Assessment 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 per plant, 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).

| 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 |
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 per plant, 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 lobs | 0= no lateral lobs, 1= very slight, 3= slight, 5= moderate, 7= deep, and 9= very deep |
| NL | Number of lobs | 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 per plant \( r = 0.998** \) 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 per plant \( (0.743**) \), weight of root per plant \( (0.998**) \), 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.

| 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 |
| Weight of salable root (kg) | 19.07 | 12.53         | 2.00| 70.00|65.72 |
| Weight of nonsalable root (kg) | 3.59  | 2.94           | 0.20| 15.60|81.96 |
| 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 |

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

| Variable | PT | LS | TL | NL | PL | WV | NNSR | NNSR | WSR | WNSR | NRP | WRP | HI |
|----------|----|----|----|----|----|----|------|------|-----|------|-----|-----|----|
| LS       | -0.050** |   |    |    |    |    |      |      |     |      |     |     |    |
| TL       | -0.195** | 0.530** |   |    |    |    |      |      |     |      |     |     |    |
| NL       | -0.089** | 0.713** | 0.719** |   |    |    |      |      |     |      |     |     |    |
| PL       | 0.354** | -0.069** | -0.032** | -0.053** |   |    |      |      |     |      |     |     |    |
| WV       | 0.016** | -0.060** | -0.028** | -0.039** | 0.021** |   |      |      |     |      |     |     |    |
| NNSR     | -0.078** | -0.058** | -0.064** | -0.025** | -0.004** | 0.090** |   |      |      |     |      |     |     |    |
| NNSR     | -0.183** | 0.037** | 0.005** | 0.001** | -0.120** | -0.020** | 0.496** |   |      |      |     |      |     |    |
| WSR      | -0.070** | -0.006** | -0.065** | -0.012** | -0.014** | 0.108** | 0.854** | 0.331** |   |      |      |     |     |    |
| WNSR     | -0.107** | 0.124** | 0.044** | 0.065** | -0.108** | -0.020** | 0.512** | 0.833** | 0.408** |   |      |      |     |     |    |
| NRP      | -0.168** | 0.003** | 0.007** | -0.021** | -0.148** | -0.053** | 0.618** | 0.697** | 0.469** | 0.635** |   |      |     |    |
| WRP      | -0.098** | 0.027** | -0.007** | 0.014** | -0.103** | 0.046** | 0.732** | 0.376** | 0.851** | 0.504** | 0.743** |   |      |     |    |
| HI       | -0.083** | 0.020** | -0.045** | -0.007** | -0.039** | -0.389** | 0.722** | 0.476** | 0.786** | 0.563** | 0.514** | 0.719** |   |     |     |
| RY       | -0.100** | 0.028** | -0.006** | 0.015** | -0.102** | 0.046** | 0.732** | 0.376** | 0.851** | 0.505** | 0.743** | 0.998** | 0.719** |   |

**significant at 1%, *significant at 5%, dan **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).

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

| Variable                  | 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 non salable root| -0.366     | -0.070     | 0.149      | 0.082      | -0.018     |
| Number of 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| -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      | 0.564      | 0.666      | 0.752      | 0.832      |
| **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.

**Table 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|
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 divide 183 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.

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