSSe)/r$$

t = the table value at 5 % or 1 % probability level

r = Number of replications.

Estimation of genetic variability parameters

Genotypic and phenotypic variances and coefficient of radiances were computed based on the expected mean sum of squares from ANOVA table as follows.

The treatment means sum of squares due to genotypes is made up of environmental variance along with ‘r’ times the genetic variances (‘r’ being number of replications).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{TMSS} - \text{EMSS}}{\text{Number of replications (r)}}$$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$
Error variance ($\sigma^2 e$) = EMSS
Where,

TMSS - Mean sum of squares for treatments

EMSS - Mean sum of squares for error

Genotypic and phenotypic coefficients of variation were calculated according to Burton (1953).

$$PCV(\%) = \frac{\sqrt{\text{Phenotypic Variance of Germplasm}}}{\text{General mean of Character}} \times 100$$

$$GCV(\%) = \frac{\sqrt{\text{Genotypic Variance of Germplasm}}}{\text{General mean of Character}} \times 100$$

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as follows.

0 – 10% : Low
10 – 20% : Moderate
>20% : High

Heritability

The broad sense heritability (h^2 *bs*) was estimated by following the procedure suggested by Weber and Moorthy (1952) as indicated here below.

$$\text{Heritability} = \frac{Vg}{Vp} \times 100$$

Where, Vp is the phenotypic variance and Vg is the genotypic variance of respective germplasm.

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949)

0 – 10% : Low
10 – 20% : Moderate
>20% : High

Genetic advance

It was predicted by using the formula provided by Johnson et al. (1955).

$$GA = h_2 bs \text{ X } \sigma_p \text{ X } k$$

Where,

$h_2 bs$ = Heritability in broad sense

σ_p = Phenotypic standard deviation of the trait

k = Standard selection differential which is 2.06 at 5 per cent selection intensity

Genetic advance as per cent mean (GAM)

Genetic advance as per cent mean (GAM) was computed by the following formula,

$$GAM(\%) = \frac{\text{Genetic advance}}{\text{General mean of the Character}} \times 100$$

The genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955).

0 – 10% : Low
10-20% : Moderate
>20% : High

Table 1: Details of black turmeric genotypes collected from provenance of the country.

#	Genotype	Place of origin	Latitude	Longitude	Altitude (m)	State
01	GKM-1	Mijar,	13° 4' 7.6764"N	74° 59' 36.9564" E	147	Karnataka
02	GKM-2	Mangalore	12°55'2.03"N	74°51'21.71"E	22	Karnataka
03	GKB-3	Bangalore	12.9716° N	77.5946° E	920	Karnataka
04	GKB-4	Sanjeevini vatika	13.0801° N	77.5785° E	924	Karnataka
05	GKJ-5	Joida	15.1688° N	74.4848° E	532	Karnataka
06	GMV-6	Vidarbha-Gadehirolli	21.1286° N	79.0964° E	1000	Maharashtra
07	GBS-8	Samastipur	25.8629679N	85.7810263E	53	Bihar
08	GBH-9	Hajipur	25.6858392N	85.2145907E	56	Bihar
09	GGR-10	Rajkote	22° 17' 30N	70° 47' 36E	252	Gujarat
10	GAB-11	Bhoka Ghat Forest	26.2006° N	92.9376°E	76	Assam
11	GAB-12	Bijuli	28.0312°N	82.9555°E	97	Assam
12	GAB-13	Bokoliya	26.0564°N	93.1955°E	600	Assam
13	GAK-14	Killing Basti	26.8140°N	82.7630°E	680	Assam
14	GMW-15	Wakhro	23° 43' 2.6256" N	92° 43' 5.2212" E	1619	Mizoram
15	GMK16	Kolasib	24.2246° N	92.6760° E	722	Mizoram
16	GMA-17	Aizwal	23.727106°N	92.717636°E	1132	Mizoram
17	GOK-18	Khurda	20.1301° N	85.4788° E	75	Odisha
18	GOK-19	Koraput	18.82°N	82.72°E	870	Odisha
19	GAP-20	Pasighat Area	28.0619° N	95.3260° E	153	Arunachal Pradesh
20	GMF-21	Manipur – Forest	24° 48' 50.2812" N	93° 57' 1.0044" E	900	Manipur
21	GMI-22	Imphal	24.8170° N	93.9368° E	786	Manipur
22	GMS-24	Sagar	23.8388° N	78.7378° E	427	Madhya Pradesh
23	GNK-25	Kohima	25.6751° N	94.1086° E	1444	Nagaland
24	GNU-26	Uhkagoronga Hill	25° 54' 22.5612" N	93° 43' 39.3312" E	3827	Nagaland
25	GNF-27	Nepal – Forest	27° 42' 2.7684" N	85° 18' 0.5040" E	330	Nepal
26	GKT-29	Thrissur-Vellanikara	10.5452° N	76.2740° E	22	Kerala
27	GKK-30	IISR Kozhikode	11.2588° N	75.7804° E	1	Kerala
28	GMR-31	Ri-Bhoi	25.8432° N	91.9856° E	485	Meghalaya
29	GAD-32	Dolamora Borpung	26° 14' 38.9616" N	92° 32' 16.2312" E	615	Assam
30	GNP-33	Peren	25.5125° N	93.7391° E	1445	Nagaland
31	GBC-34	Champaran	27.1543° N	84.3542° E	62	Bihar
32	GJG-35	Godda	24.8255° N	87.2135° E	87	Jharkhand
33	GNP-36	Phek	25.6634° N	94.4703° E	1524	Nagaland

Results and Discussion

Analysis of variance

The analysis of variance was performed individually for each character and total variation was partitioned into different sources. Mean sum of squares due to various sources of variance for different characters of black turmeric genotypes are presented in Table 02. The results indicated highly significant variation among the genotypes for the characters studied.

Analysis of variance revealed significant differences due to the genotypes for all the fourty five characters studied. The characters were days to sprouting in main field, plant height at 120, 150, 180 & 210 DAS, number of leaves per plant at 120, 150, 180 & 210 DAS, number of shoots per plant at 120, 150, 180 & 210 DAS, number of leaves on main stem at 150, 180 & 210 DAS, leaf area per plant at 150 & 180 DAS, petiole length, leaf lamina length, lamina width at 150 & 180 DAS, plant diameter at 150 & 180 DAS, fresh rhizome yield (g/plant), weight of the root tubers (g/plant), weight of the roots (g/plant), weight of the leaves & stem per plant (g), fresh biomass per plant (g), number, length, girth & weight of the mother rhizome & primary rhizomes per clump, number of secondary rhizomes per clump, rhizome internode pattern, fresh rhizome yield per plot (kg), curing percentage, cured rhizome yield per plant (g) and projected fresh rhizome yield per hectare (t).

Genetic variability, heritability and genetic advance

The data revealed that use of most influencing independent variables and existence of large amount of variability with respect to the characters studied. Phenotypic coefficient variation (PCV) was higher than genotypic coefficient variation (GCV) for all the characters studied, though differences were very less in majority cases (Table 3 and 3A). Thus, it is showing that these traits are less influenced by environmental factors. The magnitude of coefficient of variability is varied from character to character (low, moderate or high), thus indicates great diversity among the studied population.

Growth parameters

The estimate of GCV (6.68%) and PCV (9.55%) was low, moderate heritability (49.00%) was observed along with low expected genetic advance as per cent mean (9.63) for the trait number of days for sprouting in the main field. Results indicate the role and effect of environment on sprouting, apart from type of rhizomes, stage of maturity, dormancy and storage conditions (Graph 1A &1B). Significant variation among the genotypes with respect to sprouting in the main field might be due to different environmental conditions in the origin of the genotypes. Sprouting indirectly influences the establishment, growth and yield of the crop. In majority of the genotypes emergence of sprout was observed in 24 to 28 DAS. Vijay *et al.* (2015). Mishra *et al.* (2015) and Gupta *et al.* (2016) observed high GCV, PCV, heritability and high GAM in turmeric for sprouting.

Table 2 : Analysis of variance of black turmeric genotypes for different growth and yield parameters.

Sl no.	Characters	Replication (df=2)	Treatments (df=32)	Error (df=160)	Mean sum of square (df=5)	C.D.@ 5%	C.D.@ 1%	CV (%)
1.	Days to sprouting in main field	9.136	23.047**	3.413	4.609	2.11	2.78	6.82
2.	Plant height (cm) @ 120DAP	107.276	414.944**	44.917	70.854	5.96	7.86	7.18
3	Plant height (cm) @ 150DAP	0.095	0.0000***	-	0.169	7.64	10.09	7.9
4	Plant height (cm) @ 180DAP	245.081*	431.318**	63.138	100.815	9.06	11.96	7.88
5	Plant height (cm) @ 210DAP	294.630**	470.448**	49.815	124.855**	8.05	10.62	6.76
6	Number of leaves/Plant @ 120DAP	22.190	50.232**	13.728	71.397**	2.10	2.77	10.61
7	Number of leaves/Plant @ 150DAP	8.976	50.192**	9.607	5.637	4.22	5.58	12.48
8	Number of leaves/Plant @ 180DAP	3.115*	18.377**	0.921	1.951	3.53	4.67	9.15
9	Number of leaves/Plant @ 210DAP	0.864	64.778**	8.613	4.945	3.35	4.42	8.44
10	Number of shoots/Plant @ 120DAP	0.680*	1.09**	0.149	0.285	0.43	0.57	9.57
11	Number of shoots/Plant @ 150DAP	0.629	1.244**	0.234	0.765**	0.44	0.58	6.83
12	Number of shoots/Plant @ 180DAP	1.168	28.344**	3.385	7.619	0.55	0.73	7.64
13	Number of shoots/Plant @ 210DAP	0.582	1.388**	0.228	0.981**	0.54	0.72	7.51
14	Leaves on main stem @ 120DAS	0.307	1.955**	0.192	1.650**	0.51	0.68	9.14
15	Leaves on main stem @ 150DAS	0.540*	2.393**	0.171	0.230	0.50	0.66	7.81
16	Leaves on main stem @ 180DAS	1.691	43.538**	1.222	4.459**	0.47	0.62	7.14
17	Leaf area per plant(dm2) @ 150 DAP	608198.9**	2768401.398**	105563.863	262301.383*	370.46	489.01	6.90
18	Leaf area per plant(dm2) @ 180DAP	582034.6**	2837868.655**	105103.814	329001.695*	369.65	487.95	6.75
19	Leaf lamina length (cm) @ 150DAP	35.801*	226.131**	9.583	27.0143*	3.53	3.53	8.80
20	Leaf lamina length (cm) @ 180DAP	11.681*	206.354**	2.958	4.697	4.66	4.66	8.74
21	Leaf lamina width (cm) @ 150DAP	4.774	50.922**	1.832	1.994	1.53	1.54	10.51
22	Leaf lamina width (cm) @ 180DAP	0.039	0.687**	0.141	0.105	2.02	2.04	10.49
23	Leaf petiole length (cm) @ 150DAP	12.243*	206.248**	2.894	4.911	1.96	2.59	8.58
24	Leaf petiole length (cm) @ 180DAP	0.466	1.455**	0.203	1.126**	1.94	2.56	8.44
25	Plant diameter (cm) @ 150DAP	1.785	18.450**	0.957	1.315	1.09	1.44	7.91
26	Plant Diameter (cm) @ 180DAP	21.917	3663.016**	443.363	420.836	1.12	1.47	7.98
27	Fresh rhziome yield/plant (gm)	58.291	64484.125**	9549.881	36731.312**	111.43	147.08	25.45
28	Fresh weight of root tubers/plant (gm)	4160.958	105683.545**	15569.062	88543.897**	142.27	187.80	26.77
29	Fresh weight of roots/plant (gm)	29.140	1344.671**	251.762	2313.735**	18.09	23.88	18.52
30	Fresh weight of leaves & pseudo stem/plant (gm)	1217.993	29607.722**	777.662	811.724	31.80	41.97	9.59
31	Fresh biomass per plant (gm)	9015.732	483373.360**	39893.386	10630.918	227.74	300.62	16.51
32	Number of mother rhizome/plant	0.255	1.799***	0.204	0.170	0.51	0.68	10.57
33	Length of mother rhizome (cm)	1.404**	7.651***	0.285	0.676*	0.61	0.80	9.11
34	Girth of mother rhizome (cm)	0.296	15.5054***	0.408	0.717	0.73	0.96	6.90
35	Weight of of mother rhizome (gm)	24.730	2443.300***	597.919	67.574	27.88	36.80	22.53
36	Number of primary rhizome/plant	1.517	5.413**	0.580	0.837	0.87	1.15	12.39
37	Length of primary rhizome (cm)	1.811*	18.282**	0.500	0.792	0.81	1.06	8.22
38	Girth of primary rhizome (cm)	0.285	9.090**	0.413	0.309	0.73	0.97	10.56
39	Weight of primary rhizome/plant (gm)	862.213	37059.964**	4530.91642	21089.561**	76.75	101.31	24.15
40	Number of secondary rhizome/plant	49.628	193.404**	27.290	42.432	0.4	0.53	18.07
41	Rhizome internode pattern (cm)	0.002	0.491**	0.062	0.062	0.29	0.38	7.87
42	Fresh rhizome yield /plot (kg)	1.842	16.232**	0.828	4.9154**	1.04	1.37	15.91
43	Curing percentage	0.687	42.356**	0.350	0.289	0.67	0.89	3.22
44	Cured rhizome yield /plant (gm)	36.742*	224.924**	9.605	27.393*	31.69	51.16	26.69
45	Projected fresh rhizome yield (t/ha)	0.206	1.376**	0.126	0.419**	1.26	1.66	13.03

* Significant at 5 % probability level ** Significant at 1% probability level

The estimates of GCV and PCV were low, along with moderate heritability and moderate genetic advance as per cent mean was observed for plant height characters at 120, 150, 180 and 210 DAS. Whereas number of leaves per plant, number of shoots per plant, number of leaves on main stem of the plant traits exhibited low GCV, moderate PCV, along with moderate heritability and low to moderate genetic advance as per cent mean at different growth stages of crop (120, 150, 180 and 210 DAS), indicates action of both additive and non-additive gene action for the control of the these traits in black turmeric. Nirmal babu *et al.,* (1993); Singh *et al.,* (2014) and Prajapathi *et al.,* (2014) observed similar results in turmeric. Number of leaves on main stem of the plant at 210 DAS had moderate GCV, PCV, high heritability along with moderate GAM. These characters need further improvement through selection for the development of genotypes.

Leaf area per plant (cm^2), leaf lamina length (cm), plant diameter at 150 DAS and 180 DAS was observed for moderate GCV, PCV and high heritability along with high GAM. Lesser environment influence on the expression of character was observed, simple selection the trait would be effective for increase the yield. The action of both additive and non additive gene action is controlling the trait. The findings are in accordance with the reports of Sinker *et al.* (2005), Jayasree (2009) and Vamshi *et al.,* (2019) in turmeric

Leaf lamina width (cm) and petiole length (cm) at 150 & 180 DAS characters observed for high GCV, PCV, high heritability along with high GAM. High GCV and PCV indicate presence of more variation in the population to select superior genotypes. High heritability coupled with high GAM is due to presence of additive gene action with lesser environmental influence on expression of the character. These findings are in accordance with the reports of Paw *et al.,* (2020) in black turmeric. Singh *et al.*, 2014 in turmeric.

Plant diameter at 150 and 180 DAS had moderate GCV, PCV, high heritability and high genetic advance as per cent over mean (Graph.1A). The difference between GCV and PCV was relatively narrow. This results clearly shows the action of additive gene action and lesser environment influence on the expression of the character. Results are in agreement with the findings of Nirmal Babu *et al.* (1993); Rao (2000); Singh *et al.* (2012); Singh and Ramakrishna (2014) in turmeric.

Yield parameters

The economic value of the black turmeric is determined by fresh rhizome yield/plant (g). The estimates of GCV and PCV were high (24.92 and 35.62 per cent, respectively) coupled with moderate heritability (49.00 %) and high genetic advance as per cent over mean (35.92) indicates the presence of more variation and trait is controlled by additive gene action, hence the simple selection can be practiced for selecting the superior genotypes for this trait. Moreover wide range of variability with respect to the rhizome yield, may not be due to the environmental cause but due to the variation in genotypes, so simple selection can be effective based on this morphological character. Similar observations were made by Paw *et al.,*(2020) in black turmeric; Singh *et al.* (2012), Vijay *et al.,* (2015) in turmeric.

Fresh root tubers were branched, condensed; many, ovate oblong, pale, watery pearl colour, slightly aromatic. Wide variation was observed among the genotypes for weight of root tubers per clump. High estimates of GCV, PCV moderate heritability coupled with high genetic advance clearly indicates the presence of more variation in genotypes and the trait is controlled by additive gene action with lesser environmental influence on expression of character. Simple selection is sufficient for selecting superior genotypes which produces less or nil root tubers (Saba, 2006).

Fresh weight of roots (g/plant) character was controlled by both additive and non additive gene action for expression, further improvement is required to minimize the production of minimum roots per clump in rhizomes.

The estimates of GCV and PCV (23.84 and 25.70 per cent, respectively), high broad sense heritability (86.00 %) and genetic advance as per cent over mean (45.56) were high for fresh weight of leaves and pseudo stem (g/plant). Relatively narrow differences between GCV and PCV shows least environmental effects on this morphological characteristic and also evident for the presence of more variation in the population.

Table 3 : Estimates of range, mean, components of variance, heritability and genetic advance for growth and yield parameters in black turmeric

Sl. No.	Characters	Range		Mean	PCV (%)	GCV (%)	h^2 (Broad sense) (%)	GA(%) of mean
		Min	Max					
1.	Days to sprouting in main field	23.65	30.90	27.08	9.55	6.68	49.00	9.63
2.	Plant height (cm) @120DAP	56.74	85.54	72.80	10.18	7.23	50.00	10.57
3	Plant height (cm) @150DAP	67.75	103.61	84.80	12.17	9.26	58.00	14.51
4	Plant height (cm) @180DAP	81.57	122.21	100.87	11.06	7.77	49.00	11.23
5	Plant height (cm) @210DAP	88.62	124.52	104.36	10.49	8.02	59.00	12.64
6	Number of leaves/Plant @120DAP	12.00	21.37	17.33	15.84	11.76	55.00	17.99
7	Number of leaves/Plant @150DAP	22.68	36.15	29.68	15.00	8.31	31.00	9.49
8	Number of leaves/Plant @180DAP	26.38	40.52	33.88	11.94	7.68	41.00	10.16
9	Number of leaves/Plant @210DAP	27.70	41.03	34.76	12.20	8.80	52.00	13.08
10	Number of shoots/Plant @120DAP	2.90	4.80	3.92	12.27	7.69	39.00	9.92
11	Number of shoots/Plant @150DAP	4.60	6.42	5.65	9.78	7.00	51.00	10.32
12	Number of shoots/Plant @180DAP	5.53	7.22	6.32	10.02	6.49	42.00	8.65
13	Number of shoots/Plant @210DAP	5.52	7.32	6.37	10.20	6.91	46.00	9.63
14	Leaves on main stem @ 150DAS	4.05	6.17	4.93	13.01	9.27	51.00	13.59
15	Leaves on main stem @ 180DAS	4.87	7.10	5.61	12.42	9.66	61.00	15.47
16	Leaves on main stem @ 210DAS	5.02	7.27	5.79	12.71	10.51	68.00	17.91
17	Leaf area per plant(cm^2) @ 150 DAP	3720.16	6392.19	4693.98	15.79	14.19	81.00	26.28
18	Leaf area per plant(cm^2) @ 180 DAP	3804.01	6431.82	4800.44	15.60	14.06	81.00	26.11
19	Leaf lamina length (cm) @ 150DAP	26.16	46.75	35.21	19.15	17.01	79.00	31.12
20	Leaf lamina length (cm) @ 180DAP	26.42	46.94	35.40	19.09	16.97	79.00	31.08
21	Leaf lamina width (cm) @ 150DAP	9.06	18.07	12.74	24.53	22.18	82.00	41.27
22	Leaf lamina width (cm) @ 180DAP	9.22	18.27	12.89	24.54	22.18	82.00	41.30
23	Leaf petiole length (cm) @ 150DAP	12.65	29.03	20.04	30.28	29.04	92.00	25.22
24	Leaf petiole length (cm) @ 180DAP	12.72	29.18	20.15	30.10	28.89	92.00	24.89
25	Plant diameter (cm) @ 150DAP	8.93	16.01	12.14	16.12	14.05	76.00	57.38
26	Plant diameter (cm) @ 180DAP	9.09	16.16	12.26	16.05	13.92	75.00	57.13
27	Fresh rhziome yield/plant (gm)	227.01	654.87	383.92	35.62	24.92	49.00	35.92
28	Fresh weight root tubers/plant (gm)	254.49	798.97	466.12	37.52	26.29	49.00	37.95
29	Fresh weight of roots/plant (gm)	58.82	117.06	85.67	24.32	15.75	42.00	21.03
30	Fresh weight of leaves & pseudostem/plant (gm)	176.46	471.05	270.77	25.70	23.84	86.00	45.56
31	Fresh biomass per plant (gm)	749.02	1958.61	1209.63	27.89	22.48	65.00	37.31
32	Number of mother rhizome/plant	3.10	5.23	4.27	16.04	12.07	57.00	18.70
33	Length of mother rhizome (cm)	4.21	9.08	5.86	20.99	18.91	81.00	35.10
34	Girth of mother rhizome (cm)	5.66	13.49	9.26	18.47	17.14	86.00	32.75
35	Weight of of mother rhizome (gm)	74.86	161.57	108.54	27.72	16.16	34.00	19.40
36	Number of primary rhizome/plant	3.50	8.50	6.15	19.15	14.60	58.00	22.93
37	Length of primary rhizome (cm)	6.93	13.64	8.60	21.65	20.30	86.00	38.16
38	Girth of primary rhizome (cm)	3.97	9.25	6.09	22.40	19.75	78.00	35.88
39	Weight of primary rhizome/plant (gm)	177.13	485.32	278.68	35.80	26.42	55.00	40.17
40	Number of secondary rhizome/plant	1.4	3.73	1.96	29.46	23.28	62.00	37.88
41	Rhizome internode pattern (cm)	0.82	1.85	1.20	30.49	22.28	53.00	33.53
42	Fresh rhizome yield /plot (kg)	3.89	9.56	5.71	32.22	28.02	76.00	50.20
43	Curing percentage	13.72	23.44	18.36	14.77	14.42	95.00	28.98
44	Cured rhizome yield /plant (gm)	51.16	147.13	78.89	39.68	29.36	55.00	44.76
45	Projected fresh rhizome yield (t/ha)	6.07	15.81	8.48	33.91	31.31	85.00	59.54

Table 3A : Magnitude of different variability parameters of 45 characters in black turmeric genotypes.

Sl. No.	Characters	GCV (%)	PCV (%)	H (bs) (%)	GAM (%)
1	Days to sprouting in main field	Low	Low	Moderate	Low
2	Plant height (cm) @ 120DAP	Low	Moderate	Moderate	Moderate
3	Plant height (cm) @ 150DAP	Low	Moderate	Moderate	Moderate
4	Plant height (cm) @ 180DAP	Low	Moderate	Moderate	Moderate
5	Plant height (cm) @ 210DAP	Low	Moderate	Moderate	Moderate
6	Number of leaves/Plant @ 120DAP	Moderate	Moderate	Moderate	Moderate
7	Number of leaves/Plant @ 150DAP	Low	Moderate	Moderate	Low
8	Number of leaves/Plant @ 180DAP	Low	Moderate	Moderate	Low
9	Number of leaves/Plant @ 210DAP	Low	Moderate	Moderate	Moderate
10	Number of shoots/Plant @ 120DAP	Low	Moderate	Moderate	Low
11	Number of shoots/Plant @ 150DAP	Low	Low	Moderate	Moderate
12	Number of shoots/Plant @ 180DAP	Low	Low	Moderate	Low
13	Number of shoots/Plant @ 210DAP	Low	Moderate	Moderate	Low
14	Leaves on main stem @ 150DAS	Low	Moderate	Moderate	Moderate
15.	Leaves on main stem @ 180DAS	Low	Moderate	High	Moderate
16	Leaves on main stem @ 210DAS	Moderate	Moderate	High	Moderate
17	Leaf area per plant(cm^2) @ 150 DAP	Moderate	Moderate	High	High
18	Leaf area per plant(cm^2) @ 180 DAP	Moderate	Moderate	High	High
19	Leaf lamina length (cm) @ 150DAP	Moderate	Moderate	High	High
20	Leaf lamina length (cm) @ 180DAP	Moderate	Moderate	High	High
21	Leaf lamina width (cm) @ 150DAP	High	High	High	High
22	Leaf lamina width (cm) @ 180DAP	High	High	High	High
23	Leaf petiole length (cm) @ 150DAP	High	High	High	High
24	Leaf petiole length (cm) @ 180DAP	High	High	High	High
25	Plant diameter (cm) @ 150DAP	Moderate	Moderate	High	High
26	Plant diameter (cm) @ 180DAP	Moderate	Moderate	High	High
27	Fresh rhziome yield/plant (gm)	High	High	Moderate	High
28	Fresh weight of root tubers/plant (gm)	High	High	Moderate	High
29	Fresh weight of roots/plant (gm)	Moderate	High	Moderate	High
30	Fresh weight of leaves & stem/plant (gm)	High	High	High	High
31	Fresh biomass per plant (gm)	High	High	High	High
32	Number of mother rhizome/plant	Moderate	Moderate	Moderate	Moderate
33	Length of mother rhizome (cm)	Moderate	High	High	High
34	Girth of mother rhizome (cm)	Moderate	Moderate	High	High
35	Weight of of mother rhizome (gm)	Moderate	High	Moderate	Moderate
36	Number of primary rhizome/plant	Moderate	Moderate	Moderate	High
37	Length of primary rhizome (cm)	High	High	High	High
38	Girth of primary rhizome (cm)	Moderate	High	High	High
39	Weight of primary rhizome/plant (gm)	High	High	Moderate	High
40	Number of secondary rhizome/plant	High	High	High	High
41	Rhizome internode pattern (cm)	High	High	Moderate	High
42	Fresh rhizome yield /plot (kg)	High	High	High	High
43	Curing percentage	Moderate	Moderate	High	High
44	Cured rhizome yield /plant (gm)	High	High	Moderate	High
45	Projected fresh rhizome yield (t/ha)	High	High	High	High

Fresh biomass (g/plant) had high estimates of PCV (27.89 %), GCV (22.48 %), broad sense heritability (65.00 %) along with high GAM (37.31).The biomass of the plant comprises weight of the rhizomes, root tubers, roots, leaf and pseudostem. Presence of high variability among the population and relatively narrow difference between GCV and PCV denotes lesser environment influence on the expression of the character.

Length of the rhizomes (cm) had estimates of GCV and PCV were moderate to high (18.91 and 20.99 per cent, respectively) whereas, high heritability

(81.00%) coupled with high GAM (35.10) was observed for this trait. Primary finger length observed high estimates of genotypic coefficient of variability (20.30%) and phenotypic coefficient of variability (21.65%), estimates of high broad sense heritability (86.00%) and high genetic advance as per cent of mean (38.16). Results clearly shows role of additive gene for governing their expression, with lesser environmental influence on these traits. Hence selection on phenotype would be rewarding in improvement of these traits. These results were in accordance with the findings of Aarthi *et al.,* (2018) in turmeric.

Girth of the rhizomes had relatively narrow difference between GCV and PCV (17.14 and 18.47 per cent), high broad sense heritability (86.00 %) associated with high genetic advance over per cent mean (32.75). whereas primary rhizome girth had estimates of GCV and PCV were moderate to high, 19.75 and 22.40 per cent, respectively. High broad sense heritability (78.00 %) associated with high genetic advance over per cent of mean (35.88). Similar results were reported by Jayasree (2009) and Prajapathi *et al.* (2014) in turmeric.

Number of mother and primary rhizomes per clump traits in black turmeric is controlled by both additive and non additive gene action. Similar findings were reported by Nirmal babu *et al.* (1993) and Vamshi *et al.* (2019) in turmeric; Paw *et al.* (2020) in black turmeric.

Significantly number of secondary fingers per clump had high estimates of PCV (29.46%), GCV (23.28%), heritability (62.00%) and GAM (37.88). This indicating the role of additive gene governing their expression, hence selection on phenotype would be rewarding in improvement of these traits. Similar findings were given by Verma *et al.* (2014), Vijay *et al.* (2015), Aarthi *et al.* (2018) and Vamshi *et al.* (2019) for number of secondary fingers per clump in turmeric.

Both additive and non additive gene action is prominent in controlling the expression of weight of mother rhizome per clump trait. Whereas weight of the primary rhizome per clump shows prominent additive gene action with more variation, hence the simple selection can be practiced. Similar results were obtained by Nirmal babu *et al.* (1993), Rao (2000), Sinker *et al.* (2005), Singh *et al.* (2012), Prajapati *et al.* (2014) in turmeric.

Primary rhizome internode pattern trait had high estimates of PCV and GCV (30.49 and 22.28 per cent, respectively), medium broad sense heritability (53.00 %) associated with high genetic advance over per cent of mean (33.53). This clearly shows the effect of additive gene and lesser environment effect for the expression of the trait. Simple selection can be carried out for improvement of the yield through this trait.

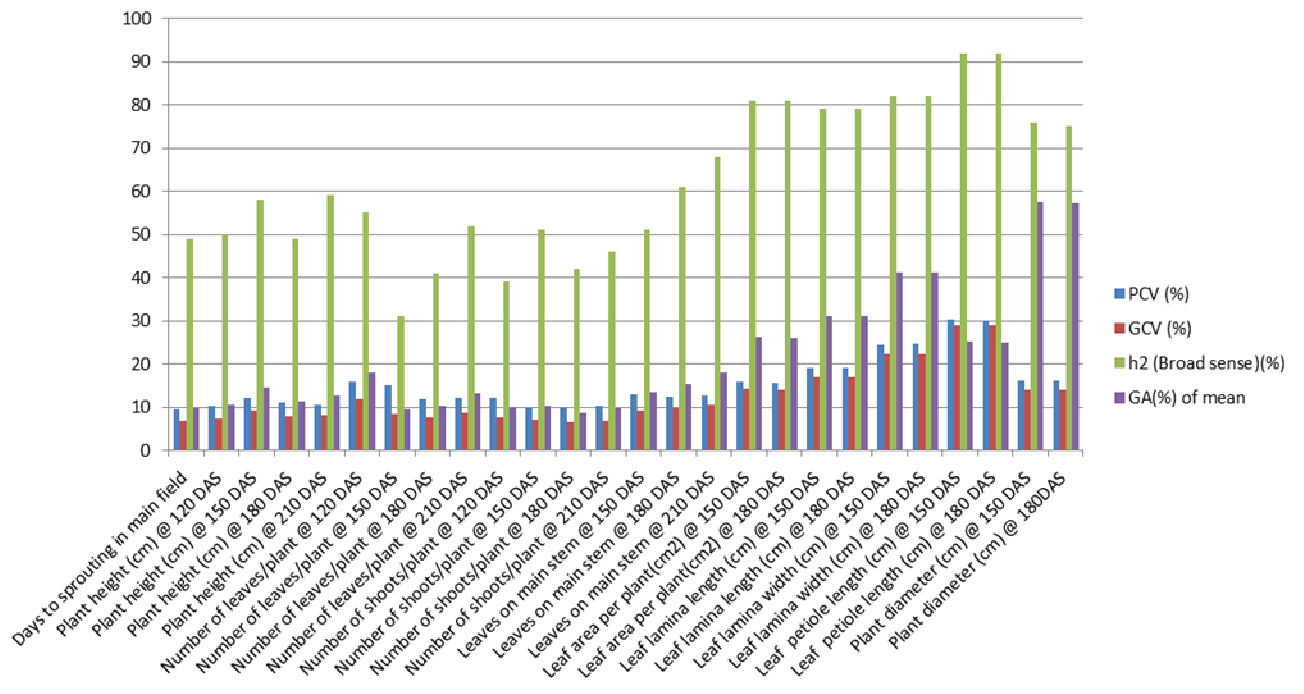

Fig. 1A: Components of variance, heritability and genetic advance for growth parameters in black turmeric

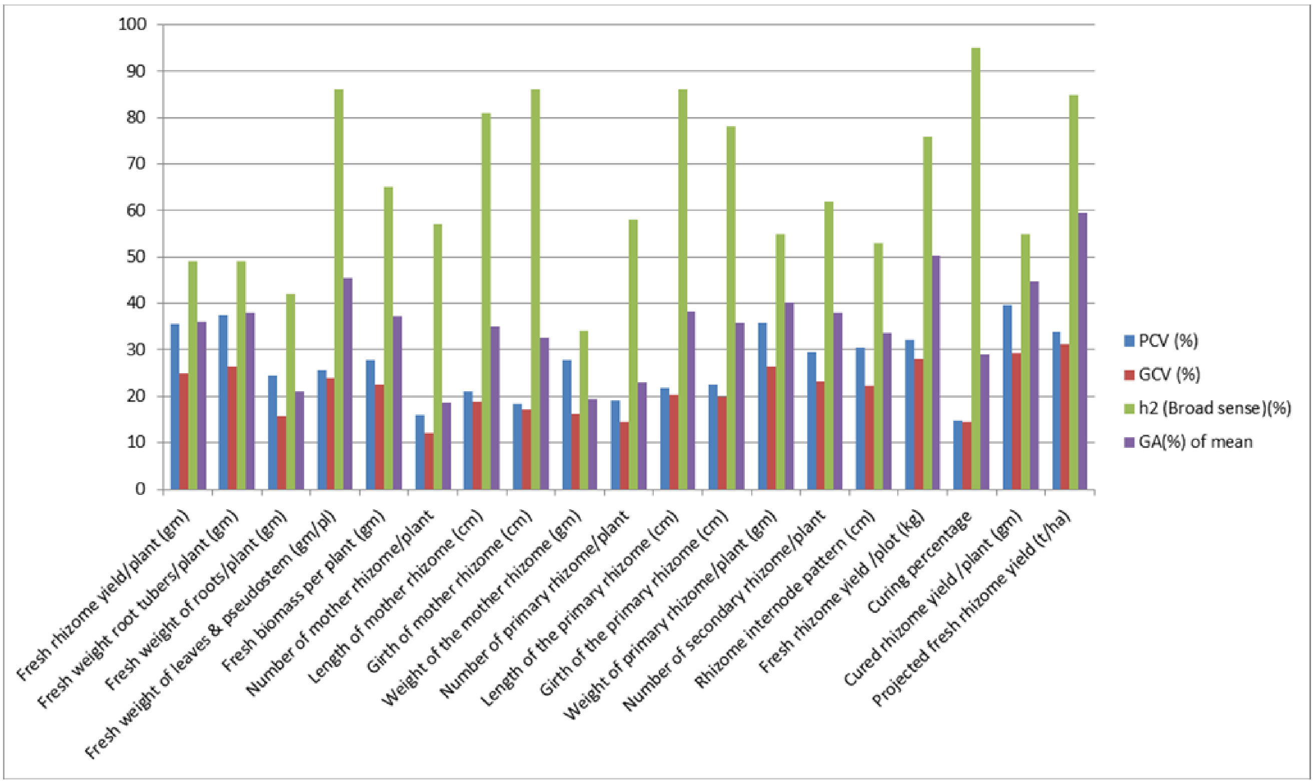

Fig. 1 B: Components of variance, heritability and genetic advance for yield parameters in black turmeric

Fresh rhizome yield per plot (kg) and projected fresh rhizome yield (t/ha) characters exhibit huge variation among the population, least environmental influence for exhibition of the traits. Hence simple selection can be made for selection of superior genotypes for these traits. The findings are in line with the observation of Nirmal babu *et al.,* (1993), Vijayalatha (2002) and Sinker *et al.,* (2005) in turmeric.

Probably this seems to be first report on curing percentage of black turmeric rhizomes. The estimates of GCV (14.42%) and PCV (14.77%) were medium and relatively narrow. High heritability (95.00 %) coupled with high genetic advance as per cent of mean (29.98) was observed. Role of additive gene for governing trait expression is prominent, in turmeric Vijayalatha (2002) and Vamshi *et al.,* (2019) reported similar results.

The cured rhizome yield mainly depends on curing percentage of the respective genotypes. An estimate of PCV and GCV (39.68 and 29.36 per cent) was high, medium broad sense heritability (55.00 %) associated with high genetic advance over per cent mean (44.76) was observed. The result clearly indicating wide variation in the population to select superior genotypes and also preponderance of additive gene action for the control of traits hence, selection based on this character would be effective.

Higher magnitude of phenotypic and genotypic coefficient of variation was observed in the following traits; leaf lamina width (cm) @ 150 and 180DAP, petiole length (cm) @ 150DAP and 180DAP, fresh rhizome yield (g/plant), weight of root tubers, roots, leaves & pseudo stem per plant, fresh biomass per plant, length and weight of the mother rhizomes, primary rhizome length (cm), girth and weight/clump, secondary rhizome numbers/clump, primary rhizome internode pattern, fresh rhizome yield /plot, cured rhizome yield /plant and projected fresh rhizome yield (t/ha).Which is suggesting that these characters are under the influence of genetic control. Hence these characters can be used for further improvement by simple selection practice.

High heritability was observed for characters, leaves on main stem (180 & 210DAS), leaf area per plant (150 & 180 DAS), leaf lamina length (150 & 180 DAS), leaf lamina width (150 & 180 DAS), petiole length (150 & 180 DAS), plant diameter (150 & 180 DAS), fresh weight of leaves and pseudostem per plant, biomass per plant, length & girth of the mother and primary rhizomes, number of secondary rhizome, fresh rhizome yield per plot, curing percentage and projected fresh rhizome yield per ha. These traits coupled with high genetic advance as per cent mean indicate, that simple selection would be sufficient for genetic improvement.

Conclusion

Genetic variation has implications for the conservation at the species level, analysis of variance revealed significant differences due to the genotypes for all the forty-five characters studied (Table 1). PCV is higher than the GCV for all the traits. Relatively narrow difference between phenotypic &genotypic coefficient of variation was evident in majority of the characters, indicated low environmental effect on expression of these traits (Table 2).

Leaf lamina width (cm) @ 150DAS& 180DAS, petiole length (cm) @ 150DAS& 180 DAS, fresh rhizome yield (g/plant), weight of root tubers (g/plant), weight of roots (g/plant), weight of leaves & pseudo stem (g/plant), fresh biomass (g/plant), length and weight of the mother rhizomes, primary rhizome length (cm), girth & weight per plant, secondary rhizome numbers, primary rhizome internode pattern, fresh rhizome yield per plot (kg), cured rhizome yield (g/plant) and fresh rhizome projected yield (t/ha) had higher magnitude of phenotypic and genotypic coefficient of variation (Fig. 1A & 1B), clearly suggesting that these characters were under the influence of genetic control. Hence, these characters can be used for crop improvement by simple selection.

High heritability along with high GAM was recorded for leaf area of the plant (at 150 & 180 DAS), leaf lamina length (at 150 & 180 DAS), leaf lamina width (at 150 & 180 DAS), petiole length (at 150 & 180 DAS), plant diameter (at 150 & 180 DAS),fresh weight of leaves & pseudo stem (g/plant), fresh biomass (g/plant),length and girth of the mother & primary rhizomes, number of secondary rhizomes, fresh rhizome yield per plot and fresh rhizome projected yield per ha (Table 7A). This is an indication of more additive gene action, shows the amount of progress expected from the selection of individual traits.

High magnitude of variance, high broad sense heritability along with high GAM was observed in leaf lamina width (at 150 & 180 DAS), petiole length (at 150 & 180 DAS), weight of leaves & pseudo stem (g/plant), fresh biomass per plant, length of the primary rhizomes, number of secondary rhizomes, fresh rhizome yield per plot and fresh rhizome projected yield per ha. Represents that these characters are under the influence of genetic control and highest amount of progress can be expect from the selection of individual traits, showing usefulness of these characters in selection programmes.

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