RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
55 (1) 61-73, 2023
http://doi.org/10.54910/sabrao2023.55.1.6
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

GENETIC VARIABILITY, HERITABILITY, AND GENETIC GAIN IN SWEET POTATO (*IPOMOEA BATATAS* L. LAM) FOR AGRONOMIC TRAITS

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SUMMARY

The study aimed to estimate the genetic variability, heritability, and genetic advance in the existing sweet potato (*Ipomoea batatas* L. Lam) populations for growth and yield traits in Peninsular Malaysia. The experiment transpired in 2020 at the Centre of Excellent Tuber Crops Research, Malaysian Agricultural Research and Development Institute (MARDI), Bachok, Kelantan, Malaysia. A total of 39 sweet potato genotypes studied consisted of introduced hybrids from the International Potato Center (CIP), Peru, Asian Vegetable Research and Development Center (AVRDC), Taiwan, and local conventional and newly released cultivars and breeding lines by MARDI, Bachok, Malaysia. Analysis of variance showed significant ($P < 0.05$) differences among the potato genotypes for almost all the traits. The phenotypic coefficient of variation (PCV) appeared higher than the genotypic coefficient of variation (GCV) for all traits. With their high heritability estimate (>60%) and a genetic advance of 5% (>20%), the other agronomic traits: storage root yield per plant, individual storage root weight, and yield per hectare, may benefit as useful selection criteria in sweet potato development. Further, recommend these characteristics for consideration while selecting high-yielding sweet potato cultivars. Thus, the findings of this study proved valuable in future breeding programs for improving cultivars and developing more genetic variations in sweet potatoes, especially in Malaysia.

Keywords: genetic variability, heritability and genetic gain, genotypic coefficient of variation, phenotypic coefficient of variation, agronomic traits

Key findings: The selected sweet potato genotypes MIb3 and MIb16 gained authentication as promising lines that can serve in future breeding programs for the development of new high-yielding sweet potato cultivars in Malaysia.

Communicating Editor: Prof. Naqib Ullah Khan

Manuscript received: November 10, 2022; Accepted: January 17, 2023.

INTRODUCTION

Sweet potato (*Ipomoea batatas* L. Lam) is a member of the Convolvulaceae family. The family has approximately 55 genera and over 1000 species (Mu and Zhang, 2019). Sweet potatoes originated in Central and South America. Based on radiocarbon dating, archaeologists found prehistoric remnants of sweet potatoes in Polynesia from about

Citation: Nurul-Afza K, Aziz A, Thiyagu D, Shahrilnizam JM (2023). Genetic variability, heritability, and genetic gain in sweet potato (*Ipomoea batatas* L. Lam) for agronomic traits. *SABRAO J. Breed. Genet.* 55(1): 61-73. http://doi.org/10.54910/sabrao2023.55.1.6.

1000 to 1100 A.D. that spread to other regions due to their great adaptability (Roullier *et al*., 2013; Munoz-Rodriguez *et al*., 2018). They hypothesized that those ancient samples came from the western coast of South America. Among the clues, one Polynesian word for sweet potato, 'Kuumala,' resembles 'kumara' and 'Cumal,' and the words for the vegetable in Quechua, a language spoken by Andean natives.

To date, sweet potato (*Ipomoea batatas* L. Lam) is the seventh most important food crop in the world after rice, wheat, potato, maize, cassava, and barley (Echodu *et al*., 2019; FAOSTAT, 2022). Sweet potato is also the third essential root crop after potato and cassava. More than 105 million MT (95%) of sweet potatoes produced globally hail in developing countries, specifically in Asia, followed by Africa. According to the United Nations Conference on Trade and Development, China is the world's largest producer and consumer of sweet potatoes, either for food, animal feed, or processing (as food, starch, and other products). In Africa, smallholder farmers value sweet potato because it grows in a cultivar of climates with few inputs and can withstand drought (Karyeija *et al*., 1998). Sweet potato is rich in carbohydrates, vitamins (A, B, and C), and minerals like phosphorus, iron, and calcium (CIP, 1996). These traits have contributed to the fact that, currently, sweet potatoes are grown in more than 100 countries (Mu *et al.,* 2017; FAOSTAT, 2022). The importance of sweet potato as a food crop flourishes rapidly in some parts of the world. It is also a good food-security crop and sells for cash by poor resource farmers (Tairo and Kullaya, 2004; Dalamu *et al*., 2012; Rawaida and Nur-Fazliana, 2019; Haq *et al*., 2021; Gins *et al*., 2022).

Nonetheless, genetic improvement in the crops is crucial for improving production on the national level. Although, the plant's inherent nature limits the genetic enhancement in sweet potatoes. The polyploid nature with a large number of chromosomes (2n = 6x = 90) and self and cross-incompatibilities provide a primary challenge to sexual recombination, seed production, and genetic improvement in sweet potatoes (Vimala and Hariprakash, 2011; Mwanga *et al.,* 2017; Munoz-Rodriguez *et al*., 2018). Self- and cross-incompatibility inhibits breeding progress because parental genotypes with desirable traits may belong to the same incompatibility group in sweet potatoes (Vimala, 1989). Sweet potato is a highly heterozygous, out-crossing polyploidy, with predominant cultivars that are self- and cross-incompatible; thus, the breeders perform grafting for flower induction followed by a screening of incompatibility groups (Katayama *et al*., 2017; Hayati *et al.,* 2020).

Crop plants often experience numerous stresses from both physical and chemical factors, influencing their growth and productivity under natural climate conditions. Climate change also plays a vital role in managing the variations in plant growth and production of crops (Iese *et al*., 2018). Seed scarcity is the principal barrier to sweet potato breeding (Abrham *et al*., 2021). The said phenomenon is also present in sweet potato production in Malaysia, a tropical country that faces high temperatures throughout the year. Alternative strategies and resources to overcome this issue are crucial for evaluating the material for cultivar development and improvement, especially for fresh consumption. Therefore, superior sweet potato cultivars need advancement through various breeding approaches to enhance productivity and improve crop quality.

Consideration of quantitative approaches for the exploitation of the extensive genetic variability available in sweet potato germplasm is essential and dependent on accurate estimations of the various genetic parameters (Tessema *et al.,* 2022). Hence, attention should look to genetic resources and determining the genes that confer beneficial growth characteristics and yield-related traits. Estimates of genetic parameters serve as a basis for selection and hybridization since the degree of variability of a particular character is a key factor for its improvement. Therefore, the pertinent study aimed to determine the nature of genetic variability among the sweet potato genotypes for yield-related and good-quality traits using genetic parameters, including genotypic and phenotypic coefficient of variations, heritability, and genetic gain.

MATERIALS AND METHODS

Breeding materials and study site

The experimental material included 39 sweet potato genotypes derived from CIP and AVRDC hybrids, as well as, conventional and newly released cultivars and breeding lines from MARDI, Bachok, Kelantan, Malaysia (Table 1). The experiment took place in 2020 at the Centre of Excellent Tuber Crops Research,

Table 1. List of sweet potato genotypes and their origin used in the study.

No.	Accession No.	Genotypes	Origin	No.	Accession No.	Genotypes	Origin
1	MIb-01	PASAR BORONG 2	Malaysia	21	MIb-29	VitAto	MARDI
2	MIb-02	CN-2067-7	AVRDC	22	MIb-30	BIRU	Malaysia
3	MIb-03	PEJABAT	Malaysia	23	MIb-31	Anggun 2	MARDI
4	MIb-08	SABAH B	Malaysia	24	MIb-32	V6 D2 15	IC01
5	MIb-09	M/BAYENG		25	MIb-33	C 76	Unknown
6	MIb-10	PASAR BORONG 1	Malaysia	26	MIb-34	GUNTUNG 2	Malaysia
7	MIb-11	PISANG KAPAS	Malaysia	27	MIb-35	JEPUN ASAL	Malaysia
8	MIb-12	SB-031	Malaysia	28	MIb-36	SABAH K	Malaysia
9	MIb-14	CN-94517-17	AVRDC	29	MIb-37	KARAK BAKAR	Malaysia
10	MIb-16	CN-254-13	AVRDC	30	MIb-38	SUNGAI CHUA 2	Malaysia
11	MIb-17	GUNTUNG 1	Malaysia	31	MIb-39	PH 4 (PURPLE)	Indonesia
12	MIb-19	TANJUNG SEPAT 1	Malaysia	32	MIb-40	Anggun 3	MARDI
13	MIb-20	V6 D1 13	IC01	33	MIb-41	BATU PAHAT 1	Malaysia
14	MIb-22	TANJUNG SEPAT 2	Malaysia	34	MIb-42	BATU PAHAT 2	Malaysia
15	MIb-23	TANJUNG SEPAT 3	Malaysia	35	MIb-43	BATU PAHAT 4	Malaysia
16	MIb-24	GENDUT	Malaysia	36	MIb-44	BANTING	Malaysia
17	MIb-25	OREN 2	Indonesia	37	MIb-45	CAMERON HIGHLAND 1	Malaysia
18	MIb-26	18G-257	Unknown	38	MIb-46	CAMERON HIGHLAND 2	Malaysia
19	MIb-27	UBI CAIRO	Egypt	39	MIb-47	CAMERON HIGHLAND 3	Malaysia
20	MIb-28	MERODA INTA	Indonesia				

*MARDI – Malaysian Agricultural Research and Development Institute; AVRDC - Asian Vegetable Research and Development Center; MIb – MARDI *Ipomoea batatas* (accession number of sweet potato germplasm collected in MARDI); IC01 – Breeding lines accessions derived from Industrial Crops breeding program).

MARDI, Bachok, Kelantan, Malaysia (5° 58' N latitude and 102° 25' E longitude). The average annual rainfall was 61.2 mm, with a relative humidity of 46.65%. At the study location, the soil type was well-drained BRIS (Beach Ridges Interspersed with Swales). The average lowest and maximum temperatures ranged from 27.5 °C to 34.8 °C in the daytime during the study.

Crop husbandry

The experimental soil was well ploughed and harrowed 30 days before planting to ensure soil exposure to sunlight, reducing soil-borne diseases and pests. During planting, the BRIS soil received a substantial amount of organic manure at a rate of 10 t/ha. The study used a randomized complete block design (RCBD) with three replications. Sweet potato vine cuttings measured 30 cm long when taken from a 3-month-old mother plant for planting. The cuttings underwent manual planting in a vertical position. Each genotype planted on a 15.00 m long and 1.20 m wide plot had a planting distance of 0.25 m × 0.60 m between plants, accommodating 60 plants per plot. The experimental plot had the variety 'Anggun' serving as a guard row plant. The application of mixed fertilizers of nitrogen (N), phosphorus (P_2O_5), and potassium (K_2O) had a ratio of 12:12:17 kg ha^{-1} at the rate of 6 g per plant, as suggested by Rosnani *et al.* (2017). In addition, fertilizer application also had a rate of 200 kg ha^{-1} in the third, fifth, and eighth weeks after planting, providing a total yield of 600 kg ha^{-1}. The experimental plants irrigated measured the ratio of 1:2 IW/CPE (amount of irrigation water [IW] applied to cumulative pan evaporation [CPE]), with 50 mm of water as recommended cultural practices for sweet potato crops (Rosnani *et al*., 2017). The pests and disease management followed the standard agronomic practices of sweet potatoes, as previously described by Rosnani *et al*. (2017).

Traits measurement

Fifteen plants randomly selected received measuring for plant growth and yield-related traits in each plot. The plant growth measurement basis included the number of plants per plot, storage root length (cm), storage root diameter (cm), and individual storage root weight (g), according to Tripathi *et al*. (2016). The traits' measurement for storage root yield per plant (g), tuber yield per plot (kg), yield per hectare (t ha^{-1}), above-ground fresh weight per plot (kg), harvest index per plot (%), and dry matter content of marketable roots (%) used the method according to Boney *et al*. (2014). Considered marketable are the tubers weighing greater than 150 g, based on the report by Slosar *et al*. (2019). The percentage of dry matter content (DMC) estimate began with drying 200 g of fresh tubers to a constant weight in an oven at 80 °C for 24 h, with calculation according to Zihin *et al*. (2011) below.

$$DMC\ (\%) = \frac{\text{dry weight of tubers}}{\text{fresh weight of tubers}} \times 100$$

Estimation of variance components

The genotype by environment (G × E) model estimated the variance components of environmental, phenotypic, and genotypic variance. The G × E phenotypic variance component model followed the work of Acquaah (2012).

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Genotypic variance $(\sigma^2 g) = (Mse - Mst)/r$

Environmental variance $(\sigma^2 e) = Mse$)

Where,
Mse = Mean square error
Mst = Mean square treatment
r = replication

The estimates of genotypic (GCV) and phenotypic coefficient of variation (PCV) calculation used the procedure outlined by Boney *et al*. (2014).

$$PCV = \sqrt{\frac{\sigma^2 p}{\bar{x}}}\ 100 \qquad GCV = \sqrt{\frac{\sigma^2 g}{\bar{x}}}\ 100$$

Where,
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance
$\bar{x}$ = grand mean

Estimation of heritability (broad sense)

Expressing the broad sense of heritability as the percentage of the ratio of the genotypic variance (g) to the phenotypic variance (p) had the genotype mean estimated as described by Boney *et al*. (2014).

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
H^2 = broad sense heritability (in percentage)
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance

Estimation of genetic advance

Calculations of the genetic advance (GA) and percentage of the mean (GAM), assuming the selection intensity at 5%, used the formula suggested by Boney *et al*. (2014):

$$G_a = \frac{(K)\left(\sqrt{\sigma^2 p}\right)(\sigma^2 g)}{\sigma^2 p} \qquad GAM = \frac{G_a}{\bar{x}}\ x\ 100$$

Where,
G_a = Expected genetic advance
K = Selection differential (2.06 at 5% selection intensity)
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 g$ = Genotypic variance
$\bar{x}$ = grand mean of a character

Statistical analysis

All standardized data underwent the analysis of variance (ANOVA) for all the agronomic traits to test the variation among the sweet potato genotypes. The analysis of variance calculation used the Statistical Analysis System (SAS) software version 9.2 (SAS, 2008). The probability levels at 5% of the treatment means' assessment used the Tukey's Studentized Range (HSD) Test (Ahmed and Huck, 2017; SAS, 2008).

RESULTS

Genetic variability in sweet potato genotypes

Results showed a wide variability among the studied sweet potato genotypes and the individual plants of the same genotype for tuber yield. The results suggested that many factors influence the phenotypic traits, such as the planting material's genetic makeup, and their propagation origin and environmental features.

The means, ranges, coefficients of variation (CV), and standard deviations of 39 sweet potato genotypes appear in Table 2. The results revealed that the trait storage root diameter showed the smallest range varied from 1.90 to 7.90 cm, with a mean value of 4.70 ± 0.13 cm. The storage root yield per plant showed the largest range (51.00–1680.00 g plant^{-1}) with a mean value of 718.65 ± 35.98 g. Following the said trait were the individual storage root weight (ranging from 32.00 to 391.00 g with a mean value of 178.88 ± 7.00 g) and the harvest index plot^{-1}

Table 2. Estimations of means, ranges, coefficient of variation (CV%), standard error, and standard deviation in sweet potato genotypes for various agronomic traits evaluated in MARDI, Bachok, Kelantan, Malaysia.

Character	Mean	Range		CV (%)	Std Error	Std Dev.
		Max	Min			
Plants per plot	53.51	60.00	33.00	11.09	0.55	5.93
Storage root length (cm)	16.90	28.65	8.04	19.92	0.31	3.37
Storage root diameter (cm)	4.70	7.90	1.90	29.75	0.13	1.40
Individual storage root weight (g)	178.88	391.00	32.00	42.33	7.00	75.72
Storage root yield plant^{-1} (g)	718.65	1680.00	51.00	54.16	35.98	389.20
Yield plot^{-1} (kg)	37.67	86.73	6.42	47.07	1.64	17.73
Yield ha^{-1} (t ha^{-1})	20.93	48.18	3.57	47.07	0.91	9.85
Fresh weight plot^{-1} (kg)	65.52	157.20	27.60	34.47	2.09	22.58
Harvest index plot^{-1} (%)	59.16	172.50	9.07	40.96	2.24	24.23
DMC marketable root (%)	30.91	49.22	19.37	18.42	0.53	5.70

(varied from 9.07% to 172.50% with a mean value of 59.16% ± 2.24%). Yield ha^{-1} and above-ground fresh weight have approximately identical ranges, ranging from 3.57 to 48.18 t ha^{-1} and 9.20 to 52.40 kg, respectively. However, the rest of the traits displayed small scales. The recorded lowest (<29%) coefficients of variation (CV) values came from the traits, viz., the number of plants plot^{-1} (11.09%), storage root length (19.92%), and dry matter content of marketable root (18.42%) indicating relatively high stability. The observed higher CV (>30%) showed for the traits of storage root diameter (29.75%), individual storage root weight (42.33%), storage root yield plant^{-1} (54.16%), root yield plot^{-1} (47.07%), tuber yield ha^{-1} (47.07%), above-ground fresh weight plot^{-1} (34.47%), and harvest index plot^{-1} (40.96%).

Mean performance of sweet potato genotypes

The results showed a wide range of mean performance of sweet potato genotypes for growth and yield-related traits, except a few ones exhibiting narrow mean ranges of variation among the genotypes (Table 3). The sweet potato genotypes did not differ significantly ($P < 0.05$) for the number of harvest plants per plot. The highest and same number of plants in plot^{-1} (60) resulted in genotypes MIb8 and MIb12. However, the lowest number of plants in plot^{-1} (43) emerged in sweet potato genotype MIb28. Generally, the genotype's performance for growth traits was excellent till harvest and not affected by environmental conditions, such as water logging during heavy rains and pests and disease attacks, which could also reduce crop yields. The genotype MIb3 produced the longest storage roots (21.88 ± 1.85 cm), whereas the genotypes MIb39 and MIb32 produced the shortest storage roots with mean values of 10.63 ± 0.62 cm and 10.50 ± 1.62 cm, respectively. Sweet potato Genotype MIb47 had the hugest storage root diameter (6.91 ± 0.67 cm), showing significantly different from other genotypes. Although, the genotypes MIb25 and MIb28 produced the minimum storage root diameter with mean values of 2.43 ± 0.07 cm and 2.42 ± 0.38 cm, respectively. Results further revealed that the maximum storage root weight occurred in the genotypes MIb47 (382.73 ± 6.82 g) and MIb41 (357.00 ± 9.53 g). However, the lowest individual storage root weight measured 46.25 ± 10.13 g for genotype MIb28 compared with other genotypes.

The sweet potato genotypes evaluated significantly differed ($P < 0.05$) for growth and yield-related traits, i.e., storage root yield plant^{-1}, yield plot^{-1}, yield hectare^{-1}, above-ground fresh weight plot^{-1}, harvest index, and dry matter content of marketable root (%). Results further revealed a wide range of mean performances occurred among the sweet potato genotypes for storage root yield plant^{-1}. Genotype MIb47 produced the highest weight (1673.34 ± 3.85 g), followed by MIb3 (1519.67 ± 24.43 g) and MIb16 (1365.83 ± 22.09 g). Meanwhile, the genotypes MIb28 (69.78 ± 3.66 g) and MIb25 (67.84 ± 9.72 g) produced the lowest storage root yield plant^{-1}. The maximum yield plot^{-1} resulted in the genotype MIb3 (79.66 ± 4.08 kg), followed by MIb16 (72.71 ± 3.76 kg). Contrastingly, genotype MIb17 displayed the lowest yield plot^{-1} (6.89 ± 0.33 kg).

In the case of yield ha^{-1}, a similar trend also surfaced, with genotype MIb3 producing the highest yield (44.25 ± 2.27 t ha^{-1}), followed by MIb16 (40.39 ± 2.09 t ha^{-1}), but the lowest showing in the genotype MIb17

Table 3. Mean values for agronomic traits in sweet potato genotypes evaluated in MARDI, Bachok, Kelantan, Malaysia.

No.	Genotypes	PP	SRL (cm)	SRD (cm)	ISRW (g)	SRYP (g)	Yield plot^{-1} (kg)	Yield (t ha^{-1})	FWP (kg)	HIP (%)	DMC (%)
1	MIb-01	58.00	18.13	4.54	156.13	630.00	49.93	27.74	82.13	61.21	31.14
2	MIb-02	54.00	18.51	4.82	158.22	837.44	42.71	23.73	76.14	56.16	33.80
3	MIb-03	54.00	21.88	3.51	133.53	1519.67	79.66	44.25	83.25	95.63	34.23
4	MIb-08	60.00	18.25	6.05	254.20	1088.33	71.70	39.83	86.40	83.40	27.43
5	MIb-09	56.00	20.47	4.45	161.33	1078.34	40.78	22.66	85.60	48.06	28.40
6	MIb-10	54.00	19.05	2.68	67.27	253.89	15.59	8.66	36.60	43.53	34.03
7	MIb-11	52.00	14.02	5.79	150.50	651.67	48.46	26.92	68.00	70.78	20.77
8	MIb-12	60.00	19.22	5.97	263.93	976.67	58.08	32.27	75.03	77.25	39.61
9	MIb-14	55.00	20.49	4.65	194.63	1257.08	41.82	23.23	63.80	65.87	35.24
10	MIb-16	57.00	17.73	4.79	168.60	1365.83	72.71	40.39	91.70	79.19	35.45
11	MIb-17	56.00	19.99	3.67	89.81	158.66	6.89	3.81	51.80	14.59	23.57
12	MIb-19	55.00	18.52	5.65	216.86	550.00	42.57	23.65	54.10	77.62	37.28
13	MIb-20	45.00	11.39	6.18	211.50	1040.75	46.41	25.78	56.80	83.25	25.67
14	MIb-22	44.00	18.18	3.79	146.67	274.33	36.42	20.23	50.60	72.52	20.80
15	MIb-23	59.00	14.62	5.33	172.63	423.44	21.11	11.73	50.20	42.95	39.30
16	MIb-24	53.00	16.09	3.04	75.60	428.50	21.99	12.22	56.00	41.49	39.54
17	MIb-25	50.00	18.92	2.43	79.59	67.84	36.81	20.45	49.40	76.05	32.81
18	MIb-26	55.00	17.50	3.75	120.90	716.66	23.98	13.32	81.80	30.05	39.69
19	MIb-27	53.00	16.89	3.97	135.73	554.83	27.37	15.20	72.40	43.60	21.40
20	MIb-28	43.00	14.37	2.42	46.25	69.78	23.16	12.87	39.60	59.35	34.11
21	MIb-29	57.00	15.97	6.36	205.10	1268.33	55.26	30.70	73.40	75.33	24.43
22	MIb-30	56.00	16.48	6.04	266.87	650.00	28.53	15.85	44.60	65.70	35.52
23	MIb-31	53.00	16.58	3.66	153.53	641.45	23.28	12.93	46.40	53.73	31.96
24	MIb-32	46.00	10.50	6.19	226.40	464.00	21.58	11.99	42.70	51.65	24.86
25	MIb-33	54.00	14.97	3.50	96.83	436.13	21.35	11.86	45.00	50.21	25.92
26	MIb-34	56.00	15.81	4.69	215.55	350.52	28.74	15.97	103.80	28.31	31.50
27	MIb-35	46.00	14.71	3.47	76.97	284.22	12.69	7.05	44.20	31.44	31.37
28	MIb-36	52.00	15.00	4.89	229.33	714.67	30.09	16.72	84.60	36.25	33.83
29	MIb-37	59.00	18.57	4.54	238.50	861.48	46.83	26.02	75.40	64.59	31.30
30	MIb-38	53.00	17.46	3.89	173.30	456.45	19.65	10.92	46.00	43.46	31.74
31	MIb-39	55.00	10.63	5.41	164.60	1101.62	32.44	18.02	94.40	34.58	29.00
32	MIb-40	57.00	13.21	6.58	199.07	1160.00	56.97	31.65	87.00	95.73	28.16
33	MIb-41	55.00	15.60	6.44	357.00	643.33	38.11	21.17	93.50	40.55	30.49
34	MIb-42	53.00	21.05	4.27	141.87	546.44	29.72	16.51	58.00	51.46	30.25
35	MIb-43	53.00	18.91	4.47	221.70	691.55	43.57	24.30	56.20	78.83	28.93
36	MIb-44	56.00	15.27	6.16	310.33	652.65	38.42	21.34	50.80	80.86	26.12
37	MIb-45	50.00	17.45	4.30	187.63	897.60	51.61	28.67	81.60	64.83	30.80
38	MIb-46	56.00	17.93	3.72	125.07	586.56	22.68	12.60	50.40	47.25	39.59
39	MIb-47	52.00	18.83	6.91	382.73	1673.34	59.38	32.99	66.00	89.89	25.45
	Mean	53.51	16.90	4.69	178.88	718.65	37.67	20.93	65.52	59.16	30.91
	S.E	0.54	0.31	0.13	7.00	35.98	1.64	0.91	2.08	2.24	0.53

Plants per plot (PP); storage root length (cm) (SRL); storage root diameter (mm) (SRD); individual storage root weight (g) (ISRW); storage root yield per plant (g) (SRYP); yield per plot (kg) (Yield P); yield per hectare (t/ha) (Yield ha^{-1}); fresh weight per plot (kg) (FWP); harvest index per plot (%) (HIP); dry matter content of marketable root (%) (DMC).

(3.81 ± 00.18 t ha^{-1}). The present findings were consistent with previous studies of Demelie and Aragaw (2016), who found a similar pattern in storage root yield traits, comparable to yield plot^{-1} and yield ha^{-1}, with the newly released sweet potato cultivar 'Maé' producing the highest yield. Nonetheless, the genotypes values for various traits were greater than those of Zihin *et al*. (2011), who planted the local Turkish cultivar 'Hatay Kirmizi' (yielded 302.9 g storage root yield per plant and 8.1 t ha^{-1}) and 'Fongsu' from China (yielded 504.8 g storage root yield plant^{-1} and 14.4 t ha^{-1}).

Genotype MIb34 produced the maximum value for above-ground fresh weight plot^{-1} (103.80% ± 12.60%), whereas the minimum value came from MIb10 (36.60% ± 3.40%). Genotypes MIb40 and MIb3 had the highest mean values for the harvest index plot^{-1} (95.73 ± 39.88 kg and 95.63 ±0.62 kg, respectively). Sweet potato genotype MIb26 (39.69% ± 0.50%) had the supreme mean value for dry matter content (DMC) of marketable roots showing significantly different from three other genotypes, viz., MIb12 (39.61% ± 0.84%), MIb46 (39.59% ± 0.17%), and MIb24 (39.54% ± 0.55%). The said genotypes for processing traits were also associated with the best agronomic traits. The high dry matter content of marketable roots is one of the most relevant factors influencing sweet potato consumer preferences and industrial use (Cervantes-Flores *et al.,* 2011; Rukundo *et al.,* 2013). However, the farmer's preference for the root dry matter content is >25% (Mbah and Eke-Okoro, 2015).

Genetic variance

The analysis of variance revealed that sweet potato genotypes showed significant ($P < 0.01$) differences for nine agronomic traits, except for the number of plants per plot (Table 4). The homogeneity of agronomic traits among all potential sweet potato genotypes could be assured at a confidence level of 95% (α=0.05).

Table 4. Analysis of variance for agronomic traits in sweet potato genotypes evaluated in MARDI, Bachok, Kelantan, Malaysia.

Source of Variation	PP	SRL (cm)	SRD (cm)	ISRW (g)	SRYP (g)	Yield plot^{-1} (kg)	Yield (t/ha)	FWP (kg)	HIP (%)	DMC (%)
Genotype	54.45	21.98**	4.50**	17207.54**	460077.24**	879.03**	271.28**	1014.14**	1228.28**	86.50**
Rep	15.08	5.73	1.19	50.97	575.26	5.63	1.73	145.82	211.53	4.52
Error	26.13	6.15	0.69	146.04	1146.55	40.24	12.42	267.57	276.39	6.14

**Significant level at $P < 0.0001$, plants per plot (PP); storage root length (cm) (SRL); storage root diameter (mm) (SRD); individual storage root weight (g) (ISRW); storage root yield per plant (g) (SRYP); yield per plot (kg) (Yield P); yield per hectare (t/ha) (Yield H); fresh weight per plot (kg) (FWP); harvest index per plot (%) (HIP); dry matter content of marketable root (%) (DMC).

Table 5. Components of variance, heritability (broad sense), genetic advance, and genetic advance (%) for agronomic traits in sweet potato genotypes evaluated in MARDI, Bachok, Kelantan, Malaysia.

Traits	σ^2p	Σ^2g	σ^2e	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (G.A.)	G.A (%)
Plants per plot	35.57	9.44	26.13	17.22	33.43	26.54	3.26	18.28
Storage root length (cm)	11.42	5.27	6.15	13.58	20.00	46.15	3.21	19.01
Storage root diameter (cm)	1.96	1.27	0.69	24.03	29.85	64.80	1.87	39.84
Individual storage root weight (g)	5833.24	5687.20	146.04	42.16	42.70	97.50	153.39	85.75
Storage root yield plant^{-1} (g)	154123.40	152976.90	1146.50	54.42	54.63	99.26	802.71	111.70
Yield plot^{-1} (kg)	319.84	279.60	40.24	133.13	142.39	87.42	32.21	256.42
Yield ha^{-1} (t ha^{-1})	98.71	86.29	12.42	44.38	47.47	87.42	17.89	85.48
Fresh weight plot^{-1} (kg)	516.43	248.86	267.57	72.23	104.05	48.19	22.56	103.29
Harvest index plot^{-1} (%)	593.70	317.30	276.40	30.11	41.19	53.44	26.83	45.34
DMC marketable root (%)	32.93	26.79	6.14	16.75	18.57	81.35	9.62	31.11

Table 5 presents the estimations for genetic variance components including phenotypic (σ^2p), genotypic (σ^2g), and environment (σ^2e) variances, genotypic (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h^2), genetic advance (GA), and per cent of the mean (GAM) for 10 agronomical traits in 39 sweet potato genotypes. The phenotypic variance (σ^2p) values ranged from 1.96 to 154123.40, while the genotypic variance (σ^2g) values ranged from 1.27 to 152976.90 for various traits, which revealed that the phenotypic variance exhibited higher values than a genotypic variance. The storage root yield plant^{-1} exhibited the highest phenotypic and genotypic variances of 154123.40 and 152976.90, respectively. Following this was the individual storage root weight with a phenotypic and genotypic variance value of 5833.24 and 5687.20, respectively. However, the lowest recorded phenotypic and genotypic variances occurred for the trait storage root diameter (1.96 and 1.27, respectively).

Among various growth and yield-related traits, the genotypic coefficient of variance (GCV) ranged from 13.58% to 133.13%, with the values for the phenotypic coefficient of variance (PCV) ranging from 18.57% to 142.39% (Table 5). Both genotypic and phenotypic coefficients of variations were the highest for yield plot^{-1} (133.13% and 142.39%, respectively), followed by above-ground fresh weight plot^{-1} (72.23% and 104.05%, respectively). In addition to these two traits, observed higher magnitudes of GCV and PCV (>20%) showed for storage root yield plant^{-1} (54.42% and 54.63%), yield ha^{-1} (44.38% and 47.47%), individual storage root weight (42.16% and 42.70%), harvest index plot^{-1} (31.11% and 41.19%), and storage root diameter (24.03% and 29.85%), respectively. However, the estimates of GCV and PCV were moderate for dry matter content of marketable roots (16.75% and 18.57%) and storage root length (13.58% and 20.00%). Low estimated values of GCV (17.22%) and medium values of PCV (33.43%) emerged in the number of plants plot^{-1}. Overall, the PCV values displayed greater than GCV values for all traits except the number of plants in plot^{-1}. It indicates a wide range of genetic variability among the sweet potato genotypes for growth and yield-related parameters.

Heritability (bs) and genetic advance

In this study, the highest heritability (broad sense) recording showed for the traits, storage root yield plant^{-1} (99.26%), individual storage root weight (97.50%), yield plot^{-1} (87.42%), yield ha^{-1} (87.42%), and dry matter content of marketable root (81.35%) (Table 5). The storage root diameter had moderately high heritability (64.80%), and the traits, harvest index plot^{-1}, above-ground fresh weight plot^{-1}, and storage root length gave medium heritability values, i.e., 53.44%, 48.19%, and 46.15%, respectively. The low value of heritability (bs) observed for the trait, the number of plants plot^{-1} scored 26.58%.

The highest estimates of genetic advance (GA) and genetic advance as a percentage of the mean (GAM) resulted for the traits of storage root yield plant^{-1} (802.71% and 111.70%, respectively) and individual storage root yield plant^{-1} (153.39% and 85.75%, respectively). The same trend also occurred for yield plot^{-1} (32.21%), harvest index plot^{-1} (26.83%), and above-ground weight plot^{-1} (22.56%). It indicates that selection made from the top 5% of genotypes could cause significant advancement and improvement of 256.42%, 45.34%, and 103.29% for those traits, respectively. A moderate estimate of GA appeared for yield ha^{-1} (17.89%), whereas the GAM was high with a value of 85.48%. In contrast, low estimates of GA emerged for the traits, viz., dry matter content of marketable roots (9.62%) and storage root diameter (1.57%); however, the GAM values were high (31.11% and 39.84%), respectively. On the other hand, the lowest estimates of GA and GAM showed for the number of plants plot^{-1} (3.26% and 18.28%, respectively) and storage root length (3.21% and 19.01%, respectively).

DISCUSSION

For crop improvement, knowledge of genetic diversity, heritability, quantitative traits association, and crop yield is crucial (Dewi *et al.,* 2019). Results of the current study demonstrated that the materials of sweet potato genotypes evaluated possessed a high level of homogeneity. These results follow the findings of Gehan (2019) that the original population exhibited high variability based on estimated coefficients of variation for storage root length; however, the storage root diameter had low coefficients of variation in sweet potato genotypes. Similarly, the local Nigerian cultivar had the highest coefficient of variation, followed by three other cultivars of sweet potato, i.e., 'Abbies,' 'Mabrouka,' and 'Beauregard' (Gehan, 2019).

Tuber size and shape are prominent agronomic traits for cultivar selection used in tubers processing sweet potatoes (Kathabwalika *et al*., 2013). In sweet potatoes, the size and shape of the tubers influenced the peeling and trimming efficiency during processing (Oke and Workneh, 2013). Furthermore, storage root length, diameter, and shape are the most significant parameters in the post-harvest processing systems of sweet potatoes (Truong *et al*., 2018). Nonetheless, the marketable size may vary between countries. In the United States, Brandenberger *et al*. (2017) stated that the ideal size for marketable tubers in sweet potatoes had the category of U.S. Extra No. 1, where the length should not measure less than three inches (7.62 cm) or more than nine inches (22.86 cm), with the maximum weight, not more than 510 g, the maximum diameter not more than 8.26 cm, and the minimum diameter not less than 4.45 cm. Rosnani *et al.* (2017) stated that the market basis for sweet potatoes in Malaysia relies on the tuber weight, which is cultivar dependent. For example, in the sweet potato cultivar 'Anggun,' purple sweet potatoes weighing more than 250 g are grade A category, tubers weighing 100 to 250 g are grade B class, and less than 150 g are grade C class. Aside from tuber quality, defects and uniformity of size and shape are crucial marketing criteria in sweet potatoes (Rosnani *et al.,* 2017). Meanwhile, the root dry matter content preference for industrial purposesis >30% suitable for flour production (Rukundo *et al*., 2013).

Badu *et al.* (2017) mentioned that in orange flesh sweet potato genotypes, the mean value for storage root per plant was 5.84 g, with a yield of only 4.91 t ha^{-1}. Compared with those studies, the current study demonstrated twice the ongoing efforts to improve yield-related traits. Yahaya *et al.* (2015) stated that root yield is one of the vital aspects influencing farmers' choice and adoption. Consequently, breeders prioritize the development of high-yielding cultivars over the improvement and development of other traits. Therefore, most breeding studies focus on developing new sweet potato cultivars containing high dry matter and starch biomass, low fibre, and high pro-vitamin A (Mbah and Eke-Okoro, 2015).

According to Boney *et al*. (2014), information about genetic variability is essential for breeders to enhance the genetic improvement of crops by adopting appropriate selection methods based on the existing variability in the breeding material. Acquaah (2012) stated that the relative magnitudes of the variance components determine the genetic properties of a population. In addition, knowing the components of variance can estimate the relative importance of the various determinants of phenotypes. The phenotypic value of the quantitative traits was the expression of genetic differences among the genotypes, as well as, environmental factors and the genotypes by environment interactions. The phenotypic variance for all the traits gets partitioned into genotypic variance, G × E variance, and error variance. Only genotypic variance got compared with total phenotypic variance to understand the magnitude of the sweet potato genotype's contribution to the improvement of the open-pollinated sweet potato. Past studies also revealed that the recorded highest values of genotypic and phenotypic variance showed growth and yield-related in sweet potatoes (Thiyagu *et al*., 2013; Sharavati *et al.,* 2018; Nurul Afza *et al*., 2022).

In this study, the PCV values were greater than GCV for almost all the traits, indicating a wide range of genetic variability in the sweet potato genotypes (Table 5). All the studied characteristics provided almost identical genotypic and phenotypic coefficients of variation. Therefore, it suggested that the environment and the available broad genetic base less influenced these traits, which would be amenable to further selection. Similar findings also came from Thiyagu *et al.* (2013), where the yield and yield components of sweet potato traits studied and observed gave higher (>20%) PCV and GCV values for various traits. Tripathi *et al.* (2016) stated PCV and GCV values greater than 20% were regarded as high, while between 10% and 20% were medium and less than 10% were low. In their study, the observed results revealed that high estimates of PCV and GCV showed for the leaf area. Recording high heritability and genetic advance also took place in the leaf area, followed by dry matter and yield plant^{-1}. Therefore, their results concluded that these traits could benefit the selection of high-yielding sweet potato genotypes based on phenotypic data (Tripathi *et al.,* 2016).

In sweet potato traits, the number of tubers per plant, tuber girth, tuber yield per plant, and tuber yield per hectare resulted in high magnitudes of PCV and GCV (Table 5). These suggest a wide range of genetic variability in the germplasm for these traits and, thus, their scope for improvement through simple selection (Badu *et al*., 2017). These findings also agree with Sharavati *et al.* (2018), where the PCV was higher than GCV for leaf area, tuber weight, dry weight of vine, total tuber yield per vine, total tuber yield per plot, and marketable yield per hectare in sweet potatoes. Singh *et al.* (2018) discovered that the number of branches per vine had the highest PCV and GCV, followed by the internodal length and vine length, with the breadth of leaves having the lowest in sweet potatoes. The results also established that the studied traits had a high degree of PCV, indicating a strong connection between phenotypic and genotypic coefficients of variation, confirming these traits were not affected by the environment and that improvement can proceed.

The genetic coefficient of variance with heritability estimates would give the best picture of the genetic advance to expect from the selection. Heritability values help predict the expected progress to result through the selection process. Yadeta-Dabalo *et al.* (2020) defined heritability values as very high (≥80%), moderately high (60%–79%), medium (40%–59%), and low (≤40%). The present study results suggested that the high and moderate heritability observed for most of the traits had less impact from environmental fluctuations and instead regulated by additive gene effects that play a significant role in the expression of these traits. As a result of the selection of these traits, the accumulation of more desirable genotypes will arise. However, the rest of the attributes appear regulated by non-additive gene effects. These findings were consistent with Badu *et al.* (2017), who reported that heritability estimates above 60% are equally enough for excellent selection, and estimations (40%) considered as low via variance-covariance analysis may regard as favourable if the selection procedures are sufficiently precise. Uniformity in the agronomic traits is one of the conditions for prospective genotypes' release as superior cultivars (Budi *et al*., 2016). This analysis of variance resulted in a significant level of genetic variability among the sweet potato genotypes, which could serve to improve crop-desired traits through selection in future sweet potato breeding programs. These findings agree with previous studies of Thiyagu *et al.* (2013), Demelie and Aragaw (2016), Badu *et al*. (2017), Wiwit and Rahayuningsih (2017), and Sharavati *et al*. (2018), who reported significant differences among the sweet potato genotypes for various growth and yield-related traits. Higher CV values showed greater levels of dispersion around the mean values for various traits (Ahmed and Huck, 2017). Therefore, the obtainable results demonstrated that the used sweet potato genotypes possess a high level of homogeneity.

Similarly, Singh *et al.* (2018) discovered that the vine length, above-ground dry weight, individual storage root weight, harvest index, storage root fresh yield plant^{-1}, storage root number, vine internode length, vine internode diameter, leaf area, storage root dry matter content, and storage root fresh yield plot^{-1} in sweet potato had moderate to high heritability estimates, indicating that these traits had less influence from the environment. In contrast, Asemie and Ali (2021) reported high heritability values for most features, signifying the possibility of progress in the selection process.

Sharavati *et al*. (2018) stated that genetic advancement is crucial to find out the genetic gain likely to attain in the next generation. Genetic advances could categorize as low (≤10%), moderate (10%–20%), and high (≥20%). The success of genetic advance under selection mainly depends on genetic variability, heritability, and selection intensity. These findings revealed the presence of high heritability for all evaluated traits, accompanied by high genetic advance that affects the contribution of additive gene action. Low estimates of genetic advance and genetic advance as a percentage of the mean for the traits of storage root length demonstrate that it might be involved in non-additive gene action. These results also got support from the past findings of Madawal *et al*. (2015), who reported that the high heritability estimates (>60%), combined with high genetic gain as a percentage of the mean (>20%), indicated that heritability attributes to additive gene effects which may improve through simple plant selection methods in sweet potato. Demelie and Aragaw's (2016) findings revealed that the traits, viz., above-ground fresh weight, tuber yield per plot, and tuber yield ha^{-1} had high heritability and genetic gain. Similarly, recorded higher values of heritability and genetic gain for dry matter, yield per plant, and yield ha^{-1} in sweet potatoes occurred (Tripathi *et al.,* 2016). According to Singh *et al*. (2018), a selection is more effective in the case of high heritability traits, whereas it is difficult in the case of low heritability traits because the environment influences the genotypes in such cases. The highest estimates of genetic gain and high heritability demonstrate the potential for improvement through selection.

CONCLUSIONS

Given the high heritability and genetic gain, the storage root yield plant^{-1}, individual storage root weight, and yield ha^{-1} may prove as effective selection criteria for sweet potato improvement. The study proposed that these traits may be beneficial for selecting high-yielding sweet potato cultivars. The identified genotypes MIb3 and MIb16 are promising accessions as parental genotypes in Malaysia's breeding program for developing high-yielding sweet potato cultivars. Thus, the present findings prove valuable in the breeding program for improving cultivars and developing more genetic variations in sweet potatoes, especially in Malaysia.

ACKNOWLEDGMENTS

The authors would like to thank the Malaysian Agricultural Research and Development Institute (MARDI), Bachok, Kelantan, Malaysia, who supported and funded this research under the project "Production of Vegetables and Sweet Potato (P21003004030001)." The first author wishes to express her appreciation to the Faculty of Science and Marine Environment, University of Malaysia, Terengganu, Malaysia, for enabling her PhD studies.

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