Morphological characterization and diversity analysis of some BARI released potato varieties

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Article Info

ABSTRACT

Twenty-nine potato varieties released by Bangladesh Agricultural Research Institute (BARI) were characterized at Breeder Seed Production Centre (BSPC), Debigonj, Bangladesh in 2012-13 and 2013-14 based on the Potato Descriptor IBPGR. Quantification of variability for each character done by Shannon-Weaver Diversity Index was subjected to Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO) and Cluster Analysis. The qualitative characters exhibited low variation while the quantitative characters showed high variation. The Pooled values showed medium variability (0.596). The genotypes were grouped into five clusters. Cluster II had thirteen genotypes, while cluster IV and V had two each. The highest inter-cluster distance was observed between II and IV, while the lowest was III and V. The highest intra-cluster distance was found in cluster I. The inter-genotype distance was the highest between BARI Alu-22 and BARI Alu-41, and the lowest was between BARI Alu-42 and BARI Alu-34. The varieties of cluster IV earned the highest mean value for days to 80% emergence, foliage coverage, plant vigor, primary stem/hill, secondary leaflet and primary leaflet pairs. First four principal components accounted for 93.35% of the total variation. From the scree plot, four sample principal components effectively summarized the total variance. Results of PCA showed a reduction of the sixteen original variables into four linear values. The first principal components (PC1) can be considered as plant height and leaf, indicated by high loadings for plant height at 60 days after planting (DAP) (0.983), leaf length (0.133) and leaf width (0.099).

INTRODUCTION

Potato (Solanum tuberosum L.), the 4th most important food crop of the world originated in the high lands of South America is now being cultivated in 157 countries of the world (Barker and Chujoy 2007). It is used as the main food in about 44 developed countries in the world. In Bangladesh, it is the 3rd most important food crop after rice and wheat. It is mainly used as a vegetable and is available in the market throughout the year. The per capita consumption of potato was about 46.40 kg per annum in Bangladesh during 2013, which could be increased substantially to reduce pressure on cereal crops (PotatoPRO 2019). In Bangladesh, potato was cultivated in about 0.477 million hectares of land, the total production was 9.74 million metric tons while the national average yield was about 20.41 t/ha during the fiscal year 2017-2018 (BBS 2019). The genetic base of potato in Bangladesh is very narrow (Rashid 1989). However, precise information about the extent of genetic divergence and variation of characters used for differentiation among the population is crucial in any crop improvement program (Ananda and Rawat 1984; De et al. 1988). Furthermore, assessment of genetic diversity becomes even more crucial if we want to maximize the amount of useful genetic variation within a collection (Bisht et al. 1999). It has become feasible to quantify the magnitude of genetic diversity among germplasm with the assist of advanced biometrical procedures, such as multivariate analysis (Rao 1952) based on Mahalanobis’ (1936) D² statistics. Variability for each qualitative and quantitative character is

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computed using the standardized Shannon-Weaver Diversity Index (Siopongco et al. 1999). No information regarding the extent of genetic divergence in these varieties is available under this condition. In view of the above, the present study has been undertaken to accumulate information on genetic divergence in these genotypes so that useful parental materials for the breeding program could be selected.

MATERIALS AND METHODS

Twenty-nine high yielding potato varieties released by Tuber Crops Research Center (TCRC) of Bangladesh Agricultural Research Institute (BARI) were evaluated during 2012-13 and 2013-14 at Breeder Seed Production Centre (BSPC), Debiganj, Bangladesh. The origin of materials and developed/breeding method and parentage are presented in Table 1. The unit plot size was 3 m x 3 m with 3 replications. The whole tubers were planted with a spacing of 60 cm × 25 cm during the second week of November 2012 and 2013. Fertilizers were applied @ 325-220-250-120 kg/ha of Urea, TSP, MOP and Gypsum, respectively (Kundu et al. 2018). Necessary intercultural operations and plant protection measures were done as per TCRC recommendation.

Analysis

At particular stages of growth, accessions were characterized and evaluated for 21 qualitative (Table 2) and 16 quantitative morpho-agronomic characters using the Descriptor for the Cultivated Potato by International Board for Plant Genetic Resources (IBPGR), Rome, Italy (Huaman et al. 1977). For each accession, ten (10) randomly selected plants were used for the scoring of the characters.

Quantification of variability for each character was done using the Shannon-Weaver Diversity Index. The estimate of variability for each qualitative character was computed using the standardized Shannon-Weaver Diversity Index, designated as $H'$ and has the formula:

$$H' = -\sum \frac{Pi}{n} \log\frac{Pi}{n}$$

Where $Pi$ is the proportion of the total number of

| Name       | Popular name | Origin | Released (Bangladesh) | Breeding Method | Parentage                                      |
|------------|--------------|--------|-----------------------|-----------------|------------------------------------------------|
| BARI Alu-5 | Petrones     | N      | 1993                  | I&S             | (Bintje x Record) x (Black 581 x Alpha)        |
| BARI Alu-6 | Multa        | N      | 1993                  | I&S             | Oberambacher Frueh x (Record x CPC 16731)      |
| BARI Alu-7 | Diamant      | N      | 1993                  | I&S             | Tulnerde Vries 54-30 x SVP 55-89               |
| BARI Alu-8 | Cardinal     | N      | 1993                  | I&S             | Tulnerde Vries 54-30-8 x SVP 55-89             |
| BARI Alu-12| Dheera       | CIP, Peru | 1993        | GE&S            | Maine- 53 x 377888.8                          |
| BARI Alu-13| Granola      | N      | 1994                  | I&S             | 333/60 x 267.04                               |
| BARI Alu-17| Raja         | N      | 2000                  | I&S             | Elvira X CB 70-162-23                           |
| BARI Alu-21| Provento     | N      | 2004                  | I&S             | Elvira X Escort                                |
| BARI Alu-22| Saikots      | CIP, Peru | 2004            | GE&S            | D79.638.1 X 575049                             |
| BARI Alu-24| Dura         | N      | 2005                  | I&S             | Seglinde x Lari                                |
| BARI Alu-25| Asterix      | N      | 2005                  | I&S             | Cardinal x VSP Ve 70-9                         |
| BARI Alu-26| Felsina      | N      | 2006                  | I&S             | Morene x Gloria                                |
| BARI Alu-27| Espirit      | G      | 2008                  | I&S             | 619/87/4796 x Marasel                          |
| BARI Alu-28| Lady         | N      | 2008                  | I&S             | Cardinal x VSP(VTN) 2 62-33-3                  |
| BARI Alu-29| Courage      | N      | 2008                  | I&S             | Lady Rosetta x HZ 81 H202                      |
| BARI Alu-31| Sagitta      | N      | 2010                  | I&S             | Gallia x RZ 86-2918                            |
| BARI Alu-32| Quincy       | N      | 2010                  | I&S             | Felsina x Asterix                              |
| BARI Alu-33| Almera       | N      | 2011                  | I&S             | BM 77-21/02 X AR 80-031-20                     |
| BARI Alu-34| Laura        | G      | 2011                  | I&S             | Saskia X MPI 495402                            |
| BARI Alu-35| 4.5W         | B      | 2012                  | H&S             | Cardinal X Unknown                             |
| BARI Alu-36| 4.26R        | B      | 2012                  | H&S             | Patronese X TPS- 67                           |
| BARI Alu-37| 4.4O         | B      | 2012                  | H&S             | 934 X TPS- 67                                  |
| BARI Alu-38| Omega        | G      | 2012                  | I&S             | 52.83.2 x Orion                                |
| BARI Alu-39| Bellini      | N      | 2012                  | I&S             | Mondial x Felsina                              |
| BARI Alu-40| 4.45 W       | B      | 2013                  | H&S             | 934 X TPS-67                                  |
| BARI Alu-41| 5.183        | B      | 2013                  | H&S             | Carlita X TPS-67                               |
| BARI Alu-42| Agila        | G      | 2013                  | I&S             | Marabell X 1.442202-89                         |
| BARI Alu-43| Atlas        | F      | 2013                  | I&S             | Spunta X Jose                                  |
| BARI Alu-44| Elger        | N      | 2013                  | I&S             | Y66-13-636 X Ve 71105                          |
| BARI Alu-45| Steffi       | N      | 2013                  | I&S             | SolaraX PO 120                                 |

N.B. Introduction and selection = I&S; Hybridization and selection = H&S; Germplasm evaluation and selection = GE&S

N = Netherlands; B = Bangladesh; G = Germany; F = France
genotypes belonging to the $i^{th}$ class.

Following the work of Siopongco et al. (1999), the same formula was applied to the quantitative characters following the construction of frequency classes, with the class boundaries equal to some function of mean and standard deviation. For each quantitative character, the overall genotype means ($\theta$) and standard deviation ($\sigma$) were used to subdivide the population values ($x_i$) into 10 frequency classes, ranging from class 1 (if $x_i \leq -2\sigma$) to class 10 (if $x_i \leq X+2\sigma$), the class interval being 0.5$\sigma$. The lowest and highest values were considered to determine the number of classes construct. The diversity considered high when $H' > 0.75$, moderate when $H' = 0.50 – 0.75$ and low when $H' < 0.50$.

The Shannon-Weaver Diversity Index has a value ranging from 0 to 1, where 0 indicates the absence of diversity and 1 indicates maximum diversity.

Mean data for each character was subjected to multivariate analyses using Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Canonical Vector Analysis (CVA) and Cluster Analysis using GENSTAT 5 (Released as 4.1) software (Copyright, 1997). The dendrogram was constructed by using SPSS statistical software (version 16).

**Principal Component Analysis**: Raw data were first standardized to zero mean unit variance followed by computation of numerical measures of likeness/similarity and construction of distance matrix using variance-covariance co-efficient. Eigenvalues and Eigenvectors of the variance-covariance matrix were then computed.

**Principal Coordinated Analysis (PCO)**: Principal Co-ordinate analysis was performed to get the inter genotypic distance and intracluster distance for all possible combinations.

**Cluster Analysis**: Using standardized data, numerical measures of likeness/similarity were computed and distance matrix constructed using Euclidean Distance Coefficients. Clustering by UPGMA (Unweighted Pair Group of Arithmetic Mean) method was executed.

Table 2. Descriptor list of qualitative characters of potato with their code

| Sl. No. | Major characters                      | Components                        |
|---------|--------------------------------------|-----------------------------------|
| 01.     | Branching habit                      | 1 Single; 2 Branching; 3 few branch at the upper part of the stem |
| 02.     | Stem: colour                         | 1 Green only; 2 Red-brown only; 3 Purple only; 4 Cream with some red–brown; 5 Cream with purple; 6 Red–brown with some green; 7 Purple with some green; 8 Other |
| 03.     | Stem: Cross Section                  | 1 Round; 2 Angular                |
| 04.     | Leaf Dissection                      | 1 Undissected; 2 Pinnatifolobed; 3 Scarcely dissected, 4 Weakly dissected; 5 Medium dissected; 6 Strongly dissected; 7 Very strong dissected; 8 Other |
| 05.     | Predominant Tuber Skin Colour        | 1 White-cream; 2 Yellow; 3 Orange; 4 Brownish; 5 Pink; 6 Red; 7 Purplish–red; 8 Purple; 9 Dark purple-black |
| 06.     | Secondary Tuber Skin Colour          | 0 Absent; 1 White-cream; 2 Yellow; 3 Orange; 4 Brownish; 5 Pink; 6 Red; 7 Purple; 8 Purple; 9 Dark purple–black |
| 07.     | Distribution of Secondary Tuber Colour| 0 Absent; 1 Eyes; 2 Eyebrows; 3 Splashed; 4 Scattered; 5 Spectacled; 6 Stippled; 7 Purple; 8 Other |
| 08.     | Tuber Skin Type                      | 1 Smooth; 2 a medium rough; 2 b Rough (flaky); 3 Partially netted; 4 Totally netted; 5 Very heavily netted; 6 Other |
| 09.     | Predominant Tuber Flesh Colour       | 1 White; 2 Cream; 3 Yellow – cream; 4 Yellow; 5 Red; 6 Violet |
| 10.     | Secondary Tuber Flesh Colour         | 0 Absent; 1 White; 2 Cream; 3 Yellow – cream; 4 Yellow; 5 Red; 6 Violet; 7 Purple; 8 Other |
| 11.     | Distribution of Secondary Tuber Flesh Colour | 0 Absent; 1 Scattered spots; 2 Scattered areas; 3 Narrow vascular ring; 4 Broad vascular ring; 5 Vascularizing medulla; 6 All flesh except medulla; 7 Other |
| 12.     | General Tube shape                   | 1 Compressed; 2 Round; 3 Oval :4 Obovate; 5 Elliptic; 6 Oblong; 7 Long-Oblong; 8 Elongate; 9 Oval |
| 13.     | Unusual Tuber Shape                  | 0 Absent; 1 Flattened; 2 Clavate; 3 Reniform; 4 Fusiform; 5 Falcate ; 6 Spiral; 7 Digitate; 8 Concertina; 9 Tuberosed |
| 14.     | Depth of Tuber Eyes                  | 1 Protruding; 2 Shallow; 3 Medium; 4 Deep; 5 Very deep |
| 15.     | Notes of Eyes per Tuber              | 1 Few (less than; 5 Intermediate; 9 Many (more than 20); |
| 16.     | Distributions of Tuber Eyes          | 1 Predominantly apical; 2 Evenly distributed |
| 17.     | Tuber Size                           | 3 Small; 4 Small to medium; 5 Medium; 6 Medium to large; 7 Large |
| 18.     | Uniformity of Tuber Size             | 3 Low; 5 Medium; 7 High; |
| 19.     | Tuber Defects:Crack                  | 0 Absent; 1 Present |
| 20.     | Secondary growth                     | 0 absent; 1 Present |
| 21.     | Lenticels                            | 0 Absent; 1 Present |
RESULTS AND DISCUSSION

The mean, range, standard deviation and coefficient of variation of the different characters of the genotypes were measured and presented in Table 3. The highest variation was found in tuber number per hill (21.41%) followed by primary stem per hill (21.33) and frequency of secondary leaflets pairs at midrib (20.79 %), and other characters also showed considerable variability. These variations indicated the scope of improved for these characters through breeding and selection.

Estimate of Variation Using the Shannon-Weaver Diversity Index

The computed diversity indices for qualitative character traits ranged from '0' (stem cross-section, secondary tuber skin color, distribution of secondary tuber color, unusual tuber shape) to 0.96 (distributions of tuber eyes) with a mean diversity value of 0.39. The diversity values showed high variation in general tuber shape (0.87), where the other characters exhibited low to medium variation. The mean diversity index of 0.39 indicated the existence of low variation within the collection, in terms of qualitative characters (Table 4).

A quantitative character trait exhibited a low diversity value of 0.44 for the plant vigor, whereas, Foliage coverage (0.75) and primary stem per hill (0.75) exhibited a medium degree of variation. All the rest gave high diversity values ranging from 0.76 (tuber number per hill) to 0.89 (plant height at 60 days after planting, terminal leaflet blade width and lateral leaflet blade width). A high degree of variation exhibited within the collection for the quantitative characters, as reflected by the mean diversity value of 0.80 (Table 4). The Pooling of

| Characters | Range | Mean | SD | CV % |
|------------|-------|------|----|------|
| Days to 80% emergence | 23.00 - 16.00 | 19.31 | 1.89 | 9.80 |
| Foliage coverage | 100.00 - 85.00 | 95.34 | 4.07 | 4.27 |
| Plant vigour | 10.00 - 7.00 | 8.62 | 0.68 | 7.85 |
| Plant height at 60 days after planting | 109.10 - 67.00 | 87.45 | 10.63 | 12.16 |
| Primary Stem per hill | 7.80 - 5.01 | 5.01 | 1.07 | 21.33 |
| Leaf length (cm) | 35.00 - 20.00 | 26.39 | 3.40 | 12.89 |
| Leaf width (cm) | 22.80 - 9.60 | 16.45 | 2.93 | 17.81 |
| Frequency secondary leaflets pairs at midrib | 9.60 - 3.90 | 6.34 | 1.32 | 20.89 |
| Terminal leaflet blade length (cm) | 10.70 - 5.90 | 8.02 | 1.07 | 13.35 |
| Terminal leaflet Blade width (cm) | 6.85 - 3.70 | 5.53 | 0.75 | 13.61 |
| Number of Primary Leaflet Pairs | 6.00 - 4.20 | 4.91 | 0.40 | 8.10 |
| Lateral leaflet blade length (cm) | 9.60 - 5.10 | 8.01 | 1.06 | 13.24 |
| Lateral leaflet blade width (cm) | 6.50 - 3.50 | 4.98 | 0.66 | 13.25 |
| Tuber number/hill | 16.28 - 6.25 | 10.48 | 2.24 | 21.41 |
| Tuber weight/hill (kg) | 0.85 - 0.44 | 0.67 | 0.09 | 13.81 |
| Tuber yield | 56.67 - 29.00 | 44.38 | 6.13 | 13.81 |

Table 3. The range, mean, standard deviation and coefficient of variation of 2 different characters of the BARI released potato varieties

| Character | H’ | Character | H’ |
|-----------|----|-----------|----|
| Branching habit | 0.37 | General tuber shape | 0.87 |
| Stem colour | 0.22 | Unusual tuber shape | 0 |
| Stem cross section | 0 | Depth of tuber eyes | 0.58 |
| Leaf dissection | 0.49 | Notes of eyes per tuber | 0.30 |
| Predominant tuber skin colour | 0.29 | Distributions of tuber eyes | 0.96 |
| Secondary tuber skin colour | 0 | Tuber size | 0.64 |
| Distribution of secondary tuber colour | 0 | Uniformity of tuber size | 0.71 |
| Tuber skin type | 0.40 | Tuber defects:crack | 0.48 |
| Predominant tuber flesh colour | 0.69 | Secondary growth | 0.22 |
| Secondary tuber flesh colour | 0.11 | Lenticels | 0.66 |
| Distribution of secondary tuber flesh colour | 0.12 | Mean diversity index = 0.39 |

| Character | H’ |
|-----------|----|
| Days to 80% emergence | 0.84 |
| Foliage coverage | 0.75 |
| Plant vigour | 0.44 |
| Plant: height at 60 days after planting | 0.89 |
| Primary stem per hill | 0.75 |
| Leaf length (cm) | 0.85 |
| Leaf width (cm) | 0.80 |
| Frequency secondary leaflets pairs at midrib | 0.78 |

Table 4. Computed diversity indices (H’) for the qualitative and quantitative characters of BARI released potato varieties

Mean Diversity Index = 0.80

Pooling of Diversity Index = 0.595
diversity values for the qualitative and quantitative characters traits gave an overall diversity index of 0.595, indicative of medium variability existing within the collection. Siopongco et al. (1999) reported that the collection exhibited medium variation for the qualitative characters and high variation was observed for the quantitative characters whereas the Pooling of diversity indices for the qualitative and quantitative characters gave medium diversity.

**Cluster analysis:**

Based on cluster analysis the 29 genotypes were grouped into five different clusters (Table 5 and Figure 1). Cluster III contained the maximum number of thirteen genotypes followed cluster II having five genotypes when cluster IV & V contained two genotypes for each cluster. BARI Alu 34 (Laura) is introduced variety in Bangladesh and it is developed in Germany, whereas BARI Alu-37 (4.4O) developed in Bangladesh but they were in the same cluster-III. In many cases, the same cluster included genotypes from different eco-geographic region indicating the geographic distribution and genetic divergence did not follow the similar trend. These findings were in agreement with the findings of other researchers (Haydar et al. 2007). Yahiya et al. (2009) and Huque et al. (2012) reported the non-correspondence of genetic and geographic diversity.

From the Canonical Variate Analysis (CVA), scattered diagram produced from canonical variate I & II, where four clusters were found. Among them clusters I, II, III, IV, and V contained 7, 5, 13, 2 and 2 genotypes, respectively (Figure 2). The results were confirmatory with the cluster pattern of the genotypes obtained through Dendrogram (Figure 1).

The genotypes from cluster I earned the highest cluster mean value for lateral leaflet blade width (5.65 cm), but the lowest cluster means for the plant height at 60 days after planting (74.29 cm), leaf length (23.85 cm), leaf width (13.79 cm), number of primary leaflet pairs (4.66) and lateral leaflet blade length (7.44 cm). On the other hand, Cluster II integrated five genotypes that produced the highest mean value for plant height at 60 days after planting (99.130 cm), primary stem per hill (5.30) and tuber number per hill (11.50). But the lowest mean value for days to 80% emergence (17.83) and foliage coverage. Cluster III had the highest mean value for tuber weight per hill (0.75 kg) and Tuber yield (50.08 t/ha). Whereas cluster IV produced the highest mean value for days to 80% emergence (21.33), foliage coverage (98%), plant vigor (9.0), primary stem per hill (5.3), frequency secondary leaflets pairs at midrib (6.87) and number of primary leaflet pairs (5.13) (Table 6).

![Figure 1. Dendrogram produced from cluster analysis of BARI released varieties of potato using morphological data and executed by UPGMA.](image)

| Cluster | No. of genotypes | Serial no. of genotypes | Name of genotypes |
|---------|-----------------|------------------------|-------------------|
| I       | 7               | 1; 3; 4; 7; 9; 18; and 28 | BARI Alu-5 (Petrones), BARI Alu-7 (Diamant), BARI Alu-8 (Cardinal), BARI Alu-17 (Raja), BARI Alu-22 (Saikot), BARI Alu-33 (Almera) and BARI Alu-44 (Elger) |
| II      | 5               | 2; 17; 21; 23 and 24 | BARI Alu-6 (Multa), BARI Alu-32 (Quincy), BARI Alu-36 (4.26R), BARI Alu-38 (Omega) and BARI Alu-39 (Bellini) |
| III     | 13              | 5; 8; 11; 12; 14; 15; 16; 19; 22; 25; 26; 27 and 29 | BARI Alu-12 (Dheera), BARI Alu-21 (Provento), BARI Alu-25 (Asterix), BARI Alu-26 (Felsina), BARI Alu-28 (Lady Rosetta), BARI Alu-29 (Courage), BARI Alu-31 (Sagitta), BARI Alu-34 (Laura), BARI Alu-37 (4.4O), BARI Alu-41 (5.183), BARI Alu-42 (Agila), BARI Alu-43 (Atlas) and BARI Alu-45 (Steffi) |
| IV      | 2               | 6 and 13 | BARI Alu-13 (Granola) and BARI Alu-27 (Espirit) |
| V       | 2               | 10 and 20 | BARI Alu-24 (Dura) and BARI Alu-35 (4.5W) |
Figure 2. Scattered distribution of 29 BARI released varieties of potato based on their Canonical variate I & II

Principal Coordinate Analysis

Inter genotypic distances ($D^2$) were obtained from Principal Coordinate analysis (PCO) for all possible combinations between pairs of genotypes. Among the possible 406 combinations, the highest inter-genotype distance (1.4122) was observed between BARI Alu-22 (Saikot) and BARI Alu-41 (5.183) followed by BARI Alu-22 (Saikot) and BARI Alu-45 (Steffi) (1.4093), and BARI Alu-22 (Saikot) and BARI Alu-12 (Dheera) and BARI Alu-22 (Saikot) (1.3585) while the lowest distance (0.3436) was observed between genotypes BARI Alu-42 (Agila) and BARI Alu-34 (Laura) (Table 7). The dissimilarity between the highest and lowest in ter genotypic distance indicated the presence of variability among the 29 BARI released varieties of potato.

The intra-cluster distance was computed by using the values of inter genotypic distance from the distance matrix according to Sing and Chaudhary (1985). The magnitude of the intra-cluster distance was not always proportional to the number of genotypes in the clusters (Huque et al. 2012), as cluster I composed of seven genotypes showed highest intra-cluster distance (0.7641) followed by cluster III (0.6168), cluster V (0.5977), cluster II (0.4938) and cluster IV (0.4327) (Table 8). The results supported by Huque et al. (2012).

The inter distances were obtained from the Canonical Variate Analysis (CVA). The values of inter-cluster distance ($D^2$) are presented in Table 8. Inter-cluster distance represents the index of genetic diversity among the clusters (Huque et al. 2012). The values of inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of the different groups. The results supported by Huque et al. (2012). The cluster II and IV were more diverse as indicated by the maximum inter-cluster distances (9.235) between them followed by the distance between cluster II and I (8.469), cluster I and IV (8.201) and cluster IV and V (6.753). The maximum values of inter-cluster distance indicated that the genotypes belonging to cluster II were far away from those of cluster IV. Similarly the higher inter-cluster value between cluster II and I, cluster I and IV and cluster IV and V indicated that the genotypes belonging to each pair of these clusters were far diverse. The minimum inter-cluster distance was found between clusters III and V (1.895) indicating that the genotypes of these clusters were genetically closed. Higher intra-cluster and inter-cluster distances indicate closeness among the genotypes of two clusters and between the clusters also.

Table 6. Cluster mean values for various quantitative characters in BARI released potato varieties

| Characters                              | Cluster-I | Cluster-II | Cluster-III | Cluster-IV | Cluster-V |
|-----------------------------------------|-----------|------------|-------------|------------|-----------|
| Days to 80% emergence                   | 19.14     | 17.83      | 19.50       | 21.33      | 19.67     |
| Foliage coverage                       | 95.86     | 92.33      | 93.75       | 98.00      | 96.78     |
| Plant vigour                           | 8.43      | 8.33       | 8.25        | 9.00       | 9.00      |
| Plant height at 60 days after planting  | 74.29     | 99.13      | 80.28       | 90.63      | 92.03     |
| Primary Stem per hill                  | 5.07      | 5.30       | 4.42        | 5.30       | 4.93      |
| leaf length (cm)                       | 23.85     | 25.99      | 24.58       | 28.37      | 28.79     |
| leaf width (cm)                        | 13.79     | 17.49      | 16.10       | 17.43      | 17.66     |
| Frequency secondary leaflets pairs at midrib | 6.37   | 6.35       | 5.80        | 6.87       | 6.38      |
| Terminal leaflet blade length (cm)     | 7.89      | 7.79       | 7.78        | 8.00       | 8.37      |
| Terminal leaflet Blade width (cm)      | 5.65      | 5.38       | 5.30        | 5.60       | 5.61      |
| Number of Primary Leaflet Pairs        | 4.66      | 5.05       | 4.90        | 5.13       | 4.96      |
| lateral leaflet blade length (cm)      | 7.44      | 8.03       | 7.52        | 8.02       | 8.64      |
| lateral leaflet blade width (cm)       | 4.79      | 4.91       | 4.63        | 5.00       | 5.32      |
| Tuber number/hill                      | 10.35     | 11.50      | 11.02       | 9.32       | 10.06     |
| Tuber weight/hill (kg)                 | 0.64      | 0.65       | 0.75        | 0.50       | 0.71      |
| Tuber yield                            | 42.40     | 43.50      | 50.08       | 33.44      | 47.61     |
Principal Component Analysis:

Principal Component Analysis (PCA) is a statistical method that attempts to describe the total variation in the multivariate sample using fewer variables than in the original data set (Bartolome et al. 1999). In the end, the analysis results in the identification of the significant attributes that are responsible for the observed variation within a given collection.

The computed Eigenvalues for the 16 variables subjected to Principal Component Analysis, together with the corresponding proportion and cumulative explained variance are given in Table 9. Following the Proportion of Variance Criterion, four principal components were retained and these are the principal components whose cumulative explained variances are equal to or more than 90%. In summary, the principal component analysis resulted in the reduction of the 16 original variables to four independent linear combinations, principal component of variables. These four principal components account for 93.35% of the total variation.

The first principal component accounted for 57.44% of the total variation while principal components PC1, PC2 and PC3 accounted for 18.96%, 11.79% and 5.16%, respectively (Table 9). Huque et al. (2012) reported that the first five axes accounted for 87.38% of the total variation whereas the first principal component accounted for 29.00%. Siopongco et al. (1999) reported that the first eight principal components accounted for 73.99% of the total variation whereas the first principal component accounted for 33.59%. Islam et al. (2009) found that the first three principal components accounted for 71% of the total diversity whereas the first principal component accounted for 29.01%.

A scree plot is a useful visual aid for determining an appropriate number of principal components. The magnitude of eigenvalues versus its number with the eigenvalues ordered from largest to smallest. To determine the appropriate number of components, we look for an elbow (bend) in the scree plot. The number of components is taken to be the point at which the remaining eigenvalues are relatively small and all about the same size (Johnson and Wichern 2008). In this case, it appears without any other evidence, that four principal sample components effectively summarized the total sample variance (Figure 3).

Table 7. Ten highest and ten lowest inter genotypic distance among 29 BARI released varieties potato

| Number* | Genotypic Combination                      | Distance (D²) value |
|---------|--------------------------------------------|---------------------|
| 1       | BARI Alu-22 (Saikot) - BARI Alu-41 (5.183)| 1.4122              |
| 2       | BARI Alu-22 (Saikot) - BARI Alu-45 (Steffi)| 1.4093              |
| 3       | BARI Alu-12 (Dheera) - BARI Alu-22 (Saikot)| 1.3585              |
| 4       | BARI Alu-22 (Saikot) - BARI Alu-34 (Laura)| 1.2896              |
| 5       | BARI Alu-22 (Saikot) - BARI Alu-37 (4.40) | 1.2168              |
| 6       | BARI Alu-13 (Granola) - BARI Alu-22 (Saikot)| 1.1789              |
| 7       | BARI Alu-22 (Saikot) - BARI Alu-42 (Agila)| 1.1644              |
| 8       | BARI Alu-7 (Diamant) - BARI Alu-13 (Granola)| 1.1406              |
| 9       | BARI Alu-22 (Saikot) - BARI Alu-25 (Asterix)| 1.1095              |
| 10      | BARI Alu-22 (Saikot) - BARI Alu-31 (Sagitta)| 1.0998              |
|        |                                            | 0.3436              |

Table 8. Average intra- (bold face) and inter-cluster distance (D²) for 29 BARI released varieties of potato

| Cluster | I   | II  | III  | IV   | V    |
|---------|-----|-----|------|------|------|
| I       | 0.7641 |     |      |      |      |
| II      | 8.469 | 0.4938 |      |      |      |
| III     | 5.060 | 3.915 | 0.6168 |      |      |
| IV      | 8.201 | 9.235 | 6.315 | 0.4327 |      |
| V       | 3.171 | 5.463 | 1.895 | 6.753 | 0.5977 |
As a summary, through PCA, it was shown that the variation in the advanced lines of potato could be explained not just by a few but several components (three principal components) and that several characters comprise each component. Furthermore, the results of the principal component analysis support the initial findings of variability estimated using the Shannon-Weaver Diversity Index. The collection is medium diverse in terms of quantitative characters and this reflected by the fact that the first three principal components were loaded by almost all of the characters. The results supported by Siopongco et al. (1999).

**CONCLUSIONS**

The overall diversity index of 0.595 indicates the existence of medium variation in the collection. This means that we still need to conduct exploration trips to acquire additional genotypes in order to enrich our collection and thus conserve maximum genetic variation. From the distance (D^2) matrix, genotypes from clusters II and IV can be selected for hybridization program, while BARI Alu 22 (Soikot) and BARI Alu 41(5.183) can subtly be chosen as parents to get the maximum heterosis from the existing collection.

**ACKNOWLEDGMENTS**

The authors thankfully acknowledged the authority of Bangladesh Agricultural Research Institute,
Gazipur-1701, Bangladesh for supporting to conduct the experiment.

CONFLICT OF INTEREST
The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

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