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Utilization of the most recent GGE biplot to locate stable genotypes in turmeric using the well-liked Eberheart Russell stability model

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ABSTRACT

GGE and AMMI biplot methods with Eberhart and Russell regression model were applied on the set of twelve indigenous turmeric genotypes grown in nine environments for quick and relevant method to delineate genotype by environment interaction, stable genotypes and environmental discrimination. The average rhizome yield over the locations was depicted as 12.01 ton/ha, which ranged from 7.87 ton/ha (Jagdalpur) to 20.02 ton/ha (Raigarh). The genotype CG Haldi 2 (16.61 ton/ha) exhibited the highest rhizome yield followed by IT 36 (15.00 ton/ha), over national checks Roma (13.53 ton/ha), Suranjana (11.73 ton/ha) and over local check CG Haldi -1 (10.57 ton/ha). As per Eberhart and Russell model, the genotypes CG Haldi 2 (IT 10), CG Raigarh Haldi-3 (IT 36), Roma, and Narendra Haldi -1 were best performing entries while the performance of BSR 2, IT 38, Suranjana, CG Haldi-1, IT 7, and IT 8 were varied with change in environments. In AMMI analysis, IPCA 1 (62.60 %), IPCA 2 (21.80 %), IPCA 3 (11.70 %), and IPCA 4 (2.60 %) were explained the interaction mean squares, respectively. While, in GGE biplot, PC 1 and PC 2 captured 47.28 % and 34.62 % interaction variation, respectively. The genotypes T-111 (CG Haldi-2), T-101 (IT 36), and national check T-106 (Roma) were high yielding and as well as found stable in GGE and AMMI-1 biplot. The test environments RG 17, RG 16 and RG 15 exhibited different niches, whereas, AM 17, AM 16, JD 16, JD 17, JD 15 and AM 15 were representative with better discriminating ability. Between biplot models applied, the GGE biplots were clear in visualization for polygon view, genotypic stability and environmental discrimination. The GGE method considered both G+GE for biplot generation and found most suitable for stability analysis.

Key words: Indigenous turmeric, AMMI and GGE biplots, genotype × environment interaction, rhizome yield.

INTRODUCTION

Turmeric or haldi (*Curcuma longa* L.) is the mainstay to livelihood of all the human beings residing in tropical, semi-arid tropics regions of the world. Although it is native to South Asia, especially India, it is grown throughout the world in many warm climates, including Latin America, Taiwan, Thailand, China, Haiti, Jamaica, Pakistan, and Peru (Weiss 12). It can be found growing widely over India, although it thrives in areas with annual rainfall between 1000- and 1500-mm. Andhra Pradesh, Karnataka, Kerala, Odisha, Maharashtra, and Tamil Nadu are the major states in India that cultivate turmeric (Muthusamy, 8). Total spices area cultivated in Chhattisgarh was 67,325 thousand hectares with production of 466.88 thousand metric tons (MT) and with productivity of 6.32 MT /ha, while turmeric is grown on 11.868 hectares producing in 106.96 thousand MT with average productivity of 9.01 ton/ha (Dept. of Agril., Govt. Chhattisgarh 2024-25). In India it is grown on 290.9 thousand hectares' area with a total production of 1116.12 thousand tons and productivity of 3.83 MT/ha (State Agri/Hort. Departments/DASD Kozhikkode).

The growing environment of turmeric has a significant impact on its performance. The turmeric plant grown in shade had high production, productivity and quality as compared to open field condition (Srikrishnah and Sutharsan, 10). the presence of significant phyto-constituents like curcumin, oleoresin, and essential oil makes turmeric a useful therapeutic medicinal plant (Suresh *et al.*, 11). Owing to its high demand and susceptibility to fertilizers, its output fluctuates constantly depending on input availability. The very limited information on genotype × environment as well as stability study of turmeric is reported in Chhattisgarh, which limits the availability of high-yielding genotypes in a variety of environments. The present study consists of evaluation of different set of selected indigenous genotypes of turmeric in different Agro-climatic zones of Chhattisgarh by using the conventional stability model developed by Eberheart and Russell, (3). Additionally, the multiplicative interaction model (AMMI), additive main effects, and genotype and genotype × environment interaction effects (GGE) model are used to know the detection of G × E

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interaction in terms of the crossover effect resulting from great changes in the ranking of the genotypes across the environments and in visualizing G × E effects in graphical representation (Anandraj *et al.,* 1; Gauch, 5; Gauch *et al*., 6). Hence, this study was conducted to identify stable genotypes of indigenous turmeric for different environments of Chhattisgarh by multilocation testing through IGKV funded project MLT Turmeric (GPB 24).

MATERIALS AND METHODS

The experimental materials comprised of twelve indigenous Turmeric genotypes (Table 1). Out of 12 genotypes, Roma, Suranjana, BSR 2 and Narendra Haldi -1 were national checks while CG Haldi 1 (CG Haldi-1) as state check/local check. The field trials were conducted during 2015-16, 2016-17 and 2017-18 at three different Agro-Climatic Zones of Chhattisgarh i.e. Chhattisgarh plains at CARS, Raigarh [21.8974° N, 83.3950° E], Bastar Plateau at SG CARS, Jagdalpur [19.0741° N, 82.0080° E] and Northern Hills at RMD CARS, Ambikapur [23.1355° N, 83.1818° E; elevation 623 m]. The experiment was conducted in Randomised Block Design (RBD) in three replications having ten rows plot with row to row spacing of 30 cm and row length of one meter). All the standard package and practices were adopted to raise the good crop. The crop was harvested at physiological maturity stage i.e. when leaves start yellowing and complete dried. The matured rhizome showed complete development of colour and distinct scales appears on rhizome. The manual harvesting is done by digging plants and clumps are collected by hand. At harvest rhizome yield was determined for each genotype at each test environments. The observations were recorded on days to maturity, number of tillers per plant and number of leaves per plant at research farm of College of Agriculture and Research Station, Raigarh. The GGE, AMMI biplots and Eberhart and Russell regression analysis were generated using R software (Gauch *et al*., 6; Kang *et al*., 7). Eberheart and Russell, 3) model is widely adapted method but with inclusion of a greater number of genotypes and simultaneously the assumption of linear response of genotypes to environments restricts its application (Flores *et al*., 4). GGE biplot method is environment centred SVD model and graphically addresses which won where, genotypic stability and environmental discrimination etc. (Yan *et al*., 15). The polygon view of GGE-biplot is very quick way to visualize the interaction patterns between genotypes and environments (Dehghani *et al*., 2; Yan *et al.,* 15).

Table 1: Origin and parentage of 12 turmeric genotypes.

Genotype No.	Entry No.	Genotype Code	Accession No.	I.C. No.
1	T-101	IT-36	RTS 36	626539
2	T-102	IT-9	RTS 13	626522
3	T-103	IT-8	RTS 10	626521
4	T-104	IT-7	RTS 8	626520
5	T-105	CG Haldi-1	RTS 2	626515
6	T-106	Roma	N.C.	-
7	T-107	Suranjana	N.C.	-
8	T-108	IT-38	RTS 38	626551
9	T-109	BSR-2	N.C.	-
10	T-110	NH	N.C.	-
11	T-111	CG Haldi-2	RTS 14	626523
12	T-112	IT-23	RTS 23	626528

N.C.= National Check

RESULTS AND DISCUSSION

The stable genotype exhibited the lowest G × E interaction and the highest economic yield. Significant genotypic mean squares were shown by the analysis of variance for each location, and the pooled analysis of variance also showed extremely significant differences between genotypes and locations ($P<0.001$), suggesting that there is significant genetic and environmental variation. The mean squares for the G × E interaction was remarkable as well, indicating the variations in genotype performance among the tested environments. Rhizome yields ranged from 4.90 tons/ha (Jagdalpur 2015) to 22.86 tons/ha (Raigarh 2015), with an average of 12.01 tons/ha across the locations. The average rhizome yield by location was found in Raigarh (20.20 tons/ha), Ambikapur (7.95 tons/ha), and Jagdalpur (7.87 tons/ha), in that order. For rhizome yield, the genotype Chhattisgarh Haldi-2 (16.61 ton/ha) showed the greatest value followed by IT 36 (15.00 ton/ha), over national checks Roma (13.53 ton/ha), Suranjana (11.73 ton/ha) and over state check CG Haldi-1 (10.57 ton/ha) Table 5.

The G × E interaction mean squares deduced additional partitioning into components classified as linear and non-linear (pooled deviation). Significant heterogeneity in genotypes across environments was seen in the linear interactions. The genotypes CG Haldi-2 (μ=16.61 ton/ha, bi = 1.16 and S^2di = -9.30, IT 36 as CG Raigarh Haldi-3 (μ=5.06 ton/ha, bi= 0.96 and S^2di = -16.15), shown consistent performance across the environments and considered as wide adaptable genotypes. While the mean rhizome yields of Roma (μ= 13.53 ton/ha, bi = 1.15, and S2di = 5.48), IT 23 (μ= 13.16 ton/ha, bi = 0.94, and S2di = 34.57), and Narendra Haldi -1 (μ= 12.47 ton/ha, bi = 1.42, and S2di = 4.06) were high, they also displayed significant deviations from the regression and will perform under high input environments, adapting their performance according to the surrounding conditions (Table 2). Conversely, the genotypes BSR 2, IT 38, Suranjana, CG Haldi-1, IT 7, IT 8 registered below average rhizome yield with regression coefficient near to unity and exhibited more deviation from the regression were found better for poor environments.

In AMMI ANOVA, there were significant mean squares for genotype (g), location (l), and genotype × location interaction (gl) (Table 3). Significant variation (97.25%) in the total mean squares was explained by the mean squares of the overall treatments (g+l+gl). The location impact accounted for 70.2% of the variation, with genotypic variation (8.92%) and the genotype × location interaction (17.96%) following closely behind (Table 3). The substantial interaction verified the altered relative genotype ranks across the sites once more. The AMMI model (Table 4) amply revealed the existence of the G × E interaction, with four of the major component axes showing statistical significance (P < 0.01). Consequently, the interaction mean squares were described by IPCA 1 (62.60%), IPCA 2 (21.80%%), IPCA 3 (11.70%), and IPCA 4 (2.60%), in that order. First two interaction principal components best explain the interaction sum of squares (Yan and Tinker 13).

Turmeric's G × E interaction effects were seen in all the three Chhattisgarh's Agroclimatic Zones, according to an AMMI statistical investigation. The environments RG 15 (22.86) showed high IPCA1 scores, whereas the genotypes T-111 (CG Haldi-2), T-112 (IT 23), and T-110 (Narendra Haldi-1) showed low IPCA 2 values. In order to assess the stability of the genotypes, AMMI stability values (ASV) were also computed; genotypes with low ASV scores were regarded as the consistent performers (Table 5). Low ASV was seen in the high producing genotypes over grand mean, T-111 (CG Haldi-2) and T-108 (IT 38) respectively. Based on the primary effects on absicca and the mapping of IPCA 1 with IPCA 2 scores of ordinates, AMMI 1 and AMMI 2 biplots

Table 3: ANNOVA for AMMI analysis of genotype by environment interaction on yield of turmeric.

Source of Variation	DF	SS	MSS	F Value	Pr > F
Env	8	12169.60	1521.20	239.04	<.0001
Rep(Env)	18	114.50	6.36	3.51	<.0001
Genotype	11	1543.90	140.36	77.40	<.0001
Env*Genotype	88	3105.80	35.29	19.46	<.0001
Residuals	198	359.00	1.81		
Total	323	17292.80			

Table 2: Stability parameters of Eberhart and Russell joint regression model.

Entry	Genotypes	Treatment mean μ (ton/ha)	REGCOF bi=1	STABPARM $S^2di=0$	Remarks
		Above average mean μ(ton/ha), Bi=1, $S^2di=0$			
11	CG Haldi-2	16.61	1.16	-9.30	Stable genotypes
1	IT 36	15.06	0.96	-16.15	
		Above average mean μ(ton/ha), Bi=1, $S^2di>0$			Responsive to high input environments
6	Roma	13.53	1.15	5.48	
12	IT 23	13.16	0.94	34.57	
10	NH-1	12.47	1.42	4.06	
		Below average mean μ(ton/ha), Bi=1, $S^2di>0$			Poor performing unstable genotypes
2	IT 9	10.88	0.67	8.56	
3	IT 8	8.99	0.85	3.49	
4	IT 7	9.46	0.50	2.73	
5	CG Haldi-1	10.57	0.71	3.42	
7	Suranjana	11.73	1.23	4.21	
8	IT 38	10.10	1.16	3.43	
9	BSR 2	11.54	1.26	5.11	

Table 4: Principal component analysis of the interaction between genotype and environment on turmeric rhizome yield.

Effect	DF	SS	MSS	F Value	Pr > F	Percent	Cumulative %
PC1	18	1943.76	107.99	59.55	<.0001	62.60	62.60
PC2	16	678.50	42.41	23.39	<.0001	21.80	84.40
PC3	14	364.10	26.01	14.34	<.0001	11.70	96.20
PC4	12	81.62	6.80	3.75	<.0001	2.60	98.80
PC5	10	23.65	2.37	1.30	0.2326	0.80	99.50
PC6	8	11.75	1.47	0.81	0.5945	0.40	99.90
PC7	6	2.18	0.36	0.20	0.9765	0.10	100.00
PC8	4	0.22	0.05	0.03	0.9983	0.00	100.00

Table 5: Genotypic and environmental rhizome yield per se with AMMI IPCA scores and ASV.

Entry No.	Genotype	Fresh rhizome yield (ton/ha)	PC1	PC2	ASV	YSI	Rank ASV	Rank Y
T-101	IT-36	15.06	1.61	1.52	4.86	12	10	2
T-102	IT-9	10.88	-1.83	0.85	5.30	19	11	8
T-103	IT-8	8.99	-1.00	-0.06	2.87	16	4	12
T-104	IT-7	9.46	-1.38	1.49	4.23	19	8	11
T-105	CG Haldi-1	10.57	0.14	1.85	1.89	10	1	9
T-106	Roma	13.53	1.26	-0.05	3.61	8	5	3
T-107	Suranjana	11.73	1.30	-0.25	3.74	12	6	6
T-108	IT-38	10.10	0.61	-0.81	1.93	12	2	10
T-109	BSR-2	11.54	1.39	-0.72	4.06	14	7	7
T-110	NH	12.47	1.50	-1.46	4.54	14	9	5
T-111	CG Haldi-2	16.61	-0.74	-0.86	2.28	4	3	1
T-112	IT-23	13.16	-2.86	-1.50	8.33	16	12	4

the genotypes, viz., T-111 (CG Haldi-2), T-101 (IT 36), T-108 (IT 38) were observed with high additive main effects and low interaction effects. While, the environments RG-16, AM-15, JD 15, JD 17, JD 16, AM 16 and AM 17 were found with high interaction and main effects.

The most G × E interactive biplot genotype with stability in the polygon "What-won-where" biplot genotype was identified as the vertex exhibiting the longest detachment from the biplot origin. Based on our analysis, a biplot of the untransformed mean seed yield data created using a standard singular value decomposition model showed that 81.90% (PC1 = 47.28%, PC 2 = 34.62%) of the total GGE variation could be explained by the environment-centered data, demonstrating the model's ability to determine genotype stability across environments.

The genotypes T-111 (CG Haldi-2) and T-101 (IT 36) were the vertex genotypes in the current investigation, and they produced more rhizome yield (Fig. 1) than the grand mean. The graph's eight environments RG-17, RG-16, AM-15, JD-15, JD-17, JD-16, AM-16, and AM-17 were all positioned in the same plane, indicating that there was no discernible difference between them. The RG-15 individual environment was situated on a different plane. The vertex genotypes for environment RG-15 were T-109 (BSR 2), T-107 (Suranjana), T-110 (Narendra Haldi-1), and T-106 (Roma). The genotypes T-104 (IT -7), T-103 (IT 8), T-109 (BSR 2), T-105 (CGH-1), T-102 (IT 9), T-112 (IT 23) were placed in same sector of the graph specifying that the said genotypes were below average rhizome yield and did not fit for cultivation in these studied environments. The nine environments were classified in to two mega environments. The mega environment one includes total eight out of nine environments (AM 15, AM 16, AM 17, JD 15, JD 16, JD 17, RG 16, and RG 17) while RG 15 created separate mega environments.

The genotypes T 111 (CG Haldi-2) > T 101 (IT

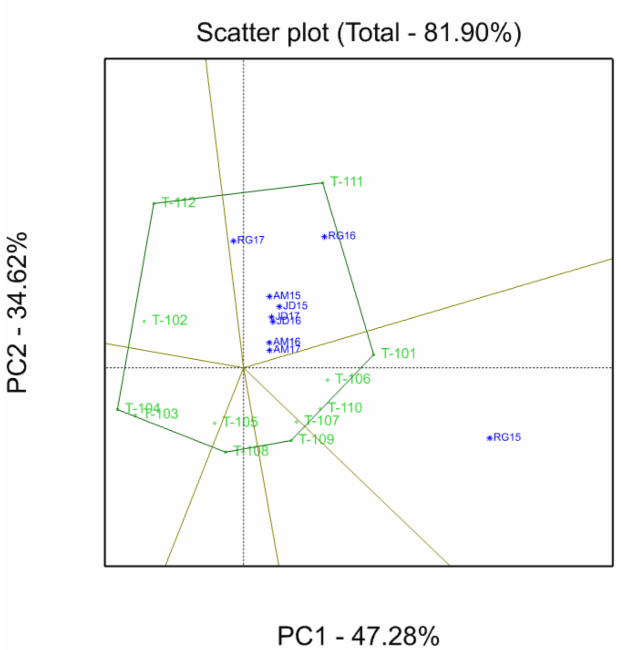

Fig. 1. Which won where pattern in polygon view in GGE model *represents environments and dot for genotypes in Fig. 1 & 2.

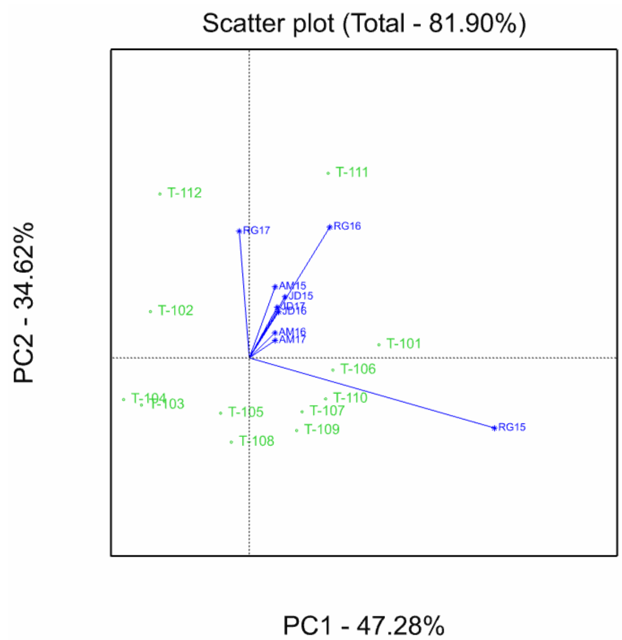

Fig. 2. Environments assessed for representativeness and discrimination in the GGE model.

36) > T 106 (Roma) were presented as having high values on absicca and low interaction with less ordinate values in the AEC (Average Environment Coordination) perspective. Low AEC absicca showed low rhizome yield per se throughout the locations, hence the genotypes T-102 (IT 9), T-112 (IT 23), T-104 (IT 7), and T 103 (IT 8) were deemed poor performers. High per se and steady performance in various situations were characteristics of the chosen genotypes (Yan and Tinker, 13). Long vectors were reported to be used for discrimination in the settings RG 17, RG 16, and RG 15, while acute angles were observed in the environments AM 15, JD 15, JD 17, JD 16, AM 16, and AM 17. (Yan *et al*., 13; Yan and Tinker, 14) also emphasized that the environments with long vectors and less cosines are more discriminating and representative for consideration in future studies. Whereas, taking in account the discriminating ability and representativeness the environments AM 17, AM 16, JD 16, JD 17, JD 15 and AM 15 were regarded as potential environments (Fig. 2). The environments RG 17, RG 16 and RG 15 found highly responsive environment and indicated superior performance of the genotypes in these environments.

In the two-dimensional scatter plot of fresh rhizome yield and its variation coefficient, a low coefficient of variation meant higher yield stability. All the genotypes evaluated in the environments RG 15, RG 16 to JD 15 and JD 16 showed decreased rhizome yield performance while to the environment RG 16, RG 17 to JD 16 and JD 17 showed higher to lower performing environments. The high mean rhizome yielding environment were RG 16, RG 17, AM 16 and AM 17 were common in two-way scatter plot matrix for rhizome yield (Fig. 3 & Fig. 4).

The chief goal of crop improvement programs

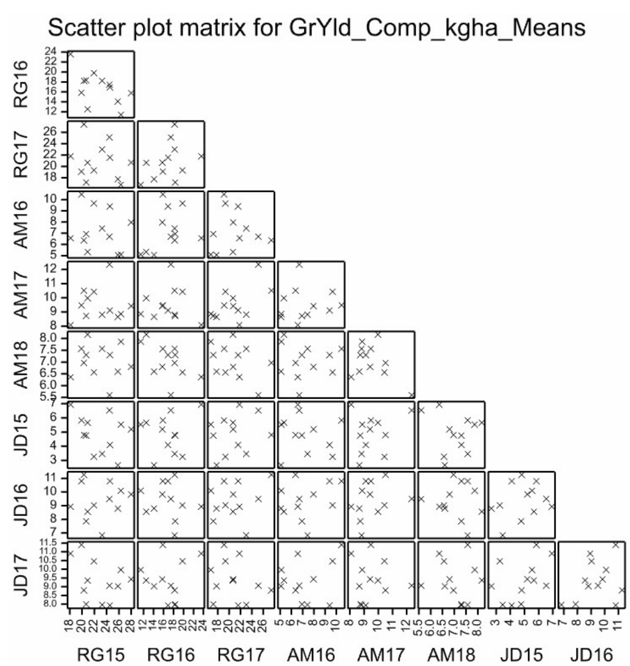

Fig. 3. Scatter plot matrix for rhizome yield (ton/ha).

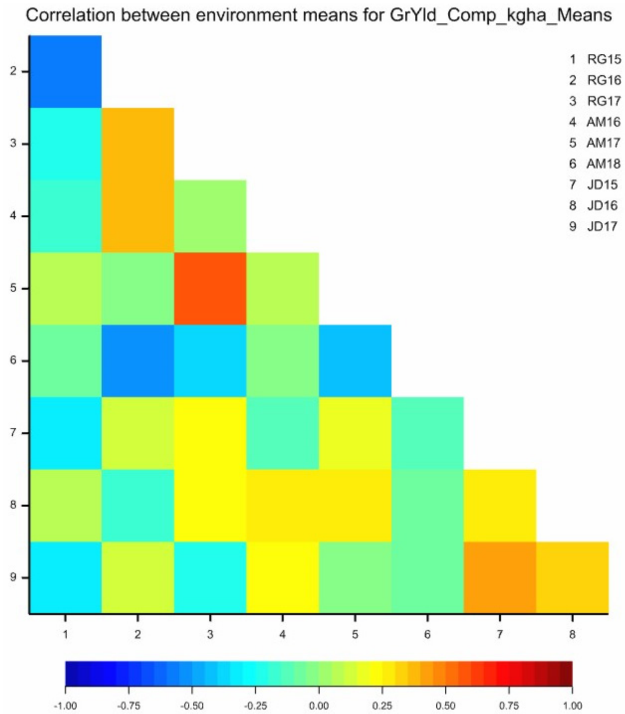

Fig. 4. The environment means and rhizome yield (ton/ha) correlation.

is to create genotypes that are stable and produce well in many environments. Low interaction effects were seen for the genotypes T 111 (CG Haldi-2), T 103 (IT 08), T -104 (IT 7), T 102 (IT 9) and T 112 (IT 23) in the AMMI study. The genotypes T-105 (CGH 1), T-108 (IT 38), T-111 (CG Haldi-2), T-103 (IT 8), and T-106 (Roma) were recognized as having high main effects, low IPCA 2 scores, and ASV while also taking AMMI stability values into account. Rad *et al*. (9), the ASV in two-dimensional views is the coordinate point's distance from the origin for IPCA 1 scores compared to IPCA 2 scores in the AMMI model. In regression model, the genotypes namely T-111 (CG Haldi-2), T-101 (IT 36), T-112 (IT 23), and T-108 (IT 38), exhibited stable performance, while no information for environmental specific genotypes and environmental interactions could be generated.

The genotypes T-111 (CG Haldi-2), T-101 (IT 36), T-103 (IT 8), and T-106 (Roma), among others, showed little interaction and high rhizome yield with less ordinate values in the current investigation (Table 6). The representative and discriminating environments were further examined using environmental vector lengths and the cosine between environments. Plant breeders can reduce costs by eliminating non-informative conditions by using discriminating and representative habitats. RG 17, RG 16, and RG 15 were representative and discriminating settings. The GGE model performed well for polygon view visualization, particularly for environmental discrimination. Yan *et al*. (15) have also highlighted that GGE biplots are superior for visualization because they can accommodate a greater number of genotypes and habitats, are representative of test environments and discriminatory, and reflect the same. In conclusion, the present study indicated the significant effects for G, E and GEI and GEI also changed genotypic ranks over the locations. The genotypic selection in consensus was difficult for stability, however the genotypes T-111 (CG Haldi-2), T-101 (IT 36), T-103 (IT 8) and checks T-106 (Roma) and T-110 (Narendra Haldi-1) were found high yielding and consistent. The environments RG 15 was different from rest of the environments and AM 17, AM 16, JD 16, JD 17, JD 15 and AM 15 were

Table 6: The AMMI stability value (ASV), PC1, PC2 scores, and mean rhizome yield (ton/ha) of turmeric to assess the performance and stability of nine test environments.

Env_ID	Environment	Fresh rhizome yield (ton/ha)	PC1	PC2	ASV	YSI	Rank ASV	Rank Y
AM15	Ambikapur_2015	7.25	-0.71	0.71	2.15	14	7	7
AM16	Ambikapur_2016	9.54	-0.16	0.33	0.56	5	1	4
AM17	Ambikapur_2017	7.06	-0.07	0.89	0.91	10	2	8
JD15	Jagdalpur_2015	4.90	-0.43	0.78	1.45	14	5	9
JD16	Jagdalpur_2016	9.36	-0.36	0.92	1.38	8	3	5
JD17	Jagdalpur_2017	9.36	-0.43	0.79	1.47	12	6	6
RG15	Raigarh_2015	22.86	4.54	-1.01	13.05	10	9	1
RG16	Raigarh_2016	16.85	-0.50	-0.16	1.43	7	4	3
RG17	Raigarh_2017	20.90	-1.89	-3.24	6.31	10	8	2

representative with better discriminating ability. The GGE model found suitable for stability analysis and biplots generated were also easy to view polygon, genotypic interactions and environmental ranks.

Reliability, mean square deviations from regression (s^2di) close to zero, regression coefficient (bi) around unity, and high mean yield (X) were used to identify stable genotypes based on AMMI analysis and the Eberhart and Russell, (3) model. An average stable genotype was defined as one that demonstrated above average mean performance, a regression coefficient close to 1.0, and a low mean square deviation. These genotypes were predicted to exhibit consistency over a range of settings and time periods. It was discovered that the genotypes T-111 (CG Haldi-2), T-101 (IT 36), and T-108 (IT 38) consistently produced large yields in the conditions that were chosen as the most stable ones for high rhizome production. As a result, it was suggested that Chhattisgarh State pursue commercial production of these five genotypes/clones.

AUTHOR'S CONTRIBUTION

Conceptualization and designing of the research work, conduction of field trials and data collection, analysis and writing manuscript. (SLS); Assisted in conduction of field trials, labour management, data recording and essential field work (AKS, MKS, SA); computerization of field data, tabulation of analysed file; and other essential work (BP).

DECLARATION

The authors confirm that they do not have any conflicts of interest.

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