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Short 1 Research Article

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3 Phenotypic Variation Analysis of Sweetpotato

4 Germplasm Resources from Different Agro-climate

5 Zones of China

The objectives of this research were to study the phenotypic diversity of sweetpotato germplasm collection using 16 agro-morphological traits. Field experiments were done with 123 cultivated varieties of sweetpotato. The varieties were cultivated at the research farm of Hubei Academy of Agricultural Sciences, Jiangxia District, Wuhan, China in the year 2015. They were evaluated in a randomized complete-block design with three replications. ~~The results were reported here: e~~ Estimates of phenotypic variation found ~~in~~ immature leaf color, mature leaf color, predominant color of vine and petiole pigmentation were in high similarity, while 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 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 vine pigmentation had highest correlation ($r=0.848$) with predominant color of leaf vine followed by base of petiole pigmentation ($r=0.832$). Base of leaf vine pigmentation, base of petiole pigmentation and predominant color of leaf vine 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 ~~from~~ 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 sweetpotato accessions in this study, ~~however~~, showed a high level of phenotypic diversity. This study could provide a reference for future ~~study research~~ and elucidate the ~~eat~~ phenotypic diversity existed ~~sited~~ in sweetpotato.

6

7 **Keywords:** sweetpotato; germplasm resources; phenotypic variation; agro-morphological; correlation
8 analysis; population component analysis; hierarchical cluster analysis

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9 1. INTRODUCTION

10 Sweetpotato (*Ipomoea batatas*(L.)Lam.) is a tuberous-rooted perennial plant belonging to
11 Convolvulacea (morning glory family) [1]. It is an important food security crop in many developing
12 countries because of its high productivity and its abundant use, ranging from the consumption of fresh
13 roots, to processing into animal feed, starch, noodles, ~~fuel~~ and ~~alcohol~~ [2]. As one of the
14 crops in poor areas, sweetpotato greatly alleviate the hunger malnutrition problems [3]. Sweetpotato
15 had been one of the most important crops in China since the late 16th Century (Ming Dynasty) [4]. Chinese
16 farmers produced about 117 million tonnes of sweetpotato annually, accounting for 90% of worldwide
17 sweetpotato ~~productivity~~ production, according to ~~the investigation by~~ International Potato Center (CIP)
18 in 2010. The growing regions of sweetpotato in China include a wide range of diverse agro-climate zones ~~in China~~,
19 from the very south Hainan province to the very north Heilongjiang province, from the plain area along
20 the coast line with an altitude of only several or tens of meters to Yunnan-Guizhou Plateau, which has a
21 altitude of over 2000 meters [5]. As referred to long cultivating history of sweetpotato in China, a
22 magnitude gene pool was reserved here. In order to avoid the lose of the elite lines, the exploitation of
23 the indigenous gene pools had always been ~~talked~~ discussed [6]. There were ~~once~~ two national-wide
sweetpotato

24 germplasm resources collection ~~conducted~~actions happend in China, the routes started from the
southeast China
25 along the coast line to the northwest area directed alongside the Yangtze river, thousands of
traditional
26 lines were collected. After that, the Sweetpotato Research Center in Xuzhou ~~cooperated~~collaborated
with CIP, ~~to collect~~
27 ~~collected~~resources from Heilongjiang, Shanxi and Hainan provinces. The
~~characterization~~identifications of these
28 traditional lines were conducted after the collection actions, ~~and~~ ~~S~~some of them were reported to be
tolerant to
29 a number of biotic stress [7]. Moreover, as more ~~and more~~ foreign resources had been introduced in
30 China, some resources made great contributions to sweetpotato breeding history. For example, it was
not
31 until 1970s that great progress was made in China leading to release of many cultivars, including the
32 excellent cultivar Xushu 18, which was the offspring of the most important exotic cultivars Okinawa
100
33 from Japan and Nancy Hall from the United States [8]. Thus, the role of a broad genetic base and
34 system~~atically~~ characteriz~~ing~~ e the germplasm had been well recognized in ~~the~~ crop improvement[9].
35 Agro-morphological characters can always be used as the first step to establish a gene-bank
36 collection [10]. Present study aimed to characterize and properly evaluate agro-morphological traits
from
37 the set of the sweetpotato germplasm resources collected from different agro-climate zones ~~of China~~.
The results
38 of this study can provide the potential materials for sweetpotato breeders by exploiting more desirable
39 characters.

40

41 2. MATERIAL AND METHODS

42 2.1 Genetic materials

43 ~~A F~~field experiments ~~were was~~ carried out to evaluate agro-morphological traits of 123 cultivated
varieties of

44 sweetpotato. Mos[OM1]t of the collections originated from China, the rest were introduced from
~~oversea~~ [OM2](Table

45 S1) . The collections were ~~cultivated~~grown at the research farm of Hubei Academy of Agricultural
Sciences,

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Jiangxia District, Wuhan, China in the year 2015. The experimental site (29°18'N 46 ~~latitude~~latitude
113°42'E

47 ~~longitude~~longitude with an altitude of 20-40 above the sea level) had a humid climate.

48 2.2 Experimental design

49 The varieties were evaluated in a randomized complete-block design with three replications. Each
50 accession was represented with a row of 10 ramets. The row was in a 2.5 meters length
~~adoping~~[OM3] a space

51 of 75 cm between rows and 25 cm between the ramets. The distance between each replication was
100

52 cm. They were raised under normal agronomic practices.

53 2.3 Sampling and traits measurement

54 The 14 qualitative traits were recorded on five individual ramets in one replication. Yield survey was
55 done with three replications. Samples were collected and submitted to the Hubei Engineering and
56 Technology Research Center of Sweetpotato at Wuhan for dry matter content (%) measuring.

57 2.4 Statistical analysis

58 The 14 qualitative traits were digitized and scored using 0-9 scale according to the ~~d~~Descriptors and
59 ~~D~~data ~~S~~standard for ~~S~~Sweetpotato (*Ipomoea batatas*(L.) Lam.) by Zhang and Fang in 2006 [11] and
the

60 standard of classification code can be seen in (Table 1). Each

61 trait counted the distribution frequency. The quantitative traits like yield and dry matter content calculated
62 the ~~m~~Maximum (~~Max~~), the ~~M~~minimum (~~Min~~), ~~M~~mean values, and estimated the standard deviation~~ivation~~ and
63 coefficient of variation. ~~by using the computer software SPSS version 20.0 [12] and Excel.~~ Data on 14
64 morphological traits and two agronomic traits were subjected to correlation analysis and principal~~alle~~
65 component analysis (PCA) ~~by using the software SPSS version 20.0,~~ too. Extracted components were
66 further used to perform hierarchical cluster analysis using SPSS 20.0. Data analysis and a ~~A~~ phenetic tree was ~~also~~

67 constructed using this SPSS version 20.0 programme.

Table 1 Classification for the registered qualitative traits of sweetpotato gemplasm 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

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Traits Classification code

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 vine

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

vine

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

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70 3. RESULTS

71 3.1 Phenotypic variation

72 The phenotypic variation of 14 qualitative traits ~~are shown were demonstrated~~ in (Table 2). 75% of the
73 accessions exhibited similarity in the foliage color of immature leaf. More than 80% of the materials had
a

74 similarity in the foliage color of mature leaf, predominant color of vine and petiole pigmentation, this
75 results indicated that simplicity existed in these traits. Other morphological traits like general mature
leaf

76 outline, general immature leaf outline, base of petiole pigmentation, base of leaf vine pigmentation,

77 predominant color of leaf vine, number of central leaf lobes, number of leaf lobes, type of central leaf

78 lobe, type of leaf lobe and abaxial leaf vein pigmentation had a series of different distribution frequencies,

79 demonstrated that these traits had more genetic diversities.

Table 2 Genetic diversity of the qualitative traits in sweetpotato 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

The base of petiole pigmentation 0.42 0.11 0.41 0.03

The base of leaf vine 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 vine 0.41 0.13 0.42

Number of central leaf lobes 0.08 0.11 0.02

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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

80

81 The mean expression of the two quantitative traits, yield and dry matter content recorded on

82 genotypes were are presented in (Table 3). The maximum dry matter content was 39.44% and the lowest

83 was 16.59%. Data with regard to yield revealed a significant difference among the genotypes ,the

84 coefficient of variance was 54.74%, the maximum yield was 11.28 kg, the minimum yield was 0.15 kg.

85

Table 3 Phenotypic variation of the quantitative traits in sweetpotato gemplasm 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

86

87 3.2 Correlation Studies

88 Correlation results of 16 agro-morphological traits were presented in (Table 4). Characters such as

89 number of central leaf lobes, general mature leaf outline showed significant positive association with

90 general immature leaf outline. The base of petiole pigmentation had a significant negative association with

91 general immature leaf outline while had a relatively low negative association with predominant color of leaf

92 vine. The base of leaf vine pigmentation showed highest correlation ($r=0.848$) with the predominant color

93 of leaf vine followed by base of petiole pigmentation ($r=0.832$). Abaxial leaf vein pigmentation was poorly

94 correlated with other agro-morphological traits. The base of leaf vine pigmentation ($r=0.306$), base of

95 petiole pigmentation ($r=0.255$) and predominant color of leaf vine ($r=0.255$) had significant positive

96 correlations with the yield. As referredreferred to dry matter content, both number of central leaf lobes and

97 immature leaf color had negative impacts on it indicating that the outline and color of immature leaf may

98 [have play](#) impacts on the dry matter accumulation by regulating the photosynthesis process efficiency.
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Table 4 Phenotypic correlation coefficients among 16 agro-morphological traits of 123 sweetpotato
 gemplasm 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 vine 105 pigmentation X7: 106 base of petiole pigmentation X8: predominant color of vine X9: predominant color of leaf vine X10: type of central leaf lobe X11: abaxial leaf vein pigmentation X12: petiole 107 pigmentation X13: number of leaf lobes X14: type of leaf lobe X15: yield X16: dry matter content
 108 *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.

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3.3 Principal Component Analysis

110 As it had been found that characters were interrelated, principal component analysis was [conducted taken](#) in

111 order to have an idea of independent impact. The first five components in the principal component

112 analysis contributed 66.05% of the total variability among collections (Table 5). Principle Component 1

113 (PC1) contributed 21.67% of the total variability, while PC2 accounted for 15.21% of the total variability.

114 PC3 contributed 10.92% of the observed variability. PC4 and PC5 contributed 9.7% and 8.53% of the

115 total variability, respectively.

Table 5 Total variance explained of the sweetpotato 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

116

117 For each principal component, there were a number of characters that contributed to the total variation

118 (Table 6). In PC1, the traits that accounts for 21.68% of the total variability included base of leaf vine

119 pigmentation, base of petiole pigmentation, predominant color of leaf vein. PC2 was related to number of

120 central leaf lobes, type of central leaf lobe, number of leaf lobes, type of leaf lobe. PC3 was more related

121 to immature leaf color, mature leaf color, predominant color of vein, yield and dry matter. PC4 was related

122 to general immature leaf outline, general mature leaf outline, abaxial leaf vein pigmentation. PC5 included

123 petiole pigmentation.

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Table 6 Principal component analysis of 16 agro-morphological traits for sweetpotato 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 vine pigmentation X7: base of petiole pigmentation X8: predominant color of vine X9: predominant color of leaf vine 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

124

125 3.4 Hierarchical Cluster Analysis

126 An attempt was made to visualize the clustering pattern using the first five principal components ~~of~~
127 ~~the principal component analysis~~ for assessing phenotypic diversity in 123 sweetpotato accessions. The

128 dendrogram based on hierarchical clustering analysis utilizing the between-groups linkage method was

129 presented in Figure 1. The taxonomic distance ranged from 0 to 25. At a Euclidean ~~dsitancedistance~~ of 25, all the

130 varieties were grouped into two major clusters. Among the different clusters-, the cluster size varied from 1

131 to 10 genotypes. The cluster II consisted of NO. 31 (Guangshu2), NO. 88 (Xuhaizi), NO. 66

132 (Nongdahong) had long distances than others. At a Euclidean ~~dsitancedistance~~ of 17, the cluster I was divided

133 into two sub-groups, namely I-1 and I-2. I-2 consisted of NO.89 (Xulv 1) only, which was a kind of
134 sweetpotato for vegetable using. At the Euclidean ~~dsitancedistance~~ of 12, I-1 was also divided into two sub135

groups, namely a and b. Group b had a long distance from group a, including NO. 102 (Yushu297), NO.
136 106 (Yusu83), NO. 18 (N3573), NO. 68 (Aya), NO.117 (Eshu3). From all the groups that can be ~~inferedinferred~~

137 from the dendrogram, none of them can reflect the phenetic structure and geographic region of origin.

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Figure 1 Hierarchical cluster analysis of 123 sweetpotato germplasm resources based on five extracted principle components

139 4. DISCUSSIONS

140 Evaluation and characterization of the genotypes, which ~~were-are~~ suitable in one or more aspects ~~wereare~~

141 the pre-~~requisites~~~~requisites~~ for breeding strategies. Phenotypic analysis in this study revealed significant variation

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among the ~~varieties~~~~[OM4]~~ indicating that high phenotypic variation existed in sweetpotato. 142 The differences

143 among varieties for all the qualitative traits were changing. There were significant variation among

144 varieties for vein and leaf descriptor characters, except immature leaf color, mature leaf color,

145 predominant color of vine and petiole pigmentation. Those traits showed less diversity indicating that

146 simplicity existed in these morphological traits, early researchers confirmed similar results [3] [13].

Other

147 ~~morphological~~[morphological](#) traits like general mature leaf outline, general immature leaf outline,
 148 base of petiole
 148 pigmentation, base of leaf vine pigmentation, predominant color of leaf vein, number of central leaf
 149 lobes,
 149 number of leaf lobes, type of central leaf lobe, type of leaf lobe and abaxial leaf vein pigmentation
 had
 150 more variation. ~~Besides, s~~Storage root characters demonstrated extremely high phenotypic
 coefficient of
 151 variation, with the yield of 54.74% and dry matter content of 13.98%, this result was in accordance
 with [those](#)
 152 ~~which~~ obtained by Tsegaye in 2007 [14]. The mean expression of yield which was recorded on
 genotypes
 153 showed all the varieties of yield varied from 11.28 kg to 0.15 kg, this results suggested that yield
 154 character was more complex and liable to have environmental influences compared to other traits.
 155 Results obtained ~~from using~~ Person correlation [studies](#) showed that correlations varied from 0.002,
 which
 156 was the lowest correlation between immature leaf color and number of leaf lobes, general mature leaf
 157 outline and yield, to 0.848, which was the highest correlation between base of leaf vine pigmentation
 and
 158 predominant color of leaf vein. Abaxial leaf vein pigmentation was poorly correlated with other
 agro159
 morphological traits, [this result \[OM5\]](#) had never been reported before. The base of leaf vine pigmentation
 160 ($r=0.306$), base of petiole pigmentation ($r=0.255$) and predominant color of leaf vine ($r=0.255$) had a
 161 significant positive correlation with the yield, as a result, it may be assumed that pigmentation in the
 leaf
 162 vine and petiole affecting yield accumulation by regulating its photosynthesis process. In addition,
 both
 163 number of central leaf lobes and immature leaf color had negative impacts on dry matter content
 indicating
 164 that the outline and color of immature leaf may [have play](#) impacts on the dry matter accumulation.
 165 The relationship among 123 sweetpotato varieties revealed by hierarchical cluster analysis based on
 166 five extracted princip[ale](#) components were presented in Figure 1. The clustering of the varieties
 based on
 167 extracted phenotypic components did not reflect their phenetic structure and geographic region of
 origin,
 168 the results of which were in agreement with those obtained in sweetpotato by Naskar in 1996 [15],
 veasey
 169 in 2007 [16], Elameen in 2011 [3] and these may be caused by the acceleration of [resources](#)
 170 communication a[OM6]mong sweetpotato research institutes. However, the results can still give us
[insightelues](#) about
 171 interrelationships [that](#) existed ~~ed~~ among the varieties.
 172 The sweetpoto varieties in this study showed a high level of phenotypic diversity.
[However](#)~~However~~, the
 173 phenotypes of sweetpotato was often influenced by ~~potential~~ environment, thus, it mak[esde](#) the
 process of
 174 evaluation more complex [17]. In addition, agro-morphological traits alone could not provide a
 thorough
 175 assessment of genetic diversity because they represented a restricted number of segregation locis [that](#)
 existed
 176 within the whole genome [17,19]. Agro-morphological traits, however, presented that each variety
 had at
 177 least one character that was quite different from the other one in the collections, thus sometimes
 agro178
 morphological characters were important traits for breeders to detect and eliminate duplicates [20-22].

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Until now, China has two national germplasm collection centers, ~~one is~~ the National 179 Sweetpotato
 180 Germplasm Resources Garden in Guangdong province, ~~the other is and~~ the National Sweetpotato
 181 Germplasm Resources Repository in Xuzhou. Establishment of a national-wide sweetpotato
 germplasm
 182 collection with various field trials in different agro-climate climatic zones will help to eliminate [OM7]
 the duplicates and
 183 detect the interaction of phenotypic plasticity, thus maintain high genetic diversity [3]. This study
 lacked
 184 multiple zones to eliminate the bias because of financial problem, we hoped this results could provide
 a
 185 reference for future ~~more sophisticated~~ study. This research will also pave a way for selecting
 superior
 186 parents to get potential hybrid combinations.
 187

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 238

239 APPENDIX

Table S1 Names and regional distribution of the 123 sweetpotato varieties

Code Origin Name

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
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 13
 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
240 **Continued**
Code Origin Name
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
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14
46 Jiao 2 USA
47 Nanfeng Japan
48 Aya Japan
49 Shamoguang Japan
50 Fengshoubai Jiangsu
51 Lizhixiang Jiangsu
52 Mengzizhenbai Jiangsu
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
241 **Continued**
Code Origin Name
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
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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

242 **Continued**

Code Origin Name

104 X Hubei

105 Eshu 3 Hubei

106 Eshu 7 Hubei

107 Eshu 8 Hubei

108 Chuanshu 73 Sichuan

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

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120 Hanshu 4 South Korea

121 Hanshu 5 South Korea

122 Hanshu 7 South Korea

123 Hanshu 8 South Korea

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