BIODIVERSITAS
Volume 25, Number 5, May 2024
Pages: 2276-2289

ISSN: 1412-033X
E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d250546

Yield performance and anthocyanin content of several purple-fleshed sweet potato clones grown in two locations in East Nusa Tenggara, Indonesia

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Manuscript received: 19 February 2024. Revision accepted: 28 May 2024.

Abstract. *Arsa IGBA, Mau YS, Ndiwa ASS, Gandut YRY, Ishaq LF, Mahayasa INW. 2024. Yield performance and anthocyanin content of several purple-fleshed sweet potato clones grown in two locations in East Nusa Tenggara, Indonesia. Biodiversitas 25: 2276-2289.* Several promising purple-fleshed sweet potato hybrid clones were identified to have high yield potential and, thus, can be evaluated for other superior traits and later be further processed for varietal registration and release. This study aimed to determine the tuber yield performance and anthocyanin content of several purple-fleshed sweet potato clones across two locations and to identify the best clones based on mean performance and stability. The study was conducted in the farmer's field in two different altitudes in West Timor, i.e., Mata Air Village, Kupang District (86 masl) and Netpala Village, Timor Tengah Selatan (TTS) District (1,090 masl) from April to September 2023. Six purple-fleshed sweet potato clones/varieties were assigned as treatment. The experiment was laid out in a complete block design in each location, and each treatment consisted of three replicates. Observed data included fresh storage root yield, number of storage roots per plant, storage root length, storage root tuber diameter, and tuber anthocyanin content. Observed data from the two trial locations were subjected to a combined ANOVA, cluster analysis, Principal Component Analysis (PCA), and GGE biplot analysis. The results showed that the genotype-by-location interaction effect was significant in all studied traits. Meanwhile, location or genotype significantly affected all traits except for the location, which did not significantly affect the anthocyanin content. The storage root yield ranged from ~19.95 t ha^{-1} to ~49.33 t ha^{-1}, while the anthocyanin content ranged from ~28,64 mg/100 g to ~157,65 mg/100 g. The ranks of the tested genotypes based on the mean performance and stability are Undana UJ 7>Undana UJ 1>JPV-1>Antin 3>Undana UJ 6>Undana UJ 3 for storage root yield and JPV-1>Antin 3>Undana UJ 7>Undana UJ 6>Undana UJ 3>Undana UJ 1 for anthocyanin content.

Keywords: Anthocyanin, growing site, purple-fleshed, storage root yield, sweet potato

INTRODUCTION

Sweet potato [*Ipomoea batatas* (L.) Lam] is Indonesia's second most important tuber crop, after cassava. The carbohydrate content of this crop is relatively high, and it is a potential staple food crop to substitute rice and corn. East Nusa Tenggara (ENT) Province is one of Indonesia's sweet potato production centers (BPS Pusat 2023), where this crop has long been cultivated and used as a staple food to substitute rice and corn. However, the productivity of this crop in the ENT Province is still very low, ranging from 6.36 to 7.09 t ha^{-1} in the last three years (2020-2023 (BPS NTT 2024). Meanwhile, the mean productivity at the national level is ~19 t ha^{-1} (BPS Pusat 2023), and that of Indonesian superior varieties is >25 t ha^{-1} (Balitkabi 2017). The use of local varieties that are mostly low-yielding (Mau et al. 2013) is among the factors contributing to low sweet potato productivity in ENT Province.

Sweet potato is rich in minerals, fiber, vitamins, and antioxidants, making it an essentially healthy food source for humans (Ginting et al. 2014; Budiman et al. 2021). Sweet potato genotypes with purple color in the flesh and the leaf contain high anthocyanin contents, which is important as an antioxidant and serves many health-promoting properties (Li et al. 2019; Kim et al. 2020; Sun et al. 2020; Wong and Tan 2020; Kurnianingsih et al. 2021; Yan et al. 2022). Purple-fleshed sweet potato is now becoming more popular along with the increased awareness of its health benefits. However, the purple-fleshed sweet potato has yet to be fully optimized as a healthy, functional food in the ENT Province due to many factors, such as low productivity at the farmer levels and low awareness of the community regarding the post-harvest handling of these products. Additionally, the purple-fleshed sweet potato in the market is limitedly available as most of the cultivated sweet potato cultivars are white, yellow, and orange-fleshed local varieties (Mau et al. 2013).

In addition to low-yielding local cultivars, other factors such as poor cultivation techniques, drought stress, and pest and pathogen infestations also contribute to the low productivity of sweet potatoes, including purple-fleshed genotypes in ENT Province. These yield-limiting factors such as drought stress, pest and pathogen infestations, and low-yielding cultivated varieties can be overcome by using superior, high-yielding, and stress-tolerant purple-fleshed varieties. These types of superior sweet potato varieties can

be generated through various breeding methods, including conventional cross-pollination breeding involving local cultivars and nationally released varieties as parental clones. We have evaluated and selected local sweet potato clones from ENT Province for several traits such as drought tolerance, yielding ability and adaptability, and resistance to pests and diseases (Mau 2011; Mau et al. 2013; Mau 2018), and the selected clones were used to produce hybrid clones and further evaluated for various traits (Mau et al. 2019; Mau et al. 2021; Mau et al. 2022). Several of the evaluated hybrid clones have purple flesh color and high potential yield (>20 t/ha), but their anthocyanin content has not been determined.

In the sweet potato breeding program, storage root yield is the most important trait to select for purple-fleshed sweet potato. Still, anthocyanin content in the storage root is also similarly important for purple-fleshed sweet potato as a specialty superior trait. Thus, the two traits are mutually important in the purple-fleshed sweet potato breeding program. Genetic and environmental factors influence sweet potatoes' storage root yield performance and anthocyanin content (Tanaka et al. 2017; Ishiguro et al. 2022). Information on the yield performance and anthocyanin content of the above-mentioned purple-fleshed clones in multi-growing locations is essential. It will help select the best clone to further test or propose as a new variety. A multi-location trial may also result in a significant genotype by environment (G x E) interaction effect, which may hamper these selections (Khalili and Pour-aboughadareh 2016; Maulana et al. 2022) as a certain genotype may be best adapted to a specific location; hence, the breeder needs to select the best genotype for a specific environment. Thus, it is important to know in advance the performance of the above-mentioned purple-fleshed clones in multi-environments to select the best genotypes based on their mean performance and stability.

Several statistical methods have been used by various authors to asses the G x E interaction effect on multi-environmental testings, which include Analysis of Variance (ANOVA), linear regression, Principal Component Analysis (PCA), and additive main effects and multiplicative interaction (AMMI) (Rakshit et al. 2012). In addition, using biplot analysis/methodology such as AMMI biplot (Gauch 2006) and GGE biplot (Yan and Kang 2003) has greatly addressed the more complex G x E interaction in a more simplistic graphical manner. This study aimed to utilize some of the methods mentioned above to determine the genotype by environmental interaction effect on yield performance and anthocyanin content of purple-fleshed sweet potato clones grown in two locations and to identify the best sweet potato clones based on their mean performance and stability across those two locations.

MATERIALS AND METHODS

Research location and date

This study was carried out in two locations, i.e., Mata Air Village, Kupang District, East Nusa Tenggara, Indonesia [10°09'02" S and 123°42'05" E, 68 masl., soil type is Grummosol (USDA) or Vertisols (FAO/UNESCO) with clay-sandy texture)] and Netpala Village, Timor Tengah Selatan (TTS) District, East Nusa Tenggara, Indonesia [09°44'35" S and 124°16'02", 1,090 masl, soil type is also Grummosol (USDA) or Vertisols (FAO/UNESCO) of clay texture]. The study was carried out from April to September 2023.

Research design

The experiment was conducted using a randomized block design in each location, employing sweet potato genotype/clones as treatment. The treatments included six purple-fleshed sweet potato clones/genotypes, consisting of four hybrid clones (Undana UJ 1, Undana UJ 3, Undana UJ 6, and Undana UJ 7), one Indonesian released variety (Antin 3), and one local clone (JPV-1). Each treatment comprised three replicates; thus, 18 experimental units were evaluated in each planting site/location. A list of the tested sweet potato clones is presented in Table 1.

Field preparation and planting

The planting field was cleared of weeds and debris, and a hand tractor was used to plow the land. The experimental field was plowed about 30 cm depth and divided into three blocks as replicates; each consisted of 6 plots of 3x1.5 m in size. The within-block distance was 100 cm, while the within-plot space was 50 cm.

The panting materials were sweet potato vine cuttings 25-30 cm long and 4-5 nodes each. The vine cuttings were planted in holes 8-10 cm deep with a planting space of 50 cm within plants and 70 cm within rows. Only one cutting was planted in a planting hole.

An NPK compound fertilizer (16:16:16) was applied at the planting time at a rate of 300 kg ha^{-1}. Irrigation was provided daily during crop growth and development. Weeding was manually controlled, while insecticide and fungicide sprays were used to control pests and diseases. Tuber harvesting was done at five months after planting. A standard sweet potato cultivation technique was applied throughout the experiment in the field (PPPTP 2012).

Table 1. List of purple-fleshed sweet potato clones employed in the present study

Genotype code	Crosses/origin/source
Undana UJ 1	Hybrid Clone, Universitas Nusa Cendana collection*
Undana UJ 3	Hybrid Clone, Universitas Nusa Cendana collection*
Undana UJ 6	Hybrid Clone, Universitas Nusa Cendana collection*
Undana UJ 7	Hybrid Clone, Universitas Nusa Cendana collection*
Antin 3	Indonesian Released Superior Variety, Balitkabi (Indonesian Legume and Tuber Crops Research Institute /ILETRI)
JPV-1	Local Cultivar, West Timor, ENT Province, Indonesia

*Note: The clones were selected from the results of Mau et al. (2022)

Observation

Variables observed at harvest included storage root yield per plot and yield-attributing traits such as storage root number per plant, storage root diameter, and storage root length. The storage root yield per plot was converted to root yield per hectare, assuming 80% land coverage for planting. Only storage roots with fresh weights of over 100 g each were included in the observations. After harvest, samples of storage roots were taken to the laboratory to determine the anthocyanin content. Anthocyanin content was analyzed using the pH differential of Koraqi et al. (2023) with a slight modification. About 5.0 g of sweet potato dry powder was extracted five times using 10 mL 15% Sodium Acetate-methanol for 30 minutes using a shaker. The extract was then centrifuged (12,000 rpm) for 10 minutes at room temperature. The supernatant was then evaporated to let it dry. The dry extract was then diluted into 25 mL methanol for the anthocyanin content analysis. About 0.05 mL of the extracted sample was each put into two reaction tubes. The first tube was added with 4.95 mL potassium chloride buffer (pH 1.0), and the second was added with 4.95 mL sodium acetate buffer (pH 4.5). After 15 minutes of equilibration at room temperature, the absorbances of the two reactions were measured using a Spectrophotometer at 520 nm and 700 nm wavelengths.

The absorbance value was calculated using the formula:

$$\mathbf{A = (A_{520} - A_{700})_{pH\ 1} - (A_{520} - A_{700})_{pH\ 4.5}}$$

Anthocyanin contents were determined as **anthocyanin (mg/100 g FW) = (A x MW x DF x 1000 x V)/(E x 1 x M)**

Where: A: Absorbance, MW: molecular weight of Cyanin-3-Glucocide (449.2), DF: dilution factor, 1: cuvette path length (1 cm), V: extraction volume, E: molar absorption coefficient (26,900), M: sample mass calibrated as fresh weight.

Data analysis

The observed data in each location was subjected to variance analysis to determine the treatment effect. A homogeneity test of variances of data from the two locations was conducted before a combined analysis of variances to analyze the effect of genotype by location interaction on the observed traits. A Least Significant Difference test (0.05) separated the treatment means. Therefore, using the Euclidean coefficient, the observed data was used to perform cluster analysis based on the Un-weighted Pair Group Method with Arithmetic Mean (UPGMA). A PCA (Principal Component Analysis) was also carried out to reveal the characters that mostly contributed to the observed variation. A GGE Biplot analysis was also carried out on the storage root yield and anthocyanin content data to determine the mean performance, stability, and ranking of the genotypes across the two locations. The combined ANOVA was carried out using Microsoft Excel, while the cluster analysis and GGE biplot analysis were performed using PAST version 4.03 and GGEbiplot version 4.1 (Yan 2001).

RESULTS AND DISCUSSION

Results of the combined ANOVA for the studied traits are presented in Table 2. The ANOVA results demonstrated that genotype-by-location interaction caused a highly significant effect ($P<0.01$) on all observed traits. Additionally, the main factors of the sweet potato genotype or location significantly affected the observed traits, except for the anthocyanin content, which was not affected by location. The highly significant effect of genotype by location interaction implies that the observed traits varied among the genotypes, and the magnitude of the variation did change following the change in planting location. In other words, different locations posed different effects on the genetic expression of the observed traits of the tested sweet potato clones. The performance of each studied trait is presented below.

Yield Attributing Traits

Number of storage roots per plant

The means of the number of storage roots per plant, storage root diameter, and storage root length are presented in Table 3. The results of the combined variance analysis showed that the Genotype by Location (G x E) interaction effect was highly significant ($P<0.01$) on the number of storage roots per plant. In addition, the main factors of the planting sweet potato genotype or the planting had a highly significant ($P<0.01$) effect on the same trait. These highly significant treatment effects indicated differences among the genotypes regarding their ability to produce storage root number per plant, and the magnitude of the difference varied significantly between the two planting locations.

Table 2. The combined ANOVA results of the studied traits of the sweet potato clones were evaluated in two locations: Mean squares and coefficients of variations of yield components, yield, and anthocyanin content

Source of variation	DF	SRN	SRD	SRL	SRY	ANTC
Location	1	77.88^{**}	8.69^{**}	107.76^{**}	5213.23^{**}	3.09^{ns}
Replication /Location	4	0.16^{ns}	0.03^{*}	1.33^{*}	7.75^{*}	15.86^{ns}
Genotype (G)	5	28.63^{**}	0.29^{**}	26.92^{**}	831.41^{**}	21979.86^{**}
G x E	20	6.96^{**}	0.04^{**}	5.31^{**}	271.74^{**}	302.54^{**}
CV (%)		6.46	1.85	3.95	4.37	3.94

Note: *=significant at 5% level, **=significant at 1% level, ns: not significant, DF: degree of freedom, SRN: storage root number, SRD: storage root diameter, SRL: storage root length, STY: storage root yield, ANTC: anthocyanin content, CV: coefficient of variation

The mean number of storage roots per plant, as presented in Table 3, varied considerably among the genotypes and locations. The highest number of roots per plant (11.69 storage roots) was produced by Undana U7 1 when grown in Kupang. The lowest (4.16 storage roots) was observed on Undana UJ 3 grown in the TTS. Over the two locations, three genotypes, i.e., Undana UJ 1, Undana UJ 6, and Undana UJ 7, produced almost similar the highest number of storage roots per plant. In contrast, Undana UJ 3 had the lowest number of storage roots yet was not significantly different from that of JPV-1. The mean number of storage roots per plant of all tested genotypes was much higher in Kupang (9.17) than in TTS (6.22).

Storage root diameter

The storage root diameter was also highly significantly influenced by the interaction of genotype with location, indicating mean storage root diameter difference among the genotypes and also among the locations, in which the rank of the storage root diameter did change with the change of the planting location. Either the main factor, genotype or location, had a significant effect on the storage root diameter. Table 3 shows that Undana UJ 3 and Undana UJ 7 produced the largest storage root diameter when grown in Kupang (4.33 cm and 4.35 cm, respectively). Over the two locations, Undana UJ 7 produced the largest tuber diameter (3.83 cm) but did not differ from that of Undana UJ 3 (3.74 cm). Meanwhile, the mean storage root diameter of all tested genotypes grown in Kupang (4.05 cm) was much larger than that of TTS (3.06 cm).

Storage root length

The interaction effect of G x E was highly significant on the storage root length. The mean storage root length presented in Table 3 shows that Undana UJ 6 grown in Kupang produced the longest tuber (18.21 cm) yet did not differ significantly from that of Undana UJ 1, Undana UJ 7, and Antin 3 grown in the same location, and also Antin 3 grown in TTS. Interestingly, Antin 3 also produced the longest storage root in the TTS location. On average, the mean tuber length of all tested genotypes grown in Kupang (16.55 cm) was much longer than that of TTS (13.08 cm). Over the two locations, the check variety Antin 3 produced the longest tuber (17.40 cm). In contrast, over the two locations, Undana UJ 3 and JPV-1 produced the lowest storage root length (12.03 and 12.45 cm, respectively) (Table 3).

Storage root yield and anthocyanin content

Storage root yield

A highly significant interaction effect of G x E was also observed in the storage root yield, indicating considerable variation among the genotypes and the change in the magnitude of the variation between planting locations. The main factors of genotype and location significantly influenced the storage root yield. The mean storage root yield of tested genotypes in Table 4 shows that the Undana UJ 1 grown in Kupang produced the highest storage root yield per ha (70.63 t ha^{-1}), followed by Undana UJ 7 (59.58 t ha^{-1}) and JPV-1 (49.52 t ha^{-1}) at the second and third places, respectively. Meanwhile, the lowest storage root yield was observed on Undana UJ 3 grown in TTS (13.00 t ha^{-1}). Consistently, over the two planting locations, Undana U J1 produced the highest storage root yield (49.33 t ha^{-1}), followed by Undana UJ 7 (42.89 t ha^{-1}) in the second place, and JPV-1 (35.70 t ha^{-1}) and Antin 3 (31.70 t ha^{-1}) in the third and the fourth places, respectively. Meanwhile, Undana UJ 6 (20.76 t ha^{-1}) and Undana UJ 3 (19.95 t ha^{-1}) produced the lowest storage root yield across the two locations. The mean storage root yield of all tested genotypes in Kupang (45.42 t ha^{-1}) was much higher than that of TTS (21.35 t ha^{-1}).

Table 3. Means of number of storage roots per plant, storage root diameter, and storage root length of six purple-fleshed sweet potato clones grown in two locations

Sweet potato clone (G)	Number of storage root			Storage root diameter (cm)			Storage root length (cm)		
	Location (L)			Location (L)			Location (L)		
	Kupang	TTS	Mean (G)	Kupang	TTS	Mean (G)	Kupang	TTS	Mean (G)
Undana UJ 1	11.06 a A	8.10 a B	**9.58 a**	4.15 b A	3.24 ab B	**3.69 b**	17.43 a A	13.37 b B	**15.40 b**
Undana UJ 3	5.19 b B	4.16 c A	**4.67 c**	4.33 a A	3.15 ab B	**3.74 ab**	14.02 b A	10.04 c B	**12.03 c**
Undana UJ 6	10.90 a B	7.33 a A	**9.12 a**	3.77 d A	2.77 c B	**3.27 d**	18.21 a A	13.90 b B	**16.05 b**
Undana UJ 7	11.69 a B	8.00 a A	**9.84 a**	4.35 a A	3.30a B	**3.83 a**	17.19 a A	13.95 b B	**15.56 b**
Antin 3	10.55 a B	4.31 bc A	**7.43 b**	3.77 d B	3.08 b A	**3.42 c**	17.34 a A	17.46 a A	**17.40 a**
JPV-1	5.67 b B	5.50 b A	**5.58 c**	3.95 c A	2.89 c B	**3.42 c**	15.10 b A	9.80 c B	**12.45 c**
Mean (L)	**9.18 A**	**6.23 B**		**4.05 B**	**3.07 A**		16.55 **A**	13.09 **B**	

Note: Values within the same column/row with similar lowercase or uppercase are not significantly different based on the LSD (0.05) post hoc test. Lowercase denotes comparison within the same column; uppercase indicates comparison within the same row

Anthocyanin content

The study revealed that the tested sweet potato clones exhibited a variation in the tuber flesh color, as presented in Figure 1. All the tested genotypes showed a purplish flesh color with a varying purple intensity. Figure 1 indicates that Undana UJ 1 (A) had the lowest purple intensity in the tuber flesh, while the highest intensity was observed in Undana UJ 7 (D), Antin 3 (E), and JPV-1 (F). The difference in the purple color intensity in the tuber flesh may reflect the difference in anthocyanin content of the tested genotypes, as presented in Table 3.

The combined analysis of variance showed a highly significant effect ($P<0.01$) of interaction between the sweet potato genotype and planting locations on the total anthocyanin content of the tested genotypes. This result suggests that anthocyanin content did vary among the genotypes, and the magnitudes of the differences among the genotypes varied within the two planting locations (Table 4). Meanwhile, the main factor of the sweet potato genotype caused a highly significant effect ($P<0.01$) on the anthocyanin content. As opposed to other observed traits, the planting locations caused no significant effect ($P>0.05$) on the anthocyanin content.

Data in Table 4 show that the highest anthocyanin content was observed on Undana UJ 7 (171.67 mg/100 g) grown in Kupang, followed by JPV-1 (156.61 mg/100 g) grown in TTS. Meanwhile, the lowest anthocyanin content was observed in Undana UJ 1 grown in either Kupang (25.43 mg/100 g) or TTS (31.85 mg/100 g). Over two locations, Undana UJ 7 produced the highest anthocyanin content (157.65 mg/100 g), which did not differ significantly from that of JPV-1 (153.58 mg/100 g), followed by the check variety Antin 3 (141.97 mg/100 g). The other three sweet potato clones produced a mean anthocyanin content of less than 100 mg/100 g over the two locations, with Undana UJ 1 being the lowest (28.64 mg/100 g). The mean anthocyanin content of all the genotypes grown in Kupang (96.30 mg/100 g) was statistically similar to that of TTS (96.88 mg/100 g).

The clustering of the sweet potato clones

The cluster analysis resulted in a dendrogram, as shown in Figure 2. The dendrogram shows that two main clusters were formed at a truncation point 45.0 (Clusters I, II). Cluster I comprises two sub-cluster; one is a stand-alone sub-cluster comprised only of Antin 3, and the other contains two clones, i.e., Undana UJ 7 and Undana JPV-1. Cluster II also consisted of two sub-clusters, the stand-alone sub-cluster of Undana UJ 1 and the other sub-cluster of Undana UJ 3 and Undana UJ 6.

The principal component analysis revealed that two PCs were responsible for most of the total observed variation in the data set. PC1 contributed 96.32%, while PC2 contributed 3.48%, amounting to 99.81% of the total variability. The scatter plot of the PCA is presented in Figure 3.

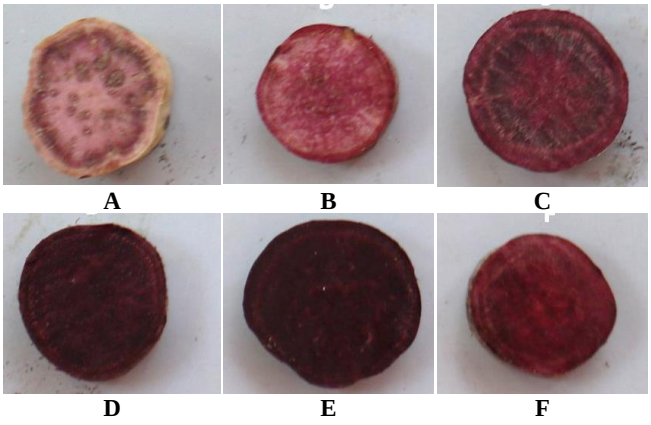

Figure 1. The storage root flesh color of tested sweet potato genotypes: A (Undana UJ 1), B (Undana UJ 3), C (Undana UJ 6), D (Undana UJ 7), E (Antin 3), F (JPV-1)

Table 4. Means of storage root yield and anthocyanin content of six purple-fleshed sweet potato clones grown in two locations

Sweet potato clone/genotype (G)	Storage root yield (t ha^{-1})			Anthocyanin content (mg/100 g)		
	Location (L)			Location (L)		
	Kupang	TTS	Mean (G)	Kupang	TTS	Mean (G)
Undana UJ 1	70.63 a A	28.04 a B	**49.33 a**	25.43 f A	31.85 e A	**28.64 e**
Undana UJ 3	26.90 e A	13.00 c B	**19.95 e**	36.90 e A	46.15 d A	**41.52 d**
Undana UJ 6	23.39 e A	18.13 b B	**20.76 e**	54.96d A	57.43 c A	**56.20 c**
Undana UJ 7	59.58 b A	26.21 a B	**42.89 b**	171.67 a A	143.62 b B	**157.65 a**
Antin 3	45.51 d A	20.88 b B	**31.70 d**	138.30 c A	145.65 b A	**141.97 b**
JPV-1	49.52 c B	21.87 b A	**35.70 c**	150.54 b A	156.61 a A	**153.58 a**
Mean (L)	**45.92** **A**	**21.36** **B**		**96.30** **A**	**96.89** **A**	

Note: Values within the same column/row with similar lowercase or uppercase are not significantly different based on the LSD (0.05) post hoc test. Lowercase denotes comparison within the same column; uppercase indicates comparison within the same row

Figure 3 shows that the six sweet potato clones are scattered almost evenly along the four quadrants, indicating variability. In PC 1, the traits that had positive loading factors included the anthocyanin content (ANTC) (0.99), storage root yield (SRY) (0.23), and storage root length (SRL) (0.15). In contrast, the contribution of storage root diameter (SRD) and storage root number (SRN) is almost negligible. In the PC2, the storage root number (SRN), storage root diameter (SRD), storage root length (SRL), and storage root yield (SRY) had positive loading scores, respectively, 0.58, 0.59, 0.22, and 0.97. Meanwhile, the anthocyanin content (ANTC) almost negligibly contributed to the PC2. Thus, the PCA indicates that anthocyanin content (ANTC) is mostly responsible for the variability in the PC1. At the same time, Storage Root Yield (SRY) is mostly responsible for variability in the PC2, as indicated by their longer biplot projection lines from the biplot origin (Figure 3).

GGE biplot analysis

Table 2 shows that the G x E interaction had a highly significant effect on all the observed traits; thus, the data complied with the requirement for biplot analysis. GGE biplot analysis was conducted only on the storage root yield and anthocyanin content as the two traits are the most important to select for in the purple-fleshed sweet potato breeding program. GGE biplot analysis was carried out for environment evaluation, identification of the which-won-where, and ranking the tested genotypes based on mean performance and stability across environments.

Environment evaluation

Evaluation of the environment helps determine the appropriate environment for a certain trait performance. In GGE biplot analysis, environment evaluation is presented as discriminativeness and representativeness of the test environments, as presented in Figure 4. Figure 4.A shows that two Principal Components (PCs) were responsible for the total observed variability in storage root yield, i.e., PC1 and PC2, which contributed 98.2% and 1.8%, respectively, to the total variability. In anthocyanin content (Figure 4.B), two PCs were also responsible for the total variability; PC1 contributed 99%, and PC2 contributed 1% to the total variability.

In Figure 4, the small red circle indicates the position of the average environment divided by the average PC1 and PC2 scores across the two environments. The average environment can be regarded as a virtual environment; the thick red line that passes through the biplot origin and the average environment, referred to as the Average Environmental Coordinate (AEC) line, is a red arrow pointing to the average environment from the biplot origin. The vector length of an environment represents its discriminating ability; the longer the vector, the more discriminative an environment is, and the closer the vector is to the biplot origin, the less discriminative an environment is. Meanwhile, the angle between an environment vector line and the AEC line represents the representativeness of an environment; the narrower the angle between the two lines, the more representative the environment is. An ideal environment should be both discriminating of the genotypes and representative of the average environment.

The GGE biplot in Figure 4.A shows that Kupang is the ideal location to discriminate the genotypes for storage root yield, as indicated by its longer vector. At the same time, that of TTS is short and close to the biplot origin, indicating its less discriminating of the genotypes for storage roots yield. In the anthocyanin content, vectors of both Kupang and TTS locations are long and far apart from the biplot origin (Figure 4.B), suggesting that both locations are highly discriminating for the trait. However, Kupang is still considered the ideal location to discriminate the genotypes for anthocyanin content. Kupang is considered the ideal location to discriminate the genotypes for anthocyanin content as the tested genotypes tested in Kupang had a wider range of anthocyanin contents (25.43-171.67 mg/100 g FW) than the TTS location (31.85-156.61 mg/100 g FW) (Table 4).

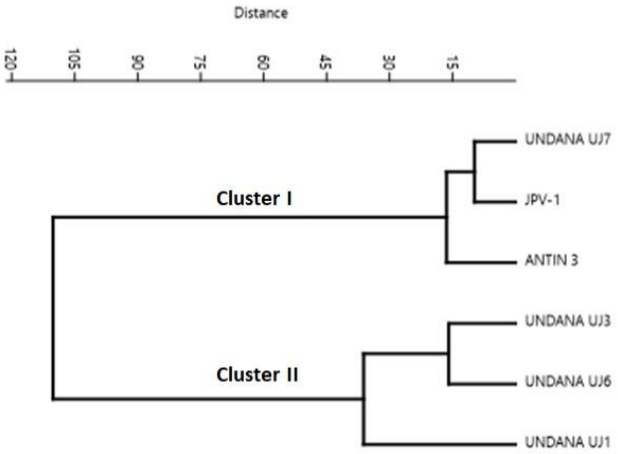

Figure 2. UPGMA Dendrogram, based on Euclidean distance coefficient, of six sweet potato genotypes generated using five agronomical characters of storage root

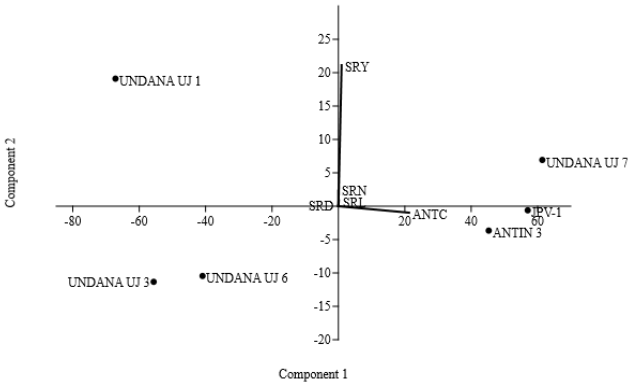

Figure 3. Scatter plots showing distribution and agronomic characters are mostly responsible for the observed variability of six purple-fleshed sweet potato genotypes in PC1 versus PC2. SRY: storage root yield, SRN: storage root number, SRD: storage root diameter, SRL: storage root length, ANTC: storage root anthocyanin content

Further, in Figure 4.A, the angle of each location's vector line with the AEC line is narrow and similar, indicating that the two locations are equally representative of the storage root yield trait. Meanwhile, Figure 4.B shows that TTS had a narrower angle with the AEC line than Kupang, indicating that TTS is more representative of the anthocyanin content trait.

In addition to discriminativeness and representativeness of location, environment evaluation is also useful in determining the relationship/association among locations. Two environments are positively correlated if the angle between their vectors is <90°, are negatively correlated if the angle between their vectors is >90°, and are independent if the angle between their vectors is 90° (0° means r =1, 180° means r = -1 Figure 4 shows that the angle of the two vectors is narrow (less than 90°), implying a close relationship (positive correlation) between the two locations for both the storage root yield and anthocyanin content. The close correlation between the two locations may suggest a redundant environment. Additionally, the two test locations in this study had the same soil type (grummosol/vertisol). Also, the study was carried out in the two locations simultaneously, i.e., during the dry season, during which the genotypes tested in both locations were exposed to almost similar weather conditions, including the sunlight duration and intensity. Additionally, the irrigation was provided similarly in both locations using pipe water as there was no rainfall during the experiment, thus the abovementioned factors presumably explain the close relationship between the two environments. The close relationship between two locations may be used in identifying traits that can be used in indirect selection for a target trait, i.e., high storage root yield that can be indirectly selected through selecting the yield-contributing attributes such as number of storage root, tuber diameter, or tuber length.

Evaluation of which-won-where and mega-environment

Mega-environment (Mega-E) is a group of environments that similarly support the performance of a set of genotypes (Crossa et al. 2002). Mega-E is indicated by a vertex genotype, i.e., the genotype performing the best in each sector/quadrant of the which-won-where GGE biplots (Yan and Hunt 2002).

Figure 5.A shows that GGE biplot analysis identified two Principal Components (PCs) contributing to the total variation. PC1 contributed 98.2%, while PC2 contributed only 1.8% to the total observed variation in the storage root yield trait. Which-won-where biplot in Figure 5.A was not well distributed; there was only one Mega-E for storage root yield. The biplot of storage root yield (Figure 5.A) is divided into four main quadrans/sectors, and the two locations fell into a single sector, indicating that a single vertex genotype had the highest storage root yield in both locations. Therefore, the winning genotype for the two locations is Undana UJ 1, located at the farthermost vertice (the largest distance from the origin of the biplot). In Addition, Undana UJ 7 is considered the second winning genotype for storage root yield as it was located at the second vertice of the same sector where Undana UJ 1 is. In a which-won-where GGE biplot method, a vertex genotype is considered more responsive to environmental change and is considered to be the specifically adapted genotype (Yan and Kang 2003; Yan and Tinker 2006). Meanwhile, Antin 3 and JPV-1 were located near the origin of the biplot, indicating that these genotypes are less responsive to environmental change concerning the storage root yield performance. Undana UJ 3 and Undana UJ 6 are the vertex genotypes of the sectors containing no environments (locations), indicating that the two genotypes were poorly adapted to the two test locations for the storage root yield.

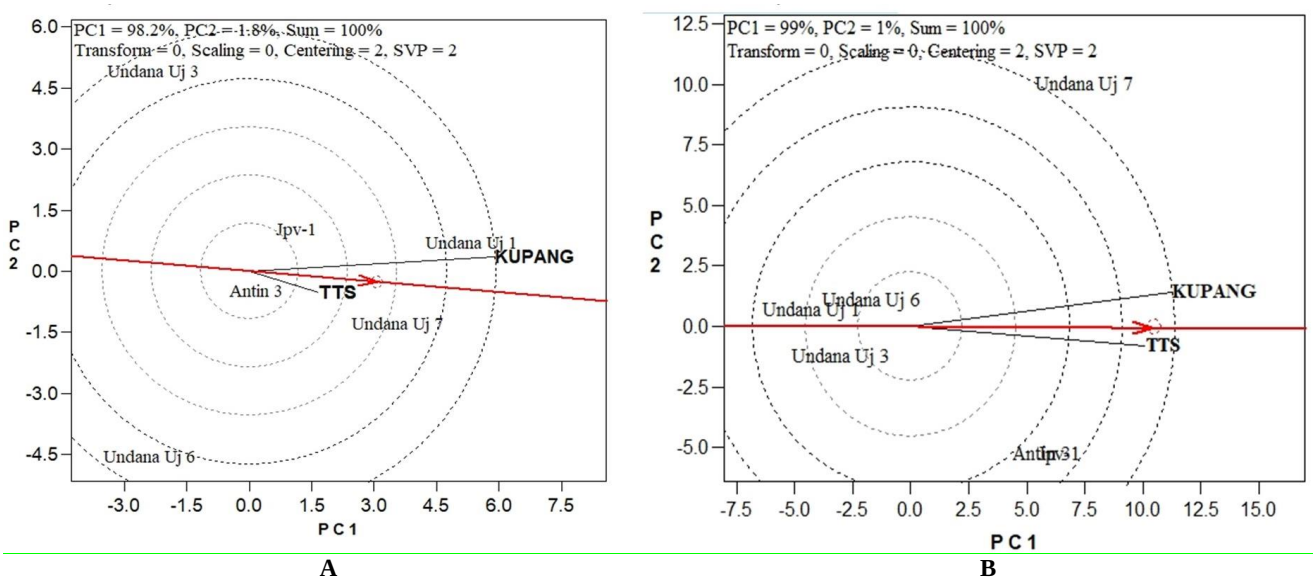

Figure 4. GGE biplot graph showing discriminativeness and representativeness of the test locations on the sweet genotypes in storage root yield and anthocyanin content. A. Root yield, B. Anthocyanin content

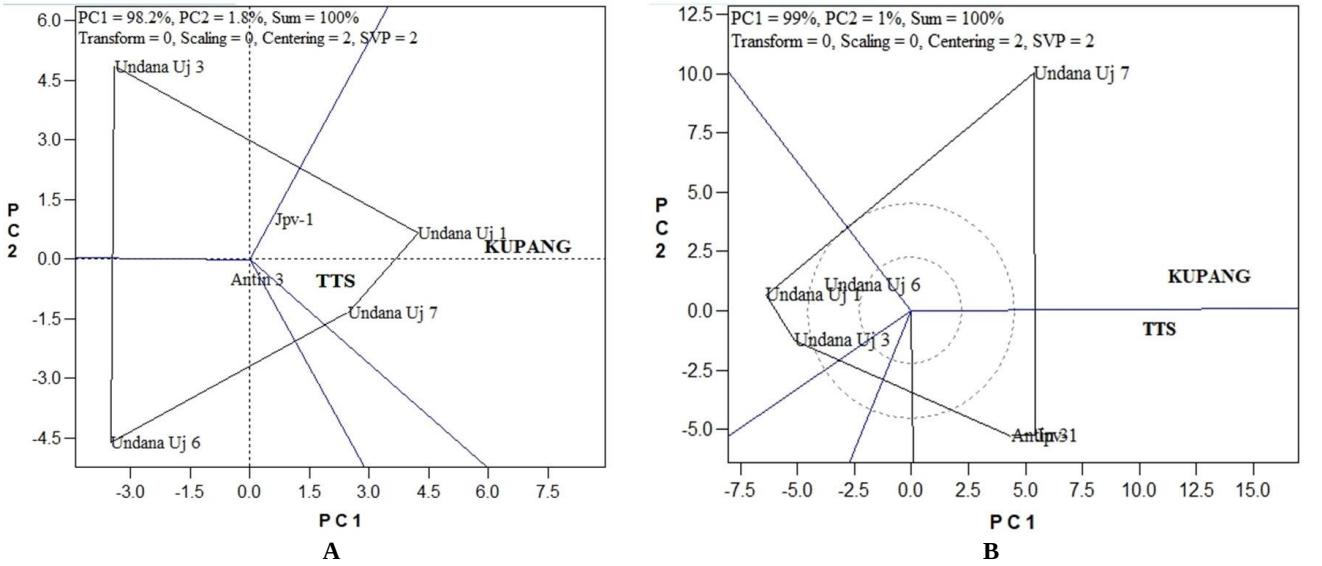

Figure 5. GGE Biplot graph showing the winning genotypes/clones in two locations in root yield and anthocyanin content. A. Root yield, B. Anthocyanin content

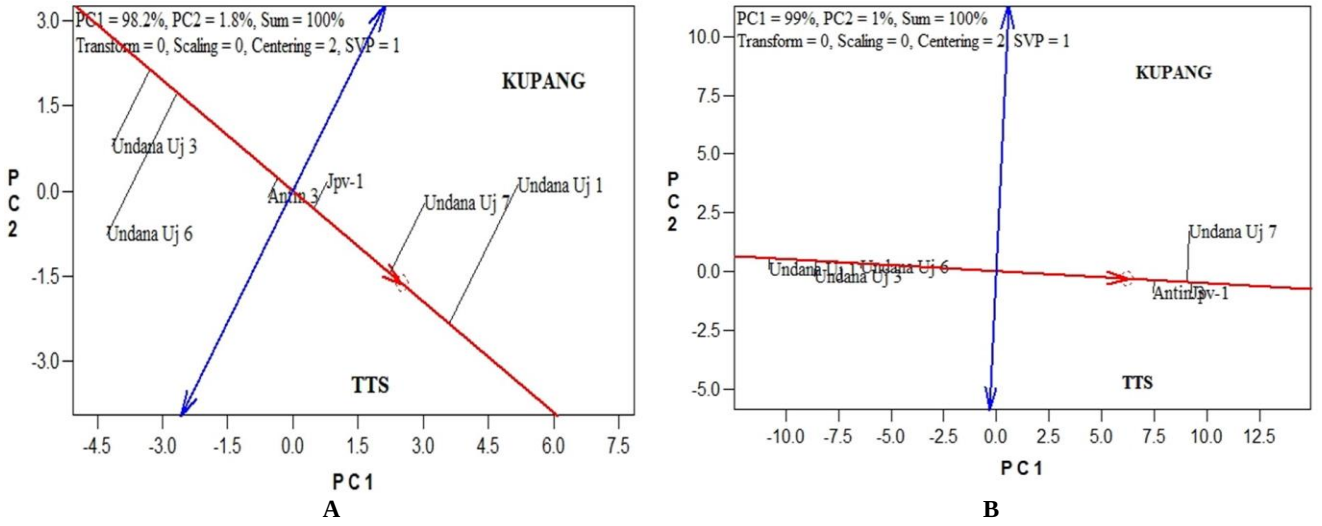

Figure 6. GGE Biplot graph shows the genotypes' mean performance and stability across two locations in root yield and anthocyanin content. A. Root yield, B. Anthocyanin content

The GGE biplot analysis revealed two PCs responsible for the observed variation in the anthocyanin content trait. At the same time, PC1 and PC2 contributed 99 and 1% to the observed variability in the anthocyanin content. The biplot is divided into five sectors, with the six genotypes falling into different sectors and the two locations falling into two sectors. Undana UJ 7 is the vertex genotype in the Kupang location, while two genotypes, i.e., Antin 3 and JPV-1, are the vertex genotypes in the TTS location. The other three genotypes (Undana UJ 6, Undana UJ 1, and Undana UJ 3) fell into sectors without any location, indicating that the three genotypes were poorly adapted to the two test locations.

Ranking of genotypes based on mean performance and stability

In the GGE biplot method, the mean performance and stability were estimated using average environmental coordinates (AEC) (Yan and Hunt 2002). The mean performance and stability of the tested genotypes across two locations are presented in Figure 6, while the rank of the genotypes is presented in Figure 7. In Figure 6 and Figure 7, the line passing through the biplot origin is the AEC line, which is defined by the mean scores of PC 1 and PC 2. Meanwhile, the blue double arrow line that passes through the origin of the biplot, and is perpendicular to the AEC line, represents the stability of the genotype, where, the farther away from the biplot origin or a longer projection to the blue line indicate greater G by E

interaction, which means more variable and less stable across environment (Yan and Kang 2003).

Based on their mean performance across the two locations, the genotypes were ranked along the AEC, with the arrow pointing to a greater value. Thus, the rank of the genotypes for the storage root yield is Undana UJ 1>Undana UJ 7>JPV-1>Antin3>Undana UJ 6>Undana UJ 3. Meanwhile, the rank of the genotypes based on anthocyanin content is Undana UJ 7>JPV-1>Antin 3>Undana UJ 6>Undana UJ 3>Undana UJ 1. The blue double arrow line also separates the genotypes with below-average means from those with above-average means. Thus, the genotype's rank for storage root yield is Undana UJ 1>Undana UJ 7>JPV-1>Mean>Antin3>Undana UJ 6>Undana UJ 3. At the same time, the anthocyanin content is Undana UJ 7>JPV-1>Antin 3>Mean>Undana UJ 6>Undana UJ 3>Undana UJ 1.

For the stability of the genotypes across two locations, the genotype with a longer projection toward the blue double arrow line or farther away from the AEC line is considered more variable or less stable and vice versa. Thus, the stability rank of the tested genotypes for storage root yield (Figure 4.A) is Antin3>JPV-1>Undana Uj 3>Undana UJ 7>Undana UJ 6>Undana UJ1 while that for anthocyanin content (Figure 4.B) is Antin 3>Undana Uj 6>Undana UJ 1>JPV-1>Undana UJ 3>Undana UJ 7.

Figure 6.A shows that Undana UJ 1 and Undana UJ 7 had the highest yield performance but were less stable, while Antin 3 and JPV-1 had yield performance around the mean yield but were stable across two locations. Meanwhile, Figure 6.B shows that three genotypes, i.e., Undana UJ 1, Undana UJ 3, and Undana UJ 6, were stable across two locations, but they had anthocyanin content less than the means of all genotypes; on the contrary, Undana UJ 7 had the highest anthocyanin content across two locations but was less stable.

An ideal genotype has high mean performance and stability across environments (Farshadfar et al. 2012; Mitrovic et al. 2012). Figure 7 shows the ranking of the genotypes relative to an 'ideal' genotype. The small red circle indicates the average environment, the red line is the AEC abscissa line, and the double arrow line is the ACT ordinate. There are also five concentric circles, with the 'ideal' entry being the concentric center. The arrow inside the concentric center is where the ideal genotypes should be. A genotype is more desirable if it is closer to the 'ideal' genotype center (Mıtrovıã et al. 2012). Thus, for storage root yield, the ranking of desirable genotypes based on the ideal genotype is Undana UJ 7>Undana UJ 1>JPV-1>Antin 3>Undana UJ 6>Undana UJ 3 (Figure 7.A). At the same time, that for anthocyanin content is JPV-1>Antin 3>Undana UJ 7>Undana UJ 6>Undana UJ 3>Undana UJ 1 (Figure 7.B).

The vector length of the average environment (the distance from the biplot origin and the average environmental marker/small red circle) is a measure of the relative importance of the genotype main effect (G) vs. the genotype by Environment Interaction (GE). The longer it is, the more important the G is; hence, the more meaningful the selection is based on mean performance. The results in Figure 7 shows that the genotype's main effect is important for root yield and anthocyanin content. The GGE Bilplot in Figure 7 confirmed the results of the combined ANOVA results in Table 2, where, for the storage root yield trait, the sum of squares of the genotype (G) (831.41) is much higher than that of the genotype by environment (GE) (271.74). Similar results apply for anthocyanin content trait, where the sum of squares of Genotype (G) (21979.86) is much higher than that of genotype by environment interaction (GE) (.302.54). In addition, data in Table 4 also showed that the rank of the genotypes for both storage root yield and anthocyanin content did not change much along with the change of the environment indicating that genotypic main effect is more important than GE effect for the traits. Thus, selecting these traits based on mean performance is effective.

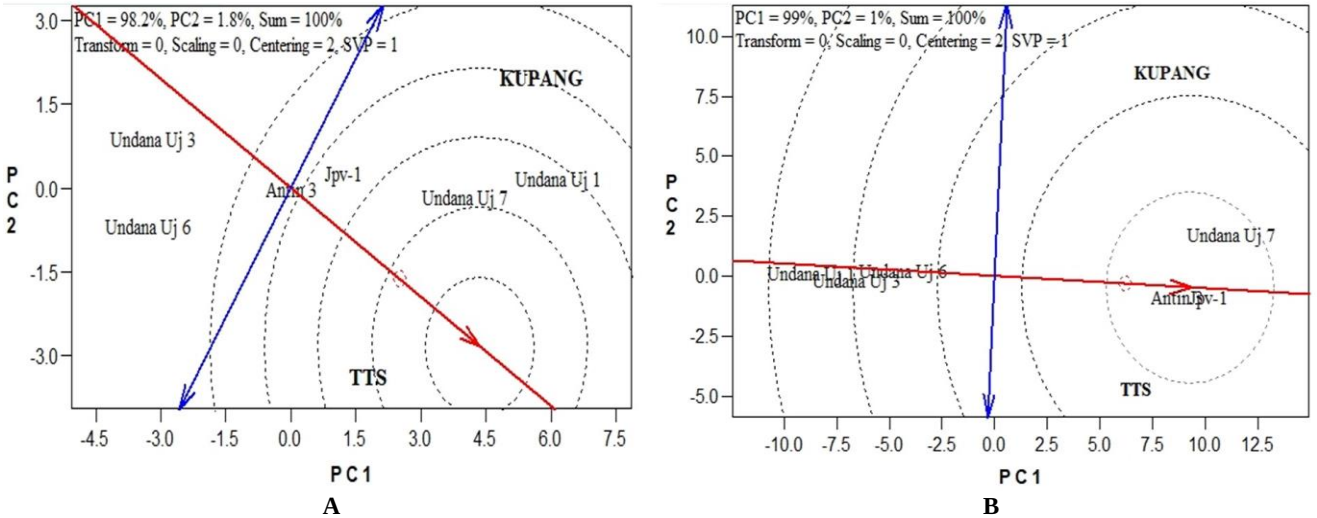

Figure 7. GGE Biplot graph showing the ranking of the genotypes relative to an ideal genotype based on mean performance and stability across two locations in root yield and anthocyanin content

Discussion

The combined ANOVA revealed that G x E interaction significantly affected (P<0.01) yield attributing traits, storage root yield, and anthocyanin content of tested sweet potato clones. The main effect of either genotype or location also significantly affected (P<0.01) the observed traits, except for the anthocyanin content, where the effect of location was not significant (P>0.05). A significant G x E interaction effect suggests that the observed traits varied according to the clones, and the magnitude of the variation did change following the change of environment/location.

The existence of significant G x E effects makes plant breeding programs inefficient (Maulana et al. 2022). Additionally, the presence of G x E effects causes the ranking of each genotype on the observed traits in each location to vary. Thus, there is a need to select the best genotype for a specific environment (Khalili and Pour-aboughadareh 2016; Maulana et al. 2022).

The presence of a significant G x E interaction effect on yield attributing components and storage root yield is presumably due to the difference in the environmental conditions of the two locations. According to Jamshidmoghaddam and Pourdad (2013), the large variation in the planting environments that influence crop growth and development contributes to the emergence of the G x E interaction effect. Environmental conditions influencing storage root production include soil fertility, altitude, temperature, humidity, etc. Soil fertility influences plant growth by providing essential nutrients for plant and storage root growth and development.

There was a significant variation in altitude (Kupang 86 masl, TTS, 1,090 masl) and some variation in soil conditions between the two locations. The soil types of the two locations were similar, i.e., grummosol/vertisol, but differed slightly in the soil texture, i.e., clay-sandy and clay, respectively, in Kupang and TTS. The acidity of the soils in Kupang (pH 6.93) and TTS (pH 6.74) were almost similar. Soil mineral fertility of the Kupang and TTS was slightly different in the mineral contents, i.e., N (0.21%), P (142 ppm), and K (0.94 me/100) in Kupang and N (0.12%), P (138.48 ppm), and K (0.56% me/100) in TTS. These differences, through their interaction with the genetic makeup of the tested clones, presumably have resulted in a highly significant effect on the observed traits of the tested sweet potato clones.

The present study confirmed the previous study reports that genotype by environment interaction effect was significant on yield components and storage root yield of sweet potato (Mau et al. 2013; Madawal et al. 2015; Gurmu 2017; Mustamu et al. 2018; Ngailo et al. 2019, Maulana et al. 2023). These findings may indicate that yield components and storage root yield are quantitative traits governed by many genes whose expressions are strongly influenced by environmental factors. The results showed that Kupang is the best location that produced the highest mean root yield of tested genotypes compared to the TTS location (Table 4). Kupang location has a more sandy-soil condition (clay-sandy) than TTS, with a higher clay content (clay) soil texture, which may have affected the plant growth and development. The higher clay content may cause the sweet potato yield less than optimal (Maulana et al. 2023). The higher fresh root yield observed in the Kupang planting location was more likely because the mineral contents of N, P, and K in this location were higher than those in TTS.

Mau et al. (2019) reported a storage root yield of Undana UJ 1, Undana UJ 3, and Undana UJ 6 of, respectively, equivalent to 34.46 t ha^{-1}, 19.08 t ha^{-1}, and 23.04 t ha^{-1} when grown in Lasiana Village, Kupang District (Alluvial, 60 masl). As a comparison, the results of the present study revealed that the mean fresh root yield of Undana UJ 1 (48.86 t ha^{-1}) was much higher than that grown in Lasiana Village, Kupang (Mau et al. 2019). Meanwhile, the storage root yields of Undana UJ 3 (19.08 t ha^{-1}) and Undana UJ 6 (23.04 t ha^{-1}), as reported by Mau et al. (2019), were not much different from those of the present study (19.24 t ha^{-1} and 20.74 t ha^{-1}, respectively). These results confirmed the previous study findings that the interaction between genotype and environmental conditions strongly influenced root yield that contributes to sweet potato characteristics (Madawal et al. 2015; Gurmu 2017; Rahajeng and Rahayuningsih 2017; Mustamu et al. 2018; Ngailo et al. 2019; Karuniawan et al. 2021; Maulana et al. 2023).

In our previous study (Mau et al. 2019), Undana UJ 1, Undana UJ 3, and Undana UJ 6 outyielded the purple-fleshed check variety Antin 2 (11.96 t ha^{-1}). Similarly, the present study results revealed that Undana UJ 1 (48.86 t ha^{-1}) and Undana UJ 7 (42.69 t ha^{-1}) also out yielded the purple-fleshed check varieties (Antin 3, 31.26 t ha^{-1}). Furthermore, Mukherjee and Naskar (2012) reported a root yield of 16 - 22 t ha^{-1} with anthocyanin content of purple-fleshed sweet potato genotypes ranging from 85-90 mg/100 g Fresh Weight (FW). Additionally, Bassey et al. (2019) evaluated the yield performances of 16 sweet potato varieties over two years. They obtained mean storage root yields ranging from 6.15-15.85 t ha^{-1}, classified into low and moderate yielding ability. A study by Saitama et al. (2017) found the root yield of several Indonesian sweet potato varieties (yellow, orange, and purple-fleshed) to range between 8.9-44.8 t ha^{-1}. Nevertheless, specific reports lack the storage root yield of purple-fleshed sweet potatoes in Indonesia. Thus, the present study results are of importance to provide information on the purple-fleshed sweet potato yields in Indonesia and to reveal that at least two purple-fleshed clones, i.e., Undana UJ 1 and Undana UJ 7 that produced considerably higher root yield as compared to the check varieties.

One of the unique traits of purple-fleshed sweet potato observed in the present study was anthocyanin content. Anthocyanins of purple-fleshed sweet potatoes are relatively stable under light conditions, temperatures, and pH levels and also resistant to processing. Thus, they can be used as a natural colorant in the food industry, food, and also in the pharmaceutical or cosmetic industries (Wang et al. 2022). Anthocyanin contents of purple-fleshed sweet potato can be easily seen from its purple color intensity. The flesh color of the tested sweet potato genotypes (Figure 1) differed considerably from light to dark purple, which may indicate variation in anthocyanin contents. Montilla et al. (2011) reported a good correlation between the purple color

intensity in the flesh and the anthocyanin content of sweet potatoes. They found that the most intense purple color of the Japanese purple-fleshed sweet potato, Chiran Murasaki, accumulated higher anthocyanin than the less intense purple color genotypes. Additionally, Ginting et al. (2020) found that anthocyanin content was negatively correlated with the lightness value (L) of the tuber flesh color; the lighter the purple color, the lower the anthocyanin content, and vice versa; the deeper the purple color, the higher the anthocyanin content. Our results are consistent with those of Montilla et al. (2011) and Ginting et al. (2020), where the genotypes with deeper or more intense purple color produced higher anthocyanin content (Figure 1, Table 3).

The results of the present study showed that the total anthocyanin content of tested sweet potato genotypes ranged from about 26 to 170 mg/100 FW (Table 4). As a comparison, the anthocyanin contents of Indonesian released varieties purple-fleshed sweet potato varieties (Antin 1, Antin 2, Antin 3) were, respectively, 33.89 mg/100 g, 130,19 mg/100 g and 150,67 mg/100 g with storage root yield potential of 33.2 t ha^{-1} (Antin 1), 37.1 t ha^{-1} (Antin 2) and 30.6 t ha^{-1} (Antin 3) (Balitkabi 2017). In addition, Ginting et al. (2020) reported anthocyanin content of 15 Indonesian purple-fleshed sweet potato genotypes of >100 mg/100 g FW, with Antin 2 and Antin 3 producing the highest anthocyanin content of about, respectively, 157 and 177 mg/100 g FW). Furthermore, a previous study by He et al. (2016) reported anthocyanin levels of purple-fleshed sweet potatoes in the range of 10-97 mg/100 g fresh weight. Mukherjee and Naskar (2012) reported anthocyanin content of purple-fleshed sweet potato genotypes ranged from 85-90 mg/100 g FW. In Japan, Ishiguro et al. (2022) reported a much higher anthocyanin content in purple-fleshed sweet potato varieties ranging from 200-800 mg/100 g FW. Besides the difference in genetic background of the sweet potato genotypes tested, the difference in anthocyanin content among the different studies was presumably due to the differences in environmental factors, more specifically, the temperature, which is assumed to influence the anthocyanin content in plants (Ishiguro et al. 2022). Similarly, Alam et al. (2022) also reported that anthocyanin contents of purple-fleshed sweet potatoes were affected by location.

Both genetic and environmental factors influence anthocyanin content in plants; the environmental factors that affect the anthocyanin content include temperature, light, plant growth regulators, and sugars (Schwartz et al. 2009; Matsushita et al. 2016). Villavicencio et al. (2007) observed that the anthocyanin content of sweet potatoes was higher when grown at lower temperatures in growth chambers. In field experiments, Ishiguro et al. (2022) also highlighted that sweet potato anthocyanin content in lower-temperature locations was higher than in higher-temperature locations. Similarly, Kurata and Kobayashi (2023) confirmed that anthocyanin content could be maximized by planting and harvesting the sweet potato at lower soil temperatures. In the present experiments, the mean anthocyanin contents of tested sweet potato clones grown in TTS (altitude 1,090 masl, lower temperature) was a bit higher than that grown in Kupang (86 masl, higher temperature). However, they were not statistically different (Table 4). Therefore, these findings align with the previous reports that the environmental conditions, such as temperature, affected the anthocyanin content, where the lower temperatures of growing conditions enhanced anthocyanin production in plants, especially the purple-fleshed sweet potato. Matsushita (2016) emphasized that the higher anthocyanin content of sweet potatoes grown in lower temperature conditions presumably through the elevation of the anthocyanin pathway. According to Tanaka et al. (2017), anthocyanins are included in a class of flavonoids synthesized via the phenylpropanoid pathway, responsible for colors ranging from pale pink to purple and deep blue. Anthocyanins are present in plant tissues, especially the flowers, fruits, and storage roots.

Genetic studies showed that a tissue-specific accumulation of anthocyanin in many plants is controlled by transcription factors belonging to the MYB family (Tanaka et al. 2017). Through a gene expression analysis using purple-fleshed sweet potato cultivars, Mano et al. (2007) revealed that one of the MYB-type transcription factors in sweet potato, i.e., *IbMYB*1, is responsible for anthocyanin accumulation in storage root. Furthermore, Park et al. (2015) confirmed that overexpression of *IbMYB1* induced anthocyanin accumulation and elevated radical scavenging activity in purple-fleshed sweet potato genotypes. Tanaka et al. (2012) also found two distinct *IbMYB1* copies, i.e., *IbMYB1-2a* and *IbMYB1-2b*, shared only in high-anthocyanin sweet potato cultivars. Thus, they can be used as molecular markers in selecting high anthocyanin sweet potato genotypes. According to Tanaka (2017), quantitative variations in anthocyanin and carotenoid content are likely to be controlled by multiple genes. Still, this needs to be confirmed by further phytochemical, biochemical, and genetic studies.

Cluster analysis placed the six sweet potato clones into two main clusters, each comprised of three genotype members, indicating high agronomic trait variability among the clones. The dendrogram shows that the separation of the six clones into two clusters of three genotypes each may be contributed mostly by two observed traits, i.e., anthocyanin content and storage root yield, as revealed in the PCA scatter plots (Figure 3), where storage root yield is mostly responsible for the variability in PC1, and anthocyanin content is responsible for most of the variability in PC2. Data in Table 4 show that the three clones placed in cluster I on the dendrogram (Figure 2) are also the same three clones that produced the highest anthocyanin content, while the other three clones placed in cluster II are those with the lowest anthocyanin content. Thus, the anthocyanin content is the trait that mostly explains the clustering of the tested sweet potato genotypes in Figure 2, implying that the trait is the most variable amongst the clones. The results indicate the usefulness and effectiveness of anthocyanin content as a grouping character of sweet potato (UPOV 2010). The effectiveness of agro-morphological characters, including anthocyanin traits as discriminators of sweet potatoes, has been reported in previous works (Tairo et al. 2018; Ochieng 2019; Mau et al. 2022).

The GGE biplot analysis was used to evaluate the discriminativeness and representativeness of the location and the ranking of the genotypes based on mean performance and stability. The results (Figure 4) showed that Kupang is the ideal location to discriminate the clones for storage root yield, while TTS is not discriminative for the trait. Kupang and TTS locations are highly discriminative for anthocyanin content, but Kupang is still the ideal location to discriminate the genotypes for anthocyanin content. The which-won-where biplot (Figure 5.A) revealed only one mega-E for storage root yield, meaning both Kupang and TTS similarly support the best performance of the best performing (vertex) genotypes where Undana UJ 1 is the vertex genotype for the two locations for storage root yield. Meanwhile, two mega-E were identified in anthocyanin content (Figure 5.B), suggesting each location had its vertex genotype for the trait. Undana Uj 7 was Kupang's winning genotype for anthocyanin content, while JPV-1 and Antin 3 were the winning genotypes for the TTS location. These results indicate that a large G x E effect was present for anthocyanin content, which may necessitate the selection of specifically adapted genotypes. The use of GGE biplot analysis for evaluation of discriminativeness and representativeness of location has been reported in other crops such as dry bean (Mndolwa et al. 2019), rice (Akmal et al. 2014; Akter et al. 2015; Susanto et al. 2015), fluted pumpkin (Fayeun et al. 2018) and soybean (Kocaturk et al. 2019).

The present study results revealed that the three highest performing genotypes above the grand mean root yield for storage root yield were Undana Uj 1>Undana UJ 7>JPV-1. In comparison, the three most stable genotypes for the trait were Antin 3>Undana Uj 6>Undana UJ 1, which indicates that the genotype with the highest mean yield is not always the most stable, and vice versa, the most stable genotype is not always the performing genotype for the traits. Similar findings were reported for various traits in sorghum (Rakshit et al. 2012), aromatic rice (Akmal et al. 2014), dry bean (Mndolwa et al. 2019), and fluted pumpkin (Fayeun et al. 2018). These results may have occurred because a different set of genes controls each trait, and the expression of these genes will vary considerably as they will be differentially affected by the environment. Thus, to select the best genotypes for certain breeding objective traits, it is necessary to rank the genotype based on both the mean performance and the stability.

Based on the mean performance and stability, the rank of the genotypes for storage root yield was Undana UJ 7>Undana UJ 1>JPV-1>Antin 3>Undana UJ 6>Undana UJ 3 (Figure 7.A). Two hybrid clones, Undana UJ 7 and Undana UJ 1, rank above the check variety Antin 3; thus, they are potential clones for registration as purple-fleshed candidate varieties with storage root yield as their superiority. Meanwhile, for the anthocyanin content, the rank was JPV-1>Antin 3>Undana Uj 7>Undana UJ 6>Undana UJ 3>Undana UJ 1. The hybrid clone Undana UJ 7 ranks below the check variety Antin 3 but ranks first in the Kupang Location for anthocyanin content (Table 4). Thus, Undana UJ 7 can still be a potential candidate for the purple-fleshed sweet potato variety with anthocyanin content as the superior trait specific to the Kupang location. However, as only two locations were tested in this study, the rank of the genotypes for the two traits may change when a higher number of tested locations are included in the evaluation. This is in line with the Indonesian Agriculture Ministry Regulation (DPTP 2021), which dictates that, for sweet potatoes, a minimum of six environments are required in Mulit-Envirnmental Testing for varietal release.

In conclusion, the results of the present study show that the observed traits were influenced by genotype, location, and genotype by location (G x E), except for anthocyanin content, which was not affected by location. Undana UJ 1 (49.33 t ha^{-1}), Undana UJ 7 (42.89 t ha^{-1}) and JPV-1 (35.70 t ha^{-1}) produced the highest mean root yield, while Undana UJ 7 (157.65 mg/100 g FW), JPV-1(153.58 mg/100 g FW) and Antin 3 (141.97. mg/100 g FW) produced the highest anthocyanin content across the two locations. The tested genotypes were grouped into two main clusters, and the trait that mostly explained the grouping was the anthocyanin content. The ranks of the tested genotypes based on the mean performance and stability are Undana UJ 7>Undana Uj 1>JPV-1>Antin 3>Undana UJ 6>Undana UJ 3 for storage root yield and JPV-1>Antin 3>Undana UJ 7>Undana UJ 6>Undana UJ 3>Undana UJ 1 for anthocyanin content.

ACKNOWLEDGEMENTS

The authors thank the Rector of Universitas Nusa Cendana, Kupang, Indonesia for funding this research through Professor Research Grant, Financial Year 2023 (Contract number: 202/UN15.19/LT/2023). We also thank Andreas Bouk, Aprianto Nana, Epol Koen, and Garvasilus V. Asa for their technical assistance during the field experiments.

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