

Analysis of Genetic Diversity in Some Potato Varieties Grown in Bangladesh

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Abstract: Genetic diversity using Mahalanobis's D^2 - technique was studied for tuber yield and its components viz., Plant Height (PH), Number of Leaves/plant (NLPP), Fresh Weight/plant (FWP), Number of Tubers/plant (NLPP), Number of Eyes/tuber (NEPT), Average Tuber Weight of Plant (ATWP) and Tuber weight/plant (TWt./P). The 30 potato genotypes were grouped into six clusters. The maximum diversity was contributed by tuber weight/plant. The cluster III and cluster IV contained the maximum number of genotype and the cluster I contained the minimum. The highest inter-cluster distance between cluster I and cluster VI followed by between cluster I and cluster v showing wide diversity among the groups. The highest intra-cluster distance was observed in cluster VI and lowest in cluster II. The inter cluster distance in most of the cases were higher than the intra-cluster distance indicating wider genetic diversity among the genotypes of different groups. Plant height, number of leaves/ plant, fresh weight/plant and tuber weight/plant showed maximum contribution towards total divergence among the genotypes.

Key words: Genetic diversity • Mahalanobis's D^2 -technique • potato • tuber

INTRODUCTION

Potato is a forth major food crop of the world in its importance after rice, wheat and maize. As a carbohydrate rich food crop in Bangladesh it ranks just after rice and wheat [1]. Potato is one of the most important tuber crop grown in Bangladesh for its high production, high nutritional values, easy digestibility and many industrial uses. For a successful breeding program, genetic diversity and variability play a vital role. Genetic diversity in a population is a prerequisite for an effective plant-breeding program. Genetic divergence is a useful tool for an efficient choice of parents for hybridization to develop high yield potential cultivars. The importance of genetic divergence in the improvement of crop has been stressed in both self and cross-pollinated crops [2, 3]. Evaluation of genetic divergence is important to know the source of genes for a particular trait within the available germplasm [4]. The main goal of potato breeding is to develop potential varieties that ensure highest and stable production in a range of environments. Genetic diversity is used for discriminating divergent populations, which are reinstated by more scientific and advanced

biometrical techniques, viz., multivariate analysis based on Mahalanobis D^2 -statistic. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for cultivation for increasing yield, wider adaptation, desirable quality, pest and disease resistance. Genetic divergence analysis estimates the extent of diversity existed among selected genotypes [5]. In addition, genetic diversity is studied to identify specific parents for wider genetic variation and heterosis when they are crossed. Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization [6]. Since published work of potato on genetic diversity is scanty. The present study was undertaken to find out the nature and magnitude of genetic diversity and the characters contributing genetic diversity of 30 potato genotypes by D^2 statistics.

MATERIALS AND METHODS

The experiment was conducted at A. H Z. Biotech Ltd, Namo Bhadhra, Rajshahi, Bangladesh during Rabi seasons of three consecutive years (2003-2005). Thirty

potato genotypes were grown for the experiment. The potato tubers were grown following Randomized Block Design with three replications and a spacing of 60 cm row to row and 20 cm plant to plant. [7] viz., 10 tons of cow dung, 326-217-250 kg of urea, TSP and MP per hectare were used. The potato tubers were planted during first week of November for three years. Intercultural operations like weeding, irrigation, mulching and earthing up were performed as and when necessary. Data on different agronomic characters were recorded on individual plant basis from 10 plants randomly selected in each row of each replication. Data were measured and recorded with 10 randomly selected plants on plant height (cm), number of tubers/plant, fresh weight/plant (g), number of tubers/plant, number of eyes/tuber, average tuber weight/ plant (g) and tuber weight/plant (g). Genetic diversity analysis was carried out using Mahalanobis D² statistics. The genotypes were grouped into clusters as per Tocher method following the formula cited by Singh and Chaudhary [8]. All the statistical analysis was carried out using GENSTAT-5 Computer software.

RESULTS AND DISCUSSION

The 30 potato genotypes were grouped into six clusters based on D² values (Table 1). Cluster III and cluster IV were contained seven genotypes, cluster II, V and IV had five genotypes and cluster I had one genotype. This finding was in agreement with the findings of other researcher [5]. The average Intra and inter cluster distances are presented in Table 2. The inter cluster distances were higher than the average intra cluster distances, which indicated wide genetic diversity among the genotypes of different groups than those of same cluster. The highest inter cluster distance was observed between cluster II and VI (26.334) and followed by cluster I and cluster V (22.926) and the lowest between cluster II and cluster III (4.226). The highest intra-cluster distance was observed for the cluster VI and minimum for the cluster II. Intra-cluster distance was much lower than the inter cluster one, suggested heterogenous and homogenous nature between and within groups, respectively [5, 9]. On the Basis of the cluster means (Table 3), the important cluster were cluster I for fresh weight/plant, number of leaves/plant and tuber weight/plan, cluster III for plant height, cluster V for number of tubers/plants. Cluster VI had the lowest mean for number of eyes/tuber. Similar reports of non correspondence between genetic and geographic diversity was also found in potato [5] in chickpea [9] and

Table 1: Distribution of 30 potato genotypes among 6 clusters

Cluster name	No. of genotypes	Name of genotypes
I	2	Diamont
II	5	Monona, Petronese, GMO, Calwhite, Cheroki
III	7	Fundy, Granulla, TPS-67, Shilbilati, 573, Japanese red, Prelude
IV	7	Multa, Raja, Elvera, Atlantic, Shepody, Conestoga, Superior
V	5	TPS-7, Atlas, Brondy, Russet burbank, Yucon gold
VI	5	Green mountain, Hagrai, Allblue, Banana, Lalpakri

Table 2: Average intra (bold) and inter cluster distance (D²) of 30 potato genotypes

Clusters	I	II	III	IV	V	VI
I	0.000	6.565	12.785	18.374	22.926	36.394
II		0.368	4.226	8.627	13.436	17.218
III			0.818	5.616	8.526	12.396
IV				0.726	6.221	10.968
V					0.852	5.382
VI						0.961

Table 3: Cluster means for 7 characters in 30 potato genotypes

Characters	Clusters					
	I	II	III	IV	V	VI
PH	46.788	44.597	40.153	44.373	40.401	34.010
NLPP	290.900	235.558	255.595	241.076	271.802	170.827
FWP	137.222	122.674	116.939	96.815	92.685	99.467
NTPP	7.300	6.562	6.228	5.689	5.536	6.207
NEPT	15.198	9.698	10.028	10.257	10.238	8.993
ATWP	28.296	29.635	26.368	24.426	21.828	12.138
Twp	179.000	157.944	136.706	114.963	89.738	58.760

PH = Plant height, NLPP = Number of leaves/plant, FWP = Fresh weight/plant, NTPP = Number of tubers/ plant, NEPT = Number of eyes/tuber, ATWP = Average tuber weight of plant, Twp = Tuber wt./plant

in mungbean [10]. It could be concluded that short plant height, less number of leaves/plant, less no. of eyes/tuber and less tuber yielding genotypes from cluster I best and high quality of plant height, number of leaves/plant, fresh weight/plant, number of tube/plant and tuber weight/plant from cluster I could be selected as parents for hybridization program. Contributing of characters towards diversity of the genotypes is given in Table 4. Group constellations were also independently developed by using Principal Component Analysis (PCA) to verify grouping obtained through D² statistics in two dimensional. Contribution of the characters towards

Table 4: Latent vectors for 7 characters of 30 potato genotypes

Characters	Vector I	Vector II
PH	0.0365	0.1456
NLPP	0.0085	0.0362
FWP	0.0156	0.0439
NTPP	-0.0526	0.0391
NEP	-0.0169	-0.0465
ATWP	0.0462	0.0635
Twp	0.1341	0.1462

PH = Plant height, NLPP = Number of leaves/plant, FWP = Fresh weight/plant, NTPP = Number of tubers/ plant, NEPT = Number of eyes/tuber, ATWP = Average tuber weight/ plant, Twp = Tuber wt./plant

diversity of the genotypes the results of Principal Component Analysis revealed that in vector I the important characters responsible for genetic diversity in the major axis of differentiation were tuber weight/plant (0.1341), average tuber weight/plant (0.0462), plant height (0.0365), fresh weight/ plant (0.0156) and number of leaves/ plant (0.0085). In vector III tuber weight/plant (0.1462), plant height (0.1456), average tuber weight/plant (0.0635), fresh weight/plant (0.0439) and number of leaves/plant (0.0362) played their role in genetic diversity. The Principal Component Analysis revealed that the vectors (I and II) for plant height, number of leaves/plant, fresh weight/plant, average tuber weight of plant and tuber weight/plant were positive. Such results indicated that those five characters contributed maximum towards diversity. The greater diversity in the present materials is due to these five characters which will offer a good scope for improvement of yield through rational selection of parents genotypes for potato producing. It could be concluded that short plant height, less number of leaves/plant, less number of eyes/tuber and less tuber yielding genotypes from cluster I, best and high quality of plant height, number of leaves/plant, fresh weight/plant, number of tuber/plant and tuber weight/ plant from cluster I could be selected as parents for hybridization program.

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