Original Research Article

Genotype×environment interaction, rhizome yield stability and selection for region specific stable genotypes in turmeric (*Curcuma longa* L.)

Raj Kishori Lal✉, Sougata Sarkar and Mohammad Zaim

CSIR-Central Institute of Medicinal and Aromatic Plants, P.O. CIMAP, Lucknow - UP 226015, India

ABSTRACT

The present investigation was carried out to determine the stability over years among seventeen genetic stocks of turmeric assembled from different localities in India for high and stable rhizomes yield. The observed differences among genetic stocks, years and g×e interactions were highly significant for rhizome yield. The stable genetic stocks were selected on the basis of stability parameters, high mean, regression coefficient (bi) around unity and mean square deviations from regression (s^2di) near zero. The environmental indices for rhizome yield also indicated clear effects over the year's, i.e. 1.85 in year I followed by 9.95 in year II; -6.31 in year III and -5.29 in the year IV. The largest AMMI1 gain of the grand mean occurs over years for picking stable genotypes/clones. Further partitioning of genotypes on the basis of AMMI and Eberhart and Russell (1966) model, the clones/genotypes T-8, T-12 and T-13 were highly stable; T-11 and T-14 adapted to the average stable in low yielding environment/year and T-9 and T-17 genotypes/clones with below average stable suitable for high yielding environment were recommended for commercialization.

1. Introduction

Turmeric (*Curcuma longa* L.) is a subtropical/tropical perennial medicinal plant belonging to family 'Zingiberaceae'. It is mainly valued as a spice in food and a natural dye or clothing. This plant is also important as a potential source of new drugs for a variety of diseases (Lekshmi et al., 2014; Alvarez et al., 2016; Dyab et al., 2016; Kim et al., 2016; Park et al., 2017; Saccol et al., 2017; Zhou et al., 2017). Its importance in medicine started with an endeavour in which the dried rhizome of the plant was a rich source of phenolic compounds, identified as curcuminoids, particularly curcumin or diferuloyl methane. Some of the biological and therapeutic activities attributed to curcumin were anti-inflammatory, antioxidant and anti-carcinogenic, wound healing, and antiviral properties (Joe et al., 2004; Elvira and Maribel, 2014; Mishra et al., 2015). Turmeric is traditionally used in Indian and Ayurvedic and Unani system of medicine as stomachic, carminative, blood purifier, vermicide and antiseptic. Wound healing antiseptic property of turmeric is well known to Indians since long years ago. Curcumin is the main biologically active phytochemical compound of turmeric with wide range of therapeutic effects (Gomathy et al., 2014). In recent years, pharmacological properties and actions of curcumin have been widely researched and its beneficial effects have been well established. Turmeric is a clonally propagated by its underground rhizomes. Though vegetative propagation is the usual means of reproduction, several studies have shown the existence of spontaneous genetic variation in this species (Mishra et al., 2015; Kim et al., 2016; Shakeri et al., 2017; Tanvir et al., 2017; Uchio et al., 2017; Wang et al., 2017). The intra-specific variation may be due to the long-term cultivation and targeted selection of desirable genotypes in turmeric, which in turn may have adaptive value to the crop (Elvira and Maribel, 2014).

Basically, the region specific stable clones/genotypes over years strategy focuses on responses of all genotypes/clones over years which help for the recommendation of stable genotypes/clones for commercial cultivation. The stable and reliable genotype is the one capable of

✉ Corresponding author: Raj Kishori Lal
Tel: +91-522-2718523; Fax: +91-522-2343666
E-mail address: rajkishorilal@gmail.com

expressing continuously high yield over the years. High yield stability usually refers to a genotype's ability to perform consistently over years (Annicchiarico, 2002; Lal, 2014, 2015). Many biometrical, univariate and multivariate methods used to assess stability among different crops (Eberhart and Russell, 1966; Akçura et al., 2005; Lal, 2012, 2014) among which the most widely used are the regression coefficient (Finlay and Wilkinson, 1963), the environmental variance, the Shukla's stability variance (Shukla, 1972) and Wricke's ecovalence (Wrike, 1962), etc. The concept of yield stability and reliability with high yield in genotypes has been demonstrated by some researchers (Eskridge, 1990; Kang and Pham, 1991) in the different crops.

The basic information on wide adaptability and stability over years in turmeric is lacking. Studies on stability by genotype×environment interaction (g×e) using AMMI and model are very meager in turmeric crop (Mishra et al., 2015). In other words, there is not any record on stability and reliability of turmeric using AMMI as well as Eberhart and Russell stability model (Eberhart and Russell, 1966). Therefore, the objective of present investigation was to determine their stability and reliability over years for the selection of stable genotypes/clones in turmeric crop.

2. Experimental

2.1. Sampling areas of 17 genotypes of turmeric

Seventeen genotypes (T-1 to T-17) of turmeric (*Curcuma longa* L.) belonging to family 'Zingiberaceae' representing fifteen states of India (Uttar Pradesh, Uttaranchal, Rajasthan, Haryana, Bihar, Punjab, Madhya Pradesh, Gujarat, Delhi, Jammu and Kashmir, Maharashtra, Karnataka, Kerala, Andhra Pradesh and Meghalaya) constituted the material for the present investigation (see Table 1 and Fig. 1). They were evaluated at the Research Farm of CSIR-Central Institute of Medicinal and Aromatic Plants, P.O. CIMAP, Lucknow, U.P. 226 015 (India).- in the four consecutive years: 2012-13, 2013-14, 2014-15 and 2015-16 in Northern Indian plain's environments using a completely randomized block design (RCBD) with three replications. The experimental location at the institute research farm was located at 26.5º N latitude and 80.50º E longitude, and 120 m above the mean sea level. The climate is semiarid /subtropical in nature. The plants were planted in 30×50 cm rows to row/ plants to plant distance with plot size=30 m². The normal intercultural operations, irrigations, and fertilizers (100 N, 50 kg P_2O_5, and 50 kg K_2O per hectare) provided in the all experiments over the years. Plants were uprooted at maturity stage as an annual crop.

2.2. Extraction of essential oils

Fresh rhizomes were sliced and washed with water and then subjected to water distillation. Hydro distillation of the rhizomes of each accession was

Fig. 1. Morphological variability in genetic stocks of *Curcuma longa* plants.

performed in Clevenger's apparatus (Clevenger, 1928) for the extraction of essential oil content.

2.3. Analysis of essential oils

Gas chromatography and mass spectroscopic (GC-MS) analyses were performed using a Variance CP3800 instrument. For mass spectrometry (MS), CPC18CB fused silica column 30×0.32 mm×1 μm cell thickness were used, oven temperature was 60 to 220 ºC at the rate of 3 ºC per min, 220 ºC. Injected temperature 280 ºC, detected temperature 290 ºC, split ratio 1:30, and hydrogen as a carrier 1 mL/min.

2.4. Statistical analysis

Stability parameter calculations were performed for rhizome yield (kg/plot) only using MATMODEL version 3.0 programme mode: fitting AMMI Model software (Gauch, 2007) and with stability model of Eberhart and Russell (Eberhart and Russell, 1966) using statistical software version 0.3 based on Singh and Chaudhary (Singh and Chaudhary, 1979) and Panse and Sukhatme (Panse and Sukhatme, 1967) available at the Department of Genetics and Plant Breeding of CSIR-CIMAP, Lucknow U.P. PIN -226 015, India.

3. Results and Discussion

3.1. Estimation of genetic variability

The analysis of variance (ANOVA) results indicated that there were highly significant differences (P<0.01) for rhizome yield among the seventeen clones/ genotypes of turmeric (Table 1, 2). This clearly accounted for the existence of substantial genetic variability among clones/genotypes of turmeric grown in four years. The genotype×environments/ years interaction was also highly significant. Such significant genotype×environment/years reveal the high differential response of the genotypes to change in years/environments (Table 2). The pooled mean rhizome yield over years ranged from 8.73-

Table 1

Genotypes/clones, identification codes, Botanical names and oil compositions of *Curcuma longa* genotypes/ clones.

No.	Genotypes/ clones	Identification Codes	Places/Origin in India	Mean Rhizome yield (kg/plot)	Oil content (%)	α-terpionelene	ar-turmerone	α-turmerone	β-turmerone	Curcumine in oil	Gingiberene
1	T-1	TUR-2	Udaipur, Rajasthan	68.87	0.32	12.882	28.790	13.616	18.043	3.26	0.288
2	T-2	TUR-11	Indaur, Madhya Pradesh	86.48	0.16	8.069	29.735	14.389	17.461	0.1579	2.64
3	T-3	AMT-3	CSIR-CIMAP,Lucknow, Uttar Pradesh	49.93	0.17	18.563	21.868	11.131	16.146	-	0.224
4	T-4	TUR-12	Haldwani, Uttarakhand	53.18	0.22	6.158	30.201	14.599	17.768	0.123	2.68
5	T-5	TUR-8	Kozhikode, Kerala	51.22	0.20	10.958	23.659	13.264	20.068	2.456	1.81
6	T-6	TUR-1UNK	Muzaffarpur, Bihar	11.50	0.21	16.537	25.924	12.931	15.884	-	2.102
7	T-7	AM-2	Jorhat, Assam	09.54	0.15	5.279	27.767	14.730	15.460	8.0266	0.19
8	T-8	TUR-5	Chennai, Andhra Pradesh	92.95	0.13	10.130	27.580	13.428	19.486	-	0.190
9	T-9	TUR-13	Phagawara, Punjab	92.59	0.20	8.946	35.996	13.339	7.341	-	4.25
10	T-10	TUR-8	Junagarh, Gujarat	92.87	0.20	10.958	23.659	13.264	20.068	2.456	1.81
11	T-11	TUR-6	Puri, Odessa	89.67	0.22	9.060	29.668	14.549	17.250	-	2.38
12	T-12	TUR-10	Krishnanagar, West Bengal	94.11	0.25	12.261	28.570	13.726	16.678	0.4556	2.875
13	T-13	TUR-4	Bangalore, Karnataka	93.84	0.23	13.379	28.388	13.176	17.521	-	2.179
14	T-14	TUR-3	Renukot, Uttar Pradesh	92.15	0.17	18.563	21.868	11.131	16.146	-	0.224
15	T-15	ST-1 (UNK)	Palampur, Himachal Pradesh	59.38	0.21	16.537	25.924	12.931	15.884	-	2.102
16	T-16	ST-2 (4)	Shilang, Meghalaya	08.73	0.23	13.379	28.388	13.176	17.521	-	2.179
17	T-17	ST3 (9)	Jammu, Jammu and Kashmir	137.09	0.19	9.120	28.874	13.817	20.541	0.1881	0.286
Total	17	Range	-	08.73-137.09	0.13-0.32	0.946-18.563	Traces-41.220	11.131-14.730	7.341-20.541	Traces-8.027	Traces-4.25

137.09 kg/plot; oil content in rhizomes=0.13- 0.32%, respectively. The genotype/clone T-17 was the highest rhizome yielder=137.09 kg/plot followed by clone T-12=94.11 and T-13=93.84 kg/plot, respectively. The lowest rhizome yielder clone was T-16=8.733 kg/plot. For oil content clone/genotype T-1=0.32% was the highest followed by T-12=0.25%; T-13 and T-16=0.23%, respectively. On the other hand, the oil composition of the rhizomes the α-terpionelene ranged from 0.946-18.563%. The best clones for α-terpionelene were T-14=18.653% followed by T-15=16.537; T-13 and T-16=13.379%. The range between other chemical constituents were ar-turmerone=traces-35.996;α-turmerone=11.131-14.730; β-turmerone=7.341-20.541;curcumine in oil=trace-8.02 and gingiberene=trace-4.25 in percent in order (Table 1). The mean rhizome yield of clones/genotypes across the years/environments ranged from in year/ environment I (4.4. to 20.833, mean 11.700 kg/plot); in year/environment II 6.833-330.933, mean 139.192 kg/plot; in year/environment III 2.233-171.367, mean 72.173 kg/plot and in year/environment IV 2.700-205.267, mean 55.545 kg/plot, respectively (Tables 4-11 and Fig. 2). The genotypic rank differences and IPCA (Interaction Principal Components Axes) axis 1 scores for AMMI model over years were expressed the highly influences of genotype×environment interactions (g×e) (Table 3, Fig. 3, 4).
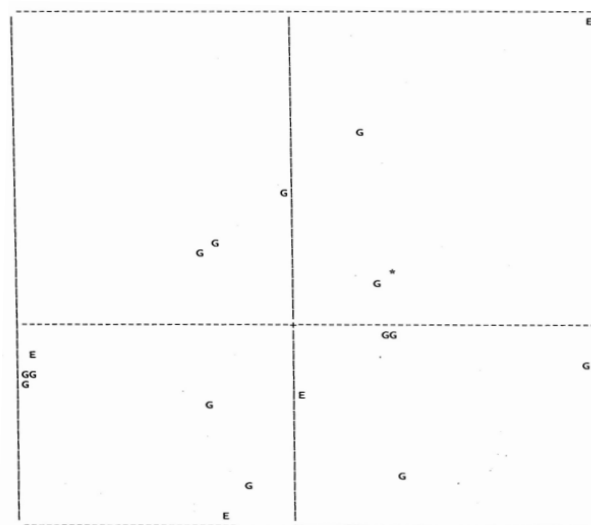
Fig. 2. Mata model version 3.0 Mega-environments for AMMI 1 Model, cultivars, switch points, including hypothetical winners in *Curcuma longa*.

3.2. Selection of stable genotypes

Selection of stable genotypes for rhizomes yield in turmeric along with the genotype×environment interaction are among important issues for plant breeders, who want to select stable clones across diverse environments. The careful perusal of results indicated that the AMMI I and AMMI F selected the

Fig. 3. Year /environment wise AMMI values in *Curcuma longa* for rhizome yield.

Table 2
Pooled analysis of variance and deviations for rhizome yield in *Curcuma longa*.

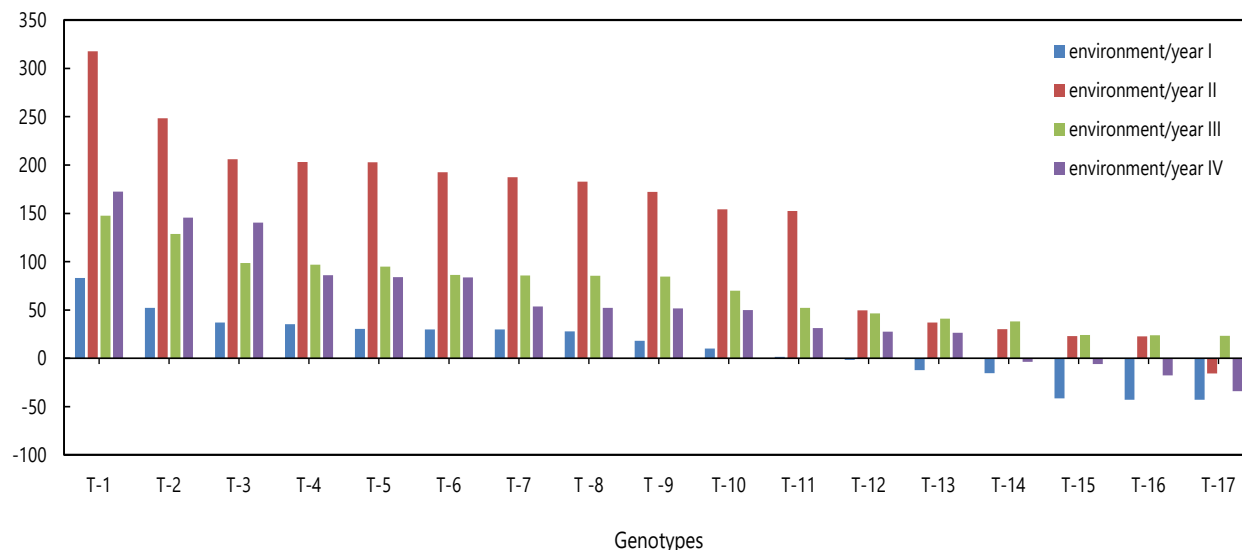| Sources of variations	d.f.	Sum of squares	Mean sum of squares
Treatments	16	396.37	24.77**
Years	3	8475.80	2825.27**++
Replications × Years	8	93.81	11.73**
Treatments × Years	48	2846.61	29.30**
Years + (Treatments × Years)	51	3774.14	74.00**++
Years (Lin.)	1	2825.27	2825.27**++
Treatments × Years (Lin.)	16	371.51	23.22**
Pooled deviation	34	577.36	16.98
Pooled error	136	250.04	1.84

**-p<0.01; ++- p<0.01 pooled deviation

same winners in the two environments, i.e. 50% and also picked different winners in other two years 50%. The average loss from selecting AMMI1 winners = 8.958 and 12.86% of the grand mean. The AMMI1 ranking
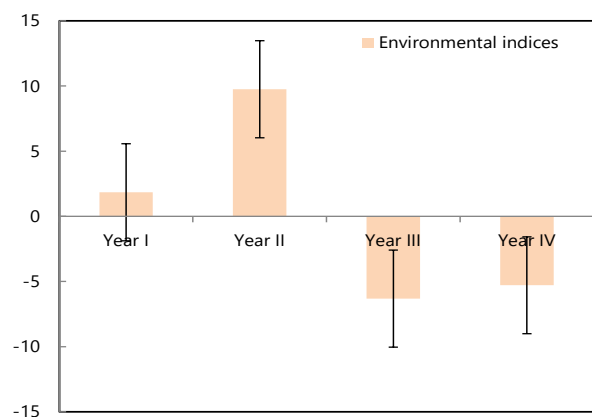
Fig. 4. Enviromental indices for rhizome yield in *Curcuma longa*.

was more to be trusted the average gain for selecting AMMI1 winners, i.e. 19.49 and 56.69% of the grand mean. The largest AMMI1 gain of 125.94 or 180.81 of the grand mean occurs in year I where AMMIF picked genotype T-16 but AMMI 1 picked genotype T-17 instead of other genotype. The environmental means and IPCA axis 1 scores for model AMMI1 are presented in the (Table 3). In the interaction the sum of square noise can be estimated as genotype×environment interaction, degree of freedom, error and mean sum of square. This value was=1294052.16 exceeded the genotype×environment interaction (g×e), sum of squares. The genotype×environment interaction (g×e), sum of square indicated about the pattern of genotype×environment interaction. The genotype and environment typical bias values for seventeen genotypes were 170.06. On the other hand, the typical bias for the seventeen genotypes was 97.58 that falls within limit and is useful for selection.

Table 3

Environmental means and IPCA Axis 1 Scores for model AMMI I in *Curcuma longa*.

No.	Environments	Means	Count	Index	Environments	Means	Count	Index	Environments	Score	Index	Name	Score
1	ENV. I (years 2010-11)	11.700	17	2	ENV. II (years 2011-12)	139.192	17	1	ENV. I (years 2010-11)	-1.877	2	ENV. II (years 2011-12)	16.358
2	ENV. II (years 2011-12)	139.192	17	3	ENV.III (years 2012-13)	72.173	17	2	ENV. II (years 2011-12)	16.358	1	ENV.I (years 2010-11)	-1.877
3	ENV.III (years 2012-13)	72.173	17	4	ENV. IV (years 2013-14)	55.545	17	3	ENV.III (years 2012-13)	-3.719	3	ENV. III (years 2012-13)	-3.719
4	ENV.IV (years 2013-14)	55.545	17	1	ENV. I (years 2010-11)	11.700	17	4	ENV.IV (years 2013-14)	-10.762	4	ENV.IV (years 2013-14)	-10.762

Grand Mean = 69.652 rhizome yield Kg/plot; AMMI = Additive Main Effects and Multiplicative Interactions; ENV = year

Table 4

Genotype IPCA axis 1 Scores for model and means for AMMI I in *Curcuma longa*.

No.	Genotypes/clones	Mean	Count	Index	Name	Mean	Count	Score	Index	Genotypes/clones	Score
1	T-1	68.87	4	17	T-17	137.09	4	6.722	2	T-2	9.879
2	T-2	86.48	4	12	T-12	94.11	4	9.879	1	T-1	6.722
3	T-3	49.93	4	13	T-13	93.84	4	3.869	4	T-4	3.960
4	T-4	53.18	4	8	T -8	92.95	4	3.960	3	T-3	3.869
5	T-5	51.22	4	10	T-10	92.87	4	-4.340	10	T-10	2.673
6	T-6	11.50	4	9	T -9	92.59	4	-2.688	9	T -9	2.491
7	T-7	9.54	4	14	T-14	92.15	4	-2.997	8	T -8	2.479
8	T -8	92.95	4	11	T-11	89.67	4	2.479	11	T-11	2.033
9	T -9	92.59	4	2	T-2	86.48	4	2.491	14	T-14	-0.564
10	T-10	92.87	4	1	T-1	68.87	4	2.673	13	T-13	-0.571
11	T-11	89.67	4	15	T-15	59.38	4	2.033	17	T-17	-2.211
12	T-12	94.11	4	4	T-4	53.18	4	-8.590	6	T-6	-2.688
13	T-13	93.84	4	5	T-5	51.22	4	-0.571	7	T-7	-2.997
14	T-14	92.15	4	3	T-3	49.93	4	-0.564	16	T-16	-3.402
15	T-15	59.38	4	6	T-6	11.50	4	-8.843	5	T-5	-4.340
16	T-16	8.73	4	7	T-7	9.54	4	-3.402	12	T-12	-8.590
17	T-17	137.09	4	16	T-16	8.73	4	-2.110	15	T-15	-8.843

Grand mean = 69.65 rhizomes yield Kg/plot; AMMI = Additive Main Effects and Multiplicative Interactions

The performance of genotypes for stability may be taken as important main effects of yield trials over the years. The AMMI model reduces the effects of genotype×environment interaction (g×e) in a very accurate and refined manner which helps for selecting suitable genotypes. After critical perusal of year wise AMMI values of the four years, it was clearly depicted that genotype T-17, followed by T-11 and T-12 T-13, T-14, T-8 and T-9 were found stable with comparisons to other genotypes (Fig. 3). The fresh rhizome yield of these clones were T-17=137.09, T-11 (89.67) and T-12 =94.11 T-13=93.84, T-14=92.15, T-8=92.95 and T-9=92.59 kg/plot in orders. The similar findings also reported by number of researchers using the AMMI model for broader information and interpretations on stability in the same and different crops (Lin et al., 1986; Purchase, 1997; Leeуvner, 2005; Prasad et al., 2007; Mishra et al., 2015; Lal et al., 2017).

3.3. Stability parameter applications in evaluation and further partitioning of genotypes of turmeric for selection

Nevertheless, there are remarkable achievements and inconsistencies observed among seventeen genetic stocks of turmeric in stability for rhizomes yield. To further confirm the results of AMMI analysis.

Table 5

Stability parameters for rhizome yield in *Curcuma longa*.

Treatments	Treatment means (⁻X)	regression coefficient (bi)	mean square deviation from linear regression (s²d)
T-1	68.87	1.11**	-0.87*
T-2	86.48	1.63**	34.04**
T-3	49.93	0.85*	-0.49
T-4	53.18	1.12**	-0.29
T-5	51.22	1.13**	1.80**
T-6	11.50	1.27**	3.86**
T-7	9.54	0.87*	1.69**
T -8	92.95	1.13**	-1.09**
T -9	92.59	1.08**	33.32**
T-10	92.87	1.30**	27.72**
T-11	89.67	0.45	-1.00**
T-12	94.11	1.42**	4.70**
T-13	93.84	1.01**	-1.00**
T-14	92.15	0.99**	-1.47**
T-15	59.38	0.17	46.90**
T-16	8.73	0.38	88.25**
T-17	137.09	1.10**	24.92**
Population mean	69.652	-	-
SE (Population mean) ±	2.38	-	-
bi (SE) ±		0.32	-

*, **-P<0.05 and P<0.01

Table 6

Genotypes mean for environment/year I in *Curcuma longa*.

No.	Genotypes	Count	Data	AMMI 1	Residual	Rank	Index	Genotype name	Data	Index	Genotype name	AMMI 1
1	T-1	4	11.433	-1.704	13.138	1	16	T-16	20.833	17	T-17	83.100
2	T-2	4	7.433	9.977	-2.544	2	17	T-17	20.300	12	T-12	52.282
3	T-3	4	9.500	-15.282	27.782	3	15	T-15	18.033	13	T-13	36.961
4	T-4	4	14.333	-12.203	26.537	4	4	T-4	14.333	14	T-14	35.256
5	T-5	4	11.667	1.412	10.255	5	13	T-13	13.033	8	T -8	30.343
6	T-6	4	11.100	-41.406	52.506	6	5	T-5	11.667	9	T -9	29.963
7	T-7	4	11.267	-42.785	54.052	7	1	T-1	11.433	10	T-10	29.897
8	T -8	4	10.833	30.343	-19.510	8	14	T-14	11.400	11	T-11	27.897
9	T -9	4	4.433	29.963	-25.530	9	7	T-7	11.267	15	T-15	18.032
10	T-10	4	5.433	29.897	-24.463	10	6	T-6	11.100	2	T-2	9.977
11	T-11	4	7.433	27.897	-20.464	11	8	T -8	10.833	5	T-5	1.412
12	T-12	4	10.433	52.282	-41.849	12	12	T-12	10.433	1	T-1	-1.704
13	T-13	4	13.033	36.961	-21.927	13	3	T-3	9.500	4	T-4	-12.203
14	T-14	4	11.400	35.256	-23.856	14	2	T-2	7.433	3	T-3	-15.281
15	T-15	4	18.033	18.032	0.001	15	11	T-11	7.433	6	T-6	-41.406
16	T-16	4	20.833	-42.841	63.674	16	10	T-10	5.433	7	T-7	-42.785
17	T-17	4	20.300	83.100	-62.800	17	9	T -9	4.433	16	T-16	-42.840

Environments I and Mean = 11.700, AMMI (Additive Main Effects and Multiplicative Interactions) gain = 125.941

Table 7

Genotypes mean for environment/year II in *Curcuma longa*.

No.	Genotypes	Count	Data	AMMI 1	Residual	Rank	Index	Genotype name	Data	Index	Genotype name	AMMI 1
1	T-1	4	255.667	248.359	6.807	1	2	T-2	330.933	2	T-2	317.613
2	T-2	4	330.933	317.614	13.319	2	1	T-1	255.167	1	T-1	248.360
3	T-3	4	183.467	182.757	0.709	3	10	T-10	192.100	10	T-10	206.129
4	T-4	4	188.600	187.502	1.099	4	9	T-9	189.633	8	T-8	203.047
5	T-5	4	20.600	49.759	-29.159	5	4	T-4	188.600	9	T-9	202.880
6	T-6	4	25.200	37.064	-11.864	6	8	T-8	187.733	11	T-11	192.467
7	T-7	4	17.800	30.061	-12.261	7	13	T-13	186.600	4	T-4	187.502
8	T -8	4	187.733	203.047	-15.313	8	17	T-17	186.533	3	T-3	182.757
9	T -9	4	189.633	202.880	-13.246	9	14	T-14	184.767	17	T-17	172.116
10	T-10	4	192.100	206.128	-14.029	10	3	T-3	183.467	13	T-13	154.044
11	T-11	4	177.200	192.467	-15.67	11	11	T-11	177.200	14	T-14	152.464
12	T-12	4	26.100	23.129	2.971	12	12	T-12	26.100	5	T-5	49.759
13	T-13	4	186.600	154.045	32.555	13	6	T-6	25.100	6	T-6	37.064
14	T-14	4	184.767	152.464	32.302	14	5	T-5	20.600	7	T-7	30.061
15	T-15	4	7.000	-15.737	22.737	15	7	T-7	17.800	12	T-12	23.129
16	T-16	4	6.833	22.612	-15.779	16	15	T-15	7.000	16	T-16	22.612
17	T-17	4	186.533	172.116	14.417	17	16	T-16	6.833	15	T-15	-15.737

Environments II and Mean = 139.192, AMMI (Additive Main Effects and Multiplicative Interactions) gain = 0.00001

Table 8

Genotypes mean for environment/year III in *Curcuma longa*.

No.	Genotypes	Count	Data	AMMI 1	Residual	Rank	Index	Genotype name	Data	Index	Genotype name	AMMI 1
1	T-1	4	3.600	46.387	-42.787	1	17	T-17	171.167	17	T-17	147.459
2	T-2	4	4.167	52.253	-48.086	2	10	T-10	170.333	12	T-12	128.578
3	T-3	4	4.067	38.065	-33.998	3	12	T-12	169.933	13	T-13	98.485
4	T-4	4	3.267	40.975	-37.708	4	8	T -8	169.833	14	T-14	96.768
5	T-5	4	169.23	69.879	99.354*	5	5	T-5	169.233	15	T-15	94.795
6	T-6	4	3.467	24.019	-20.552	6	11	T-11	169.233	8	T -8	86.249
7	T-7	4	2.233	23.208	-20.974	7	9	T -9	169.067	9	T -9	85.847
8	T -8	4	169.833	86.249	83.585	8	15	T-15	7.233	10	T-10	85.446
9	T -9	4	169.067	85.847	83.219	9	16	T-16	4.333	11	T-11	84.624
10	T-10	4	170.333	85.446	84.887	10	2	T-2	4.167	5	T-5	69.879
11	T-11	4	169.233	84.624	84.609	11	3	T-3	4.017	2	T-2	52.253
12	T-12	4	169.933	128.578	41.355	12	1	T-1	3.600	1	T-1	46.387
13	T-13	4	3.300	98.485	-95.185*	13	6	T-6	3.467	4	T-4	40.975
14	T-14	4	2.467	96.768	-94.301*	14	13	T-13	3.300	3	T-3	38.065
15	T-15	4	7.233	94.795	-87.561	15	4	T-4	3.267	6	T-6	24.019
16	T-16	4	4.333	23.899	-19.565	16	14	T-14	2.467	16	T-16	23.899
17	T-17	4	171.367	147.459	23.707	17	7	T-7	2.233	7	T-7	23.208

Environments III and Mean = 72.173, AMMI (Additive Main Effects and Multiplicative Interactions) gain = 0.00001: Large residuals exceeding this by a factor of 1.960, 2.576, or 3.291 are marked with *, **, or *** respectively. Assuming normality, 5%, 1%, and 0.1% of the residuals exceed these limits.

Table 9

Genotypes mean for environment/year IV in *Curcuma longa*.

No.	Genotypes	Count	Data	AMMI 1	Residual	Rank	Index	Genotype name	Data	Index	Genotype name	AMMI 1
1	T-1	4	5.267	-17.576	22.842	1	15	T-15	205.267	12	T-12	172.444
2	T-2	4	3.367	-33.943	37.309	2	13	T-13	172.433	17	T-17	145.691
3	T-3	4	2.700	-5.806	8.506	3	17	T-17	170.367	15	T-15	140.443
4	T-4	4	6.533	-3.539	10.073	4	12	T-12	169.967	13	T-13	85.877
5	T-5	4	3.367	83.817	-80.449	5	14	T-14	169.966	14	T-14	84.112
6	T-6	4	6.233	26.323	-20.089	6	9	T-6	7.233	5	T-5	83.817
7	T-7	4	6.867	27.684	-20.817	7	7	T-7	6.867	11	T-11	53.678
8	T -8	4	3.400	52.162	-48.762	8	4	T-4	6.533	8	T -8	52.162
9	T -9	4	7.233	51.677	-44.444	9	6	T -9	6.233	9	T -9	51.677
10	T-10	4	3.600	49.996	-46.396	10	1	T-1	5.267	10	T-10	49.996
11	T-11	4	4.800	53.678	-48.878	11	11	T-11	4.800	16	T-16	31.229
12	T-12	4	169.967	172.444	-2.477	12	10	T-10	3.600	7	T-7	27.684
13	T-13	4	172.433	85.877	86.557	13	8	T -8	3.400	6	T-6	26.323
14	T-14	4	169.967	84.111	85.855	14	5	T-5	3.367	4	T-4	-3.539
15	T-15	4	205.267	140.443	64.823	15	2	T-2	3.666	3	T-3	-5.806
16	T-16	4	2.900	31.229	-28.329	16	16	T-16	2.900	1	T-1	-17.576
17	T-17	4	170.367	145.691	24.676	17	3	T-3	2.700	2	T-2	-33.943

Environments IV and Mean = 55.545, AMMI (Additive Main Effects and Multiplicative Interactions) gain = 32.001

Table 10

Values for assessing the significance of mean separations in the data estimates and typical bias in *Curcuma longa*.

No.	Estimates	Scope	Count	First order	Typical bias	Genotypes	Years/environments
1	Genotype and environment	Gen with one Env	17	1.794	170.060	17	3
2	Environment and genotype	Env within one Gen	4	1.029	97.582	17	3
3	Treatments	All treatments	68	2.367	224.339	-	-
4	Details of estimates	Unweighted grand mean without imputed data	With 136 df the root error mean square	With 3 replications the standard of treatment means	Coefficient of variation of treatment means	Standard error of difference between two treatment means	With 136 df t .05 of 1.978 giving LSD .05
5	Data estimates % of GM	69.652	164.193	94.797	136.100 % of GM	134.06	265.118
6	Environmental indices	1.85	9.75	-6.31	-5.29		

Gen = Genotypes; Env = Environment/years; GM = Grand mean

The Eberhart and Russell (1966) model was also applied. In this model, the stable genotypes were selected based on high mean yield ($\bar{X}$), regression coefficient (bi) around unity and mean square deviations from regression (s^2di) near zero. Genotypes with high mean performance, regression coefficient approaching 1.0 and low deviation mean square were considered to be an average stable genotype, which could be expected to perform uniformity over variable environments/years. However, high mean yield, regression coefficient less than unity would indicate a genotype to have above average stability specifically adapted to low yielding environments/years and a coefficient greater than unity represents that a genotype with below average stability suitable for high yielding environments/years.

Evaluation of the obtained results and further partitioning of clones /genotypes of turmeric on the basis of Eberhart and Russell (1966) model, for individual parameters of stability ($\bar{X}$, bi and s^2d) the genotypes T-17 produced the highest rhizome yield (137.09 kg/plot) followed by T-13 (93.84 kg/plot) and T-8 (92.95 kg/plot (Table 5). The regression coefficient (bi) of these genotypes was above unity (bi>1.00) with low deviation from regression (s^2d) indicated

their responsiveness to favorable environments/years. The clones/genotypes T-8 and T-13 were the high stable; the clone T-11 and T-14 were found average stable due to high mean rhizome yield ($\bar{X}$), regression coefficient (bi) less than unity would indicate a clone/genotype to have an average stability specially, adapted low yielding environments/years. The genotypes/clones T-9 and T-17 showed high rhizome yield mean value ($\bar{X}$), regression coefficient (bi) greater than unity would indicate a clone/genotype below average stability to high yielding environments/years. The average chemical constituents in these selected clones/genotypes are presented in the (Table 1). On the other hand, genotype/clone like T-1 (68.87 kg/plot) gave mean rhizome yield below the overall mean rhizome yield (69.652 kg/plot). The regression coefficient of this genotype was bi>1.00 unity but the s^2d not found fit for selection. The genotype/clone T-14 had regression coefficient (bi) close to unity (bi≈1.0) with a mean rhizome yield 92.15 kg/plot and low s^2d value was found suitable for selection (Table 5). The rest of others genotypes showed high deviation from regression and not fit for selection as stable clones. The environmental indices for rhizome yield also indicated clear effects over the year's, i.e.

Table 11

Interval, maximum, count and histogram for AMMI I residuals in *Curcuma longa*.

Interval	Maximum	Count	Histogram
1	4.96769	6	|************************
2	9.93539	2	|********
3	14.90308	9	|************************************
4	19.87078	5	|********************
5	24.83847	13	|**
6	29.80617	4	|****************
7	34.77386	3	|************
8	39.74156	2	|********
9	44.70925	4	|****************
10	49.67694	4	|****************
11	54.64464	2	|********
12	59.61233	0	|
13	64.58003	2	|********
14	69.54772	1	|****
15	74.51542	0	|
16	79.48311	0	|
17	84.45080	3	|************
18	89.41850	5	|********************
19	94.38619	1	|****
20	99.35389	2	|********

1.85 in year I followed by 9.95 in year II; -6.31 in year III and -5.29 in the year IV, respectively (Fig. 4). The above findings are in agreement with other reports (Annicchiarico, 2002; Lal et al., 2000; 2004; Akçura et al., 2005; Leeụvner, 2005; Lal, 2008, 2012, 2014). In nut shell, the data indicated from both model that the clones/genotypes T-8, T-12 and T-13 were highly stable; T-11 and T-14 adapted to the average stable in low yielding environment/year and T-9 and T-17 genotypes/clones with below average stable suitable for high yielding environment identified for commercial cultivation in large areas.

4. Concluding remarks

In the final tally, on the basis of AMMI analysis and Eberhart and Russell (1966) model, based on individual parameters of stability ($\bar{X}$, bi and s^{2}d), the stable genotypes were selected based on high mean yield ($\bar{X}$), regression coefficient (bi) around unity and mean square deviations from regression (s^{2}d$_i$) near zero. Genotypes with high mean performance, regression coefficient approaching 1.0 and low deviation mean square were considered to be an average stable genotype, which could be expected to perform uniformity over variable environments/years. The genotypes, T-8 (92.95 kg/plot), T-12 (94.11 kg/plot), T-13 (93.84 kg/plot), T-11 (89.67 kg/plot), T-14 (92.15 kg/plot), T-9 (92.59 kg/plot) and T-17 (137.09 kg/plot) were selected as the most stable ones for high rhizome yield. Therefore, these seven genotypes/clones were recommended for further commercial cultivation.

Conflict of interest

The authors declare that there is no conflict of interest.

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