



Phenotypic Variation Analysis of Sweet Potato Germplasm Resources from Different Agro-climate Zones in the World

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Authors' contributions

This work was carried out in collaboration between all authors. Author WS designed the study, carried out the experiment and wrote the first draft of the manuscript. Author YL carried out the experiment. Authors JL, LW and SC identified the plants and gave helps during the statistical analysis. Authors CJ and XY reviewed the experimental design and all drafts of the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The objectives of this research were to study the phenotypic diversity of sweet potato germplasm collections using 16 agro-morphological traits. A field experiment was done with 123 cultivated varieties of sweet potato. The varieties were grown at the research farm of Hubei Academy of Agricultural Sciences, Jiangxia District, Wuhan, China in the year 2015. They were evaluated in a

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randomized complete-block design with three replications. Estimates of phenotypic variation found immature leaf color, mature leaf color, predominant color of vine and petiole pigmentation were in high similarity, whereas other traits demonstrated more genetic variation. The coefficient of variance in yield and dry matter content was 54.74% and 13.98%, respectively, this indicated that yield and dry matter content was liable to have environmental influences. Person correlation analysis was conducted to illustrate the interrelationships among the traits, the results showed that base of leaf vien pigmentation had highest correlation ($r=0.848$) with predominant color of leaf vien. Base of leaf vien pigmentation, base of petiole pigmentation and predominant color of leaf vien had significant positive correlations with yield. Number of central leaf lobes and immature leaf color had negative impacts on dry matter content. Principal component analysis extracted five principal components, contributed 66.05% of the total variability. The hierarchical cluster analysis based on five extracted principal components resulted in a dendrogram which was discordant with geographic origin. The sweet potato varieties in this study showed a high level of phenotypic diversity. This study could provide a reference for future research and have elucidated the phenotypic diversity that existed in sweet potato.

Keywords: Sweet potato; germplasm resources; phenotypic variation; agro-morphological; correlation analysis; principal component analysis; hierarchical cluster analysis.

1. INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a tuberous-rooted perennial plant belonging to Convolvulacea (morning glory family) [1]. It is an important food security crop in many developing countries because of its high productivity and its abundant use, ranging from the consumption of fresh roots, to processing into animal feed, starch, noodles, fule and alcohol [2]. As one of the major food crops in poor areas, sweet potato greatly alleviate the hunger malnutrition problems [3]. Sweet potato has been one of the most important crops in China since the late 16th Century (Ming Dynasty) [4]. Chinese farmers produced about 117 million tonnes of sweet potato annually, accounting for 90% of worldwide sweet potato production, according to the investigation by International Potato Center (CIP) in 2010. The growing regions of sweet potato in China include a wide range of diverse agro-climate zones, from the very south Hainan province to the very north Heilongjiang province, from the plain area along the coast line with an altitude of tens of meters to Yunnan-Guizhou Plateau, which has an altitude of over 2000 meters [5]. As referred to long cultivating history of sweet potato in China, a magnitude gene pool was reserved here. In order to avoid the lose of elite lines, the exploitation of the indigenous gene pools had always been discussed [6]. There were once two nation-wide sweet potato germplasm resources collection conducted in China, the routes started from the southeast China to the northwest area directly alongside the Yangtze river, thousands of traditional lines were collected. After that, the Sweet potato

Research Center in Xuzhou collaborated with CIP to collect resources from Heilongjiang, Shanxi and Hainan provinces. The characterization of these traditional lines was conducted after the collection action, and some of them were reported to be tolerant to a number of biotic stress [7]. Moreover, as more and more foreign sweet potato resources had been introduced into China, some resources made great contributions to sweet potato breeding history. For example, it was not until 1970s that great progress was made in China leading to release of many cultivars, including the excellent cultivar Xushu 18, which was the offspring of the most important exotic cultivars Okinawa 100 from Japan and Nancy Hall from the United States [8]. Thus, the role of a broad genetic base and systematic characterizing the germplasm had been well recognized in the sweet potato improvement [9].

Agro-morphological traits can always be used as the first step to establish a gene-bank collection [10]. Present study aimed to properly evaluate agro-morphological traits from a set of sweet potato germplasm resources collected from different agro-climate zones in the world. The results of this study could provide the potential materials for sweet potato breeders by exploiting more desirable characters.

2. MATERIALS AND METHODS

2.1 Genetic Materials

A field experiment was carried out to evaluate 16 agro-morphological traits of 123 cultivated

varieties of sweet potato. Here 108 varieties came from China, 6 varieties from Africa, 1 variety from the USA, 3 varieties from Japan, 5 varieties from South Korea, the detailed geographic information can be seen in Table S1. The varieties were grown at the research farm of Hubei Academy of Agricultural Sciences, Jiangxia District, Wuhan, China in the year 2015. The experimental site (29°18'N latitude 113°42'E longitude with an altitude of 20~40 m above the sea level) had a humid climate.

2.2 Experimental Design

The varieties were evaluated in a randomized complete-block design with three replications, a distance of 1 m was maintained between the plots. Each accession was represented on the row with 10 ramets, plant to plant distance was 25 cm. Row to row spacing was 75 cm and the row length was 2.5 m for each variety. All the varieties were grown under normal agronomic practices.

2.3 Sampling and Traits Measurement

The morphological traits were recorded on five individual ramets in one replication after 60 days of planting. Yield survey was done with three replications during harvest. Samples were collected and submitted to the Hubei Engineering and Technology Research Center of Sweet Potato at Wuhan for dry matter content (%) measuring.

2.4 Statistical Analysis

The 14 morphological traits were digitized and scored using 0 ~ 9 scale according to the descriptors and data standard for sweet potato (*Ipomoea batatas* (L.) Lam.) by Zhang and Fang in 2006 [11] and the standard of classification code was shown in Table 1. Each trait counted the distribution frequency. The agronomic traits like yield and dry matter content calculated the maximum (Max), the minimum (Min), the mean values, the standard deviation and the coefficient of variation by using the computer software SPSS version 20.0 [12] and Excel. Data on 14 morphological traits and two agronomic traits were subjected to correlation analysis and principal component analysis (PCA) by using the software SPSS version 20.0, too. Extracted components were further used to perform hierarchical cluster analysis using SPSS version 20.0. A phenetic tree was also constructed using this programme.

3. RESULTS

3.1 Phenotypic Variation

The phenotypic variation of 14 morphological traits was shown in Table 2. The frequency distribution showed that 75% of the varieties exhibited similarity in immature leaf color. More than 80% of the varieties had a similarity in mature leaf color, predominant color of vine and petiole pigmentation, this results indicated that simplicity existed in these traits. Other morphological traits had a series of different distribution frequencies, demonstrated that these traits had more genetic diversities.

The mean expression of the two agronomic traits, yield and dry matter content recorded on varieties were presented in Table 3. Data with regard to dry matter content and yield revealed significant differences among the varieties, the coefficient of variance was 13.98% and 54.74%, respectively.

3.2 Correlation Studies

Correlation results of 16 agro-morphological traits were given in Table 4. Characters such as number of central leaf lobes, general mature leaf outline showed significant positive association with general immature leaf outline. Base of petiole pigmentation had a significant negative association with general immature leaf outline while had a relatively low negative association with predominant color of leaf vein. Base of leaf vein pigmentation showed highest correlation ($r=0.848$) with predominant color of leaf vein. Abaxial leaf vein pigmentation was poorly correlated with other agro-morphological traits. Base of leaf vein pigmentation ($r=0.306$), base of petiole pigmentation ($r=0.255$) and predominant color of leaf vein ($r=0.255$) had significant positive correlations with the yield. As referred to dry matter content, both number of central leaf lobes and immature leaf color had negative impacts on it indicating that the outline and color of immature leaf may have impacts on the dry matter accumulation by regulating the photosynthesis process efficiency.

3.3 Principal Component Analysis

As it had been found that traits were interrelated, principal component analysis was conducted in order to have an idea of independent impact. The first five components in the principal component

analysis contributed 66.05% of the total variability among varieties (Table 5). Principal Component 1 (PC1) contributed 21.68% of the total variability, while PC2 accounted for 15.21% of the total variability. PC3 contributed 10.92% of the observed variability. PC4 and PC5 contributed 9.70% and 8.54% of the total variability, respectively.

Table 1. Classification for the registered 14 morphological traits of 123 sweet potato germplasm resources

Traits	Classification code
Immature leaf color	1 slightly green, 2 green, 3 purple green, 4 brown green, 5 slightly purple, 6 purple, 7 brown, 8 golden, 9 red
Mature leaf color	1 slightly green, 2 green, 3 purple green, 4 brown green, 5 slightly purple, 6 purple, 7 brown, 8 golden, 9 red
General mature leaf outline	1 rounded, 2 reniform (kidney-shaped), 3 cordate (heart-shaped), 4 hastate, 5 triangular, 6 lobed
General immature leaf outline	1 rounded, 2 reniform (kidney-shaped), 3 cordate (heart-shaped), 4 hastate, 5 triangular, 6 lobed
Number of central leaf lobes	1 single notch , 2 double notch, 3 multi-notch
Number of Leaf lobes	1 single notch, 2 double notch, 3 multi-notch
Type of central leaf lobe	1 lined, 2 toothed, 3 few toothed
Type of leaf lobe	1 lined, 2 toothed, 3 few toothed
Petiole pigmentation	1 slightly green, 2 green, 3 green with purple spots, 4 purple, 5 dark purple
Base of petiole pigmentation	1 slightly green, 2 green, 3 slightly purple, 4 purple, 5 dark purple
Base of leaf vien pigmentation	1 slightly green, 2 green, 3 slightly purple, 4 purple, 5 dark purple
Abaxial leaf vein pigmentation	1 slightly green, 2 green, 3 yellow , 4 slightly purple, 5 purple with spots
Predominant color of leaf vien	1 slightly green, 2 green, 3 yellow, 4 slightly purple, 5 purple, 6 purple spots
Predominant color of vine	1 slightly green, 2 green, 3 purple red, 4 slightly purple, 5 purple, 6 dark purple, 7 brown

Table 2. Genetic diversity of the 14 morphological traits in 123 sweet potato germplasm resources

Traits	Frequency distribution								
	1	2	3	4	5	6	7	8	9
Immature leaf color	0.01	0.75	0.14	0.00	0.01	0.06	0.01		
Mature leaf color	0.01	0.83	0.12	0.00	0.00	0.01	0.01		
General mature leaf outline		0.01	0.29	0.41	0.15	0.15	0.10		
General immature leaf outline	0.01	0.01	0.13	0.13	0.58	0.15	0.10		
Base of petiole pigmentation		0.42	0.11	0.41	0.03				
Base of leaf vein pigmentation		0.36	0.11	0.44	0.07				
Predominant color of vine		0.86	0.03	0.01	0.06	0.01			
Predominant color of leaf vien		0.41		0.13	0.42				
Number of central leaf lobes	0.08	0.11	0.02						
Number of leaf lobes	0.45	0.17							
Type of central leaf lobe	0.41	0.13	0.07						
Type of leaf lobe	0.07	0.14	0.02						
Petiole pigmentation		0.81	0.06	0.06	0.06	0.07	0.01		
Abaxial leaf vein pigmentation		0.50		0.10	0.36				

Table 3. Phenotypic variation of the two agronomic traits in 123 sweet potato germplasm resources

Traits	Mean	Standard deviation	Maximum	Minimum	Range	Coefficient of variance (%)
Dry matter content (%)	29.68	4.15	39.44	16.59	22.85	13.98
Yield (kg)	3.69	2.02	11.28	0.15	11.13	54.74

Table 4. Phenotypic correlation coefficients among 16 agro-morphological traits of 123 sweet potato germplasm resources

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16
X1		0.368**	-0.042	0.565**	-0.035	-0.211*	-0.246**	-0.037	-0.191*	-0.040	-0.126	0.019	-0.059	0.170	-0.044	-0.105
X2	0.368**		0.015	0.392**	-0.038	-0.014	-0.085	-0.085	-0.061	-0.252**	-0.004	0.137	-0.276**	0.333**	-0.165	-0.304**
X3	-0.042	0.015		-0.232**	0.395**	0.203*	0.200*	0.337**	0.155	0.041	-0.016	0.049	0.002	0.089	-0.038	-0.228*
X4	0.565**	0.392**	-0.232**		-0.232**	-0.185*	-0.220*	-0.133	-0.252**	-0.127	-0.018	0.020	-0.130	0.061	0.002	-0.100
X5	-0.035	-0.038	0.395**	-0.232**		0.205*	0.256**	0.383**	0.189*	0.248**	-0.043	-0.055	0.157	-0.018	-0.059	-0.088
X6	-0.211*	-0.014	0.203*	-0.185*	0.205*		0.832**	0.321**	0.848**	0.052	0.049	0.033	-0.004	0.028	0.306**	0.039
X7	-0.246**	-0.085	0.200*	-0.220*	0.256**	0.832**		0.365**	0.790**	0.095	-0.026	0.027	-0.008	0.006	0.255**	0.150
X8	-0.037	-0.085	0.337**	-0.133	0.383**	0.321**	0.365**		0.334**	0.005	0.029	0.045	0.023	0.130	-0.102	0.029
X9	-0.191*	-0.061	0.155	-0.252**	0.189*	0.848**	0.790**	0.334**		0.107	0.023	0.044	0.026	0.081	0.255**	0.156
X10	-0.040	-0.252**	0.041	-0.127	0.248**	0.052	0.095	0.005	0.107		-0.135	-0.088	0.785**	-0.333**	0.071	0.029
X11	-0.126	-0.004	-0.016	-0.018	-0.043	0.049	-0.026	0.029	0.023	-0.135		0.401**	-0.117	-0.056	0.065	-0.018
X12	0.019	0.137	0.049	0.020	-0.055	0.033	0.027	0.045	0.044	-0.088	0.401**		-0.015	0.044	-0.220*	-0.114
X13	-0.059	-0.276**	0.002	-0.13	0.157	-0.004	-0.008	0.023	0.026	0.785**	-0.117	-0.015		-0.516**	0.035	0.054
X14	0.170	0.333**	0.089	0.061	-0.018	0.028	0.006	0.130	0.081	-0.333**	-0.056	0.044	-0.516**		-0.036	-0.050
X15	-0.044	-0.165	-0.038	0.002	-0.059	0.306**	0.255**	-0.102	0.255**	0.071	0.065	-0.220*	0.035	-0.036		0.128
X16	-0.105	-0.304**	-0.228*	-0.100	-0.088	0.039	0.150	0.029	0.156	0.029	-0.018	-0.114	0.054	-0.050	0.128	

X1: General immature leaf outline X2: Number of central leaf lobes X3: Immature leaf color X4: General mature leaf outline X5: Mature leaf color X6: Base of leaf vein pigmentation
 X7: Base of petiole pigmentation X8: Predominant color of vine X9: Predominant color of leaf vein X10: Type of central leaf lobe X11: Abaxial leaf vein pigmentation X12: Petiole pigmentation
 X13: Number of leaf lobes X14: Type of leaf lobe X15: Yield X16: dry matter content

*and**indicated significance at 5%and 1% levels, respectively. Correlation coefficient $r > 0.185$ and $r > 0.232$ were significant at 5% and 1% level

Table 5. Total variance explained of the 123 sweet potato germplasm resources

Component	Initial eigenvalues			Extraction sums of squared loadings		
	Total	% of variance	Cumulative %	Total	%of variance	Cumulative %
1	3.47	21.68	21.68	3.47	21.68	21.68
2	2.43	15.21	36.89	2.43	15.21	36.89
3	1.75	10.92	47.81	1.75	10.92	47.81
4	1.55	9.70	57.51	1.55	9.70	57.51
5	1.37	8.54	66.05	1.37	8.54	66.05
6	0.99	6.22	72.27			
7	0.88	5.51	77.78			
8	0.70	4.34	82.12			
9	0.61	3.81	85.93			
10	0.56	3.49	89.42			
11	0.47	2.92	92.34			
12	0.39	2.45	94.79			
13	0.37	2.28	97.07			
14	0.20	1.26	98.33			
15	0.15	0.95	99.28			
16	0.12	0.72	100.00			

Extraction Method: Principal Component Analysis

Table 6. Principal component analysis of 16 agro-morphological traits for the 123 sweet potato germplasm resources

Variables	Component				
	1	2	3	4	5
X1	-0.438	0.222	0.285	0.564	0.198
X2	-0.340	0.567	0.260	0.271	0.218
X3	0.358	0.197	0.575	-0.157	-0.195
X4	-0.515	0.226	0.024	0.526	0.351
X5	0.445	-0.010	0.597	-0.003	-0.172
X6	0.816	0.337	-0.140	0.197	0.199
X7	0.838	0.276	-0.131	0.175	0.110
X8	0.491	0.253	0.380	-0.072	-0.120
X9	0.820	0.292	-0.165	0.184	0.161
X10	0.309	-0.683	0.312	0.274	0.228
X11	0.013	0.158	-0.142	-0.541	0.560
X12	-0.032	0.233	0.149	-0.469	0.650
X13	0.243	-0.772	0.286	0.183	0.299
X14	-0.116	0.673	0.020	0.044	-0.304
X15	0.293	-0.037	-0.464	0.354	0.077
X16	0.182	-0.199	-0.516	0.049	-0.146

X1: General immature leaf outline X2: Number of central leaf lobes X3: Immature leaf color X4: General mature leaf outline
 X5: Mature leaf color X6: Base of leaf vein pigmentation X7: Base of petiole pigmentation X8: Predominant color of vine
 X9: Predominant color of leaf vein X10: Type of central leaf lobe X11: Abaxial leaf vein pigmentation X12: Petiole
 pigmentation X13: Number of leaf lobes X14: Type of leaf lobe X15: Yield X16: Dry matter content

For each principal component, a number of traits that contributed to the total variation were shown in Table 6 (above). In PC1, the traits that accounts for 21.68% of the total variability included base of leaf vein pigmentation, base of petiole pigmentation, predominant color of leaf vein. PC2 was related to the traits including number of central leaf lobes, type of central leaf lobe, number of leaf lobes, type of leaf lobe. PC3 was more related to the traits including immature leaf color, mature leaf color, predominant color of vine, yield and dry matter. PC4 was related to the traits including general immature leaf outline,

general mature leaf outline, abaxial leaf vein pigmentation. PC5 included petiole pigmentation.

3.4 Hierarchical Cluster Analysis

An attempt was made to visualize the clustering pattern using the first five principal components for assessing phenotypic diversity in 123 sweet potato varieties. The dendrogram based on hierarchical clustering analysis utilizing the between-groups linkage method was given in Fig. 1. The taxonomic distance ranged from 0 to 25. At a Euclidean distance of 25, all the varieties

were grouped into two major clusters. Among the different clusters, the cluster size varied from 1 to 10 varieties. The cluster II consisted of NO. 31 (Guangshu2), NO. 88 (Xuhaizi), NO. 66 (Nongdahong) had longer genetic distances than others. At a Euclidean distance of 17, the cluster I was divided into two sub-groups, namely I-1 and I-2. I-2 consisted of NO.89 (Xulv 1) only, which was a kind of sweet potato for vegetable using. At the Euclidean distance of 12, I-1 was also divided into two sub-groups, namely a and b. Group b had a longer distance than group a, including NO. 102 (Yushu297), NO. 106 (Yusu83), NO. 18 (N3573), NO. 68 (Aya), NO.117 (Eshu3). From all the groups that can be inferred from the dendrogram, none of the varieties coming from the same region can be clustered together, hence, the dendrogram can not reflect the geographic origin of the varieties.

4. DISCUSSION

Evaluation and characterization of the varieties, which are suitable in one or more aspects are the pre-requisites for breeding strategies. Phenotypic analysis in this study revealed significant variation among the varieties, indicating that high phenotypic variation existed in sweet potato. The differences among varieties for the morphological traits were changed. There were significant variation among varieties for vine and leaf descriptor characters, except immature leaf color, mature leaf color, predominant color of vine and petiole pigmentation. Those traits were shown less diversity indicating that simplicity existed in these morphological traits, early researchers confirmed similar results [3,13]. Other morphological traits investigated in this study had more variation. Storage root characters demonstrated extremely high phenotypic coefficient of variation, with the yield of 54.74% and dry matter content of 13.98%, the result of high coefficient of variation in yield and dry matter content was in accordance with those obtained by Tsegaye in [14]. The mean expression of yield which was recorded on varieties showed all the varieties of yield varied from 11.28 kg to 0.15 kg, this results suggested that yield character was more complex and liable to have environmental influences compared to other traits.

Results obtained using Person correlation showed that correlations varied from 0.002, which was the lowest correlation between immature leaf color and number of leaf lobes, between general mature leaf outline and yield, to

0.848, which was the highest correlation between base of leaf vein pigmentation and predominant color of leaf vein. Abaxial leaf vein pigmentation was poorly correlated with other agromorphological traits. Base of leaf vein pigmentation ($r=0.306$), base of petiole pigmentation ($r=0.255$) and predominant color of leaf vein ($r=0.255$) had significant positive correlations with the yield, as a result, it may be assumed that pigmentation in the leaf vein and petiole affecting yield accumulation by regulating its photosynthesis process. In addition, both number of central leaf lobes and immature leaf color had negative impacts on dry matter content indicating that the outline and color of immature leaf may also have impacts on the dry matter accumulation.

The relationship among 123 sweet potato varieties revealed by hierarchical cluster analysis based on five extracted principal components were given in Fig. 1. The clustering of the varieties based on extracted phenotypic components did not reflect their geographic region of origin, the results of which were in agreement with those obtained in sweet potato by Naskar in [15], Veasey in [16], Elameen in [3] and these may be caused by the acceleration process of germplasm resources communication. However, the results can be given still us insights about interrelationships that existed among the varieties.

The sweet potato varieties in this study showed a high level of phenotypic diversity. However, the phenotypes of sweet potato was often influenced by environment, thus, it makes the process of evaluation more complex [17]. In addition, agromorphological traits alone could not provide a thorough assessment of genetic diversity because they represented a restricted number of segregation locis that existed within the whole genome [17,19]. Agro-morphological traits, however, presented that each variety had at least one aspect that was quite different from the other one in the collections, thus sometimes agromorphological characters were important traits for breeders to detect and eliminate duplicates [20-22]. China has two national germplasm collection centers, the National Sweet Potato Germplasm Resources Garden in Guangdong province, and the National Sweet Potato Germplasm Resources Repository in Xuzhou. Establishment of a sweet potato germplasm collection with various field trials will help to eliminate the duplicates and detect the interaction of phenotypic plasticity, thus the high

genetic diversity will be maintained [3]. This study lacked multiple zones to eliminate the bias because of financial problem and the results

were part of longer field research, we hoped these results could provide a reference for future study.

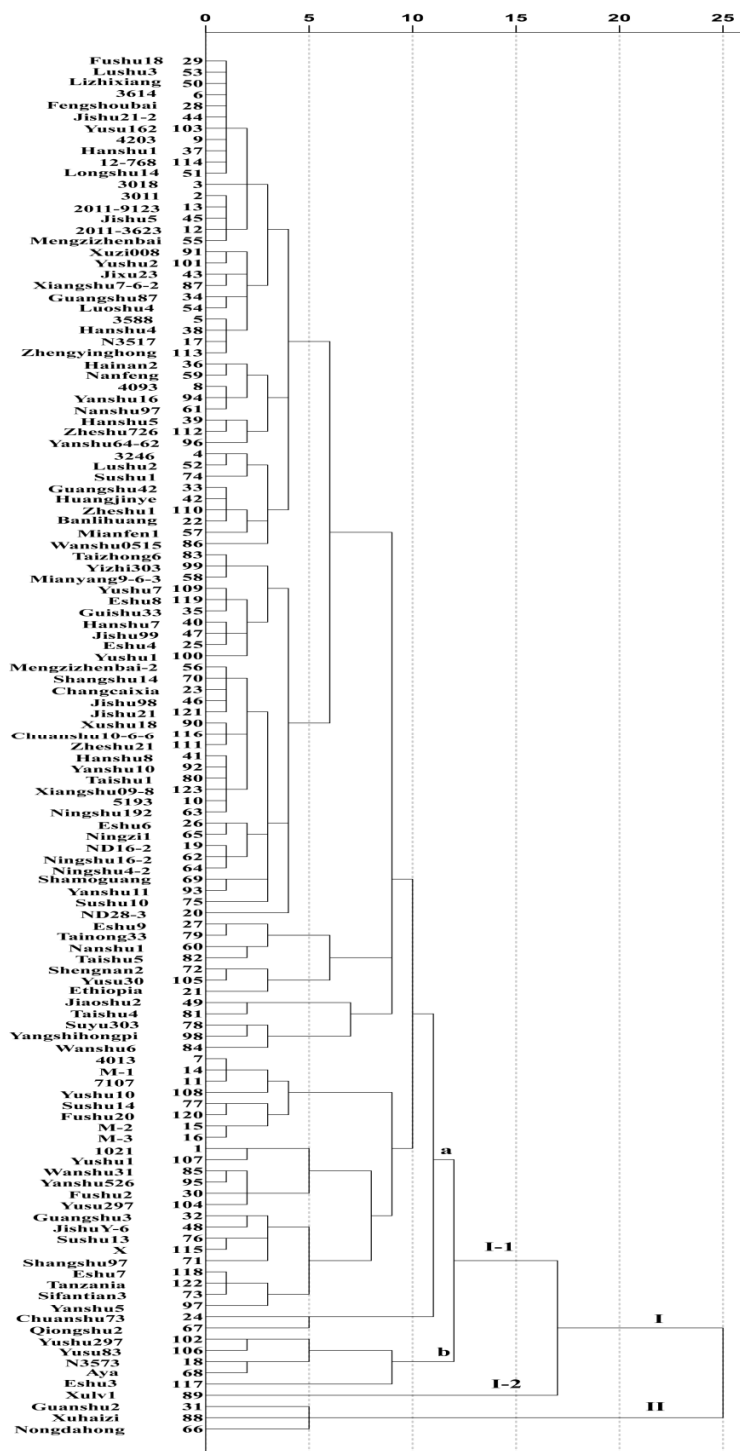


Fig. 1. Hierarchical cluster analysis of 123 sweet potato germplasm resources based on five extracted principal components

5. CONCLUSION

The present study provided a preliminary analysis of the phenotypic diversity among 123 sweet potato varieties coming from different agro-climate zones in the world. The results showed that significant phenotypic variations existed among the varieties except four traits, immature leaf color, mature leaf color, predominant color of vine and petiole pigmentation. Considering traits like yield and dry matter content, this study identified that they were liable to have environmental influences. PCA extracted five principal components, contributed 66.05% of the total variability, the hierarchical cluster analysis based on five extracted principal components resulted in a dendrogram which was discordant with geographic origin. This research will be important source for selecting superior parents to get potential hybrid combinations.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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APPENDIX

Table S1. Names and regional distribution of 123 sweetpotato germplasm resources

Code	Name	Origin
1	M-1	Africa
2	M-2	Africa
3	M-3	Africa
4	Ethiopia	Africa
5	Sifantian3	Africa
6	Tanzania	Africa
7	Wanshu61	Anhui
8	Wansu31	Anhui
9	Nongdahong	Beijing
10	Yuzi 303	Beijing
11	Yushu 1	Chongqing
12	Yushu 2	Chongqing
13	Yushu 297	Chongqing
14	Yusu 162	Chongqing
15	Yushu 297	Chongqing
16	Yushu 30	Chongqing
17	Yushu 83	Chongqing
18	Fushu 18	Fujian
19	Fushu 2	Fujian
20	Longshu 14	Fujian
21	Yanshu 5	Fujian
22	Fushu 20	Fujian
23	Guangshu 3	Guangdong
24	Guangshu 42	Guangdong
25	Guangshu 87	Guangdong
26	Huangjinye	Guangdong
27	Jishu 21-2	Hebei
28	Jishu 5	Hebei
29	Jishu 98	Hebei
30	Jishu 99	Hebei
31	Jishu Y-6	Hebei
32	Luoshu 4	Henan
33	Shangshu 14	Henan
34	Shangshu 97	Henan
35	Yushu 1	Henan
36	Yushu 10	Henan
37	Yushu 7	Henan
38	Zhengyinghong	Henan
39	Guishu 33	Guangxi
40	Guanshu 2	Hainan
41	Hainan 2	Hainan
42	Qiongshu 2	Hainan
43	Xiangshu 7-6-2	Hunan
44	Yangshihongpi	Hunan
45	Xiangshu 09-8	Hunan
46	Jiao 2	USA
47	Nanfeng	Japan
48	Aya	Japan
49	Shamoguang	Japan
50	Fengshoubai	Jiangsu
51	Lizhixiang	Jiangsu
52	Mengzizhenbai	Jiangsu

Code	Name	Origin
53	Mengzizhenbai-2	Jiangsu
54	Ningshu 16-2	Jiangsu
55	Ningshu 192	Jiangsu
56	Ningshu 4-2	Jiangsu
57	Ningzi 1	Jiangsu
58	Sushu 1	Jiangsu
59	Sushu 10	Jiangsu
60	Sushu 13	Jiangsu
61	Sushu 14	Jiangsu
62	Xuhaizi	Jiangsu
63	Xulv 1	Jiangsu
64	Xushu 18	Jiangsu
65	Xuzi 8008	Jiangsu
66	Suyu 303	Jiangsu
67	Banlihuang	Shandong
68	Changcaixia	Shandong
69	Taishu 1	Shandong
70	Taishu 4	Shandong
71	Taishu 5	Shandong
72	Jishu 21	Shandong
73	Taizhong 6	Shandong
74	Yanshu 10	Shandong
75	Yanshu 11	Shandong
76	Yanshu 16	Shandong
77	Yanshu 526	Shandong
78	Yanshu 64-62	Shandong
79	Jixu 23	Shandong
80	Lushu 2	Shandong
81	Lushu 3	Shandong
82	Tainong 33	Taiwan
83	1021	Hubei
84	3011	Hubei
85	3018	Hubei
86	3246	Hubei
87	3588	Hubei
88	12-768	Hubei
89	3614	Hubei
90	4013	Hubei
91	4093	Hubei
92	4203	Hubei
93	5193	Hubei
94	7107	Hubei
95	2011-3623	Hubei
96	2011-9123	Hubei
97	N3517	Hubei
98	N3573	Hubei
99	ND16-2	Hubei
100	ND28-3	Hubei
101	Eshu 4	Hubei
102	Eshu 6	Hubei
103	Eshu 9	Hubei
104	X	Hubei
105	Eshu 3	Hubei
106	Eshu 7	Hubei
107	Eshu 8	Hubei
108	Chuanshu 73	Sichuan

Code	Name	Origin
109	Mianfen 1	Sichuan
110	Mianyang 9-6-3	Sichuan
111	Nanshu 1	Sichuan
112	Nanshu 97	Sichuan
113	Shengnan	Sichuan
114	Wangshu 0515	Sichuan
115	Chuanshu 10-6-6	Sichuan
116	Zheshu 1	Zhejiang
117	Zheshu 21	Zhejiang
118	Zheshu 726	Zhejiang
119	Hanshu 1	South Korea
120	Hanshu 4	South Korea
121	Hanshu 5	South Korea
122	Hanshu 7	South Korea
123	Hanshu 8	South Korea

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