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Genetic divergence analysis in potato (*Solanum tuberosum* L.)

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Abstract
The experiment was conducted during the rabi season of experimental year at Botanical Research Field in Rajshahi University. A total of 48 potato genotypes were evaluated for 6 quantitative traits in RCBD with 3 replications. Genetic divergence using Mahalanobis D^2 techniques was studied for yield contributing traits. These genotypes were grouped into 6 clusters. Cluster IV showed maximum divergence with 12 genotypes followed by cluster III having 10 genotypes. The inter-cluster distance was higher than intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The highest intra-cluster value was the maximum in cluster III (3.884) and minimum in cluster IV (1.012). The highest inter-cluster distance was in between cluster I and III ($\sqrt{D^2}$ =11.847) indicating maximum exploitation of heterosis on hybridization. The maximum and minimum divergence was revealed between cluster I with III and cluster I with IV, respectively. In conclusion, according to cluster mean and principal component analysis cluster IV and cluster VI contained the best genotypes for most of the characters and could be used as parents in crossing program targeted at developing process type genotypes.

Keywords: genetic divergence, cluster, potato, RCBD

Introduction
Potato (*Solanum tuberosum* L.) is the third most important food crop in the world in terms of consumption after rice and wheat. It can be used as fresh products and commercially processed foods such as french fries and chips (Hussen *et al*., 2020) [5]. Potato is one of the most important food crops in Bangladesh as well as of many countries of the world. It ranks first among the vegetables in terms of area and production in Bangladesh. Around 320 million tons of potatoes are produced yearly and this amount is estimated to be doubled by 2020 (FAO, 2021). The yield level of this crop in Bangladesh is low compared to other potato growing countries of the world (Satter *et al*., 2011).
Estimation of genetic divergence is an important factor to know the source of genes for a particular character within the available genotypes. Genetic diversity among the segregating population also helps select suitable types as parents and also for commercial cultivation. The present investigation was carried out in order to find out the above mentioned qualities in a group of potato genotypes collected from Tuber Crops Research Centre in Bangladesh. This crop is one of the most important tuber crop grown in Bangladesh for its high production, high nutritional values, easy digestibility and many other industrial uses. Potato of an average size with skin provides about 10 percent of the recommended daily intake of fibre (Nirmodh *et al*., 2019). In Bangladesh, several improved potato varieties have been released by different research centres, different Agricultural Universities and Institutions since the establishment of the potato research and development program. However, most of the released varieties have not satisfied the farmer and consumer expectations.
Therefore, the present study was designed to explore the nature and magnitude of genetic divergence and the characters contributing in potato genotypes for tuber quality, yield and yield-related traits. To identify genetically diverse parents for developing varieties with superior traits for high yield, consumer-preferred quality attributes by using cluster and principal component analyses.

Materials and Methods
The field experiment of the present study was carried out during the Rabi season of Botany Department Research Field at University of Rajshahi, Bangladesh. The experiment was conducted in randomized complete block design (RCBD) with 48 potato genotypes (Table 2) in 3 replications. Sowing of potato tuber was done during mid-November in that year. The recommended dose of fertilizers i.e. nitrogen 250kg/ha, phosphorus 125kg/ha

and potassium 125kg/ha was applied. All the phosphorus, potassium and half dose of nitrogen were applied at the time of sowing while remaining was used at 1st and 2nd earthing up. The experimental plot was visited regularly during growing season. Irrigation and plant protection measures were carried out when required. Germination was recorded after 30 days of planting. Plant height was measured from ground level to top of the highest branch at the time of 60 days of crop growth. Five plants were selected from each plot and each replication for recording plant height, number of leaves, number of stems, plant fresh weight, plant dry weight and tuber yield were recorded.

The genetic divergence was estimated using the Mahalanobis D^2 statistics (Mahalanobis, 1936) [6]. Tracing D^2 as a generalized distance, the criterion used by Tocher as described by Rao (1952) was applied for determining the cluster in group. The mean of intra and inter cluster distances were determined using GENSTAT-5 Fifth Edition computing software. Software and suggested by Singh and Chaudhary (1985). The scattered diagram was made by using software IBM SPSS Statistics version 22.

Results and Discussions

The percentage (%) contribution of the characters towards total divergence is presented in Table I. The contribution of different characters towards the total divergence was recorded the highest for plant height followed by number of leaves and number of stems. While formulating breeding programme, these characters be given priority to explore the diversity in genotypes. The similar trend in divergence has also been reported by Rangare and Rangare (2017).

Based on the D^2 analysis, all the 48 potato genotypes were grouped into six clusters (Table 1.). The clustering pattern of genotypes in the divergence studies revealed that out of 48 maximum of 12 genotypes were recorded in cluster IV, followed by 10 in cluster III, 09 in cluster VI, 07 in cluster I, 06 in cluster V and lowest 04 genotypes in cluster II.

The highest inter-cluster distance was observed between cluster I and III (11.847) followed by cluster I and II (8.164), cluster III and VI (8.029), cluster II and IV (7.304). The minimum inter cluster distance were found between cluster I and IV (1.800). Inter-cluster distance is the main criterion for selection of genotypes on the basis of D^2 analysis. Genetic divergence is the most important tool to select prospective parents for crop improvement programmes. The genotypes belonging to the cluster separated by high estimated distance could be utilized in hybridization programmes for obtaining wide variation among the segregants. The data on intra-cluster distance suggesting that the more diverse genotypes were recorded in cluster III. The minimum intra-cluster distance exhibited by cluster IV indicating limited genetic diversity among the integrated genotypes. These findings are in agreement with the previous reports of Chandrakar (2007) [1], Singh (2008) [12], Haydar *et al* (2009) [4], Panigrahi *et al*., (2014) [7] and Probha *et al.* (2019) [8].

The genetic divergence between clusters was reflected in their cluster means. Cluster mean values for six yield related traits are presented in Table 4. Results revealed that cluster mean for number of stems cluster IV found the highest mean value (508.07) whereas, cluster III was found to the lowest value (2.71) for plant height. The similar trend in divergence have also been reported by Chandrakar (2007) [1], Haydar *et al,* (2007) [3], Singh (2008) [12], Haydar *et al,* (2009) [4], and Prabha *et al*., (2019) [8].

The canonical analysis revealed that the value for both vectors (I, II) plant height, plant fresh weight and plant dry weight were positive (Table 5). Such results indicated that these characters contributed maximum towards diversity of the genotypes. It could be concluded that the genotypes with greater divergence would offer a good scope for the improvement of potato genotypes through selection. Based on principal component axes 1 and 2, a two dimensional scattered plotting diagram (Z1 and Z2) of the genotypes are presented in Figure 1. The scattered diagram revealed that apparently there were mainly six clusters. The pattern of distribution of genotypes in the scattered diagram revealed considerable variability among the genotypes. A two dimensional scatter diagram was constructed using component 1 as X axis and component 2 as Y axis, reflecting the relative position of the genotypes (Figure 1). As per scatter diagram the genotypes were apparently distributed into six groups.

Genetic divergence is the key component for the improvement of genotypes. The accessibility of more diverse genotypes indicates the possibility of acquire desirable genes to improve the varieties.

Table 1: Percentage of contributing characters towards divergence in Potato genotypes.

Characters	Contribution by each character (%)
Plant height	48.85
Number of leaves	18.07
Number of stems	12.30
Plant fresh weight	10.90
Plant dry weight	5.79
Tuber yield	4.10

Table 2: Distribution of 48 potato genotypes among 6 clusters.

Cluster	Genotypes	Genotypes in different clusters
I	7	Prelude, lalpakri, hagri, gaforgown, banana, atlus, remarkarursset

II	4	Baraka, felcina, martin, senori
III	10	Carlita, diamond, eldina, fibula, future, lura, marrabel, petronese, raja, victoria
IV	12	Vanilla, shepodi, shaita white, shaita red, all red, blondy, blue maintain, chieftain, indurcani, multa, quency, burbank
V	6	Asterix, cardinal,challista, chipita, durby, granula
VI	9	Beleni, akria, callwhite, courage, fontany, innovator,radeo, ultra, voyager

Table 3: Inter and intra (bold) cluster distances in potato genotypes.

Clusters	I	II	III	IV	V	VI
I	1.026	8.164	11.847	1.800	6.883	3.453
II		2.571	4.786	7.304	4.090	4.911
III			3.884	10.484	5.319	8.029
IV				1.012	5.320	2.503
V					1.186	3.076
VI						1.135

Table 4: Cluster means for six characters in 48 potato genotypes.

Characters	I	II	III	IV	V	VI
Plant height	64.20	17.00	2.71	283.75	5.05	65.33
Number of leaves	120.61	20.80	3.70	435.30	8.81	321.73
Number of stems	114.20	23.61	4.12	384.2	10.50	508.07
Plant fresh weight	78.42	19.60	3.31	254.28	7.71	132.62
Plant dry weight	99.73	23.14	4.20	290.20	9.34	334.24
Tuber yield	103.90	22.30	3.12	304.73	5.48	211.19

Table 5: Latent vectors for six characters of 48 potato genotypes.

Characters	Vector I	Vector II
Plant height	0.00069	0.02025
Number of leaves	0.01008	-0.20317
Number of stems	0.02241	-0.04788
Plant fresh weight	0.01154	0.01992
Plant dry weight	0.01047	0.00737
Tuber yield	0.02363	-0.00582

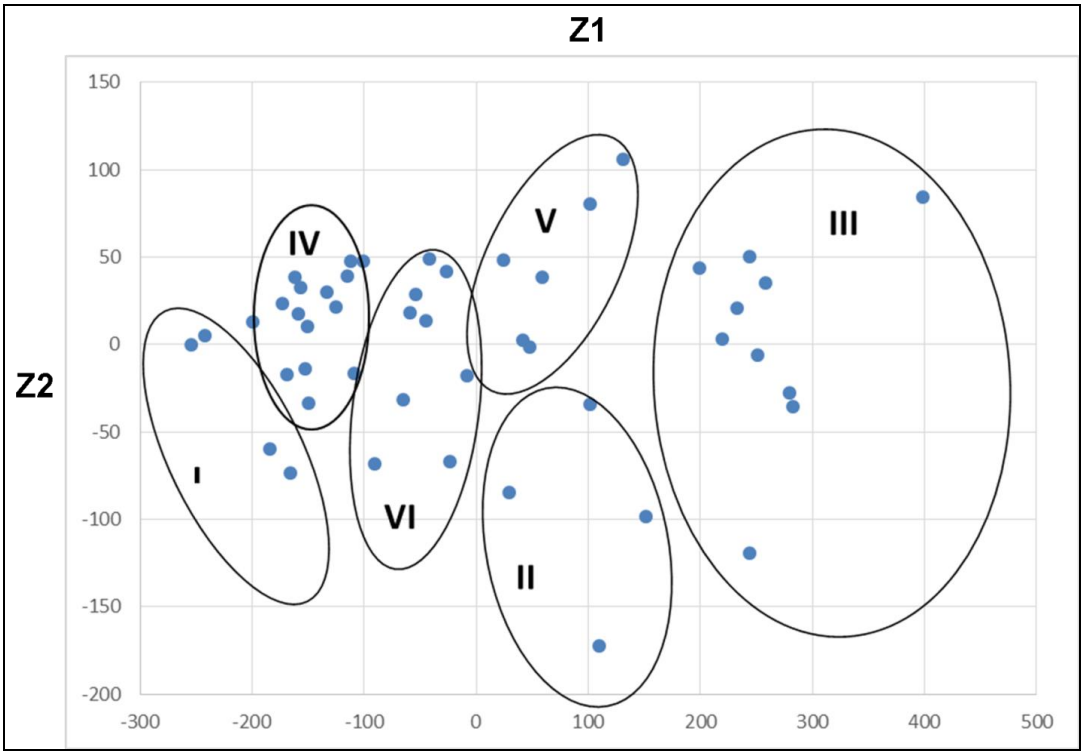

Fig 1: Scatter distribution of 48 potato genotypes based on their principal component scores superimposed with clustering.

References

1. Chandrakar A. Genetic analysis of clonal hybrids (C1 progenies) for tuber yield and its components in potato (Solanum tuberosum L). M.Sc. (Ag.) Thesis, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), 2007.
2. FAO. World Food and Fertilizer Trends and Outlook to 2021. Food and Agriculture Organization of the United Nations, Rome, Italy, 2020.
3. Haydar A, Ahmed MB, Hannan MM, Razvy MA. Analysis of genetic diversity in some potato varieties grown in Bangladesh. Middle-East J. Sci. Res,2007:2(3-4):143-145.
4. Haydar A, Uddin MS, KHOKAN EH T. Ara T, Zamman KMK, Hoque A. D2 -Analysis and Selection Criteria in Potato. Int. J. Sustain. Crop Prod,2009:4(1):91-93.
5. Hussen ES, Ali WM, Desta TA. Genetic Diversity in Potato (Solanum tuberosum L.) Genotypes for Yield and Processing Attributes at Holetta, Central Highlands of Ethiopia. East African J. Agric. Biotech,2020:2(1):24-50.
6. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Sci., India,1936:2:49-55.
7. Panigrahi KK, Sarkar KK, Baisakh B, Mohanty A. Assessment of Genetic Divergence in Potato (Solanum Tuberosum L.) Genotypes for Yield and Yield Attributing Traits. International J. Agric. Environ. Biotech,2014:7(2):247-254.
8. Prabha N, Nanda HC, Chandrakar C, Pandey KK. Analysis of genetic divergence in potato. J. Pharmacognosy and Phytochemistry,2019:8(4):1719-1723.
9. Rangare SB, Rangare NR. Classificatory analysis of Potato (Solanum tuberosum L.) genotypes for yield and yield attributing traits. The Pharma Innovation Journal,2017:6(8):94-102.
10. Rao CR. Advanced Statistical Methods in Biometric Research. John Wiley and Sons Inc., New York, 1952:15(10):130-134.
11. Sattar MA, Uddin MZ, Islam MR, Bhuiyan MKR, Rahman MS. Genetic Divergence in Potato (Solanum tuberosum L.). Bangladesh J. Agril. Res,2011:36(1):165-172.
12. Singh G. Studies on genetic variability, association and divergence in potato (Solanum tuberosum L.). M.Sc. (Ag.) Thesis, Indira Gandhi Krishi Vishwavidayala, Raipur (C.G.), 2008, 14.
13. Singh RK, Choudhary BD. Biometrical Methods in Quantitative Genetic Analysis. Revised ed. Kalyani Publishers, New Delhi, 1985, 57.
14. Singh RK, Choudhary BD. Biometric methods in quantitative genetic analysis- Kalyani publication, New Delhi, 1985, 317-319.