



Original Research Article

## Genotype x environment interaction, stability analysis for yield and quality traits in turmeric (*Curcuma longa* L.)

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### ABSTRACT

Genotype x environment interaction and stability were analyzed through the Eberhart and Russell model among seventeen accessions/germplasms of turmeric (*Curcuma longa* L.) during three environments/years. For rhizome yield the mean performance over three environments showed that yield ranged from 241.41 q/ha (CIMCH14127) to 579.67 q/ha (CIMCH14229). Six genotypes, namely CIMCH14107, CIMCH14171, CIMCH14165, CIMCH14130, CIMCH14208, and CIMCH14229 had significantly higher mean for rhizome yield as compared to the general mean. Among seventeen genotypes, five genotypes had more than 1 regression coefficient, while eight genotypes had less than 1 regression coefficient and four genotypes showed  $b_i=1$ . For CIMCH14101, CIMCH14144, CIMCH14159, CIMCH14190, CIMCH14152, CIMCH14123, and CIMCH14164,  $S^2_{di}$  was significant. The stability parameters for rhizome yield revealed that CIMCH14171 and CIMCH14229 were stable for all environments. Three genotypes viz., CIMCH14107, CIMCH14130, and CIMCH14208 genotypes were suitable for unfavorable environments having mean values,  $b_i < 1$  and  $S^2_{di}=0$ . For rhizome yield, CIMCH14107 showed suitability under only favorable environments.

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### 1. Introduction

*Curcuma longa* L. is a genus of perennial, herbaceous plants placed in the family Zingiberaceae (Kress et al., 2002). The genus, represented by approximately 126 species, is known to exhibit spontaneous genetic variation (Skornickova et al., 2007; Shakeri et al., 2017; Tanvir et al., 2017; Uchio et al., Wang et al., 2017). India is the largest producer of turmeric and contributes about 94% of the total global production (Sandeep et al., 2018). Interestingly, with a total of 6% area dedicated for spices production, turmeric is considered as one of the most important spices grown in India (Ranawat et al., 2018). According to the Bureau of Indian Standards (BIS), 63 spices are grown in tropical to temperate regions of the country. India has the highest number of spice varieties in the world (Sheikh et al., 2014). Exports in the future are expected to increase based on the steady demand for the turmeric and tur-

meric-based products both in the health sector and pharmaceutical industry (KarvyComtrade Limited 2017; Dhanalakshmi et al., 2018; Lal et al., 2020). Turmeric plants are herbaceous with the varying height ranging from 40 cm to 150 cm (Ravindran et al., 2007). Fruits are not known in the plants and the rhizomes are oblong, globular, branched or unbranched, fleshy, and aromatic. The rhizomes are usually light brown externally, but internally differ in shades such as yellow, light yellow, and light to deep orange (Shah and Raju, 1975; Sabu, 1991), and it is believed that the color quality and appearance of the whole rhizome varies according to its source of origin (Parry 1962). Turmeric improves the shelf life and delicacy of food products and is widely used as a food additive (Scotter, 2009). Rosengarten (1969) reported that finger rhizomes are always the best in comparison to split and round rhizomes. Studies on molecular, phytochemical, and pharmacological effects allow a greater perceptiveness of the factors sustaining the safe use of the medicine, including inter-

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actions with other drugs or nutritional factors (Ashraf and Sultan, 2017). It has been shown that at different concentrations, individual genotypes of turmeric show antioxidant and antimicrobial activity (Mishra et al., 2018). There are many medicinal plants having importance in a variety of scientific disciplines. Based on diversity and different climatic conditions, India, China, and Iran have more than 100 endemic and unique species of medicinal plants which show various kinds of biological and pharmaceutical properties (Ghasemi et al., 2017; Mohammadhosseini, 2017; Mohammadhosseini et al., 2017; Mohadjerani and Asadollahi, 2019; Mohammadhosseini et al., 2019; Nahar and Sarker, 2019; Nangue et al., 2019). Turmeric shows virtually no side effects and has a great potential to be considered as a reliable source of new drugs for the treatment of a number of diseases (Mishra et al., 2015; Dyab et al., 2016; Kim et al., 2016; Park et al., 2017; Saccol et al., 2017; Zhou et al., 2017). The performance of a genotype mainly depends on environmental interactions. Evaluation of genotype x environment interaction shows the buffering capacity of the population (Gupta et al., 1977). During stability analysis, the yield component is considered as the main criterion for effective improvement and the evaluation of a variety of samples by a plant breeder (Lerner, 1958). The genetic variability present in the population is responsible for the success of any plant breeding program (Gupta et al., 2015). It is an outcome of the interactions among different factors of plants and the environment. Eberhart and Russell (1966) interpreted that a stable germplasm/accession is represented by 1 having regression ( $b_i=1$ ) and  $S^2_{di}=0$ , i.e. least deviation from linearity. According to linear regression of a genotype and measure of stability, a genotype with the least deviation should be considered as the stable one and vice versa (Samuel et al., 1970; Paroda and Hayes, 1971). In the current work on G X E interaction for yield and yield traits of turmeric (*Curcuma longa* L.), we have analyzed six objectives: i) ANOVA for individual environment ii) components of variability iii) correlation coefficients iv) path coefficients v) pooled analysis of variance over three environments vi) and stability parameters.

## 2. Experimental

### 2.1. Plant material

The planting materials for the present investigation were collected from different states/place of India comprised a total of 17 genotypes/accessions of *Curcuma longa* L. of diverse origins such as CSIR-CIMAP Gene Bank (13), Narendra Dev University (2), Pantnagar (1) and Assam (1) (Table 1).

### 2.2. Experimental field and their environment/location

The present investigation was done at two locations of CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow, and one location of CSIR-CIMAP research center Pantnagar, Uttarakhand. The genotypes were grown at two different agroclimatic conditions and three different soil conditions for three consecutive years (2015-2016, 2016-2017, and 2017-2018) in a

completely RBD, replicated thrice having row length 3 m each and plant to plant distance of 50 cm. The first experimental site CSIR-CIMAP, Lucknow, Uttar Pradesh located at 26.5°N latitude and 80.50°E longitude, and 120 m above mean sea level having climate semiarid to subtropical. The soil condition was loamy soil (pH 6-7) and sandy loam soil (pH ranges from 5.8-6.0). Another experimental location was situated at the research farm of CSIR-CIMAP, Pantnagar, Uttarakhand at coordinates 29°N, 79.38°E, an altitude of 243.84 m in the foothills of Himalaya in North India with a sub-tropical and humid climate. The soil condition was clay loam (pH 7.1). The duration of monsoon started from the middle of June to September. At both locations, crops were harvested after 10 months of planting. The data were recorded for thirteen economic traits on five randomly selected representative plants per row per replications, namely length of leaves = LL; width of leaves = WL; length of petiole = LP; length of rhizome = LRz; rhizome dry weight = RzDW; rhizome fresh weight = RzFW; germination days = GD; days to leaves emergence = DLE; number of leaves = NL; stipulated tuber length = STL; height of plant = HP; rhizome thickness = RzT; stipulated tuber thickness = STT; rhizome yield = RzY.

### 2.3. Germplasm collection and evaluation by statistical analysis

The ANOVA for Randomized Block design was estimated by Statistical Software 4.0 version. Statistical analyses were done based on Panse and Sukhatme (1989) and Singh and Chaudhary (1985). Based on Burton and de Vane (1953) and Johnson et al (1955), heritability in a broad sense and expected genetic advance in percent of mean was calculated. According to Dewey and Lu (1959), the pooled mean values of all the traits were subjected to correlation and path coefficient analyses. Estimation of stability and genotype x environment interactions was analyzed using Eberhart and Russell (1966). The pooled mean values of the three years (2015-2016, 2016-2017, and 2017-2018) for all the thirteen traits in seventeen selected genotypes/accessions were subjected to stability analyses under different environments. Let us consider that there are 'v' genotypes whose performance has been tested in 'n' environments. Considering  $Y_{ij}$  as the mean observation of ith-variety in the jth environment. The field view of turmeric germplasm/accessions for all three soil conditions has been shown (Fig. 1).

## 3. Results and Discussion

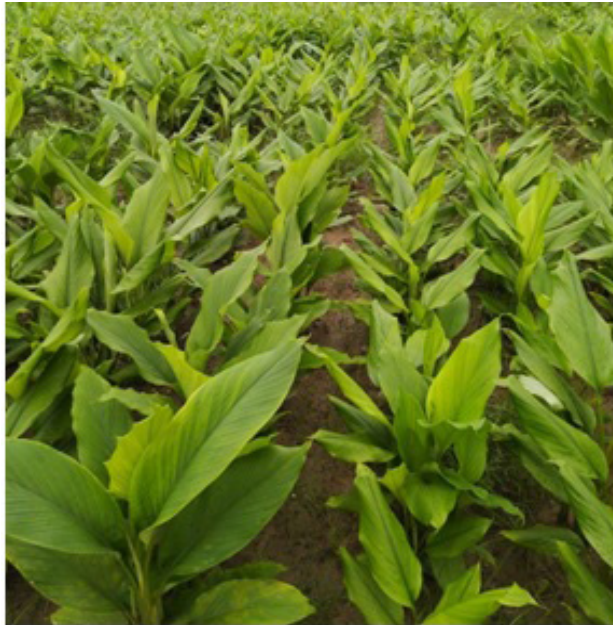
### 3.1. ANOVA and genetic parameters

The ANOVA for different traits in all three environments has been shown in Table 2. The ANOVA results were observed as highly significant differences ( $P<0.01$ ) for rhizome yield among seventeen genotypes of turmeric and their thirteen traits. This accounted for the genetic variability among genotypes/accessions of turmeric grown in three years. The significant differences

**Table 1**

Geographic distribution of 17 genotypes/accessions of *Curcuma longa* L.

S. No.	Accessions	Places of collection	Height of plant	Rhizome habit	Rhizome shape	Colour of TS of rhizome	Leaf colour
1	CIMCH14101	CSIR-CIMAP, Pantnagar, Uttarakhand (India)	tall	intermediate	oblong	orange	green
2	CIMCH14107	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	medium tall	compact	globular	orange	green
3	CIMCH14122	N.D. University, Faizabad U.P. (India)	tall	compact	oblong	orange	green
4	CIMCH14123	N.D. University, Faizabad U.P. (India)	tall	intermediate	oblong	orange	dark green
5	CIMCH14127	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	compact	oblong	orange	dark green
6	CIMCH14130	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	intermediate	oblong	orange	dark green
7	CIMCH14144	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	intermediate	oblong	orange	green
8	CIMCH14152	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	medium tall	intermediate	oblong	orange	dark green
9	CIMCH14157	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	intermediate	oblong	orange	dark green
10	CIMCH14159	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	medium tall	compact	oblong	orange	green
11	CIMCH14160	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	medium tall	loose	oblong	orange	light green
12	CIMCH14164	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	intermediate	oblong	orange	light green
13	CIMCH14165	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	compact	oblong	dark orange	green
14	CIMCH14171	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	medium tall	compact	oblong	yellow	dark green
15	CIMCH14190	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	intermediate	globular	orange	dark green
16	CIMCH14208	Assam, (India)	tall	intermediate	oblong	orange	light green
17	CIMCH14229	CSIR-CIMAP Gene Bank Lucknow U.P. (India)	tall	compact	oblong	dark orange	green



**i) Loamy soil field view**



**ii) Clay loam soil field view**



**ii) Sandy loam soil field view**

**Fig. 1.** Field view of turmeric germplasms/genotypes/accessions for all three soil conditions

for traits in a particular environment showed that the genotypes had a remarkable variation for that particular trait. The estimates of range, general mean, and coefficient of variation, heritability, genetic advance, and GAM concerning three environments viz.,  $E_1$ ,  $E_2$ , and  $E_3$  for different traits have been shown in Table 3. The results derived from this table were described according to traits. The genotypic coefficient of variation for LL (cm) was maximum in  $E_1$  (6.27%) followed by  $E_2$  (5.13%), while it was minimum in  $E_3$  (5.06%). The same pattern was followed by the phenotypic coefficient of variation. The heritability in the broad sense for this trait was high but the GAM was medium in the case of all three environments. For the width of leaves, the highest GCV (30.61%) and PCV (34.75%) were observed in  $E_1$ . In  $E_3$ , both GCV (17.69%) and PCV (17.92%) were minimum. The estimates of heritability ranged from 96.40% to 99.10% along with high GAM for each environment. In the case of the length of petiole, the highest GCV (18.03%) and PCV (20.28%) was found in  $E_1$ , whereas the lowest GCV (10.30%) and PCV (10.80%) were found in  $E_3$ . High values of heritability coupled with moderate values of GAM were found in all three environments viz.,  $E_1$ ,  $E_2$ , and  $E_3$ . For length LRz (cm), the highest GCV (9.07%) and PCV (10.10%) were observed in  $E_1$ , whereas the lowest GCV (6.87%) and PCV (8.15%) were observed in  $E_3$ . The estimate of high heritability (80.70% and 71.00%) with a low value of GAM was exhibited by  $E_1$  followed by  $E_3$ , whereas environment  $E_2$  showed medium heritability with low GAM. For RzDW (gm), the highest GCV (6.83%) and GAM (9.25%) was found in  $E_1$ , whereas the highest PCV (7.62%) was found in  $E_3$ . Additionally, heritability was medium in all three environments for this trait. For RzFW (gm), the highest GCV (7.76%) and PCV (9.72%) were observed in  $E_1$ , whereas the highest heritability, GA, and GAM were observed in the case of  $E_3$  and minimum value for these parameters were observed in  $E_2$ . For GD (n) GCV (5.13%), PCV (6.77%), heritability (73.00%), genetic advance, and the estimates of GAM was maximum in  $E_1$ , while the lowest in  $E_2$ . The heritability ranged from 51.20 to 73.00% in all three environments. For NL (n), the highest GCV (10.89%), PCV (11.24%), heritability (93.90%), GA, and the estimates of GAM were maximum in  $E_1$ . The lowest GCV (8.14%) and PCV (8.54%) were found in  $E_2$ . All three environments exhibited high estimates of heritability which ranges from 88.80 to 93.90%, coupled with high GAM. For STL, the values of GCV in  $E_1$ ,  $E_2$ , and  $E_3$  were 10.20%, 9.91%, and 7.14% respectively, whereas the values of PCV in  $E_1$ ,  $E_2$ , and  $E_3$  were 12.37%, 10.49%, and 7.61%, respectively. Each environment showed high heritability with medium GAM. The highest GCV (14.98%) and PCV (16.22%) were found in  $E_1$  for HP. The lowest value for GCV (10.50%) and PCV (11.99%) was found in  $E_2$ . The estimate of high heritability was shown in all three environments which ranged from 76.70% to 85.30%, whereas GAM was medium in all three environments. For RzT (cm), the values for GCV (17.38%), PCV (28.56%), and heritability (94.30%) were found to be maximum in  $E_1$ . The heritability for all three environments ranged from 91.70% to 94.30%. The GAM ranged from 23.18% to 33.10% and the highest value was observed in again  $E_1$ . For STT, the highest GCV (11.66%),

PCV (12.64%), heritability (85.10%), and the estimates of GAM (22.16%) were observed maximum in  $E_1$ , whereas the lowest GCV (6.36%) and PCV (8.04%) was observed in  $E_2$ . For RzY (q/ha), the highest GCV (26.28%) and PCV (28.12%) was in  $E_1$ , while the lowest value in  $E_3$ . The heritability ranged from 93.60% to 94.00%. The estimates of heritability were highly coupled with high GAM in all three environments viz.,  $E_1$  (50.39%),  $E_2$  (49.14%), and  $E_3$  (48.26%).

### 3.2. Correlations and path coefficient analysis

At phenotypic and genotypic levels, the correlation coefficients were analyzed for 13 traits of 17 accessions on a pooled basis and tested at 5% and 1% level of significance (Table 4). During analysis, it was observed that the phenotypic correlations were lower than the genotypic ones in magnitude for all traits. Despite few exceptions, the traits having a negative association at the phenotypic level generally showed a negative association at the genotypic level. The study of genotypic correlation coefficients revealed that RzY was positively and significantly associated with LL, WL, LP, LRz, RzDW, RzFW, GD, DLE, NL, STL, HP, RzT, and STT. Furthermore, correlation studies among thirteen traits of turmeric show that LL were highly significant and positively correlated with WL (0.60\*\*G, 0.52\*\*P), STL (0.49\*\*G, 0.47\*\*P) and NL (0.41\*\*G, 0.39\*\*P), whereas WL with STL (0.63\*\*G, 0.57\*\*P); LP with RzY (0.56\*\*G, 0.49\*\*P), stipulated tuber thickness (0.40\*\*G, 0.36\*\*P), RzDW (0.36\*\*G, 0.29\*\*P) and RzT (0.28\*\*G, 0.26\*\*P). In the same way, LRz correlated with RzY (0.70\*\*G, 0.63\*\*P). RzDW with STT (0.98\*\*G, 0.96\*\*P) and RzY (0.90\*\*G, 0.89\*\*P). RzFW with GD (0.97\*\*G, 0.94\*\*P), RzY (0.95\*\*G, 0.92\*\*P) and less significant and positively correlated with RzT (0.37\*\*G, 0.35\*\*P). RzT was highly significant and positively correlated with RzY (0.88\*\*G, 0.83\*\*P) and HP with RzY (0.69\*\*G, 0.62\*\*P). STL was moderately significant and positively correlated with RzY (0.57\*\*G, 0.55\*\*P), whereas STT with RzY (0.54\*\*G, 0.52\*\*P) and GD with RzT (0.43\*\*G, 0.40\*\*P). NL was less significant and positively correlated with HP (39\*\*G, 0.37\*\*P). On the other hand, LL were highly significant and negatively correlated with RzT (-0.55\*\*G, -0.44\*\*P) STL with RzT (-0.51\*\*G, -0.42\*\*P) and WL with LP (-0.58G, -0.45P), whereas GD with STL (-0.32, -0.29) and RzT (-0.57, -0.48) and RzFW with STL (-0.36, -0.32). These traits were found together as good criteria for the best selection.

### 3.3. Stability of genotypes/clones

During path coefficient analysis, it was found that RzFW (0.250) shows the highest positive direct effect followed by RzT (0.231), HP (0.216), STL (0.210), NL (0.198), RzDW (0.123) and PL (0.112) in percent (Table 5). WL (-0.204), GD (-0.125), and LL (-0.083) had a negative direct effect but showed a maximum positive indirect effect via RzDW. The residual effect of 0.150 showed 90% of yield adequacy of the traits. During the study of pooled ANOVA for different traits, highly significant differences were found among accessions/germplasms

**Table 2** Analysis of variance for 13 agro morphological traits in three different environments to evaluate 17 genotypes/germplasms of *Curcuma longa* L.

S.No.	Traits	Environment-1			Environment-2			Environment-3		
		Replication	Genotypes	Error	Replication	Genotypes	Error	Replication	Genotypes	Error
	<b>S.V.</b>	<b>2</b>	<b>16</b>	<b>32</b>	<b>2</b>	<b>16</b>	<b>32</b>	<b>2</b>	<b>16</b>	<b>32</b>
1	Length of leaves (n)	0.06	0.28**	0.03	0.07	0.20**	0.02	0.03	0.16**	0.01
2	Width of leaves (cm)	0.03	0.09**	0.01	0.02	0.08**	0.01	0.01	0.08**	0.02
3	Length of petiole (cm)	0.34	0.74**	0.04	0.22	0.92**	0.06	0.18	0.89**	0.05
4	Length of rhizome (cm)	0.04	1.20 **	0.03	0.02	0.98**	0.04	0.01	0.86**	0.04
5	Rhizome dry weight (gm)	104.23	1078.29**	76.11	95.14	856.10**	74.09	78.11	632.18**	73.06
6	Rhizome fresh weight (gm)	204.12	2187.31**	119.67	198.73	1732.04**	174.26	152.42	1197.12**	109.53
7	Germination days (n)	0.05	0.26**	0.03	0.06	0.24**	0.03	0.06	0.32**	0.02
8	Number of leaves (n)	0.18	1.64**	0.08	0.16	2.54**	0.06	0.14	1.73**	0.06
9	Stipulated tuber length (cm)	0.2	0.81**	0.05	0.19	0.73**	0.03	0.09	0.56**	0.03
10	Height of plant (cm)	106.72	840.98**	37.32	103.42	542.37**	32.09	91.23	435.21**	33.11
11	R h i z o m e thickness (cm)	0.04	0.32**	0.02	0.03	0.45**	0.01	0.02	0.17**	0.03
12	Stipulated tuber thickness (cm)	0.04	0.24**	0.01	0.03	0.12**	0.02	0.02	0.07**	0.01
13	Rhizome yield (q/ha)	976.42	22389.91**	387.72	854.28	22171.89**	318.12	470.84	21456.12**	243.52

\*Significant at 5% probability level

\*\* Significant at 1% probability level

**Table 3**

 Range, mean, coefficient of variation, heritability and genetic advance for thirteen traits and three environments in seventeen genotypes of *Curcuma longa* L.

S.No.	Traits	Environment	Range	General mean + SE	Genotypic coefficient of variation	Phenotypic coefficient of variation	Heritability in broad sense (%)	Genetic advance	Genetic advance in percent of mean
		1	2	3	4	5	6	7	8
1	Length of leaves (n)	E <sub>1</sub>	17.00-21.00	18.77 + 0.52	6.27	7.29	70.7	1.71	9.13
		E <sub>2</sub>	17.12-21.00	18.80 + 0.58	5.13	6.77	73	1.91	10.18
		E <sub>3</sub>	16.95-21.15	18.83 + 0.67	5.06	6.68	67.3	1.48	7.89
2	Width of leaves (cm)	E <sub>1</sub>	6.87-18.73	9.39 + 0.23	30.61	34.75	99.1	5.89	42.75
		E <sub>2</sub>	6.53-13.98	8.84 + 0.19	18.24	18.44	97.9	3.28	37.18
		E <sub>3</sub>	6.94-14.00	8.83 + 0.21	17.69	17.92	96.4	3.18	34.97
3	Length of petiole (cm)	E <sub>1</sub>	6.61-13.90	8.79 + 0.22	18.03	20.28	97.3	3.22	36.64
		E <sub>2</sub>	7.32-10.33	8.82 + 0.20	10.89	11.24	93.9	1.92	21.74
		E <sub>3</sub>	7.50-10.19	8.80 + 0.22	10.3	10.8	91.9	1.79	20.34
4	Length of rhizome (cm)	E <sub>1</sub>	5.19-6.57	5.90 + 0.21	9.07	10.1	80.7	0.99	16.79
		E <sub>2</sub>	5.12-6.76	5.96 + 0.39	6.93	10.68	72.2	0.55	9.27
		E <sub>3</sub>	5.30-6.63	5.94 + 0.21	6.87	8.15	71	0.71	11.92
5	Rhizome dry weight (gm)	E <sub>1</sub>	84.31-112.16	96.00 + 4.93	6.83	8.92	73.3	8.88	9.25
		E <sub>2</sub>	85.18-110.01	95.57 + 4.55	6.08	8.42	75.1	8.63	9.03
		E <sub>3</sub>	83.17-108.12	96.11 + 4.24	5.37	7.62	77.8	7.5	7.81
6	Rhizome fresh weight (gm)	E <sub>1</sub>	250.73-340.17	283.55 + 13.56	7.76	9.72	88.7	36.18	12.76
		E <sub>2</sub>	260.18-322.16	283.79 + 11.54	6.43	8.13	86.5	29.71	10.47
		E <sub>3</sub>	246.35-320.63	282.54 + 10.25	7.66	8.78	89.36	38.56	13.65
7	Germination days (n)	E <sub>1</sub>	17.12-21.00	18.80 + 0.58	5.13	6.77	53	1.91	10.18
		E <sub>2</sub>	17.50-20.05	18.73 + 0.58	3.79	5.34	51.2	1.03	5.53
		E <sub>3</sub>	16.95-21.15	18.83 + 0.67	5.06	6.68	57.3	1.48	7.89
8	Number of leaves (n)	E <sub>1</sub>	7.32-10.33	8.82 + 0.20	10.89	11.24	93.9	1.92	21.74
		E <sub>2</sub>	7.85-10.00	8.85 + 0.22	8.43	8.94	88.8	1.48	16.36
		E <sub>3</sub>	7.88-10.32	8.93 + 0.19	8.14	8.54	90.9	1.43	15.99
9	Stipulated tuber length (cm)	E <sub>1</sub>	4.48-6.22	5.21 + 0.20	10.2	12.37	68.8	0.88	16.82
		E <sub>2</sub>	4.25-6.17	5.24 + 0.15	9.91	10.49	59.2	1.01	19.28
		E <sub>3</sub>	4.36-6.01	5.21 + 0.11	7.14	7.61	67.8	0.72	13.78
10	Height of plant (cm)	E <sub>1</sub>	82.01-142.87	110.91 + 5.63	14.98	16.22	85.3	31.6	28.5
		E <sub>2</sub>	79.93-126.66	105.92 + 4.73	11.23	13.4	83.4	24.37	23
		E <sub>3</sub>	85.78-130.05	108.58 + 5.13	10.5	11.99	76.7	20.57	18.95
11	Rhizome thickness (cm)	E <sub>1</sub>	2.53-3.11	2.86 + 0.11	17.38	28.56	94.3	1.37	33.1
		E <sub>2</sub>	2.49-5.43	3.03 + 0.13	14.54	16.13	91.7	1.31	23.18
		E <sub>3</sub>	2.03-3.21	2.81 + 0.09	13.68	14.2	92.8	0.76	27.14
12	Stipulated tuber thickness (cm)	E <sub>1</sub>	2.01-2.97	2.38 + 0.10	11.66	12.64	65.1	0.53	22.16
		E <sub>2</sub>	2.11-2.80	2.41 + 0.10	7.87	9.45	69.4	0.33	13.51
		E <sub>3</sub>	2.00-2.66	2.36 + 0.09	6.36	8.04	62.5	0.25	10.35
13	Rhizome yield (q/ha)	E1	243.30-488.32	343.82 + 18.50	26.28	28.12	93.6	173.27	50.39
		E2	250.56-480.33	339.72 + 18.13	25.14	25.98	93.7	170.33	49.14
		E3	238.39-483.43	340.38 + 17.24	24.63	25.4	94	167.49	48.26

\*, \*\* Significant at 5% and 1% level, respectively. P&lt;0.05; \*\*P&lt;0.0

Length of leaves = LL; width of leaves = WL; length of petiole = LP; length of rhizome = LRz; rhizome dry weight = RzDW; rhizome fresh weight = RzFW; germination days = GD; number of leaves = NL; stipulated tuber length = STL; height of plant = HP; rhizome thickness = RzT; stipulated tuber thickness = STT; rhizome yield = RzY.

**Table 4** Genotypic (bold) and phenotypic associations/correlations among thirteen economic traits of seventeen germplasm of turmeric (*Curcuma longa* L.).

<b>Correlation</b>	<b>LL</b>	<b>WL</b>	<b>LP</b>	<b>LRz</b>	<b>RzDW</b>	<b>RzFW</b>	<b>GD</b>	<b>NL</b>	<b>STL</b>	<b>HP</b>	<b>RzT</b>	<b>STT</b>	<b>RzY</b>
LL	-	0.60**	-0.19	0.02	-0.03	-0.04	-0.05	0.41**	0.49**	-0.21	-0.55**	-0.04	-0.02
WL	0.52**	-	-0.58**	0.13	-0.15	-0.32*	-0.29*	-0.08	0.63**	-0.04	-0.57**	-0.2	-0.03
LP	-0.16	-0.45**	-	-0.03	0.36**	0.19	0.17	0.09	-0.05	0.19	0.28*	0.40**	0.56**
LRz	0.01	0.05	-0.01	-	-0.16	0.13	0.15	-0.09	-0.08	0.12	-0.23*	-0.19	0.70**
RzDW	-0.02	-0.15	0.29*	-0.12	-	0.17	0.15	0.13	-0.2	0.05	-0.09	0.98**	0.90**
RzFW	-0.02	-0.26*	0.11	0.1	0.15	-	0.97**	0.15	-0.36**	-0.21*	0.37**	0.16	0.94**
GD	-0.03	-0.25*	0.15	0.13	0.11	0.95**	-	0.05	-0.32**	-0.09	0.43*	0.18	0.06
NL	0.39*	0.004	-0.13	-0.05	0.09	0.13	0.04	-	-0.22	0.39**	0.13	0.17	0.12
STL	0.47**	0.57**	0.05	-0.07	-0.16	-0.32*	-0.29*	-0.18	-	0.05	-0.51**	0.22	0.57**
HP	-0.003	-0.06	-0.03	0.1	0.03	-0.19	-0.07	0.37**	-0.02	-	0.04	0.19	0.69**
RzT	-0.44*	-0.48**	0.26	-0.19	-0.05	0.35**	0.40**	0.12	-0.42	0.02	-	0.09	0.88**
STT	-0.03	-0.17	0.36	-0.12	0.96**	0.12	0.12	0.15	-0.19	0.13	0.05	-	0.54**
RzY	-0.02	-0.01	0.49**	0.63**	0.89**	0.92**	0.05	0.11	0.55**	0.62**	0.83**	0.52**	-



**Table 5** Direct (bold) and indirect effects on thirteen economic traits related to path analysis in turmeric (pooled basis).

	LL	WL	LP	LRz	RzDW	RzFW	GD	NL	STL	HP	RzT	STT	RzY (g)
LL	<b>-0.083</b>	-0.106	0.116	-0.15	0.076	0.047	0.061	0.219	0.03	0.105	0.09	0.157	0.562
WL	-0.065	<b>-0.204</b>	0.208	-0.163	0.183	0.12	-0.213	0.089	0.104	0.203	0.119	0.099	0.645
LP	0.058	0.202	<b>0.112</b>	-0.204	0.075	0.192	-0.17	0.246	0.059	-0.121	0.087	0.212	0.538
LRz	0.039	0.102	-0.227	<b>0.077</b>	0.115	0.163	0.091	0.069	0.078	-0.118	0.145	-0.161	0.718
RzDW	0.14	-0.218	0.104	0.155	<b>0.123</b>	0.098	-0.146	-0.157	-0.111	0.096	0.12	0.206	0.678
RzFW	0.032	-0.103	0.205	-0.111	-0.178	<b>0.25</b>	-0.21	0.224	0.103	0.19	0.089	-0.068	0.726
GD	-0.021	-0.063	0.113	0.11	0.117	0.018	<b>-0.125</b>	-0.029	0.008	0.243	-0.066	0.115	0.435
NL	0.073	0.058	0.189	0.016	0.263	-0.112	0.077	<b>0.198</b>	0.006	0.045	-0.178	0.081	0.716
STL	0.088	0.007	-0.146	0.005	0.176	0.064	-0.123	0.04	<b>0.21</b>	0.136	0.09	0.063	0.61
HP	-0.137	0.21	0.013	0.02	-0.018	-0.108	0.216	0.005	0.038	<b>0.216</b>	0.072	0.23	0.757
STT	0.085	-0.098	0.214	0.073	0.21	0.116	-0.197	-0.157	-0.121	0.013	<b>0.127</b>	0.007	0.65
RzT	0.029	0.007	-0.123	0.013	0.118	0.216	-0.098	0.104	0.007	-0.142	0.253	<b>0.231</b>	0.738

Length of leaves = LL; width of leaves = WL; length of petiole = LP; length of rhizome = LRz; rhizome dry weight = RzDW; rhizome fresh weight = RzFW; germination days = GD; number of leaves = NL; stipulated tuber length = STL; height of plant = HP; rhizome thickness = RzT; stipulated tuber thickness = STT; rhizome yield = RzY.

**Table 6**  
Pooled analysis of variance for different traits in turmeric.

Source of variation	D.F.	LL (cm)													Rh Yield (q/ha)
		1	2	3	4	5	6	7	8	9	10	11	12	13	
Genotypes (G)	16	0.48**	0.16**	0.70**	0.94**	895.35**	2123.89**	1.07**	2.64**	0.84**	641.91**	0.07**	0.32**	31401.46**	
Environments (E)	2	0.09**	0.02	0.09**	0.09*	105.23**	265.71**	0.07**	0.05	0.02	122.33*	0.01	0.16**	1229.19**	
GxE	32	0.08**	0.17	0.08**	0.13**	78.45**	200.26**	0.05**	0.09*	0.03	55.46*	0.04**	0.14**	519.50**	
E + (GxE)	24	0.08**	0.03	0.08**	0.12**	81.76**	198.46**	0.05**	0.09*	0.03	55.67*	0.04**	0.14**	520.13**	
E (linear)	1	0.28**	0.02	0.28**	0.04	421.28**	795.37**	0.22**	0.15	0.05	367.43**	0.02	0.48**	3688.80**	
GxE (linear)	16	1.00**	0.02	1.00**	0.05	107.32**	278.72**	0.11**	0.14**	0.04	53.45**	0.04**	0.36**	630.09**	
P o l l e d deviation	17	0.07	0.03	0.07	0.16	96.34	210.75	0.02	0.06	0.02	57.21	0.04	0.03	556.2	
Pooled error	96	0.02	0.03	0.03	0.06	48.56	116.18	0.04	0.06	0.06	38.15	0.02	0.02	293.03	

(Table 6). Except for WL, LL, STL, and STT, the differences amongst the environment were significant for all traits. For LL, PL, LRz, RzDW, RzFW, GD, STT, RzT, and RzY, genotype x environment interactions were highly significant, whereas the differences significant for HP and NL. Based on three stability parameters viz., high mean yield ( $X_i$ ) regression coefficient ( $b_i$ ) approaching one, and mean square deviations from regression ( $S^2d_i$ ) near zero, the stable accessions were selected. Genotypes with high mean performance, regression coefficient around one and low deviation mean square were identified as an average stable accession, which show uniformity over three environments/years. However, for any accession having ( $X_i$ ) and ( $b_i$ ) less than 1 would be responsible to show above average stability adapted to low yielding environments/years whereas when all these parameters becomes greater than 1 represents the accessions with below average stability although they are suitable for high yielding environments/years. Evaluation of the obtained results and further partitioning of clones/genotypes of turmeric-based on Eberhart and Russell (1966) model, for an individual parameter of stability ( $X_i$ ,  $b_i$ , and  $S^2d_i$ ), the genotypes CIMCH14171 produced the highest RzY per plant (397.21g) followed by CIMCH14229 (393.7g), CIMCH14130 (304.90g) and CIMCH14144 (301.65g) (Table 7). The regression coefficient ( $b_i$ ) of these accessions/genotypes was above one ( $b_i > 1.00$ ) with low deviation from regression ( $S^2d_i$ ) indicated their responsiveness inclination towards favorable environments/years. The mean performance for all three environments/year, RzFW per plant showed that it ranged from 252.54 g (CIMCH14190) to 393.73g (CIMCH14229). Out of seventeen genotypes, four genotypes, i.e. CIMCH14144, CIMCH14160, CIMCH14130, and CIMCH14229 had significantly higher mean values for RzFW per plant than the general mean, while five accessions/genotypes had a lower mean (Table 7). For nine genotypes, the  $b_i$  was greater than 1, while for eight genotypes, the  $b_i$  value was found to be less than one. For eight genotypes viz., CIMCH14101, CIMCH14144, CIMCH14160, CIMCH14159, CIMCH14190, CIMCH14122, CIMCH14123, and CIMCH14164 the  $S^2d_i$  was significantly greater than zero, while the rest of the genotypes had non-significant  $S^2d_i$ . The genotypes CIMCH14171 showed  $b_i > 1$  and  $S^2d_i = 0$  which interpret that for a favorable environment these genotypes were suitable. CIMCH14229 and CIMCH14130 showed  $b_i < 1$  with  $S^2d_i = 0$  which indicated that these genotypes were suitable for unfavorable environments. For rhizome yield, the mean performance over all the three environments showed that RzY ranged from 241.41 q/ha (CIMCH14127) to 579.67 q/ha (CIMCH14229). Six genotypes, namely CIMCH14107, CIMCH14171, CIMCH14165, CIMCH14130, CIMCH14208, and CIMCH14229 had significantly higher mean for rhizome yield as compared to their corresponding general mean. Five genotypes showed average mean values, while the remaining genotypes showed lower mean performance for this trait (Table 7). Out of seventeen genotypes, five genotypes had more than 1 regression coefficient, while eight genotypes had less than 1 regression coef-

ficient. Four genotypes showed  $b_i = 1$  viz., CIMCH14171, CIMCH14157, CIMCH14127, and CIMCH14229. For CIMCH14101, CIMCH14144, CIMCH14159, CIMCH14190, CIMCH14152, CIMCH14123, and CIMCH14164  $S^2d_i$  was significant, whereas the rest of the genotypes were characterized by  $S^2d_i = 0$ . The genotype CIMCH14190 with ( $X_i$ ),  $b_i > 1$ , and  $S^2d_i = 0$  indicated that this genotype was more responsive to favorable environments. Two genotypes, namely CIMCH14171 and CIMCH14229 with ( $X_i$ ),  $b_i = 1$ , and  $S^2d_i = 0$  were considered stable for a wide range of environments. Three genotypes viz., CIMCH14165, CIMCH14130, CIMCH14208 had mean values  $b_i < 1$  with  $S^2d_i = 0$ . In the present study, seventeen genotypes of turmeric were analyzed for three environments, i.e.  $E_1$ ,  $E_2$ , and  $E_3$  based on their agro-morphological traits. The assessment of variability in the germplasm was done by calculating range, mean, coefficients of variation at genotypic and phenotypic levels. Eberhart and Russell (1966) model were employed for stability analysis by observing genotype x environment interaction and selecting stable accessions. The ANOVA for all the thirteen traits among the seventeen genotypes in three environments showed a wide range of variation for mean performance under this study (Table 2). The genotypes showing high mean performance for various traits listed in Table 8, which may be used as a standard of genotypes for improving the traits. Genotypes CIMCH14208, CIMCH14190, CIMCH14101, CIMCH14107, and CIMCH14171 show high mean performance for LL (cm). Genotypes CIMCH14107, CIMCH14130, CIMCH14208, CIMCH14229, and CIMCH14190 show high mean performance for WL (cm). Genotypes CIMCH14130, CIMCH14101, CIMCH14208, CIMCH14107 and CIMCH14229 show high mean performance for PL (cm). Genotypes CIMCH14130, CIMCH14101, CIMCH14107, CIMCH14164, and CIMCH14229 show high mean performance for LRz (cm). Genotypes CIMCH14101, CIMCH14229, CIMCH14208, CIMCH14107, and CIMCH14190 show high mean performance for RzDW (gm). Genotypes CIMCH14208, CIMCH14122, CIMCH14127, CIMCH14107, and CIMCH14130 show high mean performance for RzFW (gm). Genotypes CIMCH14144, CIMCH14157, CIMCH14164, CIMCH14171, and CIMCH14107 show high mean performance for GD (n). Genotypes CIMCH14229, CIMCH14101, CIMCH14159, CIMCH14123, and CIMCH14107 show high mean performance for NL. Genotypes CIMCH14107, CIMCH14229, CIMCH14130, CIMCH14208, and CIMCH14127 show high mean performance for STL (cm). Genotypes CIMCH14122, CIMCH14107, CIMCH14160, CIMCH14123, and CIMCH14152 show high mean performance for HP. Genotypes CIMCH14130, CIMCH14101, CIMCH14208, CIMCH14107 and CIMCH14152 show high mean performance for STT (cm). Genotypes CIMCH14229, CIMCH14101, CIMCH14107, CIMCH14152, and CIMCH14190 show high mean performance for RzT (cm). Genotypes CIMCH14229, CIMCH14107, CIMCH14208, CIMCH14130, and CIMCH14171 show high mean performance for RzY (q/ha). During this experiment, a number of variability was observed in all genotypes of turmeric for 13 traits in

**Table 7**Stability parameters for rhizome yield in *Curcuma longa* L.

S.No.	Genotypes	Weight of fresh rhizomes/plant (g)			Rhizome yield (q/ha)		
		$\bar{X}_i$	bi	S <sup>2</sup> di	$\bar{X}_i$	bi	S <sup>2</sup> di
1	CIMCH14101	258.16	1.87	420.56**	291.72	2.18	1550.87**
2	CIMCH14107	289.85	0.41	-45.42	341.57	1.57	83.49
3	CIMCH14144	301.65	1.22	558.72**	259.3	0.52	987.57*
4	CIMCH14171	393.21	1.62	12.97	430.73	1.06	-78.06
5	CIMCH14160	267.55	1.86	562.12**	279.16	2.12	170.15
6	CIMCH14159	279	-0.54	557.71**	289	1.55	940.12*
7	CIMCH14157	261.39	0.67	14.87	302.68	1.07	59.49
8	CIMCH14190	252.54	0.2	612.97**	268.32	-0.92	1407.15**
9	CIMCH14165	288.33	1.87	-33.58	477.04	-1.27	41.53
10	CIMCH14127	258.46	0.9	142.66	241.41	1.15	-89.84
11	CIMCH14144	277.15	1.01	220.04	294.5	0.27	1511.07**
12	CIMCH14130	304.9	-0.92	-53.45	491.53	0.09	-104.88
13	CIMCH14122	283.96	1.68	439.42**	281.21	-1.37	1444.92
14	CIMCH14208	290.97	1.54	41.57	474.98	0.28	-124.36
15	CIMCH14123	269.7	-1.7	559.86**	301.11	-1.21	933.63*
16	CIMCH14229	397.73	0.91	171.85	579.67	1.02	-147.6
17	CIMCH14164	283.8	0.81	410.80**	315.12	1.87	1026.83*
	Population mean	283.37	1	-	304.3	1	-
	SE ± (Population mean)	5.56	0.89	-	6.11	0.85	-

**Table 8**

The superior genotypes of turmeric for different characters based on pooled mean performance.

S. No.	Traits	Genotypes				
		1	2	3	4	5
1	LL (cm)	CIMCH14208	CIMCH14190	CIMCH14171	CIMCH14165	CIMCH14101
2	WL (cm)	CIMCH14165	CIMCH14130	CIMCH14208	CIMCH14229	CIMCH14190
3	LP (cm)	CIMCH14130	CIMCH14165	CIMCH14208	CIMCH14171	CIMCH14229
4	LRz (cm)	CIMCH14130	CIMCH14107	CIMCH14165	CIMCH14164	CIMCH14229
5	RzDW (gm)	CIMCH14171	CIMCH14229	CIMCH14208	CIMCH14165	CIMCH14190
6	Rz FW (gm)	CIMCH14208	CIMCH14122	CIMCH14127	CIMCH14165	CIMCH14130
7	GD (n)	CIMCH14144	CIMCH14157	CIMCH14164	CIMCH14171	CIMCH14165
8	NL (n)	CIMCH14229	CIMCH14165	CIMCH14159	CIMCH14123	CIMCH14171
9	STL (cm)	CIMCH14107	CIMCH14229	CIMCH14130	CIMCH14208	CIMCH14127
10	HP (cm)	CIMCH14122	CIMCH14107	CIMCH14160	CIMCH14123	CIMCH14159
11	STT (cm)	CIMCH14130	CIMCH14107	CIMCH14208	CIMCH14165	CIMCH14159
12	RzT (cm)	CIMCH14229	CIMCH14165	CIMCH14171	CIMCH14159	CIMCH14190
13	RzY (q/ha)	CIMCH14229	CIMCH14165	CIMCH14208	CIMCH14130	CIMCH14171

three environments/years viz.  $E_1$ ,  $E_2$ , and  $E_3$ . The maximum GCV was observed for RzY, WL(cm), PL, HP, STL, RzT, STT, and NL in all environments, whereas, LL (cm), RzDW, RzFW, and GD showed lower values of GCV. The similar results were reported in the case of PCV for different traits. In general, the PCV was higher than GCV, suggesting that the environment played a crucial role in the expression of these traits (Table 3). The findings were congruent to previous studies (Mohanty (1979), Mohanty et al. (1981), Geetha and Prabhakaran (1987), Jalgoankar et al. (1990), Indiresht et al. (1992), Singh (1993), Yadav and Singh (1996), Nirmal and Yamger (1998), Pandey et al. (2002), Singh et al. (2003) and Sinkar et al. (2005). Summing up, the heritability was higher for all the traits in all environments except for GD, STL, and STT. The findings of the present study are in agreement with those of Jalgoankar and Jamdagni (1989), Lynrah et al. (1998), Shanmugasundaram et al. (2000), and Singh et al. (2003). Except for LL and RzDW, the GAM and high heritability estimates resulted in high expected GA. For RzY and HP, high heritability coupled with high GA was also found.

For the development of more efficient accessions/genotypes with increased yield potential, the modification of plant type plays a very important role. Yield is governed by polygenes which make it a complex trait and its improvement depends on the understanding of correlations among components which affect the yield. The genotypic correlation coefficients between different traits were generally similar in sign and nature to the corresponding phenotypic coefficient in the experiment. However, genotypic correlations were larger in magnitude than their corresponding phenotypic values (Table 4). The RzY was positively and significantly associated with LL, WL, PL, LRz, RzFW, RzDW, GD, NL, STL, HP, RzT, and STT. In path coefficient analysis, RzFW shows the highest positive direct effect per plant followed by RzT, HP, STL, NL, STT, RzDW, PL, and LRz, whereas WL followed by GD and LL showed a negative direct effect on RzY at the genotypic level. However, at the phenotypic level, WL, PL, NL, LRz, RzFW, RzDW, STL, HP, STT, and RzT had a positive direct effect on RzY (Table 5). The present findings were proved by Muralidharan et al. (1980), Lal et al. (1986), Singh (1993), Singh and Tiwari (1995), Hazara et al. (2000), Shanmugasundaram et al. (2001), Panja et al. (2002), Pandey et al. (2003) and Tomar et al. (2005).

The pooled analysis of variance for five traits viz., RzFW, RzDW, LRz, the thickness of rhizome, and rhizome yield exhibited highly significant mean square values for genotypes when tested against pooled error, which shows a large amount of variability amongst these accessions. The variances due to G x E interaction were also found to be significant for all five traits (Table 6). Highly significant mean squares due to G x E (linear) against pooled error for RzFW, RzDW, RzT, and RzY suggested the possibility of prediction of the performance of the traits under study. The variance due to pooled deviation was highly significant for studied traits indicating non-linear responses and based on G X E interaction. Mehta and Patel (1983) observed significant G X E interaction for RzY. Singh et al. (1995) also observed significant G X E interaction for yield and its contributing traits.

In the present investigation, we found out several stable genotypes with  $(X_i)$ ,  $(b_i = 1)$ , and  $(S^2d_i = 0)$ . Further, the genotypes with  $(X_i)$ ,  $b_i > 1$ , and  $S^2d_i = 0$  are considered more responsive for favorable environments, whereas the genotypes with  $X_i$ ,  $b_i < 1$ , and  $S^2d_i = 0$  expected to equal or exceed average performance  $(X_i)$  only under unfavorable environments. The results of the present study based on three parameters of the stability model given by Eberhart and Russell (1966) revealed that none of the genotypes had high  $X_i$ ,  $b_i = 1$ , and  $S^2d_i = 0$  for all the five traits. For RzFW, CIMCH14229 was the most desirable genotype across the three environments/year, while CIMCH14190 had  $(X_i)$ ,  $b_i > 1$ , and  $S^2d_i = 0$  were expected to be successfully grown in favorable environments (Table 7). The genotypes CIMCH14171 and CIMCH14229 had a high mean  $(X_i)$ ,  $b_i = 1$ , and  $S^2d_i = 0$  exhibited greater stability over a wide range of environments. Concerning RzFW per plant three genotypes viz., CIMCH14165, CIMCH14130, CIMCH14208 had high mean values,  $b_i < 1$  with  $S^2d_i = 0$  which indicated that these genotypes were suitable for unfavorable environments for RzY. For RzY, CIMCH14107 showed suitability under only favorable environments. The stability parameters for RzY revealed that CIMCH14171 and CIMCH14229 had  $(X_i)$ ,  $b_i = 1$ , and  $S^2d_i = 0$  were found stable for a wide range of environments. In turmeric, only a few works on phenotypic stability have been reported by Mehta and Patel (1983), Shahi et al. (1994a and 1994b), Singh et al. (1995) and Kumar and Sankaran (1998).

#### 4. Concluding remarks

The present work "stability analysis for yield and quality characters in seventeen genotypes and thirteen traits of turmeric (*Curcuma longa* L.)" was carried out to raise the normal crops. The salient findings of the study have been summarized. The ANOVA for different traits in all three environments shows significant differences by revealing a wide genetic diversity among the accessions/genotypes. Based on per se performance the genotype CIMCH14229 followed by CIMCH14171, CIMCH14130, and CIMCH14144 produced the highest rhizome yield per hectare. The PCV was higher than GCV for all the traits in all environments/years. The estimates of heritability in the broad sense were higher for all the traits in all environments with the exception of GD, STL, and STT. To conclude, rhizome yield is the most important trait which is positively and significantly associated with LL, WL, PL, LRz, RzFW, RzDW, GD, NL, STL, HP, RzT, and STT. The stability parameters revealed that no genotype exhibit average stability for all the traits. For RzFW, CIMCH14229 emerged as the most desirable genotype in all three environments/years, while CIMCH14190 was expected to be successful when grown in favorable environments. The genotypes CIMCH14171 and CIMCH14229 exhibited greater stability over a wide range of environments. For RzY, three genotypes viz., CIMCH14165, CIMCH14130, CIMCH14208 were suitable for growing in unfavorable environments. For RzY, CIMCH14107 showed suitability under only favorable environments. The stability parameters for rhizome yield revealed that CIMCH14107 and CIMCH14229 were



considered stable for a wide range of environments. Additionally, the study of genotype x environment interactions and estimation of their stability parameters available in genotypes under different environmental conditions has wide scope and application.

### Conflict of interest

The authors declare that there is no conflict of interest.

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