Scientific Research Publishing

American Journal of Plant Sciences, 2023, 14, 1235-1247
https://www.scirp.org/journal/ajps
ISSN Online: 2158-2750
ISSN Print: 2158-2742

Evaluation of Genetic Divergence in Various Potato Genotypes Grown in Bangladesh through Different Traits Assessment

Md. Mukhtar Hossain*, Md. Abdul Kaium, Md. Al Amin, Tabaraka Binte Ali, Nusrat Jahan, Md. Nasim Uddin

Department of Crop Science and Technology, Faculty of Agriculture, Rajshahi University, Rajshahi, Bangladesh
Email: *mukhtar.gpb@gmail.com

How to cite this paper: Hossain, Md.M., Kaium, Md.A., Al Amin, Md., Ali, T.B., Jahan, N. and Uddin, Md.N. (2023) Evaluation of Genetic Divergence in Various Potato Genotypes Grown in Bangladesh through Different Traits Assessment. *American Journal of Plant Sciences*, **14**, 1235-1247.
https://doi.org/10.4236/ajps.2023.1411084

Received: September 11, 2023
Accepted: November 10, 2023
Published: November 13, 2023

Abstract

The goal of the study was to quantify the genetic diversity of different potato varieties. Five groups were named to classify the 25 genres of potatoes as: Cluster I (Lalpakri, Diamond), Cluster II (Hagrai, Green Mountain, G.M.O., Elvera), Cluster III (Atlantic, Shepody, Raja, Fundy, Multa, Granulla, Shibilati, Japanese Red), Cluster IV (Atlas, Brondy, Yucon Gold, Monona, Petrones, Cheroki), and Cluster V (Calwhite, Prelude, Allblue, Russet, Burbank, TPS-67). The highest and lowest genotypes are found in Clusters III and I, respectively. The two groups' maximum inter-cluster distance (the cluster's distance between them) demonstrates the enormous diversity between Clusters II & III. Cluster III had the greatest intra-cluster distance (distance within a set), whereas Cluster V had the smallest. In most cases, the distance between gaps was more significant than the distance within the holes, showing greater genetic diversity between different groups' genotypes. The highest, second highest, and third highest eigenvalues, accompanying the positive canonical values for Vectors I and II of three characteristics: average tuber weight in each plant, the tubers number in each plant, and the eyes number in each tuber, showed the most outstanding contribution to the complete difference between genotypes. Of the nine features, the smaller leaves number in each plant, the shorter plant height, the more minor genotypes, the fewer eyes per tube generated from Cluster I, the maximum height of the plants, the high-quality tubers in each plant, the tubers number in each plant, the fresh weight in each plant, and the leaf number in each plant from Cluster II could be chosen in the role of parents in this program for hybridization. Given the size of the genetic distance, the various characteristics that contribute to the overall difference, and the average population size, Hagrai, Green Mountain, O.M.G., Elvera Cluster II and Cluster I, Lalpakri, and Diamond genotypes

can be regarded as parents of hybridization programs in the future. Thus, producers can get guidance to enhance genetic diversity by selecting materials from different relatives and reducing their vulnerability to diseases and climate change.

Keywords

Genetic Divergence, Potato Genotypes, Different Traits, Cluster Analysis, Principal Component Analysis

1. Introduction

In the list of most important food crops, potato worldwide secures the top fourth rank after rice, wheat, and corn. Bangladesh's high-carbohydrate foods are right behind wheat and rice [1]. One of the important tuber crops grown throughout Bangladesh is the potato. It is produced mainly for its high nutritional value, colossal productivity, smooth digestion, and many industrial applications [2]. Genetic variation and diversity have a significant function in the success of a reproductive program. For a fruitful plant breeding program, it is essential to have genetic diversity in the population. Genetic differences are beneficial tools for effectively selecting parents for hybridization [3]. The significance of genetic differences in improving crops has been emphasized in self-pollinated crops as well as crops of cross-pollinated [4] [5]. Knowing the genetic origins of distinct qualities in the various phenotypes is crucial for evaluating genetic differences [6]. Potato growing aims to evolve dormant varieties that secure the highest amount of stable and firm production. Genetic diversity differentiates the diverse populations restored through diversification analysis based on more scientific and advanced biometric technologies, *i.e.* Mahalanobis D^2 statistics.

For different plants to attain their goals of proliferation, genetic diversity is crucial, such as increased production, broader adaptation, the desired quality, pests, and disease resistance. The genetic divergence analysis estimates the degree of diversity between the selected genotypes [7]. Finding specific parents to get the various genetic mutations and the other sex when parents cross are additional goals of investigating genetic diversity. It will be helpful for the plant breeders in selecting varied parents for high-target hybridization if they get error-free facts and figures on the extent and nature of genetic diversity [7]. This look aims to evaluate the scope of diversity and identify the contribution of characters to the promotion of gene biodiversity in hybrid programs that are expected to be classified into different groups based on genetic differences and provide superior separation. It is, therefore, logical to carry out the current research.

2. Materials and Methods

2.1. Locale of the Experiment

During the Robi season of 2020/2021, the experiment was carried out at F.S.E.

Biotech Ltd., Bagmara, Rajshahi, Bangladesh. The land, which is part of the AEZ-11 which is also known as the High Ganges River Floodplain, is situated at 24˚22'N latitude and 88˚39'E longitude, above 14 m from sea level. The average rainfall during conducting the experiment was below 50 mm. The area soil for the experiment was silty clay which is the type of Gangetic floodplain containing a lower percentage of organic matter and boron, but iron content has significantly. The pH of the soil is 7.1 to 8.5 (Figure 1).

2.2. Planting Materials

In this study, 25 distinct varieties/lines of potato tuber were employed as materials for planting, such as Lalpakri, Diamont, Hagrai, Green-mountain, G.M.O., Elvera, Atlantic, Shepody, Raja, Fundy, Multa, Granulla, Shibilati, Japanese Red, Atlas, Brondy, Yucon Gold, Monona, Petronas, Cheroki, Calwhite, Prelude, Allblue, Russet, Burbank, and TPS-67.

2.3. Layout and Experimental Design

Spacing 20cm between plants and 60 cm between rows was followed in cultivating potato tubers. A Randomized Block Design having three replications was implemented.

2.4. Data Collection

Ten plants from each row of each replication, which were assigned randomly, were used to collect data on several agronomic criteria on an individual plant basis. The average weight of the tuber of plants (g), the tuber number in each plant, plant height (cm), the eyes number in each tuber, the weight of the tuber in each plant (g), fresh weight of each plant (g), the number of leaves in each plant, SPAD were also measured and recorded (Figure 2, Figure 3).

2.5. Data Analysis through Multivariate Analysis (D^2 Statistics)

Multivariate Analysis that is also known as D^2 statistics was used to analyze the collected data using different biometric approaches. On a computer, the following multivariate analyses were carried out using the programs GENSTAT 5.13 and Microsoft Excel 2000.

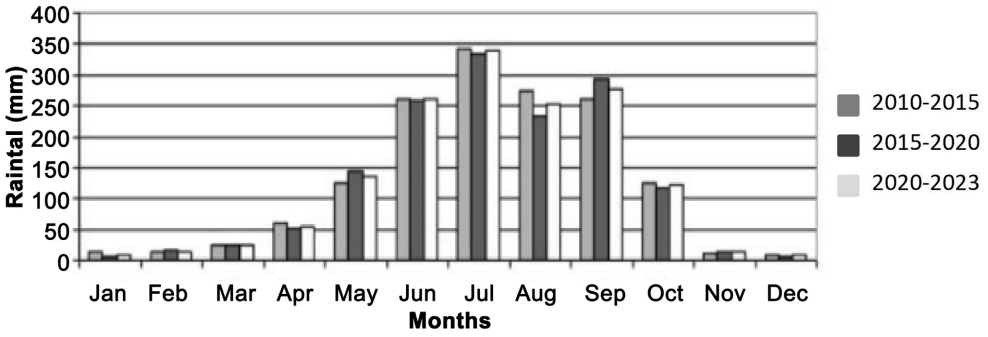

Figure 1. Average rainfall in Rajshahi region, Bangladesh.

Figure 2. SPAD meter.

Figure 3. Electric balance.

2.5.1. Cluster Analysis (CA)

Applying the D^2 analysis method, which Mahalanobis first introduced in 1928 [8] and 1936 [9] and Rao built on in 1952 [10], the genotypes were divided into roughly homogeneous groups based on the various data groupings.

The Pivotal condensation technique is used to transform correlated data into D^2, which is the sum of squares of differences between two populations for each uncorrelated variable. Clustering was carried out by using hierarchical and non-hierarchical categorization.

With the computer application GENSTAT 5.13, cluster analysis was carried out in order to determine the selection criterion's desired values. The genotypes were divided by the algorithm into several necessary groups, and after that, the group-to-group movement of genotypes was done by the algorithm until the signal value was improved by the transfer. If any more transitions did not appear that strengthened the criteria, the algorithm moved on to the next step. It looked into how the two genotypes' impulses affected many other groups, among other things.

2.5.2. Principal Component Analysis (PCA)

PCA techniques were operated to evaluate correlations between quantitative traits. The genetic scores (obtained from the first and subsequent components with latent roots greater than unity) and correlations matrix (acquired from the products matrix and the sum of squares of the characteristics) were used to identify the most important elements. "Eigenvalues" refer to the sources of latent. The first component can obtain the features that enable the maximum variance. PCA pro-

vides a one-dimensional collinear association of a collection of variables that boosts the variability within variables. Thus, it can represent the central part of the original variables on a smaller scale. The first two principal components present the effect of various attributes on diversity from the latent vectors.

2.5.3. Principal Coordinate Analysis (PCA)

To estimate the distance of the inter-genotypes and the distance that is smallest between each pair of the location N using the matrix of similarity and all P dimensions, the analysis of the principal coordinate was carried out [11].

2.5.4. Canonical Vector Analysis (CVA)

Canonical vector analysis (CVA) using as a D^2 statistic complement. Ecclesiastical roots and vectors serve as various differentiation axes in a multiple regression analysis, and the amount of variation that all the axes represent is calculated in accordance with that representation. It identifies a linear arrangement of the initial variables that intensifies the between-group to within-group variability proportion, which results in a function of the initial variable that may be utilized for differentiation between the groups. The proportion of group variances and between-group variances was, as a result, maximized in the study above using a series of transformations of orthogonal.

2.5.5. Computation of Average Intra-Cluster Distance

Every probable D^2 value found within the cluster members via the analysis of the principal coordinate was used to compute the mean of the distance of the intra-cluster for each cluster.

2.5.6. Cluster Diagram

Taking into account the values distances of inter-cluster and intra-cluster, a cluster diagram was created. The graph showed the relationship between the various genotypes found in groups and the pattern of genotype diversity.

2.5.7. Selection of Germplasm for Future Hybridization Program

Typically, analysis of the divergence is performed to identify different genotypes for the hybridization. Genotypes within a cluster are more similar to one another than those inside distinct clusters. The maximum diversity between the genotypes held in different clusters is shown in groups separated by the most significant statistical distance (D^2). The following factors should be taken into consideration when choosing genotypes for hybridization, as suggested by Singh and Chaudhury [12]: The genotypes that are chosen from the cluster were chosen to serve as parent(s) from the chosen group(s), determining a specific genotype, combining the attributes of the overall divergence, additional significant genetic features (as for performance).

3. Result

The genetic diversity degree that was collected from different potato genotypes shows their genetic dynamics. Collecting and analyzing experimental data were

carried out to examine the genotype performance of potatoes and gather genotypes into CLUSTERs based on their similarity.

3.1. Analysis of the Diversification (D^2 Statistics)

The following technique assists in explaining external changes in phenomena between genotypes. The analysis of the nine traits of 25 genotypes of potatoes was completed by studying canonical vector analysis. Principal component analysis (PCA) and cluster analysis were also examined to identify the divergent potato genotypes.

3.1.1. Non-Hierarchical Grouping

Twenty-five genotypes of potatoes were categorized into five contrasting groups using Mahalanobi's D^2 statistics and Tocher's method. The results are consistent with the sample of the genotype group obtained from the analysis of the main component. In Table 1, it is shown that in what way the genotypes are distributed into different clusters. Here, we found 32 percent of genotypes in cluster III, eight genotypes. Clusters IV, V, and II contain 6, 5, and 4 genotypes, respectively.

3.1.2. Canonical Vector Analysis

The distance of the Inter-cluster as well as the intra-cluster were the parameters for measuring the genetic divergence, which is evaluated in Table 2 using the analysis of Canonical vector. The highest and lowest distances of the inter-cluster, as well as the intra-cluster, are responsible for the variation of genes. In that case, we found Clusters II and III were accountable for the highest genetic divergence, and inter-cluster distance was the highest (22.25) and ranked second for responsible departure between III and V, which was 15.90. The distance within Cluster (bold) III (0.80) was the highest and V (0.29) was the lowest. In most cases, the magnitude of spatial separation between gaps was more significant than the magnitude of spatial separation within the holes (Figure 4).

3.1.3. Principal Component Analysis

The analysis of nine agronomic traits of twenty-five potato genotypes, the eigenvalues, and variance percentages are presented in Table 3.

Table 1. Mahalanobis D^2 values-based distribution of 25 potato genotypes into five groups.

Clusters	No. of genotypes	Total entries (%)	Genotypes
I	2	8	Lalpakri, Diamont
II	4	16	Hagrai, Green Mountain, G.M.O., Elvera
III	8	32	Atlantic, Shepody, Raja, Fundy, Multa, Granulla, Shilbilati, Japanese Red
IV	6	24	Atlas, Brondy, Yucon Gold, Monona, Petrones, Cheroki
V	5	20	Calwhite, Prelude, Allblue, Russet Burbank, TPS-67

Table 2. Average matrix of intra (bold) and inter-cluster distances (D^2 statistics) among 9 traits of 25 potato genotypes.

Cluster number	I	II	III	IV	V
I	**0.52**				
II	4.33	**0.42**			
III	10.90	22.55	**0.80**		
IV	6.50	7.50	12.13	**0.55**	
V	5.02	11.20	15.90	14.11	**0.29**

Table 3. Eigenvalues and variance percentage (%) of 9 agronomic traits towards divergence in 25 potato genotypes.

Principal components	Eigenvalues	% variance	Cumulative variance %
NTPP	5.028	31.25	31.25
NEPT	3.322	26.20	57.45
ATWP	2.877	12.45	69.90
TWP	1.323	10.03	80.20
PH	0.858	5.20	85.40
NLPP	0.656	4.56	89.96
FWP	0.382	4.05	94.01
SPAD	0.238	3.20	97.21
Biomass	0.081	2.78	99.99

NTPP = Number of tubers/plant, NEPT = Number of eyes/tuber, ATWP = Average tuber weight of plants, TWP = Tuber weight/plant, PH = Plant height, NLPP = Number of leaves/plant, FWP = Fresh weight/plant, SPAD = Chlorophyll content of leaf.

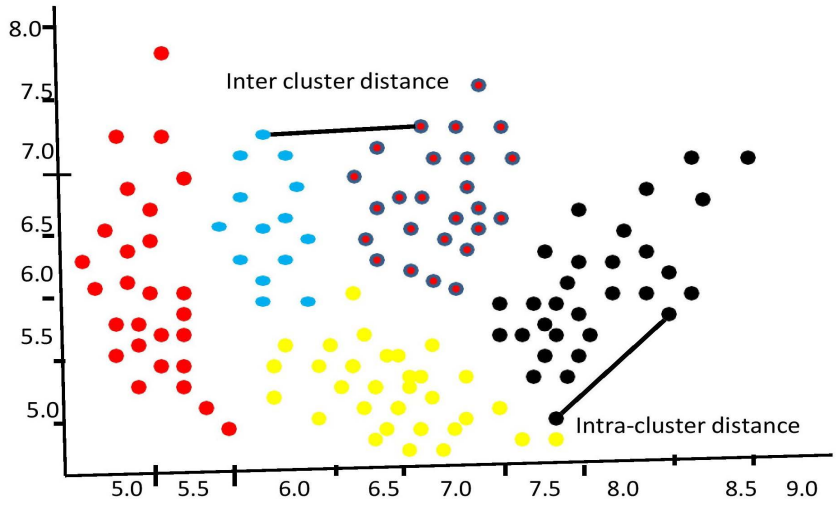

Figure 4. Cluster analysis

The highest, second highest, and third highest eigenvalues are found in the parameters: the number of tuber/plant (31.25%), the number of eyes/tuber

(26.20%), and average tuber weight (12.45%), respectively. The first four traits are responsible for 80.20% variation, and individual values were greater than one. Considering the nine traits of 25 potato genotypes, the first two traits are responsible for maximum (57.45%) variation.

3.1.4. Contribution of Traits toward Divergence

The measurement of the Latent vectors was taken to evaluate the contribution of nine traits towards divergence and the expanse of genetic variation, which are shown in Table 4.

Positive values in Vector I were demonstrated by the salient characteristics of tuber weight in each plant, the tuber number in each plant, the leaves number in each plant, the eyes number in each tuber, and the fresh weight of each plant. In Vector II, the values marked positive are the eyes number in each tuber, the average tuber weight in each plant, the tuber number in each plant, the leaves number in each plant, and biomass. The three characteristics, the eyes number in each tuber, tubers number in each plant, and average tuber weight of each plant, showed positive values in the vectors as well as in the Plant height, and SPAD showed negative values.

From the result of canonical vector analysis, it is disclosed that Vector I and Vector II carried positive values for the number of eyes/tuber, tuber/plant, and leaves/plant. On the other hand, in the case of plant height, the SPAD values were negative in not only Vector I but also in Vector II.

3.1.5. Intra-Cluster Mean

In Table 5, the clustering capacity of 9 traits is indicated as it showed differentiating potentiality for most of the nine traits in terms of the intra-cluster means. By the cluster means (Table 5), significant clusters were Cluster II for the leaves number in each plant, fresh weight of each plant, Cluster V for plant height, and

Table 4. Latent vectors for 9 traits in 25 potato genotypes.

Traits	Vector I	Vector II
NTPP	0.0382	0.0543
NEPT	0.0578	0.0585
ATWP	−0.1523	0.1311
TWP	0.0102	−0.0152
PH	−0.0238	−0.0562
NLPP	0.0563	1.3146
FWP	0.0321	−0.0528
SPAD	−0.0052	−0.4327
Biomass	−0.2436	1.2519

NTPP = Number of tuber/plant, NEPT = Number of eyes/tuber, ATWP = Average tuber weight of plants, TWP = Tuber weight/plant, PH = Plant height, NLPP = Number of leaves/plant, FWP = Fresh weight/plant, SPAD = Chlorophyll content of leaf.

Table 5. Cluster means for the nine traits of 25 potato genotypes.

Traits	Cluster mean				
	I	II	III	IV	V
NTPP	05.057	08.123	07.081	06.503	06.801
NEPT	08.152	15.558	09.027	09.082	10.957
ATWP	25.051	30.501	24.001	26.851	31.272
TWP	126.68	217.25	97.948	147.76	212.68
PH	34.566	50.078	35.002	44.316	48.578
NLPP	230.08	280.51	235.00	238.11	240.50
FWP	140.50	158.52	120.21	126.15	132.00
SPAD	44.210	49.159	40.297	48.532	50.505
Biomass	6805.0	7779.0	6529.0	5612.5	8855.6

NTPP = Number of tuber/plant, NEPT = Number of eyes/tuber, ATWP = Average tuber weight of plants, TWP = Tuber weight/plant, PH = Plant height, NLPP = Number of leaves/plant, FWP = Fresh weight/plant, SPAD = Chlorophyll content of leaf. **Order of the yield:** Cluster II > Cluster V > Cluster IV > Cluster I > Cluster III.

Cluster III for the tubers number in each plant. The lower mean was seen in Cluster I for the eyes number in each tuber. The survey reports of non-correspondence between the genetic and geographic diversity were almost identical in the case of potatoes [5].

4. Discussion

The goal of the study was to quantify the scope of genetic diversity by assessing nine characteristics of 25 types of potato genes. The above-mentioned genotypes are grouped into five categories, of which Cluster III consists of eight. The genetic distribution patterns between the different cluster groups reflect a great deal of genetic diversity in the genotypes [13] and these broader genetic variables can be caused if these species are adapted to specific environmental situations. Although the influence of geographical origins may have affected groups, the criterion for genetic diversity was not geographic distribution only. This advises against making it essential to select parents from various geographic locations [14]. According to the results of **Table 2**, the distance between the clusters was longer than the distance within the group. Analysis of the genetic diversity of grain obtained similar results, obtaining distances between clusters greater than those within the collection [7]. Cluster II and Cluster III (22.55) and Cluster III and Cluster V (15.90) have the greatest distances between them, which shows genetic diversity to a high degree, so the use of hybrid programs between different breeds may be recommended.

It has also been shown that genetic types within clusters with high differences will produce more desirable reproductive material for more excellent genetic development [15].

The highest distance within the cluster within the genetic type of Cluster III was discovered (0.80). Wider distances between and within clusters indicate more incredible genetic changes between groups and connections within groups. Because the distances within the group were much shorter than between the groups, the nature of differentiation and identity between groups became evident.

The diversity of parents indicates the potential for higher levels of heterosis to be obtained [16]. Parents for hybrids can choose by the distance between the clusters and the cluster average to separate the useful recombination from the separation generation [17]. On the contrary, the lower spaces within the group were observed in the genetic type of Cluster V (0.29), and after Cluster II (0.59), genetic diversity was reduced, allowing these to be used to improve the gene population of the potato.

The maximum eigenvalues of more than one (>1) contributed to the first four elements, *i.e.* the number of tubers/plant (5.028, variance: 31.25%), the number of eyes/tube (3.322; conflict: 26.20%), the average tuber weight/plant (2.877; the variance: 12.45%) and the tuber weights/plant (1.322, variance: 10.03%) contributed the highest variance (80.20%) for these traits (**Table 3**). Thus, these traits cause significant changes in the genetic differences of 25 varieties of potato genes in experiments. The contribution of characters to genetic diversity is shown in **Table 4**. In addition, independent development of group clusters was also done using principal component analysis (PCA) to prove the two-dimensional clustering obtained from D^2 statistics. According to the results of the analysis of the main components of the properties that contribute to genetic diversity, the crucial genetic variations on the primary axis of vector differentiation I were the tuber number in each plant (0.0382), the eyes number in each plant (0.0578), tuber weight in each plant (0.0102), the leaves number in each plant (0.0563), fresh weight (0.0321). In Vector II, the number of tubers/plants (0543), the average tuber weights/plant weight (0.1311), the number of leaves/plant (1.3146), and biological mass (1.2516) played a role in genetic diversity. The analysis of the main components revealed that the tubers number in each plant, the eyes number in each tuber, and the leaves number in each plant (I and II) were positive. These results have shown that the three characters have made the most outstanding contribution to diversity.

The plant height and SPAD attributes showed negative values in both vectors, indicating a low potential for the overall genetic difference. The characteristics that maximize the difference were used to give a greater emphasis to cluster the decision and parental choice for hybrids for further selection purposes [18]. The clustering technique was used to divide genotypes into groups based on their performance, as shown in **Table 5**. Five different clusters were identified based on the analysis of similarities and related properties. The process of grouping these genotypes has proved useful in identifying compounds with similar characteristics, thereby facilitating the process of reproduction.

Selecting the parents' genotype for the hybrid program determines the desirability of certain characteristics. These features include fewer leaves number in each plant, short plant height, fewer eyes number in each tuber, fewer tuber-yielding genotypes from Cluster I best and an increased leaves number in each plant, the high-quality height of the plant, the tubers number in each plant, an increase in the greater fresh mass of each plant, and the increasing weight of individual tubers of the plants from Cluster II considered suitable candidates for participation in the hybridization program.

Cluster II showed the highest values for the tubers number in each plant, the eyes number in each tuber, tuber weight in each plant, the leaves number in each plant, and fresh weight of each plant, and also had the second-highest average tube weights/plant, SPAD, and biomass. Compared to other clusters, Cluster I had the fewest tubers per plant. On the other hand, Cluster III demonstrated the most deficient average tuber weights/plant, fresh weight/plant, and SPAD measurement, and Cluster IV showed the lowest biomass. The selection of the cluster is essential for the strengthening of heterosexual F1. For this purpose, five groups have been considered: Clusters II and V, I and II, IV & V, II & IV, and I & III. These clusters are considered valuable assets in hybrid programs.

5. Conclusions

Potential genotypes of valuable properties are classified into various groups. There is a high diversity among the genotypes of the potatoes studied, and it may be used in multiple variety improvement programs in the future. In the winter of 2020/2021, we examined the results of the genotypes of 25 potato species for the determination of the degree of genetic diversity in various characteristics.

These genotypes have all been classified into five groups, namely Clusters I, II, III, IV, and V, and further than five groups (5 groups) have been organized by these clusters, taking into account the potential of different characteristics of Clusters II and V, I and II, IV and V, II, and IV, and I and III, respectively. The maximum number (8) was found in group III, and in group I, the minimum number. The distance between groups I and II was found to be the shortest (4.33), while the distance between groups II and III to be the longest (22.55). Eigenvalue was the highest in tubers/plant parameter number (31.25%), and the second highest (26.20%) was in eyes/tube number.

Positive canonical values were exposed by these two parameters in both Vectors I and II, and these properties can be recommended as a significant attribute to explore the maximum possibility of genetic differences. Given these two characteristics, the parents' choice had the appropriate range to obtain a broad spectrum of segregation. Cluster II found the most significant tuber number in each plant (8.123), the eyes number in each tuber (15.558), tuber weights in each plant (217), plant height (50), the leaves number in each plant (280.51), fresh weight (158.52) and the second largest average tuber weight in each plant (30.501), SPAD (49.159) and biomass (7779.0). Similarly, Cluster V obtained the largest average

weight/plant (31.272), SPAD (50.505), biological material (8855.6), and the second largest number of eyes/tuber (10.957), tuber weights/plant (212.68), plant height (48.578), the number of leaves/plant (240.50). In addition, Cluster I appeared to be the lowest producer of the tuber number in each plant (5.057), the eyes number in each tuber (8.152), plant height (34.566), and the leaves number in each plant (230.08).

The tuber number in each plant, the eyes number in each tuber, and average tuber weights contributed mainly to genetic differences. The parents' choice has the appropriate range for these three traits to obtain a wide separation. Hagrai, Green Mountain, G.M.O., Elvira in Cluster II, and Larparki and Diamond in Cluster I can be regarded as the parents of future hybrid programs due to the extent of the genetic gap, the contribution of various traits to the total separation, and the dimensions of the collective medium. Thus, this study can help farmers increase genetic diversity and reduce vulnerability to disease and climate change by choosing other related materials for cruises.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Mohan, V., *et al.* (2016) Slowing the Diabetes Epidemic in the World Health Organization South-East Asia Region: The Role of Diet and Physical Activity. *WHO South-East Asia Journal of Public Health*, **5**, 5-16.

[2] Zaheer, K. and Akhtar, M.H. (2016) Potato Production, Usage, and Nutrition—A Review. *Critical Reviews in Food Science and Nutrition*, **56**, 711-721. https://doi.org/10.1080/10408398.2012.724479

[3] Salgotra, R.K. and Chauhan, BS. (2023) Genetic Diversity, Conservation, and Utilization of Plant Genetic Resources. *Genes* (*Basel*), **14**, Article 174. https://doi.org/10.3390/genes14010174

[4] Sorrells, M.E. and Fritz, S.E. (1982) Application of a Dominant Male-Sterile Allele to the Improvement of Self-Pollinated Crops. *Crop Science*, **22**, 1033-1035. https://doi.org/10.2135/cropsci1982.0011183X002200050033x

[5] Griffing, B. and Lindsstromm, E.W. (1954) A Study of the Combining Abilities of Corn Inbreds Having Varying Proportions of Corn Belt and Non-Corn Belt Germ Plasm. *Agronmy Journal*, **46**, 545-552. https://doi.org/10.2134/agronj1954.00021962004600120004x

[6] Ross-Ibarra, J., Morrell, P.L. and Gaut, B.S. (2007) Plant Domestication, a Unique Opportunity to Identify the Genetic Basis of Adaptation. *Proceedings of the National Academy of Sciences*, **104**, 8641-8648. https://doi.org/10.1073/pnas.0700643104

[7] Hossain, Md.M., Azad, Md.A.K., Enton, T.E.-J. and Siddquie, Md.N.-A. (2021) Assessment of Different Traits to Evaluate Genetic Divergence in Some Wheat (*Triticum aestivum* L.) Genotypes under Late Sowing Condition. *American Journal of Plant Sciences*, **12**, 734-747. https://doi.org/10.4236/ajps.2021.125050

[8] Mahalanobis, P.C. (1928) A Statistical Study at Chinese Head Measurement. *Journal of Asiatic Society*, *Bangladesh*, **25**, 301-337.

[9] Mahalanobis, P.C. (1936) On the Generalized Distance in Statistics. *Proceedings of National Institute Science in India*, **2**, 49-55.

[10] Rao, C.R. (1952) Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York, 390.

[11] Digby, P., Galway, N. and Lane, P. (1989) Genstat 5: A Second Course. Oxford Science Publication, Oxford, 103-108.

[12] Singh, R.K. and Chaudhury, B.D. (1985) Biometrical Methods in Quantitative Genetic Analysis (Revised Ed.). Kalyani Publishers, Ludhiana, 318.

[13] Awad-Allah, M.M.A., Shafie, W.W.M., Alsubeie, M.S., Alatawi, A., Safhi, F.A., ALshamrani, S.M., Albalawi, D.A., Al-Amrah, H., Alshehri, D., Alshegaihi, R.M., *et al.* (2022) Utilization of Genetic Resources, Genetic Diversity and Genetic Variability for Selecting New Restorer Lines of Rice (*Oryza sativa* L.). *Genes*, **13**, Article 2227. https://doi.org/10.3390/genes13122227

[14] Rashid, M.H. (2000) Gene Effects and Selection Response of Morpho-Physiological Traits in Late Sown Bread Wheat. Ph.D. Thesis, Bangladesh Agricultural University, Mymensingh.

[15] Singh, B.N., Vishwakarma, S.R. and Singh, V.K. (2010) Character Association and Path Analysis in Elite Lines of Wheat (*Triticum aestivum* L.). *Plant Archives*, **10**, 845-847.

[16] Zaman, M.R., Paul, D.N.R., Kabir, M.S., Mahbub, M.A.A. and Bhuiya, M.A.A. (2005) Assessment of Character Contribution to the Divergence for Some Rice Varieties. *Asian Journal of Plant Sciences*, **4**, 388-391. https://doi.org/10.3923/ajps.2005.388.391

[17] Patel, F.G., Porter, S. and Mossa, M.G. (2012) Breeding Strategies for Improving Wheat Yield in Heat-Stressed Environments. In: Saunders, D.A. and Hettel, G.P., Eds., *Wheat in Heat-Stressed Environments, Irrigated, Dry Areas, and Rice-Wheat Farming*, CIMMYT, Mexico, 24-32.

[18] Jiang, C.M., Yin, Y.P., Liu, X. and Wang, Z.L. (2007) Response of Flag Leaf Lipid Peroxidation and Protective Enzyme Activity of Wheat Cultivars with Different Heat Tolerance to High Temperature Stress after Anthesis. *Acta Agronomica Sinica*, **33**, 143-148.