CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS IN POTATO (*Solanum tuberosum* L.)

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CERTIFICATE

This is to certify that thesis entitled,**“CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS IN POTATO (*Solanum tuberosum* L.)”**submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MD. MAHADY HASAN**, Registration No. **17-08208** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Date: June, 2018
Place: Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor

DEDICATED
TO
MY BELOVEDPARENTS

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ABSTRACT

The experiment was conducted with twenty genotypes of potato at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period from November2017 to March 2018 to estimate the genetic variability, correlation and diversity among the twenty (20) genotypes of potato. The experiment was conducted using Randomized Complete Block Design with three replications. All the twenty (20) genotypes varied significantly with each other for all the studied characters indicated the presence of considerable variations among the genotypes studied. The phenotypic co-efficient of variation (PCV) values were higher than the respective genotypic co-efficient of variation (GCV) values for all the characters under study. No of Secondary branches per plant, leaf breadth, no. of tuber per plant, individual weight of tuber, tuber yield per plant and yield (ton/ha) showed high heritability along with high genetic advance as percentage of mean were normally more helpful in predicting the genetic gain under selection. From the correlation analysis it was revealed that yield per ha was significantly positively correlated with secondary branches per plant, tuber per plant, individual tuber weight and tuber yield per plant at both genotypic and phenotypic levels suggesting that the selection for these traits would helpful for the improvement of yield per ha. As per principal component analysis (PCA), D^2 and clusters analysis the genotypes were grouped into five different clusters. Clusters V had the maximum nine and cluster II and IV had the minimum one genotype. The highest inter-cluster distance was observed between II and IV and the lowest was observed between I and V. Genotypes in cluster II showed maximum performance for yield per ha, tuber yield per plant, individual tuber weight, tuber number per plant, tuber breadth, no of secondary branches per plant and plant height. Cluster III showed maximum performance for no of primary branches per plant and tuber length. Cluster V showed highest value for leaf length and leaf breadth. Considering this idea and other characteristic performances, genotype G19 (BARI Alu-46) from cluster II; genotype G18 (BARI Alu-41) and G2 (BARI Alu-49) from cluster I and G12 (BARI Alu-24) from cluster IV might be considered to suggest farmer for cultivation for better yield as well as use as parent for efficient hybridization programme for further improvement.

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SOME COMMONLY USED ABREVIATIONS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	$\sigma^2{}_p$
Genotypic variance	$\sigma^2{}_g$
Environmental variance	$\sigma^2{}_e$
Heritability in broad sense	$h^2{}_b$
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Analysis of variance	ANOVA
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Centimeter	cm
Percentage of coefficient of variation	CV%
Cultivars	cv.
Degrees of freedom	df
And others	*et al.*
Etcetera	etc.
The sixth generation of a cross between two genetically dissimilar homozygous parents	F_6
Food and Agriculture Organization	FAO
Gram	g
Genotype	G
Genetic advance	GA
Genotypic coefficient of variation	GCV
Harvest Index	HI
Journal	J.
Kilogram	Kg
Meter	m
Distinctness uniformity and stability	DUS

SOME COMMONLY USED ABREVIATIONS (Continued)

Full word	Abbreviation
Mean sum of square	MS
Molecular	Mol.
Biotechnology	Biotechnol.
Science	Sci.
Murate of Potash	MoP
Ministry of Agriculture	MoA
Square meter	m^2
Phenotypic coefficient of variation	PCV
Randomized Complete Block Design	RCBD
Sher-e-Bnagla Agricultural University	SAU
Triple Super Phosphate	TSP

CHAPTER I
INTRODUCTION

Potato (*SolanumtuberosumL.*) popularly known as “Alloo”, is a member of the family Solanaceae consisting more than two thousand species, out of which, only seven are cultivated. Based on literature available, the potato is considered to be originated in the Andes Mountains of Peru and Bolivia of South America. It has been cultivated for at least 8,000 years ago (Martins, 1976) where the potato was probably first domesticated and greatest diversity of cultivated forms could be found. Potato has been disseminated throughout the world and is known as “White or Irish Potato”. All the commercial potato cultivars are tetraploid (2n = 48), which is the result of natural doubling in chromosomes. It is one of the most important crops, not only important to meet the requirement of the country in substantial manner, but can also generate more opportunities for employment, particularly, for rural landless labor through its very high industrial values. The history of potato is the testimony of the fact that whenever, there has been scarcity of food grains, potato has become the food security of people.

Potato of its great utility, occupies a pre-eminent place amongst the crops and acknowledges as the “king of vegetables”. It provides the highest dry matter per unit area and time (Anon., 2009). It contains substantial energy of edible protein (2.8 g), starch (16.3 g), total sugar (0.6 g), crude fiber (0.5 g), fat (0.14 g), carbohydrate (22.6 g) and vitamin C (25 mg) per 100 g fresh weight of tubers (Lampitt and Golden Berg, 1940). Thus, it provides more calories per unit area, per unit time than other major food crops and has many industrial uses. This makes it the most suitable non-traditional crop to world hunger. However, present per capita availability is 40.5 kg/year (Anon., 2005).

Potato is an important crop of the world and grown in about 1862 million ha area with a production of 323 million tons annually. The global average yield of potato is 17.35 t/ha (Anon., 2005). 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).

The total area under potato crop, national average yield and total production in Bangladesh are 4,62,032 hectares, 19.371 t ha^{-1}and 89,50,024 metric tons respectively. The total production is increasing over time as such consumption also rapidly increasing in Bangladesh (BBS, 2014). The yield is very low in comparison to that of the other leading potato growing countries of the world, 40.16 t ha^{-1}in USA, 42.1t ha^{-1}in Denmark and 40.0 t ha^{-1}in UK (FAO, 2013).

Genetic parameters of variation and characters association provides information about expected response of various characters. It helps in developing suitable breeding procedure for their improvement on nature and magnitude of variability in the existing plant material. The association among the various characters are pre-requisite for yield and correlation among different characters utilized in selection of better plant types and path co-efficient analysis permits further portioning of correlation co-efficient into components of direct and indirect effects facilitating important traits to be identified. These parameters, however, vary with the type of material used and the environmental conditions to which the genotypes are subjected. In India, such studies in potato have been made either under sub-tropical plains or temperate hill conditions with different sets of genotypes (Gopal, 1999).

In potato, tuber yield is a complex polygenic traits determined by interactions among genetically as well as environmental factors. The genetic variability along with heritability gives reliable information of the genetic advance expected from population during selection for a character.

Development of high yielding cultivar is a continuous process and there is an urgent need to select best hybrid or suitable for growing in Bangladesh. Considering the past increase in potato area and lack of suitable variety for this area, generation of basic information about the extent of variability, existing diversity with the available materials, association of important yield and its attributes are pre-requisite to breed suitable cultivar for the area.

The biometrical approaches used in the present investigation, for studying genetic variability, include phenotypic and genotypic co-efficient of variance, heritability, genetic advance and association analysis and genetic divergence to predict real value of genotypes under study.

Therefore, the present investigation carried out for following objectives-

1) To study the genetic parameters of variability in potato,
2) To study the association among different yield attributing traits,
3) To assess the genetic divergence in potato and
4) To find out suitable genotype of potato.

CHAPTER II

REVIEW OF LITERATURE

Proper evaluation of genotypes is very important to get higher tuber yield and ultimately good returns. The information on the important characters with tuber yield is useful in the selection of genotypes. Correlation of characters with each other and the knowledge about path through which they affect the ultimate object i.e. tuber yield, is necessary for crop improvement. So, brief knowledge about performance of potato genotypes, correlation of characters and path analysis is required. Updated available literature in the following aspects has been reviewed and presented here:

1. Performance of genotypes
2. Genetic variability, heritability and genetic advance
3. Correlation (characters association) studies
4. Genetic divergence

2.1 Performance of genotypes

Bangtratz (1990) conducted a field trial with eleven high starch containing potato varieties at five locations in France and reported that the total tuber yield ranged from 30 to 472 q/ha.

Nandekar *et al.* (1995) studied the performance of nine potato hybrids along with Kufri Chandramukhi and Kufri Badshah as control for tuber yield at 75 and 90 days harvest during 1990-91 and 1991-92 in Satpura Plateau and found MS 179-1 (285 q/ha) and JN 1758 (213 q/ha) reported to be superior among all. Rana *et al.* (1996) reported that Kufri Sutlej as mid maturing (90-95days) potato variety, based on seven locations, reported to have 5-6 shoots per plant and average yield of 27.18 t/ha.

Singh *et al.* (1997) reported that new potato hybrids MP/90-83, MP/90-94 and MP/91-23G produced mean tuber yield of 33.0, 33.6 and 32.6 t/ha, respectively, coupled with dry matter content of 20.3 per cent, 22.3 per cent and 21.6 per cent respectively.

Sharma (1999) evaluated at Raipur on eight cultures/hybrids of potato and found maximum number of leaves per plant (66.0) in Kufri Sutlej and fresh weight of shoots (148.0 g) in MS/90-542, per cent dry weight of shoots per plant was recorded in entries MS/90-542 (23.65 g) and Kufri Badshah (21.73 g), highest number of tubers per plant (11.00) in both JX-90 and JX-576. However, the higher dry weight of shoots was recorded in Kufri Pukhraj (17.21 percent) and Kufri Badshah (17.9 per cent).

Roy and Sharma (2000) reported from a field trial that 86 per cent plant emergence, 62.8 cm plant height of the plant and 22.0 to 35.3 t ha^{-1} tuber of yield recorded in potato at Jalandhar.

Painkra (2002) studied nine cultures/hybrids of potato in field trial at Raipur and observed maximum plant height in MP-90-94 (66.76 cm) and MP-91-23G (55.23 cm), higher number of shoots plant^{-1} in Kufri Sutlej (3.41), higher number of leaves plant^{-1} in MP-90-94 (64.55), higher weight of shoots plant^{-1} in MP-90-94 (195.55 g), maximum fresh weight of tubers plant^{-1} in MP-90-94 (869.16 g), maximum number of tubers in MP-90-94 (11.94), highest dry weight of shoots plant^{-1} in MP/90-94 (24.6) and both the highest total tuber yield 342.21 q ha^{-1} and marketable tuber yield 317.95 q ha-1 were reported in the Kufri Badshah.

Hossain (2011) conducted three experiments with BARI released twelve potato varieties to determine the yield potentiality, natural storage behaviour and degeneration rate for three consecutive years. He found that the highest emergence was observed in Granola at 34 DAP (Days after planting). At 50 DAP plant height (cm) of Diamant was (43.50), BARI TPS 1 (47.70), Felsina (52.00), Asterix (52.97), Granola (38.30), Cardinal (46.33). Foliage coverage (%) of Diamant was (83.33), BARI TPS 1 (85.56), Felsina (82.22), Asterix (89.44), Granola (85.56), Cardinal (81.67). No. of stems/hill of Diamant was

(4.06), BARI TPS 1 (3.21), Felsina (3.14), Asterix (4.03), Granola (3.30), Cardinal (3.89). Tuber yield/hill (g) of Diamant was (244.2), BARI TPS 1 (227.9), Felsina (300.1), Asterix (276.9), Granola (277.0), Cardinal (316.9). Under the grade 28-40 mm, the highest number (48.63%) of seed tubers was produced by Granola which was statistically identical with Asterix (46.43%). Under the same grade (28-40 mm), the highest weight (43.46%) of seed tubers was produced by Patrones followed by Asterix (37.16%), Granola (36.64%) and Multa (35.39%) among which there was no significant variation.

Behjati *et al.* (2013) conducted a field experiment to evaluate the yield and yield components on promising potato clones. Clone No. 397031-1, had the highest yield and Lady Rosetta variety had the lowest yield compared with other varieties. The lowest and highest average number of main stems per plant, related to Lady Rosetta and clone No. 397067-2. Lady Rosetta variety had the highest number of tube per plant and clone No. 397067-2 had the lowest number of tubers per plant. The lowest and highest average tuber weight per plant related to clone No. 397067-2 and Lady Rosetta variety respectively.

Karim*et al.* (2011) conducted an experiment with ten exotic potato varieties (var. All Blue, All Red, Cardinal, Diamant, Daisy, Granola, Green Mountain, Japanese Red, Pontiac and Summerset) to determine their yield potentiality. The highest total tuber weight per plant (344.60g) recorded in var. Diamant and total tuber weight plant-1 was the lowest (65.05 g) recorded in var. All red, all blue varieties showed the most potential yield in this experiment.

2.2 Genetic variability

The crop improvement programme largely depends on the extent of variability present. There are two kinds of variability in crop plants- genetic and environmental. Thus, the efficiency of selection largely depends on the extent of genetic variability present in the population for any crop improvement programme. The non-genetic variability is the result of genetic and environmental interaction. The non-genetic component of variability is not much use to breeders since it can’t be perpetuated from generation-to-generation. The study of genetic variability was made for the first time by great biologist Fisher (1918) and subsequently the estimation of genotypic and phenotypic variations were used to predict the expected genetic response. A number of other workers have also discovered several techniques for the estimation of components of variance (Wright, 1921; Lush, 1940; Robinson *et al.,* 1951 and Warner, 1952).

Dayal *et al.* (1972) observed the highest genotypic and phenotypic coefficient of variability for the traits *viz.* tuber yield, number of shoots, height of main shoot and number of nodes of main shoot. Choudhary and Sharma (1984) reported high genotypic and phenotypic coefficient of variation for tuber yield and average tuber weight followed by number of tubers/plant. Garg and Bhutani (1991) reported the highest genotypic and phenotypic variance for yield per plant followed by total tuber yield and average tuber weight.

Dixit *et al*. (1994) observed the highest genotypic variability for stem/plant and tuber yield (q/ha). Rasul *et al.* (1995) revealed high variability for plant height, foliage coverage and days to maturity. The control variety Kufri Sindhuri was the highest yielding genotype (26.8 t/ha). Further, high genotypic coefficient of variation was observed for yield ha^{-1} (37%) and it was noted moderate for plant height (19.4 cm) and tuber yield/plant (16.9%).

Yildirim *et al.* (1996) reported that hybrids 9-41 and 9-44 had the highest tuber yield. However, hybrids obtained from cross L506 x R143, Isola x NT 78, Isola x R143 and Cosima x R68 had large variation for plant height and number of stems. Lines 4-8 (Isola x NT 78), 7-1 (NT 77 x R68), 9-41 (L 506 x R 143) and R162 had high leaf length and width values.

Sandhu and Kang (1998) evaluated 286 *andigena* potato genotypes and reported high variability in shoot numbers, shoot height, node numbers, inter-nodal length, leaflet index and tuber yield. The maximum values of coefficient of variation were observed for shoot numbers, shoot height, leaflet index and tuber yield.

Sharma (1999) reported the highest genotypic coefficient of variation for dry weight of roots/plant, tuber bulking rate, tuber yield, fresh weight of shoots/plant, tuberization efficiency and dry weight of shoots/plant in potato.

Bhagowati *et al.* (2002) recorded high genotypic coefficient of variation for the characters *viz.* leaf numbers, tuber numbers and average tuber weight. Basavaraj *et al.* (2005) reported significant differences for the characters indicating the presence of sufficient genetic variation among the genotypes. Joseph *et al.* (2005) reported sufficient variation both at the phenotypic and genotypic levels for all the characters except number of leaves and tuber dry matter in potato.

Luthra *et al.* (2005) observed that there was high phenotypic and genotypic co-efficient of variations for tuber yield, tuber numbers and average tuber weight. Roy and Singh (2006) reported that co-efficient of phenotypic and genotypic variations was narrow for the character emergence percent, dry matter percent, total sugar and total starch percent.

Addisue *et al*. (2013) conducted a field experiment with thirteen potato genotypes for evaluation, genetic variability and association of agronomic characters among themselves and tuber yield. The study aimed to find out the genetic variability and interrelationships among different characters in potato. Genotypic correlation co-efficient was found to be higher in magnitude than that of phenotypic correlation co-efficients, which clearly indicated the presence of inherent association among various characters. Tuber yield was positively correlated with plant height, biological yield, harvest index and big tuber percentage at both the phenotypic and genotypic levels. In contrast, it was negatively correlated with small and medium tuber percentage at both levels.

Patel *et al*. (2013) conducted an experiment to explicated genetic variability of total 24 potato genotype for table purpose potato with two different sets viz., 75 days and 95 days of harvest. A wide range of phenotypic variability was recorded for reducing sugar, plant height, average weight of tubers, number of tuber per plant and tuber dry matter content. The high genotypic co-efficient of variation (GCV) were observed for reducing sugar, number of stem per plant, marketable tuber yield and chip color. While high phenotypic coefficient of variation (PCV) observed for marketable tuber yield and number of stem per plant. High heritability value was noted for reducing sugar (99.98% and 99.96%) in 75 days and 95 days of harvest respectively. The highest value of GA (% mean) observed for reducing sugar 95.34 (C1) and 97.24 (C2). The average weight of tuber, number of tuber per plant, number of stem per plant and marketable yield exhibited significant positive correlation with number of tuber per plant at both genotypic and phenotypic levels.

2.3 Heritability and Genetic advance

Heritability is the quantitative statement of the relative importance of heredity and environment. The partitioning of phenotypic variation and environmental variation was first done by Fisher (1918). Different methods have been revised by several workers for the estimation of heritability.

The amount of progress expected through selection for obtaining the best individual cannot be made on the basis of heritability alone. The genetic progress would be enhancing with an increase in heritability. Hence, the heritability estimate could be best utilized in conjugation with genetic advance in predicting genetic gain.

Genetic advance denotes the improvement in the genotype values of the new population. So, the knowledge of genetic advance to be expected by applying selection pressure to a segregating and variable population is useful in designing an effective breeding programme.

Johnson *et al.* (1955) the Biometrician stated that the broad sense heritability estimates may vary greatly depend upon the unit for which the variance is considered. The value of heritability depends on all the components of variance any change in any one of these components will change the estimates and further emphasized that effectiveness of genotypes can be based on the phenotypic performance.

Dayal *et al.* (1972) recorded broad-sense heritability indicating that selection of tuber yield and shoot numbers in potato could be based on the phenotype, while for node numbers and plant height, selection should be based on the progeny performance only.

Chaudhary and Sharma (1984) reported high heritability in broad sense for tuber yield, tubers/plant and average tuber weight. Dixit *et al.* (1994) revealed high heritability in broad sense for stems/shoots/plant followed by tuber yield, protein and tuber shape. Rasul (1995) recorded the highest heritability followed by crop stand and plant height. High genetic gain was observed for tuber yield/ha, tuber yield/hill and plant height.

Sharma (1999) revealed the highest value of heritability estimates for per cent dry weight of tuber followed by the fresh weight of tubers/plant, tuber yield plot (kg) while the lowest heritability value was noted for number of stolons/plant and for rest of the traits moderate heritability values were recorded.

Luthra (2001) reported high heritability estimates for plant type, dormancy period, average tuber weight, number of tubers and plant vigour. Bhagowati *et al.* (2002) recorded higher heritability of variation for the characters leaf number, tuber numbers and average tuber weight. Ikbal and Khan (2003) reported high heritability in broad sense coupled with high genetic advance for plant height and number of stems/shoots/plant.

Basavaraja *et al.* (2005) observed moderate to high heritability coupled with higher genetic advance as per cent of the mean. Luthra *et al.* (2005) reported high heritability for tuber yield, tuber numbers and average tuber weight. Roy and Singh (2006) recorded high heritability for per cent emergence, total tuber yield; harvest index, dry matter percentage, total sugar and total starch percent.

Chaudhary and Sharma (1984) found high heritability in broad sense for tuber yield, tuber/plant and average tuber yield and coupled high genetic advance. Sharma (1999) recorded the highest estimate of genetic advance as percentage of mean for fresh weight of tubers/plant whereas, medium genetic advance exhibited through number of leaves/plant. However, it was reported for plant height, tuber yield plant (kg) and dry weight of shoot/ plant.

Luthra (2001) suggested high genetic advance for tuber yield, average tuber weight, plant height and number of leaves. Bhagowati *et al*. (2002) reported higher genetic advance of variation for the characters leaf numbers, tuber numbers and average tuber weight. Ikbal and Khan (2003) reported high heritability in broad sense estimates coupled with high genetic advance for plant height and number of stems/plant.

Luthra *et al.* (2005) revealed high genetic advance for tuber yield, tuber numbers and average tuber weight. Roy and Sharma (2006) observed high genetic advance for per cent emergence, total tuber yield, harvest index, dry matter percentage, total sugar and total starch per cent.

2.4 Correlations Studies

Information on genetic association among various characters under particular environmental conditions may also help to formulate the most effective methods of breeding in any particular case and also to simplify the approach to selection. The study of the association of component characters with a complex trait like yield is pre-requisite for any of the breeding programme.

The original concept of correlation was represented by Galton (1988) who suggested the need of coefficient of correlation to describe the degree of association between variables. Later, the correlation was developed by Pearson (1904), Fisher (1918) and Wright (1921). Thereafter, Searle (1961) described the mathematical implications of correlation co-efficient at phenotypic, genotypic and environmental levels.

Dayal *et al. (*1972) reported that tuber yield was significantly and positively correlated with height of the main shoot and node numbers, while height showed a significant and positive correlation with shoots and node numbers. The node numbers had the greatest influence on yield.

Chaudhary *et al.* (1984) reported that plant height and foliage weight were positively and significantly correlated with tuber yield which are recommended as selection criteria.

Singh *et al.* (1989) reported that tuber yield and total tuber dry matter, number of tubers and total dry matter/plant, tuber dry matter content and specific gravity were all significantly and positively correlated in most environments. Tuber weight was negatively correlated with tuber numbers. Kumar *et al.* (1991) reported that tuber yield positively correlated with stem weight and LAI at 50 days after planting and with total plant weight at 50 and 110 days after planting.

Dixit *et al.* (1994) studied with the inclusion of twenty diverse strain of potato and reported that the tuber yield was positively associated with number of stem plant^{-1} and dry matter per cent. Rasul *et al.* (1995) reported that tuber yield ha^{-1} was significantly and positively correlated with yield hill^{-1}, plant vigour and foliage coverage.

Yildrim *et al.* (1995) recorded positive correlations between tuber yield, tuber size, plant height and branch numbers. Pandey and Gupta (1996) studied that tuber weight/plant and marketable tuber yield had positive correlation with total yield. Desai and Jaimini (1998) reported that tuber yield, days of maturity and plant height had significant positive correlations with all the other characters except protein and sugar contents.

Sharma (1999) at Raipur, recorded that tuber yield was positively and significantly correlated with number of shoots/plant, fresh weight of shoots/plant, fresh weight of tubers/plant at phenotypic and genotypic levels whereas, the plant height, dry weight of shoots/plant and dry weight of tubers/plant showed positive and significant correlation with tuber yield at genotypic level only.

Halwai (2000) reported that total tuber yield (q/ha) had positive and significant correlation with dry matter percentage of roots, fresh weight of shoots and roots/plant, number of shoots/plant, number of stolon/plant and dry weight of tubers/plant showed positive and significant correlation with number of shoots/plant and fresh weight of shoots/plant.

Luthra (2001) reported that association between different characteristics revealed those vigorous, erect and tall genotypes with long and wider leaves, more number of tubers and average tuber weight, shallow and medium eyes and oval and round regular shapes.

Ramanjit *et al.* (2001) revealed that tuber yield showed highly significant positive correlations with leaf area index, tuber numbers, tuber weight, dry matter production of leaves, roots, stolon and tubers at 60 and 90 days after planting. Bhagowati *et al.* (2002); reported significant positive correlations both at genotypic and phenotypic levels between plant height and leaf numbers, tuber numbers and average tuber weight, primary branch numbers and leaf numbers, tuber numbers and between leaf numbers and average tuber weight. However, they further reported negative association of tuber numbers and average tuber weight, both at genotypic and phenotypic levels.

Patel *et al.* (2002) observed significant correlations for tuber yield/plant with number of stems/plant and plant height, tuber dry matter with number of tubers/plant and number of leaves/plant. However, they observed that the number of tubers/plant was negatively associated with the average weight of tubers.

Ozkaynak *et al.* (2003) observed significant and positive correlations between tuber yield and plant height, node numbers, tuber numbers and average tuber weight. Joseph *et al.* (2005) revealed that plant height was positively associated with number of leaves and tuber yield with average tuber weight. Tuber yield was not associated with any of the foliage characters.

Joseph *et al.* (2005) reported on the basis of estimated genetic parameters and character association showed that in the population tuber yield and average tuber weight could be selected simultaneously without adversely affecting the tuber numbers.

Regassa and Basavaraja (2005) reported that the tuber yield was highly and positively correlated both at phenotypic and genotypic levels with plant height, weight of medium size tubers, weight of larger size tubers, total tuber yield, total number of tubers/plant. However, they found positive association between number of main stems/plant and tuber weight, tuber numbers and plant height.

Luthra *et al.* (2005) observed that tuber yield was significantly and positively correlated with tuber numbers and average tuber weight. Roy and Singh (2006) reported positive significant association of total tuber yield with plant height, number of tubers/plant and tuber yield/plant.

2.6 Genetic Divergence

Among several statistical methods developed for measuring divergence between populations, multivariate analysis of D^2 statistics has been effectively used for quantitative estimation of genetic variability according to Mahalanobis (1936) D^2 statistics, which can be effectively used for assessing the genetic divergence between populations and helping in selection of desirable parents for crossing programme.

Mittal and Dixit (1992) worked out genetic divergence in twenty strains of potato for seven characters. The population was grouped into seven diverse clusters out of which two clusters had only two strains each, four had three strains each and cluster-VII had four strains. Tuber yield and number of stems/plant contributed maximum towards the total divergence.

Pandey and Gupta (1997) studied genetic divergence in 52 cultivars representing *tuberosum andigena* and *rubverosum andigena*hybrid on the basis of 11 plants and tuber characters.They grouped these cultivars into 11 clusters. Indian varieties, released in past, showed considerable genetic diversity in contrast to the advanced stage pre-released hybrid indicating their development from narrow genetic base. The cultivars with wild species in their pedigree showed high genetic diversity and were distributed in almost all clusters.

Desai and Jaimini (1997) worked out on thirty six genotypes of potato in 16 environments for genetic divergence by Mahalanobis D2 statistics. Nine clusters were identified, cluster-1 being largest accommodating seven genotypes. Kumar and Kang (1998) conducted Multivariate analysis for genetic divergence among thirty *Solanumtu berosum spp. Andigena* accessions by D^2 statistics resulted in their grouping into seven clusters. Clusters-VII and V; VII and VI; IV and I and II and VII had high cluster distances. Crosses involving parents of these cluster combinations were recommended for breeding programme.

Joseph *et al.* (1999) computed genetic divergence among seventeen potato genotypes under two different climatic conditions *viz.* subtropical and temperate, using Mahalanobis D^2 statistics and grouped the genotypes into eight and six clusters, respectively. There was very little in common with regards to distribution of different genotypes into different clusters under the conditions. The genetic divergence was not related to geographic diversity as genotypes originating in different countries were grouped together in same cluster.

Sandhu and Kang (1998) evaluated 286 *andigena* potato genotypes collected and categorized into seven groups based on regression index values.

Kumar and Kang (2000) reported genetic divergence in forty five potato genotypes (*andigena)* on the basis of eight characters by non-hierarchical euclidean cluster analysis during 1998-99. Genotypes were grouped into 10 clusters based on first six principal components which explained most of the variation. Grouping of genotypes of heterogeneous origin in the same clusters indicated non-parallelism between genetic and geographical diversity..

Luthra *et al.* (2005) reported that the parental lines through morphologically diverse had narrow genetic base and could be grouped into four clusters. Further, they observed that morphological diversity was not related to geographical as well as taxonomic diversities. However, genetic divergence had a positive relationship with heterosis for tuber yield.

Sattar *et al*. (2011) conducted a field experiment in twenty eight genotypes of potato representing different sources collected from TCRC, BARI, Gazipur to study genetic divergence utilizing multivariate analysis. The genotypes were grouped into five clusters. No relationship was found between genetic divergence and geographic distribution. Number of tubers per plant and yield contributed maximum, while average weight of a tuber and weight of tubers per plant contributed high towards total divergence which offered due attention to these characters while selecting for increased tuber yield.

Sanjoy *et al*. (2015) conducted a field experiment in some potato variety. They reported experimental result was the average tuber weight of potato plant contributed maximum (31.76%), followed by number of tuber per plant (27.56%), inter nodal length (14.45%) and plant dry matter content (13.61%) for growth characters. For quality characters, ascorbic acid content (24.70%), protein content of tuber (20.84%) and TSS of tuber (20.00%) contributed effectively towards genetic divergence.

CHAPTER III

MATERIALS AND METHODS

The present investigation was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh. This chapter deals with a concise description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring, fertilizing, intercultural operations, harvesting, data recording procedure and statistical analysis etc., are presented as follows:

3.1 Experimental site

The research work relating to determine the character association and genetic diversity of Potato was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh during the period from 20 November, 2017 to 30 April, 2018. Experimental field is presented in Plate 1 and Appendix 1.

3.2 Geographical location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level (Anon., 2004).The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hill rocks of red soils as ‘islands' surrounded by floodplain (Anon., 1988b).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall

associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Design and layout of the experiment

The study was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 150 m^2. 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. The genotypes were randomly distributed to each row within each line.

3.6 Planting materials

Twenty genotypes of potato were used for the present research work. The genetically pure and physically healthy tuber of these genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur. The name and source of these genotypes are presented in Table 1.

Table 1. List of Potato genotypes with variety name

Geenotype	Variety Name
G1	BARI Alu 70
G2	BARI Alu 49
G3	BARI Alu 64
G4	BARI Alu 7
G5	BARI Alu 67
G6	BARI Alu 8
G7	BARI Alu 61
G8	BARI Alu 62
G9	BARI Alu 57
G10	BARI Alu 65
G11	BARI Alu 40
G12	BARI Alu 24
G13	BARI Alu 63
G14	BARI Alu 50
G15	BARI Alu 25
G16	BARI Alu 60
G17	BARI Alu 69
G18	BARI Alu 41
G19	BARI Alu 46
G20	BARI Alu 38

3.7 Sowing of potato tuber

The tuber were planted in the field on 26 November, 2017. The planted tuber was watered regularly to make a firm relation with roots and soil to stand along.

3.8 Intercultural operations

3.8.1 Weeding

Weeding was necessary to keep the plant free from weeds. The newly emerged weeds were uprooted carefully in all the lines after complete emergence of sprouts and afterwards when necessary.

3.8.2 Watering

Frequency of watering was done upon moisture status of soil retained as requirement of plants. Excess water was not given, because it always harmful for potato plant.

3.8.3 Earthing up

Earthing up process was done by pouring the soil in the plot at two times, during crop growing period. First pouring was done at 45 DAP and second was at 60 DAP.

3.8.4 Plant protection measures

Dithane M-45 was applied at 30 DAP as a preventive measure for controlling fungal infection. Ridomil (0.25%) was sprayed at 45 DAP to protect the crop from attack of late blight of Potato.

3.8.5 Haulm cutting

Haulm cutting was done at 26 February, 2015 at 90 DAP, when 40-50 % plants showed senescence and the top started drying. After haulm cutting the tubers were kept under soil for seven days for skin hardening. The cut haulm was collected, bagged and tagged separately for further data collection.

3.9 Harvesting of Potato

Harvesting of potato was done at 7 days after haulm cutting. The potatoes of each plot were separately harvested, bagged and tagged and brought to the laboratory. Harvesting was done manually by hand. Photograph showing harvesting of potato in Plate 2.

Plate 1. Photograph showing harvesting of potato

Plate 2. Investigation of tuber of potato genotype

3.10 Recording of data

Five plants in each line were selected randomly and were tagged. These tagged plants were used for recording observations. A brief outline of the data recording procedure followed during the study is given below. Photograph showing different morphological data collection in Plate 3.

3.10.1 Plant height (cm)

Plant height refers to the length of the plant from ground level to the tip of the tallest stem. The height of each plant of each line was measured in cm with the help of a meter scale and mean was calculated.

Plate 3.Photograph represented the morphological data collection at field level

3.10.2 No of Primary branches per plant

Total numbers of primary branches were recorded from already tagged plants.

3.10.3 No. of Secondary branches per plant

Total numbers of secondary branches were recorded from already tagged plants.

3.10.4 Leaf length (cm)

Five representative potatoes leaf were selected randomly and measurement was taken in cm from the base to the tip of leaf. It was calculated in cm.

3.10.5 Leaf breadth (cm)

The breadth of leaf at the central part was measured in cm by using a measuring tape and the average was recorded.

3.10.6 Tuber length (cm)

Five representative potatoes were selected randomly and measurement was taken in cm from the distal end to proximal end. It was calculated in cm.

3.10.7 Tuber diameter (cm)

The diameter of tuber in the middle part was measured in cm by using a measuring tape and the average was recorded.

3.10.8 No. of tuber per plant

Number of tubers per plant was recorded on plant basis. Total numbers of tubers were counted on each of plants and averaged.

3.10.9 Individual weight of tuber (g)

Average weight of tuber was measured by using the following formula-

$$\text{Average weight of tuber} = \frac{\text{Yield of tuber/plant}}{\text{Number of tubers/hill}}$$

3.10.10 Tuber weight loss (%) 20 DAH (Days after harvest)

Average weight loss measured after 20 days of harvest by using the following formula-

$$\text{Tuber weight loss (\%)} = \frac{\text{Weight loss (20 days after harvesting)}}{\text{Primary weight of potato after harvest}} x\ 100$$

3.10.11 Tuber yield per plant (g)

Tubers of each line were collected separately from which yield of tuber per plant was recorded in gram.

3.10.12 Yield ton per ha

The tuber yield per ha was recorded on individual plot at each replication at the time of harvest in kilograms. Later, it was converted in ton per ha on the basis of plant population.

3.11 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was analyzed by using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software.

3.11.1 Genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{GMS} - \text{EMS}}{r}$$

Where,

GMS = Genotypic mean sum of square
EMS = Error mean sum of square
r = number of replications

Phenotypic variance (σ^2_p)=σ^2_g + σ^2_e

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

3.11.2 Genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance
$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance
$\bar{x}$ = Population mean

For classifying, the magnitude of PCV and GCV are High (>20%), Moderate (15-20%) and Low (<15%).

3.11.3 Heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2{}_b\% = \frac{\sigma^2{}_g}{\sigma^2 p} \times 100$

Where,
h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

For classifying, the magnitude of heritability are High (>80%), Moderate (50-80%) and Low (<50%).

3.11.4 Genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.*(1955).

Genetic advance, GA = K. $h^2 . \sigma_p$

Or Genetic advance, GA = K. $\frac{\sigma^2_g}{\sigma^2 p} . \sigma_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.11.5 Genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by **Comstock and Robinson (1952):**

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean (x)}} \text{ X } 100$$

For classifying, the magnitude of genetic advance as percentage of mean are High (>40%), Moderate (25-40%) and Low (<25%).

3.11.6 Genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follow:

$$\frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Genotypic correlation, $r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} =$

Where,

$\sigma_{gxy} =$ Genotypic co-variance between the traits x and y

$\sigma^2_{gx} =$ Genotypic variance of the trait x

$\sigma^2_{gy} =$ Genotypic variance of the trait y

Phenotypic correlation (r_{pxy}) $= \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$

Where,

$\sigma_{pxy} =$ Phenotypic covariance between the trait x and y

$\sigma^2_{px} =$ Phenotypic variance of the trait x

$\sigma^2_{py} =$ Phenotypic variance of the trait y

3.12 Multivariate analysis

Mean data for each character was subjected to multivariate analysis methods viz, principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis (CLSA) using GENSTAT 5.13 program.

3.12.1 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first component and succeeding components with latent roots greater than unity (Jager*et al.*, 1983).

3.12.2 Principal coordinates analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of p it gives the minimum distances between each pair of n points using similarity matrix (Digby*et al.*, 1989). Inter-distances between genotypes were studied by PCO.

3.12.3 Canonical variate analysis (CVA)

The canonical variate analysis is based upon the roots and vectors of W-IB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix. It provides two-dimensional plots that helped in separating different populations involved.

3.12.4 Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optical values of the chosen criterion. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to second stage that examine the effect of two genotypes of different classes and so on.

3.12.5 Computation of average intra-cluster distance

Computation of average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\Sigma D^2/n$, where ΣD^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.12.6 Computation of average inter-cluster distances

The procedures of calculating inter-cluster distance between cluster II and I and between cluster III and I and between I and IV, between II and IV and so on. The clusters were taken one by one and their distances from other clusters were calculated.

3.12.7 Cluster diagram

It was drawn using the values between and within clusters distances, which presents a momentary idea of the pattern of diversity among the genotypes included in a cluster.

3.12.8 Analysis of genetic divergence

Genetic divergences among the genotypes studied were assessed by using Mahalanobis' D^2 statistics and its auxiliary analysis. Both techniques estimate divergences among a set of genotypes on multivariate scale.

Mahalanobis' D^2 statistics

First the variation among the materials were tested by Wilkin's criteria '^'.

$$\text{`}\wedge\text{'} = \frac{|W|}{|S|} = \frac{|\text{Determination of error matrix}|}{|\text{Determination of error + variety matrix}|}$$

Now, 'v' $_{(stat)}$ = $-m \log_{e\wedge} = -\{n-(p+q+1)/2\}\log_{e\wedge}$

Where,

$m = n-(p+q+1)/2$

p = number of variables or characters

q = number of varieties – 1 (or df for population)

n = df for error + varieties

e = 2.7183

Data were then analysed for D^2 statistics according to Rao (1952). Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X_1, X_2---------X_8) were transformed into a set of uncorrelated variables (Y_1, Y_2---------Y_8).

Now, the genetic divergence between two varieties/lines (suppose Vi and Vj) was calculated as –

$$D^2ij = \sum_{k=1}^{8} (Vik - Vjk)^2$$

Where,

D^2ij = Genetic divergence between ‘i’ th and ‘j’ th genotypes

Vik = Transformed mean of the ‘i’ th genotype for ‘k’ th character

Vjk = Transformed mean of the ‘j’ th genotype for ‘k’ th character

The D^2 values between all the studied genotypes were arranged in order of relative distances from each other and were used for clusters formation, as suggested by Rao, 1952.

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2 i}{n}$$

Where,

$\sum D^2 i$ = Sum of distances between all possible combinations (n) of the genotypes included in a cluster.

N = All possible combinations.

CHAPTER IV
RESULTS AND DISCUSSION

The results obtained on various parameters for twenty potato genotypes and statistical analysis are presented and discussed under following heads:

01. Analysis of variance
02. Mean performance
03. Estimation of parameters of genetic variability
04. Phenotypic and genotypic correlation coefficient
05. Genetic divergence.

4.1 **Analysis of variance**

The analysis of variance revealed that the differences due to the genotypes were highly significant for plant height, primary branches per plant, secondary branches per plant, leaf length, leaf breadth, tuber length, tuber breadth, no. of tuber per plant, individual tuber weight, tuber weight loss, tuber yield per plant and tuber yield per ha were found significant (Appendix III).

Therefore, the present findings on variance for the yield and its attributes suggest existence of substantial variance for all traits in material taken for study. All the above findings are in agreed with Choudhary and Sharma (1984) for tuber yield and number of tuber per plant; Rana *et al.* (1996) for number of shoots per plant and average tuber yield; and Roy and Sharma (2000) for plant height and tuber yield.

4.2 Mean performance for genotype for different characters

The mean performance of tuber yield and its components for all the twenty genotypes are shown in the Table 2 and findings are summarized below:

4.2.1 Plant height

The plant height varied from 29.8 cm to 39.53 cm with an overall average of 34.63 cm (Table 2). The highest plant height was recorded in genotype G18

(39.53 cm) however it was followed by genotypes G10 (39.37 cm), G14 (38.82 cm) and G19 (38.47 cm) whereas, the lowest plant height was recorded in genotype G9 (29.8 cm).

4.2.2 Number of primary branches per plant

The character number of primary branches per plant ranged from 10.8 to 15.51 with an average of 12.91 (Table 2). The maximum number of primary branches per plant was observed in genotype G13 (15.51) which was followed by genotypes G3 (15.47), G9 (14.89), G2 (14.65), G11 (14.39). The minimum number of primary branches per plant counted in genotype G7 (10.8).

4.2.3 Number of secondary branches per plant

Number of secondary branches per plant varied in between 3.22 to 11.41 with overall mean of 6.69. The highest number of secondary branches per plant was counted in genotype G10 (11.41) which was followed by G4 (11.00) and G13 (10.27) (Table 2). The lowest secondary branches per plant was observed in G17 (3.22) and it was followed by G16 (3.31).

4.2.4 Leaf length (cm)

The grand mean of leaf length of potato recorded was 6.7 cm. It was ranged from 5.13 cm to 7.73 cm (Table 3). The maximum length of leaf was recorded by G10 (7.73 cm) and the lowest was recorded by G2 (5.13 cm) (Table 2).

4.2.5 Leaf breadth (cm)

The grand mean of leaf breadth of potato recorded was 4.00 cm. It was ranged from 2.87 cm to 4.87 cm (Table 3). The maximum breadth of leaf was recorded by G9 (4.87 cm) and the lowest was recorded by G2 (2.87 cm) (Table 2).

Table 2. Mean performance of different characters of 20 potato genotypes

Genotypes	**PH(cm)**	**PBP**	**SBP**	**LL(cm)**	**LB(cm)**	**TL(cm)**	**TB(cm)**	**TPP**	**ITW (g)**	**TWL (%)**	**TYP (g)**	**Yield (Ton/ha)**
G1	31.53	12.40	4.92	7.42	4.07	73.80	52.33	14.57	83.20	3.67	761.32	24.76
G2	31.87	14.65	8.73	5.13	2.87	58.13	51.27	23.40	71.80	5.34	820.42	27.35
G3	37.33	15.47	9.40	7.00	4.67	70.20	53.40	15.13	78.00	6.68	826.67	27.56
G4	32.77	12.95	11.00	6.20	3.93	76.00	51.07	10.46	101.00	6.40	664.25	23.61
G5	32.80	12.01	7.22	5.53	3.53	65.80	55.33	13.79	80.93	4.53	748.50	24.47
G6	34.00	11.20	6.67	7.13	4.67	77.20	55.13	11.63	107.13	9.67	816.67	27.06
G7	37.27	10.80	5.08	7.05	4.67	83.35	60.45	8.13	110.47	3.96	755.00	23.14
G8	32.27	12.52	5.35	6.73	3.67	68.73	48.73	14.04	71.00	9.61	765.25	24.88
G9	29.80	14.89	4.22	7.67	4.87	73.42	48.90	12.58	89.51	5.85	774.26	27.04
G10	39.37	13.50	11.41	7.73	4.73	63.13	60.47	10.15	88.45	5.86	729.33	24.49
G11	35.66	14.39	7.63	6.93	3.41	66.60	52.60	10.62	83.73	4.60	575.08	20.46
G12	36.65	11.55	4.42	5.53	3.17	60.91	54.56	7.21	76.07	6.42	476.25	15.88
G13	35.80	15.51	10.27	6.33	3.17	67.13	59.27	9.38	90.47	6.86	839.25	27.93
G14	38.82	11.76	5.33	6.40	3.52	68.40	58.13	11.63	89.27	6.10	700.89	23.36
G15	34.27	13.82	5.47	6.20	3.84	82.05	48.35	12.63	85.93	4.61	576.25	17.71
G16	30.45	11.48	3.31	7.28	4.20	81.20	51.13	10.88	83.20	5.45	806.50	26.97
G17	33.48	11.33	3.22	7.53	4.70	83.93	53.67	8.03	95.67	3.91	747.39	25.17
G18	39.53	13.55	7.43	6.87	3.99	62.39	50.93	18.11	73.47	7.13	923.67	31.23
G19	38.47	12.76	8.35	6.80	4.34	65.13	57.67	17.08	115.26	7.19	1120.06	37.34
G20	30.47	11.77	4.38	6.60	4.08	72.07	49.47	15.96	83.87	6.74	714.90	22.19
Min	29.8	10.8	3.22	5.13	2.87	58.13	48.35	7.21	71	3.67	476.25	15.88
Max	39.53	15.51	11.41	7.73	4.87	83.93	60.47	23.40	115.26	9.67	1120.06	37.34
Mean	34.63	12.91	6.69	6.7	4	70.98	53.64	12.77	87.92	6.03	757.1	25.13
CV (%)	5.99	7.55	26.83	7.85	10.45	7.44	6.36	17.38	10.12	31.1	12.4	12.57

PH = plant height (cm), PBP = No. of primary branches per plant, SBP = NO. of secondary branches per plant, LL = leaf length (cm), LB = leaf breadth (cm), TL = tuber length (cm), TB = tuber breadth (cm), TPP = no. of tuber per plant, ITW = individual weight of tuber (g), TWL = tuber weight loss (%) 20 DAH, TYP = tuber yield per plant (g) and YPH = yield (ton/ha).

4.2.6 Tuber length (cm)

The grand mean of tuber length recorded was 70.98 cm. It was ranged from 58.13 cm to 83.93 cm (Table 3). The maximum length of tuber was recorded by G17 (83.93 cm) and the lowest was recorded by G2 (58.13 cm) (Table 2), (plate 4 and plate 5).

4.2.7 Tuber diameter

The grand mean of tuber diameter recorded was 53.64 cm. It was ranged from 48.35 cm to 60.47 cm (Table 2). The maximum diameter was recorded by G10 (60.47 cm) and the lowest was recorded by G15 (48.35 cm).

4.2. 8 No. of tuber per plant

Number of tuber per plant varied from 7.21 to 23.4 with an average of 12.77 (Table 2). The highest number of tubers per plant was counted in genotype G2 (23.40) which was followed by the genotype G18 (18.11) and G19 (17.08). The lowest number of tubers per plant was noted to be 7.21 which were observed in genotype G12.

Plate 4: Photograph showing the tuber of different variety used in this experiment.

Plate 5. Showing transverse section of different tuber of twenty potato genotypes.

4.2.9 Individual weight of tuber (g)

The individual weight of tuber ranged from 71.00 g to 115.26 with the mean of 87.92 g (Table 2). The highest individual tuber weight was observed in genotype G19 (115.26 g) which was followed by G7 (110.47 g), G6 (107.13 g) and G4 (101.00 g). The lowest individual tuber weight was recorded in genotype G8 (71.00 g).

4.2.10 Tuber weight loss percentage

Tuber weight loss percentage was observed 20 days after potato harvest. The character tuber weight loss (%) ranged in between 3.67 to 9.67 with an overall average of 6.03 % (Table 2). The highest percentage of tuber weight loss was found in genotype G6 (9.67%) which were followed by the genotype G8 (9.61%). On the other hand the minimum percent of tuber loss in potato was found in genotype G1 (3.67%).

4.2.11 Tuber yield per plant (g)

The tuber yield varied from 476.25 g to 1120.06 g with the mean of 757.1 g. The highest tuber yield per plant was found in genotype G19 (1120.06 g) which was followed by genotype G18 (923.67 g), G13 (839.25 g) whereas, the minimum yield per plant was recorded in genotype G12 (476.25 g) (Table 2).

4.2.12 Yield (ton/ha)

The character yield/ha ranged from 15.88 ton to 37.34 ton with an overall mean of 25.13 ton (Table 2). The highest yield/ha was recorded in genotype G19 (37.34 ton) which was followed by genotype G18 (31.23 ton). The lowest tuber yield per ha was recorded in genotype G12 (15.88 ton).

Based on overall findings of mean performance for various yield and its components for potato the genotypes viz. G18, G19, G0, G14 possessed high plant height; G2, G19, G18 for high number of tubers per plant; G19, G18, G13, G3, G2 for high tuber yield per plant and the genotypes G19 and G18 were overall recorded to possessed high tuber yield per ha under study. Hence, these genotypes could be considered as promising genotypes of potato.

Similar results were also found by Bantratz (1990) and Nandekar (1995) for total tuber yield, Sharma (1999) for number of tubers per plant, Roy and Sharma (2000) and Painkra (2002) for plant height, number of tubers and total tuber yield.

4.3 Genetic variability

In present investigation variability parameters for tuber yield and its components are presented in Table 3.

4.3.1 Phenotypic and genotypic co-efficient of variation

The phenotypic and genotypic coefficient of variance was calculated for all the twelve characters (Table 3 and Figure 1) and observed that phenotypic coefficient of variance was in general higher than the genotypic coefficient of variance for all the characters. Thus it suggests the substantial influence of environment besides the genetic variation for expression of these traits.

High magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was observed for secondary branches per plant 43.56% and 34.32% respectively followed by no. of tuber per plant (33.78% and 28.97%), tuber weight loss (37.38% and 20.75%) and tuber yield per ha (20.89% and 16.69%). Whereas, the moderate magnitude of PCV and GCV was observed for weight of tuber (16.50% and 13.02%), leaf breadth (17.28% and 13.77%), primary branches per plant (13.02% and 10.61%) and tuber length (12.47% and 10.01%) respectively).

Table 3. Estimation of genotypic and phenotypic variation for different characters in potato

Parameters	**σ^2p**	**σ^2g**	**$\sigma^2 e$**	**PCV**	**GCV**
Plant height (cm)	12.84	8.53	4.31	10.34	8.43
Primary branches per plant	2.83	1.88	0.95	13.02	10.61
Secondary branches per plant	8.49	5.27	3.22	43.56	34.32
Leaf length (cm)	0.71	0.43	0.28	12.56	9.80
Leaf breadth (cm)	0.47	0.30	0.17	17.28	13.77
Tuber length (cm)	78.34	50.48	27.91	12.47	10.01
Tuber breadth (cm)	22.90	11.26	11.64	8.92	6.25
No. of tuber per plant	18.61	13.68	4.93	33.78	28.97
Individual weight of tuber (g)	210.32	131.09	79.23	16.50	13.02
Tuber weight loss (%) 20 DAH	5.08	1.56	3.52	37.38	20.75
Tuber yield per plant (g)	23805.25	14992.10	8813.15	20.38	16.17
Yield ton per ha	27.55	17.58	9.97	20.89	16.69

σ^2p : Phenotypic variance
σ^2g : Genotypic variance
$\sigma^2 e$: Environmental variance

PCV : Phenotypic coefficient of variation
GCV : Genotypic coefficient of variation
ECV : Environmental coefficient of variation

The high magnitude of PCV and GCV (>20%) recorded for no. of secondary branches per plant, tuber per plant, tuber weight loss and tuber yield per ha suggesting the existence of considerable variability in potato genotypes for these traits. Hence, selection for these traits may be worthwhile for improving marketable in potato. However, the moderate PCV and GCV as recorded for the traits *viz.* weight of tuber, leaf breadth, primary branches per plant and tuber length suggest existence of considerable variability in the population. Selection for these traits may also be given the importance. These findings are in accordance with the findings Rasul*et al.* (1995) for tuber yield per ha and for average tuber weight Kumar *et al.* (2005); for tuber number, plant height and average tuber yield by Joseph *et al.* (2005); for tuber weight by Shashikamal (2006). Whereas, Roy and Singh (2006) recorded high magnitude of PCV and GCV for plant height, tuber yield, total tuber yield and dry matter percent of tuber. The moderate PCV and GCV were reported by Luthra *et al*. (2005) and Shashikamal (2006) for fresh weight of shoots/plant and plant height.

The PCV and GCV (<10 per cent) also observed in low magnitude for tuber breadth (8.92% and 6.25%) in present study. Similar finding was also reported by Joseph *et al*. (2005) in case of number of leaves.

4.3.2 Heritability

Heritability estimates in broad sense were calculated for tuber yield and its components and presented in Table 4. These are grouped into high (>60% percent) moderate (30 to 60%) and low (<30% percent) as per the classification suggested by Robinson (1966).

Estimates of high heritability was recorded for the character tuber per plant (73.53%) followed by plant height (66.43%), primary branches per plant (66.43%), tuber length (64.39), yield per ha (63.82), yield per plant (62.98), weight of tuber (62.33) and secondary branches per plant (62.07) indicated that these characters are less influenced by environmental effect and hence additive gene effect were substantially contributing for expression of these traits. These findings are similar with the finding of Choudhary and Sharma (1984) for total tuber yield per plant and average tuber weight; Luthra (2001) for average tuber weight, number of tubers; Luthra *et al.* (2005) for tuber yield, number of tuber and Roy and Singh (2006) for tuber yield.

The character tuber breadth (49.16%) and tuber weight loss (30.80%) exhibited the moderate heritability.

4.3.3 Genetic Advance

Genetic advance was worked out as percentage of mean for tuber yield and its components which is presented in Table 4 and Figure 2. Genetic advance is important to find out the genetic gains likely to be achieved in the next generation. These are classified as high (> 20%), medium (10 to 20%) and low (< 10%).

In the present study highest estimates of genetic advance as percentage of mean was obtained for characters namely no. of secondary branches per plant (55.70%) which was followed by tuber per plant (51.17%), yield per ha (27.46), tuber yield per plant (26.44), tuber weight (21.18%) and leaf breadth (22.59%). The high value of genetic advance for these traits showed that these characters are governed by additive genes and selection will be rewarding for the further improvement of such traits.

The moderate genetic advance observed in characters namely plant height (14.16%), no. of primary branches per plant (17.80%), leaf length (15.75%) and tuber length (16.55%). These findings of moderate genetic advance suggest that both the additive and non-additive variance are operating in these traits However, the low genetic advance as per cent of mean was observed for the character, tuber breadth (9.03%). This indicates significance of non-additive gene effects.

Table 4: Estimation of heritability and genetic advance for different characters in potato

Parameters	**h^2**	**GA (5%)**	**GA (% mean)**
Plant height (cm)	66.43	4.90	14.16
No. of Primary branches per plant	66.43	2.30	17.80
No. of Secondary branches per plant	62.07	3.73	55.70
Leaf length (cm)	60.56	1.06	15.75
Leaf breadth (cm)	63.46	0.90	22.59
Tuber length (cm)	64.39	11.75	16.55
Tuber breadth (cm)	49.16	4.85	9.03
No. of tuber per plant	73.53	6.53	51.17
Individual weight of tuber (g)	62.33	18.62	21.18
Tuber weight loss (%) 20 DAH	30.80	1.43	23.72
Tuber yield per plant (g)	62.98	200.17	26.44
Yield (ton/ha)	63.82	6.90	27.46

h^2 : Heritability
GA (5%) : Genetic advance (5%)
GA (% mean) : Genetic advance (% mean)

In the present investigation, high heritability estimates coupled with high genetic advance was recorded for the traits, no. of secondary branches per plant, leaf breadth, no. of tuber per plant, tuber weight, tuber yield per plant and tuber yield per ha. Hence selection for these traits will be worthwhile for improving potato. In agreement to the above results, similar findings were also supported by Luthra *et al.* (2005) for tuber yields.

4.4 Phenotypic and genotypic correlation co-efficient

Galton (1988) was first to suggest the use of correlation to describe the degree of association between the two variables. The degree of association also affects the effectiveness of selection process and helps to select desirable genotype. Crop improvement programme largely depends on availability of sufficient variability and association among different characters, which are pre-requisites for execution of selection programme. Yield, being a complex quantitative trait, is dependent on a number of component characters; therefore, knowledge of association of different components together with their relative contributions has immense value in selection.

To estimate the association between two variables, correlation co-efficient at phenotypic and genotypic levels, was worked out in all possible combination and presented in Table 5.

Table 5: Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Potato.

		PH	**PBP**	**SBP**	**LL**	**LB**	**TL**	**TB**	**TPP**	**ITW (g)**	**TWL (%)**	**TYP (g)**
PBP	G	0.022										
	P	0.146										
SBP	G	0.484**	0.597**									
	P	0.354**	0.533**									
LL	G	0.014	-0.107	-0.223								
	P	0.055	-0.012	-0.132								
LB	G	0.036	-0.261*	-0.215	0.855**							
	P	0.031	-0.092	-0.041	0.779**							
TL	G	-0.416**	-0.482**	-0.637**	0.532**	0.645**						
	P	-0.258*	-0.295*	-0.282*	0.363**	0.429**						
TB	G	0.827**	-0.268*	0.400**	0.059	0.090	-0.345**					
	P	0.471**	-0.051	0.308*	0.101	0.109	0.083					
TPP	G	-0.165	0.385**	0.215	-0.362**	-0.261*	-0.571**	-0.503**				
	P	-0.091	0.289*	0.165	-0.214	-0.160	-0.315*	-0.229				
ITW (g)	G	0.222	-0.451**	0.019	0.335**	0.561**	0.497**	0.566**	-0.467**			
	P	0.158	-0.168	0.168	0.301*	0.434**	0.420**	0.432**	-0.189			
TWL (%)	G	0.103	0.058	0.262*	-0.165	-0.065	-0.467**	-0.169	0.261*	0.014		
	P	0.096	0.005	0.159	0.101	0.076	-0.094	-0.030	0.085	-0.018		
TYP (g)	G	0.151	0.101	0.234	0.274*	0.337**	-0.184	0.177	0.507**	0.287*	0.409**	
	P	0.168	0.162	0.225	0.202	0.266*	-0.050	0.225	0.521**	0.350**	0.211	
Yield (Ton/ha)	G	0.163	0.200	0.312*	0.307*	0.327*	-0.255*	0.138	0.471**	0.274*	0.403**	0.994**
	P	0.156	0.208	0.267*	0.203	0.246	-0.083	0.213	0.517**	0.325*	0.240	0.963**

** = Significant at 1% Level. * = Significant at 5% Level.

PH = plant height (cm), PBP = No. of primary branches per plant, SBP = NO. of secondary branches per plant, LL = leaf length (cm), LB = leaf breadth (cm), TL = tuber length (cm), TB = tuber breadth (cm), TPP = no. of tuber per plant, ITW = individual weight of tuber (g), TWL = tuber weight loss (%) 20 DAH, TYP = tuber yield per plant (g) and YPH = yield (ton/ha).

4.4.1 Plant height (cm)

Plant height was highly significant positive correlation with no. of secondary branches per plant (0.484 and 0.354), tuber breadth (0.827 and 0.471) at genotypic and phenotypic level respectively. It was negatively correlated with tuber length (-0.416 and -0.258).

4.4.2 No. of Primary branches per plant

Positive highly significant correlation was observed of no. of primary branches per plant with secondary branches per plant (0.597 and 0.533) and tuber per plant (0.385 and 0.289). It was negatively correlated with tuber length (-0.482 and -0.295), tuber breadth (-0.268 and -0.051) and tuber weight (-0.451 and -0.168).

4.4.3. No. of Secondary branches per plant

No. of Secondary branches per plant showed positive and highly significantly association with tuber breadth (0.400 and 0.308) and yield per ha (0.312 and 0.267). It was negatively significant correlated with tuber length (-0.637 and -0.282) at genotypic and phenotypic level.

4.4.4. Leaf length (cm)

Leaf length was positively and highly significant associated with leaf breadth (0.855 and 0.779), tuber length (0.532 and 0.363), weight of tuber (0.335 and 0.301) and yield per ha (0.307 and 0.203) at both genotypic and phenotypic level.

4.4.5 Leaf breadth (cm)

Highly significant positive association of leaf breadth with tuber length (0.645 and 0.429), weight of tuber (0.561 and 0.434) and yield per plant (0.337 and 0.266). It was negatively correlated with tuber per plant (-0.261 and -0.160) at both level.

4.4.6 Tuber length (cm)

Tuber length was positively highly significant association with tuber weight (0.497 and 0.420) at both genotypic and phenotypic level. It was negatively significant association with tuber per plant (-0.571 and -0.315) at both genotypic and phenotypic levels. Significant negative association of tuber length with tuber breadth (-0.345), tuber weight loss (-0.467) and yield per ha (-0.255) at genotypic level.

4.4.7 Tuber breadth (cm)

Tuber breadth was positively and highly significant correlation with tuber weight (0.566 and 0.432). It was negatively significant correlation with tuber per plant (-0.503) at genotypic level and negatively correlated at phenotypic level (-0.229).

4.4.8 No. of tuber per plant

Number of tuber per plant exhibited positive and high significant correlation with yield per plant (0.507 and 0.521) and tuber yield per ha (0.471 and 0.517). It was negatively significant correlated with weight of tuber (-0.467 and -0.189).

4.4.9 Individual weight of tuber (g)

Individual tuber weight exhibited positive and significant correlation with yield per plant (0.287 and 0.350) and tuber yield per ha (0.274 and 0.325).

4.4.10 Tuber yield per plant (g)

The character tuber yield per plant had high significant and positive correlation with tuber yield per ha (0.994 and 0.963) at both genotypic and phenotypic levels.

4.5 Genetic divergence

The genetic divergence was estimated by Mahalanobis' D^2 statistics as described by Rao (1952). Based on D^2 values, the constellation of genotypes into clusters was done following Tocher'smethod (Rao, 1952).

4.5.1. Group constellations

In potato, due to stagnate and pre-petuating nature of heterosis, parental selection is a crucial step in any breeding programme. Using statistics as proposed by Mahalonobis (1936) D^2 value were calculated among twenty potato genotypes in all possible combinations.

The study of genetic divergence among genotypes under study, analysis of co-variance was performed for all possible pair of character and as an outcome, twenty genotypes grouped into five different clusters using Mahalanobis' D^2 statistics. The clustering pattern and genotypes are given in Table 6 and Figure 5. The maximum numbers of nine genotypes were included in cluster V followed by six genotypes in cluster I, three genotypes in cluster III and lowest only one genotype in both cluster II and cluster IV.

4.5.2 Intra and inter-cluster distances

The intra and inter-cluster distance of all clusters has been presented in Table 7. Intra cluster D^2 values ranged from 0.00 to 3.56. The intra cluster distance was observed highest in cluster V (3.56), followed by cluster I ((2.56) and cluster III (1.76), There was no intra cluster distance in cluster II and cluster IV because they both contained only one genotype.

However, the inter-cluster D^2 values varied from 6.12 to 39.12 (Table 8). The highest inter-cluster distance was exhibited between the cluster II and IV (39.12) followed by cluster II & III (38.71), cluster I and IV (27.28), cluster IV and V (21.29) and the minimum inter-cluster distance was observed in between cluster I and V (6.12) in Table 8. Above findings indicated that high inter-cluster distances were the main cause of diversity in composition of cluster and hence can be exploited in hybridization programme.

Table 6. Distribution of 20 genotypes of potato in different clusters

Cluster no.	Numbering of genotypes	No. of genotypes	Name of Genotypes
I	G2, G3,G 6, G13, G16, G18	6	BARI Alu49, BARI Alu64, BARI Alu8, BARI Alu63, BARI Alu60, BARI Alu41
II	G19	1	BARI Alu46
III	G4, GV11, G15	3	BARI Alu7, BARI Alu40, BARI Alu25
IV	G12	1	BARI Alu24
V	G1, G5, G7,G 8, G9, G10, G14, G17, G20	9	BARI Alu70, BARI Alu67, BARI Alu61, BARI Alu62, BARI Alu57, BARI Alu65, BARI Alu50, BARI Alu69, BARI Alu38
Total		20	

Table 7: Intra (Bold) and inter cluster distances (D^2) for 20 genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**2.56**	14.11	26.37	27.28	6.12
II		**0.00**	38.71	39.12	18.88
III			**1.76**	11.15	21.38
IV				**0.00**	21.49
V					**3.56**

Table 8: Nearest and farthest cluster distances

Cluster	Nearest cluster distance	Farthest cluster distance
I	V (6.12)	IV (27.28)
II	I (14.11)	IV (39.12)
III	IV (11.15)	II (38.71)
IV	III (11.15)	II (39.12)
V	I (6.12)	IV (21.49)

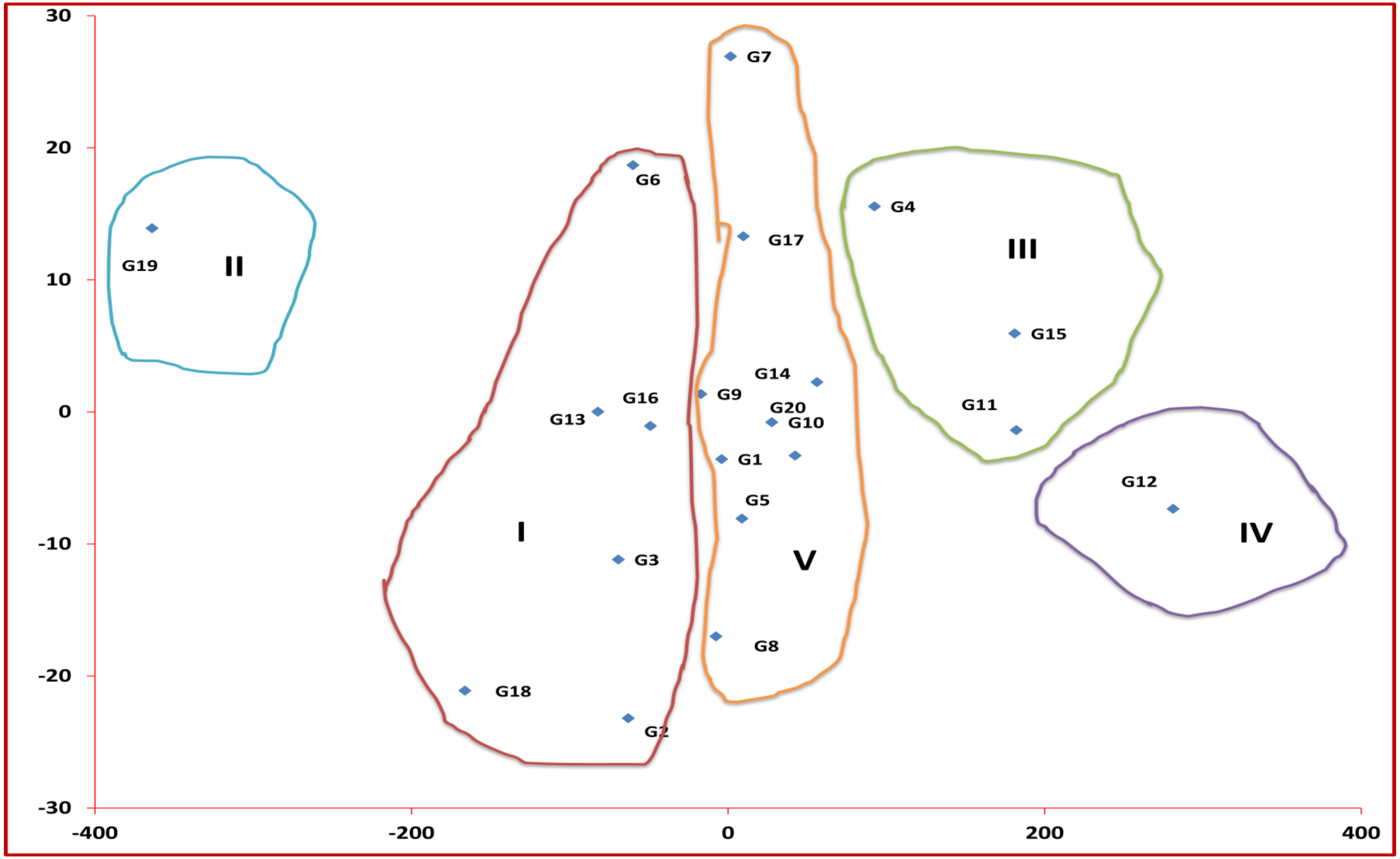


Figure 1: Cluster diagram of potato genotypes based on their principal component scores.

4.5.3 Component of cluster mean

Divergence reflecting in the material was also evidenced by an appreciable amount of desirable variation among clusters mean for different characters as shown in Table 9. The component of cluster mean for the plant height was highest in cluster III (38.47 cm) which was followed by cluster IV (36.65 cm) and lowest in cluster V (33.98 cm). As regards number of primary branches per plant, cluster III possess the highest average performance (13.72) and followed by cluster I (13.64) and lowest was observed in cluster IV (11.55). Number of secondary branches per plant showed the highest mean performance for the cluster II (8.35) followed by cluster III (8.03) and lowest in cluster IV (4.42). The character leaf length exhibited highest cluster mean for cluster V (6.96cm) followed by cluster II (6.80 cm) and lowest in cluster IV (5.53cm).

The highest mean for leaf breadth was observed in cluster V (4.20 cm) which was followed by cluster II (4.34 cm) and lowest in cluster IV (3.17 cm). Tuber length exhibited the highest mean performance for cluster III (74.88 cm) and lowest for cluster IV (60.91 cm) whereas, the highest tuber breadth (57.67 cm) and lowest (50.67 cm) was observed in cluster II and III, respectively. Tuber per plant showed highest mean performance for cluster II (17.08) which was followed by cluster I (14.76) and lowest in cluster IV (7.21). The highest individual weight of tuber (115.26 g) and lowest (76.07 g) was observed in cluster II and IV respectively.

Tuber weight loss exhibited the highest mean performance for cluster II (7.19%) which was followed by cluster I (6.86%) and lowest in cluster III (5.20%). The highest mean for tuber yield per plant was observed in cluster II (1120.06 g) followed by cluster I (838.86 g) and lowest in cluster IV (476.25 g). As regards yield per ha, the highest cluster mean was observed in cluster II (37.34 ton) followed by cluster I (28.02 ton) and lowest in cluster IV (15.88 ton).

Table 9: Cluster mean values of 12 different characters of 20 Potato genotypes

Characters	**I**	**II**	**III**	**IV**	**V**
Plant height (cm)	34.83	38.47 (H)	34.23	36.65	33.98 (L)
Primary branches per plant	13.64	12.76	13.72 (H)	11.55 (L)	12.33
Secondary branches per plant	7.64	8.35 (H)	8.03	4.42 (L)	5.68
Leaf length (cm)	6.62	6.80	6.44	5.53 (L)	6.96 (H)
Leaf breadth (cm)	3.93	4.34	3.73	3.17 (L)	4.20 (H)
Tuber length (cm)	69.37	65.13	74.88 (H)	60.91 (L)	72.51
Tuber breadth (cm)	53.52	57.67 (H)	50.67 (L)	54.56	54.16
No. of tuber per plant	14.76	17.08 (H)	11.24	7.21 (L)	12.10
Individual weight of tuber (g)	84.01	115.26 (H)	90.22	76.07 (L)	88.04
Tuber weight loss (%) 20 DAH	6.86	7.19 (H)	5.20 (L)	6.42	5.58
Tuber yield per plant (g)	838.86	1120.06 (H)	605.19	476.25 (L)	744.09
Yield ton per ha	28.02	37.34 (H)	20.59	15.88 (L)	24.39

H= High value, L= Low value

4.5.4 Desirable genotypes based on cluster performance

The better genotype selected for all the characters under consideration are presented in Table 10. Among them, G19 (BARI Alu46) included in cluster II possessed the highest tuber yield per ha (37.34 ton), highest tuber weight (115.26 g), higher plant height (38.47 cm) and higher tuber per plant (17.08) whereas, the highest plant height was observed in genotype G18 ((BARI Alu41) (39.53 cm) and higher tuber yield per ha (31.23 ton) included in cluster I. On the other hand, genotype G12 (BARI Alu24) selected from cluster IV because this cluster shown low values for maximum characters. So, for future breeding program genotype from this cluster may be included. The genotype G2 (BARI Alu49) from cluster I exhibited the highest mean value for number of tuber/plant (23.40).

All the genotypes included in present investigation, their grouping in different clusters, suggested that genotypes did not follow the geographic distribution (Desai and Jaimini, 1997). This is not unexpected since there is a free exchange of materials for various breeding programme all over the world. Further, selection of material from same origin or source for different economic characters may be contributed to divergence. Gaur *et al.* (1978), in their study with 67 and Singh *et al.* (1988) with 40 genotypes also observed that clustering pattern was not influenced by geographic distribution of genotypes. Therefore, present findings suggest the existence of true genetic divergence in population of potato.

Based on the present findings on genetic divergence and its component analysis, it can be concluded that inter-crossing among the genotype of genetically diverse clusters showing superior mean performance may be helpful for obtaining desirable segregants with higher yield, hence in view of the above findings, genotypes namely G19 (BARI Alu46) from cluster II; genotype G18 (BARI Alu41) and G2 (BARI Alu49) from cluster I and G12 (BARI Alu24) from cluster IV possessing superiority among genotypes which may be utilized as parents in hybridization programme for obtaining desirable combination.

Table 10. Selection of promising high yielding genotype based on mean performance

Genotype	Cluster No.	Yield (ton/ha)	Tuber per plant	Tuber weight (g)	Plant height (cm)
G19 (BARI Alu46)	II	37.34	17.08	115.26	38.47
G2 (BARI Alu49)	I	27.35	23.40	71.80	31.87
G18 (BARI Alu41)	I	31.23	18.11	73.47	39.53

CHAPTER V
SUMMARY AND CONCLUSION

Summary

The experiment was conducted at the research farm of Sher-e-Bangla Agricultural University. Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh during the period from November 2017 to March 2018. The experiment is carried out in randomized complete block design with three replications. All the genotypes varied significantly with each other for all the studied characters indicated the presence of considerably variations among the genotypes studied. The PCV values were higher than the respective GCV values for all the characters under study.

Secondary branches per plant, leaf breadth, no. of tuber per plant, individual weight of tuber, tuber yield per plant and yield ton per ha showed high heritability along with high genetic advance as percentage of mean were normally more helpful in predicting the genetic gain under selection.

Yield per ha was significantly positively correlated with no. of secondary branches per plant, tuber per plant, individual tuber weight and tuber yield per plant at both genotypic and phenotypic level indicating potato yield is increased with the increasing of these traits. whereas, the tuber yield per ha was recorded having positive and significant correlation at genotypic level with leaf length, leaf breadth and tuber weight loss percentage. Only positive correlation of tuber yield per ha with plant height, primary branches per plant and tuber breadth. Hence, the characters namely tuber yield per plant, number of tubers per plant, secondary branches per plant and individual tuber weight recorded to be key traits and may be given prime importance while making selections for improvement of potato.

On the basis of D^2 values, the 20 genotypes were grouped into five divergent clusters. The clusters divergence was proved by the high inter-cluster and low intra clusters D^2 values. Cluster V was the largest and consisted of nine genotypes followed by cluster I with six genotypes. The grouping pattern did not show any relationship between genetic divergence and geographical diversity. The cluster mean of 20 genotypes showed that the mean value of clusters varied in magnitude for all the twelve characters. Genotypes in cluster II showed maximum performance for yield per ha (37.34 ton), tuber yield per plant (1120.06 g), individual tuber weight (115.26 g), tuber number per plant (17.08), tuber breadth (57.67 cm), no. of secondary branches per plant (8.35) and plant height (38.47 cm). Cluster III showed maximum performance for no. of primary branches per plant (13.72) and tuber length (74.88 cm). Cluster V showed highest value for leaf length (6.96 cm) and leaf breadth (4.20 cm). Maximum inter clusters D^2 value was observed between the clusters I and IV (39.12) indicated that the genotypes belongings 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. Considering this idea and other characteristic performances, genotype G19 (BARI Alu46) from cluster II; genotype G18 (BARI Alu41) and G2 (BARI Alu49) from cluster I and G12 (BARI Alu24) from cluster IV might be considered to suggest farmer for cultivation for better yield as well as use as parent for efficient hybridization programme for further improvement.

CONCLUSION

It was concluded that genotypes namely G19 (BARI Alu-46) and G18 (BARI Alu-41) could be use as promising variety. On the other hand diverse genotypes G19 (BARI Alu-46), G18 (BARI Alu-41), G2 (BARI Alu-49) and G12 (BARI Alu-24) may be utilized as good variety for cultivation as well as use as parents in hybridization programme for obtaining desirable combination.

REFERENCES

Addisu, F., Yohannes, P. and Habtamu, Z. (2013).Genetic variability and association between agronomic characters in some potato (*Solanum tuberosum*L.) genotypes in SNNPRS, Ethiopia.*Intl. J. Bio. and Con*. **5**(8): 523–528.

Anonymous. (2009). Advanced yield trial with exotic varieties (3rd generation). Annual Report, August 2009. Tuber Crops Research Centre, BARI, Joydebpur, Gazipur. pp. 23–25.

Anonymous.(2005). Directorate of Horticulture, Govt. of Chhattisgarh, Raipur, Chhattisgarh.

Bangratz, J., (1990). Starch on potato varieties field trial result 1989.*Pomme-de-Terre-Francaise*.**52 (456):** 22–24.

BBS (Bangladesh Bureau of Statistics).(2014). Estimation of potato, 2013–2014.Agriculture Wing.Govt. People's Repub. Bangladesh.

Behjati, S., Choukan, R., Hassanabadi, H. and Delkhosh, B. (2013). The evaluation of yield and effective characteristics on yield of promising potato clones. *Annl. Biol. Res.* **4**(7): 81–84.

Bhagowati, R.R., Saikia, M. and Sut, D. (2002).Variability, heritability, genetic advance and character association in True Potato Seed (TPS) population. *J . Argil. Sci. Society of North- East India*.**15 (1)**: 119–122.

Chaudhary, S. K. and Sharma, S. K. (1984).Genetic variability for yield and its components in potato breeding material.*Indian J. Agric. Sci*. **54(10)**: 941–2.

Chaudhary, S.K., Sharma, S.K. and Sharma, H.C.(1984). Path coefficient analysis in F1C2 generation of potato crosses. *Agric. Sci. Digest*. **4(4)**: 228–230.

Dayal, T. R., Upadhyay, M.D., Malhotra, V.P. and Mehra, K. L., (1972).Heritability and correlation in yield and other quantitative characters in potato (*Solanumtuberosum*L.).*Indian J. Agric. Sci.* **42(6)**: 464–466.

Dixit, D.; Mittal, R.K.; Choubey, C.N. and Singh, P. (1994).Variability, correlations and selection indices in potato (*Solanum tuberosum*L.).*Haryana J. Hort. Sci*. **23(2)**:168–172.

FAO (Food And Agricultural Organization). (2013). Production Year Book No. 65. Food and Agriculture Organization , Rome, Italy. p. 97.

Fisher, R.A. (1918). The correlation between relatives on the supposition of Mendelian inheritance.*Trans. Roy. Soc. Edinburgh*., **52**: 399– 433.

Galton, F. (1988). Correlation and their measurements child head from antropometric data. *Proc. Roy. Soc*. **45**: 135–145.

Garg, L. P. and Bhutani, R.D. (1991).Variability and heritability studies in some important traits in potato (*Solanumtuberosum*L.). *Haryana J. Hort. Sci*. **20**: 239–243.

Halwai, R. (2000). Evaluation of potato cultures/hybrids under Chhattisgarh Plains.*M.Sc. (Ag.) Thesis*, Indira Gandhi KrishiVishwavidyalaya, Raipur (C.G.).

Hossain, M.S. (2011). Yield potential, storage behaviour and degeneration of potato varieties in Bangladesh. Ph.D. Thesis. Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur-1706, Bangladesh.

Horton, D. (1987). Potatoes: production, marketing and programs for developing countries. West view Press, London. pp. 19–24.

Iqbal, M.Z. and Khan, S.A. (2003).Genetic variability, partial regression, co-heritability studies and their implication in selection of high yielding potato genotypes.*Pakistan J. Scientific and Industrial Res.* **46 (2)**: 126–128.

Joseph, T.A., Gopal, J., Sood. S.K. (2005).Genetic parameters and character associations in potato under sub-tropical plains and temperate hill conditions.*Potato J.* **32** (1-2): 49–53.

Karim, M. R., Rahman, H., Ara, T., Khatun, M. R., Hossain, M. M. and Islam, A. K. M. R. (2011). Yield potential study of meristem derived plantlets of ten potato varieties (*Solanumtuberosum*L.). *Intl. J. Biosci.* **1**(2): 48–53.

Kassim, N.A., Nerway, Z.A.A. and Yousif, K.H. (2014).Potato virus Y (PVY) surveying and its economic importance on potato crop.*Intl. J. Res.* **2**(6): 39–46.

Kaul, A.K. (1967). Heritability, a brief review.*General P.G. School, IARI*.**5(2)**: 253–267.

Kumar R. and Kang, G. S. (2000).Characterizing genetic diversity in andigena potato using non-hierarchical Euclidean cluster analysis.Potato Global Research and Development Proceedings of the Global Conference on Potato, New Delhi.**1**: 146–149.

Kumar, V., Gopal, J. and Bhardwaj, V. (2005).Evaluation of exotic potato (*Solanumtuberosum*L. spp. Tuberosum) germplasm in North – Western Hills of India.*Indian J. Plant Genetic Resources*.**18**(1): 94–95.

Lampitt, L. H. and Goldenberg, N. (1940).*Chem. Indian.***18**: 748–61.

Lush, J. L. (1940). Intra sire correlation and regression of off spring on dams as a method of estimating heritability of characters. In: *Proc. Aimer. Soc. Animal Production.***33**: 293–301.

Luthra, S. K. (2001). Heritability, genetic advance and character association in potato.*J. Indian* Sharma, *Potato Assoc.* **28(1)**: 1–3.

Luthra, S. K., Gopal, J. and P. C. (2005).Genetic divergence and its relationship with heterosis in potato.*Potato J.* **32 (1-2)**: 37–42.

Mahalanobis, P.C. (1936). Studies on the generalized distance in statistics.*Proc. Nat. Inst. Sci. India*.**21**: 49–55.

Martins, R. (1976).New archaeological techniques for the study of ancient root crops in Peru.*Ph.D. Thesis*, University of Birmingham, England.

Mittal, R.K. and Dixit, D. (1992).Genetic divergence in potato.*Haryana J. Hort. Sci.* **21**: 72–75.

Nandekar D. N.; Sharma, R. C. and Sharma, T.R. (1995). Yield potential of potato hybrids in Madhya Pradesh. *J. Indian Potato Assoc*. **22(1-2)**: 13–16.

Ozkaynak, E.; Samanc, B. and Cetin, M.D. (2003).Correlation and path coefficient analysis of yield components in potato (*Solanumtuberosum*L.).*Turkish J. Field Crops*.**8(2)**: 51–56.

Painkra, K.S. (2002). Performance of different cultures/hybrids of (*Solanumtuberosum*L.) under Chhattisgarh Plains.*M.Sc. (Ag.) Thesis*, Indira Gandhi KrishiVishwavidyalaya, Raipur (C.G.).

Pandey, S. K. and Gupta, P.K. (1997).Genetic diversity and combining ability studies on true potato seeds (TPS) in potato (*Solanumtuberosum*L.).*J. Indian Potato Assoc*., **24**: 1–6.

Patel, A.K., Patel, N.H., Gami, R.A., Patel, C.R. and Chauhan, R.M. (2013).Assessment of potato (*Solanumtuberosum*L.) hybrids varieties for table purpose among yield and quality traits.*Trends in Biosci*.**6**(5): 669–673.

Pearson, Karl. (1904). On the generalized theory of alternative inheritance with special reference to Mendel Law. *Phil***.** *Trans***.** *Loy*. *Soc*. **203**: 53–86.

Rana, M.S., Sharma B.D., Kang, G.S., Singh, A.N., Gaur, P.C. and Pandey, S.K. (1996).Kufri Sutlej, a new medium maturing potato variety for western and central Indo-Gangetic plains of India. *J. Indian Potato Assoc*. **23(3-4)**: 108–111.

Rao, C.R. (1952).Advanced statistical methods in biometrical research, John Wiley and Sons, Newyork.

Rasul, M.G., Islam, M.A., Nahar, M.S. and Rashid, M.M. (1995). Heritability, variability and correlation in the first clonal generation of tuberlets progenies derived from true potato seed. *Bangladesh J. Scientific and Industrial Res.* **30(2/3)**: 161–170.

Reddy, M. and Heyne, E.G. (1968).Qualitative inheritance and heritability studies.*A Resume. Andhra Agric. J.* **15**: 51–56.

Regassa, D. and Basavaraja, N. (2005). Correlation and path analysis in potato (*Solanumtuberosum*L.) .*Potato J.*, **32**(3-4): 233–256.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1951).Genotypic and phenotypic correlation in corn and their implication in selection.*Agron. J*. **43**: 262–67.

Robinson, H.F. (1966). Quantitative genetics in relation to breeding on the centennial of Mendelism.*Indian J. Genet*.**26**: 171–187.

Roy, A. K. and Singh, P. K. (2006).Genetic variability, heritability and genetic advance for yield in potato (*Solanumtuberosum*L.).*International J. Plant Sci*. **1 (2)**: 282–285.

Roy, S. K. and Sharma, R.C. (2000).Effect of nitrogen, phosphorus and time schedules of haulm cutting on production of small sized (up to 40g) tuber in seed potato (*Solanumtuberosum*L.)*Crop Indian J. Agric. Sci.* **70** (7): 441–445.

Sandhu, S.K. and Kang, G.S. (1998).Genetic analysis in germplasm of *andigena*potatoes (*Solanumtuberosum*L. spp. *andigena*). Crop Improv.**25**: 181–185.

Sanjay, D., Rajib, D. and Dhirendra, S. (2015). Evaluation of genetic diversity for yield and quality parameters of different potato (*Solanum tuberosum* L.) germplasm .*J. Appl. Nat. Sci.* **7**(1): 235 – 241.

Sattar , M.A., Uddin, M.Z., Islam, M.R., Bhuiyan, M.K.R. and Rahman, M.S. (2011). Genetic divergence in potato *(Solanumtuberosum*L.).*Bangladesh J. Agril. Res*. **36**(1): 165 – 172.

Sharma, B.D. (1990). Selection criteria for early potatoes (*Solanumtuberosum*L.).*J. Indian Potato Assoc.* **17**: 219–221.

Shashikamal, (2006).Variability, character correlations and genetic divergence studies in potato (*Solanumtuberosum*L.).*Ph.D. (Ag.) Thesis*.G.B.P.U.A. & T., Pantnagar.

Singh, S.V., Kumar, D., Pandey, S. K. and Gaur, P. C. (1997).Evaluation of advanced stage potato hybrids for processing.*J. Indian Potato Assoc*. **24**(3-4): 1241– 27.

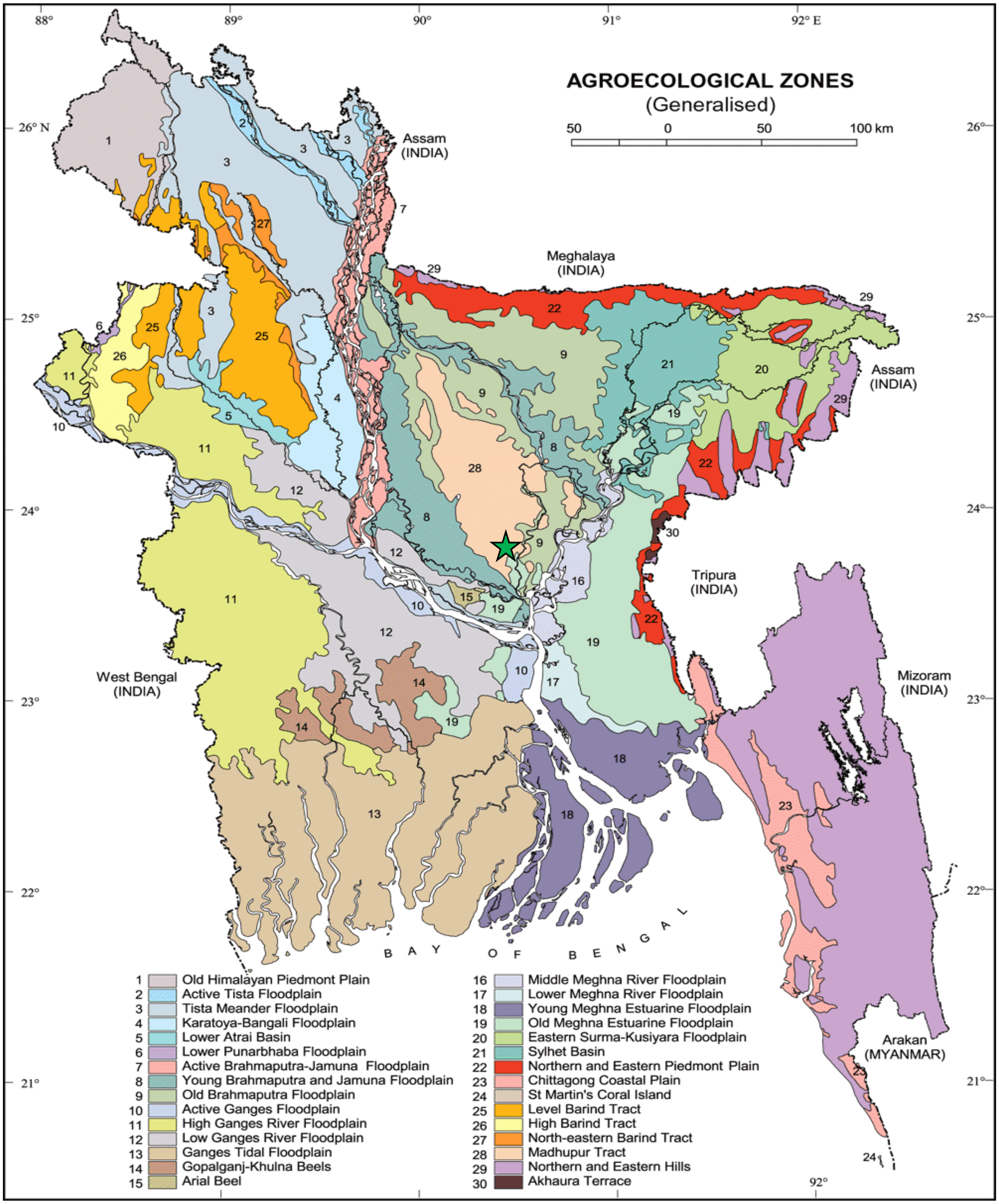
Warner, J.N. (1952). Method for estimating heritability.*Agron. J.* **44**: 427–30.

Wright, S. 1921. Correlation and causation.*J. Agric. Res.* **20**:55–7585.

Yildirim, M. B.; Budak, N.; Midikoglu, N. (1996). Genetic variability among the potato clones originated from *tuberosa*X *andigena*crosses. *Turkish J. Field crops*.**1(2)**: 48–52.

APPENDICES

Appendix I. Map showing the experimental site under the study



★ The experimental site under the study

Appendix II: Morphological, Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	**%**	**Methods employed**
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

C. Chemical composition of the soil

Sl. No.	**Soil characteristics**	**Analytical data**	**Methods employed**
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Farmgate, Dhaka

Appendix III. Analysis of variance for different characters in potato genotypes

Characters	**Mean sum of square**		
	Replication (r-1) = 2	**Genotype (g-1) = 19**	**Error (r-1)(g-1) = 38**
Plant height (cm)	11.38	29.88**	4.30
Primary branches per plant	3.07	6.58**	0.95
Secondary branches per plant	14.16	19.03**	3.22
Leaf length (cm)	0.20	1.57**	0.27
Leaf breadth (cm)	0.09	1.08**	0.17
Tuber length (cm)	16.20	179.35**	27.91
Tuber breadth (cm)	11.94	45.40**	11.64
No. of tuber per plant	2.79	45.97**	4.93
Individual weight of tuber (g)	466.27	472.51**	79.23
Tuber weight loss (%) 20 DAH	10.96	8.20**	3.51
Tuber yield per plant (g)	8,475.50	53,789.50**	8,813.13
Yield ton per ha	18.54	62.72**	9.97

**: Denote Significant at 1% level of probability

Appendix IV. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2017 to February, 2018.

	Air temperature (ºc)		**Relative humidity (%)**	**Rainfall (mm) (total)**	**Sunshine (hr)**
	Maximum	**Minimum**			
November, 2017		18.0	77	227	**5.8**
December, 2017	32.4	16.3	69	0	**7.9**
January, 2018	29.1	13.0	79	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.7**

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka – 1212