

GENETIC DIVERSITY OF POTATO (*Solanum tuberosum* L.)

M. H. Rahman, M. S. Islam and M. Sonom

Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka 1207, Bangladesh

ABSTRACT

The experiment was conducted with twenty one genotypes of potato at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period from November 2014 to March 2015 to estimate the genetic variability and diversity among the genotypes. The experiment was conducted using Randomized Complete Block Design with three replications. All the genotypes varied significantly with each other for all the studied characters indicated the presence of considerable variations among the genotypes studied. As per PCA, D² and clusters analysis the genotypes were grouped into five different clusters. Clusters III had the maximum nine and cluster II and V had the minimum one genotype. The highest inter-cluster distance was observed between I and V and the lowest was observed between IV and V. Genotypes in cluster I showed the maximum performance for number of leaves per plant, chlorophyll percentage, weight of individual potato and firmness. Cluster II showed maximum performance for total soluble sugar. Cluster III recorded the highest mean performance for dry matter. Cluster IV showed the maximum performance for number of potato per hill, weight of potato per hill and yield. Cluster V showed the maximum performance for specific gravity. Considering this idea and other characteristic performances, G₈ (Shada pakri) and G₁₇ (Shil bilati) from cluster IV; G₄ (BARI-TPS-1) from cluster II; and G₆ (Asterix), G₂₁ (Granola), G₁ (Cardinal) and G₂ (Diamant) from cluster I might be considered better parents for efficient hybridization programme.

Keywords: Genetic diversity; cluster analysis; D² statistics; potato.

INTRODUCTION

Potato (*Solanum tuberosum* L.) popularly known as ‘The king of vegetables’. It is a tuber crop belongs to the family solanaceae. It originated in the central Andean area of South America (Keeps, 1979). Potatoes have 48 chromosomes that are arranged into 24 pairs (tetraploid). It is the 4th world crop after wheat, rice and maize. Bangladesh is the 8th potato producing country in the world. In Bangladesh, it ranks 2nd after rice in production (FAO, 2013). It contributes not only energy but also substantial amount of high quality protein and essential vitamins, minerals and trace elements to the diet (Horton, 1987). In Bangladesh, potato is grown during the winter season. In our country potato is mainly used as vegetable and available in the market throughout the year with reasonable price as compared to other vegetables. Potato has also great importance in rural economy in Bangladesh. It is not only a cash crop but also an alternative of food crop against rice and wheat. Bangladesh has a great agro-ecological potential of growing potato. The area and production of potato in Bangladesh has been increasing during the last decades but the yield per unit area remains more or less static. The reasons for such a low yield of potato in Bangladesh are lack of high yielding variety, lack of disease free

seed tuber and use of low quality seed. Available reports indicated that potato production in Bangladesh can be increased by using HYV, disease free and optimal sized seed are important which influences the yield of potato (Divis and Barta, 2001). Knowledge on the nature of variability and association of yield with its components is of great importance for identification of superior parents in any breeding programme. When the variability in a population is largely of genetic nature with least environmental effect, the probability of isolating superior genotypes is high. Since information on potato progeny is not available in our country, the results reported in the study are related to select a suitable plant type having high yield with good natural keeping quality (Kanika, 2010). It has been found that the progenies derived from crossing between divergent parents give divergent and useful trait. It has been often postulated by the breeders that geographical distribution reflects genetic diversity in selecting parents for hybridization. A limited study has been made on genetic divergence in potato either at tetraploid (Gaur *et al.*, 1978; Sidhu *et al.*, 1981 and Singh *et al.*, 1988) or at diploid level (Grag, 1988). An understanding of the nature and magnitude of variability among the genetic stocks is of prime importance to the breeders. Genetic diversity is one of the important tools to qualify genetic variability in both cross and self pollinated crops (Murty and Arunachalam, 1966; Gaur *et al.*, 1978). Considering the above mentioned idea and scope, the study was taken to study the nature and extent of association of genetic variability in potato genotypes for growth, yield and quality parameters, to assess genetic diversity among the genotypes and to find out the best genotype for further use in breeding programme.

MATERIALS AND METHODS

The research work was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh during the period from 12 November, 2014 to 31 April, 2015. The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 150 m². A distance of 1.0 m from block to block, 60 cm from row to row and 25 cm from plant to plant was maintained. Twenty one (21) genotypes of potato were used for the present research work. The genetically pure and physically healthy tuber of these genotypes were collected Bangladesh Agricultural Research Institute (BARI), Gazipur, Dhaka and Dinajpur, Bogra, Joypurhat. The name and source of these genotypes are presented in Table 1. Total cow dung, vermicompost, gypsum, magnesium sulphate, borax and triple super phosphate (TSP) were applied in the field during final land preparation. Half Urea and half muriate of potash (MOP) were applied in the plot after 30 DAP. Remaining urea and muriate of potash (MOP) were applied after 50 DAP. The tuber were planted in the field on 15 November, 2014. The planted tuber were watered regularly to make a firm relation with roots and soil to stand along. All recommended agronomic package of practices were followed to grow a healthy crop. Data on ten random sample plants selected from each plot were recorded on ten characters viz., Plant height (cm), Number of leaves/ plant, Number of stems /hill, Leaf area index, Chlorophyll content of leaves (SPAD value), Stem diameter (cm), Dry matter content (%), Number of tuber /hill, Average weight of tuber (g), Yield of tuber/ plant (g), Yield /hectare (ton), Specific gravity (gcm⁻³), Total soluble solids (TSS), Firmness, Number of eye / tuber. According to Singh and Chaudhury (1985), One-way ANOVA (Completely randomized Design) was done with the mean data of all the replication subjected. Duncan's New Multiple Range Test (DMRT) was performed to test the differences between genotypes, following the method of Stel and Torrie (1960).

Table 1. List of Potato genotypes with their source

SL.No.	Genotypes No.	Name	Source
1	G ₁	Cardinal	TCRC,BARI
2	G ₂	Diamant	TCRC,BARI
3	G ₃	Laddy rosetta	TCRC,BARI
4	G ₄	BARI-TPS-1	TCRC,BARI
5	G ₅	Courage	TCRC,BARI
6	G ₆	Asterix	TCRC,BARI
7	G ₇	Lal pakri	LM,Bagura
8	G ₈	Shada pakri	LM,Dinajpur
9	G ₉	Jam alu	TCRC,BARI
10	G ₁₀	Tilok Pura	LM,Joypurhat
11	G ₁₁	Pahari Pakri	LM,Bogra
12	G ₁₂	Pakri	TCRC,BARI
13	G ₁₃	Fata pakri	LM,Bogra
14	G ₁₄	Tel pakri	LM,Bogra
15	G ₁₅	Romana pakri	LM,Joypurhat
16	G ₁₆	Bot pakri	LM,Bogra
17	G ₁₇	Shil bilati	LM,Joypurhat
18	G ₁₈	Local cardinal	LM,Dinajpur
19	G ₁₉	Patnai	LM,Dinajpur
20	G ₂₀	Lal chokha pakri	LM,Joypurhat
21	G ₂₁	Granola	TCRC,BARI

TCRC=Tuber Crop Research Centre, BARI= Bangladesh Agricultural Research Institute and LM=Local Market

RESULTS AND DISCUSSION

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 2) as suggested by Singh and Chowdhary (1985). On the basis of D^2 values, the 21 genotypes were grouped into five highly divergent clusters (Table3).The clusters divergence was proved by the high inter- cluster and low intra clusters D^2 values. Cluster III was the largest and consisted of nine genotypes followed by cluster I with seven genotypes, clusters IV, II and V had 3, 1 and 1 genotypes respectively.

Table 2. Number, percent and name of genotypes in different cluster

Cluster number	Number of genotypes	Percent (%)	Genotypes
I	7	33.33	G ₁ , G ₂ , G ₃ , G ₅ , G ₆ , G ₁₈ and G ₂₁
II	1	4.76	G ₄
III	9	42.86	G ₇ , G ₁₁ , G ₁₂ , G ₁₃ , G ₁₄ , G ₁₅ , G ₁₆ , G ₁₉ and G ₂₀
IV	3	14.29	G ₈ , G ₁₀ and G ₁₇
V	1	4.76	G ₉

Table 3 revealed that cluster II and V showed minimum intra cluster D^2 value (0.00) distance followed by cluster III (14.03), whereas, maximum intra cluster D^2 value (19.04) was shown by cluster IV followed by cluster I (18.70) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter cluster D^2 value was observed between the clusters IV and V (21.44) indicated close relationship among the genotypes

included in these clusters. Maximum inter – clusters D^2 value was observed between the clusters I and V (57.13) indicated that the genotypes belonging to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregant population (Mehta and Asati, 2008).

Table 3. Intra and inter cluster distance (D^2) for 21 genotypes

Characters	I	II	III	IV	V
I	18.70	32.89	35.65	56.82	57.13
II		0.00	31.17	42.69	46.43
III			14.03	32.83	27.99
IV				19.04	21.44
V					0.00

The cluster mean of 21 genotypes (Table 11) showed that the mean value of clusters varied in magnitude for all the fifteen characters. Genotypes in cluster I showed maximum performance for number of leaves per plant (10.63), stem per hill (3.16), chlorophyll percentage (49.73), weight of individual potato (111.69 g) and firmness (26.12). Cluster II showed maximum performance for diameter per stem (1.16), leaf area index (8.42) and total soluble sugar (45.45). Cluster III recorded highest mean performance for dry matter (1.15). Cluster IV showed maximum performance for number of potato per hill (61.92), weight of potato per hill (1598.06 gm) and yield (224.66 t/ha). Cluster V showed maximum performance for number of eyes per tuber (27.27) and specific gravity (8.00).

Table 4. Cluster mean for twelve yield and yield characters of 21 potato genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Plant height (cm)	61.14	66.55	69.86	73.63	66.55
Leaves per plant (no.)	10.63	9.11	10.08	9.37	7.78
Stem per hill (no.)	3.16	1.22	2.25	2.66	1.55
Diameter per stem (cm)	1.14	1.16	0.91	0.96	0.86
Chlorophyll (%) at 60 DAP	49.73	45.91	49.40	47.65	45.24
Leaf area index	2.22	8.42	2.44	4.38	2.41
Potato per hill (no.)	6.85	6.44	21.06	61.92	24.11
Weight of potato per hill (gm)	758.25	691.11	956.38	1598.06	238.25
Weight of individual Potato (gm)	111.69	107.26	47.24	25.83	9.88
Eyes per tuber (no.)	23.39	25.57	25.09	24.79	27.27
Dry matter %	1.09	1.02	1.15	0.96	0.99
Specific gravity	6.51	6.00	7.41	6.93	8.00
Total soluble sugar (%)	37.01	45.45	29.24	32.42	15.28
Firmness (N)	26.12	21.87	16.05	18.98	4.23
Potato yield (ton / ha)	31.79	149.00	91.40	224.66	220.11

Therefore considering the magnitude of genetic distance and agronomic performances, the genotypes from the clusters I and V should be prioritized in future breeding program for having higher fruit yield. It is suggested that selection of genotypes from these more diversified groups would give better segregation when they are crossed. The greater genetic distance among the genotypes due to these characters in cluster would also offer prime scope for the development of high yielding potato variety.

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