Received: 27 Oct 2025 | Revised: 02 Feb 2026 | Accepted: 02 Feb 2026

Electronic Journal of Plant Breeding

Research Article

Estimation of genetic variability, heritability and genetic advance as percent mean in black turmeric (*Curcuma caesia* Roxb.) genotypes

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Abstract
Genetic variability, heritability, and genetic advance were evaluated in 33 genotypes of black turmeric (*Curcuma caesia* Roxb.) to identify traits suitable for effective selection. Analysis of variance revealed highly significant differences among genotypes for all 45 growth, rhizome, and yield-related traits, indicating the presence of substantial genetic variability. Phenotypic coefficient of variation (PCV) was consistently higher than genotypic coefficient of variation (GCV) for all characters, with relatively narrow differences for most traits, suggesting limited environmental influence. High PCV and GCV were recorded for leaf lamina width (PCV: 24.53–24.54 %; GCV: 22.18%), petiole length (PCV: 30.10–30.28 %; GCV: 28.89–29.04 %), fresh rhizome yield per plant (PCV: 35.62 %; GCV: 24.92 %), fresh biomass per plant (PCV: 27.89 %; GCV: 22.48 %), and several rhizome traits. Broad-sense heritability ranged from moderate to high (49.00–95.00 %), with high heritability coupled with high genetic advance as percent of mean observed for leaf lamina width (h^2: 82.00 %; GAM: 41.27–41.30 %), petiole length (h^2: 92.00 %; GAM: 24.89–25.22 %), fresh biomass (h^2: 65.00 %; GAM: 37.31 %), primary rhizome length (h^2: 86.00 %; GAM: 38.16 %), and projected fresh rhizome yield (h^2: 85.00 %; GAM: 59.54 %). Fresh rhizome yield per plant varied widely from 227.01 to 654.87 g, indicating ample scope for selection. The predominance of additive gene action for these traits suggests that direct phenotypic selection would be effective. Overall, leaf lamina width, petiole length, biomass components, rhizome characters, and fresh rhizome yield emerged as reliable selection indices for yield improvement, conservation and genetic enhancement of black turmeric.

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

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, antioxidant activity, anxiolytic and CNS depressant activity, locomotor depressant, anticonvulsant, anthelmintic activity, anti-bacterial activity, anti-ulcer activity (Das *et al.,* 2012) was 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. 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 investigation was undertaken to assess the extent of genetic variability, heritability, and genetic advance among 33 genotypes of black turmeric.

MATERIALS AND METHODS

Plant material and experimental details: Thirty-three black turmeric genotypes were collected from different regions across India (**Table 1 and Fig.1**). The experiment was carried out at ICAR–KrishiVigyan Kendra, Chamarajanagar, Karnataka, during 2018–19 and 2019–20. The crop was planted in a randomized block design (RBD) with three replications. Each plot (3.2 × 1.8 m) accommodated 54 rhizomes planted at 30 × 30 cm spacing. Recommended agronomic and plant protection practices were uniformly adopted throughout the crop growth period. Observations were recorded from five randomly selected plants of uniform vigour from each replication.

Observations recorded: Forty-five morphological characters were recorded at different growth stages following standard turmeric descriptors. The mean value for each character was computed from individual plant observations. The range was expressed based on the minimum and maximum values observed among genotypes.

Statistical analysis: Data were analyzed using analysis of variance (ANOVA) appropriate for a randomized block design to test the significance among genotypes. Genotypic and phenotypic variances were estimated from the mean sum of squares, following the procedures outlined by Burton (1953). Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated as suggested by Burton (1953) and classified as low (<10%), moderate (10–20%), or high (>20%) according to Sivasubramanian and Menon (1973). Broad-sense heritability (h^2bs) was computed following Weber and Moorthy (1952) and categorized as per Robinson *et al.* (1949). Genetic advance (GA) and genetic advance as percent of mean (GAM) were estimated using the formula given by Johnson *et al.* (1955), considering a 5% selection intensity. All statistical analyses, were performed using Windostat software (version 9.30).

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 2**. 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 45 characters studied.

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**). Thus, it revealed that these traits are less influenced by environmental factors. The magnitude of coefficient of variability was 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

Table 1. Details of black turmeric genotypes collected from states of India

S.No.	Genotype	Place of origin	Latitude	Longitude	Altitude (m)
1	GKM-1	Mijar, Karnataka	13° 4’ 7.6764’’N	74° 59’ 36.9564’’ E	147
2	GKM-2	Mangalore, Karnataka	12°55’2.03”N	74°51’21.71”E	22
3	GKB-3	Bangalore, Karnataka	12.9716° N	77.5946° E	920
4	GKB-4	Sanjeevinivatika, Karnataka	13.0801° N	77.5785° E	924
5	GKJ-5	Joida, Karnataka	15.1688° N	74.4848° E	532
6	GMV-6	Vidarbha-Gadehirolli, Maharashtra	21.1286° N	79.0964° E	1000
7	GBS-8	Samastipur, Bihar	25.8629679N	85.7810263E	53
8	GBH-9	Hajipur, Bihar	25.6858392N	85.2145907E	56
9	GGR-10	Rajkote, Gujarat	22° 17’ 30N	70° 47’ 36E	252
10	GAB-11	BhokaGhat Forest, Assam	26.2006° N	92.9376°E	76
11	GAB-12	Bijuli, Assam	28.0312°N	82.9555°E	97
12	GAB-13	Bokoliya, Assam	26.0564°N	93.1955°E	600
13	GAK-14	Killing Basti, Assam	26.8140°N	82.7630°E	680
14	GMW-15	Wakhro, Mizoram	23° 43’ 2.6256’’ N	92° 43’ 5.2212’’ E	1619
15	GMK16	Kolasib, Mizoram	24.2246° N	92.6760° E	722
16	GMA-17	Aizwal, Mizoram	23.727106°N	92.717636°E	1132
17	GOK-18	Khurda, Odisha	20.1301° N	85.4788° E	75
18	GOK-19	Koraput, Odisha	18.82°N	82.72°E	870
19	GAP-20	Pasighat, Arunachal Pradesh	28.0619° N	95.3260° E	153
20	GMF-21	Manipur – Forest	24° 48’ 50.2812’’ N	93° 57’ 1.0044’’ E	900
21	GMI-22	Imphal, Manipur	24.8170° N	93.9368° E	786
22	GMS-24	Sagar, Madhya Pradesh	23.8388° N	78.7378° E	427
23	GNK-25	Kohima, Nagaland	25.6751° N	94.1086° E	1444
24	GNU-26	Uhkagoronga Hill, Nagaland	25° 54’ 22.5612’’ N	93° 43’ 39.3312’’ E	3827
25	GNF-27	Nepal – Forest	27° 42’ 2.7684’’ N	85° 18’ 0.5040’’ E	330
26	GKT-29	Thrissur-Vellanikara, Kerala	10.5452° N	76.2740° E	22
27	GKK-30	IISR Kozhikode, Kerala	11.2588° N	75.7804° E	1
28	GMR-31	Ri-Bhoi, Meghalaya	25.8432° N	91.9856° E	485
29	GAD-32	DolamoraBorpung, Assam	26° 14’ 38.9616’’ N	92° 32’ 16.2312’’ E	615
30	GNP-33	Peren, Nagaland	25.5125° N	93.7391° E	1445
31	GBC-34	Champaran, Bihar	27.1543° N	84.3542° E	62
32	GJG-35	Godda, Jharkhand	24.8255° N	87.2135° E	87
33	GNP-36	Phek, Nagaland	25.6634° N	94.4703° E	1524

environment on sprouting, apart from type of rhizomes, stage of maturity, dormancy and storage conditions. 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) observed high GCV, PCV, heritability and high GAM in turmeric for sprouting.

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 at 120, 150, 180 and 210 DAS (**Table 3**). 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 Prajapati *et al.* (2014) observed similar results in turmeric. Number of leaves on main stem of the plant at 210 DAS had moderate GCV (10.51%), PCV (12.71%), and high heritability along with moderate GAM (17.91%). These characters need further improvement through selection for the development of genotypes.

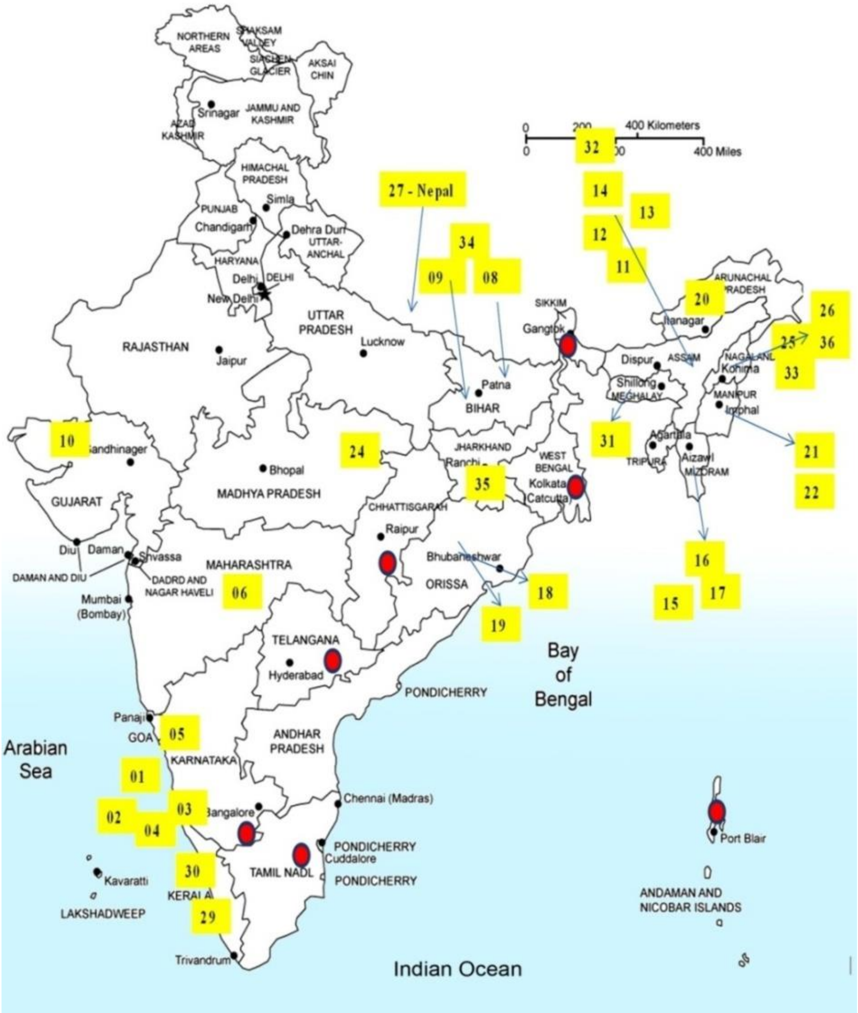

Fig. 1. Black turmeric genotypes collected from states of India

Leaf area per plant, leaf lamina length, 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 characters, 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 Vamshi *et al.* (2019) in turmeric.

Leaf lamina width and petiole length at 150 & 180 DAS observed with 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 and 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. The difference between GCV and PCV was relatively narrow. This result 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) and Singh *et al.* (2014) in turmeric.

Yield parameters: The economic value of the black turmeric is determined by fresh rhizome yield/plant. The estimates of GCV and PCV were high (24.92 and 35.62 %, 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

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

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

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

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

S.No.	Characters	Range		Mean	PCV (%)	GCV (%)	h^2 (Broad sense) (%)	GA(%) of mean
		Minimum	Maximum					
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 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

https://doi.org/10.37992/2026.1701.005

in genotypes, so simple selection can be effective based on this character. Similar observations were made by Paw *et al.* (2020) in black turmeric and 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. Fresh weight of roots 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 %, 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. 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.

Fresh biomass 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 had estimates of GCV and PCV were moderate to high (18.91 and 20.99 %, 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 show 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 %), 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 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 and 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 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. 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 Nirmalbabu *et al.*(1993), Rao (2000) and Prajapati *et al.* (2014) in turmeric.

Primary rhizome internode pattern trait had high estimates of PCV and GCV (30.49 and 22.28 %, 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. Fresh rhizome yield per plot and projected fresh rhizome yield 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) in turmeric.

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. This is the first report on curing percentage of black turmeric rhizomes. The cured rhizome yield mainly depends on curing percentage of the respective genotypes. An estimate of PCV and GCV (39.68 and 29.36%) 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 at 150 and 180DAP, petiole length at 150DAP and 180DAP, fresh rhizome yield, weight of root tubers, roots, leaves & pseudo stem per plant, fresh biomass per plant, length and weight of the mother rhizomes, primary rhizome length, 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.

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.

The study revealed substantial genetic variability among genotypes for all the characters studied, indicating good scope for improvement through selection. The consistently higher PCV than GCV for all traits, along with their narrow differences for most characters, suggests minimal environmental influence and predominant genetic control. Several growth, rhizome, and yield-related traits exhibited high variability, reflecting their strong potential for effective selection. High heritability coupled with high genetic advance as a percentage of mean for key vegetative and yield traits indicates the predominance of additive gene action and predicts substantial genetic gain through simple selection. Overall, traits such as leaf lamina width, petiole length, biomass components, rhizome characters, and fresh rhizome yield emerged as reliable selection criteria and are highly useful for genetic improvement and conservation-oriented crop improvement programmes.

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