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Assessment of rhizome yield of local Indonesian turmeric (*Curcuma longa* L.) during two growing seasons

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Abstract. *Aulia R, Maulana H, Filio YL, Shafira NA, Anindita PA, Suganda T, Concibido V, Karuniawan A. 2022. Assessment of rhizome yield of local Indonesian turmeric (*Curcuma long*a L.) during two growing seasons. Biodiversitas 23: 2534-2543.* In Indonesia, rhizome yield evaluation across diverse growing seasons is very useful for selecting turmeric genotypes that have the potential to be developed into commercial varieties. Evaluation using multiple measurements has high accuracy. This study aimed to select turmeric genotypes based on differences in agro-morphological traits, identify genotypes by season interactions (GEIs), and select stable and high-yielding turmeric during two seasons. The study was conducted for two growing seasons (Planting Season 1 in January - October 2019 and Planting Season 2 in January - October 2020) using an augmented design. Cluster analysis based on agro-morphological traits was used to select turmeric genotypes based on their proximity. A combined analysis of variance (ANOVA) was used to estimate the effect of GEIs on rhizome yield and yield attributes. Rhizome yield evaluation was analyzed using parametric and nonparametric measurements. The results showed that twenty-five turmeric genotypes were selected based on agro-morphological differences. GEIs caused the variation of rhizome yield with a contribution of 34.88%, and yield attributes of 7.04% for weight per plant (WPP), 10.97% for rhizome width (RW), 11.95% for Petiole length (PL), 47.25% for lamina length (LL), and 25.44% for lamina width (LW). The results of parametric and nonparametric measurements selected six genotypes of turmeric into ideal groups, namely G4 (CL-12), G6 (CL-20), G9 (CL-30), G12 (CL-37), G22 (CL-82), and G26 (Cek 1). They can be developed as superior local commodities and used as breeding materials for turmeric plants in the future.

Keywords: GEIs, Indonesia, selection, turmeric

INTRODUCTION

Indonesia has a high biodiversity of turmeric. Anindita et al. (2020) reported that turmeric from Indonesia has a wide genetic diversity based on agro-morphological traits. The factors that cause the extent of genetic diversity include environmental factors such as humidity, rainfall, altitude, soil nutrients, and pH (Adjebeng-Danquah et al. 2017; Sandeep et al. 2016). The origin of the population was also the cause of the high genetic variation. In addition, Indonesia is the largest cultivating country of turmeric after India (Shrishail et al. 2013). This makes turmeric one of the potential rhizome plants in Indonesia.

Turmeric is widely used as herbal medicine in Indonesia and for spices in food processing (Deanova et al. 2021). During the COVID-19 pandemic, the role of turmeric as an immune-boosting commodity is very important. Research showed that turmeric functions as antidiabetic (Shabana et al. 2015), anti-inflammatory (Choi et al. 2019), anticancer (Shakeri et al. 2019), antioxidant (Esatbeyoglu et al. 2015; Tanvir et al. 2017), and antiobesity (Jayarathne et al. 2017). The many benefits of turmeric in the health sector make this plant potential to be developed in the drug industry.

Indonesia is one of the largest turmeric producers in the world. The average production of Indonesian spices from 2012-2016 was 109,966.6 tons (FAO 2019). In Indonesia, turmeric is cultivated in almost all regions with a total harvested area of 7,481.396 ha, with the highest turmeric production in East Java Province (117,108.216 tons), followed by Central Java Province (25,747.866 tons) and West Java Province (4,183.745 tons) (CBS, 2020). A large amount of turmeric production on the Java island shows that these locations have good development potential for cultivation and research activities.

Rhizome yield and yield attributes are quantitative traits controlled by many genes and strongly influenced by environmental factors. Sareen et al. (2014) suggested that the diversity in each trait was the result of a combination of genotype (G), environmental (E), and their interactions (GEIs). According to Sharifi et al. (2017) GEIs will occur when the genotype response to various environments is unstable. Stable genotypes have the same rank in various environmental conditions (Ajay et al. 2020; Gauch, 2013; Temesgen et al. 2015). Planting in several growing seasons can be used to estimate the stability of the plant.

The phenomenon of GEIs and yield stability has become an important topic in developing varieties

worldwide. GEIs in multi-environments testing make the selection process inefficient (Andrade et al. 2016; Vaezi et al. 2017). In multi-environmental testing, genotypic selection using a single stability measure was considered less accurate (Karuniawan et al. 2021; Vaezi et al. 2019). The present used a combination of parametric and nonparametric stability measurements to select superior turmeric genotypes stable in two different growing seasons. This study aimed to select the turmeric genotypes based on agro-morphological traits, identify GEIs on rhizome yield and yield attribute traits, and select stable and high yielding genotypes in two growing seasons.

MATERIALS AND METHODS

Plant materials

This study used 92 local turmeric genotypes of Indonesia origin with six checks as controls (Table 1). The six checks are local Majalengka (check 1), local Garut (check 2), local Sumedang (check 3), local Sukabumi (check 4), local Sleman (check 5), local Tulang Bawang (check 6). The check genotypes used were a commercial accession that has been widely marketed in production center areas.

Field experiment and data collection

The experiment was carried out for two growing seasons at the Ciparanje experimental field, Universitas Padjadjaran, Jatinangor, Sumedang Regency, West Java. The experiment was carried out on dryland (6°54'59"S 107°46'17"E). The altitude of the place is 797 meters above sea level with inceptisols soil type. The experimental design used was Augmented Design. Each genotype tested was not repeated and planted in mounds measuring 5 m x 50 cm x 50 cm. The first trial season was held from January to October 2019 and the second season was held from January to October 2020.

Data were taken from each growing season. Data collection was carried out at harvest time (40 weeks after planting). The harvest data measured included rhizome yield (RY) (Kg), weight per plant (WPP) (kg), Rhizome Width (RW), and Petiole Length (PL), Lamina Length (LL), Lamina width (LW). The data collection method followed the turmeric *Guidelines for the Conduct of Test for Distinctiveness, Uniformity, and Stability.*

Table 1. Genotype list of local Indonesian turmeric and six checks used in this experiment

No.	Code	Origin	No.	Code	Origin	No.	Code	Origin
1	CL-01	West Java	36	CL-41	Maluku	71	CL-81	Bangka Belitung
2	CL-02	West Java	37	CL-42	Maluku	72	CL-82	Bangka Belitung
3	CL-03	West Java	38	CL-43	Maluku	73	CL-83	Denpasar, Bali
4	CL-04	West Java	39	CL-44	West Nusa Tenggara	74	CL-84	Banten
5	CL-06	West Java	40	CL-45	West Nusa Tenggara	75	CL-85	Lampung
6	CL-07	West Java	41	CL-46	Papua	76	CL-86	Bengkulu
7	CL-08	West Java	42	CL-47	Papua	77	CL-87	Central Kalimantan
8	CL-09	West Java	43	CL-48	Papua	78	CL-88	Bengkulu
9	CL-10	West Java	44	CL-49	West Papua	79	CL-89	North Sulawesi
10	CL-11	West Java	45	CL-50	West Papua	80	CL-90	Central Sulawesi
11	CL-12	West Java	46	CL-52	West Papua	81	CL-91	Central Sulawesi
12	CL-13	West Java	47	CL-53	West Papua	82	CL-92	Central Sulawesi
13	CL-15	Central Java	48	CL-54	West Papua	83	CL-93	South Sulawesi
14	CL-17	Central Java	49	CL-55	West Papua	84	CL-94	South Sulawesi
15	CL-19	Central Java	50	CL-56	West Papua	85	CL-95	North Maluku
16	CL-20	East Java	51	CL-57	West Papua	86	CL-96	Aceh
17	CL-21	East Java	52	CL-58	West Papua	87	CL-97	Lampung
18	CL-22	East Java	53	CL-60	West Papua	88	CL-98	West Sumatera
19	CL-23	East Java	54	CL-61	West Papua	89	CL-99	Aceh
20	CL-24	East Java	55	CL-62	Aceh	90	T1	West Java
21	CL-25	East Java	56	CL-63	Bangka Belitung	91	T2	West Java
22	CL-26	East Java	57	CL-64	South Sulawesi	92	T3	West Java
23	CL-28	South Sumatera	58	CL-65	Denpasar, Bali	93	CEK 1	West Java
24	CL-29	South Sumatera	59	CL-66	Gorontalo	94	CEK 2	West Java
25	CL-30	South Sumatera	60	CL-67	East Kalimantan	95	CEK 3	West Java
26	CL-31	North Sumatera	61	CL-68	South Sumatera	96	CEK 4	West Java
27	CL-32	North Sumatera	62	CL-69	Maluku Barat Daya	97	CEK 5	Yogyakarta
28	CL-33	North Sumatera	63	CL-70	Maluku Barat Daya	98	CEK 6	Lampung
29	CL-34	North Sumatera	64	CL-72	Southeast Sulawesi			
30	CL-35	West Kalimantan	65	CL-73	Bangka Belitung			
31	CL-36	East Kalimantan	66	CL-74	Jambi			
32	CL-37	South Sulawesi	67	CL-77	East Java			
33	CL-38	Southeast Sulawesi	68	CL-78	Banten			
34	CL-39	Southeast Sulawesi	69	CL-79	Bangka Belitung			
35	CL-40	Southeast Sulawesi	70	CL-80	West Nusa Tenggara			

Data analysis

In the augmented design, GEIs estimation was carried out on check varieties (You et al. 2013). The data for each check was adjusted based on the difference in the average value of each check used for each block and the overall plot. The estimated GxE was calculated following equation number 1 (You et al. 2013):

$$Y_{ij} = \mu + \tau_i + v_j + (\tau v)_{ij} + \varepsilon_{ij}$$

Where Y_{ij}: adjustment value of the i[th] genotype in j[th] season j; μ: average of grand rhizome yield; τ_i: effect of the i[th] genotype; v_j: effect of the j[th] season; $(\tau v)_{ij}$: interactions effect of the i[th] genotype in j[th] season, and ε_{ij}: combined error on the combined ANOVA based on check varieties.

Rhizome yield stability was estimated using parametric and nonparametric measurements. The equations number 2 (bi) and number 3 (S^2di) showed the linear regression formula expressed by Eberhart and Russell (Eberhart and Russell, 1966).

$$bi - 1 = \frac{\sum_i (x_{ij} - \bar{x}_{i.} - \bar{x}_{.j} + \bar{x}_{..})(\bar{x}_{.j} - \bar{x}_{..})}{\sum_j (\bar{x}_{.j} - \bar{x}_{..})^2} \quad [2]$$

$$S^2_{di} = \frac{1}{N-2}\left[\sum_i (\bar{X}_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..}) - (bi - 2)^2 \sum_j (\bar{X}_{.j} + \bar{X}_{..})^2\right] \quad [3]$$

Equation number 4 showed the mean-variance component (θi) following (Plaisted and Peterson 1959):

$$\theta_i = \frac{p}{2(p-1)(q-1)} \sum_{j-1}^{q} (x_{ij} - \bar{X}_{i.} + \bar{X}_{.j})^2 + \frac{SSGE}{2(p-2)(q-1)} \quad [4]$$

GE variance component ($\theta_{(i)}$) (Plaisted 1960) was calculated based on equation number 5:

$$\theta_{(i)} = \frac{-p}{(p-1)(p-2)(q-1)} \sum_{j-1}^{q} (x_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 + \frac{SSGE}{(p-2)(q-1)} \quad [5]$$

The ecovalence value (Wi^2) follows (Wricke 1962), was estimated based on equation number 6:

$$W_i^2 = \sum (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 \quad [6]$$

The equation number 7 was used to estimate the Shukla's stability variance $(\sigma^2 i)$ (Shukla 1972):

$$\sigma_i^2 = \left|\frac{p}{(p-2)(q-1)}\right| W_i^2 - \frac{\sum W_i^2}{(p-1)(p-2)(q-1)} \quad [7]$$

The Coefficient of variance (CVi) (Francis and Kannenberg 1978) was an estimate based on equation number 8:

$$CV_i = \frac{SD_i}{\bar{x}} x\ 100 \quad [8]$$

For parametric measurements, X_{ij}: total rhizome yield in the i[th] genotype in j[th] season, $\bar{X}_{i.}$average of the total rhizome yield from i[th] genotype at all seasons, $\bar{X}_{.j}$mean of the rhizome yield in the j[th] season,$\bar{X}_{..}$ average of the total rhizome yield, N: number of seasons. p and q: numbers of seasons and genotypes; SD_i: standard deviation of GEIs.

The equation number 9, 10, 11, and 12, showed the non-parametric stability measurements based on Nassar and Huhn (1987) and Huehn (1990) ($S^{(i)}$):

$$S_i^{(1)} = 2\sum_j^{n-1} \frac{\sum_{j'=j+1}^{n} |r_{ij} - r'_{ij}|}{[N(n-1)]}, \quad [9]$$

$$S_i^{(2)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_{i.})^2}{(N-1)}, \quad [10]$$

$$S_i^{(3)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_{i.})^2}{\bar{r}_i}, \quad [11]$$

$$S_i^{(6)} = \frac{\sum_{j=1}^{n} |r_{ij} - \bar{r}_{i.}|}{\bar{r}_{i.}} \quad [12]$$

Where r_{ij}: stability rank of the i[th] genotype in the j[th] season; $\bar{r}_{i.}$: average rank if i[th] genotype in all seasons; and *N* : number of seasons.

The equation number 13, 14, 15, and 16, showed the non-parametric stability measurements by Thennarasu (Thennarasu 1995):

$$NP^{(1)} = \frac{\sum_{j=1}^{n} |r_{ij}^* - M_{di}^*|}{N}, \quad [13]$$

$$NP^{(2)} = \frac{\left[\sum_{j=1}^{n} |r_{ij}^* - M_{di}^*|/M_{di}\right]}{N}, \quad [14]$$

$$NP^{(3)} = \frac{\sqrt{\frac{\sum (r_{ij}^* - r_{i.}^*)^2}{N}}}{\bar{r}_{i.}}, \quad [15]$$

$$NP^{(6)} = \frac{2x\left[\sum_{j=1}^{n-1} \sum_{j'=j+1}^{n} |r_{ij}^* - r_{i.}^*|/\bar{r}_i\right]}{N(N-1)} \quad [16]$$

Where r_{ij}^*: stability rank of the i[th] genotype in the j[th] seasons (adjusted data); M_{di}^*: adjusted data (median rank); M_{di} : unadjusted data (median rank's of the same parameters). N: number of seasons. Nonparametric stability measurement by Kang (Kang 1988) (KR) was estimated based on the rank of grain yield from each genotype and the rank of Shukla's stability variance. The rank of the two measurements was used as a selection index in KR. The genotype with high average rhizome yield and low stability variance was given a rank of 1 in KR, and vice versa. Rhizome yield stability based on parametric and nonparametric measurements was analyzed using STABILITYSOFT (online software) (Pour-Aboughadareh et al. 2019).

RESULTS AND DISCUSSION

The degree of similarity of turmeric genotypes based on agro morphological traits was presented in Figure 1. The dendrogram shows that the turmeric genotypes were divided into two main clusters. Figure 1 shows that CL-62 differed significantly from other genotypes. Likewise with the CL-23 and CL-39. Other genotypes tended to be close to each other and are thought to have similar characteristics. Based on the dissimilarity of the agro-morphological traits, twenty five genotypes were selected from each sub-cluster for further testing,i.e., CL-01, CL-07, CL-08, CL-12, CL-13, CL-20, CL-21, CL-25, CL- 30, CL-34 , CL-36, CL-37, CL-38, CL-41, CL-42, CL-43, CL-58, CL-60, CL-70, CL-72, CL-80, CL-82, CL-88, CL-91, and T2.

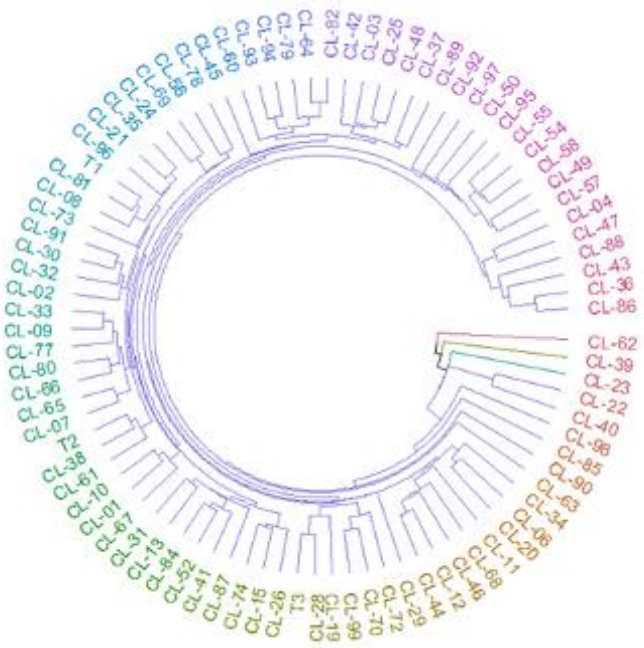

Figure 1. Genetic differences of local Indonesian turmeric based on agro-morphological traits

The results of the combined ANOVA for the six observed traits showed that the genotypes had a significant effect on the rhizome yield, WPP, RW, and LW, while environmental factors and GEIs had a significant effect on all the tested traits (Table 2). Based on the value of its contribution, the genotype effect had the greatest influence on the rhizome yield, WPP, and LW. Environmental effects contributed the highest to RW and PL traits, while GEIs showed the highest contribution to the LL trait.

The parametric and nonparametric stability measurements are presented in Table 3, while the stability ranks are presented in Table 4. In the nonparametric stability measurements $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, and $NP^{(4)}$, the genotypes G5, G16, and G22 were selected as the most stable genotypes (Table 3). The $S^{(1)}$ and $S^{(2)}$ measurements have the same power in selecting stable genotypes because they have the same stability rank for all tested genotypes. The most stable genotypes by other nonparametric measurements were G9 by $NP^{(1)}$, $NP^{(2)}$, dan $NP^{(3)}$, and G12 by *K*R. The parametric stability analysis W_i^2, σ^2_i bi, and $\theta_{(i)}$ selected the G12 genotype as the most stable. Genotypes with a small average stability rank (AR) value (close to zero) showed high and stable yields. Based on the AR values, the genotypes with the smallest values in sequence were G9, G22, G26, G6, and G4 (Table 4).

The grouping of turmeric genotypes based on the stability rating of all measurements of the tested genotypes is presented in Figure 2. The results of the dendogram visualization showed the grouping of genotypes into four groups, namely unstable low yield, unstable high yield, stable medium yield, and stable low yield (Figure 2). In addition, there were groups (clusters) of turmeric genotypes that are quite ideal, namely medium and stable yields. The group consisted of six genotypes, namely, G4, G6, G9, G12, G22, and G26.

Discussion

Turmeric genotype selections based on agro-morphological traits using cluster analysis

Cluster analysis was carried out to classify the tested genotypes that have similarities. The results of the genetic diversity analysis based on agro-morphological traits are presented in Figure 1. Cluster analysis was used to classify objects into relatively homogeneous groups (Tariq et al. 2020). In addition to grouping, cluster analysis can determine the relationship between tested genotypes. Figure 1 shows that the tested genotypes were divided into two main clusters. The genotypes in the same sub-cluster showed similar agro-morphological traits.

On the other hand, genotypes in different sub-clusters showed varying traits. Figure 1 shows that CL-62 has a very high difference from other genotypes. Likewise with the CL-23 and CL-39. According to Verma et al. (2018), genotypes separated from other clusters showed high variation. The other genotypes tended to be close to each other. Genotypes with a close distance are allegedly the same genotype because they have the same characteristics, so they need to be evaluated/selected to avoid double data from the same genotype.

Therefore, we selected one genotype from each genetically closely spaced sub-cluster. The genotypes selected for further testing were CL-01, CL-07, CL-08, CL-12, CL-13, CL-20, CL-21, CL-25, CL-30, CL-34 , CL-36, CL-37, CL-38, CL-41, CL-42, CL-43, CL-58, CL-60, CL-70, CL-72, CL-80, CL-82, CL -88, CL-91, and T2. Twenty-five accessions were then evaluated based on their rhizome yield and yield attribute traits for two growing seasons to obtain high-yielding and stable genotypes.

Genotype by environment Interactions (GEIs) on rhizome yield and yield attributes traits.

The combined ANOVA was carried out on the rhizome yield, and yield attributes to determine the effect of genotype, environment, and their interactions (GEIs) on the traits tested. The results of the combined ANOVA for the six observed traits showed that the genotype had a significant effect on the rhizome yield, WPP, RW, and LW, while environmental factors and GEIs had a significant effect on all the tested traits (Table 2). Based on the value of its contribution, the genotype effect had the greatest influence on the rhizome yield, WPP, and LW. Environmental effects contributed the highest to RW and PL traits, while GEIs showed the highest contribution to the LL trait. A highly significant genotypic effect on the observed traits indicated differences in the composition and genetic potential of each tested turmeric genotype (Lal et al. 2017; Singh et al. 2020). The highly significant influence of genotypes can be caused by differences in the genetic background of each genotype.

The turmeric genotypes studied came from different regions scattered in various parts of Indonesia. So that the opportunity to obtain genetic diversity in quantitative traits is very high. Anindita et al. (2020) reported that differences in the area of origin or geographic location might cause genetic differences in turmeric. Physical distance and geographical barriers are factors that can affect the extent of genetic diversity in an area related to migration opportunities and the introduction of genotypes from outside the area (Amien et al. 2021; Wang et al. 2013). Therefore, this difference may affect the rhizome yield potential of each turmeric which causes the response of each genotype in the different growing seasons.

The growing season factor also showed a significant difference. Genotypes planted in different growing seasons will have different responses. This is because the conditions of origin of each genotype are different from the conditions of the location and the testing season. For example, Vaezi et al. (2019) reported different responses of wheat to three different environments and growing seasons in Iran. Differences in the factors of the growing season in Sumedang can be caused by rainfall, temperature, and humidity. The difference in rainfall, humidity, and temperature in each season gave different responses to each turmeric genotype tested. Based on this, the differences in the growing season can cause different responses of each genotype tested in each season.

Table 2. Combined ANOVA on the rhizome yield and yield attributes during two growing seasons

Source		Genotype (G)	Season (E)	GEIs	Residual	Total	CV (%)
RY	SS	99.84	61.87	86.60	97.29	345.91	51.04
	MS	19.97	61.87	17.32	4.42	9.88	
	F pr.	*	**	*			
	%SS	40.21	24.92	34.88			
WPP	SS	0.86	0.01	0.07	0.66	1.60	56.38
	MS	0.17	0.01	0.01	0.03	0.05	
	F pr.	**	*	*			
	%SS	91.37	1.59	7.04			
RW	SS	6.66	29.68	4.48	48.03	97.62	28.10
	MS	1.33	29.68	0.90	2.18	2.79	
	F pr.	*	**	*			
	%SS	16.32	72.71	10.97			
PL	SS	112.07	1863.98	268.30	680.74	2997.55	45.59
	MS	22.41	1863.98	53.66	30.94	85.64	
	F pr.	ns	**	*			
	%SS	4.99	83.05	11.95			
LL	SS	77.84	326.30	362.07	933.46	1787.19	23.65
	MS	15.57	326.30	72.41	42.43	51.06	
	F pr.	ns	**	*			
	%SS	10.16	42.59	47.25			
LW	JK	204.79	168.00	127.21	737.05	1534.99	48.31
	KT	40.96	168.00	25.44	33.50	43.86	
	F pr.	*	*	*			
	%SS	40.96	33.60	25.44			

Note: SS: Sum of a square; MS: Mean of a square; F pr.: F probability; CV: Coefficient of variation; RY: Rhizome yield; WPP: weight per plant; RW: rhizome width; PL: petiole length; LL: lamina length; LW: lamina width

Table 3. Results of parametric and nonparametric stability measurement of 31 turmeric genotypes during two growing seasons

Code	Genotype	RY	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	*K*R	W_i^2	σ^2_i	s^2d_i	b_i	CVi	$\theta_{(i)}$	θ_i
G1	CL-01	1.66	12.00	72.00	4.24	0.71	6.00	0.35	0.35	0.71	33	1.39	1.35	2.0E-18	0.16	13.63	4.02	2.75
G2	CL-07	5.04	5.00	12.50	0.44	0.18	10.00	0.44	0.35	0.18	23	1.95	1.95	0.0E+00	0.01	0.14	4.00	3.04
G3	CL-08	2.25	20.00	200.00	15.38	1.54	9.00	0.77	0.69	1.54	26	1.24	1.19	2.5E-16	1.79	111.88	4.02	2.67
G4	CL-12	2.44	4.00	8.00	0.42	0.21	7.00	0.16	0.37	0.21	12	0.05	-0.08	0.0E+00	1.16	67.08	4.07	2.06
G5	CL-13	1.31	0.00	0.00	0.00	0.00	3.00	0.60	0.30	0.00	35	0.94	0.87	4.0E-18	0.31	33.05	4.03	2.52
G6	CL-20	2.84	1.00	0.50	0.02	0.04	8.00	0.32	0.34	0.04	14	0.24	0.12	-1.3E-16	1.35	66.73	4.06	2.16
G7	CL-21	1.69	8.00	32.00	1.88	0.47	4.00	0.24	0.24	0.47	29	0.99	0.92	-4.0E-18	0.29	24.27	4.03	2.54
G8	CL-25	1.27	6.00	18.00	1.50	0.50	8.00	0.33	0.67	0.50	43	1.54	1.51	0.0E+00	0.12	12.86	4.01	2.83
G9	CL-30	1.90	1.00	0.50	0.03	0.05	0.00	0.14	0.00	0.05	22	0.32	0.20	-1.6E-17	0.60	44.40	4.06	2.20
G10	CL-34	7.20	5.00	12.50	0.44	0.18	15.00	0.44	0.53	0.18	32	41.36	44.08	-1.0E-15	5.58	108.82	2.59	23.40
G11	CL-36	4.95	16.00	128.00	5.82	0.73	14.00	0.36	0.64	0.73	34	15.99	16.96	-1.0E-15	3.85	109.14	3.50	10.30
G12	CL-37	3.01	8.00	32.00	1.23	0.31	6.00	0.38	0.23	0.31	8	0.01	-0.13	6.3E-17	0.94	44.00	4.07	2.04
G13	CL-38	1.61	8.00	32.00	2.46	0.62	5.00	0.31	0.38	0.62	22	0.16	0.03	3.2E-17	0.72	62.37	4.06	2.12
G14	CL-41	1.03	2.00	2.00	0.29	0.29	5.00	1.29	0.71	0.29	42	1.16	1.11	0.0E+00	0.23	31.58	4.03	2.63
G15	CL-42	1.07	19.00	180.50	15.70	1.65	14.00	0.83	1.22	1.65	52	3.50	3.60	-4.0E-18	-0.33	43.62	3.94	3.84
G16	CL-43	5.17	0.00	0.00	0.00	0.00	12.00	0.45	0.41	0.00	30	10.33	10.91	0.0E+00	3.29	89.40	3.70	7.37
G17	CL-58	0.63	3.00	4.50	1.29	0.86	2.00	3.57	0.57	0.86	42	0.71	0.63	7.9E-18	0.40	89.38	4.04	2.40
G18	CL-60	1.81	7.00	24.50	1.58	0.45	4.00	0.23	0.26	0.45	19	0.17	0.04	-4.8E-17	0.71	55.24	4.06	2.12
G19	CL-70	1.64	5.00	12.50	0.93	0.37	1.00	0.19	0.07	0.37	26	0.27	0.15	0.0E+00	0.63	54.06	4.06	2.17
G20	CL-72	1.30	24.00	288.00	19.20	1.60	15.00	0.80	1.00	1.60	50	3.82	3.95	-1.6E-17	-0.39	42.43	3.93	4.01
G21	CL-80	0.65	5.00	12.50	3.57	1.43	11.00	3.57	3.14	1.43	51	2.61	2.65	-2.0E-18	-0.15	32.64	3.97	3.38
G22	CL-82	2.05	0.00	0.00	0.00	0.00	3.00	0.20	0.15	0.00	17	0.18	0.06	1.6E-17	0.70	47.60	4.06	2.13
G23	CL-88	3.93	24.00	288.00	18.00	1.50	13.00	0.75	0.81	1.50	34	11.93	12.62	5.1E-16	3.46	123.77	3.64	8.20
G24	CL-91	1.50	7.00	24.50	2.13	0.61	2.00	0.39	0.17	0.61	28	0.26	0.14	-1.6E-17	0.63	59.40	4.06	2.17
G25	T2	2.52	24.00	288.00	22.15	1.85	11.00	0.92	0.85	1.85	36	3.85	3.98	0.0E+00	2.40	133.56	3.93	4.02
G26	Cek-1	1.61	1.00	0.50	0.04	0.07	1.00	0.19	0.07	0.07	10	0.48	0.38	0.0E+00	0.50	43.92	4.05	2.28
G27	Cek-2	0.89	1.00	0.50	0.09	0.18	7.00	1.91	1.27	0.18	46	1.44	1.40	-9.9E-19	0.15	23.17	4.02	2.78
G28	Cek-3	3.52	11.00	60.50	2.81	0.51	10.00	0.26	0.47	0.51	29	3.32	3.41	2.5E-16	2.30	91.60	3.95	3.75
G29	Cek-4	1.14	14.00	98.00	8.91	1.27	12.00	0.64	1.09	1.27	48	2.63	2.68	9.9E-19	-0.16	19.31	3.97	3.39
G30	Cek-5	1.35	18.00	162.00	10.13	1.13	13.00	0.56	0.81	1.13	46	3.37	3.46	7.9E-18	-0.31	32.07	3.95	3.77
G31	Cek-6	1.86	16.00	128.00	6.40	0.80	9.00	0.40	0.45	0.80	33	1.74	1.72	0.0E+00	0.06	4.56	4.01	2.93

Note: RY: Rhizome yield; W_i^2: Wricke's ecovalence (Wricke, 1962); σ^2_i: Shukla's stability variance (Shukla, 1972); s^2d_i, b_i: Linear regression (Eberhart and Russell, 1966); Cvi: coefficient of variance (Francis and Kannenberg, 1978); $\theta_{(i)}$: The GE variance component (Plaisted, 1960); θ_i: The mean-variance component (Plaisted and Peterson 1959); $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$: Nassar & Huhn (1987); $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$: Thennarasu (1995); *K*R: Kang (1988).

Table 4. Stability rank's of 31 turmeric genotypes during two growing seasons

Genotype	RY	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	*K*R	W_i^2	σ^2_i	s^2d_i	bi	CVi	$\theta_{(i)}$	θ_i	SR	SD	AR
G1	17	22	22	22	20	12	12	12	20	17	16	16	22	16	4	16	16	282	4.63	16.59
G2	3	11	11	10	7	20	17	11	7	9	20	20	12	20	1	20	12	211	5.99	12.41
G3	11	28	28	27	28	18	24	22	28	10	15	15	29	15	29	15	17	359	6.69	21.12
G4	10	10	10	9	10	14	2	13	10	3	2	2	12	2	23	2	30	164	7.54	9.65
G5	23	1	1	1	1	6	21	9	1	21	12	12	23	12	11	12	20	187	8.05	11.00
G6	8	4	4	4	4	16	10	10	4	4	6	6	3	6	22	6	26	143	6.54	8.41
G7	16	18	18	17	15	8	7	7	15	13	13	13	8	13	7	13	19	220	4.04	12.94
G8	25	15	15	15	16	16	11	21	16	25	18	18	12	18	3	18	14	276	4.96	16.24
G9	13	4	4	5	5	1	1	1	5	7	9	9	5	9	16	9	23	126	5.57	7.41
G10	1	11	11	10	7	30	17	18	7	16	31	31	1	31	27	31	1	281	11.22	16.53
G11	4	24	24	23	21	28	13	20	21	19	30	30	1	30	28	30	2	348	9.57	20.47
G12	7	18	18	13	12	12	14	6	12	1	1	1	28	1	15	1	31	191	8.94	11.24
G13	19	18	18	19	19	10	9	14	19	7	3	3	27	3	21	3	29	241	8.22	14.18
G14	28	8	8	8	11	10	28	23	11	23	14	14	12	14	8	14	18	252	6.60	14.82
G15	27	27	27	28	30	28	26	29	30	31	25	25	8	25	13	25	7	411	7.19	24.18
G16	2	1	1	1	1	24	19	15	1	15	28	28	12	28	25	28	4	233	11.18	13.71
G17	31	9	9	14	23	4	30	19	23	23	11	11	24	11	24	11	21	298	7.81	17.53
G18	15	16	16	16	14	8	6	8	14	6	4	4	4	4	19	4	28	186	6.75	10.94
G19	18	11	11	12	13	2	3	2	13	10	8	8	12	8	18	8	24	181	5.62	10.65
G20	24	29	29	30	29	30	25	27	29	29	26	26	5	26	12	26	6	408	7.87	24.00
G21	30	11	11	21	26	22	30	31	26	30	21	21	10	21	10	21	11	353	7.42	20.76
G22	12	1	1	1	1	6	5	4	1	5	5	5	26	5	17	5	27	127	8.03	7.47
G23	5	29	29	29	27	26	23	24	27	19	29	29	31	29	30	29	3	418	8.06	24.59
G24	21	16	16	18	18	4	15	5	18	12	7	7	5	7	20	7	25	221	6.45	13.00
G25	9	29	29	31	31	22	27	26	31	22	27	27	12	27	31	27	5	413	7.79	24.29
G26	19	4	4	6	6	2	3	2	6	2	10	10	12	10	14	10	22	142	5.74	8.35
G27	29	4	4	7	9	14	29	30	9	26	17	17	11	17	6	17	15	261	8.50	15.35
G28	6	21	21	20	17	20	8	17	17	13	23	23	29	23	26	23	9	316	6.22	18.59
G29	26	23	23	25	25	24	22	28	25	28	22	22	21	22	5	22	10	373	5.71	21.94
G30	22	26	26	26	24	26	20	24	24	26	24	24	24	24	9	24	8	381	5.30	22.41
G31	14	24	24	24	22	18	16	16	22	17	19	19	12	19	2	19	13	300	5.34	17.65

Note: RY: Rhizome yield; W_i^2: Wricke's ecovalence (Wricke, 1962); σ^2_i: Shukla's stability variance (Shukla, 1972); s^2d_i, b_i: Linear regression (Eberhart and Russell, 1966); Cvi: coefficient of variance (Francis and Kannenberg, 1978); $\theta_{(i)}$: The GE variance component (Plaisted, 1960); θ_i: The mean-variance component (Plaisted and Peterson, 1959); $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$: Nassar & Huhn, (1987); $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$: Thennarasu, (1995); *K*R: Kang, (1988); SR: Sum Rank; AR: Average Rank; SD: Standard Deviation

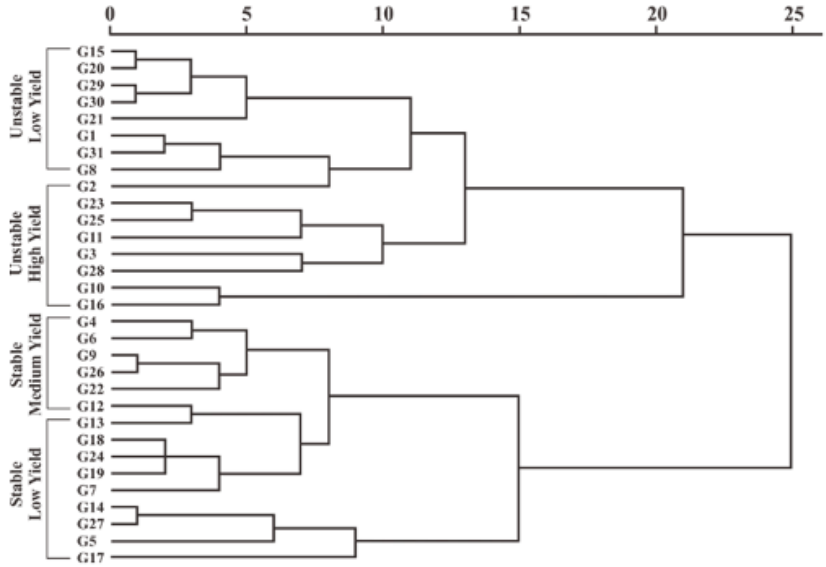

Figure 2. Grouping of Indonesian-origin turmeric genotypes based on parametric and nonparametric measurements during two growing seasons

GEIs also affected the appearance of rhizome yield and yield attribute traits. The data in Table 2 showed significant GEIs in the six traits tested, indicating different responses between the turmeric tested for the two different growing seasons. Previous studies reported that differences in seasons and planting locations could cause the emergence of the effect of GEIs on yield traits in turmeric (Anandaraj et al. 2014; Lal et al. 2017). The existence of the GEIs effect causes the plant breeding program to be less efficient. This is because the plant selection process must be carried out in different environments or seasons and conduct stability analysis on multi-location testing (Adnan et al. 2020; Khalili and Pour-Aboughadareh 2016; Nduwumuremyi et al. 2017). According to Anandaraj et al. (2014), the emergence of GEIs has hampered the turmeric breeding program. Several researchers reported the same thing, including Gurmu et al. (2013) on sweet potatoes, Ruswandi et al. (2021) on sweet corn, and Changizi et al. (2014) on hybrid corn, and Maulana et al. (2020) on sweet potatoes in West Java. This was done to obtain high-yielding and stable genotypes in various ecosystems. Therefore, it is necessary to test the stability of the rhizome yield in two different seasons to extract the effect of GEIs on this trait. Evaluation using parametric and nonparametric measurements was only carried out on rhizome yields because the yield is the main trait in selecting superior genotypes. In addition, rhizome yields are also benchmarks for farmers and researchers in large-scale development.

Rhizome yield stability based on parametric and nonparametric stability measurements

Evaluation of turmeric genotypes across seasons was needed to obtain stable and high-yielding genotypes. Rhizome yield stability was the ability of a genotype to continue to grow optimally in various environmental conditions. Therefore, stability tests were carried out to estimate the GEIs to determine whether the tested genotype was adaptive to a specific environment or stable in a wide environment (Gauch 2013; Kivuva et al. 2014; Mustamu et al. 2018). According to Abate et al. (2015), Changizi et al. (2014), Karuniawan et al. (2021). the selection of yield stability using a single measurement was considered less accurate. Therefore, an evaluation of the rhizome yield using various stability measurements was carried out to improve the measurement accuracy of the tested genotypes.

The parametric and nonparametric stability analysis results are presented in Table 3, while the stability ratings are presented in Table 4. In the nonparametric stability analysis $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, and $NP^{(4)}$, the genotypes G5, G16, and G22 were selected as the most stable genotypes. The $S^{(1)}$ and $S^{(2)}$ measurements have the same power in selecting a stable genotype because they have the same stability rank for all tested genotypes. The most stable genotypes by other nonparametric measurements were G9 by $NP^{(1)}$, $NP^{(2)}$, dan $NP^{(3)}$, and G12 by *K*R. The parametric stability analysis W_i^2, σ^2_i bi, and $\theta_{(i)}$ selected the G12 genotype as the most stable. The four parametric measurements have the same stability rank; therefore, these measurements have the same power in selecting genotypes. Therefore, we can use any of the measurements to select turmeric genotypes. Several researchers also revealed that the measurements have the same stability rank for all tested genotypes, so one can be used to select a genotype because it has the same power (Karuniawan et al. 2021; Vaezi et al. 2019). The other genotypes that were declared the most stable based on parametric stability analysis were G10 and G11 by s^2d_i and θ_i, and G2 by CVi. Several researchers have used a combination of several stability measurements to identify stable and high-yielding genotypes (Farshadfar et al. 2012; Karuniawan et al. 2021; Roostaei et al. 2014).

Table 4 also presents the value of the total sum of rank from all stability measurements (SR), the average stability rank (AR), and the standard deviation (SD) of all stability measurements (parametric and nonparametric). A combination of stability measurements was used to select a stable and high-yielding turmeric genotype. This model used an approximation of the smallest average stability rating (AR) (near zero) of all stability measurements to determine stable genotypes. Ahmadi et al. (2015) also stated that the smallest AR value indicated a stable and high-yielding genotype in grass beans. Several researchers also convey the same thing (Goksoy et al. 2019) on soybean and Karuniawan et al. (2021) on sweet potatoes. Based on the AR values, the genotypes with the smallest values in sequence were G9, G22, G26, G6, and G4. These genotypes were the most stable genotypes based on this approach.

Confirmation and grouping of the tested genotypes based on stability and rhizome yield using cluster analysis were shown in the form of dendogram visualization of the ranking value of each stability measurement (Figure 2). Grouping in cluster analysis was done based on the value of the stability rating of each genotype so that genotypes with the same or adjacent descriptions (in this case, the stability rating of each stability measurement) were combined in the same cluster. Several researchers have also used this approach to group the tested genotypes at various locations and seasons (Ahmadi et al. 2015; Karuniawan et al. 2021; Vaezi et al. 2019). The resulting dendogram is presented in Figure 2.

The dendogram grouped the genotypes into four groups, i.e., unstable low yield, unstable high yield, stable medium yield, and stable low yield. In this test, high yield stable genotype groups were not produced, but some groups were quite ideal, namely stable medium yield. The group consisted of six genotypes, namely, G4, G6, G9, G12, G22, and G26. The six genotypes have a fairly good development potential against changes in the growing season.

In conclusions the test results from 92 genotypes of turmeric, twenty-five genotypes that have agro-morphological differences were selected, i.e., CL-01, CL-07, CL-08, CL-12, CL-13, CL-20, CL-21, CL-25 , CL-30, CL-34, CL-36, CL-37, CL-38, CL-41, CL-42, CL-43, CL-58, CL-60, CL-70, CL-72, CL -80, CL-82, CL-88, CL-91, and T2. GEIs affected rhizome yield variations with a contribution of 34.88%, 7.04% of WPP, 10.97% of RW, 11.95% of PL, 47.25% of LL, and 25.44% of LW. The parametric and nonparametric measurements selected six turmeric genotypes into ideal groups, namely G4, G6, G9, G12, G22, and G26. These groups can be further developed as superior local commodities and can be used as future breeding materials for turmeric plants.

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