



RESEARCH ARTICLE

Genetic variation among biofortified and late blight tolerant potato (*Solanum tuberosum* L.) (mini tuber) production in Bangladesh

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ABSTRACT

Biofortified potato could contribute a major role in food security for millions of people. It could help to alleviate worldwide micronutrient malnutrition. An experiment was carried out during 2019-2020 growing season with 49 accessions following randomized complete block design with three replications in order to evaluate and classify agro-morphological traits in Breeder seed production centre (BSPC), Debiganj, Panchagarh. Eight quantitative characters *i.e.* germination percent, foliage coverage, stem number per hill, plant height, plant vigor, tuber number per plant, tuber weight per plant, yield per plant were measured. Principal components (PC) analysis showed three components explained 72.16 % of the total variation among traits. The first PC assigned 35.22 % and the second PC assigned 58.47 % of total variation between traits. The first PC was more related to yield per plant and weight of tuber. Forty-nine germplasm was placed on three cluster based on cluster analysis using a hierarchical classification (HCA). All accessions were discriminated and high morphological variation was observed. Thus, the outcomes of principal component analysis used in the study have revealed the high level of genetic variation and the traits contributing to the variation were identified. CIP403, CIP404, CIP405, CIP413 and CIP445 accessions identified as superior based on cluster relationship and PCA bi-plot.

Introduction

Micronutrient deficiency is a major problem, which is often termed as hidden hunger. It affects over two billion people worldwide (1). Potato could contribute to a major role in food security for millions of people. Worldwide micronutrient malnutrition could be eradicated by serving biofortified potato and ensuring nutrient security. Biofortification is the development of micronutrient or vitamin-rich crops using the traditional crop improvement practices as well as modern biotechnology tools. It is a more sustainable and cost-effective method than the food supplementation, fortification and diet diversification (2). The most popular and earliest example of a success story of transgenic biofortification research is the development of Golden Rice or β -carotene rich rice. Golden rice transgenic lines have been under field trial in the Philippines (transgenic of RC-28), Bangladesh (transgenic of BRRI Dhan-29) and will certainly help to fight against iron deficiency (3). Potato is one of the most important tuber crops grown in Bangladesh for its high production, high nutritional

values, easy digestibility and many industrial uses (4). According to a researcher (5), potato is considered as a promising candidate crop for feeding the hungry people of the world after rice and wheat. Genetic diversity and variability in a population of certain crop species is a prerequisite for an effective plant-breeding programme. A morphological tool for an efficient choice of parents is needed to initiate a hybridization programme. 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 (6). When a large number of desirable traits are involved, the application of PCA is recommended to facilitate the selection of the most relevant variables. The PCA identifies plant traits that distinguish the distinctness among the chosen genotypes for hybridization. A group of researchers (7), mentioned that these techniques aid in the classification of a population into groups of distinct orders based on similarities and thus assisting to choose parents for hybridization. The researcher and their associates (8), reported that PCA reduced the original five sensory attributes into two

independent components, which accounted for 66% of the total variability in the data. The knowledge of genetic diversity helps to avoid duplicates in the collection provides a better classification and assist in breeding selection (9). The PCA has been used to partition observed agronomic variations in genotypes of many crops such as sweet potato landraces (7), rubber, rice, sesame and durum wheat (10-13). Therefore, PCA is a very useful tool to classify genotypes of different crops. For a successful breeding programme, genetic diversity and variability are useful tool for an efficient choice of parents for hybridization to develop high-yield potential cultivars. In addition, multiple nutrition traits along with late blight tolerance will be possible to combine in a single cultivar along with high yield through hybridization (14). The purpose of this study was to investigate genetic divergence through PCA in biofortified and late blight tolerant CIP potato germplasm and the selection of desirable accession for hybridization in Bangladesh.

Materials and Methods

Forty-nine (thirty-nine high yielding biofortified and ten late blight tolerant) potato germplasm (Table 1) collected from Tuber Crop Research Centre (TCRC) of Bangladesh Agricultural Research Institute (BARI) and were evaluated during the 2019-20 growing season at Breeder Seed Production Centre (BSPC), Debiganj, Panchagarh, Bangladesh. The origin of those biofortified potato mini-tuber germplasm was collected from CIP, Bangladesh. The unit plot size was 3 m × 3 m with 3 replications. The plantlet was planted with a spacing of 40 cm × 25 cm during the

first week of November 2019. Fertilizers were applied @ 325-220-250-120 kg per hectare of urea, TSP, MOP and gypsum respectively. Intercultural operations like earthing-up and weeding were done as and when required. The experimental plots were irrigated frequently to maintain adequate soil moisture and to keep the soil cool. For each accession, ten (10) randomly selected plants were used for the scoring of the characters. Data were collected on plant stand at 45 days after planting (DAP) and foliage coverage (%) at 45 DAP and plant height (cm), stem number per plant, number of tubers per plant, the yield of tubers per plant (gm) and the grade of tubers (%) were collected during harvest at 95 DAP. Quantification of morphological variability for Tuber skin color, tuber shape, flesh colour and tuber eye depth characters were done using the Shannon-Weaver Diversity Index (Supplementary Table 1 and Supplementary Table 2). The estimate of variability for each qualitative character was computed using the standardized Shannon-Weaver Diversity Index, designated as H' and has the formula:

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

Where P_i is the proportion of the total number of genotypes belonging to the i th class. Following the work of groups of researchers (15), the same formula was applied to the quantitative characters.

Mean data for each character was subjected to multivariate analyses using FactoMineR, "Factoextra" package and "Performance Analytics" (16-18) for correlation in R Studio. The magnitude of genetic diversity among forty-nine genotypes was determined by using D^2 Mahalanobis genetic distance

Table 1. Origin and accession ID of CIP biofortified and late blight tolerant potato accessions

Name	Accession ID	Percentage of accessions	Special character
CIP-401	CIP302534.17	393371.16 × 396272.18	Late blight tolerant
CIP-402	CIP302551.26	393385.47 × 393272.18	Late blight tolerant
CIP-403	CIP304079.10	393075.54 × 800959	Late blight tolerant
CIP-404	CIP312507.311	CIP391058.175 × CIP306416.68	Iron and zinc rich
CIP-405	CIP312507.312	CIP391058.175 × CIP306416.68	Iron and zinc rich
CIP-406	CIP312535.032	CIP392025.7 × CIP306416.68	Iron and zinc rich
CIP-407	CIP312595.053	CIP393073.179 × CIP306416.68	Iron and zinc rich
CIP-408	CIP312609.247	CIP393083.2 × CIP306416.68	Iron and zinc rich
CIP-409	CIP312609.252	CIP393083.2 × CIP306416.68	Iron and zinc rich
CIP-410	CIP312633.155	CIP393536.13 × CIP306416.68	Iron and zinc rich
CIP-411	CIP312637.020	CIP393536.13 × CIP306418.69	Iron and zinc rich
CIP-412	CIP312637.069	CIP393536.13 × CIP306418.69	Iron and zinc rich
CIP-413	CIP312637.132	CIP393536.13 × CIP306418.69	Iron and zinc rich
CIP-414	CIP312682.005	CIP394600.52 × CIP306416.68	Iron and zinc rich
CIP-415	CIP312682.011	CIP394600.52 × CIP306416.68	Iron and zinc rich
CIP-416	CIP312682.042	CIP394600.52 × CIP306416.68	Iron and zinc rich
CIP-417	CIP312721.004	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-418	CIP312721.029	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-419	CIP312721.038	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-420	CIP312721.163	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-421	CIP312721.169	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-422	CIP312721.212	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-423	CIP312721.245	CIP395017.229 × CIP306416.68	Iron and zinc rich
CIP-424	CIP312725.001	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-425	CIP312725.036	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-426	CIP312725.041	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-427	CIP312725.047	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-428	CIP312725.048	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-429	CIP312725.052	CIP395017.229 × CIP306418.69	Iron and zinc rich

CIP-430	CIP312725.057	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-431	CIP312725.067	CIP395017.229 × CIP306418.69	Iron and zinc rich
CIP-432	CIP312731.004	CIP395017.242 × CIP306087.82	Iron and zinc rich
CIP-433	CIP312735.051	CIP395017.242 × CIP306416.68	Iron and zinc rich
CIP-434	CIP312735.062	CIP395017.242 × CIP306416.68	Iron and zinc rich
CIP-435	CIP312735.105	CIP395017.242 × CIP306416.68	Iron and zinc rich
CIP-436	CIP312735.114	CIP395017.242 × CIP306416.68	Iron and zinc rich
CIP-438	CIP312751.025	CIP395112.32 × CIP306418.69	Iron and zinc rich
CIP-439	CIP312751.028	CIP395112.32 × CIP306418.69	Iron and zinc rich
CIP-440	CIP312763.441	CIP395443.103 × CIP306416.68	Iron and zinc rich
CIP-441	CIP312764.013	CIP395443.103 × CIP306418.1	Iron and zinc rich
CIP-442	CIP312767.014	CIP395443.103 × CIP306418.69	Iron and zinc rich
CIP-443	CIP312871.043	CIP780278 × CIP306418.69	Iron and zinc rich
CIP-444	CIP398098.570	393371.58 × 392639.31	Late blight tolerant
CIP-445	CIP398190.200	393077.54 × 392639.2	Late blight tolerant
CIP-446	CIP398192.213	393077.54 × 392633.54	Late blight tolerant
CIP-447	CIP398192.553	393077.54 × 392633.54	Late blight tolerant
CIP-448	CIP398208.219	393371.58 × 392633.54	Late blight tolerant
CIP-449	CIP398208.620	393371.58 × 392633.54	Late blight tolerant
CIP-450	CIP398208.670	393371.58 × 392633.54	Late blight tolerant

statistics (19). Hierarchical clustering using Tocher's method, as described by (20) was followed for the grouping of genotypes into distinct clusters.

Results and Discussion

A wide range of agronomic traits has been evaluated in potato germplasm collections for their possible use in the improvement of potato cultivars. Therefore, the account of characters association between the traits themselves and with the yield is very significant for the breeding materials subjected to selection for high yielding genotypes (Fig. 1). Stronger positive and positive correlations were found between tuber yield and plant height ($r=0.34$), main stems per hill ($r=0.13$), the weight of tuber and yield ($r=0.71$), foliage coverage and tuber yield ($r=0.32$), plant vigor and plant height ($r=0.56$), plant vigor and foliage coverage ($r=0.55$), germination percentage and stem per hill ($r=0.38$), germination and foliage coverage ($r=0.29$), tuber count and stem per hill ($r=0.40$) (Fig. 1). These results revealed that any positive increase in such characters will boost the tuber yield. On the other hand, negative and significant correlations were found between tuber count and the weight of tuber ($r=-0.61$) (Fig. 1). The magnitudes of correlation coefficients were classified as based on asterisk marks (Fig. 1). Single asterisk marks were considered average; double asterisk marks were considered strong; triple asterisk marks were considered as very strong correlations. The positive correlation which means the change of the two traits be in the same direction (increase or decrease) and the negative correlation which mean the increase in the first trait combined with a decrease in the second trait (or reverse).

Another researcher (21) found a positive significant correlation between tuber weight and tuber count. We found a negative correlation between tuber weight and tuber count ($r=-0.61$). Other researchers (22) found similar results i.e., the significant correlation between tuber yield and tuber weight. PCA is commonly used to analyze phenotypic traits in crops and to select traits that contribute to

genetic improvement (23). In PCA, only the first two-component axis had eigen values up to 4.68 (Table 2) presenting a cumulative variance of 58.47%. Principal component one (PC1), with an eigen value of 2.82, contributed 35.22 % of the total variability, while PC2, with eigen value of 1.86 accounted for 58.47% of total variability observed among the 49 potato genotypes (Table 2). Another group of researchers (24) found similar results. They reported that the first three PC accounted for 71% of the total diversity whereas the first PCA accounted for 29.01%. The first PC was more related to tuber yield per plant, tuber weight and the second PC was more associated with plant height, plant emergence/germination, plant vigor, foliage coverage, stems per hill and tuber count (Fig. 2). In addition, more variations were evident relatively in the traits, which were located on the first component (Fig. 2). The Germplasm located at quadrant four had wide variability (35.2%) and most of the germplasm present in into cluster III (Fig. 3). Q1 and Q2 had least divergence and present in mostly cluster I. Quadrant Q3 had moderate variability present in cluster II.

The cluster analysis divided genotypes based on similarity and provided a hierarchical classification (HCA). The results obtained following HCA were shown as a dendrogram (Fig. 4) in which three well-defined clusters were visible. Based on the hierarchical clustering on principal components the 49 genotypes were grouped into three different clusters (Table 3 and Fig. 3). Cluster II contained the maximum number of twenty-two genotypes followed by cluster III having sixteen genotypes and cluster I having eleven genotypes (Fig. 3 and Table 3). On the basis of the cluster means, the important cluster was cluster II for percent germination, foliage coverage, stem per hill, plant height and plant vigor, cluster III for the weight of tuber and yield per plant. Cluster I had the lowest mean for germination percentage, foliage coverage, stem per hill, plant height, plant vigor, the weight of tuber, tuber count and yield per plant (Table 4). The dendrogram was cut with the most distance from the other groups and 49 cultivars were included in three clusters (Fig. 4). Researchers

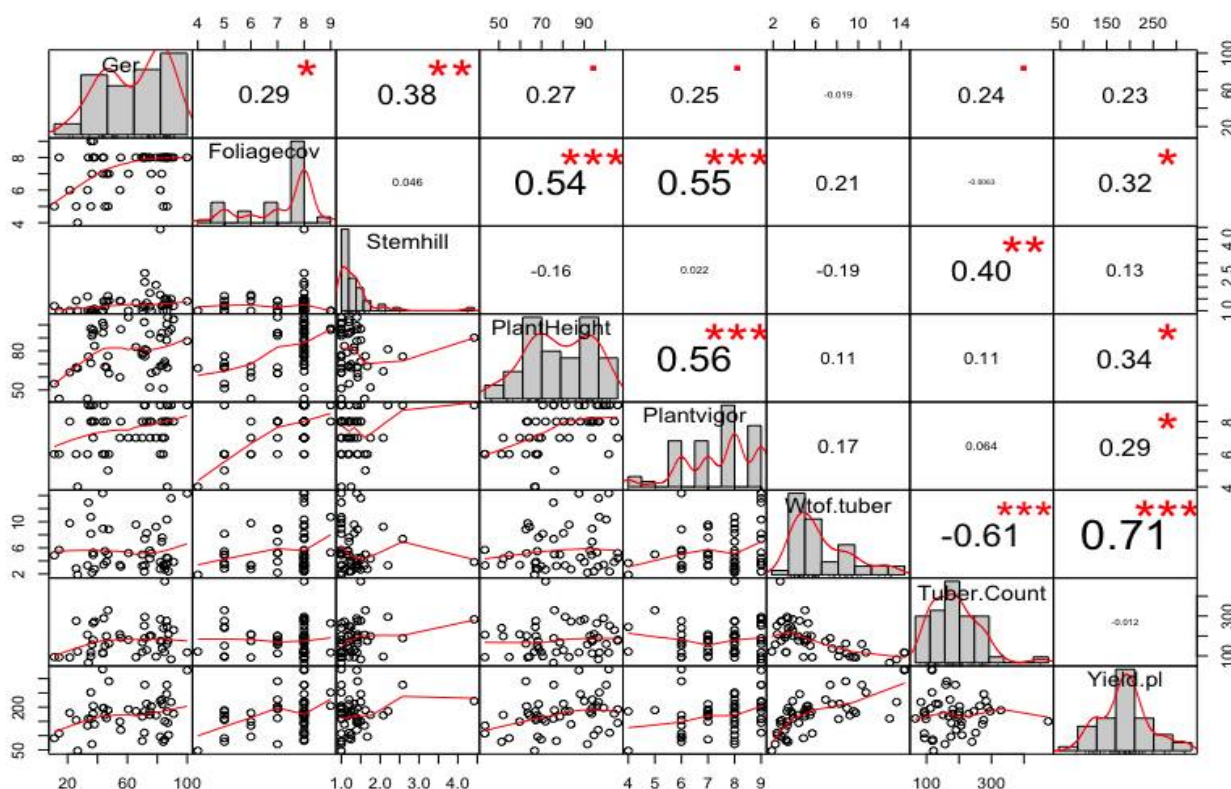


Fig. 1. Correlation coefficients among eight traits of 49 CIP biofortified and late blight tolerant potato genotypes.

(25), also found that the dendrogram obtained using highly variable morphological characters that separated 89 sweet potato genotypes into major clusters. About the distribution of tuber sizes, all the CIP clones showed a higher percentage of tubers size 25 mm and above (Table 5.). The quality of the seed depends on physiological age, uniformity and tuber size. The difference in tuber size is probably best explained by genetically different makeup of the TPS progeny. This is in agreement with (26). In addition, a researcher (27) reported that tuber size below 25 gm can successfully be used as seed tuber for next season, which gives the same potential yield as seed tubers (25-50 gm) of a standard cultivar. The Shannon-Weaver Diversity Index has a value ranging

located on the first principal component. The above variables might be taken into consideration for the effective selection of parents during the hybridization programme. We selected CIP403, CIP404, CIP405, CIP413 and CIP445 accessions for their yield potentiality and tuber weight (Supplementary Fig. 1). The lines that are superior in terms of genetic diversity and agronomical properties during the improvement studies need to be selected (28). Similarly, another researcher (29) also selected nine genotypes among sixty-three potato genotypes in terms of maturity time, tuber shape plant height.

Table 2. Computed Eigen values with corresponding proportion and cumulative explained variance

Principal component	Eigen Value	Variance	Cumulative variance
1	2.82	35.22	35.22
2	1.86	23.24	58.47
3	1.10	13.69	72.16
4	0.71	8.82	80.97
5	0.68	8.53	89.51
6	0.42	5.22	94.73
7	0.57	4.061	98.78
8	0.31	1.2121	100

from 0 to 1, where 0 indicates the absence of diversity and 1 indicates maximum diversity (Supplementary Table 1 and Supplementary Table 2). The greater diversity in the studied materials will offer good scope for the improvement of potato through rational selection of parent's genotypes. Relatively more variations were evident in the traits, which were

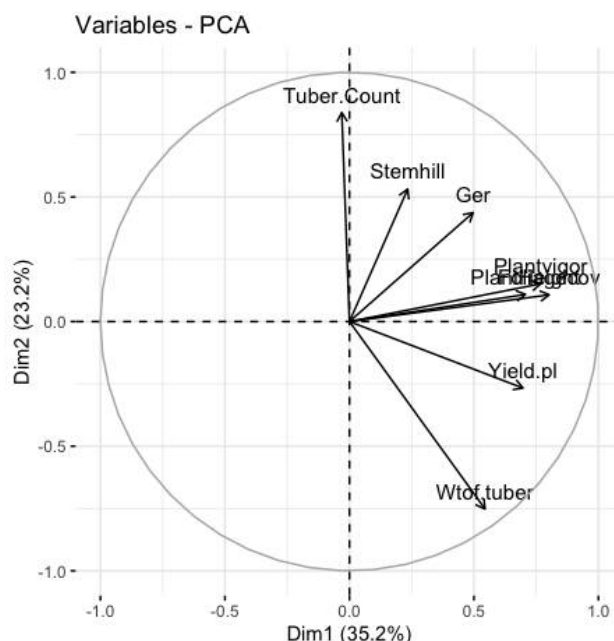


Fig. 2. Principal component analysis (PCA) plotted agronomic characters along the first two axis .

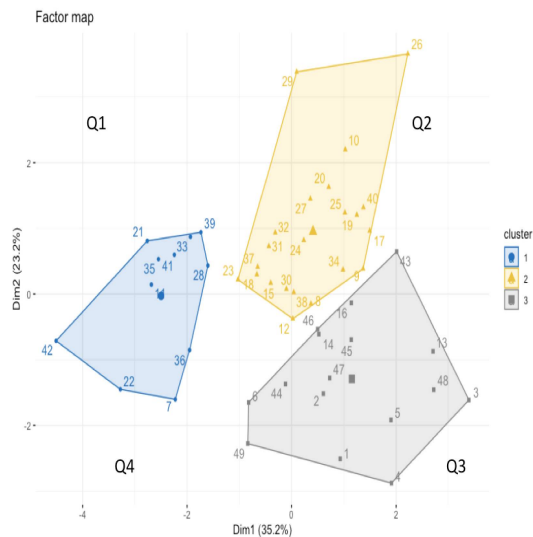


Fig. 3. Distribution of 49 biofortified and late blight tolerant potato germplasm in three clusters.

Table 3. Distribution of 49 CIP biofortified and late blight tolerant potato germplasm in three different clusters

Cluster	Number	Name of Accessions
I	11	CIP407, CIP411, CIP421, CIP422, CIP428, CIP433, CIP435, CIP436, CIP 440, CIP442 and CIP443
II	22	CIP408, CIP409, CIP410, CIP412, CIP415, CIP417, CIP418, CIP419, CIP420, CIP423, CIP424, CIP425, CIP426, CIP427, CIP429, CIP430, CIP431, CIP432, CIP434, CIP438, CIP439 and CIP441
III	16	CIP401, CIP402, CIP403, CIP404, CIP405, CIP406, CIP413, CIP414, CIP416, CIP444, CIP445, CIP446, CIP447, CIP448, CIP449 and CIP450

and will be used as parental material for fixation of heterosis in potato improvement programme.

Acknowledgements

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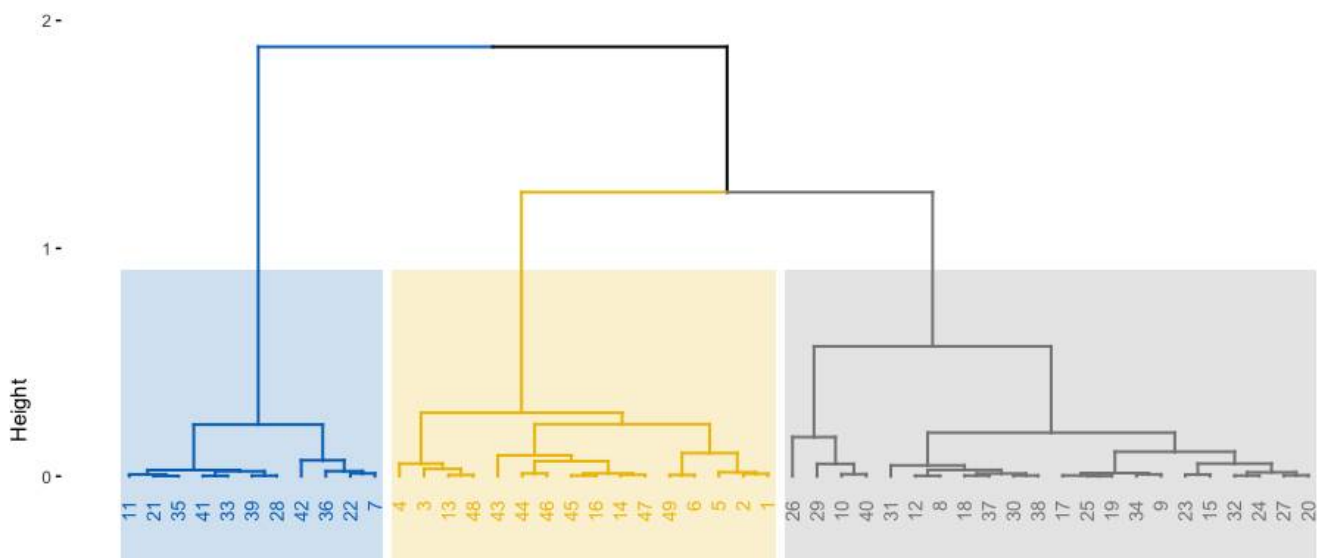


Fig. 4. Dendrogram of cluster analysis of 49 biofortified and late blight tolerant potato germplasm classified according to all the traits studied.

Thus, an improvement-breeding program involving such different cultivars may yield transgressive and heterotic segregants. Those selected clones will be used in the breeding programme after further evaluation.

Conclusion

The genetic variability among the CIP biofortified and late blight tolerant materials allows us to help the parental selection and pave the way to fortify and select blight tolerant potato for food security. The present study explored high level of morphological variation for market preferable tuber size, shape and yield among the accessions. Based on consumer preferences CIP403, CIP404, CIP405, CIP413 and CIP445 accessions present in cluster III were superior

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Authors' contributions

Md. Mushfiqur Rahman: Conceptualization, conducted the field experiments, investigation, methodology, writing original draft, formal analysis, supervision, validation, writing review and editing, Md. Nurul Amin: investigation, data analysis and drafted the part of manuscript Md. Harunor Rashid: advice and suggest to interpret the results. Md. Mazdul Islam: helped in planning, designing and

Table 4. Cluster means for eight characters in 49 CIP biofortified and late blight tolerant potato genotypes

Cluster	Parameters	Germination percent	Foliage coverage (1-9 scale)	Stem / hill (no.)	Plant Height (cm)	Plant vigor (1-9 scale)	Tuber weight / plant (g)	Tuber Count/10 plant (no.)	Yield / 10 plant (g)
Class I	Min	11.11	4.00	1.00	43.34	4.00	1.88	93.33	46.80
	Max	86.67	8.00	1.67	76.08	7.00	5.68	329.00	189.40
	Mean	46.44	5.45	1.30	60.55	5.64	3.84	194.45	127.81
	std	27.64	1.04	0.26	10.92	0.92	1.23	75.90	46.96
Class II	Min	36.36	7.00	1.00	52.00	7.00	2.21	118.63	70.10
	Max	90.91	9.00	4.42	105.80	9.00	5.58	474.67	246.00
	Mean	66.70	7.86	1.42	86.61	8.05	3.84	224.48	158.78
	std	19.02	0.47	0.73	14.86	0.72	1.06	76.46	47.46
Class III	Min	21.43	5.00	1.00	62.67	6.00	6.93	65.38	158.13
	Max	100.00	9.00	2.58	101.60	9.00	14.35	189.00	332.80
	Mean	62.04	7.56	1.31	82.22	7.94	10.05	121.22	229.88
	std	24.38	0.96	0.44	13.90	1.06	2.47	34.78	57.31

Table 5. Percentage of different CIP biofortified and late blight resistant potato accession grades of minituber by weight

Accession Name	Weight percentage				
	<5 mm	5-10 mm	15-20 mm	20-25 mm	>25 mm
CIP-401	0.27 ijklmn	1.68 rs	14.63 q	22.28 1nopq	52.7 8c
CIP-402	0.23 klmnopqr	1.62 rs	15.25 q	22.13 opqr	50.40 cd
CIP-403	0.12 s	1.18 s	8.03 r	15.38 tu	71.37 a
CIP-404	0.17 opqrs	1.42 rs	8.26 r	20.42 qrs	66.30 b
CIP-405	0.15 pqrs	1.44 rs	15.37 q	35.64 cd	40.93 hi
CIP-406	0.28 hijklm	2.43 pqrs	21.85 nop	39.85 ab	22.61 mno
CIP-407	0.35 fgghi	3.31 opqrs	21.76 nop	28.05 fgh	37.65 ij
CIP-408	0.24 klmnop	3.47 opqr	12.93 q	42.44 a	32.86 k
CIP-409	0.19 mnopqrs	6.34 ijklm	31.56 cde	18.29 rst	20.26 nop
CIP-410	0.21 mnopqr	9.73 def	37.63 ab	23.42 jklmnopq	5.64 uvwx
CIP-411	0.32 ghijkl	7.54 ghijkl	28.08 fghij	36.07 bc	7.48 uvw
CIP-412	0.23 klmnopq	4.49 mnop	23.56 lmno	34.92 cd	27.36 l
CIP-413	0.14 qrs	2.63 pqrs	19.26 p	23.10 klmnopq	42.86 fgh
CIP-414	0.17 opqrs	3.41 opqr	28.44 efghi	26.05 ghijklmn	25.46 lm
CIP-415	0.53 bc	8.07 fghi	39.53 a	20.47 qrs	14.10 qrs
CIP-416	0.17 opqrs	4.52 mnop	25.33 ijklm	25.55 ghijklmno	24.90 lm
CIP-417	0.28 ijklmn	4.40 mnop	27.62 ghijkl	26.53 ghijkl	27.78 l
CIP-418	0.25 jklmnop	7.25 ghijkl	27.48 ghijkl	35.79 c	12.47 rs
CIP-419	0.221 mnopqr	5.68 klmn	30.88 cdefg	31.89 def	13.11 rs
CIP-420	0.36 fgghi	10.51 de	37.65 ab	19.74 qrs	4.21 wxy
CIP-421	0.50 cd	9.44 defg	30.36 defgh	21.75 opqr	11.52 st
CIP-422	0.41 defg	1.85 rs	28.65 efghi	42.27 a	12.93 rs
CIP-423	0.61 b	6.42 hijklm	34.32 bc	26.91 ghijk	0 z
CIP-424	0.34 fgghij	7.70 fgghij	25.60 ijkl	24.79 hijklmnop	20.49 nop
CIP-425	0.23 klmnopq	8.12 efghi	24.92 jklmn	27.70 gh	19.55 op
CIP-426	0.18 nopqrs	5.69 klmn	24.68 jklmn	39.66 ab	15.69 qr
CIP-427	0.39 efgh	10.54 de	28.38 efghij	20.70 pqrs	9.89 stu
CIP-428	0.27 ijklmn	9.43 defg	21.91 mnop	32.68 cde	5.37 vwx
CIP-429	0.26 ijklmno	26.34 a	21.55 nop	3.86 v	3.47 xyz
CIP-430	0.19 mnopqrs	8.26 efghi	29.83 defgh	17.60 st	27.40 l
CIP-431	0.23 klmnopq	7.89 fgghij	32.38 cd	34.94 cd	0 z
CIP-432	0.31 hijkl	14.98 c	40.67 a	11.92 u	1.43 yz
CIP-433	0.24 klmnopq	8.36 efghi	32.84 cd	20.21 qrs	23.97 lmn
CIP-434	0.21 mnopqrs	6.50 hijklm	26.14 ijkl	29.30 efg	17.47 pq
CIP-435	0.24 klmnop	11.61 d	30.758 defgh	20.96 pqrs	8.54 tuv
CIP-436	0.23 klmnopq	5.79 jklmn	28.80 efghi	26.19 ghijklm	22.73 mno
CIP-438	0.46 cde	8.60 efgh	27.34 hijk	27.31 ghi	12.72 rs
CIP-439	0.23 klmnopq	6.32 ijklm	20.28 op	21.91 opqr	37.83 ij
CIP-440	0.44 cdef	11.06 d	23.29 lmno	27.03 ghij	19.85 op
CIP-441	0.19 mnopqrs	5.48 lmno	24.27 klmn	15.65 tu	37.96 ij
CIP-442	0.221 mnopqr	8.37 efghi	31.52 cdef	26.93 ghijk	13.44 rs
CIP-443	0.85 a	18.35 b	30.75 defgh	6.61 v	0 z
CIP-444	0.12 s	5.05 mno	15.67 q	25.38 hijklmno	42.35 gh
CIP-445	0.13 rs	5.49 lmno	15.33 q	23.53 ijklmnopq	43.27 fgh
CIP-446	0.18 nopqrs	4.06 nopq	23.10 lmno	34.18 cd	26.07 lm
CIP-447	0.24 klmnop	3.46 opqr	20.56 op	26.44 ghijkl	35.68 jk
CIP-448	0.24 klmnop	2.56 pqrs	15.32 q	22.83 klmnopq	49.13 cde
CIP-449	0.19 mnopqrs	2.04 qrs	14.54 q	27.18 ghij	46.68 def

CIP-450	0.23 klmnopq	5.43 lmno	15.19 q	22.48 mnopq	46.05 efg
CV (%)	21.28	20.36	8.653	9.252	9.55
Mean	0.279	6.637	24.75	25.69	24.84

Means followed by different letters are significantly different from each other

setting the experiment. Md. Mohi Uddin and Bimal Chandra Kundu: assisted in troubleshooting, provided constructive comments, suggestions and technical support to conduct the experiment. EHMS Rahaman: writing review and editing resources.

Conflict of interests

Authors declare that no conflict of interests exists regarding the publication of this paper.

Supplementary files

Table 1. Morphological characters of biofortified potato varieties.

Table 2. Code for different morphological characters of CIP biofortified and late blight tolerant accessions with shannon index.

Fig. 1. Selected Biofortified accessions for hybridization programme.

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