Assesment of Diversity in Sweetpotato Accession using Quantitative Traits by Clusters Analysis Method

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Abstract. The diversity of germplasm accession can be grouped by specific traits using cluster analysis to determine the similarity between accessions. The objective of this research was to classified the accession of sweetpotato based on quantitative characteristics using principal component analysis and cluster analysis. The research was conducted in April-August 2016 at Kendalpayak Research Station, Malang, East Java, Indonesia. The material used was 183 accessions of sweetpotato from Indonesian Legumes and Tuber Crops Research Institute (ILETRI) germplasm collection. The research was arranged in a plot size of 1 m × 5 m and 100 × 25 cm in spacing (single row). The variables observed included: plant type, leaf shape, leaf lobes types, leaf lobes number, petiole length, weight of vine, harvest index, number and weight of marketable root, number and weight of nonmarketable root, number and weight of root perplant, and root yield. The PCA identified five principal components that explained 83,2% of total variation present in the genotypes. The cluster analysis was based on 83% of similarity. It grouped 183 accessions into 13 clusters. The traits that most contributed to the diversity were petiole length, weight of vines, leaf lobes number, leaf lobes types, and leaf shape.

Keywords: cluster analysis, diversity, germplasm, *Ipomoea batatas*, PCA

1. Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam), a hexaploid crop (2n = 6x) with 90 chromosomes is a member of convolvulaceae family [1-2].Therefore, according to Laurie *et al*. [3], sweetpotato has highly genetic diversity.Tumwegamire et al. and Wassu *et al*. [4-5] state that the wide diversity of genetic resources is one of the factors that have an important role in the assembly of new varieties with superior character. The wide genetic diversity of sweetpotato germplasm requires good management of the diversity. The management of the genetic diversity within the genetic material population begins with characterization, evaluation, documentation, and conservation [6-7].

Characterization (morphological identification) is important to know the genetic diversity of germplasm accessions and to eliminate the duplication, so that the collection and conservation of germplasm can be efficient [8-10]. Morphological characterization has been used extensively in sweetpotato germplasm diversity assessment [11-14]. The diversity and the similarity of quantitative and qualitative characters will be seen between the characterized germplasm accessions,so that the grouping of germplasm accessions is required.Clustering of germplasm accessions based on the characteristics studied is one of the most appropriate methods to determine the proximity,distance, and similarity between germplasm accessions. The diversity of germplasm collection can be analyzed

using multivariate analysis. The most commonly used analyzes are Principle Component Analysis and cluster analysis. Principle Component Analysis (PCA) is a technique to identify the trait with the highest contributes to diversity, so that PCA results can be used to identify the characteristics of a variety [15]. Cluster analysis based on morphological characters is used to identify the degree of proximity, distance, and similarity between germplasm accessions [16].

The objective of this research was to classify the accession of sweetpotato based on plant quantitative characteristics using principal component analysis and cluster analysis. The desired result of this research is to obtain information on genetic diversity of 183 germplasm accessions of Iletri's sweetpotato.

2. Materials and methods

The experiment was conducted in April-August 2016 at Kendalpayak Research Station, Malang, East Java, Indonesia, using 183 accessions of sweet potato germplasm collection of Indonesian Legumes and Tuber Crops Research Institute (ILETRI), Malang, East Java, Indonesia (table 1).

Tabel 1. List of sweetpotato accessions used for characterization

No	Name	No	Name	No	Name	No	Name	No	Name
1	MLG 12501	38	MLG 12574	75	MLG 12655	112	MLG 12726	149	MLG 12795
2	MLG 12504	39	MLG 12575	76	MLG 12657	113	MLG 12727	150	MLG 12796
3	MLG 12505	40	MLG 12576	77	MLG 12658	114	MLG 12729	151	MLG 12799
4	MLG 12506	41	MLG 12577	78	MLG 12659	115	MLG 12730	152	MLG 12806
5	MLG 12509	42	MLG 12580	79	MLG 12662	116	MLG 12731	153	MLG 12807
6	MLG 12511	43	MLG 12581	80	MLG 12665	117	MLG 12734	154	MLG 12809
7	MLG 12512	44	MLG 12582	81	MLG 12669	118	MLG 12736	155	MLG 12812
8	MLG 12514	45	MLG 12583	82	MLG 12670	119	MLG 12737	156	MLG 12813
9	MLG 12515	46	MLG 12584	83	MLG 12672	120	MLG 12738	157	MLG 12816
10	MLG 12518	47	MLG 12585	84	MLG 12674	121	MLG 12739	158	MLG 12822
11	MLG 12521	48	MLG 12588	85	MLG 12676	122	MLG 12741	159	MLG 12829
12	MLG 12522	49	MLG 12594	86	MLG 12677	123	MLG 12742	160	MLG 12838
13	MLG 12523	50	MLG 12598	87	MLG 12678	124	MLG 12743	161	MLG 12840
14	MLG 12527	51	MLG 12602	88	MLG 12679	125	MLG 12747	162	MLG 12843
15	MLG 12528	52	MLG 12603	89	MLG 12682	126	MLG 12753	163	MLG 12845
16	MLG 12530	53	MLG 12608	90	MLG 12685	127	MLG 12754	164	MLG 12846
17	MLG 12531	54	MLG 12609	91	MLG 12686	128	MLG 12756	165	MLG 12849
18	MLG 12534	55	MLG 12610	92	MLG 12687	129	MLG 12757	166	MLG 12850
19	MLG 12535	56	MLG 12611	93	MLG 12689	130	MLG 12758	167	MLG 12851
20	MLG 12537	57	MLG 12612	94	MLG 12690	131	MLG 12759	168	MLG 12852
21	MLG 12538	58	MLG 12614	95	MLG 12692	132	MLG 12760	169	MLG 12853
22	MLG 12542	59	MLG 12615	96	MLG 12693	133	MLG 12761	170	MLG 12855
23	MLG 12546	60	MLG 12616	97	MLG 12694	134	MLG 12762	171	MLG 12856
24	MLG 12547	61	MLG 12626	98	MLG 12695	135	MLG 12768	172	MLG 12857
25	MLG 12548	62	MLG 12630	99	MLG 12700	136	MLG 12769	173	MLG 12858
26	MLG 12550	63	MLG 12631	100	MLG 12701	137	MLG 12772	174	MLG 12859
27	MLG 12553	64	MLG 12638	101	MLG 12705	138	MLG 12774	175	MLG 12865
28	MLG 12557	65	MLG 12639	102	MLG 12706	139	MLG 12777	176	MLG 12866
29	MLG 12558	66	MLG 12640	103	MLG 12709	140	MLG 12779	177	MLG 12868
30	MLG 12559	67	MLG 12642	104	MLG 12710	141	MLG 12780	178	MLG 12869
31	MLG 12563	68	MLG 12643	105	MLG 12711	142	MLG 12781	179	MLG 12870
32	MLG 12565	69	MLG 12644	106	MLG 12712	143	MLG 12782	180	MLG 12874
33	MLG 12566	70	MLG 12646	107	MLG 12714	144	MLG 12789	181	MLG 12875
34	MLG 12569	71	MLG 12647	108	MLG 12716	145	MLG 12790	182	MLG 12879
35	MLG 12570	72	MLG 12648	109	MLG 12719	146	MLG 12791	183	MLG 12883
36	MLG 12571	73	MLG 12652	110	MLG 12720	147	MLG 12792		
37	MLG 12573	74	MLG 12653	111	MLG 12722	148	MLG 12794		

Each accession was planted in 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 plants were

fertilized with 300 kg ha^{-1} Phonska and 2 t ha^{-1} manure. The 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 were applied to control pest and disease. The harvesting was conducted in next four months after planting. Fourteen quantitative traits (table 2) were recorded, including plant type, leaf shape, leaf lobes types, leaf lobes number, petiole length, weight of vine, harvest index, number and weight of marketable root, number and weight of nonmarketable root, number and weight of root perplant, and root yield.

Accessions diversity was identified by Principal Component Analysis (PCA) to identify principal traits. Furthermore, the value of PCA will be used for cluster analysis. Cluster analysis is used to identify the degree of proximity, distance, and similarity between germplasm accessions. PCA and cluster analysis used Minitab 14 program.

Tabel 2. Morphological traits measured in 183 sweet potato accessions.

Trait acronym	Trait/ descriptor	Score code
PT	Plant type	3= erect, 5= semi-erect, 7= spreading, and 9= extremely spreading
LS	Leaf shape	1= rounded, 2= reniform, 3= cordate, 4= triangular 5= hastate, 6= lobed, and 7 = almost divided
TL	Type of lobes	0= no lateral lobes, 1= very slight, 3= slight, 5= moderate, 7= deep, and 9= very deep
NL	Number of lobes	Direct measurement (1, 3, 5, 7, 9)
PL	Petiole length	1= very short, 3= short, 5= intermediate, 7= long, and 9= very long
WV	Weight of vine	Direct measurement (kg)
NSR	Number of salable root	Direct measurement
NNSR	Number of non salable root	Direct measurement
WSR	Weight of salable root	Direct measurement (kg)
WNSR	Weight of non salable root	Direct measurement (kg)
NRP	Number of root/plant	Direct measurement
WRP	Weight of root/plant	Direct measurement (kg)
HI	Harvest Index	Direct measurement
RY	Root Yield	Direct measurement (th^{-1})

3. Results

3.1. Descriptive statistics of quantitative traits

The morphological characteristic of 183 germplasm accessions showed that morphology varied in growth type and leaf morphology (table 3). Most germplasm accessions had semi erect type (88 accessions),erect (81 accessions) and the rest had spreading growth types (7 accessions). Leaf diversity was found in the shape, characteristics and number of lobes, and the length of the petiole. More than 50% of accessions had a lobed leaf shape, the rest had triangular, hastate, cordate, rounded, and reniform shapes. Leaf lobes were mostly very slight (teeth), slight, and moderate, while the others are deep and very deep. The numbers of lobes are 5, 3, 1, 7. More than 50% had short petiole length, the others had intermediate and very short petiole. The result of descriptive analysis of quantitative character of sweetpotato showed that all characters had high diversity coefficient value that was from 16,60-81,96% (table 3). The Weight of salable root had the greatest diversity among the quantitative characters observed, ie having a coefficient of diversity of 81.96%. Leaf shape had the lowest diversity (16.60%).

3.2. Coefficient of correlation

The correlation coefficient between quantitative characters of germplasm of sweet potato is presented in table 4. The highest positive correlation is shown by correlation between root yield with weight root perplant (r = 0.998[**]) followed by correlation between weight of salable root and number of salable root. The root yield was significantly and positively correlated with number of salable root (0.732[**]), number of nonsalable root (0.376[**]), weight of salable root (0.851[**]), weight of nonsalable root (0.505[**]), number of root perplant (0.743[**]), weight of root perplant (0.998[**]), and harvest index (0.719[**]). Meanwhile, it was not correlated with plant type, leaf shape, leaf lobes types, leaf lobes number, petiole length, and weight of vine.

Tabel 3. Descriptive statistics of sweetpotato quantitative traits.

Quantitative traits	Mean	Standard deviation	Min	Max	CV (%)
Plant type	4.27	1.24	3.00	7.00	29.16
Leaf shape	5.33	0.88	3.00	8.00	16.60
Type of lobes	3.21	2.16	1.00	9.00	67.21
Number of lobes	3.42	1.80	1.00	7.00	52.83
Petiole length	3.49	1.22	1.00	5.00	34.99
Weight of vine (kg)	5.30	2.24	1.30	13.20	42.36
Number of salable root	17.11	11.90	2.00	65.00	69.57
Number of non salable root	19.07	12.53	2.00	70.00	65.72
Weight of salable root (kg)	3.59	2.94	0.20	15.60	81.96
Weight of non salable root (kg)	0.87	0.58	0.10	3.30	66.81
Number of root/plant	2.97	1.87	0.30	14.43	63.03
Weight of root/plant (kg)	0.36	0.26	0.09	1.53	73.35
Harvest Index	0.43	0.17	0.08	0.85	41.07
Root Yield (th^{-1})	12.61	9.26	3.00	53.45	73.44

Tabel 4. Coefficient of correlation among the 14 traits measured on the 183 sweet potato accessions.

Variabel	PT	LS	TL	NL	PL	WV	NSR	NNSR	WSR	WNSR	NRP	WRP	HI
LS	-0.050[ns]												
TL	-0.195**	0.530**											
NL	-0.089[ns]	0.713**	0.719**										
PL	0.354**	-0.069[ns]	-0.023[ns]	-0.053[ns]									
WV	0.016[ns]	-0.060[ns]	-0.028[ns]	-0.039[ns]	0.021[ns]								
NSR	-0.078[ns]	-0.058[ns]	-0.064[ns]	-0.025[ns]	-0.004[ns]	0.090[ns]							
NNSR	-0.183*	0.037[ns]	0.005[ns]	0.001[ns]	-0.120[ns]	-0.020[ns]	0.496**						
WSR	-0.070[ns]	-0.006[ns]	-0.065[ns]	-0.012[ns]	-0.014[ns]	0.108[ns]	0.854**	0.331**					
WNSR	-0.107[ns]	0.124[ns]	0.044[ns]	0.065[ns]	-0.108[ns]	-0.020[ns]	0.512**	0.833**	0.408**				
NRP	-0.168*	0.003[ns]	0.007[ns]	-0.021[ns]	-0.148[ns]	-0.053*	0.618**	0.697**	0.469**	0.635**			
WRP	-0.098[ns]	0.027[ns]	-0.007[ns]	0.014[ns]	-0.103[ns]	0.046[ns]	0.732**	0.376**	0.851**	0.504**	0.743**		
HI	-0.083[ns]	0.020[ns]	-0.045[ns]	-0.007[ns]	-0.039[ns]	-0.389**	0.722**	0.476**	0.786**	0.563**	0.514**	0.719**	
RY	-0.100[ns]	0.028[ns]	-0.006[ns]	0.015[ns]	-0.102[ns]	0.046[ns]	0.732**	0.376**	0.851**	0.505**	0.743**	0.998**	0.719**

**significant at 1%, *significant at 5%, dan [tn]non significant

3.3. Principal component analysis

The results of principal component analysis (PC) in this study reduced the observed character to five principal components eigen value that were greater than 1.0 and were able to explain the material diversity tested for 83.2% (table 5). PC1 with eigen value 5.52 contributed to 39.4% of total diversity, PC2 with eigen value 2.38 contributed to 56.4% of total diversity, PC3 with eigen value 1.42 contributed to 66.6% total diversity, PC4 with eigen value 1.21 contributed to 75.2% total diversity, and PC5 With eigen value 1.12 contributed 83.2% to the total diversity among 183 accessions tested.

In PC1, the characters that contribute to diversity are plant type and petiole length colors. In PC2 the number of lobes, the type of lobes, and the leaf shape have considerable influence on the diversity. In PC3, the characters that contribute to diversity are petiole length, plant type, and weight of salable root. In PC4 the character that affects diversity is weight of vine. In PC5, the harvest index contributes to diversity (table 5).

Tabel 5. Principal component analysis of fourteen quantitative trait to classified 183 sweetpotato accession

Variabel	PC1	PC2	PC3	PC4	PC5
Plant type	0.072	-0.167	0.482	-0.314	-0.329
Leaf shape	-0.014	0.539	0.137	-0.055	-0.053
Type of lobes	0.005	0.549	0.092	0.049	-0.016
Number of lobes	-0.005	0.587	0.173	0.007	-0.023
Petiole length	0.054	-0.110	0.510	-0.311	-0.364
Weight of vine (kg)	0.014	-0.062	0.125	0.740	-0.499
Number of salable root	-0.366	-0.070	0.149	0.082	-0.018
Number of non salable root	-0.284	0.048	-0.392	-0.194	-0.439
Weight of salable root (kg)	-0.363	-0.066	0.288	0.161	0.162
Weight of non salable root (kg)	-0.310	0.084	-0.266	-0.197	-0.394
Number of root/plot	-0.348	0.012	-0.194	-0.027	-0.156
Weight of root/plot (kg)	-0.388	-0.019	0.173	0.152	0.135
Harvest Index	-0.356	-0.020	0.084	-0.307	0.267
Root Yield (t/ha)	-0.388	-0.018	0.173	0.152	0.134
Eigenvalue	5.5206	2.3807	1.4193	1.2128	1.1192
Proportion	0.394	0.170	0.101	0.087	0.080
Cumulative	0.394	0.564	0.666	0.752	0.832

3.4. Cluster analysis

The three main component factors will be used in cluster analysis, based on the variables involved in the factor, 183 accessions of sweetpotato can be categorized into 13 groups at 83% similarity (figure 1 and table 6). Group I consists of 164 accessions, groups II, III, IV, VII, VIII, IX, X, XII, and XIII each consist of 1 accession, group V and VI consist of 4 accessions and group XI consists of 2 accessions.

Tabel 6. Result of cluster analysis and mean of 183 sweet potato germplasm.

Cluster/ number of clusters	PT	LS	TL	NL	PL	WV	NSR	NNSR	WSR	WNSR	NRP	WRP	HI	RY
1/164	4	5	3	3	4	5.19	15	17	3.20	0.77	2.59	0.30	0.40	10.91
2/1	5	6	7	5	3	4.60	30	56	4.00	2.30	4.78	0.35	0.58	12.25
3/1	3	6	7	5	3	2.50	18	54	4.50	3.10	6.00	0.63	0.75	22.17
4/1	3	6	7	7	1	11.80	12	18	2.50	0.70	2.73	0.29	0.21	10.18
5/4	3	5	3	4	3	5.13	38	20	11.18	1.03	5.36	1.13	0.71	39.69
6/4	3	5	2	2	3	4.93	30	39	7.58	1.78	7.12	0.88	0.67	30.68
7/1	5	6	5	5	3	9.40	29	42	5.40	1.50	4.44	0.43	0.42	15.09
8/1	5	5	1	1	5	2.60	23	42	4.10	2.30	5.42	0.53	0.71	18.67
9/1	3	6	1	3	3	4.10	37	69	6.30	2.20	8.83	0.71	0.67	24.79
10/1	3	6	5	3	1	6.80	22	58	2.80	1.70	4.71	0.26	0.40	9.26
11/2	3	4	1	1	3	11.00	33	42	2.90	1.75	4.93	0.31	0.29	10.85
12/1	5	5	3	3	3	4.80	31	70	6.50	3.30	14.43	1.40	0.67	49.00
13/1	3	6	3	5	1	8.70	65	20	15.60	1.20	7.73	1.53	0.66	53.45
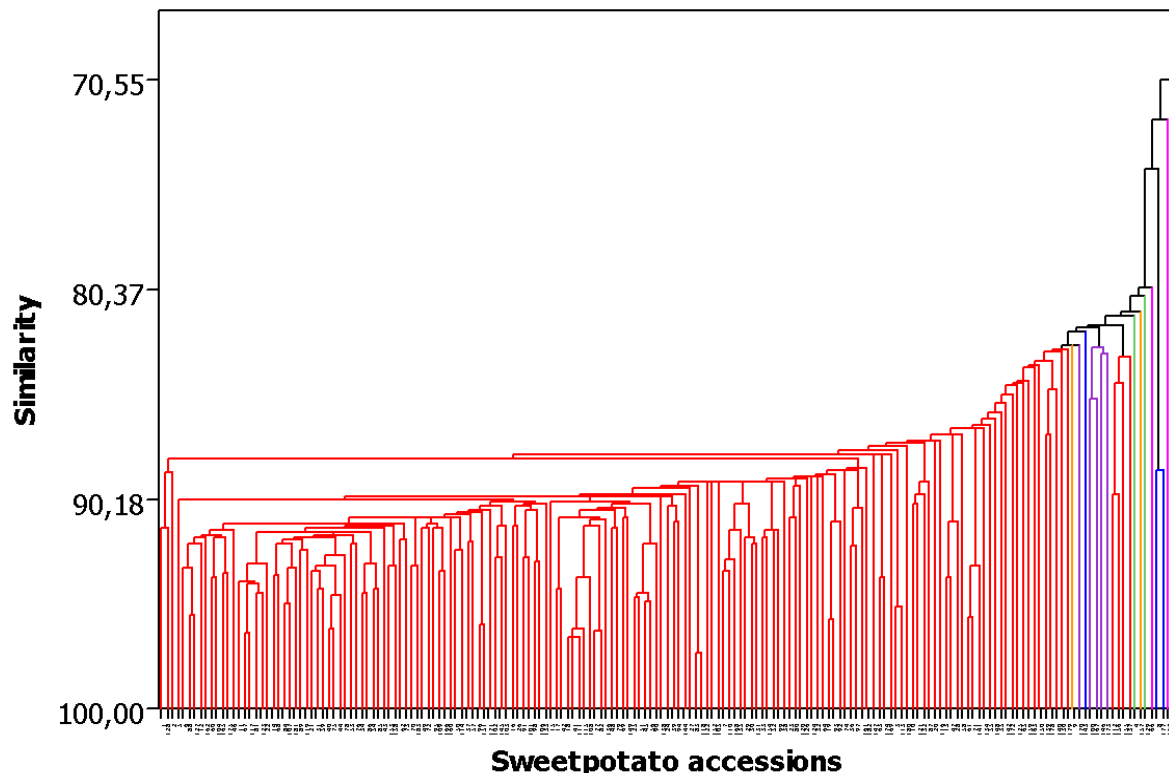
Figure 1. Dendogram of 183 sweetpotato accessions revealed by custer analysis based on fourteen traits.

4. Discussion

Sweet potato accessions have varied morphological characters (table 3). In this study, the morphological characteristic was varied in growth type and leaf morphology. It may be due partly to sexual recombination or mutation [10]. The variation in morphological characters needs to be evaluated and characterized to obtain information on genetic resources that can be used in breeding programs and to eliminate the duplication.

The significant and the positive correlation indicate that characters significantly correlated with root yields can be used as an indicator of the adaptability of sweetpotatoes in the study area to increase root yields (as indirect selection tool) [17]. In this research, the root yield was significantly and positively correlated with number of root, weight of root, and harvest index (Table 4). Meanwhile, it was not correlated with plant type, leaf shape, leaf lobes types, leaf lobes number, petiole length, and weight of vine. Similar results was also showed by previous studies, where the root yield was positively correlated with the total number of roots [15, 17-19] and harvest index [20-22].

Principal component analysis is done to find out the characters that contribute to the diversity. The use of major component analysis to study the diversity of various characters of morphology of sweetpotato has been done in several studies including Koussao *et al.* [2], they obtained four major components capable of explaining the diversity of 67.2% of the total diversity among tested accessions. In Norman et al. study, the factor of the analysis includes five factors which explain 72.79% of the total phenotypic variation in the dependence structure [10]. The result of this study reduced fourteen observed character to five principal components with eigen value that were greater than 1.0 and were able to explain the material diversity tested for 83.2%. In PC1, the characters that contribute to diversity are plant type and petiole length colors. In PC2 the number of lobes, the type of lobes, and the leaf shape. In PC3, petiole length, plant type, and weight of salable root. In PC4 weight of vine. In PC5, the harvest index. Haydar et al., state that the characters that contribute the most to the

diversity of genetic material are the characters that have the largest and positive characteristic vector values [23].

Cluster analysis based on the five principal component divide183 accessions of sweetpotato into 13 groups at 83% similarity (figure 1 and table 6). Group I was the largest group, consisted 164 accessions. Group I was characterized by inferior character. Group XIII consists of one accession with superior character (high root yield). Some previous research results show that cluster analysis divided 192 accessions into four major groups with no relationship to the district of origin [24]. Norman *et al*. [10], obtained the dissimilarity distance of 80%, the dendogram identified eight main clusters from 17 accessions. 112 accessions were grouped into eleven clusters in Koussao et al. [2]. Cluster analysis separated 12 clones tested into two major groups on the genetic similarity value of 25% [25]. Cluster analysis based on genetic grouped the 48 genotypes into three major clusters [26].

5. Conclusion

The conclusion of this study is that there was a morphological diversity in 183 germplasm accessions.The main component analysis resulted five major components with a proportion of 83.2% diversity.Based on germ analysis, 183 germplasm accessions were distributed into 13 accession groups at 83% similarity levels. The weight of vines, number of lobes, type of lobes, leaf shape, and plant type contributed the most to total diversity.

Acknowledgements

References

[1]   Mohan C, Nair A G H and Naskar K 2012 *Fruit, Veg, and Cereal Sci and Biotech* **6**(1) 57-64
[2]   Koussao S, Gracen V, Asante I, Danquah E Y, Ouedraogo J T, Baptiste T J, Jerome B and Vianney T M 2014 *African Journal of Biotechnology* **13**(6) 729–742
[3]   Laurie S M, Calitz F J, Adebola P O and Lezar A 2013 *South African Journal of Botany* **85** 10–16.
[4]   Tumwegamire S, Kapinga R, Rubaihayo P R, Labonte D R, Grüneberg W J, Burgos G, Zum Felde T, Carpio R, Pawelzik E and Mwanga R O 2011 *HortSci.* **46** 348–357
[5]   Wassu M, Solomon A, Beneberu S and Simret B 2015 *Sci. Technol. Arts Res*. **4**(1) 09-19
[6]   Karuri H W, Ateka E M, Amata R, Nyende A B, Muigai A W T, Mwasame E and Gichuki S T 2010 *Int. J. Agric. Biol.* **12** 33–38
[7]   Trustinah and Iswanto R 2014 Grouping of mungbean (*Vigna radiata* (L.) Wilczek) accession for quantitative traits *Prosiding Seminar Nasional Hasil Penelitian Tanaman Aneka Kacang dan Umbi Tahun 2013,* ed N Saleh, A Harsono, N Nugrahaeni, AA Rahmiana, Sholihin, M. Jusuf, Heriyanto, I K Sastra, M M Adie, Hermanto, D Harnowo (Indonesia) p 458—464
[8]   Huaman Z 1999 Systematic botany and morphology of the sweetpotato plant. Sweetpotato Germplasm Management (*Ipomoea batatas*). *International Potato Center (CIP)*
[9]   Veasey EA, Jurema R Q S, Mariana S R, Aline B, Eduardo A B and Nivaldo P 2007 *Sci.Agric. (Piracicaba, Braz.)* **64**(4) 416-427
[10] Norman P E, Beah A A, Samba J A, Tucker M J, Benya M T and Fomba S N 2014 *Agricultural Science Research Journal* **4**(2) 30–38
[11] Gichuru V, Aritua V, Lubega G W, Edema R, Adipala E and Rubaihayo P R 2006 *Acta Horticult.* **703** 159–164
[12] K'Opondo F B 2011 *Ann.Biol. Res.* **2**(2) 54-64
[13] Elameen A, Larsen A, Klemsdal S, Fjellheim S, Sundheim L, Msolla S, Masumba E and Rognli O 2011 *Genet. Resour. Crop. Evol.* **58** 397–407

[14] Su W, Liu Y , Lei J, Wang L , Chai S , Jiao C and Yang X 2016 *American J. of Exp. Agric.* **13**(6): 1-13

[15] Afuape S O, Okocha P I and Njoku D 2011 *Afr. J. Plant Sci.* **5**(2) 123-132

[16] Tresniawati C and Randriani E 2011 *Buletin Plasma Nutfah* **17**(1) 40—45

[17] Mekonnen B, Tulu S, Nego J 2015 *J. Plant. Sci.* **10**(5) 191-199

[18] Demelie M and Aragaw A 2015 *IJRAS* **2**(5) 362-370

[19] Egbe O M, Afuape S O and Idoko J A 2012 *Amer J Exp Agric* **2**(4) 573-586

[20] Jha G 2012 *Inter. J. Farm. Sci.* **2** 17-27

[21] Rahajeng W, Rahayuningsih S A 2015 *Proceeding of The 5th International Conference on Green Technology Maulana Malik Ibrahim Islamic State University,* ed Adi TK **5** 52-57

[22] Tirkey P L, Singh J, Chaurasia P C and Sarnaik D A 2011 *J. Plant Development Sci*. **3**(1/2) 137-143

[23] Haydar A, Ahmed M B, Hannan M M, Razvy M A, Mandal M A, Salihin M, Karim R and Hossain M 2007. *J. Sci. Res.* **2**143–145

[24] Yada B, Tukamuhabwa P, Wanjala B, Kim D J, Skilton R A, Alajo A and Mwanga R O M. 2010 *HORTSCIENCE* **45**(2) 225–230

[25] Soegianto A, Ardiarini N R and Surgiarto A N 2011 *J. Agric. Food. Technol.* **1**(9) 179-183

[26] Ngailo S, Shimelis H, Sibiya J, Amelework B and Mtunda K 2016 *South. Afr. J. of Botany*. **102** 40–45