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Research Article

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Storage root yield and sweetness level selection for new honey sweet potato (*Ipomoea batatas* [L.] Lam)

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Abstract: Multilocation experiments are the steps to determine the genotype stability being tested. Honey sweet potato is a superior agricultural product from West Java, Indonesia. High yield and sweetness are the important traits of the new honey sweet potato breeding lines. In this study, the sweetness level used was the soluble solid level (°brix). The goals of this study were to determine the effects of genotype by environment interactions (GEIs) and to select for storage root yield stability and sweetness among the new promising honey sweet potato lines. Field trials have been carried out using randomized completed block design, which was repeated thrice for the 16 genotypes, across six locations in West Java, Indonesia. To estimate GEIs, data were analyzed using combined analysis of variance. Storage root yield stability (t/ha) and sweetness (°brix) were estimated using parametric measurements, nonparametric measurements, and GGE biplot. The results showed that the genotype (G), environment (E), and GEIs have significant influences on storage root yield and sweetness. Two genotypes, SP3 and SP16, have been identified as the most stable ones with high yield and sweetness across several locations. These two superior genotypes are recommended as potential new honey sweet potato varieties for West Java, Indonesia.

Keywords: honey sweet potato, GEIs, GGE biplot, parametric, nonparametric

1 Introduction

Sweet potato is one of the tuber crops that plays an important role in Indonesia. The crop is a potential source of carbohydrates that can be used for food and feed (Mukhopadhyay et al. 2011). Furthermore, sweet potato starch has suitable characteristics for industrial materials (Grüneberg et al. 2015; Waluyo et al. 2015). The high starch content of sweet potato makes it a good source of bioethanol (Ziska et al. 2009; Waluyo et al. 2015; Lareo and Ferrari 2018). West Java is the largest area for sweet potato cultivation in Indonesia. It has the highest demand for sweet potato for both domestic and export markets. Average domestic market demand for sweet potato is approximately 40 tons per day, while the export is about 210 tons per week (Indonesian Sweet potato Farmer Agribusiness Association [ASAPUJI], personal communication). Therefore, because of its many uses and economic value, sweet potato is considered as one of the most economically important crops for West Java.

One of the most demanding characteristics of sweet potato is the sweetness level. The higher the level of its sweetness, the more precious the products. Honey sweet potato has a sweet taste when fresh and releases a liquid like honey when baked. However, for honey sweet potato breeding program, high yield and sweetness are the most important sweet potato traits. The most important stage of the breeding program is the multi-environment field trials to identify high yielding lines with stable performance across diverse environments. The existence of genotype by environment interactions (GEIs) makes it difficult to have an unbiased estimate of yield potential and yield stability, as it will uncover the varying responses of diverse genotypes to different environmental conditions (Andrade et al. 2016).

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Sweet potato yield is largely influenced by genotype or clone (G), environment (E), and GEIs. Gruneberg et al. (2005) suggested that a trait can be fully expressed under optimum environmental conditions, if the underlying favorable genes controlling this trait are present in the plant. However, under diverse environmental conditions, different genotypes may have varying or stable yield responses. Therefore, multilocation trials of yield-trait were necessary to determine the performance of each genotype in various environments.

Climate change and global warming are global problems faced by many countries. Extreme climatic events cause soil degradation, which results in low yields of agricultural crops (Agbola and Fayiga 2016), including sweet potatoes. The decline in the productivity of sweet potato yield losses to various parties, including farmers, traders, and agriculture-based industries. Therefore, superior varieties are needed that can adapt to various environmental conditions, both optimum and extreme, with high yields.

Multilocation yield trials should be conducted across established crop production areas. The chosen locations should represent all growing environments within the region to estimate adaptability, yield potential, and yield stability. In this way, widely adapted or environment-specific genotypes can be identified. Widely adapted genotypes tend to have consistent and stable performance across many environments, while environment-specific adaptation provides superior performance within a certain environment (Mustamu et al. 2018).

Various methods have been developed to analyze GEIs and select the genotypes with stable performance across environments and to determine the degree of adaptability. The most widely used measurements of stability were linear regression (Eberhart and Russell 1966), the ecovalence value (W_i^2) (Wricke 1962), Shukla's steadiness discordance (σ_i^2) (Shukla 1972), coefficient from variance (CV_i) (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) have been used in the recent GEIs studies. Numerous sweet potato development programs have adopted this method previously. For example, to determine GEIs and assess the stability of sweet potato genotypes across various environments in Turkey, the AMMI model was used successfully (Caliskan et al. 2007). Laurie et al. (2015) used GGE biplots to identify competency of sweet potato lines and emblematical environments in South Africa. Furthermore, Mustamu et al. (2018) used AMMI and GGE biplot to select stable and widely adapted sweet potato genotypes in Indonesia. Some researchers used combination of stability models to determine stable genotypes and high yields (Akcura and Kaya 2008; Farshadfar et al. 2012; Vaezi et al. 2019; Maulana et al. 2020). The goals of this study were to estimate GEIs effects and select for yield stability and sweetness on new honey sweet potato genotypes in West Java.

2 Materials and methods

2.1 Plant materials

Fifteen new promising genotypes of sweet potato (*Ipomoea batatas* L. [Lam.]) and one check variety were evaluated in this study, namely 49 (2) (SP1), 12 (133) (SP2), 57 (97) (SP3), 58 (99) (SP4), 15 (112) (SP5), 40 (136) (SP6), 68 (120) (SP7), 3 (71) (SP8), 8 (26) (SP9), 59 (15) (SP10), 50 (51) (SP11), Awachy 1 (SP12), Awachy 2 (SP13), Awachy 4 (SP14), Awachy 5 (SP15), and Rancing (SP16) as standard check. All genotypes tested were the result of crosses that had been selected previously based on consumer preference (elongated oval shape), plain fleshed storage root (not spotted), and storage root size. The storage root sizes are classified as follows: small (S = 80–150 g/tuber), medium (M = 151–300 g/tuber), and large (L = 301–600 g/tuber). Check variety used was a local variety "Rancing" belonging to Department of Food Crop Agriculture, Sumedang district, West Java, Indonesia, which is widely adapted across in diverse locations in Java and was certified as honey sweet potato variety.

2.2 Experimental design

Field experiments were conducted across six environments in West Java, Indonesia, including Bandung, Sumedang, Kuningan, Banjar, Sukabumi, and Pangandaran. The six environments have diverse agroclimatic conditions (Table 1). Field trials in each location used randomized completed block design with three replications. The 16 genotypes were planted in three experimental blocks per location. Each location was fertilized with chicken dung (dosage 5 tons/ha) and NPK (dosage 200 kg/ha).

2.3 Data collection

The observed traits were storage root yield per plot and sweetness (Huamán 1991). Data were taken when the

Table 1: Variations across six environments when the study was conducted

Locations	Coordinates	Alt.	Temp.	Rainfall	Soil parameters								
					Soil order	Textural class	Hum.	pH H_2O	OC (%)	TN (%)	C/N	P_2O_5 HCl 25% (mg/100 g)	K
Sumedang	6°52′29.0″S 107°49′14.9″E	900	24.80	0.21	Inceptisols	Clay loam	70.00	6.50	2.94	0.27	11.00	159.74	1.34
Sukabumi	6°54′34.7″S 106°44′40.2″E	510	25.83	0.39	Oxisols	Clay	74.64	6.02	2.80	0.21	5.24	55.85	1.30
Pangandaran	7°40′45.4″S 108°38′35.3″E	10	26.77	0.09	Entisols	Sandy	78.21	6.66	0.66	0.05	13.00	10.70	0.04
Kuningan	6°55′45.7″S 108°26′12.0″E	782	25.21	20.88	Entisols	Sandy loam	84.57	6.68	1.12	0.18	6.22	90.50	0.21
Bandung	6°52′45.5″S 107°44′36.8″E	753	26.42	20.38	Inceptisols	Clay loam	82.31	6.02	3.38	0.21	16.01	1.87	1.02
Banjar	7°23′34.3″S 108°36′32.5″E	16	25.37	17.91	Inceptisols	Sandy clay loam	83.31	6.74	1.11	0.12	9.25	66.70	0.18

Alt. = altitude (m.a.s.l.); Temp. = temperature (°C); Hum. = humidity; K = potassium; OC = organic carbon; TN = total nitrogen; C/N = carbon/nitrogen.

plants were 18 weeks after planting (harvest time), on a $3 \times 5\ \text{m}^2$ plot for each genotype. The storage root yield for each genotype from each plot (kg) was converted into t/ha. The sweetness of fresh storage root was measured using the digital refractometer (ATAGO-PAL1) with °brix units (Magwaza and Opara 2015). The sweetness testing using a digital refractometer starts from the calibration of the tool with aquadest, and then the liquid sample was allowed to drip onto the refractometer prism.

2.4 Data analysis

The combined ANOVA statistical model to estimate GEIs follows the equation:

$$Y_{\text{opqr}} = \mu + G_{\text{o}} + E_{\text{p}} + GE_{\text{op}} + R_{\text{q(p)}} + B_{\text{r(q)}} + \varepsilon_{\text{opqr}}, \quad (1)$$

where Y_{opqr} is the value of genotype o in plot r, and the value in location p of each replication q; μ is the grand mean both storage yield and sweetness; G_{o} is the effect of genotype o; E_{p} is the effect of the environment p; GE_{op} is the effect of GEIs on genotype o and environment p; $R_{\text{q(p)}}$ is the effect of replicate q on location p; $B_{\text{r(q)}}$ is the effect of replication q on plot r; and $\varepsilon_{\text{opqr}}$ is the error effects from genotype o in plot r and repeat q of location p, respectively. To calculate the combined ANOVA, Genstat 12th was used.

Nonparametric and parametric stability models were used to identify stable genotypes both storage yield and sweetness. Among them is the linear regressions measure following Eberhart and Russell (1966). According to Eberhart and Russell (1966), a genotype was declared stable if it has a regression deviation = 1 and the variance deviation value (S^2d_i) = 0. Mean variance component (θ_i) was estimated following Plaisted and Peterson (1959) with the formula:

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

GE variance component ($\theta_{(i)}$) was calculated as follows (Plaisted, 1960):

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

Wricke's Ecovalence (W_i^2) was estimated as follows (Wricke, 1962):

$$W_i^2 = \sum (X_{ij} - \bar{X}_i - \bar{X}_j + \bar{X}\ldots)^2. \tag{4}$$

Shukla's stability variance σ_i^2 for the genotype i was measured as follows (Shukla 1972):

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

Coefficient of variance (CV_i) follows Francis and Kannenberg (1978) with the formula:

$$CV_i = \frac{SD_g}{\bar{X}} \times 100. \tag{6}$$

For all measurements used, x_{ij}: grand yield from the genotype i across all sites; $\bar{X}_i$: mean yield from genotype i; $\bar{X}_j$: mean yield in site j; $\bar{X}\ldots$: overall average yield; p and q: the numbers of genotypes and sites; SD_g: the standard deviation of a genotype by location interaction.

Nonparametric stability ($S^{(i)}$) measures follow Nassar and Huehn (1987) and Huehn (1990) with the formula:

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

$$S_i^{(2)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_i)^2}{(N-1)}, \tag{8}$$

$$S_i^{(3)} = \frac{\sum_{j=1}^{n} (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}, \tag{9}$$

$$S_i^{(6)} = \frac{\sum_{j=1}^{n} |r_{ij} - \bar{r}_i|}{\bar{r}_i}, \tag{10}$$

where r_{ij}: rank of stability from genotype i in the location j; $\bar{r}_i$: mean rank across all location for each genotype; and N: number of location. Parametric stability ($NP^{(i)}$) measures follow Thennarasu (1995) with the formula:

$$NP^{(1)} = \frac{\sum_{j=1}^{n} |r^{*}_{ij} - M^{*}_{di}|}{N}, \tag{11}$$

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

$$NP^{(3)} = \frac{\sqrt{\frac{\sum (r^{*}_{ij} - r^{*}_{i})^2}{N}}}{\bar{r}_i}, \tag{13}$$

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

where r^{*}_{ij}: stability rank in location j from genotype i based on adjusted data; M^{*}_{di}: median rank for adjusted data both storage yield and sweetness; M_{di}: original data from the same parameters. N: number of location. Kang rank's (KR) nonparametric stability model follows Kang (1988). In this method, yield performance and stability variance identify the high yielding and stable genotypes given a weighting of 1. Stable genotypes were identified (storage root yield and sweetness) based on nonparametric and parametric stability measurements using STABILITYSOFT (online software) (Pour-Aboughadareh et al. 2019).

The model for GGE biplot follows Yan and Tinker (2006) with the formula:

$$\bar{Y}_{mn} - \mu_m = \beta_n + \sum_{k=1}^{t} \lambda_o \alpha_{mo} \gamma_{no} + \varepsilon_{mn}, \tag{15}$$

where $\bar{Y}_{mn}$; μ_m; β_n; k; λ_o; α_{mo} and γ_{no}; ε_{mn} are the performance in location "n" from genotype "m;" overall average yield; the influence of location "n;" number of primer components; the singular value from primer component "o;" value of genotype "m" and location "n" for primer component "o;" and the error of the genotype "m" in location "n," respectively.

The formula of genotype by yield*traits (GYT) follows Yan and Frégeau-reid (2018). To calculate GYT, we used the R program software v3.6.3 (R Core team 2018).

3 Results

3.1 GEIs estimation of storage root yield and sweetness in honey sweet potato

In Table 2, the three main effects (genotype [G], environment [E], and GEIs) on the combined ANOVA showed a very significant influence ($P < 0.01$) on the storage root yield and sweetness characteristics. For storage root yield, the greatest contribution was from environmental factor (40.61%), while for sweetness, GEIs showed the greatest contribution with a value of 36.46%. These results indicate that the high degree of variation for storage root yield and sweetness on honey sweet potato evaluated across six locations ranging from 3.78 to 16.73 t/ha for storage root yield, and 7.24–10.48 °brix for sweetness. The highest average storage root yield observed was in Kuningan (16.73 t/ha) and the lowest in Sukabumi (3.78 t/ha). The highest average sweetness was observed in Sukabumi (10.48 °brix) and the lowest in Kuningan (7.24 °brix). In this study, the role of GEIs on storage root yields for all genotypes used was very important. Table 2 shows that all genotypes demonstrated various responses across different locations for yield and sweetness.

Table 2: Combined ANOVA for 16 honey sweet potato genotypes storage root yields and sweetness evaluated in six locations in West Java, Indonesia

Source	Df	Storage root yield (t/ha)				Sweetness (°brix)			
		SS	MS		%TSS	SS	MS		%TSS
Environments (Env.)	5	6642.00	1328.40	**	40.61%	384.58	76916.00	**	21.35%
Replication (Env.)	12	9.70	0.81			35.09	2924.00		
Genotypes (Gen.)	15	3343.80	222.92	**	20.45%	490.96	32731.00	**	27.26%
Env × Gen	75	6247.20	83.30	**	38.20%	656.68	8756.00	**	36.46%
Minimum		0.21				4.40			
Maximum		27.38				14.70			
Means		9.92				8.85			
St. Dev.		7.55				1.96			
CV (%)		7.94				12.88			

**$p < 0.05$; St. Dev. = standard deviation; CV = coefficient of variation.

3.2 Stability of yield and sweetness of honey sweet potato across six environments based on numerical stability models

The stability analysis in this model consists of parametric and nonparametric analysis. The results of the stability analysis of the two characters are presented in Tables 3 and 4. For storage root yield (Table 3), the W_i^2, σ_i^2, and $\theta_{(i)}$ models showed the similar results in the stability ranks of the genotypes tested, as well as select the SP1, SP3, and SP10 as the most widely adapted sweet potato genotypes. Two other models, S^2d_i and $NP^{(1)}$, also revealed that SP1 is the most stable genotype, although it does not have the same pattern as the other three models. The CV_i, $NP^{(2)}$, $NP^{(3)}$, and KR models revealed that SP3 was the most stable genotype. The regression slope (bi) revealed that SP12 was the stable genotype. $S^{(1)}$ and $S^{(2)}$ expressed similar patterns in revealing stable genotypes, both stated that SP14 and SP16 were the most stable genotypes. θ_i revealed that SP15 was the most stable genotype, while SP16, SP3, SP9, and SP4 were stated to be the most stable by $S^{(3)}$, $S^{(6)}$, and $NP^{(4)}$ models.

For the sweetness (Table 4), the SP3 genotype was stated to have the most stable sweetness by the stability models $S^{(1)}$, $S^{(2)}$, $S^{(3)}$, $S^{(6)}$, $NP^{(3)}$, $NP^{(4)}$, KR, W_i^2, σ_i^2, S^2d_i, CV_i, and $\theta_{(i)}$. $S^{(1)}$, $S^{(2)}$, W_i^2, and σ_i^2 show the same patterns in determining the stability of sweetness on sweet potato genotypes. $NP^{(2)}$ models revealed that the SP8 was the genotype that had the most stable sweetness across five environments. The regression model (bi) revealed that SP11 had the most stable sweetness, followed by SP3 and SP13. SP12 had the most stable sweetness as determined by θ_i.

3.3 Spearman's rank correlations of parametric and nonparametric stability models with storage root yields and sweetness in honey sweet potato genotypes

The results of Spearman's rank correlation for the storage root yield and sweetness are shown in Tables 5 and 6, respectively. For the two characters tested, there were several stability models that are significantly correlated. Storage root yield had significant positive correlations with $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, bi, CV_i, and KR stability models. On the contrary, sweetness had significant positive correlations with $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, and KR stability models.

To classify and estimate the relationships between stability models, we used principal component analysis (PCA) for the two characters measured. The first four PCs, with eigenvalues of >1, accounted for 86.52% for storage root yield and 89.55% for sweetness of the total variation using numerical stability measures (parametric and nonparametric) (Table 7). Biplot diagrams for the two characters were drawn based on PC1 and PC2 (Figures 1 and 2), because these two components (PC1 and PC2) from the two characters had the highest eigenvalues and variability. Figure 1 shows the three main groups of numerical stability models (parametric and nonparametric) for storage root yield: (1) K1, which included storage root yield (Y) and $NP^{(2)}$, $NP^{(3)}$, and bistability measures, (2) K2, which included $NP^{(4)}$, $S^{(3)}$, $S^{(6)}$, CV_i, and KR stability measures, and (3) K3, which included $NP^{(1)}$, $S^{(1)}$, $S^{(2)}$, S^2d_i, W_i^2, σ_i^2, and $\theta_{(i)}$ stability measures. By contrast, the stability model θ_i was separate from all groups. Sweetness was

Table 3: Parametric and nonparametric stability analysis on storage root yield character of 16 honey sweet potato genotypes

Genotype	Yield	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	W_i^2	σ_i^2	s^2d_i	b_i	CV_i	$\theta_{(i)}$	θ_i	*KR*
SP1	8.28	4.47	13.37	8.18	2.12	2.33	0.42	0.40	0.55	42.72	7.78	2.45	0.57	42.57	29.10	19.43	12
SP2	7.17	4.00	10.67	9.41	2.82	2.67	0.88	0.71	0.71	129.67	27.66	17.96	0.83	92.79	27.77	28.71	19
SP3	15.87	3.93	11.77	4.47	1.29	3.33	0.24	0.29	0.30	54.28	10.42	3.50	0.54	22.59	28.92	20.66	3
SP4	12.83	4.27	12.00	5.45	1.45	3.17	0.43	0.38	0.39	132.20	28.23	17.55	1.26	64.51	27.73	28.98	12
SP5	6.08	5.33	22.40	22.40	4.80	3.83	1.80	0.93	1.07	153.25	33.04	19.43	0.65	102.48	27.41	31.22	28
SP6	7.25	4.13	13.47	12.63	3.00	2.83	0.74	0.73	0.78	73.79	14.88	10.26	1.12	96.64	28.62	22.74	17
SP7	6.60	6.80	30.67	20.91	3.82	4.83	0.76	0.80	0.93	223.60	49.13	28.58	0.59	106.70	26.34	38.73	29
SP8	10.92	5.40	19.50	11.47	2.47	3.33	0.37	0.51	0.64	143.00	30.70	20.28	1.09	71.55	27.57	30.13	18
SP9	15.25	3.87	11.87	4.81	1.41	3.67	0.26	0.39	0.31	138.93	29.77	8.27	1.77	64.87	27.63	29.69	12
SP10	11.49	4.33	12.97	7.07	2.07	4.00	0.35	0.45	0.47	65.26	12.93	6.43	1.38	68.51	28.75	21.83	8
SP11	8.48	5.67	21.10	14.07	3.07	5.00	0.48	0.72	0.76	168.04	36.43	21.92	0.68	77.58	27.19	32.80	23
SP12	11.46	5.00	16.57	8.42	1.93	4.00	0.44	0.45	0.51	150.46	32.41	15.32	1.56	82.23	27.46	30.92	18
SP13	8.34	5.80	22.70	17.46	3.23	3.83	0.64	0.64	0.89	141.96	30.46	19.39	1.21	98.78	27.59	30.02	20
SP14	4.45	2.93	5.87	6.77	2.46	3.33	0.75	1.02	0.68	67.17	13.37	2.65	0.41	64.69	28.72	22.04	20
SP15	8.97	6.73	31.10	18.29	3.41	5.33	0.60	0.68	0.79	268.07	59.29	37.50	1.20	107.13	25.66	43.47	24
SP16	15.32	3.07	6.40	2.46	0.92	3.83	0.38	0.35	0.24	129.98	27.73	18.07	1.16	51.59	27.77	28.74	9

Genotype	Rank																	SR	AR	SD
SP1	11	9	8	7	7	1	6	5	7	1	1	1	8	2	1	16	4	95	5.59	4.24
SP2	13	5	3	9	10	2	15	11	10	6	6	9	6	11	6	11	10	143	8.41	3.52
SP3	1	4	4	2	2	5	1	1	2	2	2	3	3	1	2	15	1	51	3.00	3.32
SP4	4	7	6	4	4	4	7	3	4	8	8	8	2	4	8	9	4	94	5.53	2.18
SP5	15	11	13	16	16	9	16	15	16	13	13	12	15	14	13	4	15	226	13.29	3.10
SP6	12	6	9	11	11	3	12	13	12	5	5	6	13	12	5	12	7	154	9.06	3.45
SP7	14	16	15	15	15	14	14	14	15	15	15	15	4	15	15	2	16	229	13.47	4.00
SP8	7	12	11	10	9	5	4	8	8	11	11	13	11	8	11	6	8	153	9.00	2.55
SP9	3	3	5	3	3	8	2	4	3	9	9	5	5	6	9	8	4	89	5.24	2.46
SP10	5	8	7	6	6	12	3	7	5	3	3	4	10	7	3	14	2	105	6.18	3.36
SP11	9	13	12	12	12	15	9	12	11	14	14	14	7	9	14	3	13	193	11.35	3.10
SP12	6	10	10	8	5	12	8	6	6	12	12	7	1	10	12	5	8	138	8.12	3.12
SP13	10	14	14	13	13	9	11	9	14	10	10	11	12	13	10	7	11	191	11.24	2.05
SP14	16	1	1	5	8	5	13	16	9	4	4	2	16	5	4	13	11	133	7.82	5.36
SP15	8	15	16	14	14	16	10	10	13	16	16	16	14	16	16	1	14	225	13.24	4.01
SP16	2	2	2	1	1	9	5	2	1	7	7	10	9	3	7	10	3	81	4.76	3.40

AR = average of rank; SR = sum of rank; SD = standard deviation.

Table 4: Parametric and nonparametric stability analyses on sweetness character of 16 honey sweet potato genotypes

Genotypes	Sweetness	$S^{(1)}$	$S^{(2)}$	$S^{(3)}$	$S^{(6)}$	$NP^{(1)}$	$NP^{(2)}$	$NP^{(3)}$	$NP^{(4)}$	W_i^2	σ_i^2	s^2d_i	b_i	CV_i	$\theta_{(i)}$	θ_i	KR
SP1	10.27	5.00	16.97	7.17	1.63	4.67	0.39	0.45	0.42	14.73	3.16	1.98	0.67	18.23	2.90	3.14	16
SP2	9.91	4.53	16.00	6.67	1.50	4.33	0.30	0.39	0.38	8.45	1.72	1.19	0.89	17.27	3.00	2.46	13
SP3	10.38	1.60	1.87	0.70	0.45	2.67	0.36	0.24	0.12	2.34	0.33	0.04	0.49	6.40	3.09	1.81	3
SP4	10.04	4.47	13.77	5.82	1.46	3.50	0.28	0.32	0.38	6.79	1.34	0.94	0.85	15.70	3.02	2.29	11
SP5	8.56	3.20	8.27	5.39	1.39	2.17	0.38	0.40	0.42	2.96	0.47	0.42	1.04	17.81	3.08	1.88	11
SP6	9.13	6.47	27.77	15.72	2.64	4.50	0.46	0.61	0.73	12.78	2.71	1.75	1.26	24.45	2.93	2.93	16
SP7	5.72	4.00	12.67	17.27	4.36	6.00	2.40	1.66	1.09	41.08	9.18	5.87	1.03	55.07	2.50	5.95	31
SP8	8.23	2.93	7.07	4.61	1.65	2.33	0.26	0.42	0.38	4.66	0.86	0.66	1.07	20.18	3.06	2.06	16
SP9	6.91	1.93	2.70	3.86	2.29	3.67	2.13	1.43	0.55	8.95	1.84	1.27	1.09	27.83	2.99	2.52	24
SP10	8.85	3.13	6.70	3.94	1.53	2.50	0.27	0.38	0.37	2.44	0.35	0.34	1.10	17.55	3.09	1.82	9
SP11	8.11	5.00	19.10	14.69	3.38	3.17	0.81	0.61	0.77	5.25	0.99	0.52	0.55	13.60	3.05	2.12	19
SP12	7.37	7.40	38.97	28.51	4.83	5.33	0.97	0.87	1.08	63.35	14.27	7.35	2.22	57.87	2.16	8.32	30
SP13	8.30	5.33	18.80	13.43	2.86	5.00	0.59	0.77	0.76	14.87	3.19	2.11	1.10	26.68	2.90	3.15	23
SP14	8.23	3.73	9.47	7.47	2.21	2.83	0.38	0.61	0.59	3.18	0.52	0.42	0.83	15.84	3.08	1.90	14
SP15	8.14	5.60	22.80	19.00	3.67	4.50	0.93	0.84	0.93	13.79	2.94	0.72	-0.04	12.39	2.92	3.03	24
SP16	10.54	3.73	10.27	3.85	1.15	3.50	0.37	0.33	0.28	13.25	2.82	1.08	1.85	25.02	2.93	2.98	12

Genotypes	Rank																	SR	AR	SD
SP1	3	11	11	9	7	13	9	8	8	13	13	13	7	9	13	4	8	159	9.35	3.14
SP2	5	10	10	8	5	10	4	5	5	8	8	10	5	6	8	9	6	122	7.18	2.16
SP3	2	1	1	1	1	4	5	1	1	1	1	1	2	1	1	16	1	41	2.41	3.69
SP4	4	9	9	7	4	7	3	2	4	7	7	8	9	4	7	10	3	104	6.12	2.52
SP5	8	5	5	6	3	1	7	6	7	3	3	3	10	8	3	14	3	95	5.59	3.24
SP6	6	15	15	13	11	11	10	9	11	10	10	12	13	11	10	7	8	182	10.71	2.47
SP7	16	8	8	14	15	16	16	16	16	15	15	15	8	15	15	2	16	226	13.29	4.13
SP8	11	3	4	5	8	2	1	7	6	5	5	6	4	10	5	12	8	102	6.00	3.04
SP9	15	2	2	3	10	9	15	15	9	9	9	11	14	14	9	8	13	167	9.82	4.35
SP10	7	4	3	4	6	3	2	4	3	2	2	2	6	7	2	15	2	74	4.35	3.28
SP11	13	11	13	12	13	6	12	10	13	6	6	5	1	3	6	11	11	152	8.94	3.93
SP12	14	16	16	16	16	15	14	14	15	16	16	16	11	16	16	1	15	243	14.29	3.67
SP13	9	13	12	11	12	14	11	12	12	14	14	14	3	13	14	3	12	193	11.35	3.43
SP14	10	6	6	10	9	5	8	11	10	4	4	4	16	5	4	13	7	132	7.76	3.54
SP15	12	14	14	15	14	11	13	13	14	12	12	7	15	2	12	5	13	198	11.65	3.62
SP16	1	6	7	2	2	7	6	3	2	11	11	9	12	12	11	6	5	113	6.65	3.82

AR = average of rank; SR = sum of rank; SD = standard deviation.

Table 5: Spearman's correlation rank between storage root yield character with stability models

	Yield	**S$^{(1)}$**	**S$^{(2)}$**	**S$^{(3)}$**	**S$^{(6)}$**	**NP$^{(1)}$**	**NP$^{(2)}$**	**NP$^{(3)}$**	**NP$^{(4)}$**	**W_i^2**	**σ_i^2**	**s^2d_i**	**bi**	**CV$_i$**	**KR**	**$\theta_{(i)}$**	**θ_i**
Yield	1.00																
S$^{(1)}$	0.27	1.00															
S$^{(2)}$	0.28	**0.96**	1.00														
S$^{(3)}$	**0.67**	**0.83**	**0.87**	1.00													
S$^{(6)}$	**0.77**	**0.73**	**0.76**	**0.97**	1.00												
NP$^{(1)}$	−0.10	**0.56**	**0.57**	0.39	0.32	1.00											
NP$^{(2)}$	**0.88**	0.29	0.32	**0.70**	**0.78**	0.05	1.00										
NP$^{(3)}$	**0.91**	0.33	0.38	**0.74**	**0.83**	0.19	**0.84**	1.00									
NP$^{(4)}$	**0.82**	**0.68**	**0.73**	**0.96**	**0.99**	0.27	**0.83**	**0.85**	1.00								
W_i^2	0.16	**0.71**	**0.75**	**0.67**	**0.59**	**0.72**	0.37	0.36	**0.55**	1.00							
σ_i^2	0.16	**0.71**	**0.75**	**0.67**	**0.59**	**0.72**	0.37	0.36	**0.55**	**1.00**	1.00						
s^2d_i	0.16	**0.72**	**0.71**	**0.69**	**0.63**	**0.61**	0.39	0.34	**0.57**	**0.89**	**0.89**	1.00					
bi	**0.51**	0.06	0.17	0.38	**0.50**	0.04	0.39	**0.59**	**0.50**	0.02	0.02	0.12	1.00				
CV$_i$	**0.54**	**0.69**	**0.76**	**0.90**	**0.86**	0.49	**0.70**	**0.68**	**0.86**	**0.73**	**0.73**	**0.71**	0.33	1.00			
KR	**0.75**	**0.64**	**0.66**	**0.86**	**0.89**	0.43	**0.81**	**0.82**	**0.89**	**0.75**	**0.75**	**0.69**	0.35	**0.81**	1.00		
$\theta_{(i)}$	0.16	**0.71**	**0.75**	**0.67**	**0.59**	**0.72**	0.37	0.36	**0.55**	**1.00**	**1.00**	**0.89**	0.02	**0.73**	**0.75**	1.00	
θ_i	−0.16	−**0.71**	−**0.75**	−**0.67**	−**0.59**	−**0.72**	−0.37	−0.36	−**0.55**	−**1.00**	−**1.00**	−**0.89**	−0.02	−**0.73**	−**0.75**	−**1.00**	1.00

Bold numbers correlate positively and significantly at the 5% level.

also divided into three main groups (Figure 2), namely: (1) C1, sweetness (°brix) and NP$^{(3)}$ stability measure, (2) C2 contains stability measures NP$^{(2)}$, NP$^{(4)}$, S$^{(3)}$, S$^{(6)}$, KR, and CV$_i$, (3) C3 contains stability measures S$^{(1)}$, S$^{(2)}$, NP$^{(1)}$, S^2d_i, W_i^2, σ_i^2, and $\theta_{(i)}$. For this trait, there were two stability measurements that were far from all other groups, i.e., bi and θ_i. The bistability model did not have any significant correlation with all other measurements, while the θ_i model had a significant negative correlation with the other measurements.

To classify the honey sweet potato genotypes, we used hierarchical cluster analysis (HCA). The results of dendrogram analysis classify the honey sweet potato genotypes tested into two clusters for storage root yield (Figure 3) and sweetness (Figure 4). For storage root yield, there were two subclusters in the first group (KI): (1) first subcluster consisted of SP4, SP9, SP16, SP3, SP1, and SP10, which has a high rank of storage root yield (above the overall average yield) and had high average stability ranks; and (2) genotypes that were in the second subcluster, i.e., SP2, SP6, and SP14, which had low average storage root yields (below the overall average yield) and low stability parameters rank. Other group (KII) was also divided into two subclusters: (1) in the first subcluster, there were two genotypes, namely SP8 and SP12, which were the unstable genotypes but had high storage root yields and lowest average rank (AR); (2) second subcluster consisted of genotypes SP11, SP15, SP7, SP5, and SP13, which were the unstable genotypes with storage root yields below the overall average yield. For sweetness, the first group (CI) had the stable genotypes, SP2, SP4, SP16, SP5, SP10, SP8, SP14, and SP3, and had the high sweetness level. The other genotypes were in the second group (CII). They had a high and low sweetness in specific environments (unstable).

3.4 Stability of storage root yield and sweetness in honey sweet potato across six environments based on GGE biplot

GGE biplot was used to measure the stability of storage root yield and sweetness among honey sweet potato genotypes. The value of the first (PC1) and the second (PC2) main components for storage root yield accounted for 44.3 and 31.5% of the total variation, respectively (Figure 5a). For sweetness, PC1 accounted for 59.8%, while PC2 accounted for 18.7% of the total variation (Figure 5b). Figure 6 showed that location 5 had the longest and location 3 had the shortest vector for storage root yield. For sweetness, location 3 showed the longest, while locations 4 and 5 had the shortest vectors from the biplot center point. Thus, location 5 was identified as the most ideal environment for selecting honey sweet potato genotypes for storage root yield, and location 3 for sweetness.

Table 6: Spearman's correlation rank between sweetness characters with stability models

	Sweetness	**$S^{(1)}$**	**$S^{(2)}$**	**$S^{(3)}$**	**$S^{(6)}$**	**$NP^{(1)}$**	**$NP^{(2)}$**	**$NP^{(3)}$**	**$NP^{(4)}$**	**W_i^2**	**σ_i^2**	**s^2d_i**	**bi**	**CV_i**	**KR**	**$\theta_{(i)}$**	**θ_i**
Sweetness	1.00																
$S^{(1)}$	0.13	1.00															
$S^{(2)}$	0.16	**0.99**	1.00														
$S^{(3)}$	**0.53**	**0.86**	**0.85**	1.00													
$S^{(6)}$	**0.82**	**0.61**	**0.62**	**0.85**	1.00												
$NP^{(1)}$	0.27	**0.71**	**0.67**	**0.68**	**0.65**	1.00											
$NP^{(2)}$	**0.67**	0.45	0.45	**0.63**	**0.77**	**0.69**	1.00										
$NP^{(3)}$	**0.86**	0.39	0.39	**0.68**	**0.90**	**0.61**	**0.88**	1.00									
$NP^{(4)}$	**0.79**	**0.64**	**0.65**	**0.90**	**0.95**	**0.65**	**0.84**	**0.91**	1.00								
W_i^2	0.31	**0.70**	**0.68**	**0.64**	**0.64**	**0.93**	**0.67**	**0.63**	**0.65**	1.00							
σ_i^2	0.31	**0.70**	**0.68**	**0.64**	**0.64**	**0.93**	**0.67**	**0.63**	**0.65**	**1.00**	1.00						
s^2d_i	0.28	**0.61**	**0.59**	**0.55**	**0.57**	**0.91**	**0.59**	**0.59**	**0.57**	**0.94**	**0.94**	1.00					
bi	0.17	0.14	0.12	0.20	0.18	0.16	0.33	0.35	0.24	0.23	0.23	0.16	1.00				
CV_i	0.36	0.16	0.14	0.18	0.39	**0.51**	0.43	**0.52**	0.36	**0.64**	**0.64**	**0.76**	0.20	1.00			
KR	**0.79**	**0.51**	**0.53**	**0.71**	**0.91**	**0.73**	**0.84**	**0.94**	**0.90**	**0.78**	**0.78**	**0.73**	0.22	**0.55**	1.00		
$\theta_{(i)}$	0.31	**0.70**	**0.68**	**0.64**	**0.64**	**0.93**	**0.67**	**0.63**	**0.65**	**1.00**	**1.00**	**0.94**	0.23	**0.64**	**0.78**	1.00	
θ_i	−0.31	**−0.70**	**−0.68**	**−0.64**	**−0.64**	**−0.93**	**−0.67**	**−0.63**	**−0.65**	**−1.00**	**−1.00**	**−0.94**	−0.23	**−0.64**	**−0.78**	**−1.00**	1.00

Bold numbers correlate positively and significantly at the 5% level.

Table 7: PCs, percent, and cumulative values of parametric and nonparametric stability measures in the storage root yield and sweetness characters

PCs	1	2	3	4
Yield				
Eigenvalue	6.24	4.66	1.72	1.22
Percent (%)	39.01	29.14	10.72	7.65
Cumulative (%)	39.01	68.15	78.87	86.52
Sweetness				
Eigenvalue	6.54	3.80	2.42	1.57
Percent (%)	40.86	23.77	15.11	9.81
Cumulative (%)	40.86	64.63	79.74	89.55

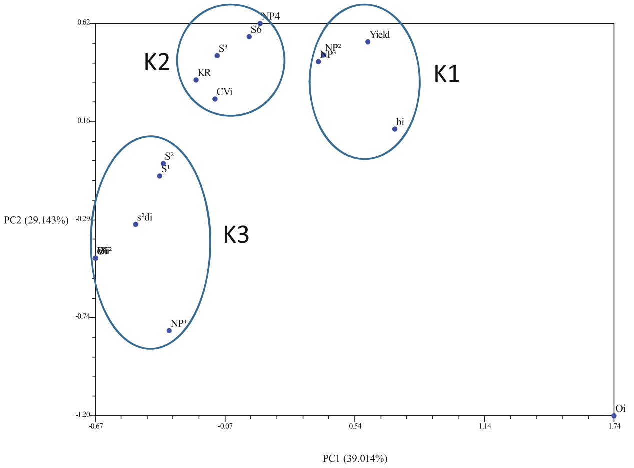

Figure 1: PCA biplot for depicting the relationship between storage root yield and numerical stability measurements in 16 genotypes of honey sweet potato at six locations in West Java, Indonesia.

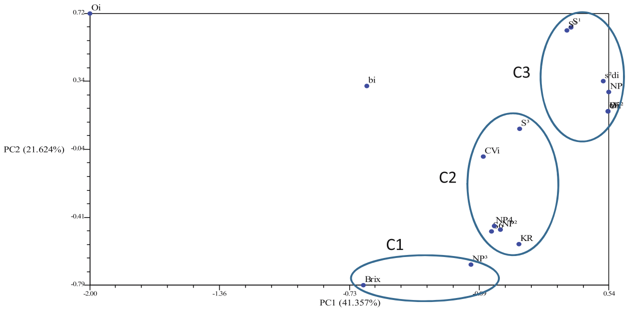

Figure 2: PCA biplot for depicting the relationship between sweetness and numerical stability measurements in 16 genotypes of honey sweet potato at six locations in West Java, Indonesia.

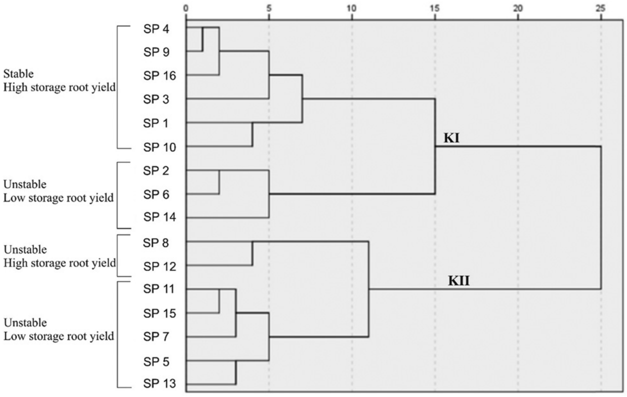

Figure 3: Dendrogram of storage root yield character on 16 honey sweet potato genotype based on stability ranks.

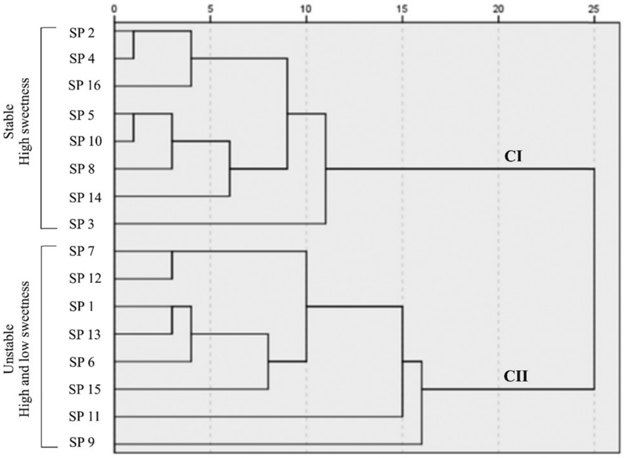

Figure 4: Dendrogram of sweetness character on 16 honey sweet potato genotype based on stability ranks.

Figure 6 shows the storage root yield stability and sweetness among honey sweet potato genotypes. Genotypes were ranked along the coordinates of the average environment with arrows that indicate the highest value based on the average across all environments for both storage root yield and sweetness. Genotype SP3 was closest to the arrow and had the highest storage root yield, while genotype SP14 was furthest from the arrow and had the lowest storage root yield. Genotype SP3 with the shortest line projection had the most stable storage root yield, while genotype SP15 had the longest line projections with the most unstable storage root yield. For sweetness, genotype SP3 had the shortest line projection and was stable across all environments, while genotype SP 12 was the most unstable one because it had the longest line.

Figure 7 shows the “which-won-where” graph of the genotypes tested on the environment. For storage root yield, there were seven sectors with two mega-environments. For this trait, the genotypes that were in top position were SP16, SP9, SP8, SP3, SP14, SP7, and SP15, and the two mega environments identified were M1 (locations 1, 2, and 4) and M2 (locations 3, 5, and 6) (Figure 7a). The

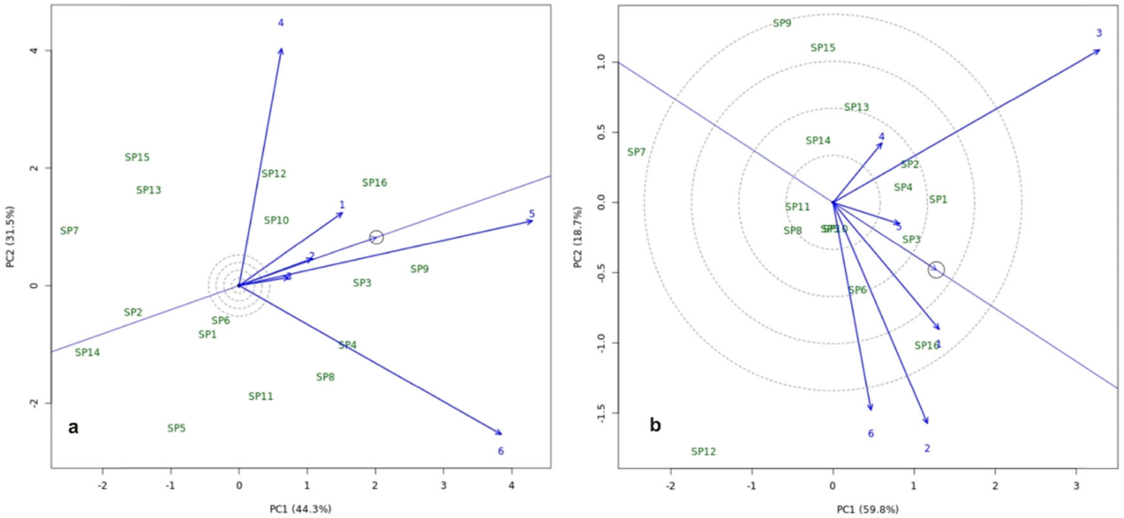

Figure 5: Biplot of 16 new honey sweet potato genotypes against average storage root yields and sweetness in six locations. (a) Storage root yield character and (b) sweetness character.

genotypes at each mega-environment were identified as having storage root yield above the overall average, while the genotypes at the top of a sector had the highest storage root yield in that sector. For sweetness, two mega locations were identified, namely M1 (locations 3 and 4) and M2 (locations 1, 2, 5, and 6) (Figure 7b). Six environmental sectors were identified with peak genotypes of SP1, SP16, SP12, SP7, and SP9. In addition to the peak genotypes, there were genotypes that were close to the axis point, namely SP1, SP2, SP6, SP13, SP3, and SP10 for yield, and SP3, SP4, SP6, SP2, SP8, SP11, and SP14 for sweetness. These genotypes were identified as more stable genotypes.

3.5 Genotype selection of new honey sweet potato which has high storage root yield and sweetness, and stability based on genotype by yield*traits (GYT)

Figure 8 represents a polygon view "Which/Whom/Where/What" of a GYT biplot resulted from combination of storage root yield with sweetness of 16 honey sweet potato genotypes in multi-locations data. The GYT biplots accounted for 73.46% of the total variation. In six locations, the highest B*Y values were in the SP16 and SP3 genotypes. This shows that the two genotypes have the

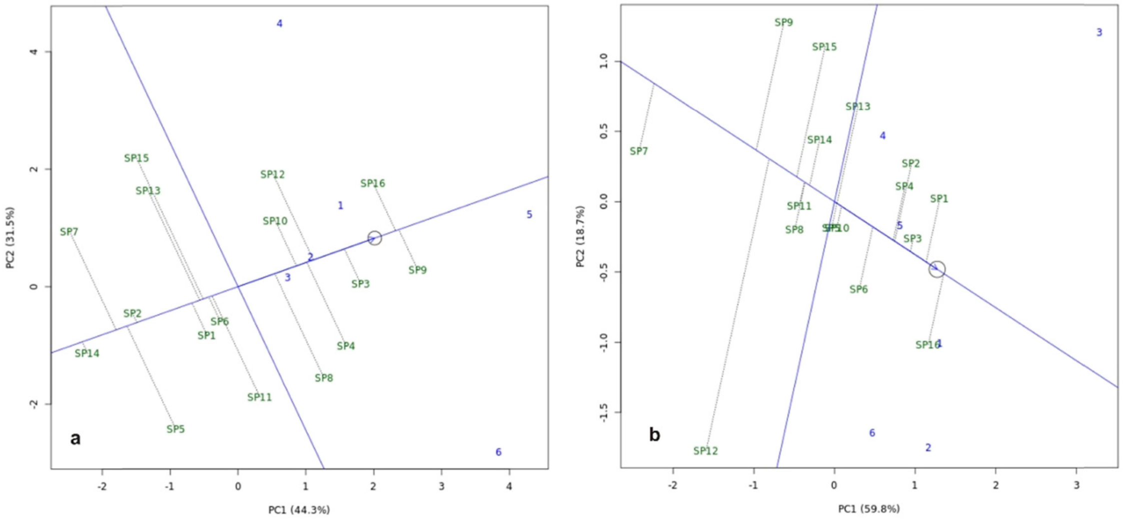

Figure 6: Biplot of average and stability of new honey sweet potato genotypes. (a) Storage root yield character and (b) sweetness character.

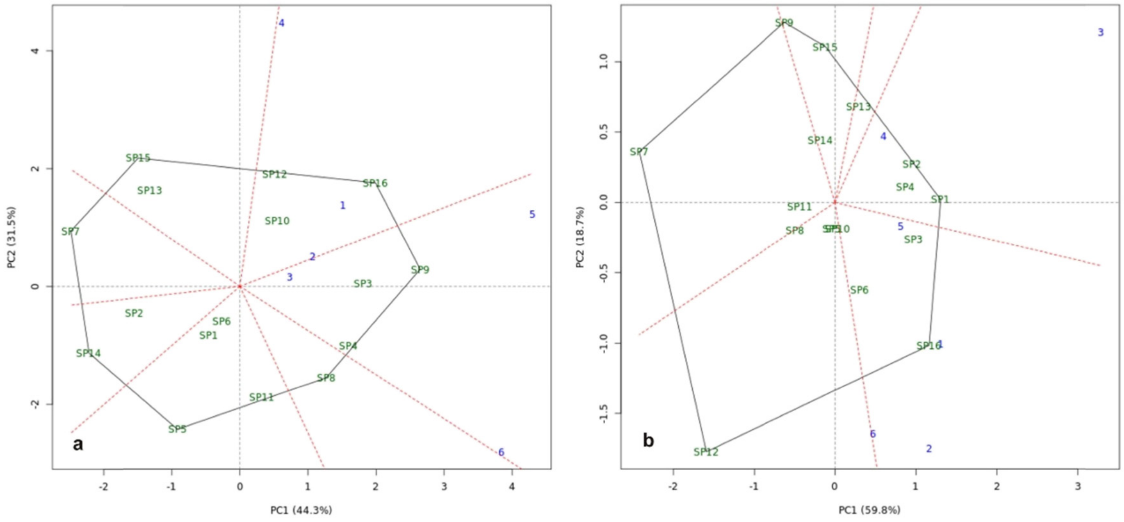

Figure 7: Biplot of mega-environments on new honey sweet potato genotypes. (a) Storage root yield character and (b) sweetness character.

best combination in terms of storage root yield and sweetness. The SP1 genotype was a stable genotype (both storage root yield and sweetness) in the six test environments; however, this genotype has low yield and sweetness.

Figure 9 shows that the combination of storage root yield with sweetness on the GYT biplot tends to be positively correlated. Based on this biplot, genotypes were ranked graphically based on the yield-trait combinations tested. In six locations, most obvious correlations were: positive correlations between B*Y1, B*Y2, B*Y3, and B*Y4, and between B*Y5 and B*Y6; this is because they are in the same quadrant. In this figure, high correlations were observed between B*Y1, B*Y2, B*Y3, and B*Y4, which showed that the combination of the storage root yield and sweetness (°brix) traits was very suitable to select yield performance and sweetness as in the SP3 and SP16 genotypes. At B*Y5 and B*Y6, there were no significant correlations observed. The different responses of each genotype tested to the environment caused the combination of storage root yield and sweetness to be different in the six planting locations.

Figure 10 shows the rank of the tested genotypes based on the storage root yield and sweetness combinations. The best ranked sequence of genotypes tested was: SP16 > SP3 > SP4 > SP10 > SP9 > SP12 > SP8. By contrast, SP14, SP7, SP5, and SP2 were ranked the lowest. Figure 10 also shows that the SP16, SP3, SP4, SP10, and SP9 genotypes were stable for various traits and locations, while SP8 had a strong performance in locations 5 and 6 in combination with storage root yield and sweetness, but had a poor performance in locations 1 and 4. In Figure 10, there was also the average tester coordinate (ATC) line. The genotypes that were below the ATC line tended to have a good rank relatively of locations 1, 2, 3, and 4, but relatively low in locations 5 and 6. SP16 and SP3 genotypes had the highest mean values and broad adaptability. Both genotypes exhibited the best characteristics in storage root yield, sweetness, and stability.

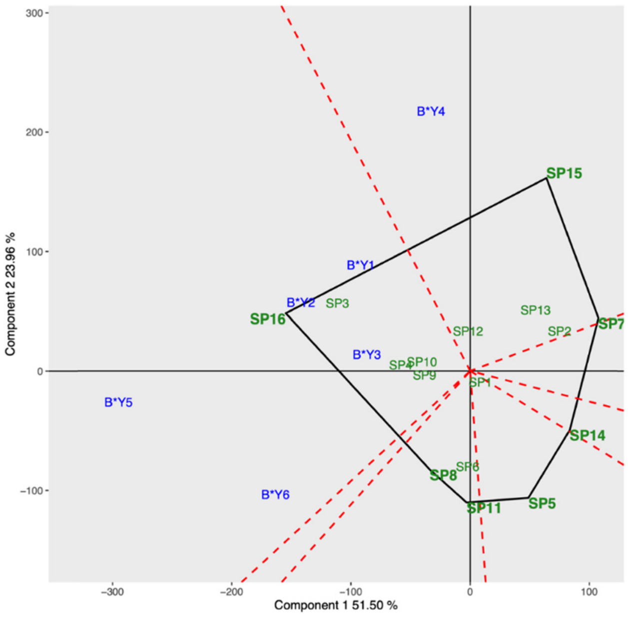

Figure 8: The genotype by yield*trait (GYT) biplot "which-won-where/what" of the honey sweet potato genotypes in multilocation data.

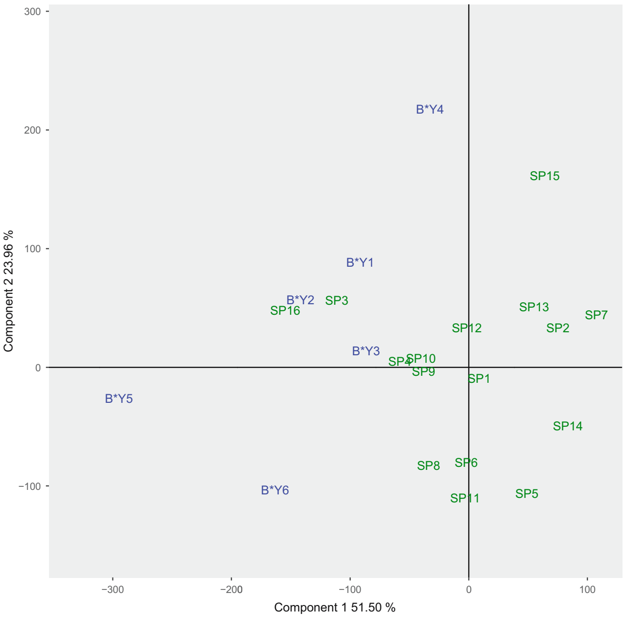

Figure 9: GYT biplot among the yield-trait combination based on multilocation data.

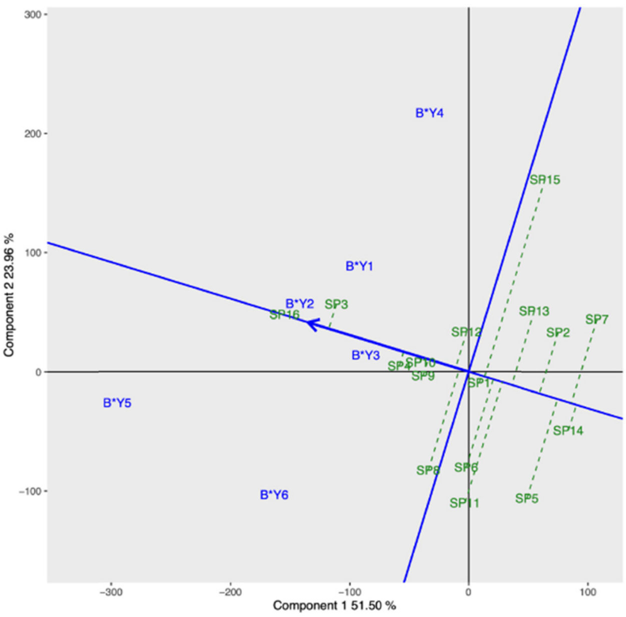

Figure 10: GYT biplot "mean vs stability" to rank the genotypes tested based on their superiority across all locations.

4 Discussion

The development of new honey sweet potato which should have a sweet taste, stable storage root yield, and acceptable to most consumers is one of the goals of the breeding program. The effects of GEIs occur mostly on quantitative characters, especially storage root yield (Gruneberg et al. 2005). The effect of GEIs can reduce the relationship between genotypic and phenotypic values, making it difficult for breeders to select the desired superior genotype (Andrade et al. 2016). This study shows that the G, E, and GEIs significantly affected storage root yield and sweetness. The combined ANOVA showed that the G, E, and GEIs effects accounted for 20.45, 40.61, and 37.47% of the total variation in storage root yield, respectively. By contrast, G, E, and GEIs for sweetness accounted for 21.35, 27.26, and 36.46% of the total variation, respectively. The highly environmental influence on storage root yield and sweetness can be attributed to the differences among the each trial site in terms of rainfall, soil type, and altitude. Besides, the contribution of GEIs was larger than the genotypes. Because the combined ANOVA showed a considerably large GEIs effect, another statistical model is warranted for selecting desired genotypes. This was also expressed by several researchers (Laurie et al. 2015; Erdemci 2018; Mustamu et al. 2018; Ngailo et al. 2019; Vaezi et al. 2019). The use of stability models can help breeders select for stable and adaptive genotypes. Thus, it is very important to have an in-depth study of storage root yield and sweetness, stability, and adaptability of honey sweet potato genotypes across locations. This study demonstrates that the GEIs had a significant effect for storage root yield and sweetness of honey sweet potato genotypes across environments. This is evident with the presence of significant differences among genotypic responses and their rank orders across environments.

Overall, genotype, environment, and GEIs have a significant effect on sweet potato storage root yield and sweetness. Solihin et al. (2018) reported that differences in planting locations can cause differences in storage root yield and quality of sweet potato. In other studies, the environment also affects canola oil content (Pavlista et al. 2011) and single cross-hybrid corn performance (Mafouasson et al. 2018). Oliveira et al. (2014) also stated that the presence of GEIs made it difficult to select for yellow passion fruit in Brazil. In cassava, low rainfall intensity and soil moisture reduced the level of root enlargement (Mcharo and Ndolo, 2013). As the presence of environmental and GEIs effects was very significant, the use of parametric and nonparametric stability models, and GGE biplots is imperative to describe GEIs and to determine the stability of storage root yield and sweetness of sweet potato.

The effects of GEIs have been widely studied by plant breeders in developing models for selecting genotypes that have high yield and adapt to various environment. There have been many approaches used to select genotypes with above-average storage root yields. Some researchers have incorporated a stability model in selecting stable, high-yielding genotypes, including Ahmadi et al. (2015) in grass pea, Vaezi et al. (2019) in barley, and Maulana et al. (2020) in sweet potato. In this study, numerical stability measures and GGE biplot are used to identify stability of storage root yield and sweetness levels on honey sweet potato genotypes.

To select for stable genotypes with high yield and sweetness, we used AR number of all stability models with low values (near zero). The SP3 genotype followed by SP16, SP9, and SP4 have had the smallest AR value in storage root yield characters. For sweetness, SP3 also has the smallest AR value and followed by SP10, SP5, SP8, and SP4. To confirm this, we used a dendrogram to classify genotypes tested based on storage root yield and sweetness, as well as stability measurements. The dendrogram generated with the storage root yield revealed that the honey sweet potato genotypes were divided into two main groups (Figure 1). Cluster I contains stable genotypes and cluster II contains unstable genotypes. Each cluster has two subclusters, namely low and high yielding stable genotypes, and low and high yielding unstable genotypes. The genotypes in the high yield stable subcluster were SP4, SP9, SP16, SP3, SP1, and SP10, while the high yield unstable cluster includes SP8 and SP12. With the sweetness trait, the dendrogram was divided into two main clusters (Figure 2) consisting of a stable sweetness cluster and an unstable sweetness cluster. The genotypes in the stable sweetness cluster were SP2, SP4, SP16, SP5, SP10, SP8, SP14, and SP3. Other genotypes showed unstable sweetness or had a high sweetness only in specific environments. Based on this study, we identified SP3, SP4, and SP10 as new promising genotypes of sweet potato that were stable, sweet, and have high yields.

Several numerical stability measures and GGE biplot were used to identify storage root yield stability and sweetness on honey sweet potato genotypes. To graphically understand the relationship between the stability models and the tested characters, we used a PCA biplot that was evaluated from the first two PCs (Figure 3). All stability measurements on the tested traits were divided into three groups by PCA. In storage root yield character, group 1 (K1) included storage root yield (Y) and NP2, NP3, and bistability measures. Group 2 (K2) included $NP^{(4)}$, $S^{(3)}$, $S^{(6)}$, CV_i, and KR stability measures, and group 3 (K3) included $NP^{(1)}$, $S^{(1)}$, $S^{(2)}$, S^2d_i, W_i^2, σ_i^2, and $\theta_{(i)}$ stability measures, while the stability model θ_i was separate from all groups. The sweetness character was also divided into three main groups. The first group (C1) consisted of sweetness (°brix) and $NP^{(3)}$ stability measure. The second group (C2) consisted of $NP^{(2)}$, $NP^{(4)}$, $S^{(3)}$, $S^{(6)}$, KR, and CV_i stability measures, and the third group (C3) contains stability measures $S^{(1)}$, $S^{(2)}$, $NP^{(1)}$, S^2d_i, W_i^2, σ_i^2, and $\theta_{(i)}$. With this trait, there were two stability measurements that are far from all groups, i.e., bi and θ_i. The bistability measure does not have a significant correlation with all other measurements, while the θ_i measure has a negative and significant correlation with other measurements. Stability measures that are not in the same group with the characters tested showed that they represent the static concept of stability and can be used to identify genotypes with moderate results (either storage root yield or other characters) in unfavorable environments (Ahmadi et al. 2015; Vaezi et al. 2019). The results of Spearman's rank correlations analysis showed that $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, bi, CV_i, and KR were significantly and positively correlated with storage root yield (Y); and $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, and KR stability measures were significant and positively correlated with sweetness (°brix). In another study, Vaezi et al. (2017) reported that $S^{(3)}$, $S^{(6)}$, $NP^{(2)}$, $NP^{(3)}$, $NP^{(4)}$, and KR were significantly correlated with yield on barley in Iran. This shows that these measurements demonstrate the concept of dynamic sense of stability and can be used to recommend genotypes in favorable environments (Mohammadi and Amri 2008). The grouping of stability measures can be used to recommend genotypes in adapted locations.

To visualize the distribution of genotypes and environments, we used GGE biplot model. The outcome of such a stability and adaptability model was the "which-won-where" graph. According to Yan et al. (2007), an important feature of this biplot is the environmental grouping that enables the presence of mega-environments from the test sites. Each sector usually has a peak genotype that has the highest storage root yield for the environment included in that sector (Mustamu et al. 2018). Our results showed that, in terms of storage root yield and sweetness characters, locations fall into different groups and are divided into two mega-environmental groups. The first two PCs explain 75.8% and 78.5% of the total variation caused by the effects of G, E, and GEIs on storage root yield and sweetness (Figures 4 and 5). Evaluation of data from the two characters tested showed that there were more than one mega-environment for honey sweet potato breeding programs in various locations in West Java. Based on our test results, each of the two mega environments was selected with a different winning genotype for each character tested. This finding implied that there was a specific adaptation of genotype in the mega-environment as it is stated by Vaezi et al. (2019). Our results also showed that some genotypes have better yields and performed specific adaptations that exceed the check variety, namely SP9.

In this study, the representation of representative versus discriminative from the GGE biplot revealed that Pangandaran was the least ideal location in testing storage root yields, and Kuningan for sweetness of new honey sweet potato. Therefore, it had to be moved to other more representative locations so that testing or development costs could be more efficient. According to Yan et al. (2007) and Vaezi et al. (2019), the ideal testing environment must be able to distinguish the genotypes tested and be able to represent all test environments. Among the six locations tested, Kuningan and Bandung have high distinguishing features and representativeness for yields, as well as Sumedang and Sukabumi for sweetness. These locations were ideal locations for selecting superior genotypes based on storage root yield (Kuningan and Bandung) and sweetness (Sumedang and Sukabumi) (Figure 3). In a plant breeding program, plant breeders expect stable genotypes and high yields. According to Zhang et al. (2016), such a genotype is an ideal genotype and has a small response to GEIs. The SP3 genotype was identified as an ideal genotype in both storage root yield and sweetness. This is also confirmed by parametric and nonparametric models, which separate the genotype as a stable, high-yield, and sweet taste (Figures 1 and 2). Based on our analysis using numerical and visual methods, the patterns produced in identifying stable genotypes were the same. For example, numerical stability measurements identify several genotypes, namely SP3, SP16, SP9, SP4, and SP10 on yield characters, and SP3, SP10, SP5, SP8, and SP4 in sweetness characters, and they were more stable than other genotypes. In the visual stability analysis using GGE biplot, several stable genotypes were identified in the yield characters, namely SP1, SP2, SP6, SP13, SP3, SP4, and SP10, while the sweetness characters identified were SP3, SP4, SP6, SP2, SP8, SP10, SP14, and SP14. Some researchers also reported that both test models have relatively similar contributions in selecting stable high-yielding genotypes (Jamshidmoghaddam and Pourdad 2013; Vaezi et al. 2019). To confirm the results of stability measurements and select genotypes based on these two characters, we use GYT.

The GYT results showed that the biplots from “Which/Who/Where/What” accounted for 73.46% of the total variation (Figure 1). In six locations, SP16 followed by SP3 had the highest value for B*Y, which means that these two genotypes were the best at combining yields with sweetness in different environments. Figure 1 also shows that the SP1 genotype was the most stable one in both yield and sweetness in the six test environments, but this genotype had storage root yield and sweetness below the overall average.

In Figure 2, combinations of yield-traits that have the most striking correlations were: a positive correlation between B*Y1, B*Y2, B*Y3, and B*Y4, while there was no correlation between B*Y5 and B*Y6. According to Mohammadi (2019), the combination of yield-traits in the same quadrant shows a strong correlation between these combinations. In this figure, a high correlation was observed between B*Y1, B*Y2, B*Y3, and B*Y4, indicating that the combination of storage root yield and sweetness (°brix) would be suitable for selecting high-performance genotypes for the two characters. The genotypes that have the best performance are SP3 and SP16. Figure 3 shows the best ranking of genotypes tested based on a combination of yield-trait, which were as follows: SP16 > SP3 > SP4 > SP10 > SP9 > SP12 > SP8. On the contrary, SP14, SP7, SP5, and SP2 were ranked as the poorest ones. According to Yan and Frégeau-reid (2018) and Mohammadi (2019), the genotype that has the closest distance to the ideal point is the best genotype. Based on these appearances, SP16 and SP3 are the best genotypes that present the highest and stable average values.

5 Conclusions

Environmental factors, genotype, and GEIs have significant positive effects on storage root yields and sweetness of honey sweet potato, with an influence of 20.45, 40.61, and 37.47% of the total variation in storage root yield, whereas the sweetness character explained 21.35, 27.26, and 36.46% of the total variations, respectively. Two genotypes (SP3 and SP16) that had weak GEIs were identified as stable on storage root yield and sweetness (°brix) in diverse environments. These two genotypes can be used as optimal genotypes in West Java.

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