



## **Patterns in genetic variation and character association of yield components in turmeric (*Curcuma longa* L.)**

Raghuv eer Silaru<sup>1,2</sup>, Yuvaraj Kotha Madduri<sup>2</sup>, Aarthi Sounderarajan<sup>1</sup> & Prasath Duraisamy<sup>1\*</sup>

<sup>1</sup>ICAR-Indian Institute of Spices Research, Kozhikode, Kerala.

<sup>2</sup>Dr. YSRHU College of Horticulture, Anantharajupeta, Andhra Pradesh.

Email: dprasath@gmail.com

Received 01 June 2023; Revised 21 June 2023; Accepted 30 June 2023.

---

### **Abstract**

Understanding genetic variability patterns of turmeric yield traits is essential to develop new genotypes with improved traits. The objective of the present study was to investigate the genetic variability, heritability, genetic advance and association of various yield components in turmeric genotypes. The experiment was conducted for two seasons during 2021-22 and 2022-23 using 21 turmeric genotypes at ICAR-IISR, Experimental farm, Peruvannamuzhi, Kerala. The results indicate that the genotypes exhibited significant variation across two seasons for most traits, with the exception of collar girth, weight of primary rhizomes per clump, and number of primary rhizomes per clump, which suggests the presence of genetic variability in the genotypes. Maximum fresh rhizome yield per clump was recorded in the genotype, IISR Pragati. The Genotypic Coefficient of Variation (GCV) was found to be moderate to high for most of the traits except plant height, leaf lamina length, collar girth and fresh rhizome yield per plant, whereas, Phenotypic Coefficient of Variation (PCV) was found to be moderate to high for all the traits except plant height. Heritability was observed moderate to high for all the traits except collar girth, number of primaries per clump, weight of primary rhizomes per clump and fresh rhizome yield per plant. The petiole length, total leaf area, weight of mother rhizomes per clump and number of mother rhizomes per clump showed high heritability along with genetic advance. Correlation analysis suggested that weight of mother rhizomes per clump had a strong positive association with plant height, number of leaves, leaf lamina length, leaf lamina width, leaf area, total leaf area, and collar girth and had a weak positive relationship with fresh rhizome yield per plant and petiole length. The path analysis revealed, total leaf area, fresh rhizome yield per plant and number of primaries per clump have high direct positive effects with weight of mother rhizomes per clump. The high heritability and genetic advance observed for above mentioned traits suggest that exercising a simple selection could indirectly improve the low heritable, low genetic advance traits such as fresh rhizome yield per plant as indicated by correlation and path analysis.

**Keywords:** Correlation, genetic variability, heritability, path analysis

---

## Introduction

Turmeric (*Curcuma longa* L.) is an important spice crop in the family Zingiberaceae. India leads in terms of turmeric production, consumption and export. Maximum area and production in India were reported from Maharashtra (84,000 ha and 2.78 million tons) followed by Telangana (40,000 ha and 2.50 million tons) (Spices Board, 2023). Turmeric is valued for its culinary, medicinal and therapeutic properties such as antimutagenic, antimicrobial, antioxidant, chemopreventive, bioprotectant, anti-angiogenic, anticancer, antithrombotic, hepatoprotective, anti-inflammatory, hypoglycaemic properties and immune modulatory potential (Iweala *et al.*, 2023; Jyotirmayee & Mahalik 2022; Razavi *et al.*, 2021). Apart from this, natural colours extracted from turmeric is being used in the textile industry, food industry, confectionary, cosmetics and pharma industry (Dawson 2009; Bijauliya *et al.*, 2017; Dey & Nagababu 2022; Kaur & Chopra 2023).

Turmeric is mainly regarded as triploid ( $2n = 63$ ) which has a speculated origin by dibasic amphiploidy or secondary polyploidy. Even though the crop has the ability to set true seed and germinate well, its commercial cultivation relies on propagation by means of seed rhizomes (Nair and Sasikumar 2009). Crop improvement in turmeric mainly depends on identifying variability through germplasm selection, polyploidy, and mutation breeding. Wide genetic diversity has been reported in turmeric earlier by several researchers (Ratnambal & Nair 1986; Sasikumar 2005; Gupta *et al.*, 2015 and Prasath *et al.*, 2016). The yield in turmeric is the most complex trait influenced by multiple factors viz.,

genetic and environment (Prasath *et al.*, 2014). Information related to genetic variability parameters such as GCV and PCV and heritability on morphological and yield traits is the key for developing an efficient breeding strategy in turmeric. Correlation analysis helps in understanding the association of two or more variables and also the magnitude of the association. It gives valuable insights for plant breeders to identify the most important traits for improving overall yield. This study was conducted to understand the genetic variability of traits influencing the yield components and their association. The findings from this study will provide valuable insights for future breeding programs focused on improving yield in turmeric.

## Materials and methods

Experiment was conducted using 21 turmeric genotypes (IISR Pragati, IISR Prathiba, IISR Alleppey Supreme, Rajendra Sonali, Megha Turmeric 1, Waigon Turmeric, Roma, CIM Pitambar, Uttar Rangini, Chhattisgarh Haldi 2, NDH 8, Co 3, Acc. 1545, Erode Local, Mydukur Local, Acc. 849, Acc. 379, Acc. 14, Acc.179, Acc. 214 and Acc. 69/5/22/13) collected from National Active Germplasm Site, ICAR- Indian Institute of Spices Research (ICAR-IISR), Kozhikode, Kerala. The experiment was laid following randomised completely block design with two replicates at ICAR-IISR Experimental Farm, Peruvannamuzhi (11°36'34"N, 75°49'12"E), Kozhikode, Kerala for two seasons during 2021-22 and 2022-23. The experimental plot was maintained by following the standard turmeric management practices (Prasath *et al.*, 2022). Observations on 15 different

morphological and yield characters were recorded based on Distinctness, Uniformity and Stability (DUS) guidelines (PPV & FRA 2009).

All the statistical analysis viz., ANOVA genetic variability, correlation (Pearson's) and path analysis were carried out using Rstudio developed by the R Core Team (2022). Variability parameters like phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated according to Burton (1952, 1953) and categorised (Sivasubramanian and Menon 1978). Broad-sense heritability (H<sup>2</sup>) was measured as per Lush (1940) and categorised (Robinson 1966). Genetic advance (GA) and genetic advance over mean (GAM) was estimated and categorised (Johnson *et al.*, 1955). ANOVA and genetic variability parameters were measured using "TraitStats" package (Devaraja *et al.*, 2022). Simple correlation coefficient (Pearson's) among the characters and path analysis (Wright 1921; Dewey & Lu 1959) were measured using "Metan" package (Olivoto & Lúcio 2020).

### Results and discussion

The mean performance of 21 genotypes was evaluated for two seasons (2021-22 and 2022-23) which has been summarized in Table 1. The results revealed that the genotype, Roma (149.90 cm) recorded maximum plant height followed by Erode Local (143.43 cm), Megha Turmeric 1 (137.98 cm) and Acc. 1545 (137.90 cm). The Acc. 1545 and Roma also recorded the maximum petiole length (26.49 cm), leaf lamina length (68.61 cm) and leaf area (817.38 cm). Acc. 849 produced highest number of leaves (11.73) along with leaf lamina width (17.13 cm) and total leaf area (9183.34 cm<sup>2</sup>). The tiller

number per plant was found to be maximum in IISR Alleppey Supreme (4.53). Number of primary rhizomes per clump was maximum in Megha Turmeric 1 (12.50) whereas, maximum number of mother rhizomes per clump was recorded in Acc. 1545 (2.83) and weight of mother rhizomes in Acc. 849 (177.19 g). The weight of primary rhizomes per clump and fresh rhizome yield per clump showed non-significant differences among the genotypes. The maximum fresh rhizome yield per clump was recorded in IISR Pragati (635.96 g). High genetic variation among the genotypes offers scope for crop improvement through selection. The findings of this study are in agreement with previous reports of Kandiannan *et al.* (2015); Aarthi *et al.* (2018); Vinodhini *et al.* (2019) and Suresh *et al.* (2020), where high genetic variability for yield and yield-contributing characteristics in turmeric were reported.

The combined analysis of variance for morphological and yield traits over a period of two years is given in Table 2. Significant variation was observed for most traits among the genotypes over the two-year period, indicating that genotypes are divergent and environment also played a major role. The significant variation for the traits over years showed the effect of environment. The genotypes showed highly significant variation for two seasons for all the traits except for collar girth, weight of primary rhizomes per clump and number of primary rhizomes per clump and fresh rhizome yield which revealed the presence of genetic variability among the genotypes. The GCV ranged from 6.51-52.51% in which plant height, leaf lamina length, collar girth, and fresh

rhizome yield were found to have low GCV (<10%). The PCV ranged from 9.93% to 58.38% where only plant height was found to have low PCV (<10%). High PCV compared to GCV is attributed to non-additive gene action genetic constitution or influence of environmental factors. Moderate to high heritability for broad sense (46.99-84.39%) was observed for the majority traits except for collar girth, weight of primary rhizomes per clump and fresh rhizome yield per plant. The present results are in agreement with earlier reports of Mishra *et al.* (2015); Gupta *et al.* (2016) and Aarthi *et al.* (2018). High heritability combined with genetic advance were observed for the traits petiole length, total leaf area, weight of mother rhizomes per clump and number of mother rhizomes per clump. The findings of this study suggest that the genetic makeup of the genotypes had significant effect on the above-mentioned traits than the environment.

Therefore, these traits could serve as important criteria for selecting superior genotypes in future turmeric breeding programs.

Positive significant correlation towards fresh rhizome yield was observed for plant height, collar girth, and weight of primary rhizomes per clump. The highest positive significant correlation for fresh rhizome yield was noticed for the weight of primary rhizomes per clump (0.921). Interestingly, all the morphological traits had highly significant positive correlation with other traits. Weight of mother rhizomes per clump had significant positive correlation with plant height, number of leaves, petiole length, leaf lamina length, leaf lamina width, leaf area, total leaf area, collar girth and fresh rhizome yield per plant. The collar girth had significant positive correlation with almost all traits except number of tillers, number of mother rhizomes per clump and number of primaries per clump as represented in Fig. 1.

**Table 1.** *Per se* performance of different morphological and yield components of 21 turmeric genotypes

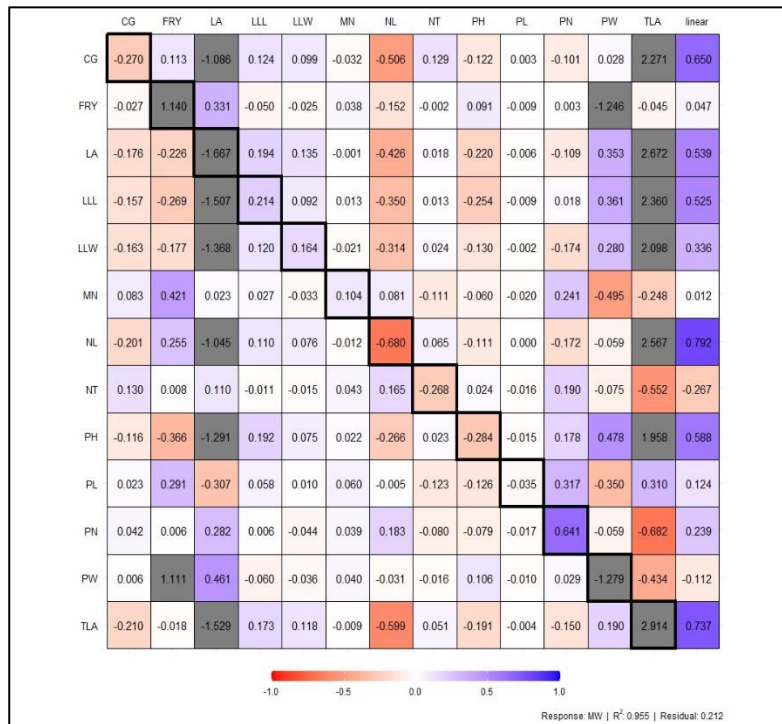
Genotype	PH	NL	NT	PL	LLL	LLW	LA	TLA	CG	PN	PW	MN	MW	FRY
IISR Pragati	112.93	8.30	3.35	23.64*	48.36	13.55	491.81	4087.95	8.21	7.45	624.53*	2.63	28.34	635.96*
IISR Prathiba	133.30	9.23	3.43	20.46	56.82	15.05	644.22	5879.22	8.79	9.74*	453.22*	3.68*	87.81	489.34*
IISR Alleppey Supreme	122.88	8.68	4.53*	20.03	56.99	15.23	661.89*	5752.87	9.02	10.31*	353.81	2.13	80.31	367.31
Rajendra Sonali	107.20	7.65	3.53	20.21	46.56	11.36	422.14	3232.26	7.60	9.55*	548.97*	2.50	39.97	536.63*
Megha Turmeric 1	137.98*	6.73	2.38	18.61	57.46	12.56	540.40	3631.13	8.44	12.50*	352.38	2.30	61.22	327.66
Waigon Turmeric	121.08	9.63	1.90	14.49	57.80	15.96	692.79*	6693.25	11.32*	5.93	535.22*	1.63	94.47	552.61*
Roma	149.90*	9.18	3.38	26.49*	68.61*	16.74	817.38*	7483.33	9.65	7.28	430.56*	3.25	70.69	427.06*
CIM Pitambar	130.68	8.65	3.25	24.78*	59.81*	14.99	677.85*	5846.72	10.50*	10.70*	571.44*	2.63	53.06	559.44*
Uttar Rangini	125.95	8.40	3.18	15.92	60.03*	15.16	697.99*	5924.42	8.93	5.64	328.97	1.53	33.06	327.26
Chhattisgarh Haldi 2	126.48	8.33	3.03	16.75	58.08	15.29	657.27	5389.32	9.26	6.35	327.44	2.40	39.06	352.79
NDH 8	104.53	7.73	2.85	18.14	45.70	12.95	431.43	3331.81	8.73	9.03*	500.56*	2.25	33.81	503.29*
Co 3	125.78	8.20	2.83	21.70*	51.24	13.71	527.76	4322.18	8.65	8.66*	283.96	1.88	63.17	298.56
Acc. 1545	137.90*	8.78	3.15	24.14*	61.04*	16.11	724.79*	6346.79	10.46*	10.88*	462.97*	4.03*	99.47	482.56*
Erode local	143.43*	8.65	3.18	23.34*	61.34*	15.25	688.94*	5909.90	10.20*	11.88*	324.72	1.60	98.97	360.83
Mydukur selection	136.15*	8.88	3.10	25.32*	60.44*	15.59	710.72*	6386.09	10.22*	8.78*	435.70*	2.45	71.81	449.74*
Acc. 849	139.93*	11.73*	2.03	17.90	62.39*	17.13*	784.17*	9183.34*	13.04*	7.51	380.81	1.00	177.19*	451.56*
Acc. 379	123.68	8.50	2.88	18.72	53.67	15.82	645.29	5476.45	8.77	8.15*	389.06	1.25	45.09	390.18*
Acc. 14	120.93	8.03	2.95	17.39	53.43	16.01	644.49	5181.56	8.82	6.40	340.88	1.63	29.16	351.92
Acc. 179	124.93	7.85	2.65	18.70	53.15	16.09	638.25	5065.65	9.57	7.00	380.05	1.83	45.58	400.10*
Acc. 214	125.58	8.05	3.13	20.09	56.46	19.59	702.85*	5678.17	10.85*	8.50*	418.34*	1.30	45.19	409.24*
Acc. 69/5/22/I <sub>3</sub>	121.48	8.73	2.68	15.74	57.17	13.77	586.30	5245.70	11.22*	6.68	403.71*	1.38	34.00	416.76*
Trait mean	127.27	8.56	3.02	20.12	56.50	15.14	637.56	5526.10	9.63	8.52	421.30	2.15	63.40	432.89*
SE(m)	5.57	0.34	0.33	1.64	3.02	0.83	54.03	561.77	1.03	1.48	77.37	0.23	11.44	84.91
CV (%)	6.19	5.70	15.51	11.51	7.56	7.75	11.99	14.38	15.11	24.52	25.97	15.22	25.51	27.74
CD (0.05)	16.43	1.02	0.98	4.83	8.91	2.45	159.40	1657.21	3.04	4.36	228.23	0.68	33.74	250.48

PH=Plant height (cm), NL=Number of leaves, NT=Number of tillers, PL=Petiole length (cm), LLL=Leaf lamina length (cm), LLW=Leaf lamina width (cm), LA=Leaf area (cm<sup>2</sup>), TLA=Total leaf area (cm<sup>2</sup>), CG=Collar girth (cm), PN= Number of primaries per clump, PW= Weight of primaries rhizomes per clump, MN=Number of mother rhizomes per clump, MW=Weight of mother rhizomes per clump (g), FRY=Fresh rhizome yield per plant (g), SE(m)=Standard error mean, CV=Coefficient of variation (%) and CD=Critical difference at 0.05 \*- genotypes at par.

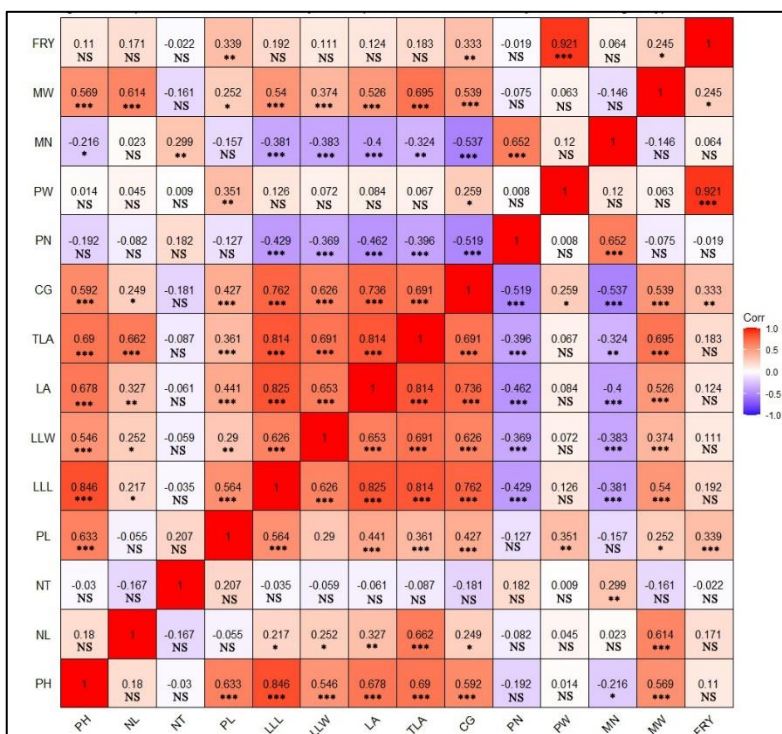
**Table 2.** Pooled components of genetic parameters and analysis of variance for different yield attributing components in turmeric

Traits	Pooled ANOVA for two seasons			Grand mean	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability (broad sense) %	Genetic advance	Genetic advance over % of mean				
	Mean sum of square												
	Seasons df=1	Genotypes Df=20	Error Df=20										
PH	2629.92***	257.1**	62.01	127.27	7.76	L	9.93	L	61.14	H	15.91	12.50	M
NL	0.4821	1.83982***	0.2379	8.56	10.45	M	11.90	M	77.10	H	1.62	18.90	M
NT	0.00292	0.60631*	0.21867	1.25	14.60	M	21.30	H	46.99	M	0.62	20.62	H
PL	283.252***	23.328***	5.36	20.12	14.90	M	18.82	M	62.64	H	4.89	24.29	H
LLL	1762.06***	60.83**	18.26	56.50	8.17	L	11.13	M	53.82	M	6.97	12.34	M
LLW	47.956***	6.252***	1.377	15.14	10.31	M	12.90	M	63.90	H	2.57	16.98	M
LA	492278***	21742**	5839	637.56	13.99	M	18.42	M	57.66	M	139.48	21.88	H
TLA	28987067***	3820526***	631166	5526.10	22.85	H	27.00	H	71.64	H	2201.88	39.85	H
CG	216.331***	3.312	2.118	9.63	8.02	L	17.11	M	21.98	L	0.75	7.75	L
PN	141.736***	7.73	4.363	18.52	15.23	M	28.87	H	27.84	L	1.41	16.56	M
PW	41895.	16845	11971	421.30	11.72	H	28.50	H	16.91	L	41.83	9.93	L
MN	2.65006***	1.26916***	0.10743	2.15	35.39	H	38.52	H	84.39	H	1.44	66.97	H
MW	5609***	2478.4***	261.7	63.40	52.51	H	58.38	H	80.90	H	61.69	97.29	H
FRY	8253	16008.1	14419.1	432.90	6.51	L	28.49	H	5.224	L	13.27	3.07	L

Significance codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*'; PH=Plant height (cm), NL=Number of leaves, NT=Number of tillers, PL=Petiole length (cm), LLL=Leaf lamina length (cm), LLW=Leaf lamina width (cm), LA=Leaf area (cm<sup>2</sup>), TLA=Total leaf area (cm<sup>2</sup>), CG=Collar girth (cm), PN= Number of primaries per clump, PW= Weight of primary rhizomes per clump, MN=Number of mother rhizomes per clump, MW=Weight of mother rhizomes per clump (g), FRY=Fresh rhizome yield per plant (g), L stands for Low, M for Moderate & H for High.



**Fig. 1.** Path analysis of yield components with independent variable weight of mother rhizome per clump



**Fig. 2.** Simple correlation of agro morphological traits components with fresh rhizome yield (significance codes NS  $p \geq 0.05$ , \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ )

The path coefficient analysis was carried out for weight of mother rhizomes per clump using 13 morphological and yield components to compute the direct and indirect effects of the component traits as it showed strong correlation and is the crucial part of the study. High direct positive effect was exhibited by total leaf area (2.914) followed by fresh rhizome yield (1.140), number of primary rhizomes per clump (0.641), leaf lamina length (0.214), leaf lamina width (0.164) and number of mother rhizomes per clump (0.104). The indirect effects with weight of mother rhizomes per clump had positive association with all the traits except number of tillers per plant and weight of primary rhizomes per clump. Our results are in line with previous studies of Mishra *et al.* (2015); Aarthi *et al.* (2022) and Aarthi *et al.* (2018). Therefore, these traits should be duly considered while selecting superior genotypes as represented in Fig. 1.

### Conclusion

In summary, this study aimed to examine the genetic variability for morphological and yield traits in turmeric genotypes. The pooled analysis of variance showed that there was significant genetic variability among the genotypes for most traits. The characters such as petiole length, total leaf area, weight of primary rhizomes per clump and number of mother rhizomes per clump exhibited high heritability and genetic advance, which are least influenced by environmental factors. Path analysis revealed that weight of mother rhizomes has strong direct impact on most traits and will be the key for future breeding programs. These parameters, along with the trait association network, will be

helpful for selecting superior turmeric genotypes.

### References

- Aarthi S, Suresh J & Prasath D 2022 Estimates of genetic variability, inter character association and path analysis in turmeric over environments. *J. Spices Arom. Crops.* 31(1): 56–64.
- Aarthi S, Suresh J & Prasath D 2018 Variability and association analysis of curcumin content with yield components in turmeric (*Curcuma longa* L.). *Electron. J. Plant. Breed.* 9(1): 295–303.
- Bijauliya R K, Alok S, Kumar M, Chanchal D K & Yadav S 2017 A comprehensive review on herbal cosmetics. *Int. J. Pharm. Sci. Res.* 8(12): 4930–4949.
- Burton G W 1952 Quantitative inheritance in grasses. *Proceedings of international grassland congress.* 1: 277–283.
- Burton G W & De Vane G M. (1953). Estimating heritability in tall fescus (*Festuca arundinaceae*) from replicated clonal material. *Agron. J.* 45:478–481.
- Dawson T L 2009 Biosynthesis and synthesis of natural colours. *Color. Tech.* 125(2): 61–73.
- Devaraja N S, Patroti P & Parashuram S 2022 TraitStats: Statistical Data Analysis for Randomized Block Design Experiments. R package version, 1.0.2, <<https://CRAN.R-project.org/package=TraitStats>>.
- Dewey D R & Lu K H 1959 A correlation and path coefficient analysis of components of wheat grass seed production. *Agron. J.*, 51: 15–18.
- Dey S & Nagababu B H 2022 Applications of food color and bio-preservatives in the food and



- its effect on the human health. *Food Chem. Adv.* 1:100019.
- Gupta A K, Mishra R & Lal R K 2016 Genetic variability and character interrelationship among indigenous germplasm of turmeric (*Curcuma longa*). *J. Herbs Spices Med.* 22(2): 190–201.
- Gupta A K, Mishra R, & Lal R K 2015 Genetic resources, diversity, characterization and utilization of agronomical traits in turmeric (*Curcuma longa* L.). *Ind. Crop. Prod.* 77:708–712.
- Iweala E J, Uche M E, Dike E D, Etumnu LR, Dokunmu TM, Oluwapelumi A E, Okoro B C, Dania O E, Adebayo A H & Ugbogu E A 2023 *Curcuma longa* (Turmeric): Ethnomedicinal uses, phytochemistry, pharmacological activities and toxicity profiles- a review. *Pharmacol. Res.-Modern Chinese Medicine.* 100222.
- Johnson H W, Robinson J F & Comstock R E 1955 Estimates of genetic and environmental variability in soybean. *Agron. J.* 47: 314–318.
- Jyotirmayee B & Mahalik G 2022 A review on selected pharmacological activities of *Curcuma longa* L. *Int. J. Food Prop.* 25(1):1377–1398
- Kandiannan K, Anandaraj M, Prasath D & Zachariah J 2015 Evaluation of short and tall true turmeric (*Curcuma longa*) varieties for growth, yield and stability. *Indian J. Agric. Sci.* 85(5): 718–20
- Kaur Y & Chopra L 2023 Natural dyes - An eco-friendly approach to textile industry. *AIP Conference Proceedings* 2558 (2023): 020041.
- Lush J H 1940 Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. *Proceedings of the American Society of Animal Nutrition*, 1940(1): 293–301.
- Mishra R, Gupta A K, Lal R K, Jhang T & Banerjee N 2015 Genetic variability, analysis of genetic parameters, character associations and contribution for agronomical traits in turmeric (*Curcuma longa* L.). *Ind. Crops. Prod.* 76: 204–208.
- Nair R R & Sasikumar B 2009 Chromosome number variation among germplasm collections and seedling progenies in turmeric, *Curcuma longa* L. *Cytologia* 74(2): 153–157.
- Olivoto T & Lúcio A D 2020 Metan: An R package for multi-environment trial analysis. *Methods Ecol. Evol.* 11: 783–789.
- PPV & FRA 2009 Guidelines for the conduct of test for distinctiveness, uniformity and stability on turmeric (*Curcuma longa* L.). India. <http://plantaauthority.gov.in/pdf/Turmeric.pdf>.
- Prasath D, Dinesh R, Srinivasan V, Senthil Kumar C M & Anandaraj M 2014 Research Highlights 2013-14 of Indian Institute of Spices Research. IISR. pp.20.
- Prasath D, Eapen S J & Sasikumar B 2016 Performance of turmeric (*Curcuma longa*) genotypes for yield and root-knot nematode resistance. *Indian J. Agric. Sci.* 86 (9): 1189–92.
- Prasath D, Krishnamurthy K S, Praveena R, Jayashree E, Leela N K, Sellaperumal C & Aarthi S 2022 Turmeric (extension

- pamphlet). ICAR-Indian Institute of Spices Research, Kozhikode, Kerala.
- R Core Team 2022 R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.
- Ratnambal M J & Nair M K 1986 High yielding turmeric selection PCT 8. J. Plant. Crops. 14: 91–98.
- Razavi B M, Rahbardar M G & Hosseinzadeh H 2021 A review of therapeutic potentials of turmeric (*Curcuma longa*) and its active constituent, curcumin, on inflammatory disorders, pain, and their related patents. *Phytother. Res.* 35(12):6489–6513.
- Robinson H F. (1966). Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian. J. Genet. Plant. Breed.* 171.
- Sasikumar B 2005 Genetic resources of *Curcuma*: diversity, characterization and utilization. *Plant Genet. Res.* 3:230–251.
- Sivasubramanian S & Menon PM 1973 Genotypic and phenotypic variability in rice. *Madras. Agric. J.* 60: 1093–1096.
- Spices Board 2023 Available at <http://www.indianspices.com/sites/default/files/Major%20spice%20state%20wise%20area%20production%202022-23.pdf>.
- Suresh R, Ramar A, Balakrishnan S, Rajeswari S & Kumaravadivel N 2020 Performance and evaluation of turmeric (*Curcuma longa* L.) genotypes based on quantitative traits for tropical regions of Tamil Nadu. *Electron. J. Plant. Breed.* 11(3): 735–741.
- Vinodhini V, Selvi BS, Balakrishnan S & Suresh R 2019 Evaluation of turmeric (*Curcuma longa* L.) genotypes for yield and curcumin content. *J. Agric. and Ecol.* 07(01):88–95.
- Wright 1921 Correlation and causation. *J. Agric. Res.* 20:557–585.