Identification and phylogenetic analysis of local yellow and orange sweet potatoes genotypes in Sumatera Utara

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Abstract. The objectives of this research was to identify and create database about the diversity of local yellow and orange sweet potatoes accessions in Sumatera Utara, have diversity accession local sweet potatoes genotype in Sumatera Utara selection for classifying populations get high production and good fruit quality. The experiment was conducted in areas of production centers of sweet potatoes in the exploration survey methods in 2 districts in Sumatera Utara, which is in the Kabupaten Simalungun and Dairi. The study was conducted on June to July 2017. Observations were made based on the identification and characterization Description List of International Board for Plant Genetic Resources standard and purposive random sampling technique. The result of this research indicate there 15 genotype of sweet potato yellow and orange in KabupatenSimalungun consistedof KecamatanPurba (G3, G4 and G7), Silimakuta (G5, G6 and G14), and Pamatang Silimahuta (G15) in Kabupaten Dairi consists of Kecamatan Parbuluan (G1, G2, G8 and G9), Sidikalang (G10 and G13), Sumbul (G11), and Sitinjo (G12) with nearest relationship is G13 and G15 with a coefficient similarity 23.908 and farthest relationship is G2 and G7 with a coefficient similarity 140.029.

1. Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.) from the family Convolvulaceae, is an important food crop, which is widely grown in tropical, subtropical and warm temperate regions [1]. The Sweet potato was originally domesticated at least 5000 years ago in Tropical America [2; 3]. Based on the analysis of key morphological characters of sweet potato and the wild Ipomoea species, Austin [2] postulated that sweet potato originated in the region between the Yucatan Peninsula of Mexico and the Orinoco River in Venezuela. Using molecular markers the highest diversity was found in Central America, supporting the hypothesis that Central America is the primary center of diversity and most likely the center of origin of sweet potato [4; 5].

Sweet potato are rich in starch, sugar, vitamin C, β-carotene, iron, and several other minerals [6; 7]. The root reported to usually have higher protein content than other roots and tubers, such as cassava and yams. In addition, some varieties of sweet potatoes contain colored pigments, such as β-carotene, anthocyanin, and phenolic compounds. These pigments form the basis for classifying the foods as nutraceuticals [7]. Orange flesh sweet potatoes are high in carotenoids and beta carotene [8]. Consumption of orange flesh sweet potato roots can provide sustainable vitamin A, which plays a major role in preventing night blindness [9].

Germplasm of the world's sweet potato plants is estimated to number over 1000 species, but only 142 species are identified by the researchers. In the 1960s sweet potato planting had spread to all

provinces in Indonesia. Production center of sweet potato is West Java Province, Central Java, East Java, Irian Jaya, and North Sumatra [10].

Sumatera Utara is one of sweet potato production center in Indonesia. According to Central Agency on Statistics (BPS) (2016), the area of sweet potato harvest in North Sumatera in 2015 is 8,952 ha with sweet potato production of 122,362 tons and productivity 136.69 Ku / ha. The largest production center of sweet potato in Sumatera Utara is in Simalungun Regency (35,080 tons) and Dairi Regency (27,818 tons).

Morphological characterization has been used extensively on various crop plants diversity assessments in many places of the world [11; 12; 13; 14; 15]. Despite the environmental influences on plant morphology, this direct inexpensive and easy to use method of estimations was perceived as the strongest determinant of the agronomic value and taxonomic classification of plants [14] and the first step in the assessment of plant diversity. On sweet potato, this tool has been used successfully to analyse genetic diversity necessary for the germplasm conservation, to reduce accession number by identification and elimination of duplicates and to enhance crop breeding[14; 16; 17; 18; 19; 20].

Based on the above description, the authors intend to conduct research on morphological identification and phylogentic relationship of sweet potato located in Sumatera Utara namely Simalungun and Dairi regencies, especially yellow and orange sweet potato containing β-carotene which is higher than other genotypes of sweet potatoes.

2. Materials and methods

The research was conducted in Simalungun Regency and Dairi Regency. Starting from June 2017 to July 2017. Determination of research location is determined based on the highest production of sweet potato data located in Sumatera Utara namely Simalungun Regency and Dairi Regency. There were 15 accessions were grown in these regencies (Table 1).

The materials used in this study were sweet potato crops with yellow and orange tuber color grow in Simalungun Regency and Dairi Regency.Observations were made based on the identification and characterization Description List of International Board for Plant Genetic Resources standard and purposive random sampling technique. The location of the study is determined based on the area of harvested area and production data from the Central Agency of Statistics (BPS), then searching the location of the study by accidental sampling. Qualitative and quantitative data were scored and processed using SPSS 21 program with cluster analysis to determine the level of relationship between genotypes. Cluster analysis   is used to construct dendogram used to assess the diversity patterns of survey data. The technique used is Agglomerative Hierarchical Clustering, the method of average linkage (between group) with euclidien distance as follows :

$$d_{(i,j)} = \sqrt{\sum_{k=1}^{p} (x_{ik} - x_{jk})^2}$$

$d_{i,j}$ =the distance between object i and object k

x_{ik} = object value i on the variable$k$

x_{jk} = object value$j$ on the variable$k$

p = the number of cluster variables[21]

The parameters observed were: 1) winding, 2) stem morphology: stem type, stem diameter, stem length, main stem color, bar hair, 3) leaf morphology: leaf general shape, lobe type, lobe number, leaf size, Leaf repeating color, old leaf color, shoot leaf color, long petiole, leaf color,4) tuber morphology: tuber formation, tuber length, tuber shape, tuber defect, cortical thickness, tuber skin color, skin color

intensity, secondary skin of tuber bulbs, main color of tuber meat, secondary color of tuber meat, secondary color distribution Meat, sap rate, oxidation reaction, average number of tubers, and average tuber weight.

Table 1. List of accessions collected in Sumatera Utara the varieties introduced used for the characterization.

Code	Regency	District	Village	Folk name
G1	Dairi	Parbuluan	Parbuluan 1	Ubi Jepang
G2	Dairi	Parbuluan	Parbuluan 1	Ubi Sibolu
G3	Simalungun	Purba	Nagori Ritongah	Ubi Jepang
G4	Simalungun	Purba	Nagori Ritongah	Ubi Taiwan
G5	Simalungun	Silimakuta	SaribuDolok	Ubi Sibolu
G6	Simalungun	Silimakuta	Kasemak	Ubi Sibolu
G7	Simalungun	Purba	TigaRunggu	Ubi Taiwan
G8	Dairi	Parbuluan	Simallopuk	Ubi Jepang
G9	Dairi	Parbuluan	Simallopuk	Ubi Sibolu
G10	Dairi	Sidikalang	BatangBeruh	Ubi Sibolu
G11	Dairi	Sumbul	LaeSiboban	Ubi Jepang
G12	Dairi	Sitinjo	Sitinjo	Ubi Sibolu
G13	Dairi	Sidikalang	LaeMungkur	Ubi Jepang
G14	Simalungun	DolokSilou	Perasmian	Ubi Sibolu
G14	Simalungun	PematangSilimahuta	Mardinding	Ubi Sibolu

3.Results and discussion

A comprehensive analysis of the extent and distribution of the genetic variation in sweet potato is essential for sound genetic conservation strategies. Conservation and sustainable use of genetic resources is essential to meet the demand for future food security. Successful conservation of any given gene pool is largely dependent on understanding the diversity and its distribution in a given region [22]. In this study, high level of genetic diversity was exhibited in sweet potato. Morphological characters were highly variable among the genotypes studied. The morphological characterization of accessions in the collection is essential not only to have a description of each accession but also to use this information to identify duplicate accessions. The genotypes exhibited high morphological diversity in aerial and storage tuber characters.

The results of surveys conducted in Simalungun and Dairi regencies have found 15 genotypes of yellow and orange tuber plant consisting of 3 types of sweet potato (Ubi Jepang, Sibolu and Taiwan). The morphological characteristics of sweet potato plants are observed visually. Each of the sweet potato genotypes is present in several locations that have different altitudes from different types of sweet potatoes that have different morphological characteristics. Based on morphological character of sweet potato in Regency of Simalungun and Regency of Dairi obtained value of kinship relation which can be seen in table 2.

Table 2 shows if the value of coefficient smaller between variables one with other variables, then the relationship between the two variables are closer or the greater the similarity and vice versa. So it can be seen that the highest level of similarity or nearest kinship on 33 qualitative and quantitative characters is found in G13 and G15 is 23.908, whereas the lowest similarity level or the furthest kinship relationship is found in G2 and G4 is 140.029. Genetic diversity study is necessary to understand the genetic relationships among populations and to assign accessions to specific heterogeneous groups that help to identify parental lines for best combinations with maximum genetic potential for further selection [23]

Based on the morphological character of sweet potato in Simalungun and Dairi districts, it is found that all the genotypes of sweet potato can be grouped into two groups, three groups and four groups of members from each group (Table 3)

Table 2. Kinship relationship of 15 sweet potatoes genotypes in Simalungun and Dairi Districts Based on Dissimilarity Matrix

No.	Kinship relationship		Coefficient Value	No.	Kinship relationship		Coefficient Value	No.	Kinship relationship		Coefficient Value
1.	G13	G15	23.908	13.	G1	G12	38.812	25.	G4	G5	98.062
2.	G5	G15	26.694	14.	G8	G10	39.254	26.	G2	G7	98.428
3.	G5	G6	27.741	15.	G8	G11	40.083	27.	G4	G7	98.521
4.	G11	G12	29.066	16.	G11	G14	40.404	28.	G3	G13	100.663
5.	G12	G14	29.105	17.	G11	G15	42.131	29.	G1	G8	101.032
6.	G5	G14	34.765	18.	G1	G2	88.315	30.	G4	G9	104.256
7.	G14	G15	35.487	19.	G1	G13	89.159	31.	G4	G8	106.368
8.	G8	G15	36.502	20.	G2	G12	89.339	32.	G4	G10	109.660
9.	G6	G11	37.207	21.	G4	G6	90.679	33.	G4	G13	132.067
10	G5	G13	37.989	22.	G4	G14	91.054	34.	G2	G4	140.029
11.	G9	G12	38.184	23.	G2	G3	94.960				
12.	G5	G8	38.783	24.	G4	G15	98.033				

Table 3. The grouping of sweet potato genotypes in 33characters in Simalungun and Dairi districts

Code	4 Group	3 Group	2 Group
G1	1	1	1
G2	2	2	1
G3	3	1	1
G4	4	3	2
G5	1	1	1
G6	1	1	1
G7	1	1	1
G8	1	1	1
G9	1	1	1
G10	1	1	1
G11	1	1	1
G12	1	1	1
G13	1	1	1
G14	1	1	1
G15	1	1	1

The identified variations are expected to form a pattern of genetic relationship useable in grouping accessions. In grouping of accessions, cluster analysis has ability to identify crop accessions with highest level of similarity using the dendrogram [24] (Aliyu et al., 2000). Result of survey of sweet potato in Regency of Simalungun and Dairi Regency on 33 characters obtained dendogram kinship relationship which can be seen in Figure 1.

Analysis of kinship relationships based on 33 characters on a 25-degree scale formed into two groups. Where the first group (I) consists of G1, G2, G3, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, and G15 while the second group (II) consists of an accession of G4. In the first group (I) is divided into two sub-groups namely the subgroups IA and IB, the first group (IA) consists of G1, G3, G5, G6, G11, G12, G13, G14, And G15 while the second group (IB) consists only of G2.
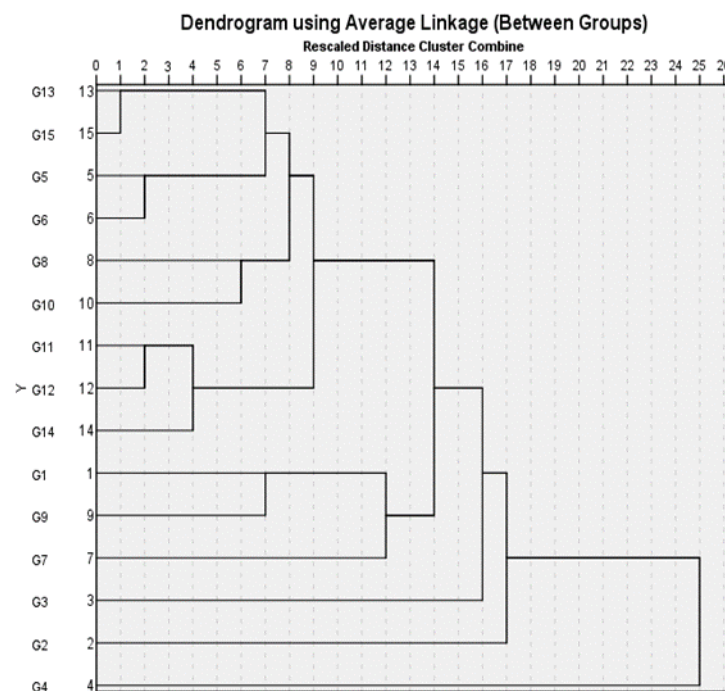
Figure 1. Dendrogram of the 15 sweet potato accessions revealed by average linkage cluster analysis based on the 33 discriminant phenotypic characters.

The further the kinship relationship will be the higher the level of diversity and the lower the level of uniformity, and vice versa [25]. The influence of environmental factors such as climate, temperature, soil type, altitude and humidity will cause the variation of plant morphology. This is not the case when the environmental factor conditions are the same [26]. Survey showed the planting area of sweet potato in Simalungun ranged from 1.160 – 1.407 m above sea level, while the area of sweet potato planting in Dairi ranged from 1.120 – 1.718 m above sea level. In Simalungun, in June the average temperature was 19, rainfall 190 mm, relative humidity 75.33%, in July average temperature 18.60, rainfall 176 mm and relative humidity 75%. While In Dairi, in June the average temperature was 18.30, rainfall 153.5 mm and relative humidity 82.5, in July average temperature 17.80, rainfall 23,5 mm and relative humidity 76,5%.

4..Conclusions

Yellow and orange sweet potatoes that have been found 15 genotypes are found in Simalungun District consisting of PurbaSubdistrict (G3, G4 and G7), Silimakuta (G5 and G6), DolokSilou (G14) and PamatangSilimahuta (G15) at Dairi Regency consists of Parbuluan sub-districts (G1, G2, G8 and G9), Sidikalang (G10 and G13), Sumbul (G11), and Sitinjo (G12) with nearest kinship values obtained at G13 with G15 of 23.908 and kinship value With the farthest distance obtained at G2 and G4 is 140.029.

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