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Genetic and phenotypic diversity, heritability, and correlation between the quantitative characters on 30 sweet potato germplasms in Lampung, Indonesia

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Abstract. *Dewi R, Utomo SD, Kamal M, Timotiwu PB, Nurdjanah S. 2019. Genetic and phenotypic diversity, heritability, and correlation between the quantitative characters on 30 sweet potato germplasms in Lampung, Indonesia. Biodiversitas 20: 380-386.* Local food commodities such as sweet potato is an alternative rice substitute food which has high nutritional content. Estimating the value of genetic diversity, heritability and correlation between quantitative characters with the weight of large storage root per plant, is needed in the selection program for the development of quality sweet potato varieties. The purpose of this study was to find out information about genetic diversity, heritability, and correlation between quantitative characters with the weight of large storage root in 30 local Lampung sweet potato germplasm, introduction and national superior genotypes. The study was carried out in the Politeknik Negeri Lampung experimental garden from September 2017 to January 2018. Using 30 genotypes of sweet potato germplasm. The study was arranged in a randomized block design (RBD) with two replications. The results showed that all characters (weight of large storage root, number of large storage root, storage root length, storage root diameter, vines length, segment length, vines diameter, and weight of vines) had a value of genetic diversity, whereas wide phenotypic diversity and has a high value of heritability. Genetic factors more influence all characters in this study compared to environmental factors. The results of the correlation analysis showed that the characters of the weight of large storage root, storage root length, and storage root diameter were positively correlated with the weight of the storage root. Whereas, the length of vines is negatively correlated with the weight of large storage. The character of the segment length, vines diameter and weight of vines did not correlate with the weight of large storage root. The character of the segment length, vines diameter and weight of vines did not correlate with the weight of large storage root. Cluster analysis results from 30 sweet potato genotypes were grouped into 13 clusters. Based on similarity of character and provenance. The germplasm of 30 Sweet potato genotypes found in Politeknik Negeri Lampung can be selected and crossed to create the desired superior characters.

Keywords: Correlation, diversity, heritability, sweet potato

INTRODUCTION

Sweet potato (*Ipomoea batatas* L.) is an important food commodity after wheat, rice, corn, potatoes, barley, and cassava (FAOSTAT. 2012; Were et al. 2014) is an important local food for food sovereignty in Indonesia (Rahajeng and Rahayuningsih . 2017). The content of the glycemic index found in sweet potatoes is low (Burri, 2011), and a source of vitamin such as vitamin A, Zn, Fe, Ca, and K as well as antioxidants (Aywa et al. 2013; Pradhan et al. 2015).

Sweet potatoes have a very high diversity (Laurie et al. 2013). High level of genetic diversity is needed by plant breeders in assembling and creating new varieties. The more diverse breeding materials, the more diverse genes can be selected and the higher the possibility of obtaining the desired genes. Agro-morphological characteristics are an important first step in the assessment of genetic diversity in plants, including sweet potato plants (Ahiakpa et al. 2013; Amoatey et al. 2015). Genetic and phenotypic diversity are very important information during the selection of the desired character. In addition to diversity, the estimated value of heritability is also very important in knowing inheritance and the selection method used for the character to be developed (Bello 2012). Heritability is needed to assess whether certain morphological/agronomic character is influenced by genetic factors or environmental factors (Ayalneh et al. 2012). If such characters are predominantly influenced by genetic factors, heritability value will be high. Extensive genetic diversity and high heritability is an indication of the high chance of success in assembling new superior sweet potato varieties that have better potential in quality and quantity. Information about genetic diversity, heritability and character relationships between quantitative characters and crop yields are very important in crop improvement (Ritonga et al. 2018).

Lampung region has variety of local sweet potatoes spread across the capital city and sub-district districts in Lampung province. Dewi and Nurman (2015) have identified several characters these local sweet potatoes, but no information on genetic diversity and its related traits.

The purpose of this study was to assess genetic diversity, heritability, and the correlation between quantitative characters with weight of large storage root in 30 genotypes of Lampung sweet potatoes.

MATERIALS AND METHODS

The study was carried out in an experimental garden of the Politeknik Negeri Lampung, Bandar Lampung, Indonesia from September 2017 to January 2018. This study used 30 genotypes of sweet potatoes from the germplasm collections of the Politeknik Negeri Lampung (Table 1 and Figure 1).

Procedures

This study used 30 sweet potato genotypes, consisted of 24 clones, one introduced clones and fives national's superior clones (Table 1). Each genotype was planted in a mound with a size of 1m x 3 m, one cutting per planting hole. The planting distance was 100 cm x 25 cm, so that one roll had 12 plants. The experimental design used was a randomized block design (RBD) with 2 replications. The application of manure was carried out above the mounds at the time before planting, with a dose of 2 tons per ha. Plants were fertilized with 300 kg of NPK. One-third part was given at planting, and 2/3 of it was given at 1.5 months after planting. Weed control was carried out at 4, 7 and 10 weeks after planting (MST).

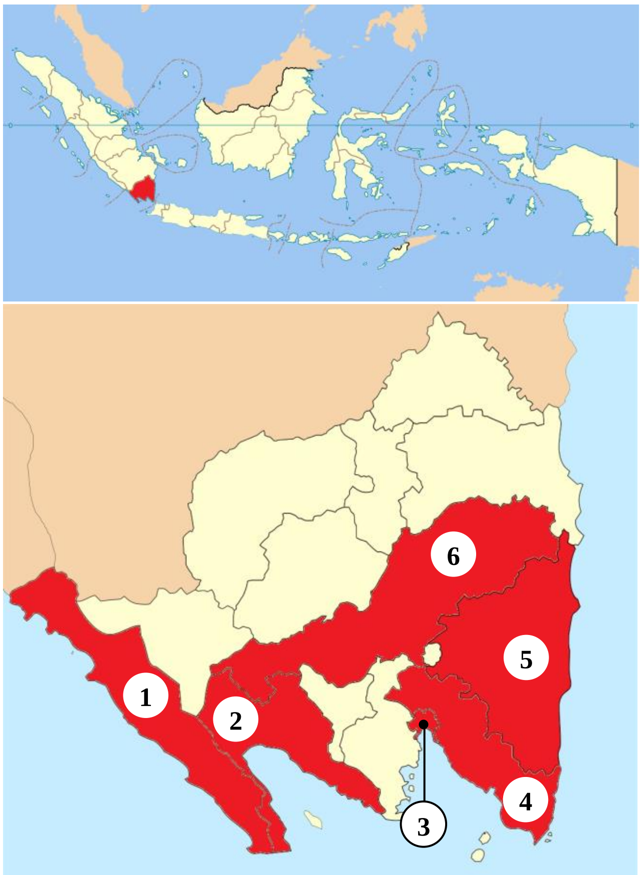

Figure 1. Study site and location of origin of Lampung's local sweet potato. 1. West Lampung, 2. Tanggamus, 3. Bandar Lampung, 4. South Lampung, 5. East Lampung, 6. Central Lampung

Table 1. List of sweet potato genotypes used in this study

Genotype	Explanation	Place of origin
LPG -01	Lampung's local	East Lampung
LPG-02	Lampung's local	Tanggamus
LPG-03	Lampung's local	Central Lampung
LPG-04	Lampung's local	South Lampung
LPG-05	Lampung's local	West Lampung
LPG-06	Lampung's local	West Lampung
LPG-07	Lampung's local	Bandar Lampung
LPG-09	Lampung's local	Bandar Lampung
LPG-10	Lampung's local	Bandar Lampung
LPG-11	Lampung's local	Bandar Lampung
LPG-12	Lampung's local	South Lampung
LPG-13	Lampung's local	South Lampung
LPG-14	Lampung's local	Bandar Lampung
LPG-15	Lampung's local	Bandar Lampung
LPG-16	Lampung's local	Bandar Lampung
LPG-17	Lampung's local	South Lampung
LPG-18	Lampung's local	South Lampung
LPG-19	Lampung's local	South Lampung
LPG-20	Lampung's local	West Lampung
LPG-21	Lampung's local	West Lampung
RD-01	Lampung's local	Bandar Lampung
RD-03	Lampung's local	Bandar Lampung
RD-04	Lampung's local	Bandar Lampung
RD-07	Lampung's local	Bandar Lampung
Aya-murasaki	Introduced	Jepang
Sari	Nasional Superiority, SK Mentan 525/Kpts/TP.240/10/2001	Balitkabi Malang
Cilembu	Nasional Superiority, SK Mentan 124/Kpts/TP.240/2/2001	West Jawa
Beta-1	Nasional Superiority, SK Mentan 2217/Kpts/SR.120/5/2009	Balitkabi Malang
Beta-2	Nasional Superiority, SK Mentan 2216/Kpts/SR.120/5/2009	Balitkabi Malang
Jago	Nasional Superiority, SK Mentan 530/Kpts/TP.240/10/2001	Balitkabi Malang

Pest and disease control was carried out at 1 and 2 months after planting. Irrigation was carried out according to conditions in the field. Harvesting was done at the age of 3 months after planting. Observations were made at the age of 3 months after planting (at harvest). The characters observed were vines length, segment length, vines diameter, weight of vines, number of large storage root, weight of large storage root, storage root length, and storage root diameter.

Data analysis

Data obtained from this study were analyzed using variance analysis and the Tukey test following Gomez and Gomez (1984). Analysis of variance and the Tukey test were used to determine the effect and differences in each quantitative character between the 30 observed sweet potato genotypes. To genetic variability (σ^2g) and phenotypic variety (σ^2f) among the genotypes was estimated by using the method of Burton and DeVane (1953). The phenotypic diversity criteria were stated broadly if the phenotypic values are equal to or greater than twice the standard deviation value. The phenotypes ($\sigma^2f \geq 2\sigma\sigma^2f$) and the phenotypic variance were narrow if the phenotypic values were equal to or less than twice of the standard deviation value of the phenotype ($\sigma^2 f \leq 2\sigma\sigma^2 f$) (Lestari et al. 2006).

The standard deviation of genetic variance and phenotype was calculated by using the formulas of Anderson and Bancroft (1952). The heritability (H) was estimated by using Petersen formula (1994). Sweet potato heritability was calculated to determine whether the characters found in sweet potatoes were influenced by genetic factors or influenced by environmental factors. The broad mean heritability was calculated by using the formula of H = ($\sigma^2 g$ / $\sigma^2 p$) x 100%. Heritability criteria were grouped by following (Petersen, 1994), i.e.: low heritability if H = <20%; moderate heritability if H = 20% - 50%; high heritability if 50% <H 100%. The correlation between quantitative characters with weight of large storage root per plant was using correlation analysis (Gomez and Gomez,1984). A cluster analysis was performed by using Minitab software version 17 to classify the level of closeness and similarity based on observed quantitative characters.

RESULTS AND DISCUSSIONS

Variety analysis and Tukey Test

The results of the variance analysis (Table 2) showed that genotypes have a very significant effect on all observed characters (vines length, segment length, vines diameter, weight of vines, number of large storage root, weight of large storage root, storage root length, and storage root diameter). The average character of vines length has a range from 55.00 cm to 292.00 cm (average 124.67 cm), segment lengths from 2.25 cm to 4.75 cm (average 3.18 cm), vines diameter from 3.25 cm to 6.25 cm (average 4.89 cm), weight of vines from 425 g to 1,625.00 g (average 940.42), the number of large storage root is greater than 0.5 storage root up to 4.5 storage root (an average of 2.17 tubers), the weight of large storage root from 40 g to 1,010.00 g (average 328.54 g), storage root length from 12.375 cm to 23.625 cm (average 16.80 cm), storage root diameter from 2.375 cm to 8.00 cm (average 5.14) (Table 3).

There is a difference between 30 sweet potato genotypes in each observed character (Tabael 3). The longest vines are found in the LPG 09 genotype (292.00 cm) and the shortest vines are found in the LPG 03 genotype (55.00 cm), the longest segment length is in the LPG 09 genotype and 07 LPG (4.75 cm) and the shortest segment is found in genotypes of LPG 01 and Jago (2.25 cm), the largest vines diameter were found in genotype LPG 12, LPG 14 and LPG 16 (6.25 mm) and the smallest vines diameter were found in the Sari genotype (3.25 mm), the heaviest weight of vines found in genotype LPG 06 (1,625.00 g) and the lightest weight of vines found in RD 07 genotype (425.00 g), the highest number of large storage root was found in LPG 03 genotype (4,50 storage root) and the smallest number of large storage root was found in genotype of LPG 14 (0.5 storage root), the heaviest weight of large storage root is found in the genotype LPG 03 (1,010.00 g) and the highest is found in the 14 LPG genotype (40.00 g), the longest storage root is in the Beta-1 genotype (23.625 cm) and the shortest was found in the 12 LPG genotype (13.25 cm), the largest storage root diameter was found in the 11 LPG (8,00 cm) genotype and the smallest found in 14 LPG genotypes (2.375 cm). This situation shows that there is significant diversity among the 30 sweet potato genotypes observed, which can be seen from the differences in each character. This supports the statement of Ahiakpa et al. (2013) and Amoatey et al. (2015) which states that agro morphological characters are the first step in the assessment of diversity in plants, including sweet potato plants.

Estimated genetic variability, phenotypic variability and heritability

The results showed that all the characters observed (vines length, segment length, vines diameter, weight of vines, number of large storage root, weight of large storage root, storage root length and storage root diameter) had extensive genetic diversity and phenotypes diversity, where the values of $\sigma^2 g \geq 2\sigma\sigma^2 g$ for genetic variability and $\sigma^2 f \leq 2\sigma\sigma^2 f$ values for various phenotypes (Table 4). The results of previous studies on sweet potatoes also revealed a wide variety of genes in the character of vines length, storage root number, storage root weight, storage root length, storage root diameter (Wahyuni et al. 2004), storage root weight, storage root number, vines length, storage root length, and storage root diameter (Fajriani et al. 2012; Solankey et al. 2015), weight of vines, storage root number, storage root weight, storage root length, storage root diameter (Rahajeng and Rahayuningsih. 2015).

Table 2. Summary of analysis of phenotypic characters of 30 sweet potato genotypes (as of Tabel 1)

Character	KT Genotype	KT Error	F- test	Coeff. of Variation
Vines length (cm)	5802.11	626.48	9.26**	20.07%
Segment length (cm)	0.94	0.26	3.61**	16.17%
Vines diameter (mm)	1.19	0.08	14.87**	5.81%
Weight of vines (g)	211372.50	58786.28	3.59**	25.78%
Number of large storage root (bulbs)	1.71	0.72	2.37**	39.19%
Weight of large storage root (g)	116113.80	12804.67	9.07**	34.44%
Storage root large (cm)	17.91	4.49	3.98**	12.62%
Storage root diameter (cm)	2.85	0.61	4.67**	15.23%

Note: ** Very significant effect at 1% level; KT = center square

Table 3. Average value of phenotypic measurements

Genotype	VL (cm)	SL (cm)	VD (mm)	WV (g)	NLS (bulbs)	WLS (g)	SL (cm)	SD (cm)
LPG-01	75.00 de	2.25 c	5.25 a-c	875.00 a-c	4.25 ab	996.30 a	18.125 a-d	7.025 ab
LPG-02	95.00 de	3.75 a-c	4.50 b-e	1.025.00 a-c	2.25 a-c	435.00 b-e	17.625 a-d	5.875 a-c
LPG-03	55.00 e	2.50 b-c	3.75 d-f	825.00 a-c	4.50 a	1.010.00 a	21.000 a-d	5.875 a-c
LPG-04	77.50 de	2.75 a-c	5.25 a-c	925.00 a-c	1.75 a-c	487.50 b-e	22.500 ab	5.875 a-c
LPG-05	120.00 b-e	3.10 a-c	5.25 a-c	1.050.00 a-c	1.25 a-c	112.50 e	14.500 b-d	3.750 cd
LPG-06	87.50 de	3.25 a-c	5.25 a-c	1.625.00 a	1.25 a-c	137.50 c-e	16.750 a-d	5.250 a-d
LPG-07	205.00 ab	4.75 a	3.50 ef	775.00 a-c	2.25 a-c	317.50 b-e	16.750 a-d	4.875 a-d
LPG-09	292.00 a	4.75 a	5.00 bc	1.200.00 a-c	2.00 a-c	232.50 c-e	13.500 cd	5.375 a-d
LPG-10	80.00 de	2.60 bc	5.50 ab	575.00 bc	4.00 a-c	702.50 ab	18.250 a-d	6.125 a-c
LPG-11	100.00 c-e	4.25 a-c	5.50 ab	675.00 a-c	2.75 a-c	582.50 a-d	16.750 a-d	8.000 a
LPG-12	105.00 b-e	2.75 a-c	6.25 a	1.325.00 a-c	1.75 a-c	95.00 e	13.250 cd	3.625 cd
LPG-13	110.00 b-e	3.25 a-c	5.25 a-c	1.050.00 a-c	2.50 a-c	242.50 b-e	14.500 b-d	5.125 a-d
LPG-14	200.00 a-c	3.25 a-c	6.25 a	1.075.00 a-c	0.50 c	40.00 e	13.500 cd	2.375 d
LPG-15	115.00 b-e	3.50 a-c	5.25 a-c	650.00 a-c	2.25 a-c	597.50 a-c	21.500 a-c	6.625 a-c
LPG-16	57.50 e	2.50 bc	6.25 a	900.00 a-c	2.25 a-c	340.00 b-e	15.250 a-d	4.500 b-d
LPG-17	64.00 e	2.60 bc	5.25 a-c	975.00 a-c	3.00 a-c	242.50 b-e	17.375 a-d	3.625 cd
LPG-18	134.50 b-e	2.75 a-c	4.75 b-d	475.00 c	2.50 a-c	287.50 b-e	20.125 a-d	6.250 a-c
LPG-19	144.00 b-e	3.10 a-c	4.25 c-f	600.00 bc	0.75 bc	145.00 c-e	14.375 b-d	4.375 b-d
LPG-20	155.50 b-e	2.60 bc	4.50 b-e	1.550.00 ab	2.00 a-c	205.00 c-e	15.125 a-d	4.625 b-d
LPG-21	96.00 de	3.10 a-c	5.25 a-c	900.00 a-c	2.50 a-c	160.00 c-e	12.375 d	4.000 b-d
RD-01	132.00 b-e	2.75 a-c	5.25 a-c	475.00 c	1.50 a-c	197.50 c-e	20.375 a-d	3.625 cd
RD-03	109.50 b-e	2.75 a-c	4.20 c-f	950.00 a-c	1.75 a-c	117.50 de	16.125 a-d	4.125 b-d
RD-04	205.00 ab	3.50 a-c	3.75 d-f	475.00 c	2.75 a-c	250.00 b-e	14.000 b-d	6.000 a-c
RD-07	95.00 de	2.75 a-c	5.25 a-c	425.00 c	1.50 a-c	190.00 c-e	4.250 b-d	4.500 b-d
Ayamurasaki	205.00 ab	4.50 ab	4.50 b-e	800.00 a-c	2.00 a-c	300.00 b-e	15.125 a-d	5.375 a-d
Sari	170.00 b-d	3.75 a-c	3.25 f	825.00 a-c	1.00 a-c	140.00 c-e	15.625 a-d	6.000 a-c
Cilembu	101.00 c-e	3.50 a-c	4.50 b-e	1.175.00 a-c	2.25 a-c	402.50 b-e	20.625 a-d	5.625 a-c
Beta-1	150.50 b-e	3.10 a-c	5.50 ab	1.425.00 a-c	2.50 a-c	347.50 b-e	23.625 a	4.625 b-d
Beta-2	97.50 c-e	3.25 a-c	4.25 c-f	1.312.00 a-c	2.00 a-c	275.00 d-e	15.875 a-d	5.125 a-d
Jago	106.00 b-e	2.25 c	4.50 b-e	1.300.00 a-c	1.50 a-c	267.50 b-e	15.375 a-d	6.125 a-c

Note: WLS = weight of large storage root; NLS = number of large storage root; SL = storage root length; SD = storage root diameter; VL = vines length; SL = segment length; VD = vines diameter; BT = weight of vines

This is an indication that the character of vines length, segment length, vines diameter, weight of vines, number of large storage root, weight of storage root, storage root length and storage root diameter in 30 genotypes used in this study, can be used for selection programme. Qosim et al. (2013) considered selection is an important step in the formation of the expected superior cultivars. The selection process will only succeed if a character has extensive genetic variability (Jalata et al. 2011). The improvement of crops is a function of diverse genetic material, the presence of diverse genetic material guarantees a higher probability of getting the desired gene in enhancing plants. Characters that have extensive genetic diversity will also have a wide variety of phenotypes as well (Mohammed et al. 2015). Extensive genetic diversity will provide flexibility in the process of selecting genotypes in the selection process, so that the selection process becomes effective (Allard 1960). This statement is supported by Sigrist et al. (2011) who stated that narrow genetic diversity can hinder the selection process, resulting in low selection efficiency, whereas Singh et al. (2012) stated that extensive genetic diversity in germplasm is a decisive factor in the development of superior crops.

The estimated heritability in 30 local Lampung sweet potato genotypes, showed high mean heritability values on all observed characters (Table 5). This shows that the influence of genetic factors is greater than the influence of the environment on the phenotypic appearance on the character of tendrils length, segment length, tendrils diameter, canopy weight, number of large tubers, bulb weight, tuber length and tuber diameter of sweet potato. In accordance with the research of Rahajeng and Rahayuningsih (2017) who reported that the character of tendrils length, crown weight, tuber length, tuber diameter and number of tubers have a broad value of heritability. The heritability of an important character is known to determine selection efficiency (Seyoum et al. 2012). The ease of inheritance can be seen from the value of heritability (Borojevic 1990). High heritability values indicate that these characters are more genetically influenced, so character selection will be effective in the early generations (Bernardo 2002; Afuape et al. 2015; Sutjahjo et al. 2015).

Table 4. Estimated values of genetic and phenotypic diversity of 30 sweet potato genotypes (as of Tabel 1)

Character	σ²g	2σσ²g	Criteria	σ²f	2σσ²f	Criteria
Vines length (cm)	2587.82	1482.30	Wide	2901.06	1473.74	Wide
Segment length (cm)	0.34	0.23	Wide	0.47	0.24	Wide
Vines diameter (mm)	0.55	0.30	Wide	0.59	0.30	Wide
Weight of vines (g)	76293.10	5726.38	Wide	105686.24	8488.89	Wide
Number of large storage root (bulbs)	0.49	0.47	Wide	0.85	0.43	Wide
Weight of large storage root (g)	51654.57	29671.72	Wide	58056.91	29492.93	Wide
Storage root large (cm)	6.70	4.69	Wide	8.95	4.55	Wide
Storage root diameter (cm)	1.12	0.74	Wide	1.43	0.72	Wide

Note: σ²g = genetic diversity, σ²f = phenotypic diversity, 2σσ²g = standard deviation of genetic diversity, 2σσ²f = standard deviation of phenotypic diversity

Table 5. Estimated value of heritability in 30 sweet potato genotypes (as of Tabel 1)

Character	Heritability (%)	Criteria
Vines length (cm)	89.00	High
Segment length (cm)	72.00	High
Vines diameter (mm)	93.00	High
Weight of vines (g)	72.00	High
Number of large storage root (bulbs)	58.00	High
Weight of large storage root (g)	89.00	High
Storage root large (cm)	75.00	High
Storage root diameter (cm)	78.00	High

Correlation analysis

The results of the correlation analysis showed that the characters of number of large storage root, storage root length, and storage root diameter were positively correlated to the character of weight of large storage root, while the character of vines length is negatively correlated with the character of weight of large storage root. Character of segment length, vines diameter and weight of vines did not correlate with weight of large storage root (Table 6). The characters that correlate and have an impact on the increase in storage root yield are the characters used for the selection of sweet potato genotypes in the program to increase sweet potato yield (Gurmu et al., 2017).

The results of similar studies were shown by previous researchers stating that the characters were positively correlated and very real with storage root yields were the number of storage root per plot, storage root weight, storage root diameter, and storage root length, while weight of vines was not correlated (Rahajeng and Rahayuningsih 2015; Gurmu et al., 2017). Kuswantoro (2017) reported that the correlation between characters is important in plant breeding programs, because it can predict an increase in a character through other characters.

Cluster analysis

The results of cluster analysis of 30 sweet potato genotypes showed that these genotypes were grouped into 13 clusters based on 80% quantitative character (Figure 2). Cluster I consists of 2 genotypes (LPG 1 and LPG 3) leading to similarity in character of the weight of large storage root, number of large storage root, storage root length, and weight of vines per plant; cluster II consists of 3 genotypes (10 LPG, LPG 11, LPG 15) leading to similarities in the character of vines diameter, weight of vines, storage root, storage root weight, and storage root diameter; cluster III consists of 3 genotypes (LPG 02, LPG 04, LPG 16) leading to similarities in the character of vines length, weight of vines, storage root number, and storage root weight; cluster IV consists of 2 genotypes (LPG 07, Ayamurasaki) leading to similarities in the character of vines length, segment length, weight of vines, storage root number, storage root weight, storage root length, and storage root diameter; cluster V consists of 2 genotypes (LPG 05, LPG 14) leading to similarities in the character of segment length, weight of vines, and storage root weight; cluster VI consists of 2 genotypes (LPG 13, LPG 17) leading to similarities in the character of vines diameter, weight of vines, number of large storage root, and weight of large storage root; cluster VII consists of 3 genotypes (LPG 21, RD 03, Sari) leading to similarities in the character of segment length, weight of vines, and number of large storage root; cluster VIII consists of 5 genotypes (LPG 18, RD 04, RD 01, RD 07, LPG 19) leading to similarities in the character of segment length, weight of vines, and number of large storage root; cluster IX consists of 2 genotypes (LPG 06, LPG 20) leading to similarities in characters of weight of vines, number of large storage root, weight of large storage root, and storage root length; cluster X consists of 1 genotype (LPG 09); cluster XI consists of 1 genotype (Cilembu); cluster XII derived from 1 genotype (LPG 12); cluster XIII consisted of 3 genotypes (Beta-1, Beta-2, Jago) leading to similarities in characters of weight of vines and number of large storage root.

Table 6. Correlation coefficient of 30 sweet potato genotypes (as of Table 1)

Characters	WLS	NLS	SL	SD	VL	SL	VD	WV
NLS	0,83062 **	1						
SL	0,55466 **	0,36392 *	1					
SD	0,66703 **	0,49084 **	0,35198	1				
VL	-0,39733 *	-0,36046 *	-0,31715 ns	-0,12477 ns	1			
SL	-0,16096 ns	-0,19520 ns	-0,17814 ns	0,18338 ns	0,68423 **	1		
VD	-0,06104	-0,04732 ns	-0,03954 ns	-0,29640 ns	-0,26715	-0,29428 ns	1	
WV	-0,23181 ns	-0,19741 ns	-0,08801 ns	-0,22036 ns	-0,00446 ns	-0,04681 ns	0,15105 ns	1

Note: ** = very real effect at 1% level; * = significant effect at the level of 5%; ns = non significant at 5% level; WLS = weight of large storage root; NLS = number of large storage root; SL = storage root length; SD = storage root diameter; VL = vines length; SL = segment length; VD = vines diameter; BT = weight of vines

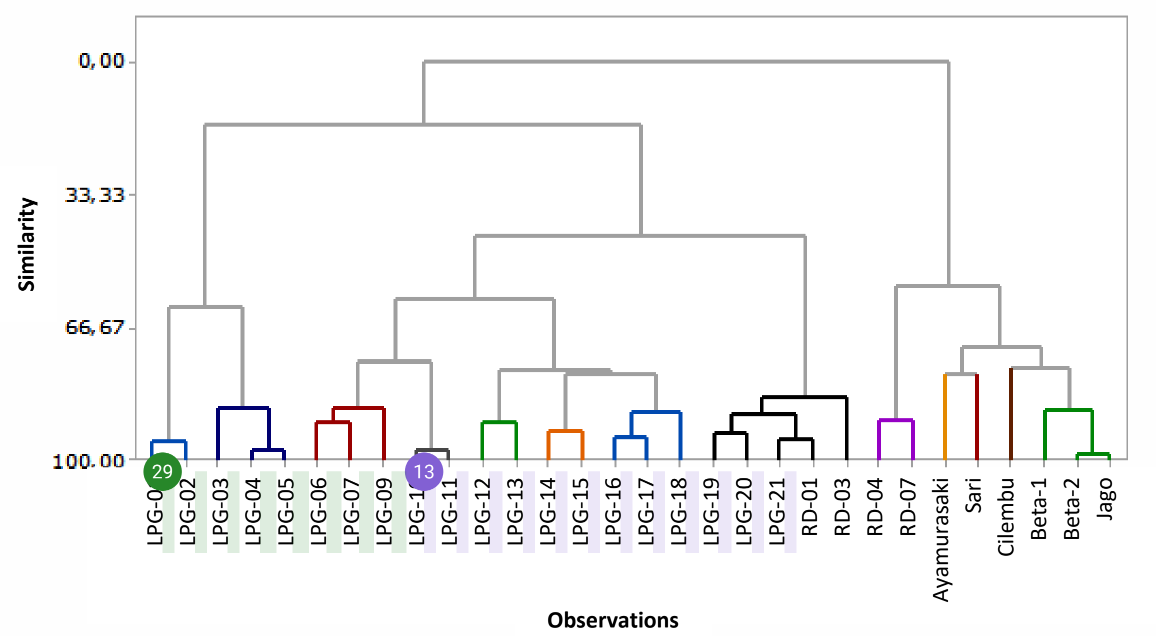

Figure 2. Dendrograms of 30 sweet potato genotypes are based on similarity quantitative characters

Genotypes that have many similarities in character, means having a close kinship relationship, while genotypes which have little or no similarity in character, means having a distant kinship relationship (Jan et al. 2012). In addition to the similarity of characters, kinship relationships can be caused due to the same place (Table 1) or close together. This can be seen from the results of research in cluster I, where LPG 01 and LPG 03 came from adjacent places (East Lampung and Central Lampung). Cluster II, where 10 LPG, 11 LPG, and 15 LPG come from one region (Bandar Lampung). Cluster V, where LPG 05 and LPG 14 come from one region (Bandar Lampung), Cluster VI, where LPG 13 and LPG 17 come from one region (South Lampung), Cluster IX, where LPG 06 and LPG 20 come from one region (West Lampung). Cluster XI, Cilembu originating from West Java has a far-reaching relationship with the local Lampung genotype, so in cluster XIII, where the Beta-1, Beta-2, and Jago genotypes come from one region (Malang, East Java) and have a distant kinship with local Lampung genotype. Genotypes which have far-reaching kinship and have superior character can be selected to be crossed in realizing the desired blend of superior characters.

It is concluded that all phenotypic characters (vines length, segment length, vines diameter, weight of vines, number of large storage root, weight of large storage root, storage root length, and storage root diameter) in 30 sweet potato genotypes found at the Politeknik Negeri Lampung have an extensive genetic and phenotypic diversity and high heritability. Genetic factors more influenced the characters found in 30 sweet potato genotypes observed in this study compared to environmental factors. These characters can be used in selecting sweet potato plants for better results in accordance with the desires of breeders. The results of the correlation analysis showed that the characters of number of large storage root, storage root lengths, and storage root diameters were positively correlated to the character of weight of large storage root, while the character of vines length is negatively correlated with the character of weight of large storage root. Character of segment length, vines diameter and weight of vines did not correlate with weight of large storage root. The results of cluster analysis of 30 sweet potato genotypes were grouped into 13 clusters in accordance to the similarity of character and place of origin. Germplasm of 30 sweet potato genotypes found in the Politeknik Negeri Lampung can be selected to be crossed to create the desired superior characters.

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