

# Genetic Parameters of Agronomic Traits in Sweetpotato Accessions

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**Abstract.** Germplasm as a source of genes in sweetpotato breeding requires information on appearance and genetic parameters. The objectives of this research were to determine the performance and genetic parameters of sweet potato accessions. The research was conducted at Kendalpayak Research Station, Malang, East Java, Indonesia. The materials used were thirty sweet potato accessions from Indonesian Legumes and Tuber Crops Research Institute (ILETRI) germplasm collection. The research was arranged in a Randomized Block Design (RBD) with two replications. The variables observed included: the vines length, the weight of vines, the number and weight of the saleable root per plot, the number and weight of the non-saleable root per plot, the number and weight of root per plant, the root yield, the harvest index, and the dry matter content. The results of ANOVA showed a significant difference among the tested genotypes in almost all traits observed except on weight of non-saleable root. PCV estimation was higher than GCV estimation for all the observed characters. The weight of the saleable root per plot, the weight of root per plant, and the root yield that showed a wide range of PCV and GCV as well as high broad-sense heritability indicated that these traits had additive gene effect and more reliable for effective selection. The broad GCV in a population is effective for selection to obtain the superior variety.

**Key words:** Genetic Advance; Genetic Variation; Heritability; *Ipomoea batatas*; Sweet Potato

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## INTRODUCTION

Sweet potato (*Ipomoea batatas* L.) is one of the important staples food in Indonesia. It is the fourth source of carbohydrate after rice, corn and cassava. It also contain fiber, vitamins, minerals, antioxidants, and have a low glycemic content. Sweet potatoes play an important role in the supply of industrial raw materials and animal feed (Wera et al., 2014; Pradhan et al., 2015). The development and improvement of sweet potato's productivity is needed to meet those needs. Productivity improvements can be made through the breeding programs.

Breeding programs will succeed if supported by information of economic value, wide diversity, and high inheritance of the character to be corrected. Therefore, understanding the diversity of sweet potato genotypes based on agronomic traits is very important in planning sweet potato breeding programs and determining effective selection criteria (Ngailo et al., 2016; Selaocoe et al., 2019). Selection in breeding programs is the basis of all improvements to get new superior varieties. Efficient selection will be obtained by using several genetic parameters and heritability as considerations. According to Palumbo et al., (2019) and Irwan et al., (2019), wide genetic diversity is one of the conditions for an effective selection program, and selection for a desired character will be more meaningful if the character is easily inherited.

Another important component that determines the success of a variety assembly program is information about inheritance (heritability values) and characters that are positively correlated with root yields. Breeders need this information to determine their selection strategies and criteria. Studies on parameters genetic and heritability has been done by researchers. Shaumi et al., (2012); Madawal et al., (2015); Rahajeng and Rahayuningsih (2016); EL-Sharkawy (2019) reported that jumlah dan bobot umbi serta hasil umbi adalah the characters with the high and moderate heritability and genetic advance can be considered for direct selection for sweet potato improvement.

The objectives of this research were to determine the performance and genetic parameters of sweet potato accessions from the germplasm bank of Indonesian Legumes and Tuber Crops Research Institute (ILETRI). Information about the performance and genetic parameters of sweet potato accessions from this study is expected to be utilized for sweet potato breeding programs.

## METHODS

The research was conducted in February-June 2017 at Kendalpayak Research Station, Malang, East Java, Indonesia. Kendalpayak Research Station lies at 8° 2' 56.4"LS 112° 37' 30"BT with an altitude of 445

m a.s.l. The average annual rainfall was 2191 mm with a minimum/maximum mean air temperature of 17.5/30 °C. The soil was classified as Entisol and the textural class was clay with pH of 5.8.

The material used was thirty sweet potato accessions from Indonesian Legumes and Tuber Crops Research Institute (ILETRI) germplasm collection. The research was arranged in a Randomized Block Design (RBD) with two replications. Each

accession was planted on 5 m x 1 m (single row), which accommodated 20 plants (the spacing between plants was 25 cm). Fertilizer (300kg/ha of NPK Phonska) was applied at planting (2/3 dose) and 5 weeks after planting (1/3 dose). Weeding was done at 4, 7, and 10 weeks after planting. Irrigation, pest, and disease control was applied as needed. Harvesting was done after 4 months of planting.

**Table 1.** List of the sweet potato accessions from ILETRI germplasm collection

Accessions	Origin	Flesh Color	No. Accessions	Origin	Flesh Color
MLGI 0001	Probolinggo, E-Java	White	16.	MLGI 0037 Klungkung, Bali	White
MLGI 0004	Bondowoso, E-Java	White	17.	MLGI 0046 Bangli, Bali	White
MLGI 0005	Banyuwangi, E-Java	White	18.	MLGI 0047 Bangli, Bali	Yellow
MLGI 0006	Banyuwangi, E-Java	Yellow-Purple	19.	MLGI 0048 Bangli, Bali	White
MLGI 0009	Banyuwangi, E-Java	Yellow	20.	MLGI 0050 Gianyar, Bali	White
MLGI 0011	Jember, E-Java	Yellow	21.	MLGI 0057 Tabanan, Bali	White
MLGI 0012	Jember, E-Java	Yellow	22.	MLGI 0058 Tabanan, Bali	White
MLGI 0014	Lumajang, E-Java	White	23.	MLGI 0059 Tabanan, Bali	Yellow
MLGI 0018	Blitar, E-Java	White	24.	MLGI 0065 Donor BORIF	White
MLGI 0021	Kediri, E-Java	White	25.	MLGI 0066 Donor BORIF	Yellow
MLGI 0023	Kediri, E-Java	White	26.	MLGI 0070 Donor BORIF	Yellow-Purple
MLGI 0027	Buleleng, Bali	Yellow	27.	MLGI 0076 Donor BORIF	White
MLGI 0030	Karangasem, Bali	White	28.	MLGI 0077 Donor BORIF	White
MLGI 0031	Karangasem, Bali	Purple	29.	MLGI 0079 Donor BORIF	Yellow-Orange
MLGI 0035	Karangasem, Bali	White	30.	MLGI 0080 Donor BORIF	Yellow

The variables observed included: the vines length (cm), the weight of vines (kg/plot), the number of the saleable root per plot, the number of the non-saleable root per plot, the number of root per plant, the weight of the saleable root per plot (kg), the weight of the non-saleable root per plot (kg), the weight of root per plant (kg), the root yield (t/ha), the harvest index, and the dry matter content (%).

Data were analyzed by analysis of variance (ANOVA) using PKBT-STAT 1.0 program. Genetic parameter analysis (genotypic and phenotypic coefficients of variation, heritability, and genetic advances) was performed according to Syukur et al. (2009) and Demelie and Aragaw (2016). The deviation of genetic variance was used to determine the criteria of genetic variability.

## RESULT AND DISCUSSIONS

### Analysis of Variance (ANOVA) and Mean Performance of Genotypes

The ANOVA test for eleven characters showed significant differences among the genotypes for almost all characters observed except weight of the non-saleable root (Table 2). This may indicate that each accession showed a different genetic, especially for the vines length, weight of vines, number of the

saleable root per plot, the number of root per plant, the weight of the saleable root per plot, the weight of the non-saleable root per plot, the weight of root per plant, the root yield, the harvest index, and the dry matter content and also had a wide variability among genotypes.

The performance of the agronomic traits in thirty sweet potato accessions are presented in Table 3. Each trait of the accessions had a wide range of mean values. MLGI 0037 produce the highest yield, harvest index, and weight of root while MLGI 0031 showed the lowest value. The root dry matter content of thirty accessions had range between 23.64% (MLGI 0014) and 34.93% (MLGI 0006) with an average 28.70%. Dry matter content of root is a critical parameter in the selection because it can be used as an indicator of root quality. According to Kathabwalika et al., (2013), the root dry matter content indicates mealiness in the roasted or boiled sweet potato, so that it becomes an important quality parameter in the food processing industry and determines consumer preferences. The farmer preference of the root dry matter content is > 25% (Mbah and Eke-Okoro, 2015). Meanwhile for industry, the root dry matter content preference is > 30% (Rukundo et al., 2013).



**Figure 1.** Morphological diversity of leaves and tubers of sweet potato accessions

**Table 2.** Analysis of variance for 11 characters in 30 sweetpotato accessions

Characters	Mean square			CV (%)
	Block	Genotype	Error	
Vines length (VL)	545.78 <sup>ns</sup>	8,526.22 <sup>**</sup>	261.34	8.88
Weight of vines (WV)	52.45 <sup>*</sup>	15.71 <sup>*</sup>	7.18	19.67
Number of the saleable root (NSR)	2,419.35 <sup>**</sup>	328.26 <sup>**</sup>	86.94	36.16
Number of the non-saleable root (NNSR)	437.40 <sup>*</sup>	287.58 <sup>*</sup>	138.71	47.81
Number of root per plant (NRP)	3.35 <sup>*</sup>	2.88 <sup>**</sup>	0.90	32.26
Weight of the saleable root (WSR)	63.63 <sup>**</sup>	25.36 <sup>**</sup>	4.13	39.99
Weight of the non-saleable root (WNSR)	0.22 <sup>ns</sup>	0.51 <sup>ns</sup>	0.31	54.87
Weight of root per plant (WRP)	0.20 <sup>**</sup>	0.09 <sup>**</sup>	0.02	37.20
Root yield (RY)	326.01 <sup>**</sup>	141.68 <sup>**</sup>	27.95	37.22
Harvest index (HI)	0.01 <sup>ns</sup>	0.03 <sup>**</sup>	0.01	25.38
Dry matter content (DMC)	0.14 <sup>**</sup>	17.00 <sup>**</sup>	0.01	0.33

Note: \*\* significant at  $p < 0.01$ , \* significant at  $p < 0.05$ , ns= non significant

### Estimation of Genetic Variance Component

In breeding programs, selection is the main activity to obtain superior varieties. Selection will run effectively if a population with a broad genetic diversity is available. So the opportunity to get the desired traits increases.

Table 4 shows eight characters (weight of vines, number and weight of root per plant, weight of saleable and non-saleable root per plot, root yield, harvest index, and dry matter content) of eleven characters observed which had broad genotypic coefficient of variation (GCV). These results are similar to the results of a study by Badu et al., (2017) and Sharavati et al., (2018) which obtained broad GCV for weight of vines, weight of root, and root yield. Vine length and number and weight of non-saleable root per plot showed narrow GCV. In breeding program, broad GCV will expand the opportunity to improve these characters through selection, because it indicates the large amount of variation (Badu et al., 2017; Narasimhamurthy et al., 2018). A rigorous selection method should be done to select the characters with narrow GCV (Addisu et al., 2013; Kuswanto et al., 2018).

Phenotypic coefficients of variation values were higher than genotypic coefficient of variation values with slight difference values for all the observed characters. Akinwale et al., (2010) and Baafi et al., (2016)

stated that the diversity is also influenced by environmental factors besides the genetic factors. The slight difference in value between PCV and GCV shows that the influence of genetic factors is more dominant than the influence of environmental factors. The research of Demelie and Aragaw (2016) and Rahajeng and Indiaty (2018) also showed the same results, PCV values were greater than GCV with a slight difference in values. If the value of PCV and GCV has a significant difference, it means that environmental factors have a high influence.

In addition to the coefficient of variance, information about inheritance is also important to determine the criteria for efficient selection. Kuswanto et al., (2018) stated that the coefficient of variance only shows the variability of genotypes of the observed characters but does not provide information about the proportion of inheritance. Therefore, the value of heritability needs to be known to determine the pattern of inheritance. Heritability indicates the amount of influence of genetic factors or environmental factors on a character. The high heritability value shows that the character is more influenced by genetic factors. A character that has a high heritability value can be used as an effective selection criteria in the early generations (Chahal & Gosal 2010; Afuape et al., 2015; Dewi et al., 2019).

**Table 3.** Agronomic traits of thirty sweet potato accessions

No	Genotype	VL	WV	NSR	NNSR	NRP	WSR	WNSR	WRP	RY	HI	DMC
1	MLGI 0001	97.80 <sup>mn</sup>	12.55 <sup>c-h</sup>	68.00 <sup>a</sup>	38.50 <sup>a-f</sup>	6.48 <sup>a</sup>	9.82 <sup>b-d</sup>	1.92 <sup>ab</sup>	0.72 <sup>a-c</sup>	28.60 <sup>a-c</sup>	0.49 <sup>ab</sup>	29.88 <sup>cd</sup>
2	MLGI 0004	128.30 <sup>k-m</sup>	13.70 <sup>a-g</sup>	48.50 <sup>b</sup>	41.50 <sup>a-e</sup>	4.95 <sup>ab</sup>	6.95 <sup>c-f</sup>	1.45 <sup>a-d</sup>	0.46 <sup>c-e</sup>	18.47 <sup>c-e</sup>	0.38 <sup>b-d</sup>	29.49 <sup>e</sup>
3	MLGI 0005	159.90 <sup>h-k</sup>	14.20 <sup>a-g</sup>	41.00 <sup>bc</sup>	47.50 <sup>a</sup>	4.97 <sup>ab</sup>	6.19 <sup>d-h</sup>	1.89 <sup>ab</sup>	0.46 <sup>c-e</sup>	18.38 <sup>c-e</sup>	0.35 <sup>b-e</sup>	28.15 <sup>g</sup>
4	MLGI 0006	186.10 <sup>f-h</sup>	12.40 <sup>d-h</sup>	19.00 <sup>d-i</sup>	23.50 <sup>a-h</sup>	2.86 <sup>c-g</sup>	3.21 <sup>f-j</sup>	0.98 <sup>a-e</sup>	0.29 <sup>e-h</sup>	11.66 <sup>e-h</sup>	0.26 <sup>d-k</sup>	34.93 <sup>a</sup>
5	MLGI 0009	160.20 <sup>h-k</sup>	19.15 <sup>a</sup>	30.00 <sup>b-g</sup>	24.00 <sup>a-h</sup>	3.41 <sup>b-e</sup>	9.02 <sup>b-e</sup>	1.12 <sup>a-e</sup>	0.64 <sup>b-d</sup>	25.61 <sup>b-d</sup>	0.34 <sup>b-f</sup>	30.04 <sup>c</sup>
6	MLGI 0011	184.20 <sup>f-h</sup>	15.00 <sup>a-g</sup>	26.00 <sup>c-i</sup>	14.50 <sup>f-h</sup>	2.39 <sup>c-g</sup>	5.27 <sup>e-j</sup>	0.54 <sup>de</sup>	0.34 <sup>e-h</sup>	13.62 <sup>e-h</sup>	0.28 <sup>d-j</sup>	31.23 <sup>b</sup>
7	MLGI 0012	166.30 <sup>h-j</sup>	16.80 <sup>a-d</sup>	36.50 <sup>b-d</sup>	19.00 <sup>c-h</sup>	3.21 <sup>b-f</sup>	6.74 <sup>d-g</sup>	1.32 <sup>a-e</sup>	0.47 <sup>c-e</sup>	18.65 <sup>c-e</sup>	0.32 <sup>c-g</sup>	28.79
8	MLGI 0014	301.90 <sup>b</sup>	11.50 <sup>d-h</sup>	14.50 <sup>e-i</sup>	12.00 <sup>h</sup>	1.51 <sup>e-g</sup>	3.40 <sup>f-j</sup>	0.46 <sup>de</sup>	0.23 <sup>e-h</sup>	8.89 <sup>e-h</sup>	0.25 <sup>d-k</sup>	23.64 <sup>m</sup>
9	MLGI 0018	155.60 <sup>h-k</sup>	11.70 <sup>d-h</sup>	23.50 <sup>c-i</sup>	6.50 <sup>h</sup>	1.64 <sup>e-g</sup>	6.85 <sup>c-g</sup>	0.30 <sup>e</sup>	0.40 <sup>d-g</sup>	15.71 <sup>d-g</sup>	0.34 <sup>b-f</sup>	31.25 <sup>b</sup>
10	MLGI 0021	68.96 <sup>n</sup>	12.20 <sup>d-h</sup>	9.00 <sup>i</sup>	16.50 <sup>f-h</sup>	1.40 <sup>fg</sup>	1.78 <sup>j</sup>	0.62 <sup>de</sup>	0.13 <sup>gh</sup>	5.22 <sup>gh</sup>	0.16 <sup>h-l</sup>	28.15 <sup>g</sup>
11	MLGI 0023	115.30 <sup>lm</sup>	13.40 <sup>b-g</sup>	15.50 <sup>e-i</sup>	42.50 <sup>a-d</sup>	3.32 <sup>b-f</sup>	2.75 <sup>g-j</sup>	1.79 <sup>a-c</sup>	0.26 <sup>e-h</sup>	10.37 <sup>e-h</sup>	0.25 <sup>d-k</sup>	27.92 <sup>h</sup>
12	MLGI 0027	215.30 <sup>ef</sup>	16.60 <sup>a-e</sup>	14.50 <sup>e-i</sup>	15.00 <sup>f-h</sup>	2.04 <sup>d-g</sup>	1.87 <sup>ij</sup>	0.49 <sup>de</sup>	0.16 <sup>f-h</sup>	6.49 <sup>f-h</sup>	0.13 <sup>kl</sup>	33.77
13	MLGI 0030	149.20 <sup>i-k</sup>	13.00 <sup>b-g</sup>	13.50 <sup>f-i</sup>	19.00 <sup>c-h</sup>	2.01 <sup>d-g</sup>	1.84 <sup>j</sup>	0.47 <sup>de</sup>	0.14 <sup>f-h</sup>	5.71 <sup>f-h</sup>	0.15 <sup>i-l</sup>	27.76 <sup>h</sup>
14	MLGI 0031	127.80 <sup>k-m</sup>	16.50 <sup>a-f</sup>	10.50 <sup>hi</sup>	9.50 <sup>h</sup>	1.25 <sup>g</sup>	1.53 <sup>j</sup>	0.30 <sup>e</sup>	0.11 <sup>h</sup>	4.51 <sup>h</sup>	0.10 <sup>l</sup>	29.54 <sup>e</sup>
15	MLGI 0035	177.70 <sup>g-i</sup>	13.75 <sup>a-g</sup>	33.00 <sup>b-e</sup>	18.50 <sup>d-h</sup>	3.37 <sup>b-e</sup>	10.93 <sup>bc</sup>	0.90 <sup>a-e</sup>	0.76 <sup>ab</sup>	30.41 <sup>ab</sup>	0.44 <sup>a-c</sup>	24.53 <sup>k</sup>
16	MLGI 0037	264.50 <sup>c</sup>	13.70 <sup>a-g</sup>	38.50 <sup>bc</sup>	23.00 <sup>b-h</sup>	3.15 <sup>b-g</sup>	16.71 <sup>a</sup>	1.34 <sup>a-e</sup>	0.92 <sup>a</sup>	36.89 <sup>a</sup>	0.56 <sup>a</sup>	24.61 <sup>k</sup>
17	MLGI 0046	172.30 <sup>h-j</sup>	14.80 <sup>a-g</sup>	23.00 <sup>c-i</sup>	21.00 <sup>b-h</sup>	2.54 <sup>c-g</sup>	5.16 <sup>e-j</sup>	0.93 <sup>a-e</sup>	0.35 <sup>e-h</sup>	14.12 <sup>e-h</sup>	0.29 <sup>c-i</sup>	32.26
18	MLGI 0047	253.30 <sup>cd</sup>	15.20 <sup>a-g</sup>	11.00 <sup>g-i</sup>	17.50 <sup>e-h</sup>	2.09 <sup>d-g</sup>	1.88 <sup>ij</sup>	0.66 <sup>c-e</sup>	0.18 <sup>f-h</sup>	7.23 <sup>f-h</sup>	0.14 <sup>j-l</sup>	34.88 <sup>a</sup>
19	MLGI 0048	282.60 <sup>bc</sup>	13.50 <sup>b-g</sup>	19.00 <sup>d-i</sup>	14.00 <sup>gh</sup>	1.88 <sup>d-g</sup>	3.08 <sup>f-j</sup>	0.57 <sup>de</sup>	0.21 <sup>e-h</sup>	8.29 <sup>e-h</sup>	0.21 <sup>e-l</sup>	27.27 <sup>i</sup>
20	MLGI 0050	346.10 <sup>a</sup>	17.90 <sup>a-c</sup>	22.50 <sup>c-i</sup>	23.00 <sup>b-h</sup>	2.57 <sup>c-g</sup>	5.45 <sup>e-j</sup>	1.13 <sup>a-e</sup>	0.37 <sup>d-h</sup>	14.97 <sup>d-h</sup>	0.26 <sup>d-k</sup>	26.69 <sup>j</sup>
21	MLGI 0057	75.20 <sup>n</sup>	12.20 <sup>d-h</sup>	25.50 <sup>c-i</sup>	27.50 <sup>a-h</sup>	3.22 <sup>b-f</sup>	3.18 <sup>f-j</sup>	1.09 <sup>a-e</sup>	0.26 <sup>e-h</sup>	10.35 <sup>e-h</sup>	0.30 <sup>c-i</sup>	26.80 <sup>j</sup>
22	MLGI 0058	228.70 <sup>de</sup>	18.20 <sup>ab</sup>	30.50 <sup>b-f</sup>	45.00 <sup>ab</sup>	4.20 <sup>bc</sup>	2.44 <sup>h-j</sup>	1.39 <sup>a-e</sup>	0.21 <sup>e-h</sup>	8.51 <sup>e-h</sup>	0.18 <sup>g-l</sup>	29.85 <sup>cd</sup>
23	MLGI 0059	208.90 <sup>e-g</sup>	11.90 <sup>d-h</sup>	13.50 <sup>f-i</sup>	24.00 <sup>a-h</sup>	2.19 <sup>d-g</sup>	1.99 <sup>ij</sup>	0.82 <sup>b-e</sup>	0.16 <sup>f-h</sup>	6.55 <sup>f-h</sup>	0.19 <sup>f-l</sup>	29.36 <sup>ef</sup>
24	MLGI 0065	108.30 <sup>m</sup>	7.30 <sup>h</sup>	29.50 <sup>b-h</sup>	43.00 <sup>a-c</sup>	3.73 <sup>b-d</sup>	4.82 <sup>f-j</sup>	1.96 <sup>a</sup>	0.35 <sup>e-h</sup>	13.95 <sup>e-h</sup>	0.48 <sup>ab</sup>	26.06
25	MLGI 0066	162.70 <sup>h-j</sup>	16.70 <sup>a-d</sup>	30.00 <sup>b-g</sup>	21.00 <sup>b-h</sup>	2.87 <sup>c-g</sup>	3.17 <sup>f-j</sup>	0.90 <sup>a-e</sup>	0.23 <sup>e-h</sup>	9.10 <sup>e-h</sup>	0.20 <sup>e-l</sup>	29.75 <sup>d</sup>
26	MLGI 0070	213.88 <sup>ef</sup>	11.00 <sup>gh</sup>	33.50 <sup>b-e</sup>	22.00 <sup>b-h</sup>	3.14 <sup>b-g</sup>	11.29 <sup>b</sup>	1.35 <sup>a-e</sup>	0.73 <sup>a-c</sup>	29.06 <sup>a-c</sup>	0.53 <sup>a</sup>	27.13 <sup>i</sup>
27	MLGI 0076	224.60 <sup>de</sup>	11.10 <sup>f-h</sup>	19.00 <sup>d-i</sup>	8.00 <sup>h</sup>	1.76 <sup>e-g</sup>	4.55 <sup>f-j</sup>	0.30 <sup>e</sup>	0.31 <sup>e-h</sup>	12.43 <sup>e-h</sup>	0.31 <sup>c-h</sup>	24.16 <sup>l</sup>
28	MLGI 0077	141.60 <sup>j-l</sup>	7.50 <sup>h</sup>	15.00 <sup>e-i</sup>	21.00 <sup>b-h</sup>	2.17 <sup>d-g</sup>	1.80 <sup>j</sup>	0.70 <sup>c-e</sup>	0.16 <sup>f-h</sup>	6.31 <sup>f-h</sup>	0.25 <sup>d-l</sup>	28.23 <sup>g</sup>
29	MLGI 0079	219.20 <sup>e</sup>	14.10 <sup>a-g</sup>	35.50 <sup>b-d</sup>	43.00 <sup>a-c</sup>	4.30 <sup>bc</sup>	6.00 <sup>d-i</sup>	1.51 <sup>a-d</sup>	0.41 <sup>d-f</sup>	16.33 <sup>d-f</sup>	0.35 <sup>b-e</sup>	25.74
30	MLGI 0080	182.80 <sup>f-h</sup>	11.20 <sup>e-h</sup>	24.50 <sup>c-i</sup>	38.00 <sup>a-g</sup>	3.71 <sup>b-d</sup>	2.86 <sup>f-j</sup>	1.32 <sup>a-e</sup>	0.25 <sup>e-h</sup>	9.83 <sup>e-h</sup>	0.28 <sup>d-k</sup>	29.24 <sup>f</sup>
LSD 5%		33.06	5.48	19.07	24.09	1.94	4.16	1.14	0.27	10.81	0.15	0.19
Minimum		68.96	7.30	9.00	6.50	1.25	1.53	0.30	0.11	4.51	0.10	23.64
Maximum		346.10	19.15	68.00	47.50	6.47	16.71	1.96	0.92	36.88	0.57	34.93
Standard deviation		65.29	2.80	12.81	11.99	1.20	3.56	0.50	0.21	8.42	0.12	2.92
Mean		182.64	13.63	25.78	24.63	2.94	5.08	1.01	0.36	14.21	0.29	28.70

Note: Means within a column followed by the same letters are not significantly different at p<0.05 according to LSD test.

**Table 4.** Phenotypic coefficient of variation, Genotypic coefficient of variation, and genetic standard deviation of some agronomical characters of thirty sweet potato accessions

Characters	PCV	GCV	SD <sub>g</sub>	Criteria
Vines length	35.75	35.20	1083.34	Narrow
Weight of vines	20.57	15.16	2.19	Broad
Number of the saleable root	49.69	42.60	43.13	Narrow
Number of the non-saleable root	48.68	35.02	40.55	Narrow
Number of root per plant	40.79	33.82	0.38	Broad
Weight of the saleable root	70.06	64.10	3.26	Broad
Weight of the non-saleable root	49.78	31.17	0.08	Broad
Weight of root per plant	59.73	52.68	0.01	Broad
Root yield	59.25	53.08	18.34	Broad
Harvest index	42.07	34.35	0.00	Broad
Dry matter content	10.16	10.15	2.16	Broad

Note: PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation SD<sub>g</sub>= standard deviation of genotype

**Table 5.** Genotypic variance, phenotypic variance, environment variance, and heritability of some agronomical characters of thirty sweet potato accessions

Characters	$\sigma_g^2$	$\sigma_p^2$	$\sigma_e^2$	H <sup>2</sup> (%)	Criteria
Vines length	4132.44	4263.11	261.34	96.93	High
Weight of vines	4.27	7.86	7.18	54.28	High
Number of the saleable root	120.66	164.13	86.94	73.52	High
Number of the non-saleable root	74.44	143.79	138.71	51.77	High
Number of root per plant	0.99	1.44	0.90	68.71	High
Weight of the saleable root	10.62	12.68	4.13	83.71	High
Weight of the non-saleable root	0.10	0.26	0.31	38.88	Medium
Weight of root per plant	0.04	0.05	0.02	80.39	High
Root yield	56.87	70.84	27.95	80.27	High
Harvest index	0.01	0.015	0.01	81.27	High
Dry matter content	8.50	8.50	0.01	99.95	High

Note:  $\sigma_g^2$  = genotypic variance  $\sigma_p^2$  = phenotypic variance,  $\sigma_e^2$  = environment variance, H<sup>2</sup> = broad-sense heritability

In this study, heritability value showed that almost all of the characters observed have high broad-sense heritability except for the weight of the non-saleable root (Table 5). This result means that the phenotypic appearance of the other 10 characters are more influenced by genetic factors rather than by environmental factors. While the medium heritability value on the character shows that the influence of the environment and genotype is at the same level. The similar result were obtain by Dewi et al., (2019) that reported the weight of vines, number of large root, and weight of root that showed high heritability values. Root yield, harvest index, and root dry matter content also show high heritability values on study by Shumbusha et al., (2019)

High heritability coupled with broad GCV indicated that the characters had additive gene effect and more reliable for effective selection. In this study, the weight of the saleable root per plot, the weight of root per plant, and the root yield showed broad GCV and high broad sense heritability. These results are in agreement with study by Wera et al., (2014), Rahajeng and Rahayuningsih (2016), and Narasimhamurthy et al., (2018).

The broad GCV in a population is effective for selection to obtain a superior variety. PCV estimation was higher than GCV estimation for all the observed characters. Inheritance information is important to determine the criteria for efficient selection in addition to the coefficient of variance. Almost all of the characters observed have high broad-sense heritability except for the weight of the non-saleable root.

Results of this study showed that based on broad GCV dan high heritability, the weight of the saleable root per plot, the weight of root per plant, and the root yield are more reliable for effective selection. The benefit of this study are the 30 accessions can be

utilized in sweet potato breeding programs especially for characters which have a broad GCV (the weight of the saleable root per plot, the weight of root per plant, and the root yield) since they can be combined as crossing parents and used these characters as the selection criteria.

## CONCLUSIONS

The results of ANOVA showed the significant difference among the tested genotypes in almost all traits observed except on weight of non-saleable root. PCV estimation was higher than GCV estimation for all the observed characters. The weight of the saleable root per plot, the weight of root per plant, and the root yield showed a wide range of PCV and GCV as well as high broad-sense heritability that indicated these traits to have additive gene effect and more reliable for effective selection. The broad GCV in a population is effective for selection to obtain superior variety. A total of 30 accessions can be utilized in assembling varieties especially for characters which have a broad GCV value.

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