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Estimation of Genetic variability, Correlation and Path analysis in Turmeric (*Curcuma longa* L.) genotypes in Chambal region of Gwalior

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ABSTRACT

The experiment was conducted to analyze variation, heritability, genetic advance, correlation and path analysis among 15 diverse genotypes of turmeric for rhizome yield and its contributing traits. Analysis of variance revealed highly significant differences among genotypes for the entire trait studied indicating presence of high genetic variability among the genotypes for various traits. The genotypes Rajapuri, ACG-79 and ACC-48 were promising with respect to rhizome yield per plant and some of the yield contributing traits. High GCV and PCV were observed for the traits number of leaves, leaf lamina width, petiole length, number of mother rhizome and rhizome weight, The characters like number of leaves, plant height, leaf lamina length, leaf lamina width, petiole length, number of mother rhizome and rhizome weight recorded high genetic advance as a per cent of mean coupled with high heritability. Rhizome yield per plant exerted significant and positive correlation with number of mother rhizome and rhizome weight showed major contribution of both these traits in rhizome yield. High positive direct effect on rhizome yield were produced by the rhizome weight followed by number of mother rhizome and number of shoots hence due weightage should be given to these traits for further improvement of rhizome yield in turmeric.

Key words : *Turmeric, Variation, Heritability, GA, Correlation, Path analysis*

Introduction

Turmeric scientifically known as *Curcuma longa*, belongs to the Zingiberaceae family and is a triploid in nature (2n = 3x = 63). Most of the countries that cultivate turmeric include India, Pakistan, Myanmar, Japan, and China. Turmeric is the second most produced spice in India after chilli, and it takes up the fifth most space among spices. It accounts for 6.3% of the total spice acreage and 16.91% of the total spice production.

Curcuma longa L. is the *Curcuma* species that has been recorded and studied the most frequently and significantly thus far. As a sign of health and prosperity, turmeric is frequently used in religious rituals and festivities.

When selection is based on two or more characters simultaneously, estimation of genotypic and phenotypic correlation among distinct characters may provide information needed in a breeding plan. When one attribute is chosen, several other traits respond in a connected manner. An easy way to

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describe path analysis is to think of it as a standardized partial regression coefficient that divides the correlation coefficient into measures of the direct and indirect effects of a set of independent factors on the dependent variable.

Heritability is used to determine the genetic progress, which shows the level of improvement in a character attained under a specific selection pressure. Genetic advancement is a crucial selection factor that helps breeders in their selection process. High genetic progress and high heritability estimates imply that additive gene effects prevail, making direct selection advantageous for enhancing these characteristics (Harshwardhan *et al.*, 2016).

For studies on species evolution, variety identification, parent selection, variety protection, and ultimately better germplasm utilization and breeding effectiveness, genetic diversity provides a crucial scientific foundation.

Materials and Methods

The present investigation was carried out during monsoon season 2022-2023 at school of agriculture ITM University, Gwalior at Chambal region of Madhya Pradesh. The experimental material comprised of 15 diverse genotypes of turmeric. The experiment was laid out in randomized complete block design with three replications. The genotypes were Pitamber, Rajendra Sonia, Rajendra Sonali, Duggirala Red, Salem, Rajapuri, Mydukar, Kasturi, ACG-79, ACC-48, Aleppy Supreme, Mango, Nizamabad Local, Armour and Guntur. The package of practices was followed as per the recommendations for raising the good and healthy crop. Observations were recorded for nine different characters *viz.*, number of leaves, plant height, leaf lamina length, leaf lamina width, number of shoots, petiole length, number of mother rhizome, rhizome weight and rhizome yield per plant. The experimental plot wise mean values of five randomly selected plants were used in each statistical analysis for different characters. Variability parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance as per cent mean were calculated (Johnson *et al.*, 1955). PCV and GCV were categorized as low, moderate or high following Sivasubramanian and Menon (1973). Heritability percentage was classified as suggested by Robinson *et al.* (1949). Genetic advance as per cent of mean (GAM) was categorized according to Johnson *et al.* (1955). Correlation and path analysis were carried out as per Goulden (1952) and Dewey and Lu (1959) respectively.

Analysis of variance, genetic variability, correlation, and path analysis were done using variability for plant breeding package in Rstudio version 4.3.0.

Results and Discussion

The analysis of variance for all nine characters are presented in Table 1. The mean square due to genotypes were highly significant for all the characters indicating the presence of a sufficient amount of variability in the experimental material used and the presence of sufficient variability among the genotypes for all traits. Similar finding has been reported by Singh *et al*. (2020); Suresh *et al*. (2020); Sivakumar *et al.* (2021); Bindu *et al.* (2022) and Nandakumar *et al*. (2022).

The estimates of phenotypic coefficient of variation were generally higher in magnitude than that of genotypic coefficient of variation for all the characters studied, indicating the influence of environment on the expression of the traits. The estimates of GCV and PCV were high for number of leaves, leaf

Table 1. Analysis of variance (mean sum of squares) for different characters in turmeric

Sr. No.	Characters	Mean Sum of Squares		
		Replications (df : 02)	Genotypes (df : 14)	Error (df : 28)
1.	Number of leaves	0.157	16.190**	0.502
2.	Plant height	1.029	784.179**	96.360
3.	Leaf lamina length	0.243	211.768**	19.470
4.	Leaf lamina width	8.812**	50.813**	1.080
5.	Number of shoots	16.719**	0.249**	0.076
6.	Petiole length	11.539**	51.038**	1.751
7.	Number of mother rhizome	0.060	0.621**	0.022
8.	Rhizome weight	0.145	33.413**	11.010
9.	Rhizome yield per plant	110.230	48818.394**	4583.952

lamina width, petiole length, number of mother rhizome and rhizome weight. Low GCV and PCV was recorded for number of shoots. Rest of the characters *viz*., plant height, leaf lamina length and rhizome yield per plant showed moderate estimates of GCV and PCV. These findings are in line with the earlier reports of Prajapati *et al.* (2014); Bahadur *et al.* (2016) and Suresh *et al.* (2020); Meenakshi *et al.* (2021), Dev and Sharma (2022) and Gayatri *et al.* (2022).

High heritability estimates were observed for number of leaves, plant height, leaf lamina length, leaf lamina width, petiole length, number of mother rhizome and rhizome weight. Similar results were reported by Prajapati *et al.* (2014); Singh *et al.* (2020), Meenakshi *et al.* (2021) and Gayatri *et al.* (2022).

High heritability coupled with high genetic advance as a per cent of mean were observed for number of leaves, plant height, leaf lamina length, leaf lamina width, petiole length, number of mother rhizome and rhizome weight. These findings are in accordance with the reports of Bahadur *et al.* (2016), Poonam *et al.* (2018); Suresh *et al.* (2020); Sivakumar *et al.* (2021); Dev and Sharma (2022) and Gayatri *et al.* (2022).

The genotypic and phenotypic correlation results for ninerhizome yield and its contributing traits among 15 genotypes of turmeric are presented in Table 4. Correlation estimates revealed that, rhizome yield per plant exerted significant and positive correlation with number of mother rhizome and rhizome weight. Except for plant height and petiole length all the other traits were positively correlated with yield but not significant. Similar results were earlier reported by Prajapati *et al.*(2014) and Verma *et al.*(2014).

Path analysis revealed that high positive direct effect on rhizome yield were produced by the rhi-

Table 2. Relationship of genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance, and genetic advance as a % of mean of nine characters in turmeric

Sr. No.	Characters	GCV(%)	PCV(%)	Heritability (H^2_b)	Genetic Advance (GA)	Genetic Advance as a % of mean (GAM)
1.	Number of leaves	32.57	34.09	91.00	4.50	64.08
2.	Plant height	12.69	15.13	70.00	26.17	21.94
3.	Leaf lamina length	14.55	16.62	77.00	14.44	26.25
4.	Leaf lamina width	29.93	30.89	94.00	8.13	59.73
5.	Number of shoots	7.36	11.22	43.00	0.32	9.94
6.	Petiole length	26.71	28.10	90.00	7.94	52.31
7.	Number of mother rhizome	24.78	26.09	90.00	0.88	48.50
8.	Rhizome weight	21.56	24.68	76.00	218.48	38.79
9.	Rhizome yield per plant	11.66	18.34	40.00	3.58	15.27

*GCV: Genotypic Coefficient ofVariation, PCV: Phenotypic Coefficient of Variation, H^2_b: Heritability, GA: Genetic Advance, GAM: Genetic Advance as a % of Mean

Table 3. Genotypic correlation coefficients for different characters in turmeric

Characters	NL	PH	LL	LW	NS	PL	NMR	RW	RYP
NL	1.00	0.42	0.001	-0.10	0.40	-0.49	0.40	0.77**	0.10
PH		1.00	-0.65**	-0.17	-0.17	-0.24	-0.12	0.30	-0.28
LL			1.00	0.07	0.40	0.07	0.07	0.07	0.15
LW				1.00	0.06	0.11	-0.05	-0.01	0.04
NS					1.00	0.05	0.59*	0.29	0.25
PL						1.00	-0.33	-0.61*	-0.37
NMR							1.00	0.47	0.50*
RW								1.00	0.33*
RYP									1.00

*NL – Number of Leaves, PH – Plant Height, LL – Leaf lamina Length, LW – Leaf lamina Width, NS – Number of Shoots, PL – Petiole Length, NMR – Number of Mother Rhizome, RW –Rhizome Weight, RYP – Rhizome Yield per Plant

Table 4. Genotypic path coefficients analysis showing direct and indirect effects of different characters on rhizome yield in turmeric

Characters	NL	PH	LL	LW	NS	PL	NMR	RW	RYP
NL	-0.3193	-0.1592	-0.0005	-0.0001	0.0710	0.1690	0.0873	0.2522	0.1004
PH	-0.1337	-0.3801	0.1141	-0.0002	-0.0307	0.0830	-0.0270	0.0972	-0.2773
LL	-0.0009	0.2468	-0.1757	0.0001	0.0707	-0.0247	0.0147	0.0222	0.1531
LW	0.0317	0.0662	-0.0116	0.0010	0.0113	-0.0374	-0.0118	-0.0049	0.0445
NS	-0.1273	0.0655	-0.0697	0.0001	0.1781	-0.0185	0.1279	0.0957	0.2516
PL	0.1561	0.0913	-0.0126	0.0001	0.0095	-0.3455	-0.0716	-0.2016	-0.3743
NMR	-0.1273	0.0468	-0.0118	-0.0001	0.1040	0.1130	0.2190	0.1538	0.4974*
RW	-0.2445	-0.1122	-0.0119	0.0000	0.0517	0.2115	0.1023	0.3293	0.3263*

*NL – Number of Leaves, PH – Plant Height, LL – Leaf lamina Length, LW – Leaf lamina Width, NS – Number of Shoots, PL – Petiole Length, NMR – Number of Mother Rhizome, RW –Rhizome Weight, RYP – Rhizome Yield per PlantResidual effect – 0.563

zome weight followed by number of mother rhizome, number of shoots and leaf lamina width. Direct contributions of remaining traits to rhizome yield were negative. The trait number of mother rhizome also has positive indirect effect on rhizome yield via rhizome weight, petiole length and number of shoots. While rhizome weight has higher direct effect than their correlation with rhizome yield which indicate true correlation between rhizome weight and rhizome yield. Apart from that rhizome weight also has positive and high indirect effect on rhizome yield via petiole length and number of mother rhizome which is nullify by its negative indirect effect via other traits. The residual effect was 0.563 which indicate that 45% variability explained by the characters included in the study. The results are in accordance with the findings of Singh and Ramakrishna (2014), Verma *et al.*(2014); Mishra *et al.* (2015); Gupta *et al.* (2016) and Aarthi *et al.* (2022).

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