Morphological characterization and diversity analysis of some BARI released potato varieties

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ABSTRACT

Twenty-nine potato varieties released by Bangladesh Agricultural Research Institute (BARI) were characterized at Breeder Seed Production Centre (BSPC), Debiganj, 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), Debigonj, 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 x 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:

$$H' = -\sum P_i (\log_2 P_i) / \log_2 n$$

Where P_i is the proportion of the total number of

Table 1. Popular name, origin, released year in Bangladesh, breeding method and parentage of BARI developed varieties of potato.

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 Fruhe 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	Saikot	CIP, Peru	2004	GE&S	D79.638.1 X 575049
BARI Alu-24	Dura	N	2005	I&S	Seglinde x Lori
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 SVP(VTN) 2 62-33-3
	Rosetta				
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 77-2102 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

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 Pinnatilobed; 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 Purplish-black; 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; 2a 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 Vascularring medulle; 6 All flesh exept medulla; 7 Other
12.	General Tube shape	1 Compressed; 2 Round; 3 Ovate ;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

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 ($\bar{x}$) and standard deviation (σ) 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 0.5σ . 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.

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

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

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 - 3.50	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 4. Computed diversity indices (H') for the qualitative and quantitative characters of BARI released potato varieties

Character	H'	Character	H'
Qualitative			
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	
Quantitative			
Days to 80% emergence	0.84	Terminal leaflet : blade length (cm)	0.85
Foliage coverage	0.75	Terminal leaflet : blade width (cm)	0.89
Plant vigour	0.44	Number of primary leaflet pairs	0.86
Plant: height at 60 days after planting	0.89	Lateral leaflet blade length (cm)	0.80
Primary stem per hill	0.75	Lateral leaflet blade width (cm)	0.89
Leaf length (cm)	0.85	Tuber number/hill	0.76
Leaf width (cm)	0.80	Tuber weight/hill (kg)	0.87
Frequency secondary leaflets pairs at midrib	0.78	Tuber yield (t/ha)	0.84
		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 I having seven genotypes and 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 (4.40) 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.

Table 5. Distribution of 29 BARI released potato variety in five different clusters

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 (4.40), 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-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 inter 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

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

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

Number*	Genotypic Combination	Distance (D ²) value
Higher inter-genotypic distance		
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
.....		
406	BARI Alu-42 (Agila) - BARI Alu-34 (Laura)	0.3436

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 components accounted for 29.00%. Siopongco et al. (1999) reported that the first eight principal components accounted for

73.99% of the total variation where the first principal components 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).

Figure 3. Scree plot constructed for 16 principal components

Analysis of the factor loading of characters in the retained four components identified the major

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

Table 9. Computed Eigen values with corresponding proportion and cumulative explained variance

Principle Component	Eigen value	Proportion %	Cumulative %
01	116.45	57.44	57.44
02	38.43	18.96	76.40
03	23.90	11.79	88.19
04	10.47	5.16	93.35
05	5.48	2.70	96.05
06	2.93	1.45	97.50
07	1.90	0.94	98.44
08	1.21	0.60	99.04
09	0.78	0.38	99.42
10	0.58	0.29	99.71
11	0.35	0.17	99.88
12	0.12	0.06	99.94
13	0.07	0.03	99.97
14	0.04	0.02	99.99
15	0.03	0.01	<100.00
16	0.01	0.00	100.00

Table 10. Eigen vector / latent vectors / Factor Loadings for Component character traits in Principal Component 1-4.

Characters	PC 1	PC 2	PC 3	PC4
Days to 80% emergence	-0.01517	-0.00980	-0.02173	-0.22219
Foliage coverage	-0.04073	-0.11299	0.69099	0.63721
Plant vigour	0.00430	-0.03089	0.11317	0.00506
Plant height at 60 days after planting	0.98325	-0.01689	-0.08909	0.14014
Primary Stem per hill	0.01213	-0.00097	-0.01721	0.14224
leaf length (cm)	0.13329	-0.13110	0.44685	-0.56522
leaf width (cm)	0.09857	-0.15932	0.38509	-0.36543
Frequency secondary leaflets pairs at midrib	-0.00055	-0.03287	-0.02366	-0.15385
terminal leaflet blade length (cm)	-0.00419	-0.02982	0.14981	-0.08704
terminal leaflet Blade width (cm)	-0.00549	-0.03444	0.09859	-0.02652
Number of Primary Leaflet Pairs	0.01327	-0.00638	-0.00439	-0.01519
lateral leaflet blade length (cm)	0.02920	-0.02982	0.14087	-0.09586
lateral leaflet blade width (cm)	0.00769	-0.02425	0.09359	-0.05184
Tuber number/hill	-0.01459	0.05033	-0.19620	-0.04867
Tuber weight/hill (kg)	0.00072	0.01451	0.00345	-0.00111
Tuber yield	0.04828	0.96742	0.23064	-0.07251

characters responsible for maximum variability (Table 10). The first principal component (PC1) can be considered as the component of plant height, leaf, indicated by high loadings for plant height at 60 days after planting (0.983), leaf length (0.133) and leaf width (0.099). Principal component II (PC2) indicated the importance of foliage coverage and tuber yield. High loadings observed for foliage coverage (0.113), tuber weight per hill (0.015) and tuber yield (0.967). Principal component III (PC3) indicated the importance of leaflet and tuber number per hill. High loadings observed for plant vigour (0.113), terminal leaflet blade length (0.150), lateral leaflet blade length (0.141) and tuber number per hill (0.196). Principal component IV (PC4) on the other hand indicated the importance of Days to 80% emergence and Frequency secondary leaflets pairs at midrib (Table 10).

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 select 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.

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CONFLICT OF INTEREST

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

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