

# Agronomic performance, variance component, and diversity of sixty-two sweet potato accessions

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Manuscript received: 2 March 2016. Revision accepted: 17 November 2016.

**Abstract.** Rahajeng W, Rahayuningsih SA. 2017. Agronomic performance, variance component, and diversity of sixty-two sweet potato accessions. *Biodiversitas* 18: 95-100. Sweet potato is an alternative carbohydrate source to overcome the shortage of rice due to the impact of the global change. The objectives of this research were to determine the performance, the genotypic and phenotypic variance, and the diversity of agronomic characters of sixty-two germplasm accessions of sweet potato. The research was conducted in April-August 2013 at Muneng Research Station, Probolinggo, East Java, Indonesia. The material used was sixty-two accessions of sweet potato from Indonesian Legumes and Tuber Crops Research Institute (ILETRI) germplasm collection. The research was arranged in a randomized complete block design (RCBD) with two replications with a plot size of 1 m × 5 m and 100 × 25 cm in spacing (single row). The variables observed included: the vines length, the branch number, the chlorophyll index, the weight of the canopy, the harvest index, the storage root length, the storage root diameter, the number of the storage root per plot, the storage root yield, and dry matter content. The analysis of variance showed the high significant genotype at all the traits observed. All the traits showed a wide range of phenotypic variance and genotypic variance and high broad sense heritability. The PCA identified four principal components that explained 79.00% of total variation present in the genotypes. The traits that most contributed to the diversity were the chlorophyll index, the weight of vines, the vines length, and the branch number. The cluster analysis based on 69% similarity grouped sixty-two accessions into ten clusters, genotypes with superior traits currently on the first cluster. MLG 12695 and MLG 12505 were potentially used as a source of genes in the superior sweet potato varieties improved for the high yield potential purpose.

**Keywords:** agronomic characters, diversity, *Ipomoea batatas*, sweet potato, variance

## INTRODUCTION

Due to the increasing in population growth and the impact of climate change, the sustainability of agricultural products, especially rice, cannot be predicted. As a result, there is an anxiety that it will lead to the shortages of rice as a source of carbohydrate in Indonesian society. Therefore, alternative sources of carbohydrates other than rice are needed. Sweet potato is one of the most promising alternatives.

According FAOSTAT (2012) and Wera et al. (2014) sweet potato is an important food crop in the world after wheat, rice, maize, potatoes, barley, and cassava. Sweet potato has a high carbohydrate content and low glycemic level (Burri 2011). Besides that, sweet potato is a source of vitamin A, micronutrients (Zn, Fe, Ca, and K), as well as anti-oxidants (Aywa et al. 2013; Pradhan et al. 2015). Additionally, sweet potato has the appropriate to be used as raw materials for the food industry because it is a source of starch (Cho and Yoo 2010; Zhao et al. 2015; Trancoso-Reyes et al. 2016).

In spite of this, sweet potato has prospects and opportunities to ensure food security and industrial raw materials, in Indonesia the average yield is 16.00 t ha<sup>-1</sup> (MoA 2015), which is far beyond the potential yield of 25-30 t ha<sup>-1</sup> of fresh storage roots. This is mainly related to the choice of appropriate varieties for breeding.

Allard (1960), stated that in sweet potato breeding programs the presence of germplasm is needed. Germplasm is a provider or source of genes that necessary to assemble a new variety with a certain advantage. The success of the breeding program is largely determined by the genetic diversity as well as by key parameters related to adaptation and productivity. Therefore, these activities need information about evaluation of the economic value, estimation of genotypic and phenotypic variance, heritability value, and genetic advance on the character to be repaired, as well as the important characters (the content of nutrients and tolerance to biotic and abiotic stresses) Wera et al. 2014; Azevedo et al. 2015).

The most important activity in the sweet potato breeding program is the selection activity, the selection activity has an important role to select and determine the genotypes which are compatible with the purpose of breeding. So the success of the breeding program is determined by the effectiveness of selection activities. Tsegaye et al. (2007), argues that one of the requirements effective in the selection for new varieties improvement is wide genetic diversity, which is inherited character (high heritability), and the high value of genetic advance. High heritability value (comparison of the genetic variance and phenotypic variance) indicates that the character is easy to be inherited. While genetic advance is one of the indicators of success in plant breeding. When the value of genetic advance of certain character is a high, it means that

character improvement through selection has a great opportunity to do.

In addition to the above information, diversity information in germplasm collections also needs to be known. This diversity can be analyzed using a multivariate analysis, the analysis is frequently used principal component analysis (Principle Component Analysis) and cluster analysis (cluster analysis). Principal component analysis is a technique to determine how much a character contribute to diversity so that the results can be used to identify the characters that characterize a variety (Afuape et al., 2011). Cluster analysis based on morphological characters is used to identify the level of closeness and distance and similarity between germplasm accessions.

The objectives of this research were to evaluate the agronomic performance, genotypic and phenotypic variance, and diversity of the sixty-two accessions of sweet potato from Indonesia for breeding purpose.

## MATERIALS AND METHODS

### Study area

The experiment was conducted in April-August 2013 at Muneng Research Station, Probolinggo, East Java, Indonesia, using sixty-two accessions of a sweet potato germplasm collection of Indonesian Legumes and Tuber Crops Research Institute (ILETRI), Malang, East Java, Indonesia (include Table 1).

### Procedures

The research was arranged in a randomized complete block design (RCBD) with two replications with a plot size of 1 m × 5 m (single row). The row length was 5 m, the space between rows was 100 cm and within the row 25 cm (20 plants per row). The fertilization was done by 300 kg ha<sup>-1</sup> of fertilizer Phonska and 2 t ha<sup>-1</sup> of manure. Weeding was scheduled at four weeks, seven weeks, and ten weeks after planting when needed. The irrigation was done every 2-3 weeks or as required to prevent drought or water shortages. Pesticides applied to control pest and disease. The harvesting was conducted in next four months after planting. Data yield and yield components were recorded, including vines length, branch number, chlorophyll index, the weight of vines, harvest index, storage root length, storage root diameter, the number of storage root per-plot, storage root yield, and dry matter content.

### Data analysis

Individual parameters were analyzed by using the procedure suggested by Gomez and Gomez (1984). The phenotypic and genotypic variance were calculated by using the formula adopted by Johnson et al. (1955). The broad sense heritability was calculated by using the formula adopted by Allard (1960). Accessions diversity identified by Principal Component Analysis (PCA) to identify principal traits. Furthermore, the value of PCA will be used for cluster analysis. PCA and cluster analysis used Minitab 14 program.

## RESULTS AND DISCUSSION

### Analysis of variance and mean performance of accessions

Analysis of variance for ten traits showed the highly significant difference ( $p < 0.01$ ) among genotypes for all traits (Table 1). The performance of the agronomic traits in sixty-two sweet potato accessions is presented in Table 2. Each trait of the accessions had a wide range of mean values. Based on the observation of sixty-two sweet potato accessions, the vines length had a range between 83.08 and 283.80 cm with 178.65 cm on average, the number of branches ranged between 0.80 and 1.60 (average 1.10), the chlorophyll index varied from 29.95 to 48.05 (average 37.61), the weight of vines had a range between 1.7 and 9.9 kg per plot (average of 5.33 kg per plot).

The storage root length ranged from 5.50 to 18.15 cm with an average of 12.76 cm, and the diameter of storage root was between 3.30 and 8.60 cm (average 5.55 cm). Whereas the harvest index ranged from 0.01 to 0.65 with an average of 0.29, the number of storage root per plot ranged between 1 and 74 (average 21.46), storage root yield varied from 0.11 to 25.84 t ha<sup>-1</sup> (average 7.90 t ha<sup>-1</sup>). MLG 12505 produce the highest yield and number of storage root per plot while MLG 12707 showed the lowest value. Dry matter content is a critical parameter in the selection because it determines whether or not the storage roots are tasty. The performance of storage root dry matter content of sixty-two accessions from 21.70 to 39.58%, but there were some accessions which could not be analyzed because the storage roots did not have sufficient contents (Table 2).

### Phenotype variance, genotype variance, and heritability

All the traits observed showing the value of genetic variance and phenotypic variance with wide criteria (Table 3). The genetic variance and the phenotypic variance ranged from 0.03 to 1750.73 and 0.03 to 1771.18. The highest and the lowest values were recorded for vines length and harvest index. The value of phenotypic variance was higher than genotypic variance.

The heritability value of a character is estimated whether the character is more influenced by genetic or environmental factors. The results presented in Table 3 shows that the estimated value of the broad sense heritability was high (ranging from 51.33% to 100%) in all the traits observed.

### Principal component analysis

The results of the principal component analysis (PCA) on this research was used to reduce the observed characters into four main components that have eigenvalue up to 1.0 and was able to explain the variety of material that was tested at 79.0% (Table 4). PC1 with the eigenvalue 5.191 contributed to 41.9% of the total diversity, PC2 with the eigenvalue 1.483 contributed to 14.8% of the total diversity, PC3 with the eigenvalue of 1.175, 11.7% contributed to the total diversity, and PC4 with the eigenvalue 1.050, contributed to 10.5% of the total variation among the sixty-two accessions tested.

**Cluster analysis**

The four principal components which had the eigenvalue up to one were further used in the cluster analysis. The cluster analysis based on 69% similarity grouped sixty-two accessions into ten clusters (Figure 1).

**Discussions**

The highly significant difference ( $p < 0.01$ ) among the genotypes for all traits indicates the high variability among the accession used in this study. It also shows that each clone or the variety shows a different genetic, especially for these traits. The efficiency of the ability to assimilate usage is illustrated by harvest index. Harvest index ranged from 0.01 to 0.65, with an average of 0.29. According to Gardner et al. (1985), the harvest index showed the ratio of assimilation distribution between economic and the overall biomass. The high harvest index showed the efficiency of the assimilate material utilization. It could be seen from the high production. This was proved by MLG 12505 that presented highest harvest index (0.65), also had the highest storage root yield ( $28.90 \text{ tha}^{-1}$ ).

The heritability value of a character is estimated whether the genetic or environmental factors was more influenced the character. All the traits had high broad sense heritability with a range from 51.33% to 100%. The results are indicating that they are more influenced by genetic factors (Chahal and Gosal 2010; Naidoo et al. 2016). According to Bernardo (2002) and Afuape et al. (2015) selection will be effective on the characters that have high heritability values, so that the selection can be made in early generations because this character is inherited and the performance is relatively the same. Borojevic (1990), states that the ease of inheritance character can be known from the value of heritability. It can be estimated by comparing the magnitude of the genetic variance of the phenotypic variance. Some previous research on sweet potato showed that the predictive value of broad sense heritability was high for the number of branches, storage root weight, storage root length, storage roots diameter, harvest index, storage root yield, and storage root dry matter content (Tsegaye et al. 2007; Tumwegamire et al. 2011).

Wide genetic diversity is a requirement for the effectiveness of the process of selection because it will provide flexibility in the process of selecting a genotype (Allard 1960). Mohammed et al. (2015) stated that the character which has a broad genetic diversity would also have a wide diversity of phenotypes. Almost the same results are shown by some previous research on sweet potato. There is wide genetic diversity for the vines length, storage root number, storage root weight, storage root length, storage root diameter, harvest index, dry matter content of storage roots, and storage root yield (Fajriani et al. 2012; Solankey et al. 2015).

According to Afuape et al. (2011), within the group of genotypes, PCA is a technique to identifies which plant traits the most contributing to the observed variation. The cumulative variance of 79% by the first four axes with the eigenvalues of  $>1.0$  indicates that the identified traits within these axes exhibited great influence on the phenotype of accessions, and could effectively be used for

selection among them. In PCA, Haydar et al. (2007), states that the maximum characters that contribute to the diversity of the genetic material are traits that have the greatest value and positive feature vector. On PC1, the traits that most contributed to the diversity were the harvest index, storage root yield, and storage root diameter. On PC2, the weight of vines and vines length had a considerable influence on diversity. On PC3, the traits that contributed to diversity were the chlorophyll index and branch number, at PC4, the trait that contributed to diversity is vines length.

Afuape et al. (2011), who reported a cumulative variance of 76.00% for the first three axes in the evaluation of twenty-one sweet potato genotypes, had found stand count at harvest, unmarketable root number, and smallest root length as the important traits that distinguished the group of genotypes they worked with. Four principal components (PC) were identified which accounted for 67.22% of the total variation among the accessions (Koussao et al. 2014). Placide et al. (2015) also used PCA to study the variability among fifty-four sweet potato genotypes and found the cumulative variance of 77.83% got from the first seven principal component axes. Our findings among 79.00% were up to the variance with the findings of these authors as there was enough variability to aid the selection among the genotypes.

**Table 1.** Analysis of variance and coefficient of variance of sweet potato accessions

Traits	Mean			CV (%)
	Block	Genotype	Error	
Vines length	2.12	3.521.90**	20.45	2.53
Branch number	0.31**	0.08**	0.02	14.07
Chlorophyll index	0.71	38.00**	12.22	9.29
Weight of vines	0.04	5.79**	0.34	10.96
Harvest index	0.00	0.06**	0.00	15.05
Storage root length	1.26	17.45**	2.15	11.50
Storage root diameter	1.14	4.51**	0.88	16.94
Number of storage root per-plot	0.01	487.09**	2.73	7.70
Storage root yield	3.47	81.07**	0.99	12.78
Storage root dry matter content	0.09	187.00**	0.85	3.45

Note: \*\* significant at  $p < 0.01$

**Table 4.** Principal component analysis of sweet potato accessions

Traits	PC1	PC2	PC3	PC4
Vines length	0.133	0.619	0.202	0.169
Branch number	-0.033	-0.345	0.614	0.056
Chlorophyll index	0.100	-0.102	0.675	0.094
Weight of vines	0.035	0.658	0.257	-0.199
Harvest index	0.456	-0.167	-0.071	0.050
Storage root length	0.425	0.042	-0.059	0.018
Storage root diameter	0.438	0.038	-0.195	0.046
Number of storage root per-plot	0.426	-0.146	0.090	-0.104
Storage root yield	0.455	-0.003	0.043	0.022
Dry matter content	0.041	-0.048	0.061	-0.951
<i>Eigen values</i>	5.191	1.483	1.175	1.050
Proportion	0.419	0.148	0.117	0.105
Cumulative	0.419	0.567	0.685	0.790

**Table 2.** The mean of agronomic traits sweet potato accessions

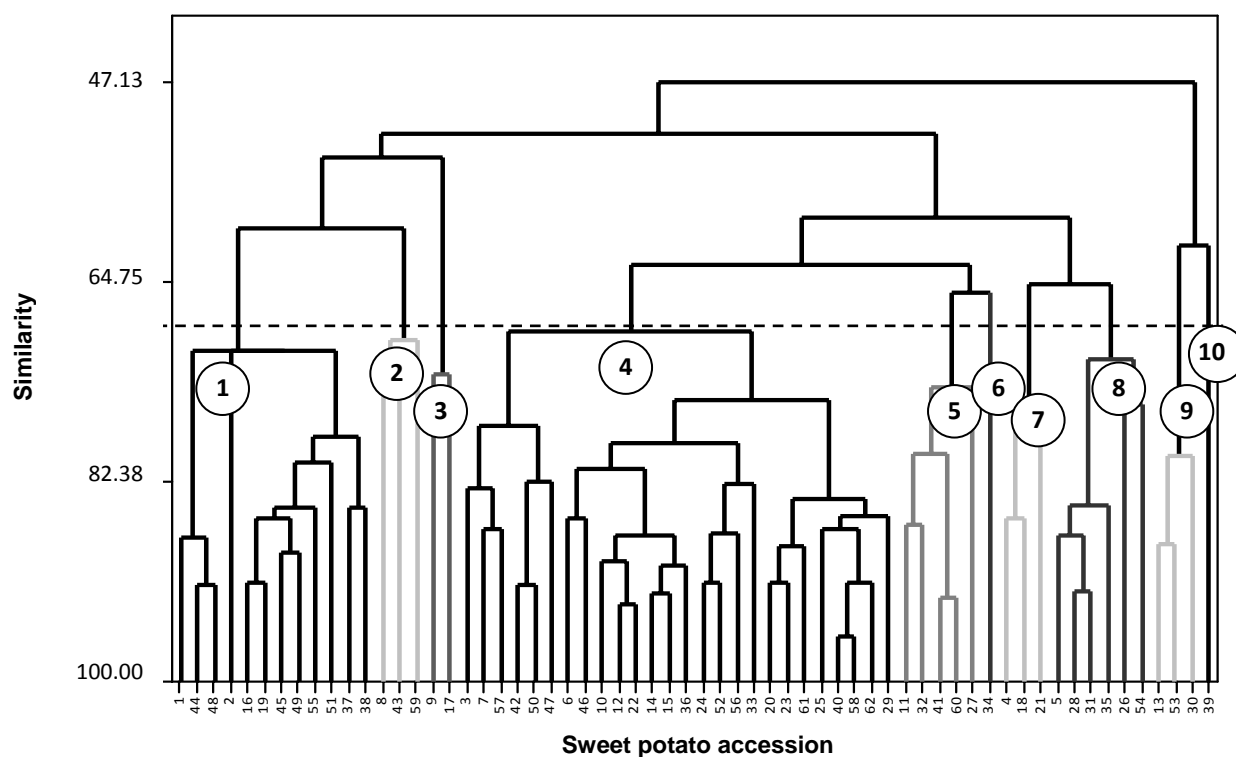
Genotype	VL (cm)	BN	CI	WV (kg)	HI	RL (cm)	RD (cm)	NRP	Y (t ha <sup>-1</sup> )	DMC (%)
MLG 12504	180.90 <sup>i-w</sup>	1.50 <sup>ab</sup>	38.55 <sup>e-p</sup>	4.55 <sup>q-x</sup>	0.52 <sup>c-g</sup>	17.25 <sup>a-c</sup>	5.10 <sup>j-u</sup>	31.50 <sup>l</sup>	18.02 <sup>bc</sup>	32.08 <sup>h-j</sup>
MLG 12505	236.40 <sup>c</sup>	1.30 <sup>a-d</sup>	40.60 <sup>b-m</sup>	4.80 <sup>o-w</sup>	0.65 <sup>a</sup>	17.65 <sup>ab</sup>	7.05 <sup>a-i</sup>	74.00 <sup>a</sup>	25.22 <sup>a</sup>	28.90 <sup>m-q</sup>
MLG 12512	195.20 <sup>k-q</sup>	1.10 <sup>c-f</sup>	34.90 <sup>k-q</sup>	7.45 <sup>c-f</sup>	0.40 <sup>i-m</sup>	16.85 <sup>a-f</sup>	6.50 <sup>c-m</sup>	30.50 <sup>fg</sup>	12.80 <sup>h-j</sup>	30.80 <sup>j-l</sup>
MLG 12514	90.80	1.10 <sup>c-f</sup>	40.65 <sup>b-m</sup>	1.65	0.40 <sup>i-m</sup>	11.10 <sup>p-y</sup>	4.65 <sup>m-u</sup>	17.50 <sup>op</sup>	6.23 <sup>r-u</sup>	30.86 <sup>l-i</sup>
MLG 12522	157.60	1.30 <sup>a-d</sup>	36.75 <sup>g-p</sup>	4.70 <sup>p-w</sup>	0.09 <sup>z</sup>	8.75 <sup>w-z</sup>	3.65 <sup>r-u</sup>	7.50 <sup>w-z</sup>	1.65 <sup>yz</sup>	30.66 <sup>l-m</sup>
MLG 12523	196.20 <sup>j-p</sup>	1.30 <sup>a-d</sup>	43.70 <sup>a-g</sup>	5.65 <sup>k-r</sup>	0.20 <sup>x</sup>	15.05 <sup>b-k</sup>	4.65 <sup>m-u</sup>	12.00 <sup>r-u</sup>	5.14 <sup>s-v</sup>	30.04 <sup>k-o</sup>
MLG 12535	226.50 <sup>de</sup>	1.00 <sup>d-f</sup>	33.60 <sup>n-r</sup>	8.75 <sup>ab</sup>	0.39 <sup>j-n</sup>	12.35 <sup>k-t</sup>	6.15 <sup>e-p</sup>	29.50 <sup>fh</sup>	13.99 <sup>fh</sup>	23.36
MLG 12540	125.00	1.20 <sup>b-e</sup>	33.60 <sup>n-r</sup>	2.90 <sup>z</sup>	0.53 <sup>b-g</sup>	10.00 <sup>z</sup>	6.55 <sup>b-l</sup>	42.00 <sup>c</sup>	12.70 <sup>h-j</sup>	30.12 <sup>k-o</sup>
MLG 12546	192.30 <sup>m-r</sup>	0.80 <sup>fg</sup>	44.85 <sup>a-e</sup>	5.55 <sup>k-s</sup>	0.46 <sup>l-j</sup>	16.75 <sup>a-g</sup>	7.30 <sup>a-g</sup>	27.50 <sup>g-k</sup>	14.67 <sup>e-h</sup>	30.84 <sup>l-l</sup>
MLG 12550	201.70 <sup>i-l</sup>	1.30 <sup>a-d</sup>	35.75 <sup>i-q</sup>	5.50 <sup>k-s</sup>	0.28 <sup>o-t</sup>	11.35 <sup>o-x</sup>	5.25 <sup>i-t</sup>	22.00 <sup>mn</sup>	8.88 <sup>m-o</sup>	35.34 <sup>c-e</sup>
MLG 12559	250.80 <sup>b</sup>	1.10 <sup>c-f</sup>	36.00 <sup>h-q</sup>	7.80 <sup>b-e</sup>	0.12 <sup>x-z</sup>	11.65 <sup>p-w</sup>	4.35 <sup>p-u</sup>	15.00 <sup>p-r</sup>	3.23 <sup>v-y</sup>	31.42 <sup>i-l</sup>
MLG 12562	193.20 <sup>l-r</sup>	0.80 <sup>fg</sup>	41.70 <sup>a-k</sup>	6.15 <sup>h-m</sup>	0.27 <sup>p-u</sup>	13.60 <sup>h-q</sup>	5.00 <sup>j-u</sup>	28.50 <sup>fi</sup>	6.60 <sup>p-s</sup>	29.72 <sup>l-p</sup>
MLG 12564	132.40	1.30 <sup>a-d</sup>	34.95 <sup>k-q</sup>	4.55 <sup>q-x</sup>	0.19 <sup>u-y</sup>	9.40 <sup>u-z</sup>	4.90 <sup>k-u</sup>	10.50 <sup>t-w</sup>	4.53 <sup>t-w</sup>	0.00
MLG 12566	188.60 <sup>p-u</sup>	1.20 <sup>b-e</sup>	36.75 <sup>g-p</sup>	7.10 <sup>d-i</sup>	0.25 <sup>q-v</sup>	14.85 <sup>b-l</sup>	5.50 <sup>g-r</sup>	13.00 <sup>ft</sup>	7.36 <sup>o-r</sup>	26.38 <sup>s-w</sup>
MLG 12576	179.70 <sup>u-x</sup>	1.20 <sup>b-e</sup>	38.05 <sup>e-p</sup>	8.75 <sup>ab</sup>	0.22 <sup>r-h</sup>	11.53 <sup>n-x</sup>	6.80 <sup>aj</sup>	18.00 <sup>op</sup>	6.07 <sup>r-u</sup>	27.90 <sup>p-t</sup>
MLG 12579	221.20 <sup>ef</sup>	1.20 <sup>b-e</sup>	39.10 <sup>d-o</sup>	4.65 <sup>p-x</sup>	0.50 <sup>d-h</sup>	16.90 <sup>a-e</sup>	5.50 <sup>g-r</sup>	56.00 <sup>b</sup>	12.79 <sup>h-j</sup>	32.14 <sup>g-j</sup>
MLG 12583	251.10 <sup>b</sup>	1.30 <sup>a-d</sup>	41.65 <sup>a-l</sup>	7.45 <sup>c-f</sup>	0.30 <sup>o-r</sup>	15.30 <sup>a-j</sup>	6.20 <sup>d-p</sup>	17.00 <sup>o-q</sup>	8.26 <sup>n-q</sup>	0.00
MLG 12584	83.00	1.30 <sup>a-d</sup>	40.50 <sup>b-n</sup>	1.70	0.22 <sup>r-v</sup>	10.10 <sup>t-y</sup>	4.20 <sup>q-u</sup>	13.00 <sup>ft</sup>	2.30 <sup>x-z</sup>	27.68 <sup>q-t</sup>
MLG 12585	150.10	1.00 <sup>d-f</sup>	42.20 <sup>aj</sup>	6.85 <sup>e-j</sup>	0.48 <sup>e-l</sup>	14.70 <sup>c-m</sup>	7.90 <sup>a-e</sup>	29.00 <sup>fh</sup>	16.52 <sup>c-e</sup>	25.80 <sup>u-x</sup>
MLG 12593	167.50 <sup>z</sup>	1.10 <sup>c-f</sup>	39.50 <sup>c-o</sup>	5.25 <sup>l-u</sup>	0.21 <sup>s-w</sup>	11.85 <sup>m-v</sup>	4.20 <sup>q-u</sup>	12.50 <sup>ft</sup>	3.72 <sup>v-x</sup>	33.66 <sup>e-h</sup>
MLG 12598	107.80	1.60 <sup>a</sup>	38.95 <sup>d-p</sup>	5.35 <sup>l-u</sup>	0.22 <sup>r-h</sup>	14.30 <sup>d-n</sup>	4.60 <sup>n-u</sup>	10.00 <sup>b-x</sup>	3.92 <sup>v-x</sup>	32.12 <sup>g-j</sup>
MLG 12603	205.80 <sup>g-l</sup>	1.10 <sup>c-f</sup>	36.15 <sup>h-q</sup>	5.95 <sup>t-o</sup>	0.31 <sup>n-r</sup>	12.00 <sup>u</sup>	5.40 <sup>h-s</sup>	24.00 <sup>lm</sup>	9.49 <sup>l-n</sup>	35.92 <sup>bc</sup>
MLG 12608	182.70 <sup>s-w</sup>	1.20 <sup>b-e</sup>	35.15 <sup>k-q</sup>	5.90 <sup>l-o</sup>	0.11 <sup>yz</sup>	11.20 <sup>p-x</sup>	3.30 <sup>u</sup>	13.00 <sup>ft</sup>	2.50 <sup>x-z</sup>	31.28 <sup>i-l</sup>
MLG 12626	234.80 <sup>cd</sup>	1.20 <sup>b-e</sup>	33.15 <sup>o-r</sup>	4.30 <sup>t-y</sup>	0.28 <sup>o-u</sup>	13.20 <sup>i-r</sup>	8.40 <sup>ab</sup>	10.00 <sup>b-x</sup>	11.09 <sup>j-l</sup>	32.84 <sup>fi</sup>
MLG 12634	126.00	1.10 <sup>c-f</sup>	33.20 <sup>o-r</sup>	5.10 <sup>l-v</sup>	0.13 <sup>w-z</sup>	10.38 <sup>r-y</sup>	5.00 <sup>j-u</sup>	15.00 <sup>p-r</sup>	3.31 <sup>v-y</sup>	29.72 <sup>l-p</sup>
MLG 12645	174.20 <sup>w-z</sup>	1.30 <sup>a-d</sup>	44.60 <sup>a-l</sup>	5.40 <sup>k-u</sup>	0.03	5.50	3.55 <sup>s-u</sup>	1.50	0.48	28.09 <sup>p-s</sup>
MLG 12650	171.10 <sup>x-z</sup>	1.10 <sup>c-f</sup>	37.15 <sup>g-p</sup>	9.90 <sup>a</sup>	0.12 <sup>x-z</sup>	6.55	3.35 <sup>u</sup>	2.00	0.68	35.57 <sup>cd</sup>
MLG 12653	159.90	1.20 <sup>b-e</sup>	34.15 <sup>m-q</sup>	3.35 <sup>yz</sup>	0.10 <sup>z</sup>	7.10 <sup>z</sup>	3.30 <sup>u</sup>	8.00 <sup>v-z</sup>	1.07 <sup>z</sup>	31.84 <sup>h-k</sup>
MLG 12655	142.50	1.20 <sup>b-e</sup>	36.90 <sup>g-p</sup>	5.45 <sup>k-t</sup>	0.12 <sup>x-z</sup>	11.80 <sup>m-v</sup>	3.40 <sup>tu</sup>	12.00 <sup>ft</sup>	3.42 <sup>v-y</sup>	21.70
MLG 12657	125.10	1.10 <sup>c-f</sup>	33.45 <sup>o-r</sup>	2.25	0.35 <sup>k-p</sup>	12.40 <sup>it</sup>	5.80 <sup>f-q</sup>	7.00 <sup>x-z</sup>	7.06 <sup>o-s</sup>	0.00
MLG 12662	97.90	1.10 <sup>c-f</sup>	37.75 <sup>l-p</sup>	3.50 <sup>x-z</sup>	0.05	14.15 <sup>d-o</sup>	5.05 <sup>j-u</sup>	2.50	0.71	27.18 <sup>q-v</sup>
MLG 12663	185.50 <sup>r-v</sup>	0.90 <sup>e-g</sup>	37.30 <sup>g-p</sup>	8.60 <sup>bc</sup>	0.13 <sup>w-z</sup>	11.75 <sup>n-v</sup>	4.45 <sup>o-u</sup>	14.00 <sup>q-s</sup>	3.02 <sup>w-z</sup>	30.82 <sup>l-i</sup>
MLG 12667	139.90	1.20 <sup>b-e</sup>	35.40 <sup>j-q</sup>	5.60 <sup>k-r</sup>	0.32 <sup>m-q</sup>	15.05 <sup>b-k</sup>	6.80 <sup>aj</sup>	19.50 <sup>no</sup>	9.38 <sup>l-n</sup>	37.66 <sup>b</sup>
MLG 12670	167.60 <sup>z</sup>	0.80 <sup>fg</sup>	29.50 <sup>qr</sup>	3.80 <sup>w-z</sup>	0.10 <sup>z</sup>	10.20 <sup>s-y</sup>	4.45 <sup>o-u</sup>	7.00 <sup>x-z</sup>	1.47 <sup>yz</sup>	35.66 <sup>cd</sup>
MLG 12675	121.00	1.30 <sup>a-d</sup>	36.25 <sup>h-q</sup>	4.40 <sup>s-y</sup>	0.07	8.95 <sup>v-z</sup>	3.50 <sup>tu</sup>	11.50 <sup>s-u</sup>	0.96	35.22 <sup>c-e</sup>
MLG 12682	199.80 <sup>i-n</sup>	1.00 <sup>d-f</sup>	45.55 <sup>a-d</sup>	6.20 <sup>g-m</sup>	0.12 <sup>w-z</sup>	13.65 <sup>h-q</sup>	5.60 <sup>g-q</sup>	5.50 <sup>z</sup>	3.35 <sup>v-y</sup>	34.32 <sup>c-f</sup>
MLG 12693	186.90 <sup>q-u</sup>	1.10 <sup>c-f</sup>	34.70 <sup>l-q</sup>	7.25 <sup>d-h</sup>	0.52 <sup>c-g</sup>	17.65 <sup>ab</sup>	7.70 <sup>a-e</sup>	48.00	19.66 <sup>b</sup>	34.78 <sup>c-e</sup>
MLG 12695	219.20 <sup>ef</sup>	1.20 <sup>b-e</sup>	36.00 <sup>h-q</sup>	8.25 <sup>b-d</sup>	0.42 <sup>h-l</sup>	17.00 <sup>a-d</sup>	8.25 <sup>a-c</sup>	25.50 <sup>ji</sup>	25.84 <sup>a</sup>	30.78 <sup>l-i</sup>
MLG 12707	218.70 <sup>ef</sup>	1.30 <sup>a-d</sup>	39.70 <sup>b-o</sup>	5.65 <sup>k-r</sup>	0.01	9.80 <sup>l-z</sup>	3.45 <sup>tu</sup>	1.00	0.11	0.00
MLG 12712	206.60 <sup>g-l</sup>	1.00 <sup>d-f</sup>	33.45 <sup>o-r</sup>	4.55 <sup>q-x</sup>	0.24 <sup>r-v</sup>	13.90 <sup>g-p</sup>	4.45 <sup>o-u</sup>	22.00 <sup>mn</sup>	3.41 <sup>v-y</sup>	26.24 <sup>t-w</sup>
MLG 12714	205.10 <sup>h-j</sup>	0.90 <sup>e-g</sup>	35.10 <sup>k-q</sup>	6.55 <sup>l-k</sup>	0.02	12.05 <sup>l-u</sup>	4.90 <sup>k-u</sup>	1.50	0.52	22.78
MLG 12725	177.40 <sup>v-y</sup>	0.80 <sup>fg</sup>	33.15 <sup>o-r</sup>	5.75 <sup>l-p</sup>	0.33 <sup>l-q</sup>	15.20 <sup>b-k</sup>	6.40 <sup>c-n</sup>	20.00 <sup>no</sup>	8.31 <sup>n-q</sup>	28.40 <sup>o-r</sup>
MLG 12726	169.00 <sup>yz</sup>	1.00 <sup>d-f</sup>	32.05 <sup>p-r</sup>	4.40 <sup>y-z</sup>	0.59 <sup>a-c</sup>	15.75 <sup>a-i</sup>	7.90 <sup>a-e</sup>	28.00 <sup>g-j</sup>	15.77 <sup>d-f</sup>	22.18
MLG 12730	157.00	1.60 <sup>a</sup>	40.85 <sup>b-m</sup>	6.00 <sup>l-n</sup>	0.56 <sup>a-e</sup>	11.75 <sup>n-v</sup>	7.10 <sup>a-i</sup>	58.50 <sup>b</sup>	17.43 <sup>cd</sup>	30.50 <sup>l-n</sup>
MLG 12731	283.80 <sup>a</sup>	1.00 <sup>d-f</sup>	42.85 <sup>a-h</sup>	4.25 <sup>u-y</sup>	0.55 <sup>b-e</sup>	14.80 <sup>b-l</sup>	6.10 <sup>e-p</sup>	38.50 <sup>de</sup>	13.45 <sup>g-i</sup>	26.16 <sup>l-w</sup>
MLG 12734	158.80	1.00 <sup>d-f</sup>	48.05 <sup>a</sup>	5.05 <sup>m-v</sup>	0.22 <sup>r-v</sup>	13.25 <sup>i-r</sup>	4.70 <sup>l-u</sup>	24.50 <sup>km</sup>	2.88 <sup>w-z</sup>	39.58 <sup>a</sup>
MLG 12738	136.20	0.60 <sup>g</sup>	32.85 <sup>o-r</sup>	5.60 <sup>k-r</sup>	0.42 <sup>h-l</sup>	12.40 <sup>it</sup>	8.60 <sup>a</sup>	25.50 <sup>ji</sup>	10.62 <sup>k-m</sup>	25.08 <sup>w-z</sup>
MLG 12739	140.70	1.30 <sup>a-d</sup>	46.50 <sup>ab</sup>	3.95 <sup>w-z</sup>	0.54 <sup>b-f</sup>	14.00 <sup>e-p</sup>	6.25 <sup>d-o</sup>	56.50 <sup>b</sup>	14.27 <sup>l-h</sup>	33.96 <sup>d-g</sup>
MLG 12747	247.40 <sup>b</sup>	1.10 <sup>c-f</sup>	40.90 <sup>b-m</sup>	3.75 <sup>w-z</sup>	0.62 <sup>ab</sup>	14.70 <sup>c-m</sup>	7.70 <sup>a-e</sup>	36.00 <sup>e</sup>	14.88 <sup>e-g</sup>	24.12 <sup>x-z</sup>
MLG 12761	214.50 <sup>fg</sup>	0.80 <sup>fg</sup>	34.75 <sup>k-q</sup>	5.75 <sup>l-p</sup>	0.29 <sup>o-s</sup>	13.95 <sup>f-p</sup>	6.10 <sup>e-p</sup>	25.00 <sup>ji-m</sup>	6.90 <sup>o-s</sup>	26.38 <sup>s-w</sup>
MLG 12762	129.10	1.00 <sup>d-f</sup>	42.40 <sup>ai</sup>	4.50 <sup>r-y</sup>	0.62 <sup>ab</sup>	16.35 <sup>a-h</sup>	7.65 <sup>a-f</sup>	43.00 <sup>e</sup>	15.83 <sup>d-f</sup>	23.88 <sup>yz</sup>
MLG 12770	201.10 <sup>i-m</sup>	1.00 <sup>d-f</sup>	37.10 <sup>g-p</sup>	3.95 <sup>v-z</sup>	0.43 <sup>h-k</sup>	13.25 <sup>i-r</sup>	5.55 <sup>g-q</sup>	25.00 <sup>ji-m</sup>	6.35 <sup>q-t</sup>	26.94 <sup>r-v</sup>
MLG 12771	197.80 <sup>j-o</sup>	1.40 <sup>a-c</sup>	34.05 <sup>m-q</sup>	4.00 <sup>v-z</sup>	0.07	10.85 <sup>q-y</sup>	4.15 <sup>q-u</sup>	6.00 <sup>yz</sup>	0.98	0.00
MLG 12780	189.30 <sup>o-t</sup>	1.20 <sup>b-e</sup>	43.70 <sup>ag</sup>	6.25 <sup>g-l</sup>	0.17 <sup>v-z</sup>	13.10 <sup>l-s</sup>	5.75 <sup>g-q</sup>	9.00 <sup>u-y</sup>	3.83 <sup>v-x</sup>	27.82 <sup>q-t</sup>
MLG 12781	181.40 <sup>l-w</sup>	0.90 <sup>e-g</sup>	39.05 <sup>d-o</sup>	5.20 <sup>l-u</sup>	0.56 <sup>a-d</sup>	18.15 <sup>a</sup>	7.20 <sup>a-h</sup>	41.00 <sup>cd</sup>	16.40 <sup>c-e</sup>	25.66 <sup>v-y</sup>
MLG 12787	191.30 <sup>n-s</sup>	0.80 <sup>fg</sup>	46.10 <sup>a-c</sup>	3.75 <sup>w-z</sup>	0.45 <sup>g-j</sup>	10.35 <sup>r-y</sup>	6.70 <sup>b-k</sup>	35.50 <sup>e</sup>	8.46 <sup>n-p</sup>	27.58 <sup>q-u</sup>
MLG 12791	213.40 <sup>l-h</sup>	0.80 <sup>fg</sup>	34.00 <sup>m-q</sup>	7.35 <sup>d-g</sup>	0.41 <sup>i-m</sup>	16.70 <sup>ag</sup>	8.05 <sup>a-d</sup>	22.00 <sup>mn</sup>	11.77 <sup>k</sup>	23.62
MLG 12792	203.70 <sup>j-k</sup>	0.90 <sup>e-g</sup>	36.85 <sup>g-p</sup>	3.70 <sup>w-z</sup>	0.13 <sup>w-z</sup>	8.60 <sup>x-z</sup>	4.10 <sup>q-u</sup>	11.00 <sup>s-v</sup>	1.52 <sup>yz</sup>	25.48 <sup>v-z</sup>
MLG 12807	131.80	1.00 <sup>d-f</sup>	26.95 <sup>r</sup>	2.90 <sup>z</sup>	0.36 <sup>k-o</sup>	11.80 <sup>m-v</sup>	5.25 <sup>i-t</sup>	26.50 <sup>h-l</sup>	4.30 <sup>u-x</sup>	28.72 <sup>n-r</sup>
MLG 12816	222.30 <sup>ef</sup>	0.90 <sup>e-g</sup>	34.65 <sup>m-q</sup>	5.70 <sup>l-q</sup>	0.06	8.80 <sup>w-z</sup>	3.50 <sup>tu</sup>	8.00 <sup>v-z</sup>	1.11 <sup>z</sup>	30.12 <sup>k-o</sup>
MLG 12825	180.90 <sup>l-w</sup>	1.10 <sup>c-f</sup>	34.40 <sup>m-q</sup>	5.05 <sup>m-v</sup>	0.22 <sup>r-v</sup>	13.40 <sup>l-q</sup>	4.80 <sup>l-u</sup>	18.50 <sup>o</sup>	3.70 <sup>v-x</sup>	33.64 <sup>e-h</sup>
MLG 12840	150.90	0.90 <sup>e-g</sup>	34.00 <sup>m-q</sup>	4.85 <sup>n-w</sup>	0.17 <sup>v-z</sup>	8.25 <sup>yz</sup>	3.60 <sup>s-u</sup>	5.50 <sup>z</sup>	2.74 <sup>w-z</sup>	23.68 <sup>z</sup>
LSD 5%	9.04	0.31	6.99	1.17	0.09	2.93	1.88	3.30	1.99	1.84

Note: Means within a column followed by the same letters are not significantly different at p<0.05 according to LSD test, VL = vine length, BN = branch number, CI = chlorophyll index, WV = weight of vines, HI = harvest index, RL = storage root length, RD = storage root diameter, NRP = number storage root per plot, Y = yield, DMC = dry matter content

**Table 3.** Criteria of variance and heritability on sweet potato accessions

Traits	$\sigma^2_p$	2 x $SD_p$	Criteria	$\sigma^2_g$	2 x $SD_g$	Criteria	H <sup>2</sup> (%)	Criteria
Vines length	1771.18	3.64	Wide	1750.73	627.52	Wide	98.85	High
Branch number	0.05	0.004	Wide	0.03	0.01	Wide	60.00	High
Chlorophyll index	25.11	2.18	Wide	12.89	7.11	Wide	51.33	High
Weight of vines	3.07	0.06	Wide	2.73	1.03	Wide	88.91	High
Harvest index	0.03	0	Wide	0.03	0.01	Wide	100.00	High
Storage root length	9.80	0.38	Wide	7.65	3.13	Wide	78.06	High
Storage root diameter	2.70	0.16	Wide	1.82	0.82	Wide	67.35	High
Number of storage root per-plot	244.91	0.49	Wide	242.18	86.79	Wide	98.89	High
Storage root yield	41.03	0.18	Wide	40.04	14.45	Wide	97.59	High
Storage root dry matter content	93.93	0.15	Wide	93.08	33.32	Wide	99.10	High

Note:  $\sigma^2_f$  = phenotypic variance,  $SD_f$  = standard deviation of phenotype,  $\sigma^2_g$  = genotypic variance,  $SD_g$  = standard deviation of genotype, H<sup>2</sup> = broad sense heritability



**Figure 1.** Dendrogram from cluster analysis of sixty two accessions

The cluster analysis grouped sixty-two accessions into ten clusters. Cluster 1 consisted of 6 accessions, each of clusters 2, 7, and 9 had 3 accessions, cluster 3 had 2 accessions, cluster 4 consisted of 26 accessions, cluster 5 had 5 accessions, each of clusters 6 and 10 had 1 accessions each, whereas cluster 8 had 6 accessions. Cluster 1 was entirely constituted by accessions mostly with superior traits in sized of storage root, chlorophyll index, harvest index, and yield. Cluster 8 was consisted accessions with inferior traits in size of storage root, harvest index, storage root number, and yield. Cluster 5 was characterized by accessions with large canopy.

Whereas cluster 4 showed little branch characteristic. Accession MLG 12695 and MLG 12505 (cluster 1) had the highest value of harvest index, the number of storage root and yield. The both accession may potentially be used as a source of genes in a superior sweet potato varieties improved for the high yield potential purpose. In the previous research of Solankey et al. (2015), Cluster analysis divided twenty genotypes into two main groups, indicating a genetic relationship among accessions. Whereas in other research, cluster analysis of 116 genotypes resulted in 12 clusters (Mohammed et al. 2015).

From the research can be concluded that the results of analysis of variance showed highly significant genotype at all the characters observed. All the characters showed a wide range of phenotypes and genotypes variety. All the characters also showed high broad sense heritability values. The PCA identified four principal components that explained 79.00% of total variation presented in the genotypes. The traits that most contributed to the diversity are chlorophyll index, weight of vines, vines length, and branch number. The cluster analysis based on 69% similarity split sixty two accessions into ten clusters, genotypes with superior traits currently on the first cluster. MLG 12695 and MLG 12505 potentially are used as a source of genes in a superior sweet potato varieties improved for high yield potential purposed.

### ACKNOWLEDGEMENTS

The authors would like to thank “Indonesian Legumes and Storage Root Crops Research Institute (ILETRI)”, Prof. Astanto Kasno as a person in charge of legumes and storage root crop germplasm research 2013, Head of Muneng Research Station and Technicians, and those who have helped this research. This research is part of the conservation and the characterization of sweet potato germplasm and financed by the state budget in 2013.

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