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Research article

Combined stability analysis to select stable and high yielding sweet potato genotypes in multi-environmental trials in West Java, Indonesia

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Abstract

Importance of the work: The yield is an important component when determining the probability of success of new high-yielding plant varieties.

Objectives: To estimate the influence of genotype-by-environment interactions (GEIs) on sweet potato yields, to select stable genotypes using various methods in multi-environments and to estimate the relationship between environmental factors and sweet potato yields in West Java, Indonesia.

Materials & Methods: The genetic materials used were eight new breeding genotypes and two commercial varieties as checks. Field experiments were conducted in five environments (Karawang, Garut, Jatinangor, Cileles and Bandung) in West Java, Indonesia, using a randomized completed block design. Data were analyzed using: combined analysis of variance, parametric and non-parametric stability measurements, genotype plus genotype-versus-environment interaction (GGE) biplots and Pearson's correlation.

Results: The environments and GEIs had an effect on sweet potato yields at 37.89% and 45.09%, respectively. The GGE biplot analysis showed that of the five environments, Garut and Karawang were the most discriminative and representative. Therefore, these two environments are recommended as being ideal in West Java for the selection of optimal sweet potato genotypes. The numerical and graphical methods produced the same results, identifying genotypes 57/97(G2) and Rancing (G6) as the optimal genotypes in West Java. The correlation analysis showed that each genotype had a different correlation with the various environmental factors.

Main finding: Information on GEIs can be used as a basis for research on sweet potato development in wider environments. The two genotypes have the potential to be developed into new sweet potato superior genotypes.

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Introduction

Fleshy roots are widely used as basic substantial sources of food, feed and industrial applications in Indonesia (Mukhopadhyay et al., 2011). The various uses of sweet potatoes cannot be separated from its nutritional value; it has high contents of starch, vitamins A and C and is a natural source of fiber, which is a primary reason why people consume this crop (Teow et al., 2007; Burri, 2011). In addition, the contents of beta-carotene, anthocyanins and other minerals are beneficial for health (Hariadi et al., 2018). Sweet potatoes play an important role in reducing hunger due to their carbohydrate and vitamin contents (Food and Agriculture Organization of the United Nations, 2014). The use of sweet potatoes in industry requires a large supply of tubers as raw material; however, these applications require various specifications. Therefore, new genotypes that are in accordance with industrial specifications are needed to fulfill the raw material requirements.

Universitas Padjadjaran (UNPAD) has developed various types of new sweet potato genotypes that can be matched to consumer preferences. These genotypes have been tested initially based on their physical and chemical characteristics. Some of them have been tested for use as natural dyes and other products (Hariadi et al., 2018; Sunyoto et al., 2019). However, these genotypes have not been assessed for the stability and adaptability of their yield in multi-environmental conditions. West Java is one of the provinces with the largest, sweet potato production in Indonesia (Karuniawan et al., 2021). Therefore, testing involving multiple locations in West Java was required to assess the stability and adaptability of the yields of new genotypes for further consideration and development.

Analysis of genotype–environment interactions (GEI) is an initial stage in the procedure of plant selection. The occurrence of GEIs indicates that different genotypes can have different responses to environmental changes, making the selection process inefficient (Rukundo et al., 2013; Kivuva et al., 2014; Andrade et al., 2016). In some cases, sweet potato yields are strongly influenced by GEIs due to the influence of environmental changes (Gruneberg et al., 2005; Gurmu, 2017; Mustamu et al., 2018; Ngailo et al., 2019). Studies have found that GEIs complicated the selection process for yellow passionfruit in Brazil (Oliveira et al., 2014), barley in Turkey (Kendal, E., 2016), finger millet in India (Sood et al., 2016) and cotton in China (Shahzad et al., 2019). Therefore, GEI analysis plays a major part in evaluating the increasing genetic resources that can further promote sweet potato genotypes.

Various methods have been applied in stability and adaptability studies. Recent GEI studies have used statistical methods such as linear regression (Eberhart and Russell, 1966; Ruswandi et al., 2020), eco-valence value (Wi^2) (Wricke, 1962), Shukla's steadiness discordance ($\sigma^2 i$; Shukla, 1972), coefficient of variance (Cvi; Francis and Kannenberg, 1978), additive main effects and multiplicative *interaction* (AMMI; Gauch, 1988) and GGE biplot analysis (Yan and Tinker, 2006; Yan et al., 2007; Ruswandi et al., 2020). Numerous sweet potato development programs have utilized these methods. For example, an AMMI model was successfully applied to determine GEIs and to evaluate the stability of the yield of sweet potato clones in various environments in Turkey (Caliskan et al., 2007). Laurie et al. (2015) used GGE biplots to identify the competency of sweet potato genes and problematical environments in South Africa. However, the use of a single stability measurement was considered less accurate in selecting the ideal genotype (stable and high yielding), so another selection model was needed to obtain the ideal genotype. Karuniawan et al. (2021) used AMMI, GGE biplot and parametric and nonparametric measurements to select stable and high yielding genotypes of honey sweet potato in Indonesia. Mustamu et al. (2018) used AMMI and GGE biplot to select stable as well as adaptable sweet potato genotypes in Indonesia. In another study, Tolorunse et al. (2018) successfully selected soybeans in Nigeria under rhizobium inoculation using AMMI and GGE biplot. Thus, the objectives of the current research were to estimate the influence of GEIs on sweet potato yields, to select stable genotypes using various methods in multi-environments and to estimate the relationship between environmental factors and sweet potato yields in West Java, Indonesia.

Materials and Methods

Plant material

The genetic materials used consisted of eight new breeding genotypes—Awachy 1, 57(97), IND OF7, IND OF8, IND 93(407), MZ119, MZ462 and MZ496—and two commercial varieties as checks (Rancing and Beta-2). These tubers were selected based on consumer preferences according to Maulana et al. (2016). The selected genotypes were chosen based on tuber production in the initial growth phase.

Experimental design

Field experiments were conducted in five environments in West Java, Indonesia: Karawang, Garut, Jatinangor, Cileles and Bandung (Fig. 1). The five locations used represented the sweet potato production centers in West Java, Indonesia. Information about the field trials is presented in Table 1. Each genotype was planted on a plot measuring 5m × 5 m, with a spacing of 25 cm × 100 cm, so that the area used in each environment was 750 m^2. Each genotype was planted in mounds with a length of 5 m and a height of 40 cm. Each genotype was planted as 100 cuttings. Each cutting was planted in an ‘L’ shape at a distance of 25 cm between holes in one mound. The distance between the mounds was 30 cm and the width of the mounds was 75 cm. The experiments were carried out using a randomized block design planting in three blocks. Fertilizer was applied using chicken dung at a dosage of 5 t/ha and NPK (consisting of nitrogen (16%): phosphorus (16%): potassium (16%)) at 200 kg/ha in each location. Chicken dung was applied at the beginning of planting to provide nutrient reserves for the growing period. NPK fertilizer was applied to plants at 6 week after planting (WAP).

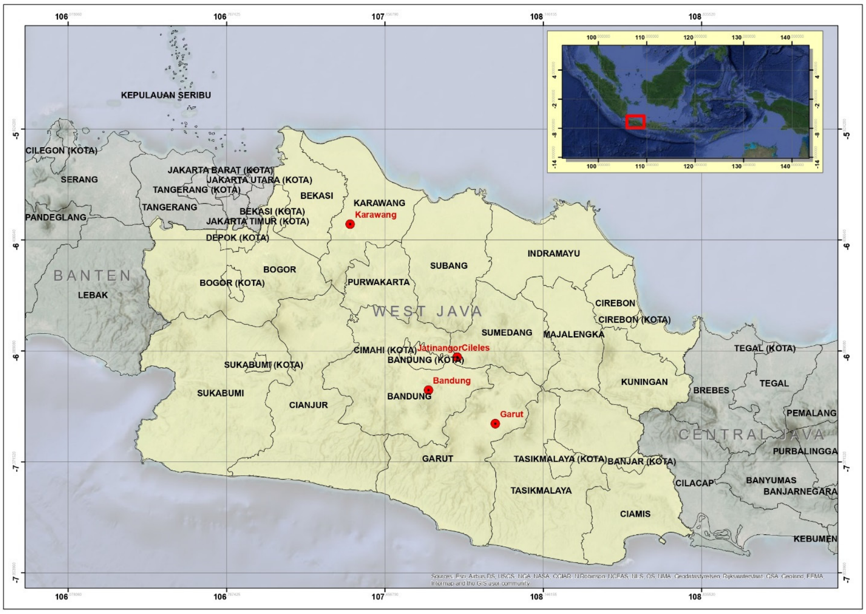

Fig. 1 Map of multi-environments trial in West Java, Indonesia, where 5 trial sites are in red

Table 1 Trial location information

Loc	Alt	Temp	Rf	Hum	Year	Season	Coordinates	pH	K	P	N	C-O
Karawang	24	27.82	173.73	72.67	2018	Dry	6°20'15.1"S 107°18'20.2"E	4.42	0.30	17.77	0.13	1.33
Garut	729	22.14	53.82	76.72	2019	Dry	7°12'20.2"S 107°56'15.0"E	5.01	0.36	70.46	0.15	7.00
Jatinangor	753	21.14	116.52	86.57	2017	Dry	6°55'00.6"S 107°46'18.3"E	5.92	0.37	26.68	0.18	1.70
Cileles	755	23.08	270.00	91.50	2019	Wet	6°54'59.6"S 107°46'14.5"E	5.60	0.33	31.29	0.13	1.41
Bandung	996	26.00	817.86	78.80	2018	Wet	7°03'35.3"S 107°38'46.5"E	4,81	0.69	45.49	0.21	2.17

Loc = location; Alt = altitude; (m.a.s.l.= meters above sea level); Temp= temperature (°C); Rf = rainfall (millimeters per month); C-O = carbon organic (%); K = potassium (%); P = phosphorous (%); N = nitrogen (%)

Data collection

The observed trait was tuber yield per plot (Huamán, 1991). The data were collected at the time of harvest (18 WAP). The weight (in kilograms) of the sample obtained from each 5 m × 5 m plot of each genotype was converted into tonnes per hectare.

Data analysis

Estimation of the GEIs was carried out for all genotypes. The statistical model for combined analysis of variance of the environments is shown in Equation 1:

$$Y_{efgh} = \mu + G_e + E_f + GE_{ef} + R_{g(f)} + B_{h(g)} + \varepsilon_{efgh} \quad (1)$$

where Y_{efgh} is the value in plot h of genotype e and the value in location f of each replication g; μ is the grand mean; G_e is the influence of genotype e; E_f is the influence of the location; GE_{ef} is the influence of interaction between genotype e and location f; $R_{g(f)}$ is the influence of replicate g on location f; $B_{h(g)}$ is the influence of repeat g on plot h; and ε_{efgh} is the influence error of genotype e in plot h and repeat g of location f, respectively.

Identification of the stable genotypes was conducted using parametric and nonparametric stability models. Linear regression was done following Eberhart and Russell (1966). Based on this model, genotype was indicated as stable if the regression slope (bi) was equal to 1 and the variance deviation (S^2di) was 0. The mean variance component (θi) was estimated according to Plaisted and Peterson (1959) using Equation 2:

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

The GE variance component ($\theta_{(i)}$) was calculated according to Plaisted (1960), as shown in Equation 3:

$$\theta_{(i)} = \frac{-p}{(p-1)(p-2)(q-1)} \sum_{j-1}^{q} (x_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 + \frac{SSGE}{(p-2)(q-1)} \quad (3)$$

Wricke’s ecovalence (Wi^2) was calculated according to Wricke (1962), as shown in Equation 4:

$$W_i^2 = \sum (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 \quad (4)$$

Shukla’s stability variance ($\sigma^2 i$) was calculated according to Shukla (1972), as shown in Equation 5:

$$\sigma_i^2 = \left|\frac{p}{(p-2)(q-1)}\right| W_i^2 - \frac{\sum W_i^2}{(p-1)(p-2)(q-1)} \quad (5)$$

and the coefficient of variance (CVi) was calculated according to Francis and Kannenberg (1978), as shown in Equation 6:

$$CV_i = \frac{SD_g}{\bar{X}} x\ 100 \quad (6)$$

where x_{ij} is the yield of genotype i in location j; $\overline{X}_i$ is the yield of genotype i; $\overline{X}_j$ is the average yield of location j; $\overline{X}..$ is the average overall yield; p and q are the numbers of genotypes and environments, respectively; and SDg is the standard deviation of a genotype mean across locations.

Stability nonparametric ($S^{(i)}$) models were applied according to Nassar and Huhn (1987) and Huehn (1990), as shown in Equations 7–10:

$$S_i^{(1)} = 2\sum_j^{n-1} \frac{\sum_{j'=j+1}^{n} \left|r_{ij} - r'_{ij}\right|}{[N(n-1)]} \quad (7)$$

$$S_i^{(2)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_{i.})^2}{(N-1)} \quad (8)$$

$$S_i^{(3)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_{i.})^2}{\bar{r}_i} \quad (9)$$

$$S_i^{(6)} = \frac{\sum_{j=1}^{n} \left|r_{ij} - \bar{r}_{i.}\right|}{\bar{r}_{i.}} \quad (10)$$

where r_{ij} is the rank in location j from genotype i; $\bar{r}_i$ is the mean rank across all locations for each genotype; and N is the number of environments. Stability parameters ($NP^{(i)}$) were calculated according to Thennarasu (1995), as shown in Equations 11–14:

$$NP^{(1)} = \frac{\sum_{j=1}^{n} \left|r_{ij}^* - M_{di}^*\right|}{N} \quad (11)$$

$$NP^{(2)} = \frac{\left[\sum_{j=1}^{n} \left|r_{ij}^* - M_{di}^*\right| / M_{di}\right]}{N} \quad (12)$$

$$NP^{(3)} = \frac{\sqrt{\frac{\sum (r_{ij}^* - r_{i.}^*)^2}{N}}}{\bar{r}_{i.}} \quad (13)$$

$$NP^{(6)} = \frac{2x\left[\sum_{j=1}^{n-1} \sum_{j'=j+1}^{n} \left|r_{ij}^* - r_{i.}^*\right| / \bar{r}_{i.}\right]}{N(N-1)} \quad (14)$$

where r^*_{ij} is the rank of genotype ‘I’ in location ‘j’ based on adjusted data; M^*_{di} is the median rank of adjusted data; M_{di} is the same parameter obtained from the unadjusted data; and N is the number of locations. Kang’s nonparametric stability measure (KR) was assessed according to Kang (1988). In this method, the yield performance and stability variance to identify stable and high-yielding genotypes were given weightings of 1. To calculate the parametric and nonparametric statistics, the online software STABILITYSOFT (Pour-aboughadareh et al., 2019) was used.

The model for GGE biplot applied Equation 15 (Yan and Tinker, 2006):

$$\bar{Y}_{ef} - \mu_e - \beta_f = \sum_{k=1}^{t} \lambda_g \alpha_{eg} \gamma_{fh} + \varepsilon_{ef} \qquad (15)$$

where $\bar{Y}_{ef}$; μ_e; β_f; k; λ_g; α_{eg} and γ_{fh}; ε_{ef} were the performance in location 'f' from genotype 'e'; overall average yield; the influence of location 'f'; number of primer components; the singular value from primer component 'g'; value of genotype 'e' and location 'f' for primer component 'g'; and the error of the genotype 'e' in location 'f', respectively.

Ethics statements

This study was approved by the Ethics Committee of UNPAD. The plant material used in the study was a cultivated plant that involved non-lethal collecting and did not impact any threatened species. In addition, the material used was sweet potato derived from cross breeding by the Plant Breeding Laboratory of UNPAD, in an effort to increase crop production to meet domestic needs.

Results

Genotype responses to environments

Table 2 presents the combined variance of yield in the five environments. The environmental factors, genotypes and GEIs showed significant differences ($p < 0.01$) with SS explaining approximately 37.89%, 17.02% and 45.09%, respectively. This showed that the yield of sweet potato was affected by environmental factors, genotypes and GEIs. The environmental factors were significant because the five locations had different environmental conditions and characteristics (Table 1). Variances in altitude, soil category, temperature, humidity and rainfall along the experimental gradient resulted in different responses by each tested genotype.

Parametric and nonparametric stability of sweet potatoes in five growing environments

The average yields and the parametric stability parameters of the fleshy root genotypes are shown in Table 3. The average yields were in the range 13.19–30.37 t/ha, with genotypes 57(97), IND OF8, Rancing and Beta-2 having higher average

Table 2 Combined analysis of variance of yield in five agro-ecosystems

	df	SS	MS	*F*-value
Environments (E)	4	8951	2237.75	4.81**
Replication/E	10	4648	464.80	3.66**
Genotypes (G)	9	4022	446.89	3.52**
Interactions (GEIs)	36	10652	295.89	2.33**
Minimum (t/ha)	0.11			
Maximum (t/ha)	80.66			
CV (%)	32.53			

** = highly significant ($p < 0.01$); df = degrees of freedom; SS = sum squares; MS = mean squares; CV = coefficient of variation

Table 3 Parametric stability measurements of 10 sweet potato genotypes in five environments

Genotype	AY	W_i^2	σ^2_i	s^2d_i	b_i	CVi	$\theta_{(i)}$	θ_i
Awachy 1	21.31	248.72	65.40	29.02	0.61	41.57	102.32	90.02
57(97)	23.83	20.85	-5.81	1.74	0.83	30.94	110.23	58.37
IND OF7	16.47	252.72	66.65	27.87	1.44	86.59	102.18	90.58
IND OF8	23.07	1012.01	303.93	113.31	0.14	61.28	75.81	196.03
IND 93(407)	18.72	106.22	20.87	10.33	1.34	65.73	107.26	70.23
MZ119	21.00	139.85	31.38	1.26	0.34	15.58	106.10	74.90
MZ462	18.86	244.46	64.07	29.56	0.65	48.23	102.46	89.43
MZ496	13.19	174.50	42.20	14.49	0.51	50.50	104.89	79.71
Rancing	30.02	302.18	82.10	17.40	1.78	54.34	100.46	97.45
Beta-2	30.37	1048.92	315.46	69.13	2.38	76.67	74.53	201.16
Rank								
Awachy 1	5	6	6	7	4	3	6	5
57(97)	3	1	1	2	1	2	1	10
IND OF7	9	7	7	6	5	10	7	4
IND OF8	4	9	9	10	9	7	9	2
IND 93(407)	8	2	2	3	2	8	2	9
MZ119	6	3	3	1	7	1	3	8
MZ462	7	5	5	8	3	4	5	6
MZ496	10	4	4	4	6	5	4	7
Rancing	2	8	8	5	8	6	8	3
Beta-2	1	10	10	9	10	9	10	1

AY = average yield (tonnes/hectare); 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); $\theta_{(i)}$ = GE variance component (Plaisted, 1960); θ_i= mean variance component (Plaisted and Peterson, 1959) yields (>21.68 t/ha), while IND OF7, IND93(407) and MZ496 had lower yields. The Eberhart and Russel (1996) model, genotype stability was determined by regression coefficients (b_i) and variance deviance (S^2d_i), with estimates of $b_i = 1$ and low S^2d_i. Genotypes 57(97), IND 93(407) and MZ462 had values of $b_i = 1$, whereas IND93(407) and MZ462 had lower yields than the overall average yield. Therefore, these latter two genotypes were less adaptable to the range of planting sites. Genotypes IND OF7, Rancing and Beta-2 ($b_i > 1$) had low average levels of stability, indicating that they adapted specifically to a particular environment and produced high yields in certain environments. Genotypes Awachy 1, IND OF8, MZ119 and MZ496 had b_i values <1 and an average yield that was lower than the overall yield, which are specific to a low-production environment. Based on the S^2d_i measurements, the MZ119 genotype had the lowest value, similar to 57(97) and IND 93(407); therefore, MZ119 was found to be the most stable according to this approach. Based on Francis and Kannenberg's parametric stability (CV_i) variance stability model, genotypes MZ119, 57(97) and Awachy 1 were classified as very well-established genotypes. The mean variance component of Plaisted and Peterson's (θ_i) established Beta-2, IND OF8 and Rancing as the most stable genotypes. Three other parametric stability models (Wricke ecovalence (Wi2), Shukla stability variance (σ_i^2) and the GE Plaisted variance component ($\theta_{(i)}$)) indicated that 57(97), IND 93(407) and MZ119 were also the most stable genotypes.

Stability estimates for each genotype using the non-parametric stability models of Huehn and Nassar ($S^{(i)}$), Thennarasu ($NP^{(i)}$) and the Kang rank-sum (KR) method are presented in Table 4. All non-parametric stability models showed that the 57(97) genotype had the lowermost value and represented the most stable genotype. On the other hand, the constancy parameters of $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, $NP^{(1)}$ and $NP^{(4)}$ identified IND OF8 as the most unstable genotype. The $NP^{(2)}$ and $NP^{(3)}$ parameters estimated MZ496 as the most unstable genotype, while the KR parameter estimated IND OF7 as the most unstable. Table 4 also presents information on the rank number, average rank, the standard deviation of the stability ranking and the genotypic stability ranking of all parametric and nonparametric stability parameters. Based on Table 4, the 57(97) genotype had the smallest average rank (AR) value; hence, it was the most stable genotype. IND OF8 had the largest AR value and was the most unstable or adaptive genotype in a particular region.

Table 4 Nonparametric stability measurements models of 10 sweet potato genotypes in five environments

Genotype	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	*K*R			
Awachy 1	3.20	8.00	5.33	2.00	3.00	0.25	0.54	0.53	11.00			
57(97)	0.60	0.30	0.18	0.36	0.60	0.09	0.07	0.09	4.00			
IND OF7	4.00	10.70	10.19	3.14	2.60	0.60	0.63	0.95	16.00			
IND OF8	5.40	20.30	15.04	3.41	4.20	0.46	0.71	1.00	13.00			
IND 93(407)	2.60	4.80	4.17	1.65	2.40	0.56	0.48	0.57	10.00			
MZ119	3.20	6.70	4.32	1.48	2.60	0.37	0.40	0.52	9.00			
MZ462	3.60	8.20	6.31	2.15	3.20	0.54	0.58	0.69	12.00			
MZ496	2.00	2.80	4.67	2.67	2.80	1.87	1.07	0.83	14.00			
Rancing	3.00	5.80	3.14	1.30	2.80	0.20	0.42	0.41	10.00			
Beta-2	3.80	10.50	6.00	2.00	3.60	0.31	0.50	0.54	11.00			
Rank										SR	AR	SD
Awachy 1	5	6	6	5	7	3	6	4	5	89	5.24	1.20
57(97)	1	1	1	1	1	1	1	1	1	30	1.76	2.19
IND OF7	9	9	9	9	3	9	8	9	10	130	7.65	2.09
IND OF8	10	10	10	10	10	6	9	10	8	142	8.35	2.34
IND 93(407)	3	3	3	4	2	8	4	6	3	72	4.24	2.51
MZ119	5	5	4	3	3	5	2	3	2	64	3.76	1.99
MZ462	7	7	8	7	8	7	7	7	7	108	6.35	1.46
MZ496	2	2	5	8	5	10	10	8	9	103	6.06	2.70
Rancing	4	4	2	2	5	2	3	2	3	75	4.41	2.37
Beta-2	8	8	7	5	9	4	5	5	5	116	6.82	3.03

$S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$ = Nassar and Huhn (1987); $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ = Thennarasu (1995); *K*R = Kang (1988); SR = sum rank; AR = average rank

Spearman's rank correlations of parametric and nonparametric stability parameters with yield and sweet potato genotypes

The Spearman rank correlation coefficients revealed that the average yield was positively and significantly correlated with $NP^{(2)}$ ($p < 0.01$) and with $NP^{(3)}$, $NP^{(4)}$, and KR ($p < 0.05$) (Table 5). The other positive and significant correlations were: W_i^2 with σ^2_i, s^2d_i, bi, $\theta_{(i)}$, $S^{(1)}$, $S^{(2)}$, $S^{(3)}$ and $NP^{(1)}$ ($p < 0.01$); σ^2_i with s^2d_i, bi, $\theta_{(i)}$, $S^{(1)}$, $S^{(2)}$, $S^{(3)}$ and $NP^{(1)}$ ($p < 0.01$); S^2d_i with $\theta_{(i)}$, $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(3)}$ and $NP^{(1)}$ ($p < 0.01$); bi with $\theta_{(i)}$ and $NP^{(1)}$ ($p < 0.01$) and with $S^{(1)}$ and $S^{(2)}$ ($p < 0.05$); CVi with $\theta_{(i)}$ ($p < 0.01$) and with $NP^{(4)}$ and KR ($p < 0.05$); $\theta_{(i)}$ with $S^{(1)}$, $S^{(2)}$ and $S^{(3)}$ and with $NP^{(1)}$ ($p < 0.01$); $S^{(1)}$ with $S^{(2)}$, $S^{(3)}$ and $S^{(6)}$ and $NP^{(1)}$ ($p < 0.01$), $NP^{(4)}$ and with KR ($p < 0.05$); $S^{(2)}$ with $S^{(3)}$, $S^{(6)}$ and $NP^{(1)}$ ($p < 0.01$) and with $NP^{(4)}$ and KR ($p < 0.05$); $S^{(3)}$ with $S^{(6)}$, $NP^{(1)}$, $NP^{(3)}$, $NP^{(4)}$ and KR ($p < 0.01$); $S^{(6)}$ with $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ and KR ($p < 0.01$); and $NP^{(1)}$ with $NP^{(3)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ and KR ($p < 0.01$). In contrast to the above results, θ_i had a negative and significant correlation with $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $NP^{(1)}$, W_i^2, σ^2_i ,Cvi, S^2d_i, bi and $\theta_{(i)}$ ($p < 0.01$), as shown in Table 5.

Cluster analyses (dendrograms) were used to classify sweet potato genotypes. The dendrograms in this analysis divided the sweet potato genotypes into two main groups (Fig. 2). The first group (KI) was the unstable group and was divided into two subclusters: 1) the genotypes Awachy 1, MZ462, MZ496 and IND OF7, which had low average yields (below the overall average yield) and low average stability ranks; and 2) the genotypes IND OF8 and Beta-2, which had yields that were greater than the overall average but had low average stability ranks. The second group (K2) was the stable group and was also divided into two subclusters: 1) the genotypes IND 93(407), MZ119 and 57(97), where IND 93(407) and

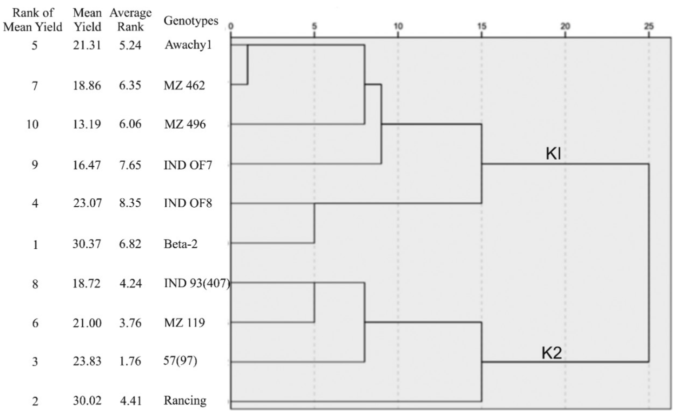

Fig. 2 Dendrogram of hierarchical classification of 10 sweet potato genotypes, where AR indicates the average sum of ranks for all parametric and nonparametric measures

Table 5 Spearman's coefficients rank correlation between mean yield and different parametric and nonparametric stability statistics of 10 sweet potato genotypes evaluated in five environments

	AY	W_i^2	σ^2_i	s^2d_i	Bi	CVi	$\theta_{(i)}$	θ_i	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	*KR*
AY																	
W_i^2	-0.43																
σ^2_i	-0.43	1.00**															
s^2d_i	-0.27	0.83**	0.83**														
Bi	-0.41	0.81**	0.81**	0.47													
Cvi	0.07	0.58*	0.58*	0.49	0.33												
$\theta_{(i)}$	-0.43	1.00**	1.00**	0.83**	0.81**	0.58**											
θ_i	0.43	-1.00**	-1.00**	-0.83**	-0.81**	-0.58**	-1.00**										
$S^{(1)}$	-0.11	0.75**	0.75**	0.76**	0.55*	0.48	0.75**	-0.75**									
$S^{(2)}$	-0.12	0.77**	0.77**	0.79**	0.53*	0.49	0.77**	-0.77**	1.00**								
$S^{(3)}$	0.20	0.62**	0.62**	0.79**	0.38	0.45	0.62**	-0.62**	0.89**	0.90**							
$S^{(6)}$	0.46	0.48	0.48	0.66**	0.30	0.49	0.48	-0.48	0.67**	0.69**	0.91**						
$NP^{(1)}$	-0.30	0.80**	0.80**	0.90**	0.65**	0.23	0.80**	-0.80**	0.67**	0.69**	0.70**	0.58**					
$NP^{(2)}$	0.87**	-0.05	-0.05	0.07	-0.03	0.43	-0.05	0.05	0.20	0.19	0.48	0.71**	0.03				
$NP^{(3)}$	0.52*	0.42	0.42	0.60*	0.25	0.43	0.42	-0.42	0.46	0.48	0.77**	0.95**	0.56*	0.72**			
$NP^{(4)}$	0.55*	0.36	0.36	0.55*	0.21	0.58*	0.36	-0.36	0.60*	0.60*	0.83**	0.96**	0.45	0.82**	0.90**		
KR	0.51*	0.49	0.49	0.60*	0.26	0.55*	0.49	-0.49	0.55*	0.57*	0.81**	0.94**	0.49	0.72**	0.96**	0.89**	

* = significant ($p < 0.05$); ** = highly significant ($p < 0.01$); AY = average yield (tonnes/hectare); 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); $\theta_{(i)}$ = GE variance component (Plaisted, 1960); θ_i= mean variance component (Plaisted and Peterson, 1959); $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$ = Nassar and Huhn (1987); $NP^{(1)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ = Thennarasu (1995); *KR* = Kang (1988)

MZ119 had yields below the overall average and high average stability ranks, while the 57(97) genotype had a yield that was above the overall average yield and the highest average rank (most stable); and 2) the Rancing genotype with yields above the overall average and a fairly high average rank.

GGE biplot analysis of 10 sweet potato genotypes

For the GGE biplot of the 10 sweet potato genotypes in West Java, principal component (PC) 1 and PC 2 explained 55.90% and 24.70%, respectively, of the whole variation, accounting in total for 80.60% of all differences in the sweet potato yield (Fig. 3). Fig. 3 is divided into six sectors, but only three sectors had environment coordinates, namely, sector 1 (Jatinangor), sector 2 (Cileles, Garut and Karawang), and sector 3 (Bandung). Jatinangor was located in sector 1 and the peak genotype in this sector was IND OF8. Cileles, Garut and Karawang were in sector 2 and the mega environment; the peak genotypes in this sector were Beta-2 and Rancing. Bandung was in sector 3 with the IND 93(407) peak genotype. The genotypes located in the peak of the graph (MZ462 and MZ496), that were not included in the environment within the sector, were considered as the lowest yielding within all environments. Genotypes 57(97), IND 93(407) and MZ119 were the closest to the center of the axis; these genotypes showed stable yields in all environments and a low GEI effect.

According to Yan et al. (2007), the experimental environment in the GGE biplots can be categorized into three kinds. The class I environment had a short vector and limited information about the genotype; thus, it was rejected as a test environment. Class II resulted in extended vectors and little viewpoints, with an average environment coordinate abscissa, so they were the best model for selecting excellent genotypes. Class III had no short vectors and produced considerable angles, with an average environment coordinate abscissa; therefore, it was rejected for assessment of the perfect genotype. However, this class entries were valuable in selecting adaptive individuals. Fig. 4 indicated Cileles as a class I environment; thus it could not be used as a trial environment. Garut and Karawang were perfect environments (class II) for selecting superior genotypes because of their high differentiation and representation. Jatinangor was a class III environment and could not be used to select main genotypes. In addition, ideal genotypes should have high yields and high stability levels (closer to the center point in the GGE biplot). The average yield data from the five locations were used to select the ideal genotype. The rankings of the ideal genotypes were, in descending order, Rancing, Beta-2, IND 93(407) and 57(97), as shown in Fig. 3. The IND OF8 genotype had a high yield. This genotype, along with MZ462 and MZ496, was categorized as less favorable because of their distance from the biplot origin.

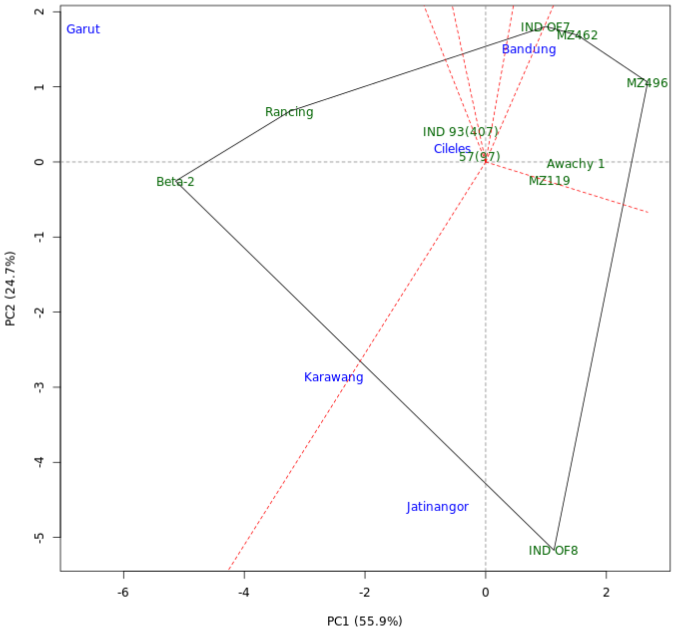

Fig. 3 Mega-environments biplot of 10 sweet potato genotypes at five locations

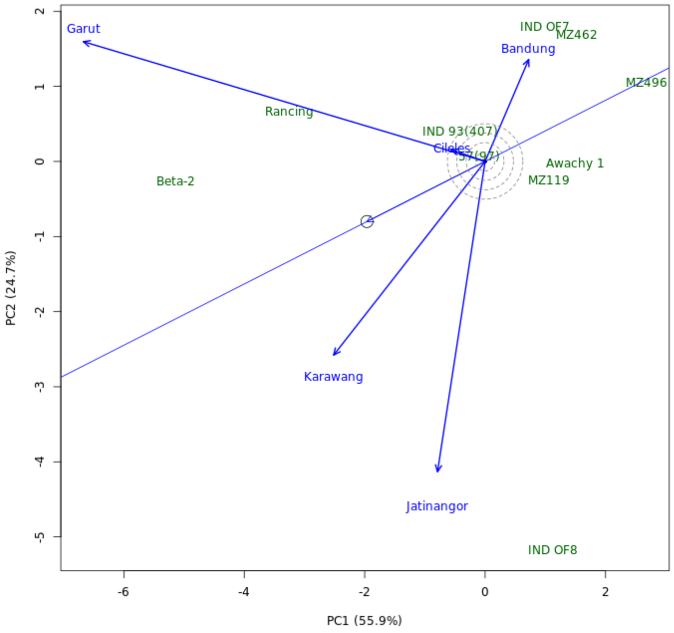

Fig. 4 Biplot of 10 sweet potato genotypes against average yields at five locations

Pearson's correlation between yield and environment factors

In Table 6, 80% of the tested genotypes was correlated with P and 60% with C-Organic. This shows that P and C-Organic each had a substantial effect on sweet potato yields. A positive and significant correlation was found for Awachy1 with altitude, humidity and soil pH ($p < 0.01$); for 57(97) with air temperature ($p < 0.05$), P and C-Organic ($p < 0.01$); for IND OF7 with ($p < 0.05$); for IND 93(407), MZ119, Rancing and Beta-2 with P and C-Organic ($p < 0.01$); for MZ496 with altitude, P and C-Organic ($p < 0.01$) and with pH ($p < 0.05$). There were strong negative correlations for Awachy 1 and MZ496 with air temperature ($p < 0.01$); for IND OF8 with rainfall, K ($p < 0.01$) and with N ($p < 0.05$); for IND 93(407) with air temperature and rainfall ($p <0.01$); for Rancing with rainfall and N ($p <0.05$); and for Beta-2 with rainfall ($p < 0.01$) and K ($p <0.05$). The differences in relationships for each genotype indicated that the responses of genotypes to environmental factors were not the same. Therefore, the development of new superior sweet potato genotypes must be adapted to the appropriate environmental conditions.

Discussion

Environmental factors, genotypes and GEIs had significant impacts on the yield of sweet potatoes. There was greater variation contributed by GEIs than by either the genotype or environment. Several other studies have found that differences in planting locations can lead to differences in the yield potential and yield quality of sweet potatoes (Solihin et al., 2018; Maulana et al., 2020). In addition, differences in planting locations have an impact on the development of sweet potato disease, which affects the quality of the yield (Dewayani et al., 2021). In other studies, the significance of environment was also shown in canola oil (Pavlista et al., 2011) and maize single-cross hybrids (Mafouasson et al., 2018). Oliveira et al. (2014) stated that the existence of GEIs made it difficult to select yellow passionfruit in Brazil. In addition, the low intensity of rainfall and low soil moisture reduce the level of cassava enlargement (Mcharo and Ndolo, 2013; Sokoto and Gaya, 2016). In the current study, the genotypes Awachy1, 57(97), IND OF8, IND 93(407), MZ496, Rancing and Beta-2 were influenced by weather and soil factors, while the genotypes IND OF7, MZ119 and MZ462 were only influenced by soil factors (Table 6). Therefore, the highly significant GEIs for sweet potato yield justified the use of parametric stability parameters, nonparametric stability parameters and GGE biplots to reduce the GEIs and to estimate the potential yield as well as the stability of the evaluated sweet potato genotypes.

In plant breeding, the presence of GEIs complicates the sweet potato selection process. This situation indicates that the selection of sweet potato clones based on yield must be conducted in a specific environment, making the breeding program inefficient. Andrade et al. (2016) reported that GEIs caused in-efficiencies in the sweet potato breeding program in Mozambique. If a sweet potato plant breeding program was carried out on a broad scale, the sweet potato genotypes that were assessed will have different advantages when planted in different locations. The influence of GEIs also led to the sub-optimal potential of the genotypes under dissimilar environmental conditions. However, the presence of GEIs can also provide opportunities for selecting sweet potato genotypes that have a high yield in specific areas. Mustamu et al. (2018) suggested this same idea in different environmental conditions in West Java. These conditions indicated that the selection of appropriate sweet potato genotypes must be carried out in each environment. Shahzad et al. (2019) reported that the environment and GEIs had very high impacts on the yield and fiber value characters of cotton in China. Therefore,

Table 6 Pearson correlations between yield and environmental factors

Genotype	AY	Alt	Temp	Rf	Hum	pH	K	P	N	C-O
Awachy 1	21.31	**0.76**	**-0.82**	-0.08	**0.79**	**0.76**	0.01	0.45	0.05	0.29
57(97)	23.83	0.25	**-0.52**	-0.42	0.15	0.16	-0.32	**0.74**	-0.41	**0.78**
IND OF7	16.47	0.08	-0.35	-0.39	0.35	0.18	-0.46	0.40	**-0.66**	0.42
IND OF8	23.07	-0.48	-0.34	**-0.75**	0.36	**0.51**	**-0.81**	**-0.62**	**-0.51**	-0.35
IND 93(407)	18.72	0.06	**-0.60**	**-0.69**	-0.05	0.16	-0.48	**0.70**	-0.39	**0.87**
MZ119	21.00	0.25	-0.34	-0.25	-0.05	-0.07	-0.14	**0.85**	-0.31	**0.85**
MZ462	18.86	0.30	-0.04	0.14	0.20	-0.10	0.03	**0.52**	-0.33	0.38
MZ496	13.19	**0.81**	**-0.78**	-0.03	0.48	**0.55**	0.17	**0.76**	0.22	**0.61**
Rancing	30.02	-0.07	-0.30	**-0.54**	-0.14	-0.11	-0.45	**0.68**	**-0.56**	**0.82**
Beta-2	30.37	-0.13	-0.44	**-0.72**	-0.24	-0.02	**-0.53**	**0.65**	-0.45	0.87

Numbers in bold denote significant correlation ($p < 0.05$); AY = average yield (tonnes/hectare); Alt = altitude; m.a.s.l. = meters above sea level; Temp= temperature (°C); Rf = rainfall (millimeters/month); C-O = carbon organic (%); K = potassium (%); P = phosphorous (%); N = nitrogen (%)

plant breeding activities should be directed in accordance with appropriate environmental conditions so that the developed plant varieties are able to adapt well to specific environments.

Various methods have been proposed for selecting stable individuals with great productivity. The use of a single stability model remains difficult, so another selection model is needed to obtain the ideal genotype. Several studies have reported the selection of stable genotypes and high yields by applying a combination of stability models, including Farshadfar et al. (2012) for chickpea genotypes, Ahmadi et al. (2015) for grass pea genotypes, Vaezi et al. (2019) for barley genotypes and Ruswandi et al. (2022) for a maize hybrid. In the current research, parametric and non-parametric stability models and GGE biplots were applied to identify sweet potato genotypes that were high yielding and stable in five environments. The average rank (AR) of all stability models was used to select high-yielding and stable sweet potato genotypes (that is with low AR values). The 57(97) and Rancing genotypes had the lowest AR values and were known to be stable and high yielding (above the overall average yield), as shown in Table 4.

To confirm this result, hierarchical clustering analysis (HCA) using a dendrogram was developed based on the average yield rank as a multivariate method to examine the genotypes. The dendrogram of sweet potato genotypes divided the genotypes into two primer groups (Fig. 2). Class I (KI) consisted of genotypes that have a low average yield (below the overall average yield) and greater than average yield but a high average stability rank, indicating that certain genotypes have undergone specific adaptation in some environments. Class II (K2) consisted of genotypes that have low and high yields with a low average stability rank (the most stable). Therefore, these genotypes can be used to improve the performance and adaptation of sweet potato breeding programs.

Overall, the results of Spearman's rank correlation analysis revealed that the measures of stability $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ and KR were clearly associated with average yields, thus providing a measure of stability in a dynamic sense. According to Mohammadi and Amri (2008), stability models that are positively correlated with yield can be used to recommend genotypes within a particular environment. In another study, Ahmadi et al. (2015) and Vaezi et al. (2019) reported that CVi, b_i and Fox-rank (TOP) were significantly correlated to yield; thus, these are three parameters that are useful to identify sweet potatoes with high average yields in environments with favorable growth conditions. Based on this, the $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$ and KR models can also be used as stability models to identify sweet potato yields in a favorable environment.

In the "which won where" GGE biplot, the polygons represent genotypic markers that are positioned utmost from the source of the biplot in numerous ways, so that whole genotype markers are convened in polygons. The genotype at the top of each sector is the genotype with the highest yield in the environment in that sector. Yan et al. (2007) stated that this biplot can indicate the existence of a mega-environment. The current results showed that there were various environmental groupings throughout the trials. The first PC explained 50.90% of the total variation caused by environmental effects (E) and GEIs during the experiment (Fig. 3). The grouping of the environment and mega-environment in various regions in West Java with different peak genotypes indicated the existence of specific adaptations of the genotypes to the mega-environment and the positive utilization of GEIs (Vaezi et al., 2019). The current findings revealed that some sweet potato genotypes have adapted to different environments in West Java better than other genotypes. The ideal environment must distinguish genotypes and represent all environments in the trial (Yan et al., 2007). In the current study, the discriminativeness versus representativeness of the GGE biplot revealed that Cileles was a class I environment, or a less than ideal location that must be replaced or moved. Among the five environments, Garut and Karawang were class II environments that had high selective influence power and representativeness; hence, they were ideal locations for selecting superior genotypes (Fig. 4). Based on Ahmadi et al. (2015), ideal genotypes have a high yield and are stable in various environments. The Rancing genotype, followed by Beta-2, IND 93(407) and 57(97), were identified as ideal genotypes. The dendrogram identified 57(97) and Rancing as genotypes with high and stable yields (Fig. 2). The current results using both numerical (parametric and nonparametric) and graphical (GGE biplot) methods produced the same pattern to identify stable genotypes. For example, numerical methods identified several stable and high yield genotypes: 57(97) and Rancing, whereas the graphical method identified genotypes 57(97), IND 93(407), Rancing and Beta-2 as the most stable and ideal genotypes. Some studies have also used numerical approaches and GGE biplots to select ideal genotypes for chickpea (Farshadfar et al., 2012), grass pea (Ahmadi et al., 2015) and soybean (Goksoy et al., 2019) in various regions in Iran. Those studies reported the relative contribution of the two methods in identifying the ideal genotypes.

Each genotype has a different correlation with environmental factors (Table 6). This is caused by the origin of each genotype, which is the result of crossing with different elders. Some studies have mentioned that adequate water intake during planting will affect sweet potato yields (Mcharo and Ndolo, 2013; Laurie et al., 2015; Lestari and Ricky, 2015; Opafola et al., 2018). In addition, Sokoto and Gaya (2016) commented that elevated air temperature, low nutrient contents and sparse rainfall will cause plant stress and inhibit crop development. In another study, environmental differences (weather and soil factors) caused variations in yield and yield attributes in the *Stevia* genotype (Amien et al., 2021). The current study supported adjusting the cultivation methods according to the genotype in suitable environments. Therefore, the right planting environment for the sweet potato development program could increase the genetic potential.

Conflict of Interest

The authors declare that there are no conflicts of interest.

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