

**GENETIC VARIABILITY, HERITABILITY AND GENETIC
ADVANCE STUDIES IN TURMERIC (*CURCUMA LONGA L.*) IN
KRISHNA-GODAVARI AGROCLIMATIC ZONE OF
ANDHRAPRADESH**

A. MOUNIKA

Faculty, Dept of Genetics and plant breeding

Bharatiya Engineering Science & Technology Innovation University, Andhra Pradesh, India.

Abstract: The present experiment was carried out to assess the genetic variability, heritability and genetic advance for different characters in 46 diverse genotypes of turmeric. The experiment was carried out in ABD (Augmented Block Design) during *kharif* 2017-18. The genetic parameters, *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense genetic advance and genetic advance as per cent mean were estimated for all the twenty four characters in this study. The highest percentage of phenotypic and genotypic coefficient of variation was observed for characters like PAL activity (in dry leaves), weight of primary rhizomes, curcumin yield, ferulic acid, PAL activity (in dry leaves) and number of primary rhizomes *i.e.*, 58.51% and 58.96%, 49.99% and 50.50%, 49.95% and 51.07%, 46.05% and 46.77%, 42.03% and 44.17%, 38.98% and 40.40% respectively. Selection in these characters may be effective as the environment influence on these characters is limited. High heritability was observed for all the characters have exhibited high heritability except leaf width and carbohydrate content which recorded moderate heritability. High GAM values were recorded in plant height, number of tillers per plant, number of leaves per plant, leaf length, weight of mother rhizome, number and weight of primary rhizomes, number and weight of secondary rhizomes, clump weight, protein content in leaves, PAL activity (fresh and dry), total phenolics in leaves, curcumin content in leaf at 150, 180 DAS, curcumin content and curcumin yield.

Keywords: Turmeric, Genetic variability, Heritability, curcumin, DAS- Days after sowing PAL, Genetic advance.

1. Introduction

Turmeric (*Curcuma longa L.*) is one of the most widely grown spice crops in India due to its agro-climatic suitability and genetic diversity. Turmeric is also referred to as the "golden spice"

(Ravindran et al. 2007). Turmeric has significant connections to the socio-cultural life of the Indian subcontinent's people. The Vedic period considered this plant with the orange-yellow rhizome to be the "herb of the Sun" (Ravindran et al.

2007). Turmeric has received a lot of attention because of its medicinal properties all over the world (Cousins et al. 2007). Turmeric has anti-inflammatory, hepatoprotective, antitumor, antiviral, wound healing, and anti-cancer properties, and it is also useful for the treatment of gastrointestinal and respiratory disorders (Polasa et al., 1994; Joe et al., 1994). The performance of any crop or variety is primarily determined by its genetic makeup. Besides that, crop performance is affected by the climatic conditions of the region in which the crop or variety is grown. As a result, genotypes that perform well in one region may not perform well in others with varying climatic conditions. As a result, it is essential to collect and evaluate all available genotypes in order to select suitable and high yielding genotypes for a specific agro-climatic condition. Given the importance of turmeric, research on this crop is pivotal in order to determine the suitability of various genotypes for a specific area. Characterization of available germplasm is a necessary step to facilitate breeding efforts; it especially benefits a plant breeder in choosing proper parental materials (Sarutayophat *et al.* 2007). Understanding variability is important for developing and advancing breeding programmes to improve yield potentials in existing crops (Johnson et al. 1955). Corresponding heritability, genetic progress, and genotypic and phenotypic coefficients of variation within a crop will aid in the selection of superior genotypes, which is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Because many economic traits are quantitative in nature and highly influenced by the environment, and breeding progress is governed by the character of genetic and non-genetic variations, it will be useful to partition overall variability into heritable and non-heritable components to determine

whether selection superiority is inherited by progenies. Effective selection of genotypes for desirable traits is determined by the estimates of heritability coupled with genetic advance. Therefore, the present investigation was undertaken to evaluate promising genotypes to estimate the variability, heritability and genetic advance in 46 turmeric genotypes.

2. Materials and methods

The present experimental investigation was carried out during *kharif* in 2017-2018 at Horticultural research station, Guntur District, Andhra Pradesh. The experimental site was situated at an altitude of 31.5 meters above mean sea level, 16° 18' N latitude, 80° 29' E longitude and about 8 km away from the Guntur town in the Krishna-Godavari Agro-climatic zone of Andhra Pradesh India. The soil of the experimental site is rich black cotton soil and has PH of 8.4, EC of 0.16 mmhos/cm and good moisture retentive capacity. The available NPK contents were 200-250, 70-90 and 800-850 kg/ha⁻¹, respectively. The entire experimental area was leveled and divided into plots with a dimension of 2 m x 1.2 m. with a spacing of 60 cm x 20 cm. Seed material (rhizomes) was obtained from last season's crop grown at Horticultural Research Station Lam, Guntur. The healthy seed material was procured. Primary rhizomes were used for planting the crop. The seed material was treated with 1 g l⁻¹ Carbendazim and 1 ml l⁻¹ Malathion solution for thirty minutes before sowing. The seed material was shade dried for one day and used for planting. The crop is supplied with 25 t ha⁻¹ FYM at the time of preparatory cultivation. The recommended dose of 300 kg N, 125 kg P₂O₅ and 200 kg K₂O per hectare was applied as per the package of practices given by Dr YSR Horticultural University to raise a healthy

crop. The data was recorded from five randomly selected plants from each treatment in each replication.

Mean data were used for statistical analysis for 24 traits i.e., plant height (cm), number of tillers, leaf length (cm), leaf width (cm), number of mother rhizomes, weight of mother rhizomes(g), number of primary rhizomes, weight of primary rhizomes (g), number of secondary rhizomes, weight of secondary rhizomes(g), clump weight (g/plant), dry recovery(%), carbohydrate in leaves (mg/g), protein in leaves (mg/g), PAL activity in leaves(fresh and dry). The analysis of variance was carried out and was used for calculating other genetic parameters. The genetic parameters viz., Genotypic Coefficients of Variation (GCV) and Phenotypic Coefficients of Variation (PCV) were calculated as per the formula suggested by Sivasubramanian and Madhavamenon (1973).

Heritability in the broad sense and expected genetic advance were calculated as per formula is given by Allard (1960), Johnson *et al.* (1955) respectively. Robinson *et al.* (1949) categorized heritability (%) into low (0-30%), moderate (30-60%) and high (above 60%). Higher heritability indicates the least environmental influence on the characters. The genetic advance was categorized into low (1-10%), moderate (11-20%) and high (>20%) as suggested by Johnson *et al.* (1955). High GA indicates that additive genes govern the character and low GA shows that non-additive gene action is involved. Heritability along with GA helps us in predicting the gene action and the method of breeding to be practiced.

3. Results And Discussion

The genetic parameters, viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense genetic advance and genetic advance as per cent mean were estimated for all the characters under study and presented in Table 1. The genotypes

evaluated exhibited a wide range of variability for all the characters.

Low genotypic and phenotypic coefficients of variation were recorded for Carbohydrate content, Dry recovery, leaf width, leaf length, plant height, number of mother rhizomes and protein content i.e., 7.49% and 10.83%, 9.19% and 10.20%, 12.93% and 18.02%, 16.22% and 17.42%, 19.69% and 21.60%, 17.78% and 20.34%, 14.60% and 14.80% respectively, indicating that there is narrow range of variability and high influence of environment in the expression of these characters with a little scope for selection. Among the recorded low GCV and PCV parameters, all the PCV values were higher than GCV indicating that the apparent variation is not only due to genotypes but also due to influence of environment, selection for these characters may be difficult and misleading.

Moderate GCV and PCV were recorded for leaf curcumin content at 150,180 and 210 DAS and also for the characters like curcumin content in rhizomes, clump weight and number of leaves i.e., 32.84% and 34.27%, 31.20% and 33.63%, 30.38% and 30.83%, 30.45% and 31.11%, 23.89% and 25.21% respectively.

High genotypic and phenotypic coefficient of variation is recorded in characters like PAL (dry), weight of primary rhizomes, curcumin yield, ferulic acid, PAL (fresh) and number of primary rhizomes i.e., 58.51% and 58.96%, 49.99% and 50.50%, 49.95% and 51.07%, 46.05% and 46.77%, 42.03% and 44.17%, 38.98% and 40.40% respectively. Selection in these characters may be effective as the environment influence on these characters is limited.

Among the recorded low, moderate and high GCV and PCV parameters all the PCV values were higher than GCV, it means that the apparent variation is not only due to genotypes but also due to influence of environment in all the characters studied. The variability pattern

was similar to those reported by earlier workers Pathania *et al.*(1988), Indires *et al.*(1992), Babu *et al.*(1993), Lynrah *et al.*(1998), Singh *et al.*(2003), Sinker *et al.*(2005), Rao *et al.*(2004), Jan *et al.*(2011), Jan *et al.* (2012), Rajyalakshmi *et al.*(2013), Singh *et al.*(2012), Singh and Ramakrishna (2014), Prajapati *et al.*(2014) and Verma *et al.* (2015) and Jayasree *et al.* (2014).

Heritability describes the proportion of total phenotypic variation in a population due to genetic factor. It can be high, medium or low (Johnson *et al.*, 1955). Burton (1952), Swarup and Chaugle (1962) indicated that genetic variability with heritability estimates would give a better idea on the amount of genetic advance expected out of selection. Panse (1957) suggested that magnitude of heritable variability is the most important aspect of the breeding material which has close relationship on its response to selection. PCV and GCV reveal the extent of genetic variability present; they do not indicate the extent of heritable variation. Genetic advance is the improvement of mean genotypic values of selected plants over parental population under each cycle of selection. Allard (1960) indicated that high genetic advance coupled with high heritability offers most suitable conditions to decide the criteria of selection. According to Singh (2001), heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40-59% are medium and values less than 40% are low. Johnson *et al.* (1955) classified genetic advance as percentage of mean (GAM); values from 0-10% are low, 10-20% are moderate and 20% and above are high

Out of 24 characters studied, all the characters have exhibited high heritability except leaf width and carbohydrate content which recorded moderate heritability. Philip & Nair (1985) reported high heritability for number of primary rhizomes and Singh *et al.* (2012) reported low heritability for number of mother

rhizomes. These differences in Heritability estimates by different authors are due to Heritability (broad sense) estimates depend on the type of genetic material, sample size, sampling method, experimental conditions and method of estimation

In the present study, genetic advance as percentage mean ranged from 10.77 (Carbohydrate) to 115.78 PAL (DRY). High GAM values were recorded in plant height, number of tillers per plant, number of leaves per plant, leaf length, weight of mother rhizome, number and weight of primary rhizomes, number and weight of secondary rhizomes, clump weight, protein content in leaves, PAL activity (fresh and dry), total phenols in leaves, curcumin content in leaf at 150, 180 DAS, curcumin content and curcumin yield. Moderate GAM was recorded in leaf width, dry recovery and carbohydrate content in leaves. None of the traits under study recorded low GAM values, indicating all the traits are governed by additive gene action; selection is efficient in most cases.

Heritability along with genetic advance is more helpful in predicting the gains under selection than heritability estimated alone (Johnson *et al.*, 1955). In the present investigation, high heritability and high genetic advance as per cent mean was observed for plant height, number of tillers per plant, number of leaves per plant, leaf length, weight of mother rhizome, number and weight of primary rhizomes, number and weight of secondary rhizomes, clump weight, protein content in leaves, PAL activity (fresh and dry), total phenols in leaves, curcumin content in leaf at 150, 180 DAS, curcumin content and curcumin yield indicating that high heritability in these traits is was contributed by additive gene effects and hence improvement, can be made by simple selection. Similar findings were reported by Pathania *et al.* (1998) and Babu *et al.* (1993).

Moderately high heritability and high GAM was recorded in number of

mother rhizomes and leaf curcumin content at 210 DAS indicated that these traits are also governed by additive gene action and selection can be effective. However, leaf width recorded moderately high heritability and medium genetic advance indicating that though the trait is governed by additive gene action, environment effects are considerable, hence selection would be ineffective. Moderate heritability and medium GAM was observed in carbohydrate content in leaves, though the trait is governed by additive gene action, environment effects are considerable, hence selection would be ineffective. The genetic advance as per cent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The traits with high heritability and high genetic advance indicate the control of additive gene action and selection may be effective for these

characters. Lynrah et al. (1998) Singh et al. (2003), Singh et al.(2012), Rajyalakshmi et al. (2013), Singh and Ramakrishna (2014), Jayasree et al. (2014) and Verma et al. (2015). High heritability for plant height and leaf width as well as moderate to low heritability for yield have been reported by Babu et al.(1993), while, Prajapati et al. (2014) registered low heritability for plant height, leaf length, leaf width, number of leaves, number of tillers and curcumin content. The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection.

Table 1 : Genetic variability, Heritability and Genetic advance

Characters	Heritability (broad)	Genetic advance at 5%	Genetic advance as
Plant height (cm)	82	28.91	36.63
Number of tillers	87	1.50	44.11
Number of leaves	89	7.87	47.35
Leaf length (cm)	86	11.88	30.87
Leaf width (cm)	51	2.37	18.79
Number of mother rhizomes	76	1.03	31.49
Weight of mother rhizome (g)	84	40.71	40.15
Number of primary rhizomes	93	5.40	77.58
Weight of primary rhizomes (g)	98	106.08	98.56
Number of secondary rhizomes	91	3.70	50.96
Weight of secondary rhizomes (g)	94	25	62.79
Clump weight (g/Plant)	95	148.67	59.75
Dry recovery (%)	81	3.42	17.03
Carbohydrate in leaves (mg/g)	47	40.07	10.77
Protein in leaves (mg/g)	97	44.73	29.31
PAL Activity in leaves	90	1.61	80.09
PAL Activity in leaves	98	0.22	95.78
Total phenols in leaves (mg/g)	87	8.04	44
Ferulic acid in leaves (mg/g)	96	1.47	88.55
Leaf curcumin (mg/g) at 150 DAS	91	14.90	63.67
Leaf curcumin (mg/g) at 180 DAS	86	10.31	58.77
Leaf curcumin (mg/g) at 210 Das	79	7.85	56.07
Curcumin content in rhizome	97	21.61	61.99
Curcumin yield (g/Plant) (dry)	95	1.76	98.32

References:

- [1].Allard RW (1960) Principles of Plant Breeding, John Wiley and Sons, Inc, New York, pp 145.
- [2].Babu, K. N, Sasikumar, B, Ratnambal, J, George, J. and Ravindran, P. N. 1993. Genetic variability in turmeric (*Curcuma longa* L.) Indian Journal Of Genetics. 53(1): 91-93.
- [3].Burton, G. N. 1952. Quantitative Inheritance in Grasses. Proceedings Of Sixth International Grassland Congress 1: 277- 83.
- [4].Cousins M, Adelberg J, Chen F, Rieck J 2007. Antioxidant capacity of fresh and dried rhizomes from four clones of turmeric (*Curcuma longa* L.) grown in vitro. Ind Crop Prod 25: 129-135.
- [5].Indiresh, K.M, Uthaiiah, B.C, Reddy, M.J. and Rao, K.B. 1992. Genetic variability and heritability studies in turmeric (*Curcuma longa* L.). Indian Cocoa, Arecanut and Spices Journal. 26: 50-53.
- [6].Jan, H. U, Rabbani, M. A. and Shinwari, Z. K. 2011. Assessment of genetic variability in turmeric (*Curcuma longa* L.) germplasm using agromorphological traits. Pakistan Journal of Botany. 44(1): 231-38.
- [7].Jayasree, M, Radhakrishnan, V. V. and Mohannan, K. V. 2014. Assessment of variability and selection of promising genotypes in mango ginger (*curcuma amada* Roxb.) accessions from Kerala. Indian Journal of Plant Genetic Resources. 27(1): 54-58.

- [8]. Joe B, Vijaykumar M, Lokesh BR 2004. Biological properties of curcumin-cellular and molecular mechanisms of action. *Critical Rev Food Sci Nutr* 44: 97-111.
- [9]. Johnson HW, Robinson HF, Comstock RE 1955. Estimates of genetic and environmental variability in soyabean. *Agron J* 47: 314-318.
- [10]. Lynrah, P. G. and Chakrabarthy, B. K. 2000. Performance of turmeric and its close genotypes. *Journal of Agriculture Science Society of North East India*. 13: 32-37.
- [11]. Prasad Rongali, L., & Kumar Budda, G. A. (2020). Architecting Scalable and Secure Infrastructure for DevOps, Patterns and Practices for Cloud, Hybrid, and On-Premise Environments. *International Journal of Enhanced Research In Science Technology & Engineering*, 09(10), 32–40. <https://doi.org/10.55948/ijerste.2020.1004>.
- [12]. Philip, P.J. and Nair, P.C.S. 1985. Studies on variability, heritability and genetic advance in turmeric. *Indian Cocoa, Arecanut and Spice Journal*. 8:23-30.
- [13]. Panse VG, Sukhatme PV (1985) Statistical methods for agricultural workers. ICAR, New Delhi (India).
- [14]. Naga Charan Nandigama, "Data-Driven Cyber-Physical Customer Experience Management In Iort-Enabled Banking Infrastructures," *International Journal of Data Science and IoT Management System*, vol. 2, no. 3, pp. 22–27, Aug. 2023, doi: 10.64751/ijdim.2023.v2.n3.pp22-27.
- [15]. Polasa K, Raghuram TC, Krishna TP 1994. Turmeric (*Curcuma longa* L.) induced reduction in urinary mutagens. *Food Chem Toxicol* 29: 699-706.
- [16]. Vikram, S. (2023). Enhancing Credential Security in Distributed Manufacturing: Machine Learning for Monitoring and Preventing Unauthorized Client Certificate Sharing. *JOURNAL OF ADVANCE AND FUTURE RESEARCH*, 1(7). <https://doi.org/10.56975/jaifr.v1i7.501709>
- [17]. Rao, A. M, Rao, P. V, Reddy, Y. N. and Ganesh, M. 2005. Genetic divergence in germplasm collections of turmeric (*Curcuma longa* L.). *Journal of Spices and Aromatic Crops*. Vol. 14 (2) : 165-68.
- [18]. Ravindran PN, Nirmal Babu K, Shiva KN (2007) *Turmeric: The Genus Curcuma: Medicinal and Aromatic Plants-Industrial Profiles*. CRC press, Boca Raton.
- [19]. Nandigama, N. C. (2016). Scalable Suspicious Activity Detection Using Teradata Parallel Analytics And Tableau Visual Exploration.
- [20]. Sarutayophat T, Nualsri C, Santipracha Q, Saereprasert V 2007. Characterization and genetic relatedness among 37 yard long bean and cowpea accessions based on morphological characters and RAPD analysis. *Songklanakarin J Sci Tech* 29 (3): 591- 600.
- [21]. Singh, B. D. 2001. *Plant Breeding: Principles and Methods*. Kalyani Publishers, New Delhi, India, Pages: 896.
- [22]. Singh, A. K. 2013. Evaluation of turmeric (*Curcuma longa* L.) genotypes for yield attributes, yield and reaction to foliar diseases. *Journal of Spices and Aromatic Crops*. 22 (2) : 238–40.
- [23]. Singh, Y, Pankaj, M. and Viveka, K. 2003. Genetic variability and heritability in turmeric (*Curcuma longa* L.). *Himachal Journal of Agricultural Research*. 29 (1) : 31-34.
- [24]. Todupunuri, A. (2023). The Role of Artificial Intelligence in Enhancing Cybersecurity Measures in Online Banking Using AI. *International Journal of Enhanced Research in Management & Computer Applications*, 12(01), 103–108. <https://doi.org/10.55948/ijermca.2023.01015>.
- [25]. Sivasubramanian, S. and Madhavamenon, P. 1973. Genotypic and phenotypic variability in rice. *Madras agricultural journal* 60:1093-96.
- [26]. Singh BK, Ramakrishna Y 2014. Indian collections of turmeric (*Curcuma longa* L.): Genetic variability, inheritance, character association and performance. *Ind J Pl Genet Resour* 27 (3): 263-270.
- [27]. Verma RK, Pandey VP, Solankey SS, Verma RB 2014. Genetic variability, character association and diversity analysis in turmeric. *Ind J Hort* 71: 367–372.