



Genetic variability, correlation and cluster analysis in potato genotypes

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Abstract

The characters association and cluster analysis between yield and yield components of 48 potato genotypes were studied. Most of the characters showed significant differences among the genotypes indicating their wide genetic variance. High genotypic and phenotypic variance coupled with high heritability and genetic advance as percentage of mean were observed for most of the characters indicating largely controlled by additive gene action. Tuber yield were found as a significant positive correlation with plant height, number of leaves, number of stems and plant fresh weight. The maximum genotypes were incorporated in cluster IV and minimum in cluster II. The genotypes of cluster IV were found minimum intra cluster distance which represent that the genotypes within this cluster highly similar to each other. Our findings revealed that selection of these characters could be used as parents for further breeding program for varietal improvement of potato.

Keywords: association, cluster analysis and potato genotypes

Introduction

Potato (*Solanum tuberosum* L.) is a solanaceaeus species, autotetraploid ($2n=4x = 48$), vegetatively propagated, short-day and a C3 plant grown in temperate, subtropical and tropical regions (Bali *et al.*, 2018) ^[4]. It is one of the most important vegetable crops, which ranked fourth after rice, wheat and maize in the world (Reddy *et al.*, 2018). After rice potato is the second most important crop in Bangladesh (Rahman, 2015) ^[18]. In Bangladesh, it is consumed as vegetable contributing alone as much as 54% of the total annual vegetable production of this country. The total production of potato is 109.494 lakh metric tons, total area is 4,69,245 hectare and yield is about 23.3 metric tons per hectare and ranking first among the vegetables in terms of area and production in Bangladesh (AIS, 2020) ^[2].

Potato has the capacity to produce maximum calories, vitamins, minerals and proteins per hectare per day than any other food crops. It is considered as a nourishing and wholesome food. Its low energy density is advantageous when eaten without much added fat. Hence, potato is readily accepted as a major part of a meal, and meal without potato is considered incomplete (Rizvi *et al.*, 2020) ^[22].

There are 91 potato varieties are available here in Bangladesh. The most popular potato varieties are: Diamant, Cardinal, Asterix, Courage, Granola and Lady Rosetta (BARI, 2019) ^[5]. More than a billion people eat potato worldwide, and global total production exceeds 300 million metric tons. Potato is an asexually propagated crop by tubers, which are underground and modified stems. Tubers are also stock pile organs, mainly starch, and show dormancy right after harvesting. The dormancy level greatly varies among cultivars, growing and storage conditions and tuber physiological age at harvest (Dilson *et al.*, 2012) ^[6]. Bangladesh is a highly populated country to feed this ever growing people there is a need to increase productivity. Thus, more potato can be produced from the same area of land. In Bangladesh, several improved potato varieties have been released by different potato research centers since the establishment of the potato research and development program. However, most of the released varieties have not satisfied the farmer and consumer expectations.

Heritability, genetic advance as percentage of mean, correlation coefficient and cluster analysis of the yield contributing characters on yield is very helpful for effective selection in crop improvement. Estimation of correlation coefficient among the yield contributing variables is necessary to understand the direction of selection and to maximize yield in shortest period of time (Rizvi *et al.*, (2020) ^[22]. Genetic correlation indicates the relative importance of variables on which greater emphasis should be made in selection for yield. Johnson *et al.* (1955) found that genotypic correlation coefficients provide a measure of association between various traits and help to identify the traits that may be useful in selection. For a successful breeding program, heritability, genetic advance as percentage of mean, correlation coefficients and cluster analysis play a vital role in obtaining the desirable variables for developing new varieties.

The present study explore the genetic variability, correlation and cluster analysis of 48 potato genotypes to identify genetically diverse parents for developing a superior varieties.

Materials and Methods

Experimental Site, Design and Materials

Forty eight potato genotypes (Table 3) were grown in the research field of Botany Department, Rajshahi University, Rajshahi. The experimental design was RCBD with three replications. Each replication consists of 48 plots. Each plot having two rows of 30 plants. Row to row and tuber to tuber distance was 50 and 20 cm, respectively. Recommended dose and application methods of fertilizers were used. To get good crop conditions irrigation, intercultural operations, spraying of insecticide and fungicides were performed. The planting was done in mid- November and the harvesting was made after 90 days of planting.

Observations were recorded and calculated on ten randomly selected plants from each plot during the course of experiment on plant height (PH), number of leaves/plant (NL), number of stems/plant (NS), number of tubers/plant (NT), plant fresh weight (PFW), plant dry weight (PDW) and tuber yield (TY).

Data Analysis

Analysis of variance

The data was subjected to analysis of variance (ANOVA) using the SPSS statistical software. The comparison of the mean performance of genotypes was done the significance of mean squares using least significance difference (LSD). The characters that exhibited significant mean squares in general ANOVA was further subjected to genetic analyses.

The statistical procedure which separates or splits the total variance into different components is known as analysis of variance. It has two main advantages: such as: it is useful in estimating the components of variance and it provides basis for the test of significance (Singh and Narayanan, 2013).

The genotypic and phenotypic variability of each quantitative traits was estimated as genotypic and phenotypic variances and coefficients of variation. The genotypic and phenotypic variance was determined by the formula as described by Singh and Choudhury (1985). Genotypic variance (σ^2g) = (MSg-MSe)/r Where, σ^2g = genotypic variance, MSg = mean square of genotype, MSe = mean square of error, r= number of replications and Phenotypic variance (σ^2p) = σ^2g + EMS. High Heritability and Genetic Advance Broad sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996) as follows: $H_2 = (\sigma^2g/\sigma^2p) \times 100$. Where, H_2 = heritability in broad sense, σ^2p = Phenotypic variance and σ^2g = genotypic variance The heritability percentage was categorized as low, moderate and high, as suggested by Robinson and Callbeck (1955). 0-30% = low, 30-60% = moderate and > 60% = high Expected genetic advance under selection (GA): Expected genetic advance (GA) at 5% percent selection intensity and genetic advance as percentage of mean (GAM) was calculated through the method of Johnson *et al.* (1955).

$GA = K \cdot \sqrt{\sigma^2p} \cdot H_2$ Where, GA = Genetic advance, $\sqrt{\sigma^2p}$ = square root of phenotypic variance, H_2 = Heritability in the broad sense and K= standardized selection differential at 5% selection intensity (K= 2.063). Genetic advance as percentage of the mean (GAM) was estimated as follows: $GAM = (GA/X) \cdot 100$.

Where, GAM = Genetic advance as percentage of the mean, GA = genetic advance and X= Population mean of the character being evaluated the magnitude of genetic advance as percentage of mean was categorized as low (0-10%), moderate (10-20%), and high (> 20%), as suggested by Johanson *et al.* (1955). Data were subjected to cluster analysis of Mahalanobis (1936) ^[12] D² analysis extended by Rao (1952) ^[20] using GENSTAT-5 fifth edition Computer programme.

Results and Discussions

The variability components (mean, genotypic and phenotypic variance, heritability in broad sense and genetic advance as percentage of mean) were estimated for six characters and results are presented below in Table 1. However, the results excluded the one character (number of stems) because of absence of significant difference at both 1% and 5% level of significant. Heritability estimates were more than 95% for the characters of plant height, number of stems, plant fresh weight and tuber yield, and more than 75% were observed in number of leaves and plant dry weight. The heritability estimates were more than 95% for most of the traits. Heritability and genetic advance as percentage of mean values were high for number of leaves, plant fresh weight and tuber yield. Heritability and genetic advance as percentage of mean values moderate for number of leaves and plant dry weight. All the characters with high heritability and genetic advance as percentage of mean were equally effective for selection. These findings are in agreement with the previous reports of Dilson *et al.* (2012) ^[6], Addisu *et al.* (2013) ^[1], Panigrahi *et al.*, (2014) ^[15], Rahman (2015) ^[18], Getachew *et al.* (2016) ^[10], Tripura *et al.* (2016) ^[26], Hajam *et al.* (2018) ^[11], Ebrahim *et al.* (2020) ^[7, 8] and Zeleke *et al.*, (2021) ^[27].

The correlation coefficients between the six characters are presented in Table 2. In this study 09 associations were highly significant (considering both 1 and 5% level of significance) out of 30 associations. Among them 07 associations were positively significant and rests of the 14 associations were non-significant. Significant positive correlations among the characters were suggested additive genetic model thereby less affected by the environmental fluctuation. The correlation analysis between genotypes gave a good estimation of the heritability, similar to the variance components. Therefore, data set from field evaluations of a high number of clones can be used to estimate the heritability and the gain from selection to identify the best breeding strategy. The significant

positive genotypic correlation coefficient ($r_g=0.616^{**}$ and $r_g=0.643^{**}$, respectively,) of plant height with number of leaves and tuber yield indicated strong genotypic relationship between them. Tuber yield showed significant positive relationship ($r_g=0.682^{**}$) with number of stems. Positive significant relationship of tuber yield with plant height ($r_p=0.763^{**}$), number of stems ($r_p=0.821^{***}$) and plant fresh weight ($r_p=0.921^{**}$) at phenotypic level suggested that the tuber yield can be increased by simple selection of these characters. The characters exhibiting the strong positive genotypic correlation coefficients with tuber yield and among themselves might be taken into consideration during the selection process for effective improvement in the breeding programme. This emphasis should be given on variables like plant fresh weight and tuber yield for the development of high yielding genotypes in potato. The smallest correlation (0.073) was between number of stems and plant fresh weight, which is also important. The similar trend in correlation coefficient has also been reported by Dilson *et al.*, (2012) [6], Al-jarmuoz (2012) [3], Moussa (2013) [13] and Rizvi *et al.*, (2020) [22].

Group consultation was also independently derived by principal component analysis to verify grouping obtained through D^2 statistic in a two dimensional chart (Z1-Z2). Therefore, scores obtained for the first two components were plotted against two main axes and then super imposed with clustering (Figure 1). The graphical presentation of the potato genotypes how are we classified into 6 clusters according to the first two discriminatory functions (Figure 1). The genotypes scattered on the right side of the diagram had higher plant fresh weight and plant height compared to that of the varieties on the left side based on X ordinate. Therefore, function 1 separated cluster II and cluster III very clearly from cluster VI and cluster V based on plant fresh weight and plant height. On the other hand, the genotypes scattered on the upper part of the diagram had higher plant fresh weight than that of the genotypes on the lower part based on Y ordinate. Therefore, function 2 separated clusters IV and cluster VI very clearly from cluster I followed by group VI. These results indicated that the genotypes in cluster IV and VI had a close relationship. The six clusters showed the minimum intra cluster distance (1.0120) which revealed that the genotypes within the cluster were very much similar to each other (Figure 1). The similar results have also been reported by Panigrahi *et al.*, (2014) [15], Rangare and Rangare (2017) [19] and Probha *et al.* (2019).

The use of heritability and genetic advance as percentage of mean is used to determining the degree of genetic gain from the selection of a variable. The yield-related variables like number of stems, fresh and dry weight and tuber yield recorded high genotypic and phenotypic values were $\geq 20\%$ with high genetic advance as percentage of mean also a low relative difference. It is evident from this present study that the enhancement of yield and other yield-related variables can be attained through effective selection based on estimates of heritability and genetic advance as percentage of mean. The result from the cluster analyses illustrate that 12 accessions from cluster IV and 10 accessions from cluster III considered high-yielding accessions and can be suggested as large-sized tuber associated with high yield potentials in potato.

Table 1: Estimation of variability components for six variables in 48 potato genotypes.

Statistic	PH	NL	NS	PFW	PDW	TY
Heritability	0.992	0.893	0.972	0.987	0.756	0.998
Genotype Variance	669.931	8.546	3.659	4831.089	22.024	25787.392
Residual Variance	13.455	3.233	0.392	177.833	21.301	151.986
Phenotypic variance	683.386	11.779	4.051	5008.922	43.325	25939.381
GAM	56.208	29.450	115.237	45.442	132.098	129.001
Grand mean	94.855	21.082	3.495	314.583	7.760	256.673
LSD	5.951	2.914	1.016	21.618	7.482	19.986
CV	3.878	8.529	17.848	4.239	59.478	4.803
Replicates	3	3	3	3	3	3
Genotype significance	1.540	2.760	1.906	2.355	2.980	6.149

Table 2: Estimation of correlation coefficients among various characters in Potato.

Genotypic correlation coefficient						Phenotypic correlation coefficient					
Traits	PH	NL	NS	PFW	PDW	Traits	PH	NL	NS	PFW	PDW
NL	0.616**					NL	0.650*				
NS	0.314*	0.204				NS	0.034	0.176			
PFW	0.491*	0.357*	0.073			PFW	0.014	0.016	0.623**		
PDW	0.236	0.409*	0.315*	0.169		PDW	0.114	0.005	0.033	0.327*	
TY	0.643**	0.682**	0.256	0.602**	0.317*	TY	0.763**	0.621**	0.083	0.912**	0.029

Table 3: Grouping of Potato Genotypes Based on 6 Clusters for six Characters.

cluster	frequency	%	Cluster membership
I	7	48.85	Atlas,banana,gaforgown,hagri, lalpakri,prelude, remarkarursset;
II	4	18.07	Baraka, felcina, martin, senori;
III	10	12.30	Carlita,diamond,eldina,fibula,futuri,lura,marrabel,petronese,raja,victory;

IV	12	10.90	Vanilla, shepodi, shaita white, shaita red, all red, blondy, blue maintain, chieftain, indurcani, multa, quency, burbank;
V	6	5.79	Asterix, cardinal, challista, chipita, durby, granula;
VI	9	4.103	Beleni, akria, callwhite, courage, fontany, innovator, radeo, ultra, voyager.

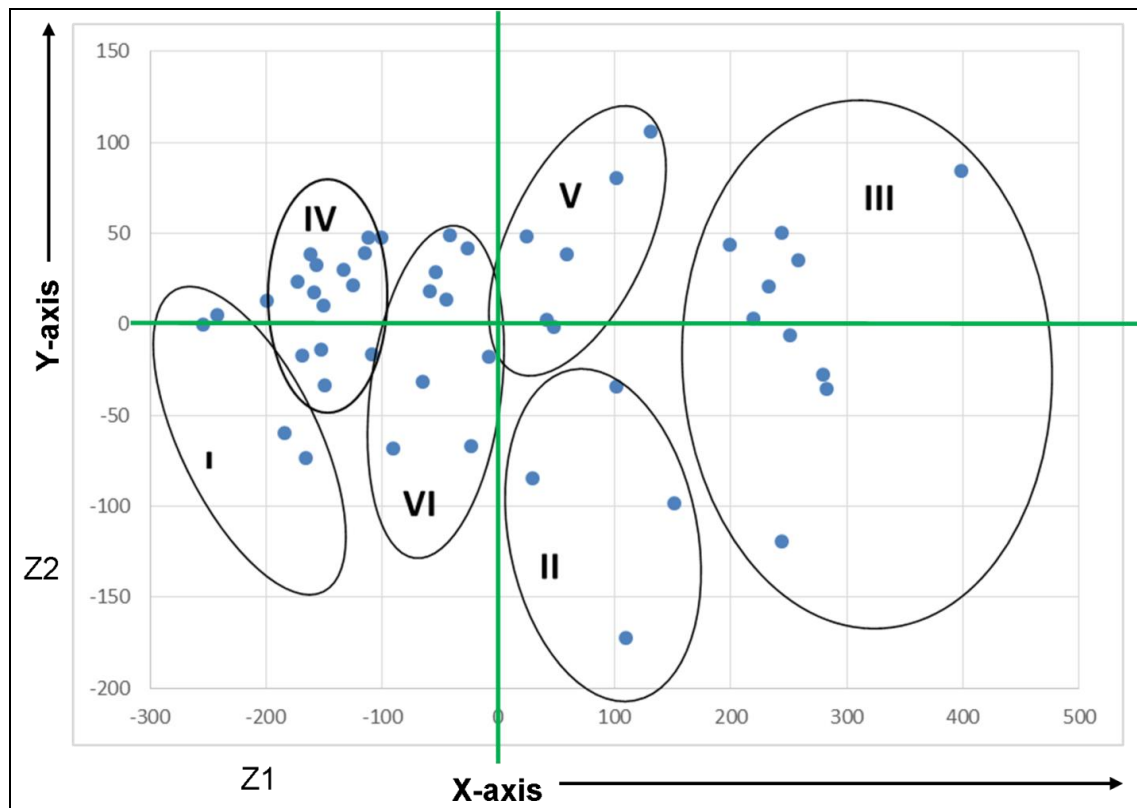


Fig 1: Graphic illustration of the discriminatory analysis in 6 clusters of potato genotypes.

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