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MORPHOPHYSIOLOGICAL CHARACTERIZATION OF POTATO (*Solanum Tuberosum* L.) GENOTYPES PREVAILING IN THE CORE AREA OF PUNJAB, PAKISTAN

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SUMMARY

Potato (*Solanum tuberosum* L.) is one of the most important vegetable crops and the fourth most important edible crop after the three major cereal crops. It is considered as an approximately complete diet food because of its nutritional value. Its center of origin is Peru, South America. In Punjab, Pakistan, the districts of Sahiwal and Okara serve as the core areas of potato cultivation. Thirty-three potato genotypes were collected from the core areas of Punjab for characterization. The genetic diversity of potato germplasm was assessed on the basis of morphophysiological traits. This experiment was conducted with a randomized complete block design and three replications. The data on 14 morphological and physiological traits were recorded. Analysis of variance indicated the presence of highly significant variation for each physiological and morphological trait. Correlation analysis showed that plant yield was highly correlated with the number of tubers per plant (0.484), tuber weight (0.648), and chlorophyll contents (0.365). By contrast, tuber dry matter exhibited a significant highly negative association with tuber moisture content (−0.753). Algorithmic hierarchical cluster analysis allocated the genotypes into four distinct clusters. Cluster 2, which was the largest cluster, comprised 18 genotypes. By contrast, cluster 4 was the smallest cluster and contained only two genotypes. The results of diversity analysis obtained through hierarchical clustering were further validated through principal component analysis (PCA). PCA provided five significant principal components that contributed 72.39% of the total variation. The principal components of the biplot explained 41.95% of the total variation, with tuber moisture content and tuber dry matter as distinct traits. Cultivars 'SH-5', 'SH 7-18', 'Simply Red,' and 'Ruby' were the vertex genotypes in the biplot. Results indicated the prevalence of significant variation in the tested germplasm. Furthermore, the assessment of diversity at the molecular level is recommended for the further validation of genetic diversity.

Keywords: Genetic diversity, Punjab, morphophysiological traits, principal component analysis, hierarchical clustering, *Solanum tuberosum* L.

Key findings: A high level of genetic diversity for all 14 morphophysiological traits was observed in the 33 tested potato varieties. Plant yield was associated with tuber-related

traits, i.e., the number of tubers per plant and tuber weight. Therefore, improving tuber-related traits will enhance the yield of potato.

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INTRODUCTION

Potato (*Solanum tuberosum* L.) belongs to the Solanaceae family, which is also known as the nightshade family, of plants. It is considered as the most important edible crop worldwide after the three important cereals, namely, wheat, rice, and maize (Akkale *et al*., 2010). The total global production of potato is 370.43 million tons (FAO, 2019). China is the largest potato producer (91.88 million tons), followed by India (50.1 million tons) and Russia (22.07 million tons). Pakistan accounts for only 1% of the world's total potato production and has an average yield of 24.88 tons per hectare (FAO, 2019). Although most potato cultivars are tetraploid, cultivars with variable polyploidy levels, i.e., diploidy, triploidy, and pentaploidy, also exist (Watanabe, 2015). In various ecological zones of Pakistan that span from the plains of Punjab to the hilly areas of Khyber Pakhtunkhwa and Gilgit Baltistan, the potato crop is grown during three different seasons, i.e., spring, summer, and autumn (Khan and Akhtar, 2006). In Punjab, Sahiwal and Okara are the two districts that serve as the core area of potato cultivation.

Potato is one of the most preferred diet food crops because of its nutritional value and diverse value chain. Potato tubers contain carbohydrates, resistant starch, beneficial proteins, vitamin C, vitamin B6, and potassium that are important for human metabolic function (Camire *et al*., 2009). In cooked potatoes, the quantity of vitamins C and B6 decreases significantly, whereas that of anthocyanins and carotenoids has a high recovery rate due to the improved release of these compounds from food during meal preparation (Tian *et al*., 2016). The energy provided by 100 g of boiled potato tubers ranges from 96.33 kcal to 123.17 kcal and is approximately equal to the energy provided by 100 g of cooked rice (130 kcal) and 100 g of cooked cassava (160 kcal) (King and Slavin, 2013; De-Haan *et al*., 2019). Genetic variation is one of requirements of breeding programs for the development of genetically diverse plant varieties (Flajoulot *et al*., 2005). Improving the yield levels of potato in Pakistan is direly needed.

The assessment of genetic diversity provides useful information on diverse genetic material that could be used in programs for the development of new varieties for different targeted regimes. A plant's genetic makeup and response after interaction with stress are the key essence of plant resistance (Pedley and Martin, 2003). In South America, local farmers have developed improved cultivars through selection by exploiting the naturally prevailing diversity of existing potato varieties (Bradshaw *et al*., 2006). Among various factors, crop genotype is the main factor for crop improvement (Aremu, *et al*., 2007). Mendoza and Haynes (1974) proposed that a high level of heterozygosity is the basis of high heterosis that leads to increased potato yield. Characterization studies are necessary for the selection of the best parental lines with maximum genetic potential for new cultivar development (Aremu *et al*., 2007). Singh *et al*. (2006) revealed that the identification of genetic variability among genotypes is the most important step in the breeding of desired crop cultivars. Therefore, this study was designed for the identification of potato genotypes with superior performance that

can be utilized as parental lines in future breeding programs.

MATERIAL AND METHODS

Plant materials and experimental site

This experiment was conducted at the research area of Plant Pathology Research Institute, Ayub Agricultural Research Institute, Faisalabad, Pakistan (31.4504°N, 73.1350°E) during the 2019–2020 winter season. Thirty-three potato genotypes were provided by the Potato Research Institute Sahiwal, Pakistan, which is located in the core area of potato cultivation in Punjab (Table 1, Figure 1). This trial was conducted with a randomized complete block design (RCBD) and three replications.

Table 1. Potato genotypes collected from the core area in Punjab, Pakistan.

No.	Genotypes	No.	Genotypes	No.	Genotypes
1	FD 75-47	12	FD 1-3	23	FD 76-72
2	Safayada	13	FD 76-6	24	FD 73-73
3	FD 71-1	14	Simply Red	25	Karoda
4	Ruby	15	SH 7-18	26	FD 77-4
5	Bar	16	FD 74-30	27	FD 73-49
6	FD 76-55	17	FSD Red	28	FD 81-1
7	FD 74-38	18	PRI Red	29	FD 73-44
8	Sante	19	SL 9-14	30	SH-5
9	FD 78-51	20	FD 51-5	31	Cere Za
10	Asterix	21	FSD White	32	FD 73-110
11	Sadaf	22	FD 35-36	33	SL 28-51

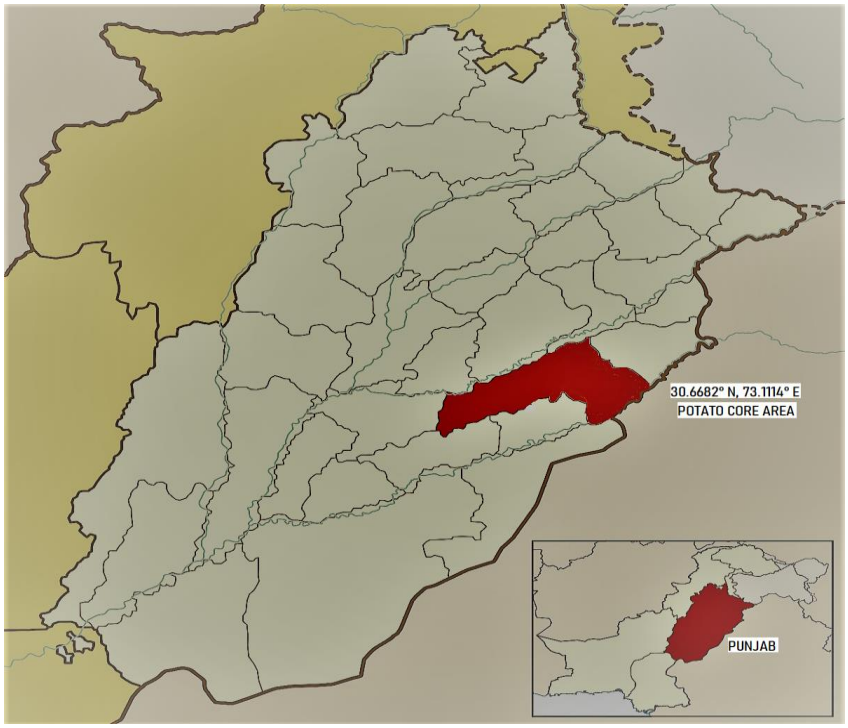

Figure 1. Geographical location of the core area of potato cultivation in Punjab, Pakistan.

Data collection

Data were collected on various morphophysiological attributes as follows: the number of tubers per plant; plant height; the number of compound leaves; the number of aerial stems; plant yield; tuber weight; tuber dry matter; tuber length; tuber girth; tuber moisture content, which was determined with the help of a pH–moisture meter (Westland Company, Northern Ireland); chlorophyll content, which was quantified with a chlorophyll concentration meter (MC-100, Apogee Instruments, USA); total soluble solids, which was determined with a UV–visible spectrophotometer (V-730, Mary's Court Easton, MD 21601 United States); and relative leaf water content, which was measured in accordance with Yamasaki and Dillenburg (1999).

Statistical analysis

The recorded data were subjected to analysis of variance (ANOVA), correlation coefficient analysis, algorithmic hierarchical clustering, and principal component analysis (PCA) by using XLStat 2014 software (Sneath and Sokal, 1973; Wold *et al.*, 1987; Steel *et al.*, 1997).

RESULTS

ANOVA and correlation analysis

ANOVA revealed significant genotypic variation among all potato genotypes for the morphophysiological traits under consideration (Table 2). High significant variation among the genotypes indicated the presence of genetic diversity within the germplasm. Correlation analysis was performed to explore the association between observed attributes (Table 3). Chlorophyll contents had positive associations with tuber weight (0.442), plant height (0.398), tuber length (0.353), and plant yield (0.365). By contrast, chlorophyll contents had a negative correlation with the number of aerial stems (−0.365). Plant yield had a highly significant association with the number of tubers (0.648) and tuber weight (0.494). By contrast, tuber weight had a significantly negative correlation with the number of compound leaves (−0.482). Tuber dry matter had a highly positive correlation with tuber weight (0.730) and a negative correlation with the number of compound leaves (−0.339). Tuber moisture content had a highly negative relation with tuber dry matter (−0.753). Leaf area had a positive association with tuber girth (0.607) and tuber moisture content (0.356). Relative leaf water content had a significantly negative association with total soluble solids (−0.463).

The mean performance of all genotypes for each trait is given in Table 4. 'Sadaf' had the highest plant height (49.75 cm). 'Safayada' had the highest number of aerial stems (7.00). 'Simply Red' had the highest number of compound leaves (106). 'FD 75-47' had the highest chlorophyll contents (26.65 SPAD). 'FD 73-49' had the highest plant yield (978.5 g). 'FD 1-3' had the highest number of tubers (14.5). 'SH-5' had the highest tuber weight (107.15 g) and tuber dry matter content (27.53%). 'Ruby' had the highest leaf area (cm^2). 'FD 81-1' had the highest relative leaf water content (63.25). 'Asterix' had the highest tuber moisture content (93.4%) and tuber length (10.0 cm). 'FD 76-6' had the highest leaf area (56.9 cm^2). 'FD 78-51' had the highest tuber girth (6.45 cm). 'FSD Red' had the highest total soluble solids (11.7 Brix°).

Algorithmic hierarchical clustering

Algorithmic hierarchical clustering was performed to classify genotypes into various categories based on dissimilarities. The genotypes were grouped into four distinct clusters. The distance between cluster centroids is given in Table 5. The cluster centroid distances between clusters 1 and 2, clusters 1 and 3, and clusters 1 and 4 were 212.12, 190.01, and 506.12, respectively. The cluster distance between clusters 2 and 3 and clusters 2

Table 2. ANOVA for the morpho-physiological traits of potato.

Source of variation	d.f.	PH	NS	NCL	CC	PY	NT	TW
Replication	2	0.835	0.54	230.68	7.56	1082	0.27	9.15
Genotypes	32	159.4**	4.14**	888.31**	51.79**	107328**	18.81	981.18**
Residual	64	10.51	0.82	91.46	3.55	4069	0.71	32.4
Grand Mean		36.78	5.09	61.67	16.99	589.73	9.09	67.77
SOV	Df	LA	RLWC	TMC	TDM	TL	TG	TSS
Replication	2	91.18	3.07	2.01	2.99	0.16	0.01	0.06
Genotypes	32	470.66**	371.52**	80.69**	73.87**	1.7**	1.3**	5.86**
Residual	64	18.57	15.71	6.75	5.2	0.28	0.1	0.18
Grand Mean		38.95	37.22	83.45	11.36	8.3	5.29	7.5

Significance levels: <0.01 '**'<0.05 '*'

SOV = Sources of variation, Df = Degree of freedom, PH = Plant height (cm), NS = Number of aerial stems, NCL = Number of compound leaves, CC = Chlorophyll content (SPAD), PY = Plant yield (g), NT = Number of tubers, TW = Tuber weight (g), LA = Leaf area (cm^2), RLWC = Relative leaf water content (%), TMC = Tuber moisture content (%), TDM = Tuber dry matter (%), TL = Tuber length (cm), TG = Tuber girth (cm), TSS = Total soluble solids (BRIX).

Table 3. Coefficients of correlation among 14 potato morphophysiological traits.

Variables	PH	NS	NCL	CC	PY	NT	TW	LA	RLWC	TMC	TDM	TL	TG	TSS
PH	1.000													
NS	−0.124	1.000												
NCL	0.184	0.111	1.000											
CC	0.398*	−0.365*	−0.327	1.000										
PY	0.198	0.036	−0.256	0.365*	1.000									
NT	0.208	0.230	0.131	0.086	0.648**	1.000								
TW	0.019	−0.145	−0.482**	0.442**	0.494**	−0.266	1.000							
LA	0.082	−0.114	−0.171	0.085	0.185	0.252	−0.030	1.000						
RLWC	0.209	−0.034	−0.091	0.260	0.130	−0.208	0.325	−0.090	1.000					
TMC	0.236	0.179	0.132	−0.001	0.108	0.241	−0.145	0.356*	0.003	1.000				
TDM	−0.134	−0.284	−0.339*	0.297	0.189	−0.355	0.730**	−0.271	0.185	−0.753**	1.000			
TL	0.116	−0.149	−0.216	0.353*	0.185	−0.012	0.183	0.214	0.026	0.003	0.089	1.000		
TG	0.089	0.112	−0.136	0.184	0.262	0.302	−0.024	0.607**	−0.031	0.256	−0.252	0.111	1.000	
TSS	−0.274	−0.033	0.020	0.004	−0.081	−0.079	0.045	−0.143	−0.463**	−0.164	0.141	0.176	0.006	1.000

Significance levels: <0.01 '**'<0.05 '*'

Table 4. Mean performance of 33 genotypes for 14 morpho-physiological traits.

Genotypes	PH	NS	NCL	CC	PY	NT	TW	LA	RLWC	TMC	TDM	TL	TG	TSS
FD 75-47	49.00	3.25	68.50	26.65	689.75	8.75	79.04	40.85	49.38	76.60	18.63	9.55	5.75	6.45
Safayada	26.13	7.00	60.25	9.70	415.50	7.00	58.92	29.66	34.08	83.30	9.78	7.65	5.20	4.75
FD 71-1	45.50	6.50	46.50	19.38	751.50	9.00	87.62	25.20	33.93	88.55	10.06	7.75	4.50	7.80
Ruby	42.75	4.75	52.75	20.40	728.75	12.50	58.30	63.15	34.62	90.45	5.46	8.50	6.20	7.65
Bar	37.50	4.25	60.00	20.15	572.75	7.25	78.94	27.40	48.27	77.25	17.97	7.70	4.75	7.40
FD 76-55	31.75	5.25	58.25	22.95	560.25	9.50	65.41	60.15	42.41	92.00	5.27	9.25	5.90	7.70
FD 74-38	36.00	5.25	59.00	10.68	562.25	8.00	70.29	33.65	32.03	82.90	12.02	7.60	4.10	5.65
Sante	22.75	6.00	62.75	9.53	803.25	11.50	70.10	57.30	27.94	90.90	6.25	7.90	6.25	8.85
FD 78-51	47.75	5.50	46.00	23.58	581.25	7.50	88.80	27.25	41.91	87.85	11.14	8.00	6.45	7.15
Asterix	38.50	5.25	39.75	18.43	705.00	11.75	59.97	49.25	33.06	93.40	3.95	10.00	5.50	8.20
Sadaf	49.75	5.50	83.50	15.58	512.50	9.25	53.12	57.70	29.06	90.00	5.56	7.95	5.95	7.50
FD 1-3	42.13	6.00	79.00	15.23	741.00	14.50	51.23	35.95	26.32	82.05	9.21	7.55	4.80	7.30
FD 76-6	48.13	4.75	66.75	14.98	410.00	4.50	91.13	56.90	54.31	82.75	15.72	9.35	5.00	7.00
Simply Red	35.50	5.00	106.00	11.98	177.50	4.75	45.87	18.45	42.17	88.50	5.53	8.10	4.45	7.25
SH 7-18	45.50	4.25	100.75	15.80	467.25	13.00	35.87	40.90	26.02	92.70	2.61	7.20	4.95	6.10
FD 74-30	28.63	5.50	60.00	13.48	390.25	8.75	45.03	44.50	19.73	75.50	11.05	8.05	5.60	10.40
FSD Red	34.75	5.75	102.50	16.08	505.50	8.25	60.77	16.10	21.33	81.15	11.55	8.80	4.65	11.70
PRI Red	35.50	4.25	53.75	15.33	371.00	6.75	55.02	54.15	26.60	80.50	10.71	9.10	5.45	6.55
SL 9-14	41.13	5.25	45.75	16.25	564.00	9.25	60.83	45.70	31.28	79.95	12.18	8.10	5.40	6.75
FD 51-5	33.00	5.00	79.75	11.55	691.25	11.75	58.79	34.25	33.63	76.15	14.00	8.65	5.45	7.55
FSD White	36.75	3.25	58.25	22.15	649.00	10.50	61.87	48.80	25.28	80.50	12.09	7.65	5.85	7.10
FD 35-36	35.00	8.50	65.75	17.48	514.00	12.00	47.49	30.30	42.46	78.30	10.27	8.35	5.80	7.40
FD 76-72	40.25	3.75	62.75	21.40	965.25	9.75	98.85	34.80	61.79	83.20	16.53	8.15	5.25	7.00
FD 73-73	45.00	6.00	61.25	15.03	846.25	12.00	70.19	31.10	57.41	82.50	12.36	7.65	5.40	6.60
Karoda	37.50	5.00	39.00	20.33	887.25	9.50	99.04	29.75	30.07	81.05	18.58	9.80	4.85	8.35
FD 77-4	32.75	3.50	47.25	20.90	702.50	10.00	70.73	29.75	37.14	78.80	14.87	9.50	4.05	7.05
FD 73-49	33.75	6.25	62.00	17.05	978.50	11.75	88.47	53.90	33.43	86.35	11.81	8.85	6.75	7.15
FD 81-1	29.00	6.50	57.50	17.05	535.25	7.25	74.24	43.20	63.25	85.30	10.67	7.80	5.10	5.15
FD 73-44	31.63	4.25	62.00	15.13	514.50	8.75	58.24	34.70	46.73	81.65	10.89	7.25	4.90	6.90
SH-5	22.13	5.00	43.50	17.98	444.25	5.25	107.15	31.05	27.53	76.05	25.97	7.65	4.50	10.15
Cere Za	35.88	4.75	51.75	19.15	484.25	7.75	62.03	30.60	42.39	86.05	8.59	8.50	4.90	7.95
FD 73-110	30.75	2.75	39.50	18.28	511.50	6.00	85.25	43.35	35.27	80.75	16.36	7.95	5.80	8.40
SL 28-51	32.00	4.50	53.25	11.25	228.00	6.00	37.97	25.70	37.59	80.90	7.26	8.30	5.30	8.85
Means	36.79	5.10	61.67	16.99	589.73	9.09	67.77	38.95	37.22	83.45	11.36	8.31	5.30	7.51
Maximum	49.75	8.5	106.00	26.65	978.50	14.5	107.15	63.15	63.25	93.4	25.97	10.00	6.75	11.7
Minimum	22.12	2.75	39.00	9.52	177.50	4.50	35.87	16.10	19.73	75.5	2.61	7.20	4.05	4.75

Table 5. Inter-cluster distance between cluster centroids.

Clusters	1	2	3	4
1	0.00	212.1237	190.0061	506.1246
2	212.1237	0.00	401.2722	294.7955
3	190.0061	401.2722	0.00	695.4067
4	506.1246	294.7955	695.4067	0.00

and 4 were 401.27 and 294.79, respectively. The highest cluster distance (695.40) was found between clusters 3 and 4. A dendrogram was generated based on Euclidean distance and the unweighted pair group average method with arithmetic mean (UPGMA). The dendrogram was based on dissimilarities among clusters and genotypes (Figure 2).

The variance decomposition within clusters was 12.48% and that among clusters was 87.52%. Cluster 1 comprised eight genotypes. Cluster 2 was the largest cluster and included 18 genotypes. Cluster 3 contained five genotypes, whereas cluster 4 was the smallest cluster with two genotypes. A profile plot showing the contribution of the traits to clustering was generated for each cluster (Figure 3). The profile plot revealed that compared with other traits, plant yield, followed by tuber weight, had a greater contribution to the grouping of genotypes into different clusters.

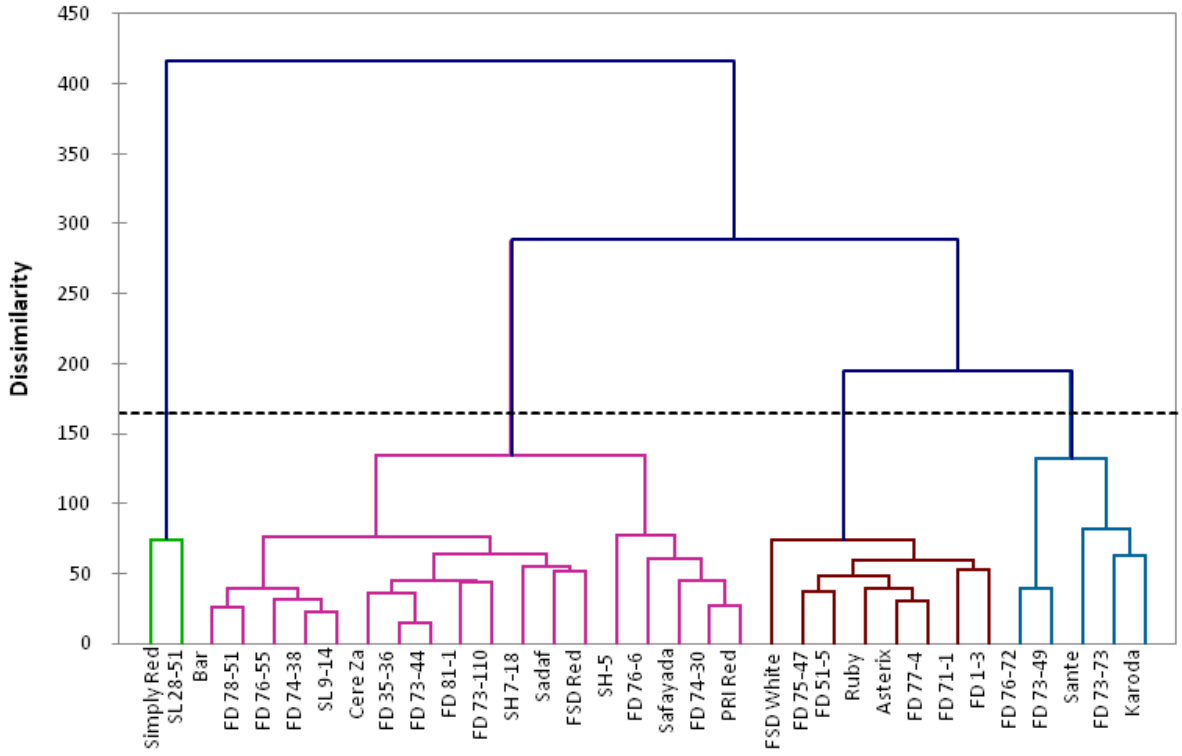

Figure 2. Dendrogram of 33 potato genotypes based on morphophysiological parameters. The dendrogram was obtained by using Euclidean distance with the UPGMA method.

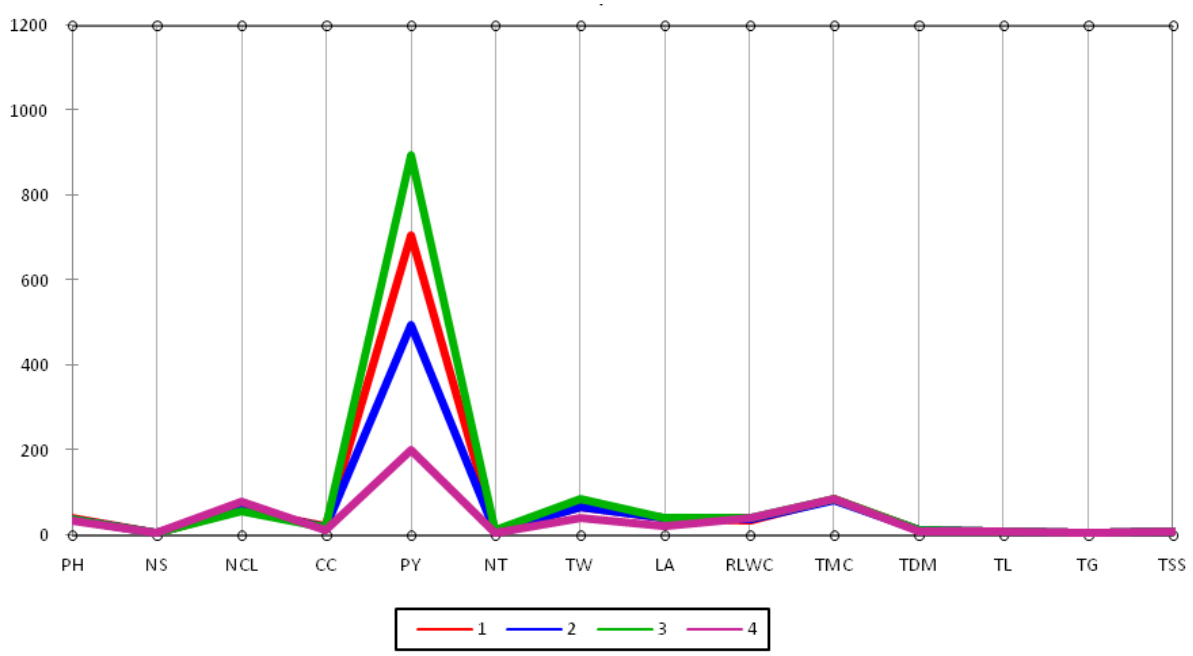

Figure 3. Profile plot of clusters based on morphophysiological traits.

PCA

PCA extracted 14 principal components (PCs) on the basis of morphophysiological attributes. Among these PCs, five had eigenvalues exceeding 1 with the cumulative variation of 72.38% (Table 6). The PC1, PC2, PC3, PC4, and PC5 had contributions of 22.1%, 19.79%, 11.97%, 9.64%, and 8.82%, respectively. PC1 was largely represented by tuber dry matter, tuber weight, the number of compound leaves, and tuber moisture content. All parameters exhibited positive factor loadings for PC1, and most were traits related to tuber quality. In PC2, plant yield, tuber girth, leaf area, and the number of tubers were the traits presenting major variation. PC2 was related to plant yield. Total soluble solids, relative leaf water content, and plant height represented most of the variation explained by PC3. However, the number of aerial stems, plant yield, and the number of tubers represented most of the variation in PC4, whereas PC5 had no significant contribution from any parameter (Table 7). Eight genotypes, viz., 'FD 75-47', 'Bar', 'Sadaf', 'SH 7-18', 'FD 76-72', 'Karoda', 'SH-5', and 'FD 73-110', contributed significantly to the variation represented by PC1 (Table 8). Eight genotypes, namely, 'Ruby', 'FD 76-55', 'FD 74-38', 'Asterix', 'Simply Red', 'FD 73-49', 'FD 73-44' and 'SL 28-51' largely contributed towards the total variation in PC2. Only two genotypes, namely, 'Sante' and 'FD 74-30', were contributors to the variation in PC3. The remaining 15 genotypes were distributed in the two remaining PCs.

The biplot of PC1 and PC2 explained 41.95% of the variation. Tuber moisture content, tuber dry matter, plant yield, chlorophyll contents, and tuber weight had the longest vectors, which represented the maximum contribution. By contrast, total soluble solids, the number of aerial stems, and plant height provided the minimum contribution. Tuber moisture content and tuber dry matter content were the most discriminating attributes considering that they had the longest vectors with a negative association between them (Figure 4). 'Simply Red', 'SH 7-18', 'Ruby', 'FD 73-

Table 6. Eigen value, variability, and factor loadings of five PCs.

Traits	PC1	PC2	PC3	PC4	PC5
Eigen value	3.1018	2.7707	1.6758	1.3507	1.2351
Variability (%)	22.156	19.790	11.970	9.6481	8.8221
Cumulative%	22.1561	41.946	53.916	63.565	72.387
Plant height	−0.0077	0.4734	−0.5155	−0.1780	0.4779
Number of aerial stems	−0.4157	−0.0164	0.0274	0.5953	−0.2629
Number of compound leaves	−0.5589	−0.2372	−0.2704	−0.0058	0.4644
Chlorophyll content	0.5689	0.5217	−0.0877	−0.2133	0.2952
Plant yield	0.3005	0.6937	0.0933	0.5535	0.1617
Number of tubers	−0.3705	0.5949	0.1514	0.4950	0.3487
Tuber weight	0.8299	0.1997	−0.0018	0.1924	−0.1649
Leaf area	−0.1858	0.6384	0.2714	−0.3383	−0.3497
Relative leaf water content	0.3580	0.1651	−0.7044	0.0247	−0.2870
Tuber moisture content	−0.5348	0.5038	−0.1545	−0.1648	−0.1352
Tuber dry matter	0.8927	−0.2522	0.0743	0.1840	0.0370
Tuber length	0.3042	0.3376	0.2759	−0.3743	0.1819
Tuber girth	−0.1769	0.6423	0.3138	−0.0980	−0.2923
Total soluble solids	0.0843	−0.2535	0.7233	−0.0699	0.3422

Table 7. Variance in 14 morpho-physiological traits explained by five PCs.

Traits	PC1	PC2	PC3	PC4	PC5
Plant height	0.0019	8.0880	15.8585	2.3468	18.4917
Number of aerial stems	5.5716	0.0098	0.0447	26.2395	5.5954
Number of compound leaves	10.0697	2.0298	4.3622	0.0025	17.4600
Chlorophyll content	10.4354	9.8249	0.4593	3.3690	7.0574
Plant yield	2.9109	17.3678	0.5196	22.6811	2.1163
Number of tubers	4.4250	12.7724	1.3685	18.1418	9.8425
Tuber weight	22.2066	1.4396	0.0002	2.7410	2.2017
Leaf area	1.1126	14.7081	4.3951	8.4709	9.8995
Relative leaf water content	4.1320	0.9837	29.6055	0.0452	6.6679
Tuber moisture content	9.2198	9.1600	1.4250	2.0102	1.4800
Tuber dry matter	25.6931	2.2963	0.3292	2.5061	0.1105
Tuber length	2.9833	4.1131	4.5413	10.3737	2.6788
Tuber girth	1.0089	14.8875	5.8749	0.7109	6.9181
Total soluble solids	0.2293	2.3190	31.2161	0.3613	9.4803

Table 8. Variance in 33 genotypes explained by five PCs.

Genotypes	PC1	PC2	PC3	PC4	PC5
FD 75-47	2.9756	1.6967	−1.1619	−1.3595	1.5765
Safayada	−1.5142	−1.9468	−0.7619	1.0919	−2.2832
FD 71-1	0.4845	0.3528	−0.7969	1.3814	0.5285
Ruby	−1.2845	3.2178	0.6916	−0.7442	−0.0045
Bar	2.1875	−1.2486	−1.1256	0.2305	0.3294
FD 76-55	−0.7110	2.2591	0.6399	−1.5393	−0.8840
FD 74-38	−0.3390	−1.6606	−1.0940	0.8281	−0.5472
Sante	−2.2320	1.0918	2.4257	1.1876	−1.6678
FD 78-51	1.0481	1.5474	−0.9362	−0.2930	−0.3029
Asterix	−0.9756	2.5609	1.2311	−0.9047	0.1103
Sadaf	−2.5704	1.3389	−0.3369	−1.1055	0.3954
FD 1-3	−1.8347	0.2462	−0.1363	1.9476	1.7317
FD 76-6	1.5827	0.0460	−1.4465	−1.9639	−0.7524
Simply Red	−2.3567	−3.1502	−2.0178	−1.4358	0.5045
SH 7-18	−3.8835	0.4359	−1.5679	−0.4747	1.7643
FD 74-30	−1.0167	−1.8879	2.8063	−0.2784	0.0742
FSD Red	−0.7425	−2.5671	1.6236	0.2006	2.8991
PRI Red	−0.2395	−0.3836	0.7306	−1.9933	−0.7433
SL 9-14	0.0197	0.1785	0.1420	−0.0277	−0.3549
FD 51-5	−0.3789	−0.6788	0.7154	1.1331	0.7968
FSD White	0.3181	0.9309	0.7062	−0.6261	0.5449
FD 35-36	−1.2921	−0.1514	0.0709	1.8833	−0.1971
FD 76-72	2.7050	1.5265	−1.6209	0.9109	0.3521
FD 73-73	0.1152	1.0163	−1.7841	2.0874	0.0835
Karoda	3.0559	0.7432	1.2586	0.7978	0.9516
FD 77-4	2.1830	−0.3574	0.0834	−0.1950	1.1986
FD 73-49	0.0069	2.9073	1.3937	1.3824	−0.8441
FD 81-1	0.1748	−0.1217	−2.0478	0.6131	−2.5131
FD 73-44	−0.2052	−1.2204	−0.9526	0.1691	−0.5567
SH-5	3.5880	−3.1392	2.0559	0.6812	−0.6987
Cere Za	0.1401	−0.4582	−0.3776	−0.7894	0.0191
FD 73-110	2.1279	−0.5321	1.1076	−1.3525	−0.9970
SL 28-51	−1.1365	−2.5926	0.4820	−1.4427	−0.5134

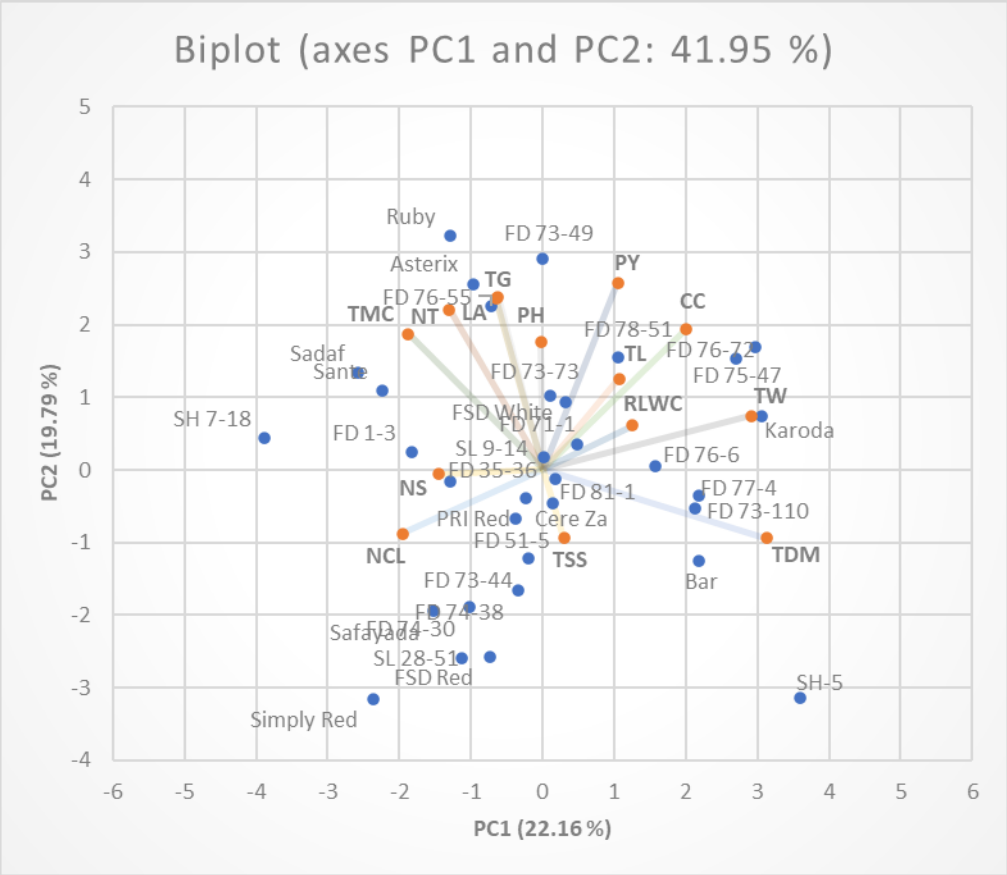

Figure 4. Biplot of PC1 and PC2 for agromorphological traits.

49', 'SH-5', 'FSD Red', and 'SL 28-51' were highly variable genotypes. 'FD 81-1', 'FD 35-36', and 'SL 9-14' were the genotypes with the least variation.

DISCUSSION

Potato, one of the most diverse crops with a wide distribution across the globe, can be used to address food security (Haverkort *et al*., 2014). In the Indo-Pakistan plains, potatoes are cultivated either in monoculture or in rotation and is regarded as a cash and staple crop. The potato yield in India has increased significantly at an average rate of 2% per year owing to successful breeding programs and quality seed systems (Scott and Suarez, 2011). In Bangladesh, potato is the second most important food and cash crop after rice and is widely distributed across the country (Scott and Suarez, 2012). In the United States, nutritionists endorse the application of potato as a staple food because of its nutritive value and its contribution to a balanced diet (Bohl and Johnson, 2010). By addressing micronutrient deficiency, the potato combats a global health issue, namely, hidden hunger, that affects almost two billion people (Bailey *et al*., 2015). The content of health-promoting components, such as vitamin C, phenolic compounds, iron, and protein, in potato is comparable with that in cereals (Burlingame *et al*., 2009).

Plant breeders are constantly searching for genetically diverse germplasm for the breeding of improved crop cultivars. High germplasm diversity is beneficial for trait-targeted crop

improvement, i.e., breeding materials with high diversity have a high probability that they will contain desirable genes for the trait of interest, thus providing additional room for crop improvement. The assessment of genetic diversity in germplasm (accessions, landraces, advance breeding lines, and segregating populations) relies on agronomic, morphological, biochemical, and molecular analyses (Mohammadi and Prasanna, 2003). Various studies have already been conducted to characterize the genetic diversity of potato germplasm (Ahmadizadeh and Felenji, 2011; Arslanoglu *et al*., 2011).

A particular statistical method or a combination of statistical methods is utilized to reveal variation in available accessions and classify genotypes into various heterogeneous groups (Aremu, 2005). In this work, ANOVA indicated the presence of highly significant genetic diversity for all morphophysiological attributes in the genotypes. Correlation analysis showed that plant yield was significantly associated with the number of tubers per plant, chlorophyll contents, and tuber weight. Tuber yield and tuber-related parameters have also been reported to be significantly positively associated (Gunel *et al*., 1991; Ruiz-de-Galarreta *et al*., 2006). Tuber moisture content was highly correlated with tuber weight but was negatively correlated with tuber dry matter. Similar findings have also been reported by previous studies on the morphophysiological traits of potato (Solis *et al*., 2007; Khan *et al*., 2013). Roy and Singh (2006) recommended the application of some tuber-yield-related traits, i.e., plant height, number of tubers per plant, and tuber yield per plant, as selection criteria for yield improvement in potato because of their significant associations. 'FD 73-49', 'SH-5', 'FD 1-3', and 'Asterix' can be utilized as the parents for the improvement of plant yield, tuber weight, the number of tubers, and dry matter content, respectively.

The estimation of genetic diversity in germplasm is the key step in the selection of suitable genotypes for breeding (Bose and Pradhan, 2005). Previously, De Mello *et al*. (2016) performed PCA to characterize potato genotypes. In this study, PCA identified five significant PCs that indicated the existence of diversity among genotypes on the basis of morphophysiological traits. The biplot of PC1 and PC2 revealed that tuber moisture content, tuber dry matter, plant yield, chlorophyll contents, and tuber weight were the main traits representing diversity. Khan *et al*. (2013) previously applied cluster analysis to classify potato genotypes into various clusters depending on morpho-physiological traits. In a following study, cluster analysis distributed 33 potato genotypes into five distinct clusters. All statistical analyses validated the existence of genetic diversity among genotypes. This diversity is very useful for trait-targeted potato improvement. Biswas *et al.* (2010) utilized 20 inbred lines and 30 F_1 progenies that were developed with the line × tester mating design for characterization and combining ability studies. These 50 genotypes were classified into seven distinct clusters.

Cultivar selection by assessing available potato germplasm is considered as one of the most important practices that can be used to develop improved cultivars (Park *et al*., 2002). The assessment of locally available germplasm should be the initial step in any crop improvement scheme (Williams *et al*., 1991). The inclusion of local potato germplasm in breeding programs would ensure the development of climate-smart cultivars (Ortiz, 2001). Genetic diversity studies help breeding programs identify genetically diverse breeding material that facilitates developing the improved cultivars of different crops (Aremu, 2005). Genetically distinct or diverse genotypes are required as breeding material to improve heterosis for a specific trait (Cruz, 2001). One of the success stories of potato crop improvement via diversity exploitation is the development of the potato variety 'Freedom Russet' through selection and hybridization between the disease-resistant parent 'ND 14-1' and

'W1005 rus', a parent with high processing quality (Groza *et al*., 2009).

CONCLUSIONS

High genetic diversity for morphophysiological traits was found in the investigated potato genotypes. Plant yield was associated with tuber-related attributes. Cluster analysis allocated the germplasm into four heterogeneous groups. Significant variation was found for all the morphophysiological traits of the genotypes. The findings of this study could be used by breeding programs for the selection of parents for the further improvement of potato varieties.

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