International Journal of Bio-resource and Stress Management https://pphouse.org/ijbsm.php

Crossref

IJBSM June 2022, 13(6):595-604 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR2941b

Research Article *Natural Resource Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2022.2941b

Genetic Variability in Turmeric (*Curcuma longa* L.)

H. Dev and Vipin Sharma

Dept. of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh (173 230), India

Open Access

Corresponding happydev21@yahoo.in

0000-0002-4688-5815

ABSTRACT

The investigation was carried out in the Department of Vegetable Science, Dr. YSPUHF, Nauni, Solan, HP, India during *kharif* May, 2011-January, 2012. The objective of the study was to assess the genetic variability of 40 diverse genotypes of turmeric collected from different parts of the country including 2 recommended varieties as checks viz. Palam Lalima and PalamPitambar.This research work can be valued of immence importance over the time, as it may be of use for global breeders through exchange of germplasm in future.The observations were recorded on various growth, yield and quality parameters. High GCV and PCV were found for weight of mother and primary rhizomes, incidence of rhizome rot and curcumin content, indicating wide range of variations and offered better scope for improvement through clonal selection. High heritability coupled with high genetic gain were estimated for weight of mother and primary rhizomes and girth of primary rhizome, indicating that these characters were under additive gene effects and more reliable for effective clonal selection. High heritability coupled with moderate genetic gain for length and core diameter of mother, primary and secondary rhizomes, girth and weight of secondary rhizome and yield plant^{-1}, plot^{-1} and ha^{-1} were also observed, which indicated that clonal selection for these characters can also be effective. The overall assessment showed that there was wide variability among turmeric genotypes which has important implication for clonal selection of turmeric genotypes for yield and quality attributes.

KEYWORDS: *Curcuma longa*, heritability, quality, turmeric, variability, yield

Citation* (VANCOUVER)*: Dev and Sharma, Genetic Variability in Turmeric (*Curcuma longa* L.). *International Journal of Bio-resource and Stress Management,* 2022; 13(6), 595-604. HTTPS://DOI.ORG/10.23910/1.2022.2941b.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 23rd February 2022 RECEIVED in revised form on 07th June 2022 ACCEPTED in final form on 20th June 2022 PUBLISHED on 30th June 2022

1. INTRODUCTION

Turmeric (*Curcuma longa* L.) is one of the important spice crops in India belonging to the family Zingiberaceae and plays a vital role in the national economy. It originated in the west coast of south India. Turmeric oleoresin is used in brine pickles and to some extent in non-alcoholic beverages, gelatins, butter and cheese, etc. Curcumin extracted from turmeric is used as a colorant which hasantioxidant (Tanvir et al., 2015; Tanvir et al., 2017; Akter et al., 2019.), anti-inflammatory, antifungal and antitumoral activities (Siju et al., 2010, Tomeh et al., 2019). Curcumin is also beneficial in treating viral disorders (Prasad and Tyagi, 2015; Kocaadam and Anlier, 2017) and play a great role in protecting against COVID-19 (Ciavarella et al., 2020). India is largest producer, consumer and exporter of turmeric in the world. Annual global production is 1.1 mt. India dominates the world production scenario contributing 80% followed by China (8%), Myanmar (4%), Nigeria (3%) and Bangladesh (3%). In 2020–21 India had exported 1.71 lakh tones of turmeric compared to 1.37 lakh tones in the previous year. The export demand of turmeric witnessed a rise as orders are pouring in from the middle east, USA, Europe and Southeast Asia. Right after the Covid-19 outbreak, turmeric sales have been continuously increasing in 2020-21 (Anonymous, 2020–2021). Out of the total turmeric produced in India 90% is consumed locally. Remaining 10% of the production is exported to various countries like US, UK, Middle East, Japan, Singapore, Malaysia, South Africa, Australia and other countries. Andhra Pradesh followed by Odisha, Tamil Nadu and Maharashtra states in India constitutes the lion's share in India's turmeric production. In Himachal Pradesh, turmeric has not attained significant status among spice crops probably due to poor yield and being a long duration crop. But increasing monkey menace and engagement of farmers in other occupations offer better opportunities for increasing acreage under this crop in the state. The scope of improvement depends upon the magnitude of genetic variability present in the available germplasm.Genetic diversity is used as source of genes in crop improvement for production of high yielding varieties (Jan et al., 2012; Kumar et al., 2013 and Kumar, 2014). Greater the variability in the available germplasm better would be the chances of selecting superior genotypes (Ravishanker et al., 2013 and Simmonds, 1962). Wide genetic variability exists in this crop with regard to the yield, yield contributing traits and quality. Relative composition of turmeric varies considerably (Sandeep et al., 2015,Gomes et al., 2018, Gomes et al., 2019) with the geographical origin and different agroclimatic zones. Hence, for effective selection, a thorough study on genotypic and phenotypic variability is essential (Kumari et al., 2017). Correlation studies and further partitioning into various components of yield and other characters are rational approaches to understand the nature and magnitude of their relationship (Dey et al., 2021).

However, not much work has been done on crop improvement through the selection of superior types with high yield in the state. So, there is a great need of screening turmeric germplasm to select elite genotypes with higher yield and improved quality for direct selection (Sigrist et al., 2012; Xiang et al., 2012 and Arya et al., 2016). Keeping in view the above facts, therefore it was important to study/screen the germplasm of turmeric collected from the different turmeric growing areas of Himachal Pradesh and India.

2. MATERIALS AND METHODS

The present investigations were carried out at the Experimental Farm of the Department of Vegetable Science, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India during *kharif* May, 2011–January, 2012, which is located at Nauni, about 13 km from Solan, at an altitude of 1276 meters above mean sea level, lying at 77 11' 30" East and 30 52' 30" North.The research work carried out during 2011–2012 has great importance over time and again, as it can be used for breeders around the globe through exchange of germplasm in future. 40 diverse genotypes of turmeric collected from different parts of the country including two recommended varieties as checks viz.PalamLalima and Palam Pitambar were used for the present investigations. Uniform size of rhizomes was directly sown in the field in the month of April, 2011 at a spacing of 30×20 cm^2 in raised beds of 3×1 m^2 size, accommodating 50 plants plot^{-1}. Drainage channels were also made between plots. Each collection was sown in a Randomized Block Design with three replications. The standard cultural practices recommended in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand (Anonymous, 2009). Data were recorded from the mean of ten plants tagged randomly from each genotype in each replication on different characters, viz. emergence, number of tillers and leaves plant^{-1}, leaf length and breadth, plant girth and height, length, girth, core diameter and weight of mother, primary and secondary rhizomes, number of primary and secondary rhizomes plant^{-1}, yield plant^{-1}, plot^{-1} and ha^{-1}, incidence of rhizome rot, dry matter recovery and curcumin content.Genotypic and phenotypic variances were estimated according to Johnson et al. (1955). The genotypic and phenotypic coefficients of variation were calculated according to the formula suggested by Burton and De-Vane (1953). Heritability in broad sense was done according to Allard (1960). The expected genetic advance for different characters under selection was estimated using the formula suggested by Allard (1960). Genetic gain expressed as per cent ratio of genetic advance and population mean was calculated by the method given by Johnson et al. (1955).

3. RESULTS AND DISCUSSION

The results revealed highly significant differences for all the characters (Table 1 and 2). The germplasm provided wide variation for emergence (84.62–100.00), number of tillers (2.39–7.00) and leaves plant^{-1} (16.51–24.97), leaf length (48.49–76.43 cm) and breadth (11.83–18.64 cm), plant girth (9.04–28.70 cm) and height (95.73–144.85 cm), length (4.38–11.90 cm), girth (4.13–11.17 cm), core diameter (1.31–3.57 cm) and weight of mother rhizome (52.27–189.59 g),

Table 1: Mean performance of turmeric genotypes for growth, yield and quality characters

Genotype	Emergence (%)	No. of tillers-plant^{-1}	No. of leaves-plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Plant girth (mm)	Plant height (cm)	Yield			IRR	DMR	CC
								plant^{-1} (g)	plot^{-1} (kg)	ha^{-1} (t)			
ST10-01	95.83 (9.79)*	5.75	21.92	64.92	15.83	23.57	127.13	221.57	10.71	21.516	2.84 (1.68)*	16.84 (4.10)*	2.51 (1.58)*
ST10-02	97.91 (9.89)	6.37	24.68	76.43	18.64	26.13	143.16	243.18	12.53	25.159	1.42 (0.97)	20.44 (4.52)	3.11 (1.76)
ST10-03	96.87 (9.84)	6.06	22.84	62.33	15.20	24.85	132.47	257.56	12.51	251.32	2.13 (1.42)	19.48 (4.41)	2.26 (1.50)
ST10-04	94.79 (9.74)	5.44	19.34	55.60	13.56	22.29	112.18	200.46	10.21	20.498	4.21 (2.04)	16.04 (4.00)	6.30 (2.50)
ST10-05	97.91 (9.89)	6.37	23.55	67.20	16.39	26.13	136.60	219.64	10.68	21.462	1.42 (0.97)	20.04 (4.48)	2.53 (1.59)
ST10-06	98.96 (9.95)	6.69	20.02	57.99	14.14	27.42	116.12	197.17	10.23	20.545	0.71 (0.49)	18.60 (4.31)	4.58 (2.14)
ST10-07	88.54 (9.41)	3.56	19.97	55.97	13.65	14.60	115.83	176.56	8.96	18.007	8.38 (2.88)	21.56 (4.64)	2.71 (1.65)
ST10-08	89.58 (9.46)	3.87	23.22	66.53	16.23	15.88	134.65	222.66	10.83	21.764	7.95 (2.79)	21.32 (4.62)	2.36 (1.53)
ST10-09	94.79 (9.73)	5.44	19.48	51.69	12.61	22.29	112.97	200.24	10.36	20.820	4.21 (1.94)	17.16 (4.13)	3.89 (1.97)
ST10-10	95.83 (9.79)	5.75	21.36	62.80	15.32	23.57	123.87	195.58	9.48	19.045	3.17 (1.74)	16.24 (4.03)	5.29 (2.30)
ST10-11	93.75 (9.68)	5.13	23.19	69.02	16.83	21.01	134.50	262.88	12.84	25.802	5.25 (2.21)	17.48 (4.18)	2.70 (1.64)
ST10-12	95.83 (9.79)	5.75	20.10	58.00	14.15	23.57	116.58	199.06	10.11	18.309	3.17 (1.74)	17.32 (4.16)	4.90 (2.21)
ST10-13	91.67 (9.57)	4.50	23.08	64.40	15.71	18.45	133.87	228.57	11.78	23.666	6.67 (2.58)	16.28 (4.03)	3.25 (1.80)
ST10-14	94.79 (9.73)	5.44	22.23	68.03	16.59	22.29	128.93	325.54	16.63	33.403	4.21 (1.94)	16.84 (4.10)	1.53 (1.20)
ST10-15	96.87 (9.84)	6.06	21.28	62.53	15.25	24.85	123.40	375.09	18.75	37.676	2.46 (1.51)	21.08 (4.59)	3.30 (1.81)
ST10-16	97.92 (9.89)	6.38	22.14	65.07	15.87	26.14	128.41	250.26	12.70	25.507	1.42 (1.17)	17.48 (4.18)	2.09 (1.44)
ST10-17	94.79 (9.74)	5.44	19.30	54.32	13.25	22.29	111.93	183.69	9.12	18.315	4.21 (2.01)	16.60 (4.07)	3.63 (1.90)
ST10-18	93.75 (9.68)	5.12	19.89	55.79	13.61	21.01	115.35	211.14	10.39	20.873	5.25 (2.22)	20.36 (4.51)	2.89 (1.70)

IRR: Incidence of rhizome rot (%); DMR: Dry matter recovery (%); CC: Curcumin content (%)

Table 1: Continue...

Genotype	Emergence (%)	No. of tillers-plant^{-1}	No. of leaves-plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Plant girth (mm)	Plant height (cm)	Yield			IRR	DMR	CC
								plant^{-1} (g)	plot^{-1} (kg)	ha^{-1} (t)			
ST10-19	92.71 (9.63)	4.81	24.61	72.70	17.73	19.73	142.73	195.16	9.67	19.440	6.29 (2.49)	24.76 (4.98)	2.26 (1.50)
ST10-20	91.66 (9.57)	4.50	24.24	69.15	16.87	18.45	140.60	256.37	12.54	25.186	7.34 (2.69)	22.48 (4.74)	1.86 (1.36)
ST10-21	93.75 (9.68)	5.12	16.51	48.49	11.83	21.01	95.73	181.13	9.02	18.128	5.25 (2.22)	17.48 (4.18)	3.87 (1.97)
ST10-22	98.96 (9.95)	6.69	18.36	56.36	13.75	27.42	106.49	370.42	18.52	37.207	0.71 (0.49)	17.32 (4.16)	3.45 (1.86)
ST10-23	96.87 (9.84)	6.06	20.22	57.96	14.14	24.85	117.29	196.07	9.60	19.286	2.46 (1.25)	16.68 (4.08)	2.95 (1.72)
ST10-24	95.83 (9.79)	5.75	18.52	51.07	12.46	23.57	107.42	228.01	11.30	22.702	3.17 (1.74)	15.88 (3.98)	2.65 (1.63)
ST10-25	92.71 (9.63)	4.81---	19.23	55.67	13.58	19.73	111.53	234.87	11.59	23.291	4.96 (2.16)	15.52 (3.94)	5.45 (2.33)
ST10-26	97.91 (9.89)	6.37	18.39	52.00	12.68	26.13	106.65	204.69	10.43	20.967	1.42 (0.97)	15.64 (3.95)	5.16 (2.27)
ST10-27	100.00 (10.00)	7.00	22.34	64.98	15.85	28.70	129.60	427.18	20.51	41.198	0.00 (0.00)	16.64 (4.08)	3.39 (1.84)
ST10-28	98.96 (9.95)	6.69	21.89	62.39	15.22	27.42	126.97	222.86	11.04	22.186	0.71 (0.49)	15.88 (3.98)	3.09 (1.76)
ST10-29	94.79 (9.74)	5.44	23.17	62.11	15.15	22.29	134.37	205.42	10.65	21.402	4.21 (2.01)	17.32 (4.16)	2.77 (1.66)
ST10-30	95.83 (9.79)	5.75	23.78	67.74	16.52	23.57	137.94	233.50	12.06	24.222	3.17 (1.74)	20.20 (4.49)	2.73 (1.63)
ST10-31	91.66 (9.57)	4.50	20.42	58.81	14.34	18.45	118.43	180.59	9.16	18.409	7.34 (2.69)	19.12 (4.37)	4.65 (2.16)
ST10-32	92.71 (9.63)	4.81	20.92	58.47	14.26	19.73	121.33	230.10	11.42	22.949	6.29 (2.49)	16.36 (4.04)	2.94 (1.71)
ST10-33	84.62 (9.20)	2.39	20.83	56.04	13.67	9.04	120.80	202.55	10.51	21.121	9.77 (3.12)	15.96 (3.99)	4.33 (2.06)
ST10-34	92.71 (9.63)	4.81	22.47	64.27	15.68	19.73	130.32	216.63	10.88	21.858	6.29 (2.50)	21.60 (4.65)	1.92 (1.38)
ST10-35	95.83 (9.79)	5.75	21.23	62.53	15.25	23.57	123.15	206.32	10.37	20.827	2.50 (1.57)	16.00 (4.00)	2.17 (1.47)
ST10-36	95.83 (9.79)	5.75	23.51	67.05	16.35	23.57	136.33	254.04	12.75	25.614	3.17 (1.74)	17.00 (4.12)	2.78 (1.67)
ST10-37	94.79 (9.74)	5.44	24.97	70.40	17.17	22.29	144.85	230.19	11.66	23.425	4.21 (2.01)	16.68 (4.08)	3.12 (1.76)
ST10-38	96.87 (9.84)	6.06	19.69	59.07	14.41	24.85	114.21	181.27	9.06	18.208	2.13 (1.43)	16.44 (4.05)	4.05 (2.01)
Palam Lalima	95.83 (9.79)	5.75	23.80	70.13	17.11	23.57	138.01	323.95	16.51	33.175	2.84 (1.66)	20.68 (4.55)	3.57 (1.87)

IRR: Incidence of rhizome rot (%); DMR: Dry matter recovery (%); CC: Curcumin content (%)

Table 1: Continue...

Genotype	Emergence (%)	No. of tillers plant^{-1}	No. of leaves plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Plant girth (mm)	Plant height (cm)	Yield			IRR	DMR	CC
								plant^{-1} (g)	plot^{-1} (kg)	ha^{-1} (t)			
Palam Pitambar	96.87 (9.84)	6.06	20.28	61.79	15.07	24.85	117.65	360.41	18.27	36.704	2.13 (1.46)	18.92 (4.35)	2.98 (1.71)
Mean	94.95	5.49	21.42	61.70	15.05	22.47	124.26	237.82	11.91	23.875	3.89	18.14	3.30
Range	84.62–100.00	2.39–7.00	16.51–24.97	48.49–76.43	11.83–18.64	9.04–28.70	95.73–144.85	176.56–427.18	8.96–20.51	18.007–41.198	0.00–9.77	15.52–24.76	1.53–6.30
SEm±	(0.08)	0.46	0.98	2.69	0.86	1.84	5.38	12.13	0.55	1.156	(0.33)	(0.07)	(0.09)
CD (p=0.05)	(0.22)	1.30	2.79	7.61	2.43	5.20	15.22	34.35	1.56	3.273	(0.93)	(0.20)	(0.25)

IRR: Incidence of rhizome rot (%); DMR: Dry matter recovery (%); CC: Curcumin content (%); *Figures in the parenthesis are square root transformed values

Table 2: Mean performance of turmeric genotypes for rhizome characters

Genotype	Mother rhizome					Primary rhizome					Secondary rhizome			
	L	G	CD	W	NP	L	G	CD	W	NP	L	G	CD	W
ST10-01	7.03	6.49	2.11	75.03	10.50	6.86	10.42	3.27	163.64	8.40	5.48	8.09	2.61	57.93
ST10-02	6.59	6.12	1.98	69.57	11.75	7.32	10.81	3.49	175.46	9.40	6.20	9.37	2.95	67.72
ST10-03	7.90	7.51	2.37	86.86	11.12	7.74	11.44	3.69	186.40	8.90	6.42	9.76	3.05	71.16
ST10-04	5.79	5.47	1.74	61.72	9.87	5.71	8.60	2.72	139.46	7.90	5.72	8.48	2.72	61.00
ST10-05	7.03	6.64	2.11	75.39	11.75	6.81	10.22	3.24	163.37	9.40	5.34	8.12	2.54	56.27
ST10-06	5.26	4.89	1.58	57.40	12.37	5.73	8.46	2.73	140.07	9.90	5.41	7.89	2.58	57.10
ST10-07	5.14	4.84	1.54	56.62	6.12	5.57	8.40	2.65	137.32	4.90	3.58	5.45	1.70	39.24
ST10-08	6.35	5.98	1.90	66.91	6.75	6.79	10.05	3.23	162.90	5.40	5.63	8.35	2.68	59.76
ST10-09	5.78	5.48	1.73	61.88	9.87	6.14	9.25	2.92	147.88	7.90	4.94	7.32	2.35	52.36
ST10-10	6.04	5.65	1.81	64.07	10.50	5.88	8.73	2.80	144.20	8.40	4.90	7.16	2.33	51.37
ST10-11	8.08	7.58	2.42	90.13	9.25	8.03	11.61	3.83	192.88	7.40	6.41	9.48	3.05	70.01
ST10-12	6.28	5.86	1.88	66.79	10.50	5.87	8.57	2.79	142.66	8.40	5.35	7.95	2.55	56.40
ST10-13	7.18	6.66	2.15	77.14	8.00	6.71	10.14	3.20	160.13	6.40	6.29	9.17	3.00	68.44
ST10-14	10.26	9.62	3.08	136.95	9.87	8.45	12.56	4.02	204.85	7.90	9.33	14.05	4.44	120.70
ST10-15	7.95	7.39	2.39	88.45	11.12	11.69	17.47	5.57	313.16	8.90	5.79	8.71	2.76	61.93
ST10-16	6.47	6.09	1.94	68.22	11.75	7.79	11.48	3.71	186.56	9.40	5.93	8.70	2.82	63.71
ST10-17	5.28	5.04	1.58	58.16	9.87	5.80	8.74	2.76	141.35	7.90	3.96	5.82	1.89	42.34
ST10-18	6.32	5.97	1.89	68.07	9.25	6.26	9.42	2.98	150.57	7.40	5.70	8.42	2.71	60.57
ST10-19	5.88	5.46	1.76	62.42	8.62	6.33	9.40	3.02	151.91	6.90	4.08	5.93	1.94	43.25
ST10-20	8.48	8.05	2.54	97.51	8.00	8.25	12.50	3.93	199.64	6.40	5.38	8.18	2.56	56.73
ST10-21	4.38	4.13	1.31	52.27	9.25	5.21	7.69	2.48	130.22	7.40	4.86	7.37	2.31	50.91
ST10-22	6.61	6.23	1.98	69.60	12.37	11.66	17.44	5.55	312.31	9.90	5.48	8.20	2.61	58.11
ST10-23	6.11	5.86	1.83	64.62	11.12	5.79	8.80	2.76	141.08	8.90	5.23	7.92	2.49	54.98

L: Length (cm); G: Girth (cm); CD: Core diameter (cm); W: Weight (g); NP: No. plant^{-1}

Table 2: Continue...

Genotype	Mother rhizome					Primary rhizome					Secondary rhizome			
	L	G	CD	W	NP	L	G	CD	W	NP	L	G	CD	W
ST10-24	6.70	6.20	2.01	71.04	10.50	6.00	8.77	2.86	145.11	8.40	7.26	10.96	3.46	82.90
ST10-25	7.99	7.59	2.40	88.53	8.62	6.33	9.33	3.01	151.81	6.90	7.26	10.92	3.46	83.06
ST10-26	6.89	6.54	2.07	73.16	11.75	5.73	8.43	2.73	139.73	9.40	6.03	8.88	2.97	64.96
ST10-27	11.90	11.17	3.57	189.59	13.00	12.82	19.24	6.10	361.78	10.40	6.06	9.09	2.88	65.41
ST10-28	7.75	7.30	2.33	84.60	12.37	6.49	9.63	3.09	155.57	9.90	6.20	9.34	2.95	67.29
ST10-29	7.06	6.65	2.12	75.93	9.87	6.22	9.17	2.96	149.65	7.90	5.30	7.79	2.52	55.77
ST10-30	7.05	6.64	2.12	74.92	10.50	7.27	10.74	3.46	173.19	8.40	5.66	8.56	2.70	60.31
ST10-31	5.36	5.15	1.61	58.58	8.00	5.39	8.19	2.57	135.04	6.40	4.30	6.50	2.05	45.54
ST10-32	6.65	6.33	2.00	70.69	8.62	6.43	9.48	3.06	154.22	6.90	6.81	10.08	3.24	75.87
ST10-33	6.63	6.24	1.99	70.77	3.77	5.98	8.91	2.85	144.82	3.02	5.45	8.05	2.60	57.73
ST10-34	7.05	6.77	2.11	75.19	8.62	6.69	9.77	3.19	159.98	6.90	5.34	8.08	2.54	56.65
ST10-35	6.66	6.28	2.00	71.61	10.50	6.26	9.46	2.98	150.53	8.40	5.30	7.82	2.52	55.79
ST10-36	8.28	7.89	2.48	94.50	10.50	7.88	11.92	3.75	189.40	8.40	6.00	9.00	2.86	64.64
ST10-37	8.23	7.78	2.47	92.35	9.87	6.92	10.41	3.30	164.81	7.90	6.05	9.11	2.98	65.38
ST10-38	5.68	5.51	1.70	60.94	11.12	5.57	8.43	2.65	136.81	8.90	4.21	6.36	2.00	44.47
Palam Lalima	8.41	7.86	2.52	95.73	10.50	10.10	15.07	4.81	255.59	8.40	6.29	9.34	3.00	68.36
Palam Pitambar	9.10	8.44	2.73	109.56	11.12	10.80	16.22	5.14	279.69	8.90	7.11	10.56	3.39	80.72
Mean	6.99	6.58	2.10	78.34	9.97	7.13	10.63	3.40	175.89	7.98	5.70	8.51	2.72	61.92
Range	4.38–11.90	4.13–11.17	1.31–3.57	52.27–189.59	3.77–13.00	5.21–12.82	7.69–19.24	2.48–6.10	130.22–361.78	3.02–10.40	3.58–9.33	5.45–14.05	1.70–4.44	39.24–120.70
SEm±	0.37	0.38	0.12	5.84	0.92	0.36	0.54	0.18	10.20	0.73	0.28	0.42	0.14	3.85
CD (*p*=0.05)	1.05	1.09	0.33	16.53	2.59	1.02	1.53	0.50	28.89	2.08	0.80	1.20	0.39	10.91

L: Length (cm); G: Girth (cm); CD: Core diameter (cm); W: Weight (g); NP: No. plant^{-1}

length (5.21–12.82 cm), girth (7.69–19.24 cm), core diameter (2.48–6.10 cm) and weight of primary rhizome (130.22–361.78 g) and length (3.58–9.33 cm), girth (5.45–14.05 cm), core diameter (1.70–4.44 cm) and weight of secondary rhizomes (39.24–120.70 g), number of primary (3.77–13.00) and secondary rhizomes plant^{-1} (3.02–10.40), yield plant^{-1} (176.56–427.18 g), plot^{-1} (8.96–20.51 g), ha^{-1} (180.07–411.98), incidence of rhizome rot (0.00%–9.77%), dry matter recovery (15.52%–24.76%) and curcumin content (1.53%–6.30%) which warrants the scope for isolating the genotypes on the basis of these characters.

The estimates of variability parameters viz. range, coefficients of variation (GCV and PCV), heritability (broad sense), genetic advance and genetic gain were worked out andpresented in Table 3. Significant differences were found among the genotypes for all the characters studied.

A rough estimate of degree of variation can be made from the range but the coefficients of variation are more reliable. The estimates of phenotypic and genotypic coefficients of variability gave a clear picture of amount of variations present in the available germplasm. For all the characters studied, phenotypic coefficients of variability were higher in magnitude than genotypic coefficients of variability, though differences were very less in majority of the cases. Thus, showing that these traits are lesser influenced by environmental factors. Coefficients of variability varied in magnitude from character to character (either low or moderate or high). Therefore, it indicated that there was a great diversity in the experimental material used.

The phenotypic coefficients of variability (PCV) were found high for incidence of rhizome rot, curcumin content, weight of mother and primary rhizomes. This reflects greater genetic variability among the genotypes for these

Table 3: Estimates of phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain for different traits in ginger

Characters	Range	Mean±SE(m)	Coefficients of variability (%)		Heritability (%)	Genetic advance	Genetic gain (%)
			Phenotypic	Genotypic			
1. Emergence (%)	84.62– 100.00	94.95±0.08	3.94	2.81	51.00	3.93	4.14
2. No. of tillers plant^{-1}	2.39– 7.00	5.49±0.46	20.50	14.54	50.30	1.17	21.31
3. No. of leaves plant^{-1}	16.51– 24.97	21.42±0.98	11.55	8.38	52.60	2.68	12.51
4. Leaf length (cm)	48.49– 76.43	61.70±2.69	12.09	9.45	61.10	9.39	15.22
5. Leaf breadth (cm)	11.83– 18.64	15.05±0.86	13.16	8.71	43.80	1.79	11.89
6. Plant girth (cm)	9.04– 28.70	22.47±1.84	20.63	15.01	53.00	5.06	22.52
7. Plant height (cm)	95.73– 144.85	124.26±5.38	11.34	8.52	56.30	16.35	13.16
8. i) Length of mother rhizome (cm)	4.38– 11.90	6.99±0.37	21.83	19.78	82.10	2.58	36.91
ii) Girth of mother rhizome (cm)	4.13–11.17	6.58±0.38	21.92	19.44	78.70	2.34	35.56
iii) Core diameter of mother rhizome (cm)	1.31–3.57	2.10±0.12	21.88	19.71	81.10	0.77	36.67
iv) Weight of mother rhizome (g)	52.27–189.59	78.34±5.84	32.85	30.21	84.60	44.85	57.25
9. i) Number of primary rhizome plant^{-1}	3.77–13.00	9.97±0.92	22.58	16.01	50.30	2.33	23.37
ii) Length of primary rhizome (cm)	5.21–12.82	7.13±0.36	26.99	25.53	89.50	3.55	49.79
iii) Girth of primary rhizome (cm)	7.69–19.24	10.63±0.54	27.18	25.71	89.40	5.32	50.05
iv) Core diameter of primary rhizome (cm)	2.48–6.10	3.40±0.18	27.03	25.45	88.70	1.68	49.41
v) Weight of primary rhizome (g)	130.22–361.78	175.89±10.20	31.85	30.22	90.00	103.85	59.04
10. i) Number of secondary rhizome plant^{-1}	3.02– 10.40	7.98±0.73	22.58	15.99	50.10	1.86	23.31
ii) Length of secondary rhizome (cm)	3.58– 9.33	5.70±0.28	19.42	17.40	80.30	1.83	32.11
iii) Girth of secondary rhizome (cm)	5.45– 14.05	8.51±0.42	19.63	17.63	80.70	2.78	32.67
iv) Core diameter of secondary rhizome (cm)	1.70–4.44	2.72±0.14	19.47	17.43	80.10	0.87	31.99
v) Weight of secondary rhizome (g)	39.24–120.70	61.92±3.85	24.33	21.82	80.40	24.95	40.29
11. i) Yield plant^{-1} (g)	176.56–427.18	237.82±12.13	26.11	24.56	88.50	113.18	47.59
ii) Yield plot^{-1} (kg)	8.96–20.51	11.91±0.55	25.54	24.24	90.10	5.64	47.36
iii) Yield ha^{-1} (t)-Converted	18.007–41.198	23.875±1.156	2.582	2.442	8.950	11.366	4.761
12. Incidence of rhizome rot (%)	0.00–9.77	3.89±0.33	72.47	53.84	55.20	3.21	82.52
13. Dry matter recovery (%)	15.52–24.76	18.14±0.07	13.34	12.09	82.10	4.09	22.55
14. Curcumin content (%)	1.53–6.30	3.30±0.09	35.90	31.52	77.10	1.88	56.97

characters for making further improvement by clonal selection. Whereas, moderate PCV were recorded for length, girth and core diameter of mother, primary and secondary rhizomes, yield plant^{-1}, plot^{-1} and ha^{-1}, weight of secondary rhizome, number of primary and secondary rhizomes plant^{-1}, plant girth and number of tillers plant^{-1}. For dry matter recovery, leaf length and breadth, number of leaves plant^{-1}, plant height and emergence, phenotypic coefficients of variability (PCV) were low in magnitude. Similar results were reported by Babuet al. (1993) and Singh et al. (2003). Sinkar et al. (2005) also reported high PCV for curcumin content. However, in contradictory to present studies, Babu et al. (1993) found high PCV for number of tillers and secondary rhizomes plant^{-1}, weight of secondary rhizome and yield plot^{-1} and Singh et al. (2003) found high PCV for number of secondary rhizomes plant^{-1}, length of primary and secondary rhizomes, girth, core diameter and weight of secondary rhizome and moderate PCV for plant height and number of leaves plant^{-1}. The genotypic coefficients of variability (GCV) were high for incidence of rhizome rot, curcumin content, weight of mother and primary rhizomes. This reflects existence of genetic variability among the genotypes for these characters for making further improvement through clonal selection. Whereas, moderate GCV were recorded for length, girth and core diameter of mother, primary and secondary rhizomes, yield plant^{-1}, plot^{-1} and ha^{-1}, weight of secondary rhizome, number of primary and secondary rhizomes plant^{-1} and plant girth. For number of tillers and leaves plant^{-1}, dry matter recovery, leaf length and breadth, plant height and emergence, GCV were low. Similar results were reported by Babu et al. (1993) and Singh et al. (2003). It is also reported that moderate GCV for width and length of rhizome. High GCV for curcumin content similar to present study is reported by Sinkar et al. (2005). In contradictory to present studies, Babu et al. (1993) found high GCV for number and weight of secondary rhizomes plant^{-1}, whereas, moderate GCV for number of tillers plant^{-1} and Singh et al. (2003) found high GCV for length of primary rhizome, number plant^{-1}, girth, core diameter and weight of secondary rhizomes and moderate GCV for plant height, number of tillers and leaves plant^{-1}. This may be due to different experimental material studied under different environmental conditions. The genotypic coefficient of variation does not offer full scope to estimate the variations that are heritable and therefore, estimation of heritability becomes necessary. The success of any selection programme depends upon the extent of heritability as well as on genetic gain which usually changes from population to population and environment to environment. Burton (1952) and Burton and De-Vane (1953) was of the opinion that the genetic coefficients of variation along with heritability gave the best picture of genetic advance to be expected from selection whereas, Johnson et al. (1955) advocated that heritability together with genetic advance is more useful than the heritability alone in predicting the resultant effect in selecting best individual.

The estimates of heritability (broad sense) were found high for the characters viz. yield plant^{-1}, plot^{-1} and ha^{-1}, length, girth, core diameter and weight of primary and secondary rhizomes, length, core diameter and weight of mother rhizome and dry matter recovery and moderate for girth of mother rhizome, curcumin content, leaf length, plant girth and height, incidence of rhizome rot, number of tillers and leaves plant^{-1}, emergence, number of primary and secondary rhizomes plant^{-1}, while, it was low for leaf breadth only. The results of present findings are in line with those reported by Singh et al. (2003) who revealed high heritability estimates for length of mother and secondary rhizomes, girth of primary and secondary rhizomes, core diameter and weight of mother, primary and secondary rhizomes and yield ha^{-1}; Babu et al. (1993) who reported high heritability for weight of secondary rhizome and moderate heritability for plant girth and height, number and length of leaves and number of primary rhizomes and low for leaf breadth, length and width of rhizomes showed high heritability; Lynrah et al. (1998) who reported that mother and finger rhizome yield components showed high broad-sense heritability; Jana et al. (2001) reported that yield ha^{-1} and weight of secondary fingers clump^{-1} showed high magnitude of heritability; Chattopadhyay et al. (2004) also reported that weight of secondary rhizome have high heritability; Singh et al. (2012) reported high heritability estimates for weight of mother, fresh and secondary rhizomes per plant, length and width of mother rhizome, rhizome girth and dry matter recovery. In the light of results obtained in the present studies, it is concluded that selection can be performed at phenotypic performance for highly heritable characters *viz.* length, core diameter and weight of mother, primary and secondary rhizomes, girth of primary and secondary rhizomes, yield plant^{-1}, plot^{-1} and ha^{-1} and dry matter recovery.

Genetic gain (expressed as % of population mean) was low to high in nature for different characters. It was found high for incidence of rhizome rot, weight of primary and mother rhizomes, curcumin content and girth of primary rhizome. Moderate genetic gain was observed for length and core diameter of mother, primary and secondary rhizomes, girth of mother and secondary rhizomes, weight of secondary rhizome and yield plant^{-1},plot^{-1} and ha^{-1}. Whereas, it was recorded low for number of primary and secondary rhizomes plant^{-1}, dry matter recovery, plant girth and height, number of tillers and leaves plant^{-1}, leaf length and breadth, and emergence. These findings are in line with Babu et al. (1993). Singh et al. (2003) who also reported high genetic gain for weight of mother and primary rhizomes and moderate genetic gain for length, girth and core diameter of mother rhizome and yield ha^{-1}. In contradictory to present studies, Babu et al. (1993) reported high genetic gain for number and weight of secondary rhizomes and moderate genetic gain for plant girth and number of primary rhizomes. This may be due to different environmental conditions and experimental material used.

High heritability estimates coupled with high genetic gain were observed for weight of mother and primary rhizomes and girth of primary rhizome which indicated that these characters are under additive gene effects and are more reliable for effective clonal selection (Panse, 1957). Similar results for weight of mother and primary rhizomes have been reported by Singh et al. (2003). High heritability coupled with moderate genetic gain was observed for length and core diameter of mother, primary and secondary rhizomes, girth and weight of secondary rhizomes, yield plant^{-1}, plot^{-1} and ha^{-1} which indicated that clonal selection for these characters can also be effective. Similar results were reported by Singh et al. (2003) for length and core diameter of mother rhizome and yield ha^{-1} and Singh et al. (2003) also reported similar results for length and core diameter of mother rhizome.

4. CONCLUSION

High GCV and PCV for weight of mother and primary rhizomes, rhizome rot and curcumin, indicated wide range of variations. High heritability coupled with high genetic gain were estimated for weight of mother and primary rhizomes and girth of primary rhizome, whereas high heritability coupled with moderate genetic gain for length and core diameter of mother, primary and secondary rhizomes, girth and weight of secondary rhizome and yield indicated that clonal selection for these characters can be effective.

5. REFERENCES

Akter, J., Hossain, M.A., Takara, K., Islam, M.Z., Hou, D.X., 2019. Antioxidant activity of different species and varieties of turmeric (*Curcuma* spp): Isolation of active compounds. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology 215, 9–17.

Allard, R.W., 1960. Principles of plant breeding. John Wiley and sons, New York, 485.

Anonymous, 2009. Package of practices for vegetable crops. Directorate of extension education, Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, 202.

Anonymous, 2019. Indian horticulture database. Available at http://www.nhb.gov.in. Accessed on 27th May, 2019.

Anonymous, 2021. Turmeric Outlook June 2021. Available at.https://pjtsau.edu.in/files/AgriMkt/2021/june/Turmeric-june-2021.pdf. Accessed on 27th May, 2021.

Arya, N., Prakash, O., Kumar, S., Pant, A.K., 2016. Curcumin profiling and genetic diversity of different accessions of *Curcuma longa* L. Asian Pacific Journal of Tropical Disease 6, 70–74. https://doi.org/10.1016/S2222-1808(15)60987-2.

Babu, K.N., Sasikumar, B., Ratnambal, M.J., George, J., Ravindran, P.N., 1993. Genetic variability in turmeric (*Curcuma longa* L.). Indian Journal of Genetics and Plant Breeding 53, 91–93.

Burton, G.W., 1952. Quantitative inheritance in grasses. In: Proceeding of the 6th International Grassland Congress 1, 277–278.

Burton, G.W., De-Vane, E.W., 1953. Estimating heritability in tall fescue (*Festuca arundiancea*) from replicated clonal material. Proejtunniens9, 12–15.

Chattopadhyay, N., Hore, J.K., Bandopadhyay, A., 2004. A Studies on character association and genetic variability in turmeric. Horticultural Journal 17, 259–266.

Ciavarella, C., Motta, I., Valente, S., 2020. Pharmacological (or synthetic) and nutritional agonists of PPAR-γ as candidates for cytokine storm modulation in COVID-19 disease. Molecules 25, 2076.

Dey, S., Kumar, R., Battan, K.R., Chhabra, A.K., Reddy, A.L., 2021. Study of coefficient of variation, heritability and genetic advance for different traits of rice genotypes grown under aerobic condition. International Journal of Bio-resource and Stress Management 12(5), 426–430.

Gomes, A.F., Almeida, M.P., Leite, M.F., Schwaiger, S., Stuppner, H., Halabalaki, M., Amaral, J.G., David, J.M., 2019. Seasonal variation in the chemical composition of two chemotypes of *Lippia alba*. Food Chemistry 273, 186–193.

Gomes, A.F., Ganzera, M., Schwaiger, S., Stuppner, H., Halabalaki, M., Almeida, M.P., Leite, M.F., Amaral, J.G., David, J.M., 2018. Simultaneous determination of iridoids, phenylpropanoids and flavonoids in *Lippia alba* extracts by micellar electrokinetic capillary chromatography. Microchemical Journal 138, 494–500.

Gupta, S.C., Sung, B., Kim, J.H., Prasad, S., Li, S., Aggarwal, B.B., 2013. Multitargeting by turmeric, the golden spice: From kitchen to clinic. Molecular Nutrition and Food Research 57(9), 1510–1528.

Jan, H.U., Rabbani, M.A., Shinwari, Z.K., 2012. Estimation of genetic variability in turmeric (*Curcuma longa* L.) germplasm using agromorphological traits. Journal of Botany 44, 231–238.

Jana, J.C., Dutta, S., Chatterjee, R., 2001. Genetic variability, heritability and correlation studies in turmeric (*Curcuma longa* L.). Research on Crops 2, 220–225.

Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybean. Agronomy Journal 47, 314–318.

Kocaadam, B., Anlier, N., 2017. Curcumin, an active component of turmeric (*Curcuma longa*), and its effects on health. Critical Reviews in Food Science and Nutrition 57, 2889–2895.

Kumar, B., Singh C.M., Jaiswal, K.K., 2013. Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). Bioscan 8, 143-47.

Kumar, R., 2014. Evaluation of chrysanthemum genotypes for flowering traits under open grown condition. Journal of Ornamental Horticulture 3(4), 388–389.

Kumari, P., Kumar, R., Rao, T.M., Dhananjay, M.V., Bhargav, V., 2017. Genetic variability, character association and path coefficient analysis in China aster (*Callistephus chinensis* L.). Journal of Horticultural Sciences 7(2), 3353–3362.

Lynrah, P.G., Barua, P.K., Chakrabarty, B.K., 1998. Pattern of genetic variability in a collection of turmeric (*Curcuma* spp.) genotypes. Indian Journal of Genetics and Plant Breeding 58, 201–207.

Panse, V.S., 1957. Genetics of quantitative characters in relation to plant breeding. Indian Journal of Geneticsand Plant Breeding 17, 318–328.

Prasad, S., Tyagi, A.K., 2015. Curcumin and its analogues: A potential natural compound against HIV infection and AIDS. Food Function 6, 3412–3419.

Ravishanker, Kumar, S., BaranwalD.K.,Chatterjee, A. and Solankey, S.S., 2013. Genetic diversity based on cluster and principal component analyses for yield and quality attributes in ginger (*Zingiber officinale* Roscoe). International Journal of Plant Breeding and Genetics 7(3), 159–168. DOI: 10.3923/ijpbg.2013.159.168.

Sandeep, I.S., Kuanar, A., Akbar, A., Kar, B., Das, S., Mishra, A., Sial, P., Naik, P.K., Nayak, S., Mohanty, S., 2016. Environmental factors influencing yield and quality of essential oils in *Curcuma Longa* cv. Lakadong. In: Proceedings of the National Academy of Sciences, India- Section B. Biological Studies 85, 229.

Siju, S., Dhanya, K., Syamkumar, S., Sasikumar, B., Sheeja, T.E., Bhat, A.I., Parthasarathy, V.A., 2010. Development, characterization and cross species amplification of polymorphic microsatellite markers from expressed sequence tags of turmeric (*Curcuma longa* L.). Molecular Biotechnology 44, 140–147.

Simmonds, N.M., 1962. Variability in crop plants, its use and conservation. Botanical Review 37, 422–465.

Singh, Y., Mittal, P., Katoch, V., 2003. Genetic variability and heritability in turmeric (*Curcuma longa* L.). Himachal Journal of Agricultural Research 29, 31–34.

Sigrist, M.S., Pinheiro, J.B., Filho Azevedo, J.A., Zucchi, M.I., 2012. Genetic diversity of turmeric germplasm (*Curcuma longa*; Zingiberaceae) identified by microsatellite markers. Genetics and Molecular Research 10, 419–428. https://doi.org/10.4238/vol10-1gmr1047.

Sinkar, P.V., Haldankar, P.M., Khandekar, R.G., Ranpise, S.A., Joshi, G.D., Mahale, B.B., 2005. Preliminary evaluation of turmeric (*Curcuma longa* L.) varieties at Konkan region of Maharashtra. Journal of Spices and Aromatic Crops 14, 28–33.

Tanvir, E.M., Afroz, R., Karim, N., 2015. Antioxidant and antibacterial activities of methanolic extract of BAU kul (*Ziziphus mauritiana*), an improved variety of fruit from Bangladesh. Journal of Food Biochemistry 39, 139–147.

Tanvir, E.M., Hossen, M.S., Hossain, M.F., Afroz, R., Gan, S.H., Khalil, M.I., Karim, N., 2017. Antioxidant properties of popular turmeric (*Curcuma longa*) varieties from Bangladesh. Journal of Food Quality. 2017, 1–8.

Tomeh, M.A., Hadianamrei, R., Zhao, X., 2019. A review of curcumin and its derivatives as anticancer agents. Molecular Science 20, 1–26. DOI https://doi.org/10.3390/ijms20051033.

Xiang, Z., Wang, X.Q., Cai, X.J., Zeng, S.U., 2012. Metabolomics study on qualitycontrol and discrimination of three curcuma species based on gaschromatograph-mass spectrometry: metabolomics quality control and discrimination of curcuma. Phytochemical Analysis 22, 411–418.