

## D<sup>2</sup>-ANALYSIS AND SELECTION CRITERIA IN POTATO

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### ABSTRACT

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The experiment was conducted at Botanical Research Garden of Rajshahi University, Rajshahi during rabi season of November 2006 to March 2007 to ascertain the nature and magnitude of genetic diversity present in the material which would ultimately help to identify parents for future breeding program. Genetic divergence among 30 potato genotypes based on tuber yield and its component characters were estimated using D<sup>2</sup> statistic. Divergence analysis grouped these genotypes in to five clusters. 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 maximum in cluster II (1.73) and minimum in cluster IV (0.43). The highest inter-cluster distance was in between cluster II and IV ( $\sqrt{D^2}=8.123$ ) indicated maximum exploitation of heterosis on hybridization. Cluster II showed the highest mean values for most of the characters and clusters III and V showed the maximum mean values for plant height, number of leaves/plant and tuber yield, while cluster IV revealed the lowest mean value for all the characters. Three characters e.g. plant height, number of leaves/plant and fresh weight/plant showed maximum contribution towards total divergence among different characters. Genotypes were much in use having the above mentioned characters in cluster II and III would offer a good scope for the improvement of this crop through hybridization and rational selection.

**Key words:** D<sup>2</sup>-analysis, selection criteria, potato

### INTRODUCTION

Potato (*Solanum tuberosum* L) is the most important food crop of the world. Potato has a huge prospect in Bangladesh. Though potato is being eaten as an item of vegetables at present, it can be used as complementary food. Because it contains all the characteristics of a staple food. The potato is a crop which has always been the 'poor man's friend'. For vegetable purposes it has become one of the most popular crops in this country. Potatoes are used for several industrial purposes such as for the production of starch and alcohol.

Potato starch is used in laundries and for sizing yarn in textile mills. Potatoes are also used for the production of dextrin and glucose. As a food production itself, potatoes are converted into died products such as 'potato chips', 'sliced' or 'shredded potatoes'. Bangladesh is a country with high population density. To feed this ever growing number of people there is a need to increase productivity so that more potato crops can be produced from the same area of land. The importance of genetic diversity in the selection of suitable genotypes for hybridization has been stressed by several scientists in different crops (Ivy *et al.* 2007, Mondal *et al.* 2007 and Haydar *et al.* 2007). For a successful breeding program, genetic diversity and variability play a vital role. The qualification of genetic diversity has made it possible to choose genetically diverse parents for a successful hybridization program. With the development of advanced biometrical methods such as multivariate analysis (Rao,1952) based on Mahalanobis's (1936)D<sup>2</sup> statistic, the magnitude of genetic diversity among all the possible pairs of populations at genotypic level before effecting actual crosses in modeling the genotypes in a desired genetic architecture has become possible. The present study was taken up with 30 potato genotypes to ascertain the nature and magnitude of genetic diversity present in the material which would ultimately help to identify parents for future breeding program.

### MATERIALS AND METHODS

The experiment was conducted at Botanical Research Garden of Rajshahi University, Rajshahi-6205 during rabi season of November 2006 to March 2007. Thirty potato genotypes were collected from Biotech Seeds Limited, Namu Bhadra, Rajshahi, Bangladesh. The experiment was laid following randomized block design with three replications. The potato tubers were planted on November 2006. The unit plot size was 15 m X 3 m with row to row spacing was 25 cm. Fifteen plants were grown in each row (line). The intercultural operations were done timely to raise a good crop. Observations were recorded from 10 randomly selected plants in each line for plant height (cm), number of leaves/plant, fresh weight/plant (g), number of tubers/plant and tuber yield/plant(g). Genetic diversity was studied following Mahalanobis's(1936) generalized distance (D<sup>2</sup>) extended by Rao (1952). Clustering of genotypes was done according to Tocher's method (Rao, 1952) and Principal Component Analysis for graphical representation of the genotypes. All the statistical analysis was carried out using Genstat-5 computer software.

## RESULTS AND DISCUSSION

The analysis of variance on the basis of potato plant revealed significant difference among the genotypes for all the characters and therefore, diversity analysis was carried out. Thirty potato genotypes were grouped into five different clusters using clustering technique. 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 5 groups. This clustering pattern confirmed the results obtained by D<sup>2</sup>-statistic. The distribution pattern in the D<sup>2</sup>-analysis indicated that 30 genotypes were grouped into five clusters (Table 1).

The maximum number of genotypes (9) was grouped into cluster II followed by cluster I (8), where as minimum number (3) in clusters IV and V. The cluster III consists of 7 genotypes. Mondal *et al.* (2007) reported five clusters (groups) in a divergence study of 31 potato genotypes. Statistical distances represent the index of genetic diversity among the clusters. The intra and inter- cluster values among the five clusters are presented in Table 2.

The results revealed that the inter-cluster distance was longer than the intra-cluster distance which suggested wider genetic diversity among the genotypes of different groups. The inter-cluster (D<sup>2</sup>) values varied from 2.573 to 8.123 indicating range of diversity present among the genotypes. The highest inter-cluster distance was observed between cluster II and IV (8.123) and followed by cluster I and IV (6.349) and the lowest between I and II (2.573). The intra-cluster distance ranged from 0.43 to 1.73. The highest intra- cluster distance was observed for the cluster II and minimum for the cluster IV. The intra-cluster distances in all the five clusters were low indicating the genotypes within the same cluster were closely related. These relationships were also reflected in the scatter diagram. The highest inter cluster divergence indicated that the genotypes grouped in these cluster were highly divergent from each other. Selection of parents from the highly divergent clusters is expected to manifest high heterosis and also wide variability in genetic architecture.

The cluster means for five characters are presented in Table 3. The genetic differences between the clusters were reflected in the intra cluster means. The characters contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization. The cluster II had the highest mean values for the selective five characters.

The highest mean values for fresh weight/plant and number of tubers/plant were observed in cluster II indicating the grouping of high yielding varieties. On considering cluster means genotypes in cluster II were important for these selective characters.

The canonical analysis revealed that the value for both vectors (VI, VII) fresh weight /plant was positive. Such results indicated that fresh weight/plant 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 through selection.

Table 1. Genotypic grouping of thirty potato genotypes based on morphological characters

| Cluster (Group) | Number of Genotypes | Genotypes   |
|-----------------|---------------------|---|
| I               | 8                   | Calwhite, Shilbilati, Cheroki, Fundy, GMO, TPS-67, Elvera, Monona             |
| II              | 9                   | Petronese, Conestoga, Granula, Raja, Japanese red, Atlas, 573, Diamond, TPS-7 |
| III             | 7                   | Hagri, Russet Burbank, Green mountain, Atlantic, Blondy, Superior, Shepody    |
| IV              | 3                   | Banana, Lalpaki, Allblue  |
| V               | 3                   | Prelude, Yucon gold, Multa  |

Table 2. Average intra (bold value) and inter cluster distance (D<sup>2</sup>) in 360 potato genotypes

|     | I           | II          | III         | IV          | V           |
|-----|-------------|-------------|-------------|-------------|-------------|
| I   | <b>1.53</b> |             |             |             |             |
| II  | 2.573       | <b>1.73</b> |             |             |             |
| III | 2.75        | 3.302       | <b>0.78</b> |             |             |
| IV  | 6.349       | 8.123       | 5.075       | <b>0.43</b> |             |
| V   | 3.428       | 5.759       | 3.759       | 3.392       | <b>1.23</b> |

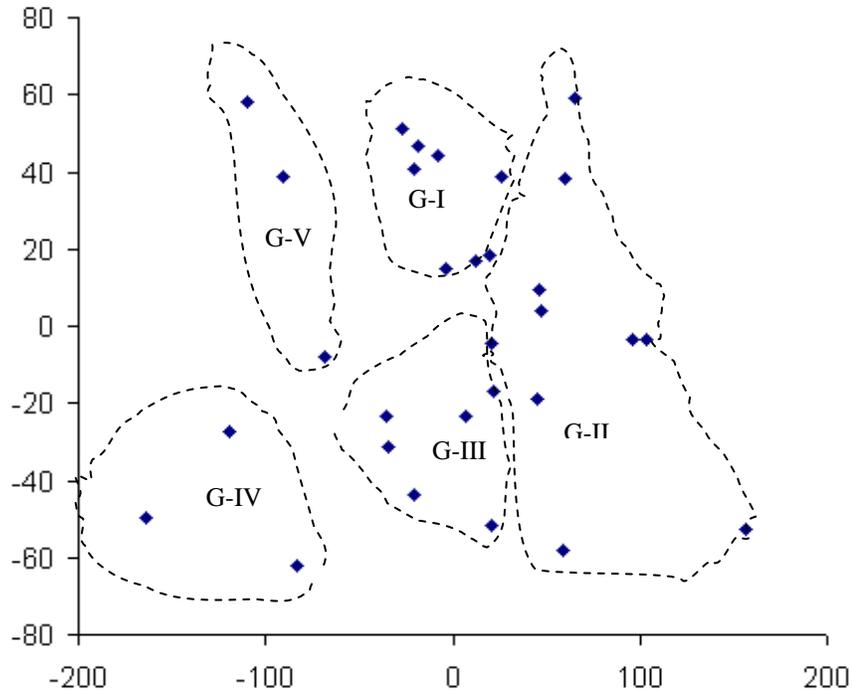


Figure 1. Scatter diagram of 30 potato genotypes

Table 3. Cluster mean values for different characters in potato

| Cluster (Group) | PH    | NLPP   | FWP    | NTPP  | TYP    |
|-----------------|-------|--------|--------|-------|--------|
| I               | 42.7  | 229.3  | 121.56 | 10.25 | 145.37 |
| II              | 43.37 | 312.48 | 104.12 | 10.04 | 130.34 |
| III             | 43.45 | 240.67 | 93.06  | 10.4  | 91.2   |
| IV              | 30.28 | 127.96 | 82.42  | 7.74  | 51.45  |
| V               | 35.34 | 147.66 | 133.15 | 11.14 | 114.7  |

PH = Plant height, NLPP = Number of leaves / plant, FWP = Fresh weight / plant, NTPP = Number of tubers / plant, TYP = Tuber yield / plant.

Table 4. Relative contribution of the five characters to total D<sup>2</sup>-analysis in potato

| Sl. No. | Characters               | Vector-I | Vector-II |
|---------|--------------------------|----------|-----------|
| 1       | Plant height             | 0.0411   | -0.0771   |
| 2       | Number of leaves / plant | 0.0294   | -0.0077   |
| 3       | Fresh weight / plant     | 0.0026   | 0.0237    |
| 4       | Number of tubers / plant | 0.0427   | -0.2013   |
| 5       | Tuber yield / plant      | 0.0252   | 0.0336    |

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