ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN AGRO-MORPHOGENIC TRAITS OF TOMATILLO (*Physalis ixocarpa* Brot.) GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled, " ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN AGRO-MORPHOGENIC TRAITS OF TOMATILLO (*Physalis ixocarpa* Brot.) GENOTYPES." 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. REJAUL KARIM, Registration No. 09-03676, 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 been duly acknowledged.

Dated: June, 2016
Place: Dhaka, Bangladesh

Prof. Dr. Naheed Zeba
Supervisor

Dedicated to

My

Beloved Parents

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
and others (*at elli*)	*et al.*
Bangladesh Agricultural Research Institute	BARI
Centimeter	cm.
Days After Sowing	DAS
Days After Transplanting	DAT
Days to 1st flowering	DFF
Days to 50% flowering	D50%F
Days to maturity	DM
Degree Celcius	^{o}C
fruit diameter	FD
fruit length	FL
Fruit yield/plant	FYP
gram (s)	g
Horticulture Research Centre	HRC
Kilogram	Kg
Kilogram/hectare	Kg/ha
Least Significant Difference	LSD
Lycopene content	LC
Meter	M
Muriate of Potash	MP
negative log of the activity of the hydrogen ion	P^{H}
No. of branches/plant	BPP
No. of fruits/plant	FPP
Number of cluster/plant	NCP
Number of fruits/cluster	FPC
Percent	%
Plant height	PH
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Single Fruit weight	SFW
ton/hectare	t/ha
Triple Super Phosphate	TSP
Vitamin C content	VCC

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MD. REJAUL KARIM

Abstract

An experiment was conducted at experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, during the period from October 2014 to April 2015 to estimate genetic variability, heritability and genetic advance in agro-morphogenic traits of tomatillo (*Physalis ixocarpa* brot.) genotypes. Four genotypes were used in the study. The genotypes were PI001, PI002, PI003 and PI004. Data were collected on days to first flowering, days to 50% flowering, number of branch per plant, number of fruits per plant, average fruit weight, fruit length, fruit diameter and fruit yield per plant. Genotype 3 (PI003) was the highest performer in terms yield (3.07 kg/plant). Genotype 1 (PI001) and genotype 2 (PI002) show earliness in flowering. No. of branch per plant and fruits per plant were highest in genotype 4 (PI-4) while the highest average fruit wt. was shown in genotype 1 (PI001). Av. fruit wt., FL, FD show significant positive correlation with yield while days to flowering, no. of branch per plant and no. of fruits per plant correlate negatively. Least difference between GCV and PCV for NBPP, AFW and FYPP indicate that variation is due to the environment.

CHAPTER I

INTRODUCTION

The tomatillo (*Physalis ixocarpa* Brot.) is a fruit vegetable and belongs to the family solanaceae bearing round or spherical and green or green-purple fruit. The basic chromosome number of Tomatillo is n=12 and most species are diploid (Menzel, 1951). The tomatillo fruit is surrounded by an inedible, paper-like husk formed from the calyx (Waterfall, 1967). From outside it looks like a common weed of our country "Foshka Begun". At maturity stage, it fills the husk and can split it open by harvest. The husk turns brown gradually. The freshness and greenness of the husk are quality criteria. Inside the husk, tomatillo fruits look same as green tomato but inside the fruit it is compact, firm and bright green. From inside, it has juicy pulp and tiny seeds. Green and Purple color and tart flavor are the main culinary contributions of tomatillo fruit. Tomatillos originated in Mexico and distributed in India, Australia, South Africa and Kenya. About ten years ago the crop began to be industrialized in Mexico and agro-industries are currently estimated to process 600 tonnes per year (FAO, 2015). Recently it was also introduced in Bangladesh by the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University in 2013. In this research tomatillo was evaluated and compared with a similar species tomato (*Solanum lycopersicum* L.).

Tomatillo contain Energy 32 Kcal, Carbohydrates 5.84 g, Protein 0.96 g, Total Fat 1.02 g, Dietary Fiber 1.9g, Vitamins (Folates7 µg, Niacin 1.850 mg, Pyridoxine 0.056 mg, Thiamin 0.044 mg, Vitamin A 114 IU, Vitamin C 11.7 mg, Vitamin E 0.38 mg, Vitamin K 10.1 µg), Sodium 1 mg, Potassium 268 mg, Calcium 7 mg, Copper 0.079 mg, Iron 0.62 mg, Magnesium 20 mg, Manganese 0.153 mg, Phosphorus 39 mg, Selenium 0.5 µg, Zinc 0.22 mg, Carotene-ß 63 µg, Carotene-α 10 µg, Lutein-zeaxanthin 467 µg (Yamaguchi, 1983).

A recently-discovered set of naturally occurring phytochemical compounds called withanolides, such as Ixocarpalactone-A, is one of the compounds in tomatillo found to be not only antibacterial, but also a natural cancer fighter. Traditional healers in India have been known to prescribe foods containing these compounds as a tonic for arthritis and other musculoskeletal conditions, even if they didn't know why it worked.

Tomatillo can be used as cooking vegetables, fried vegetables, salad and in processing industries like sauces, pickles etc. Mexican salsa is very popular in Mexico, USA and other adjacent countries. The total volume of table sauces, pickled, and other items processed in Louisiana is around 22,277,000 kg with an estimated value of $58,427,000. Table sauces accounted for approximately 77% of the total volume (Broussard and Hinson, 1988). *P. ixocarpa* is gaining ground as a new crop in California due to the increased popularity of Mexican food in the United States (Quiros, 1984).

Information regarding genetic variability, heritability and genetic advance among different genotypes of tomatillo is very important for their improvement. Analysis of genetic variability, heritability and genetic advance of agro-morphogenic traits are useful in selecting genetically diverse parental combinations, dependable classification of accessions and for intra and inter-genus crossing. Considering the above facts, the present study was therefore undertaken,

- to evaluate the performance of yield and yield contributing traits of tomatillo and compare with tomato,
- to recognize the genetic variability among various tomatillo and tomato genotypes,
- to study the genetic relationship between yield and yield contributing characters among the various tomatillo and tomato genotypes,
- to select parental materials for future breeding package.

CHAPTER II

REVIEW OF LITERATURE

High degree of genetic variability in tomatillo cultivars made demand for more research. There are a number of cultivated and wild species of tomatillo which show some similarities and also some dissimilarity. But scientists from around the world are now noticing the wild tomatillo, and wondering if it might provide a major medicinal breakthrough. They have found compounds from the wild tomatillo that have strong anticancer properties against breast cancer, skin cancer, thyroid cancer and brain cancer in their early studies (Pearce, 2012).

The need for the maintenance of wild species, local varieties and outdated genotypes in gene banks is evident, which have become an important form of gene maintenance (Gepts, 2006). However, in order to determine the extent of genetic diversity the accessions in gene banks should be characterized and evaluated, which would allow the selection of genotypes of interest in breeding program. (Balestre *et al.*, 2008; Terzopoulos and Bebel, 2008).

Tomato is a well-studied crop species for breeding, genetics and genomics in plants. Various resources are accessible now for its research, which can lead to uprising in evaluation of tomato biology (Barone *et al*., 2008). Many studies have been done using different genes to examine its genetic diversity (Asamizu and Ezura, 2009; Carelli *et al*., 2006; Martinez *et al*., 2006).

2.1 Nomenclature, Origin and distribution

The tomatillo (*Physalis ixocarpa* Brot.) is widely cultivated in Mexico from the pre-Columbian time and it is there an indispensable vegetable for preparing hot sauces with chilli and for other dishes (Estrada-Trejo *et al*., 1994). It is also cultivated in Russia, in home gardens from the time of Vavilov expeditions (Medvedev, 1958). This species is native to Mexico and Central America, and it is presently one of the most important crops in Mexico (Cantwell *et al*., 1992).

According to Plata (1984), tomatillos originated in Mexico and were cultivated in the pre-Columbian era.

The tomato (*Solanum lycopersicum L.*), is a species with a narrow genetic base. The introduction of the species in Europe, from Mexico, was pivotal in the reduction of genetic variability, since in the European habitat tomatoes were generally cultivated in protected environments. This protected the wild forms, then allogamous, from the action of wind and insect pollinators, culminating in the maintenance of a germplasm adapted to autogamy only (Foolad, 2007).

According to "International Plant Name Index" and "Slow Food ® Upstate", in 1753, Linnaeus placed the tomato in the genus *Solanum* as *Solanum lycopersicum* and in 1768 Philip Miller moved it to its own genus, naming it *Lycopersicon esculentum*. This name came into wide use, but was in violating of the plant naming rules. Genetic evidence has now shown that Linnaeus was correct to put the tomato in the genus *Solanum*, making *Solanum lycopersicum* the correct name (Natural History Museum; Peralta and Spoonar, 2001). Both names, however, will probably be found in the literature for some time.

The word "tomato" comes from the Spanish word, *tomate*, which in turn comes from the Nahuatl (Aztec language) word *tomatotl*. It first appeared in print in 1595. A member of the deadly nightshade family, tomatoes were erroneously thought to be poisonous (although the leaves *are* poisonous) by Europeans who were suspicious of their bright, shiny fruit. Native versions were small, like cherry tomatoes, and most likely yellow rather than red (Filippone, 2014).

The scientific species epithet *lycopersicum* means "wolf peach", and comes from German werewolf myths. These legends said that deadly nightshade was used by witches and sorcerers in potions to transform themselves into werewolves, so the tomato's similar, but much larger, fruit was called the "wolf peach" when it arrived in Europe (Hammerschmidt and Franklin, 2005).

Tomato originated from South America, which is widely grown in both temperate and tropical regions of the world and constitutes a major agricultural industry. Tomato is an excellent model system for plant genetic studies (Benor *et al*., 2008).

The tomato is native to western South America and Central America (Filippone, 2014). The cultivated tomato originated in the Peru-Ecuador-Bolivia area of the South American (Vavilov, 1951). Genetic variation in modern cultivars or hybrids is limited (Chen *et al*., 2009). It is estimated that cultivated tomato genome contains less than 5% of the genetic variation of the wild relatives (Miller and Tanksley, 1990).

2.2 Variability

The fundamental key to achieve the genetic improvement of a crop through a proper breeding programme is to assess the amount and nature of variation of plant characters in breeding population. It helps the breeder for improving the selection efficiency. For this reason, many researchers studied variation in tomatillo and tomato. It has been suggested by Yi *et al*. (2008) that domestication and inbreeding dramatically reduced the genetic variation.

The success of any crop improvement programme depends on the presence of genetic variability and the extent to which the desirable trait is heritable. Genetic variability can be estimated using both morphological and molecular markers. The presence of genetic variability in the breeding material has been emphasized by previous researchers (Reddy *et al*., 2013; Singh, 2009; Shuaib *et al*., 2007).

A field experiment was carried out to study the genetic variation among twenty five tomato genotypes that helped in the reliable varietal selection programme for breeding. All tomato accessions were analyzed by two parameters e.g. morphological and molecular parameters. This study showed that plant height, fruit size and color show variability (Naz *et al*., 2013). Another experiment using nineteen exotic collections of tomato, Reddy *et al*. (2013) revealed considerable genetic variability for characters which was pertaining to the growth, earliness, yield and quality. Fruit weight, plant height and number of fruits per plant contributed to the total variation.

A field experiment was conducted at CCSHAU, Hisar during spring-summer 2013 to study the genetic variability, Heritability and Genetic Advance for quantitative and qualitative traits in tomato. With 27 genotypes including two checks in randomized block design with three replications. A high degree of significant variation was observed for all the characters studied except for number of branches, ascorbic acid and equatorial diameter of fruit (Nalla *et. al*., 2016)

Singh *et al.* (2005) conducted a field experiment on 15 advance generation breeding lines of tomato, to study the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter content and observed significant differences among the genotypes under normal conditions, whereas differences were not significant under high temperature conditions. The population mean was higher during November than February planting for all the characters except acid content and TSS.

A field experiment was carried out by Shashikanth *et al.* (2010) to study the genetic variation among 30 tomato genotypes and observed that the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight.

Multivariate and biochemical analysis of genetic affinity among tomato genotypes are necessary before setting any experiment for their improvement (Alam *et. al*., 2012).

Estimation of Morphological traits can provide a simple technique of quantifying genetic variability and simultaneously assessing genotypic performance under relevant growing environments (Shuaib *et al*., 2007).

An experiment was conducted by Kumari *et al*. (2007) for days to flowering, days to maturity, number of fruits per branch, plant height etc. and found that there were highly significant differences for all the characters among parents except early yield, total yield and days to flowering.

The Kenyan tomato germplasm evaluation by Agong *et al.* (2001) showed a significant variation in the quantitative traits among the accessions. The average fresh and dry weight of fruit varied significantly among the accessions. Most of the landraces gave lower fresh and dry fruit weight than the market cultivars.

Considerable genetic variability was found in an experiment among 18 indigenous and exotic tomato cultivars for five economic characters (plant height, number of branches per plant, number of fruits per plant, average fruit weight and yield) in Orissa, India during rabi 1998-99 conducted by Mohanty and Prusti (2001).

The fundamental key to achieve genetic improvement of a crop through a proper breeding program is to find out the amount and nature of variation among the population. The assessment helps breeder for improving the selection efficiency. Many researchers studied variation in tomato but in case of tomatillo it is not widely studied. Therefore some researchers found similar growth habit and characters between tomato and tomatillo. Here, some of the results are discussed on tomato as such research materials on Tomatillo are not available.

2.2.1 Days to first flowering

Abak *et al.* (1994) found earliness in first flowering in *P. ixocarpa* (Brot.) and *P. peruviana* L. species of tomatillo in green house, low tunnel and open field experiment where Cuartero *et al*. (1983) found 4 days earliness in first flowering under cultivation condition.

Farzaneh *et al.* (2013) showed earliness in days to first flowering while studying combining abilty from a 9x9 diallele cross, whereas no significant differences were found for this character (Monamodi *et al.*, 2013). Remarkable variation were reported among the 26 tomato genotypes for days to first flowering ranging between 49.67 and 68.33 days (Matin and Kuddus, 2001).

Kumari *et al.* (2007) recorded data for total soluble solids, dry matter content, reducing sugars, titratable acidity, ascorbic acid, lycopene, days to flowering, days to maturity, number of fruits per bunch, weight per fruit, fruit length, fruit width, number of fruit bearing branches, total number of fruits per plant, plant height, early yield and total yield and found that there were highly significant differences for all the characters among parents except acidity, early yield, total yield, and days to flowering. Pre-flowering periods of the varieties ranged from 56 to 76 days were reported by Geogieva *et al.* (1969). The phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering (Matin, 2001; Aditya, 1995).

2.2.2 Days to 50% flowering

No significant difference was found in days to 50% flowering among 23 genotypes of Tomatillo (Abak *et al.*, 1994). A field experiment was done using 27 tomato genotypes and reported days to 50% flowering (1.14%) contributed very little for variability (Nalla *et al.*, 2014). Narolia (2012), studied in 55 genotypes of tomato and found high variability for all the characters studied except number of branches per plant and days to 50% flowering. Significant genotype x environment interaction was observed for number of days to 50% flowering (Ravindra *et al.*, 2003).

Baishya *et al.* (2001) conducted a 9 × 9 half diallel analysis in tomato and observed that most of the crosses out of 36 exhibit desirable negative heterosis over better parent for days to 50% flowering.

2.2.3 Number of branches per plant

Cuartero *et al.* (1983) found positive correlation with yield and no. of branch per plant. Menzel (1951), in an experiment observed that no. of fruits, no. of flowers, no. of fruits increase with no. of primary branches per plant. Singh *et al.* (2005) conducted a field experiment with 30 tomato and five genotypes among them showed higher number of primary branches than the control. The maximum number of fruits per plant was obtained from one of the five higher branching genotypes. Singh (2005), observed PCV was slightly higher than GCV for number of branches per plant.

An experiment was conducted with 30 tomato genotypes to study their genetic variability and significant difference for number of primary branches per plant was reported among them (Shravan *et al*., 2004). Ravindra *et al.* (2003) observed significant genotype × environment interaction for number of primary branches.

2.2.4 Number of Fruits per plant

Abak *et al.* (1994) found positive correlation between no. of primary branches and no. of fruits per plant in Tomatillo, where, Moriconi *et al.* (1990) found profuse flowering and fruit setting in Louisiana. Cuartero *et al.* (1983) observed that no. of fruits per plant of Tomatillo increases in cultivated condition where Mulato-Brito *et al.* (1985); found that no. of fruits per plant varies among different species of Tomatillo.

Prajapati *et al.* (2015) evaluated 39 diverse genotypes of tomato at Vegetable Research Farm, Rewa (Madhya Pradesh) during the *Rabi* session of 2011. Analysis of variance showed significant variation among the genotypes for all evaluated traits. Number of fruits plant^{-1} showed the highest genotypic and phenotypic variance. Twenty-six genotypes of tomato were assessed to determine the nature and magnitude of variability, correlation, and path coefficient analysis between yield and yield-contributing characters. Correlation indicated that yield was significantly and positively associated with number of fruit per plant and per cluster (Kumar *et al.*, 2013).

Seventeen diverse genotypes of tomato were evaluated by Thakur (2009) for their performance and interaction with changing environments through the characters like fruit yield, number of fruits/plant. The analysis of variance indicated highly significant differences between the genotypes and environments for all the characters studied. Saeed *et al*. (2007) observed that coefficient of variation was greater in traits such as number of fruits per plant followed by number of flowers per plant and yield per plant. Joshi *et al.* (2003) observed the number of fruits per plant show the highest phenotypic and genotypic coefficient of variation. The number of fruits per plant had positive effects on the yield and negative effects on average fruit weight (Mohanty, 2003).

Brar *et al.* (2000) studied phenotypic and genotypic co-efficient of variation in tomatoes and observed high variability in the number of fruits per plant. Wide range of genotypic variation for number of fruits per plant was reported by Islam *et al.* (1996). Hundred thirty nine genotypes of tomatoes were evaluated and estimated phenotypic and genotypic variances, phenotypic and genotypic co-efficient of variation. Number of fruits per plant show significant variation (Reddy and Reddy, 1992)

2.2.5 Fruit weight

Cantwell *et al*. (1992) observed that both the variances were high for individual fruit weight in the study of genetic variability with different tomatillo genotypes. Abak *et al*, (1994) found direct positive relationship with yield and no. of fruits per plant.

Twenty-six genotypes of tomato were assessed to determine the nature and magnitude of variability, correlation, and path coefficient analysis between yield and yield-contributing characters. The analysis of variance (ANOVA) revealed highly significant differences among all genotypes for the characters. Path analysis at the genotypic level indicated that fruit weight had the most positive direct effect on yield per plant (Kumar *et al.*, 2013).

Shravan *et al.* (2004) analyzed genetic variability with 30 tomato genotypes in Utter Pradesh of India and reported remarkable difference for average fruit weight among the genotypes. A field experiment was carried out by Mohanty *et al.* (2003) to study genetic variability of 18 tomato genotypes and observed that the average fruit weight had direct positive effects on the yield and indirect negative effects on number of fruits per plant.

Singh *et al.* (2002) in an experiment with heat tolerant tomato found that average fruit weight has the highest phenotypic (PCV) and genotypic (GCV) coefficients of variation.

Matin and Kuddus (2001), reported that varietal differences were significant among different cultivars of tomato for average fruit weight. Similar results for average fruit weight were found by Brar *et al*. (2000). A field experiment with 4 genotypes of tomato, Ahmed (1987), reported that a wide range of variation was observed for individual fruit weight.

2.2.6 Fruit length

Mulato-Brito *et al.* (1985); found fruit length and fruit diameter has direct positive correlation with yield per plant. Similar results was also observed by Cantwel *et al.*, (1992). Twenty-six genotypes of tomato were assessed to determine the nature and magnitude of variability, correlation, and path coefficient analysis between yield and yield-contributing characters. The analysis of variance (ANOVA) revealed highly significant differences among all genotypes for the characters. Path analysis at the genotypic level indicated that fruit weight had the most positive direct effect on yield per plant followed by number of fruits per plant, fruit diameter, and number of fruits per cluster (Kumar *et al.*, 2013).

Kumari *et al.* (2007); conducted an experiment and recorded data for fruit length and found highly significant differences among parents. High PCV for fruit length was reported by Singh *et al*. (2002).

2.2.7 Fruit diameter

An experiment was done by Kumar *et al.* (2013) with twenty-six genotypes of tomato to determine the nature and magnitude of variability, correlation, and path coefficient analysis between yield and yield-contributing characters. The analysis of variance (ANOVA) revealed highly significant differences among all genotypes for the characters. Path analysis at the genotypic level indicated that fruit weight had the most positive direct effect on yield per plant followed by number of fruits per plant, fruit diameter, and number of fruits per cluster.

Saleem *et al.* (2013) examined twenty-five F_1 hybrids generated from 5×5 diallel crosses to study the quantitative genetics of yield and some yield related traits and found fruit diameter was the most heritable trait. Similar results were observed by Anupam *et al.* (2002) evaluated 30 genotypes of tomato. Singh *et al.* (2002); also reported that PCV was highest for fruit diameter.

2.2.8 Yield per plant

Abak *et al.* (1994) found highest GCV for yield per plant in *P. ixocarpa* (Brot.) and *P. peruviana* L. species of tomatillo in green house, low tunnel and open field experiment. Procelli and Proto (1991), found direct positive correlation in yield per plant with no. of flower per plant, fruits per plant and fruit weight.

Evaluation of five tomatillo Mexican landraces including altogether 13 accessions was performed under environmental conditions of Ontario, Canada and Chapingo in central Mexico. The measured traits were: beginning of flowering and harvest, total number of harvested fruits and the yield. In both localities accessions 1 and 3 of the Rendidora landrace as well as the accession 1 of the Manzano landrace were the earliest and the highest yielding (Mulato-Brito and Pena-Lomeli, 2007).

Fourty eight genotypes of tomato were evaluated for their genetic variation using Mahalar statistics by Singh *et al*. (2006) and observed that characters like number of fruits per plant, av. fruit wt., plant height and fruit yield per plant have highest contribution on genetic variations.

Significant differences for yield plant^{-1} was reported by Matin and Kuddus (2001) among the genotypes tested. Sachan (2001), conducted an experiment with several tomato genotypes and observed remarkable differences among the genotypes for yield plant^{-1}. Higher genotypic co-efficient of variation for average yield plant^{-1} was reported by Kumar and Tewari (1999) among thirty two genotypes of tomato.

2.3 Heritability and genetic advance

Plant Selection based on phenotypic characteristics is the most important tools for all breeding practices. Selection efficiency for yield depends on heritability. Character with higher heritability has higher selection efficiency. To judge the potentiality for breeding of a population for further improvement through selection, heritability and genetic advance are the most important parameters. Researchers of the world have studied heritability and genetic advance of yield and yield contributing characters. The literatures very relevant to the present study are reviewed below:

Saleem *et al.* (2013) conducted an experiment of quantitative genetics of yield and yield contributing traits. Number of fruits per plant shows the highest estimates of GCV and PCV while fruit diameter was the most heritable trait. In an experiment, Buckseth *et al*. (2012) found high heritability with high genetic advance for the number of fruits plant^{-1}, av. fruit wt., yield plant^{-1} and pericarp thickness indicate that the heritability is most likely due to the additive gene effects and selection may be effective.

Narolia (2012) conducted an experiment with 55 genotypes of tomato and found high heritability and high genetic advance as percent of mean for all the characters except days to 50% flowering. High genotypic variance for most of the characters indicating a larger contribution of the genetic component for total variation (Shashikanth *et al.*, 2010).

Twelve varieties of tomatoes were evaluated by Ponnusviamy *et al.* (2010) to determine heritability and observed that high heritability with high genetic advance as percentage of mean for average fruit weight. High heritability with high GCV and genetic gain for fruit weight and fruit yield were found in an experiment with 20 tomato genotypes conducted by Nardar *et al.* (2007). Broad sense heritability was the highest for number of fruits per plant, followed by number of flowers per plant was observed by Padda *et al*. (2007).

Pandit *et al.* (2010) conducted an experiment with twelve tomato varieties to determine heritability and noticed that high heritability along with high genetic advance as percent of mean for average fruit weight. Heritability were high for all the characters and genetic advance was high for plant height in an experiment was observed by Kumari *et al.* (2007). Golani *et al.* (2007) evaluated twenty genotypes of tomato and reported that high heritability with high GCV and genetic gain for fruit weight and fruit yield.

2.4 Correlation co-efficient analysis

2.4.1 Correlation between the characters

To evaluate the relationships between the characters, correlation is the best estimate. It will help the breeder to decide about selection methods. Many of the cases, correlation between yield and yield contributing characters was studied as yield is one of the basic targets to most of the breeders. Yield contributing characters are also interlinked. So, to plan effective breeding program for obtaining maximum yield, association of characters with yield and with its components is very much important.

Correlation analysis may vary due to agro-climatic variations from year to year and place to place. Higher heritability than yield shows that there is positive correlation between these, then there may be chance to increase in total yield by proper selection of that component. Negative correlation co-efficient among yield components indicate selection for any component might not bring change for yield improvement. Many researchers have studied correlation between yield and yield contributing characters. Some of the likely cases are described here.

Kumar *et al.* (2013) evaluated forty nine genotypes of tomato (*Solanum lycopersicum* L.) for various quantitative and quality characters and the analysis indicated that total numbers of fruits per plant were positively correlated with gross yield, marketable yield, number of marketable fruits per plant and plant height and was significant.

Mahapatra *et al.* (2013) found Fruit yield has significant positive correlation with plant height, number of primary branches/plant, number of flower clusters/plant, number of fruits/plant, fruit length, fruit diameter and average fruit weight. Number of primary branches per plant increase with the increase in plant height. Monamodi *et al*. (2013) found positive and significant correlation between no. of branches/ plant with no. of fruits/plant. Fourty genotypes of tomato were studied to find out the correlation among different different traits by Buckseth *et al*. (2012) and found highly significant dissimilarities among the genotypes.

Kumar and Dudi (2011) studied thirty diverse genotypes of tomato and observed that correlation coefficients at the genotypic level were higher than the phenotypic ones and yield/plant was positively and significantly correlated with plant height, fruit number/plant.

Fruit weight is positively and significantly correlated with yield per plant, while number of fruits per plant and fruit weight have negative correlation (Rani *et al*., 2010). A field experiment was conducted by Golani *et al*. (2007) and found that fruit weight and fruit length were significantly and positively correlated.

Correlation co-efficient study was performed by Kumar *et al.* (2006) with 30 tomato genotypes and noticed that number of fruits plant^{-1} had significant and positive correlation with fruit yield plant^{-1}. Manivannan *et al*. (2005) conducted an experiment with cherry for correlation coefficient analysis and perceived that fruit yield was meaningfully and absolutely correlated with the number of leaves and fruit weight.

Joshi *et al*. (2004) done correlation analysis with 37 tomato genotypes and revealed that yield per plant was significantly correlated with average fruit mass, fruit size, plant stature and harvest spell. In case of tomato, Arun *et al.* (2003) detected that, yield per plant was absolutely correlated with average fruit mass and plant tallness. Harer *et al*. (2002) considered correlation of thirty seven tomato genotypes and disclosed that the number of fruits per bunch and number of fruits per plant were expressively and completely correlated with fruit yield per plant.

2.5 Genetic divergence

Genetic divergence has been considered as an essential parameter in crop improvement program to identify the most diverse parents. Highly heterotic F_1 generation can only be found from genetically diverse parents. Many researchers have studied genetic divergence based on Mahalanobis' D^2-statistics. Among them the most relevant current publications are reviewed below:

Nalla *et al*. (2014) carried out an experiment and recorded data on fifteen characters and observed high divergence from fruit yield plant^{-1}, TSS and diameter. Reddy (2013) found that fruit weight show maximum diversity followed by plant height and number of fruits plant^{-1}. Xiaorong *et al*. (2012) in an experiment used 26 phenotypic characters to explore genetic diversity in 67 tomato cultivars. Cluster analysis showed that tomato varieties could be categorized into three clusters at phenotypic levels.

A field experiment was carried out by Shashikanth *et al*. (2010) to perform study on genetic divergence of 30 tomato genotypes and categorized into 10 clusters. He observed no parallelism between genetic diversity and topographical divergence in

Zhu *et al*. (2004) observed large phenotypic variations and significant genetic diversity in wild types. These variations offer great prospective for crop advancement.

CHAPTER III

MATERIALS AND METHODS

This chapter clarifies information regarding methodology, used in implementation of the experiment. It describes a brief statement of experimental site, planting materials, climate and soil, seed bed preparation, design of the experiment, other operations done, data collection methods, statistical analysis procedure etc., which are presented as follows:

3.1 Experimental site

The experiment was conducted at experimental field, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh, during the period from Oct 2014 to April 2015. Location of the site is 23°75' N latitude and 90°34' E longitude with an elevation of 8 meter from sea level under AEZ-28. The experimental site is indicated on the map of AEZ of Bangladesh in (Appendix I).

3.2 Planting materials

Four genotypes were used in the experiment. Among the studied materials, tomatillo seeds of the genotypes were collected from research supervisor. The name and source of collection of these genotypes are presented in Table 1.

3.3 Climate and soil

Experimental site was situated in the subtropical climatic zone, where moderately low temperature prevails during October to March (Rabi season), suitable for tomato cultivation in Bd. The soil was sandy loam in texture and pH was 5.45- 5.61. Information regarding Weather and physico-chemical properties of the soil are presented in Appendix II and Appendix III respectively.

Table1. Name and source of collection of genotypes used in the study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G1	PI001	Mexico
2	G2	PI002	Mexico
3	G3	PI003	Mexico
4	G4	PI004	Mexico

Table 2. Doses of manures and fertilizers used in the study

Sl. No.	Fertilizers/ Manures	Dose (Quantity/ha)
1.	Urea	550 kg
2.	TSP	450 kg
3.	MOP	250 kg
4.	Cow dung	10 ton

3.4 Seed bed preparation and raising of seedling

Seed sowing was done on Oct 19, 2014 in the seedbed. Before sowing, seed treatment was done with Provax. All cultural practices necessary for seed bed were done properly. 23 day old seedlings were transplanted in the main field. Seedlings in the seedbed are shown in Plate 1A.

3.5 Design and layout of the experiment

The experiment was designed in Randomized Complete Block Design (RCBD). Layout of the land is presented in Plate 1C. There were 4 genotypes, 5 replications, spacing was 60 cm × 40 cm and plot size was 70 m^2.

3.6 Land preparation

Land was well ploughed at tilth condition. All fertilizers and cow dung except urea were applied during final land preparation. Land preparation is shown in Plate 1B.

3.7 Transplanting of seedlings

The seedlings were raised in seedbed and 23 days old seedlings were transplanted in the main field on November 12, 2014. Transplanting of seedlings is shown in Plate 1D.

3.8 Manure and fertilizers application

All fertilizers and cow dung except urea were applied during final land preparation. Urea was applied in three split doses. The rate of application is presented in Table 2.

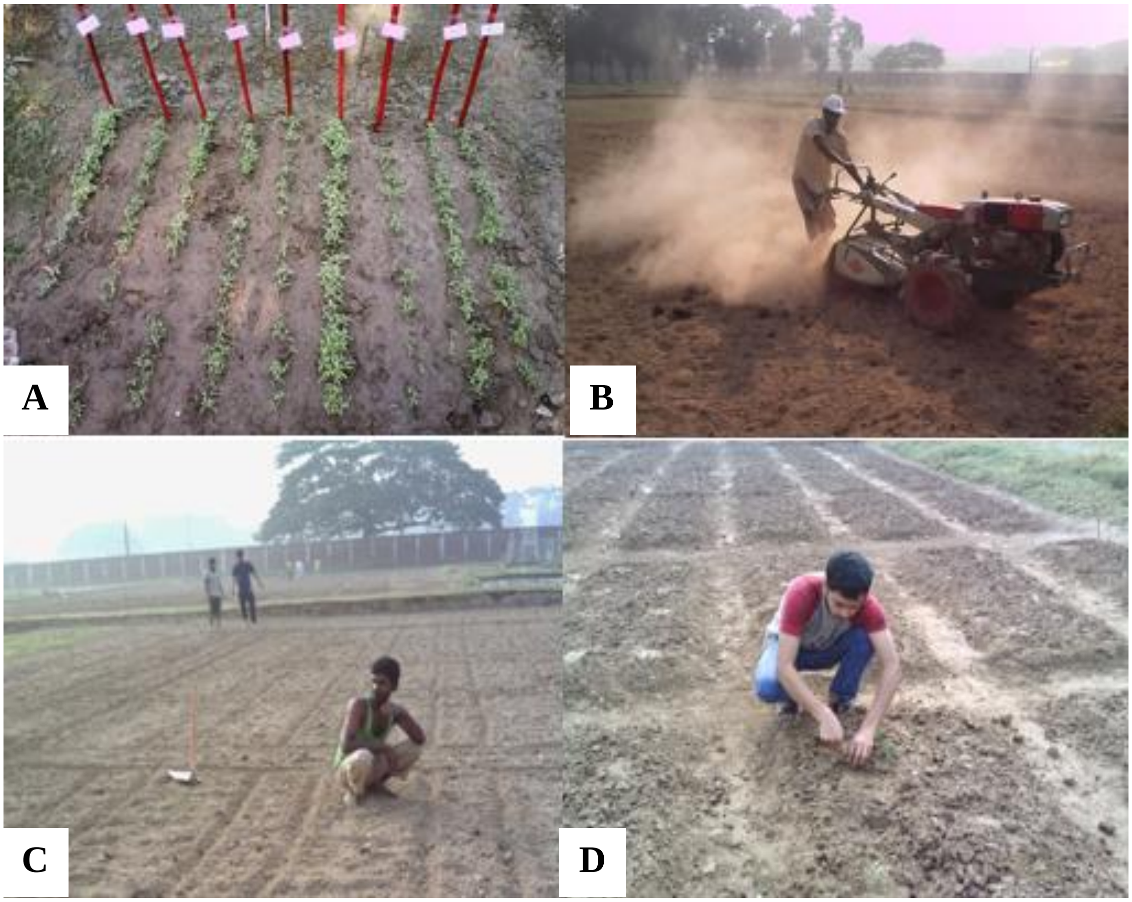

Plate 1. Raising to transplanting of tomatillo seedlings. (A) Seedlings in the seed bed, (B) Main experimental land preparation, (C) Laying out of the main plot, (D) Transplanting of seedlings

3.9 Intercultural operations

Irrigation, weeding, mulching, staking, pesticide application was done properly when required. Different intercultural operation is shown in Plate 2.

3.10 Harvesting and processing

Harvesting was done regularly and time to time.

3.11 Data recording

Five plants from each genotype were selected and tagged. Thus was done in all the three replication. Data were recorded from those plants. The vegetative stage, flowering and fruiting stage for data recording is presented in Plate 3.

3.11.1 Days to first flowering

No. of days from sowing to first flower opening was recorded as days to first flowering.

3.11.2 Days to 50% flowering

Days to 50% flowering were recorded when flower open in nearly about half of the plant.

3.11.3 Number of branches per plant

The number of branches per plant was recorded at 70 days after transplanting. The

3.11.4 Number of fruits per plant

Total number of marketable fruits harvested from each of the five tagged plants was counted and the number of fruits per plant was calculated as average.

3.11.5 Fruit weight (g)

Fruits from the tagged plant harvested and individual fruit weight were calculated as average weight and expressed in grams (g).

3.11.6 Fruit length (cm)

Fruit length was measured from stalk end to bottom end by slide calipers.

Plate 2. Intercultural operation. (A) Watering the seedlings, (B) Stalking the seedling

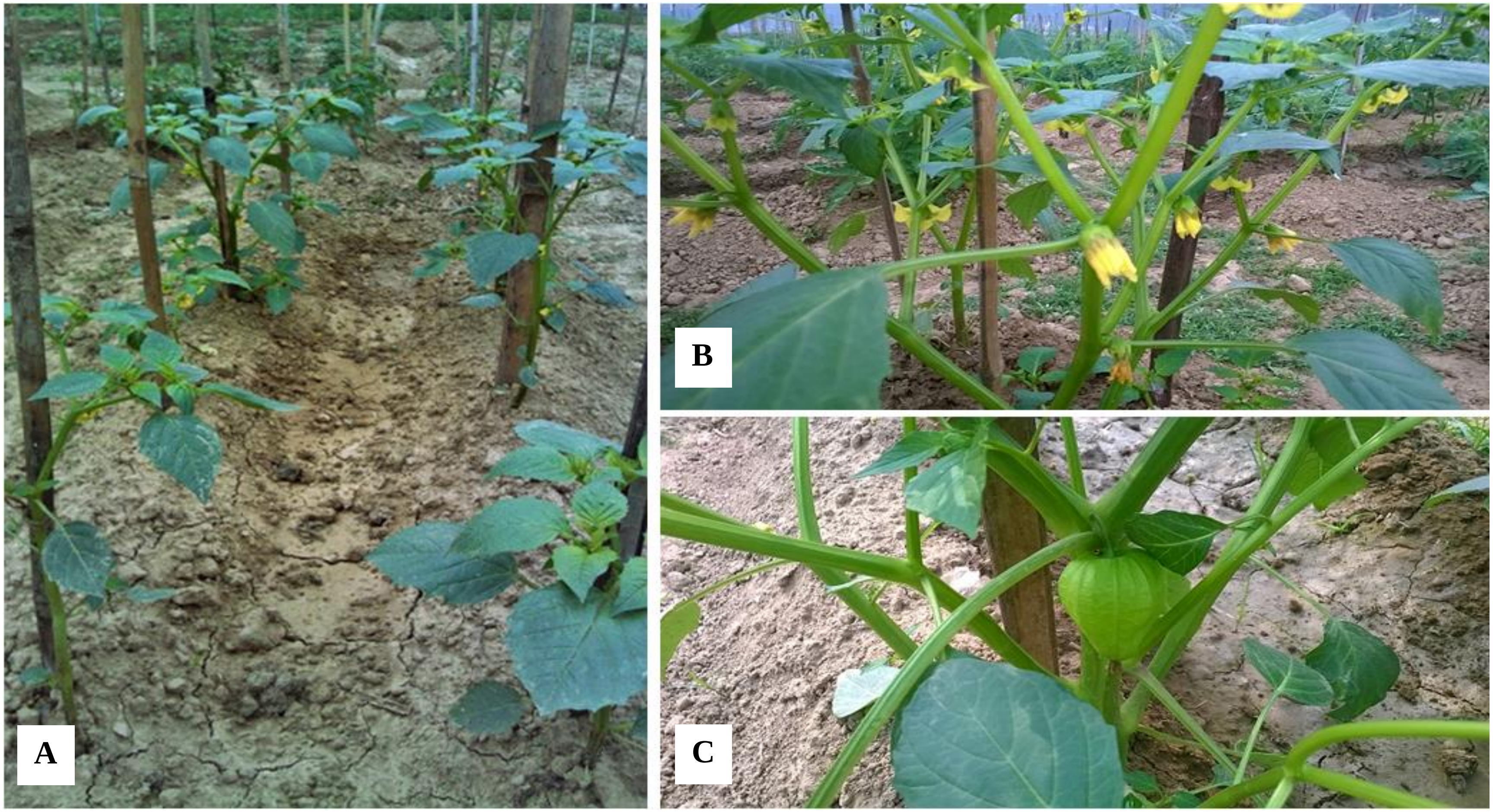

Plate 3. Different stages of tomatillo plant. (A) Flowering stage, (B) Fruiting stage

3.11.7 Fruit Diameter (cm)

Fruit diameter was measured at middle of the stalk end and bottom end by slide caliper.

3.11.8 Fruit yield per plant (kg)

From each picking, weight data was recorded for each of the tagged plant and total weight was calculated and expressed as fruit yield per plant.

3.12 Statistical analysis

Mean data of the characters were exposed to multivariate analysis. Univariate analysis of the individual character was also done for all characters under study using the mean values and was assessed using MSTAT-C computer program. For all the characters, Duncan's Multiple Range Test (DMRT) was performed to test the differences between the genotypic means. Using MSTAT-C, mean, range and co-efficient of variation (CV %) were also estimated. GENSTAT 5.13 and Microsoft Excel 2000 software were used to perform multivariate analysis.

3.12.1 Estimation of genotypic and phenotypic variances

The formula to estimate genotypic and phenotypic variances given by Johnson *et al.* (1955).

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance, $\sigma^2_{ph} = \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

Environmental variance ($\sigma^2 e$) =EMS

Where,

EMS = Mean Square Error

3.12.2 Estimation of genotypic and phenotypic co-efficient of variation

Burton (1952), proposed the following formula to estimate genotypic and phenotypic co-efficient of variation;

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

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 of variation, PCV % = $\frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.12.3 Estimation of heritability

The following formula was used to estimate broad sense heritability, suggested by Johnson *et al.* (1955);

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

Where,

$h^2{}_b$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.12.4 Estimation of 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. σ_p

Or Genetic advance, GA = K. $\frac{\sigma^2{}_g}{\sigma^2{}_{ph}}.\sigma_{ph}$

Where,

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

σ_{ph} = Phenotypic standard deviation

$h^2{}_b$= Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ = Phenotypic variance

3.12.5 Estimation of genetic advance mean's percentage

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

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

3.12.6 Estimation of simple correlation co-efficient:

Simple correlation co-efficients (r) was estimated with the following formula (Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x.\sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.12.7 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations 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 follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

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

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to perform the variability analysis of different genotypes of tomatillo (Physalis ixocarpa Brot.) using yield contributing traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment. The fruits were harvested when they began the color change. The data pertaining to 8 common characters between tomatillo have been presented and statistically analyzed with the possible interpretations.

4.1 Genetic variability, heritability and genetic advance

The mean values for each character of all the genotypes are shown in Table 3. Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of fifteen characters was studied and mean sum of square, phenotypic variance (σ2p), genotypic variance (σ2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 4. The variation in tomatillo fruits are presented in Plate 4.

4.1.1 Days to first flowering

The genotypic variance and phenotypic variance for this trait were 0.54 and 10.5 respectively (Table 4). The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The genotypic co-efficient of variation (GCV) (1.39) and phenotypic co-efficient of variation (PCV) (6.11) were different, indicated presence of high variability in this trait (Table 4). Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Similar findings were reported by Farzaneh *et al.* (2013) and Kumari *et al.* (2007). Matin *et al*. (2001) also found similar results in tomato. In contrast Monamodi *et al.* (2013) and Aditya *et al*. (1995) found in significant difference in days to first flowering. The heritability estimates for days to first flowering was low (5.14%) with low genetic advance (1.11%) and genetic advance in percentage of mean (2.10%) (Table 4). Thus indicating this trait was mostly controlled by non-additive gene. Genetic advances in per cent of mean were low which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for days to first flowering.

4.1.2 Days to 50% flowering

Significant variation was found for days to 50% flowering and it is ranged from 57 days after sowing (DAS) (PI002 and PI003) to 60 DAS in PI004 with mean value 58 (DAS) (Table 3).Present study observed low variance for days to 50% flowering. Similar findings for days to 50% flowering were also observed by Narolia (2012). On the other hand Nalla *et al*., (2014) found dissimilar result with very low variability for this trait. Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low (1.18 and 5.42 respectively) (Table 4). The phenotypic variance appeared to be high than the genotypic variance advised significant influence of environment on the expression of genes governing days to 50% flowering. Many author also found higher PCV than GCV (Singh, 2005 and Samadia *et al*., 2006). Therefore, it can be referring that selection based upon phenotypic expression of this character wouldn't be productive for the improvement of tomato. The heritability estimates for this trait was low (4.75%) with low genetic advance (0.97%) and genetic advance in per cent of mean (1.67%), indicating this trait was controlled by non-additive gene (Table 4). Singh *et al.* (2005) and Kumar *et al.* (2004) support the findings.

4.1.3 Number of branches per plant

Number of branches per plant showed significant difference where maximum number of branches was found 30 in PI-4 and the minimum was recorded 20 in PI001 with mean value 26 (Table 3). The phenotypic variance (17.8) was higher than the genotypic variance (15.63). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 15.21 and 16.23 respectively (Table 4) indicating that the phenotypic expression of this trait is highly governed by the environment. Singh *et al*. (2002) also showed that the PCV was higher than GCV for number of primary branches per plant. The heritability estimates for this trait was high (87.81), genetic advance was moderate (32.20%) and genetic advance in per cent of mean (123.84) (Table 4) were found high, revealed that this trait was governed by non-additive gene. Moderate heritability and low genetic advance for this character was also observed by Kumar *et al.* (2004).

4.1.4 Number of fruits per plant

From the current study we observed that the maximum range for number of fruits per plant was found 378 in PI-4 and the minimum was recorded 69 in PI001 (Table 3). The difference between genotypic (20207.10) and phenotypic (20397.9) variances indicate low environmental influence (Table 4). The phenotypic coefficient of variation (88.85) and genotypic coefficient of variation (88.84) was high, which indicated presence of high variability among the genotypes (Table 4). Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi and Singh (2003) supported the findings. The heritability estimates for this trait was high (99.06), genetic advance (41626.63%) and genetic advance in percent of mean (25895.26%) were found high, revealed that this character was governed by additive gene and selection for this character would be effective (Table 4). This character showed high heritability coupled with high genetic gain which is supported by Ara *et al.* (2009) and Saeed *et al.* (2007).

4.1.5 Average fruit weight (g)

The maximum single fruit weight was recorded 41.35 g in PI001 and where the minimum was recorded 4.9 g in PI004 with mean value 25.97 g (Table 3). The genotypic variance (298.99) and phenotypic variance (300.1) for fruit weight was high (Table-4). The genotypic co-efficient of variation and phenotypic co-efficient of variation were high (67.5 and 67.17 respectively) and similar, proved that environment has little influence of the expression of this character (Table 4). Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High GCV and PCV for average fruit weight were also noticed by Manivannan *et al*. (2005) and Singh *et al*. (2002). High heritability (99.63%) associated with high genetic advance in percent of mean (2388.21%) is and high Genetic advance (615.92%) (Table 4) was observed indicating fruit weight governed by additive gene. Pandit *et al.* (2010), Ara *et al.* (2009) and Singh *et al.* (2006) also supported the present findings.

4.1.6 Fruit Length (cm)

The mean fruit length was noticed as 3.45 cm with a range of 4.9 cm to 1.5 cm. The genotypic and phenotypic variance were very high (286.48 and 290.2 respectively) and genotypic co-efficient of variation (490.60) and phenotypic co-efficient variation (493.78) were close to each other (Table 4), indicating minor environmental influence on this character that would be effective for the improvement of this crop. Singh *et al*. (2002) showed that the phenotypic coefficient of variation was greatest for this character which support the present study. High heritability estimates (98.72%) with high genetic advance (590.15%) over percent of mean (17105.76%) (Table 4) indicate that effective selection may be made for fruit length. Moderate heritability and moderate genetic gain for this character was observed by Joshi *et al.* (2004).

4.1.7 Fruit Diameter (cm)

The mean fruit diameter was 3.93 cm with a range of 5.7 cm to 1.7 cm (Table 3). The phenotypic and genotypic variance were very high (373.92 and 377.0 respectively) and genotypic co-efficient of variation (492.04) and phenotypic co-efficient variation (494.06) (Table 4) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement. Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character which does not support the present study. High heritability estimate (99.18%) with high genetic advance (770.28%) over high percent of mean (19599.88%) (Table 4) indicate that effective selection may be made for fruit length. High heritability coupled with low genetic gain for this character was observed by Pandit *et al*. (2010).

4.1.8 Fruit yield per plant (kg)

Fruit yield per plant was found 3.07 kg in PI-3 which is highest and the lowest was recorded 1.86 kg in PI004 with mean value 2.14 kg (Table 3). The phenotypic variance (0.35) is similar to genotypic variance (0.4) (Table 4), suggested no influence of environment on the expression of the genes controlling this character. The phenotypic coefficient of variation and genotype coefficient of variation were 25.50 and 23.86, respectively for fruit yield per plant, which indicating that significant variation exists among different genotypes which made the trait effective for selection (Table 4). Similar findings supported by Singh *et al*. (2006) and Manivannan *et al*. (2005). Estimation of high heritability (87.50%) for fruit yield per plant with low genetic advance (0.72%) and moderate Genetic advance of % mean (29.07%) (Table 4) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding programme. High heritability and high genetic advance was also observed by Ara *et al.* (2009) and Anupam *et al.* (2002).

Table 3. Mean analysis of growth, yield and yield contributing parameters

G	DFF	D50F	NBPP	NFPP	AFW	FL	FD	FYPP
G1	52	58	20	69	41.35	4.9	5.7	2.87
G2	53	57	25	119	17.81	2.6	2.9	2.12
G3	52	57	29	77	39.83	4.8	5.4	3.07
G4	55	60	30	378	4.90	1.5	1.7	1.86
Min	52	57	20	69	4.9	1.5	1.7	1.86
Max	55	60	30	378	41.35	4.9	5.7	3.07
Mean	53	58	26	160.75	25.97	3.45	3.93	2.48
$LSD_{0.05}$	2.17	2.12	1.01	9.52	0.73	1.33	1.21	0.08
CV%	5.94	5.35	5.55	8.63	4.11	5.47	4.36	4.94

DFF= Days to first flowering, D50F= Days to 50% flowering, NBPP= no. of branch per plant, NFPP= Number of fruits per plant, AFW= Average fruit weight (g), FL= Fruit length, FD= Fruit Diameter, FYPP= Fruit yield per plant (kg) and YIELD= Yield per Ha (Ton)

Table 4: Estimation of genetic parameters in eight characters of tomatillo

Traits	MS	$σ^2g$	$σ^2e$	$σ^2P$	GCV	ECV	PCV	h^2b (%)	GA (5%)	GA(% mean)	CV(%)
DFF	7.25**	0.54	9.96	10.5	1.39	5.95	6.11	5.14	1.11	2.10	5.94
D50F	7.12**	0.47	9.45	9.9	1.18	5.30	5.42	4.75	0.97	1.67	5.35
NBPP	80.33**	15.63	2.17	17.8	15.21	5.67	16.23	87.81	32.20	123.84	5.55
NFPP	101226.27**	20207.10	190.77	20397.9	88.43	8.59	88.85	99.06	41626.63	25895.26	8.63
AFW	1496.06**	298.99	1.13	300.1	67.05	4.12	67.17	99.63	615.92	2388.21	4.11
FL	1436.14**	286.48	3.73	290.2	490.60	55.98	493.78	98.72	590.15	17105.76	5.47
FD	1872.68**	373.92	3.06	377.0	492.04	44.51	494.06	99.18	770.28	19599.88	4.36
FYPP	1.75**	0.35	0.02	0.4	23.86	5.70	25.50	87.50	0.72	29.07	4.94

DFF- Days to 1st flowering, **D50F**- Days to 50% flowering, **NBPP**- No. of branches/plant, N**FPP**-No. of fruits/plant, **AFW**- Average Fruit weight (g), **FL**- fruit length (cm), **FD**- fruit diameter (cm), **FYPP**- Fruit yield/plant (g), **YIELD=** Yield per Ha (Ton)

Plate 4. Fruits of four different genotypes of tomatillo. A. PI001, B. PI002, C. PI003, D. PI00

4.2 Correlation Co-efficient

Correlation studies provide a better understanding of the association of different characters with fruit yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). As we know yield is a complex product being influence by several inter-dependable quantitative characters. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Phenotypic and genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomato are given in Table 5 and Table 6.

4.2.1 Days to first flowering

Days to first flowering had nonsignificant negative correlation with fruit yield per plant at genotypic level (-0.492) (Table 5). Patil and Bojappa (1993), Mayavel *et al.* (2005) and Samadia *et al.* (2006) observed positive correlation which does not support the present findings. This character showed highly significant positive association at both genotypic and phenotypic levels with days to 50% flowering (1.000 and 0.996) (Table 5 and Table 6). Days to first flowering had positive but non-significant correlation with average fruit weight, fruit length and fruit diameter at both level. This trait had non-significant negative correlation at both levels for number of branch per plant, number of fruits per plant and average fruit weight.

4.2.2 Days to 50% flowering

Days to 50% flowering showed non-significant negative association with no. of branch per plant, number of fruits per plant, and fruit yield per plant (kg) at both levels (Table 5 and Table 6). Dhankhar *et al.* (2006) and Samadia *et al.* (2006) observed positive correlation. Non-significant positive relation found with with average fruit weight (g), fruit length and fruit diameter at genotypic and phenotypic level. Non- significant association of this trait with yield indicated that the association was largely influenced by environment. Improvement can be achieved by selection for days to 50% flowering were reported by Wright *et al*. (2007).

4.2.3 Number of branches per plant

The number of branches per plant had positive and highly significant correlation with no. of fruit per plant (0.696 and 0.680) at genotypic and phenotypic levels (Table 5 and Table 6). Monamodi *et al*. (2013) found more branch number in a plant will produce more fruits. But a negative correlation between the number of branches per plant and number of fruits per plant was noticed by Singh *et al*. (2005). The number of branches per plant showed highly significant negative relation for average fruit weight (-0.840 and -0.820) at both levels indicated that the association between these traits is largely influenced by genetic factors. It showed non-significant negative relation with fruit length, fruit diameter and fruit per plant at both level indicating environmental effect. A positive correlation between yield of fruits per plant and number of branches per plant was observed by Singh *et al*. (2006) and Ara *et al.* (2009).

4.2.4 Number of fruits per plant

It had nonsignificant and negative association with yield per plant (-0.288 and 0.281) at genotypic and phenotypic levels respectively (Table 5 and Table 6). Rani *et al.* (2010) reported that the number of fruits per plant was negatively associated

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

	DFF	D50F	NBPP	NFPP	AFW	FL	FD	FYPP
DFF	1.00**	0.86**	0.18	0.37	-0.35	-0.29	-0.31	-0.26
D50F		1.00**	0.07	0.38	-0.32	-0.30	-0.31	-0.24
NBPP			1.00**	0.52*	-0.45	-0.42	-0.43	-0.26
NFPP				1.00**	-0.88**	-0.84**	-0.85**	-0.81**
AFW					1.00**	0.99**	0.99**	0.96**
FL						1.00**	1.00**	0.95**
FD							1.00**	0.95**
FYPP								1.00**

* = Significant at 5%, ** = Significant at 1%

DFF- Days to 1st flowering, **D50%F**- Days to 50% flowering, **NBPP-** No. of branches/plant, N**FPP-**No. of fruits/plant, **AFW**- Average Fruit weight (g), **FL**- fruit length (cm), **FD**- fruit diameter (cm), **FYPP**- Fruit yield/plant (g), **YIELD** = Yield per Ha.

Table 6. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomatillo

	DFF	D50F	NBPP	NFPP	AFW	FL	FD	FYPP
DFF	0.96**	0.71**	0.15	0.30	-0.29	-0.24	-0.28	-0.22
D50F		0.85**	0.04	0.31	-0.26	-0.25	-0.28	-0.20
NBPP			0.97**	0.51*	-0.39	-0.37	-0.40	-0.22
NFPP				0.93**	-0.82**	-0.79**	-0.82**	-0.77**
AFW					0.94**	0.94**	0.96**	0.92**
FL						0.95**	0.97**	0.91**
FD							0.97**	0.91**
FYPP								0.96**

* = Significant at 5%, ** = Significant at 1%

DFF- Days to 1st flowering, **D50%F**- Days to 50% flowering, **NBPP**- No. of branches/plant, **NFPP**-No. of fruits/plant, **AFW**- Average Fruit weight (g), **FL**- fruit length (cm), **FD**- fruit diameter (cm), **FYPP**- Fruit yield/plant (g), **YIELD** = Yield per Ha.

with yield per plant. The number of fruits per plant had significant negative correlation average fruit weight,fruit length and fruit diameter at both level. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight (Table 5 and Table 6).

4.2.5 Average fruit weight (g)

Average fruit weight showed highly significant and positive correlation with fruit length (0.677 and 0.670) for both levels (Table 5 and Table 6). Matin *et al*. (2001) found that individual fruit weight had significant positive correlations with yield per plant. Arun *et al*. (2004) and Joshi *et al*. (2004) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight. Megha *et al*. (2006) also found similar results for this trait in tomato. It had non-significant positive effect at both levels for fruit diameter and yield per plant. Matin *et al*. (2001) found significant negative correlations between number fruits per plant and individual fruit weight.

4.2.6 Fruit length (cm)

Fruit length had highly significant and positive correlation with fruit diameter (0.966 and 0.960) and average fruit wt. (0.677) at both level and non-significant positive correlation with yield per plant (0.521 and 0.506) at both level (Table 5 and Table 6).

4.2.7 Fruit diameter (cm)

Fruit diameter showed positive relation with fruit yield per plant (0.505 and 0.499) at both level (Table 5 and Table 6). Fruit diameter also showed significant positive relation with fruit length at both level and nonsignificant positive relation with average fruit weight at both level. On other hand, fruit diameter was highly negatively associated with number of fruits per plant at both the levels. So, with increase in fruit length, increase in fruit diameter and increase in no. of fruit per plant, decrease in fruit diameter.

4.2.8 Fruit yield per plant

In general, fruit yield is the main target of improvement breeding. Thereby its correlation study is utmost important. From Table 5 and 6 it is observed that, fruit yield per plant (FYP) was positively correlated with Average fruit weight (AFW), fruit length and fruit diameter at both genotypic and phenotypic level. Similar result was also reported by several authors. Rani *et al*. (2010) conducted an experiment with tomato and found average fruit weight (AFW) along with some other fruit quality (like pericarp thickness and lycopene content) was positively and significantly associated with fruit yield per plant (FYP). Findings' of Weber *et al.* (2010) also evidenced the positive and strong association between FYP and AFW. Singh and Cheema (2006) reported positive indirect effects through AFW mainly contributed towards its strong association with yield. This study also revealed positive and significant correlation between FYP and fruit length (FL) and fruit diameter (FD) at genotypic level (0.105 and 0.110 respectively). Strong association between FYP and FD and FL were reported earlier (Susic, 2002).

Again, fruit yield per plant (FYP) showed negative association with days to first flowering, days to 50% flowering, no. of branch per plant and no. of fruit per plant at both genotypic and phenotypic level. Inconsistently, number of fruits per plant (FPP) manifested strong positive association with fruit yield per plant (FYP) in several earlier investigations (Kumar *et al*., 2004; Kumar *et al*., 2003 and Singh *et al*., 2004). Dhankar and Dhankar (2006) reported number of fruit per plant had the highest direct effect on yield per plant. But, in more recent study, Rani *et al*. (2010) investigated negative association between numbers of fruit per plant with fruit yield. Less fruit number enabled high single fruit weight and thereby high positive correlation between SFW and FYP established in the present study.

CHAPTER V

SUMMARY AND CONCLUSION

The present study was undertaken at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh, with four genotypes of tomatillo (*Physalis ixocarpa* Brot.) during October 2014 to April 2015. Seeds were sown in seed bed and then transferred to the main field in Randomized Complete Block Design (RCBD) with five replications. Data on various yield attributing characters such as, days to first flowering, days to 50% flowering, days to maturity, number of branch per plant, number of fruit per plant, fruit weight (g), fruit length (cm), fruit diameter (cm) and yield per plant (kg) were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

Tomatillo is an eco-friendly crop as there is no need of pesticide spray for insect and pest control. It was found that the yield of tomatillo is almost three times more in Bangladesh than in its origin Mexico. Tomatillo plants are highly self-incompatible and require cross- pollination, so we have to plant at least two plants for the blooms to be pollinated and fruit to be produced. Tomatillo becomes ready to be cut from the plant when the fruit is green, but has filled out the husk. Left to ripen further, the fruit will frequently split the husk and turn yellow.

The number of fruit yield per plant showed highest range of variation (1.28 to 3.07 kg) that means wide range of variation present for this character.

In case of days to first flowering, days to 50% flowering, number of fruits per plant, fruit length and fruit diameter, showed higher influence of environment for the expression of these characters. On the other hand, branch per plant, Av. Fruit wt., and fruit yield per plant showed least difference in phenotypic and genotypic variance suggesting additive gene action for the expression of the characters. All the characters under the present study exhibit the highest value of heritability.

Correlation coefficients among the characters were studied to define the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study. Significant positive correlation with yield was found in AFW, FL and FD. Significant negative correlation with yield was found in NFPP. Non-significant negative correlation with yield per plant was found in days to first flowering, days to 50% flowering and no. of branch per plant at genotypic and phenotypic level, respectively.

From the findings of the present study, the following conclusions could be drawn:

i. Tomatillo could be a promising crop in Bangladesh as they are high yielding

ii. Selection should be applied for desired characters such as lowest days to first flowering and increased number of fruits per plant, fruit weight, fruit diameter and fruit length to develop high yielding varieties.

iii. Inter genotypic crosses program could be taken.

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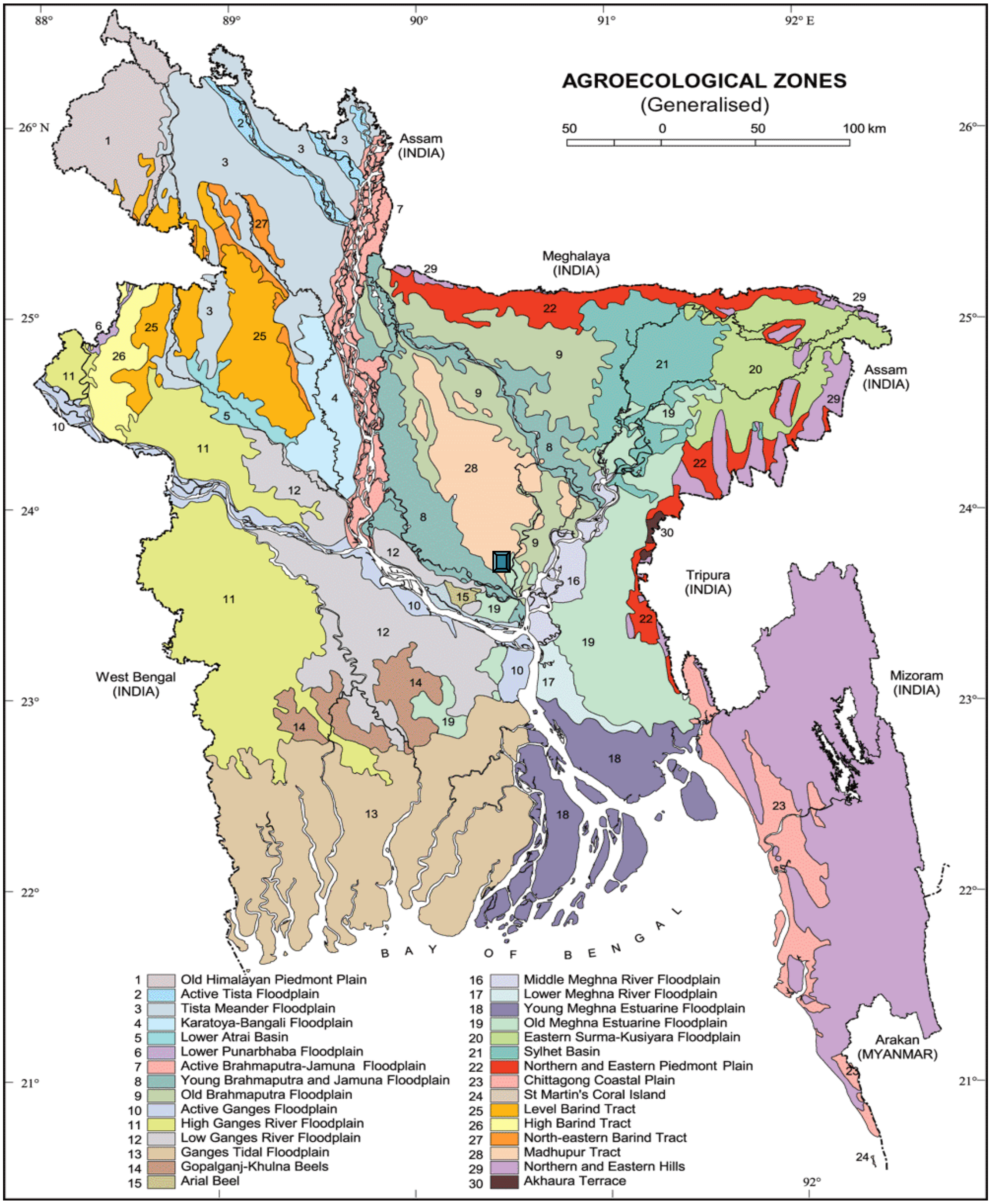
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from October 2014 to March 2015

Month	Year	Monthly average air temperature (^{o} C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum	Mean			
Oct	2014	29.36	18.54	23.95	74.80	Trace	218.50
Nov	2014	28.52	16.30	22.41	68.92	Trace	216.50
Dec.	2014	27.19	14.91	21.05	70.05	Trace	212.50
Jan.	2015	25.23	18.20	21.80	74.90	4.0	195.00
Feb.	2015	31.35	19.40	25.33	68.78	3.0	225.50
Mar.	2015	32.22	21.25	26.73	72.92	4.0	235.50

Source: Bangladesh Meteorological Department (Climate division), Agargaon Dhaka-1212.

Appendix III. **The mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 - 15 cm depth).**

Mechanical composition:

Particle size constitution

Sand	:	40%
Silt	:	40%
Clay	:	20%
Texture	:	Loamy

Chemical composition:

Soil characters	:	Value
Organic matter	:	1.44 %
Potassium	:	0.15 meq/100 g soil
Calcium	:	3.60 meq/100 g soil
Magnesium	:	1.00 meq/100 g soil
Total nitrogen	:	0.072
Phosphorus	:	22.08 µg/g soil
Sulphur	:	25.98 µg/g soil
Boron	:	0.48 µg/g soil
Copper	:	3.54 µg/g soil
Iron	:	262.6 µg/g soil
Manganese	:	164 µg/g soil
Zinc	:	3.32 µg/g soil

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka

Appendix IV. Showing tomatillo plant with profuse branching and fruit setting at SAU experimental field.

Appendix V. Showing a part of experimental field of the present study

Appendix VI. Showing a part of experimental field of the present study with research supervisor