GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN F_1 AND F_2 POPULATIONS OF TOMATILLO (*Physalis ixocarpa* Brot. / *Physalis philadelphica* Lam.)

S. M. AHSAN-WZ-ZAMAN

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

December, 2020

GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN F_1 AND F_2 POPULATIONS OF TOMATILLO (*Physalis ixocarpa* Brot. / *Physalis philadelphica* Lam.)

BY

S. M. AHSAN-WZ-ZAMAN

REGISTRATION NO: 17-08220

A Thesis
submitted to the Faculty of Agriculture
Sher-e-Bangla Agricultural University, Dhaka
in partial fulfillment of the requirements
for the degree of

DOCTOR OF PHILOSOPHY

IN

GENETICS AND PLANT BREEDING

Approved by:

Prof. Dr. NaheedZeba
Chairman
Advisory Committee

Prof. Dr. MD. Sarowar Hossain Member Advisory Committee	Prof. Dr. Jamilur Rahman Member Advisory Committee	Prof. Dr. A.K.M. Ruhul Amin Member Advisory Committee

Naheed Zeba, PhD
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh
Tel: 88-02-44814079
Mobile: +8801913091772
E-mail: naheed0359@yahoo.com
zeban@sau.edu.bd

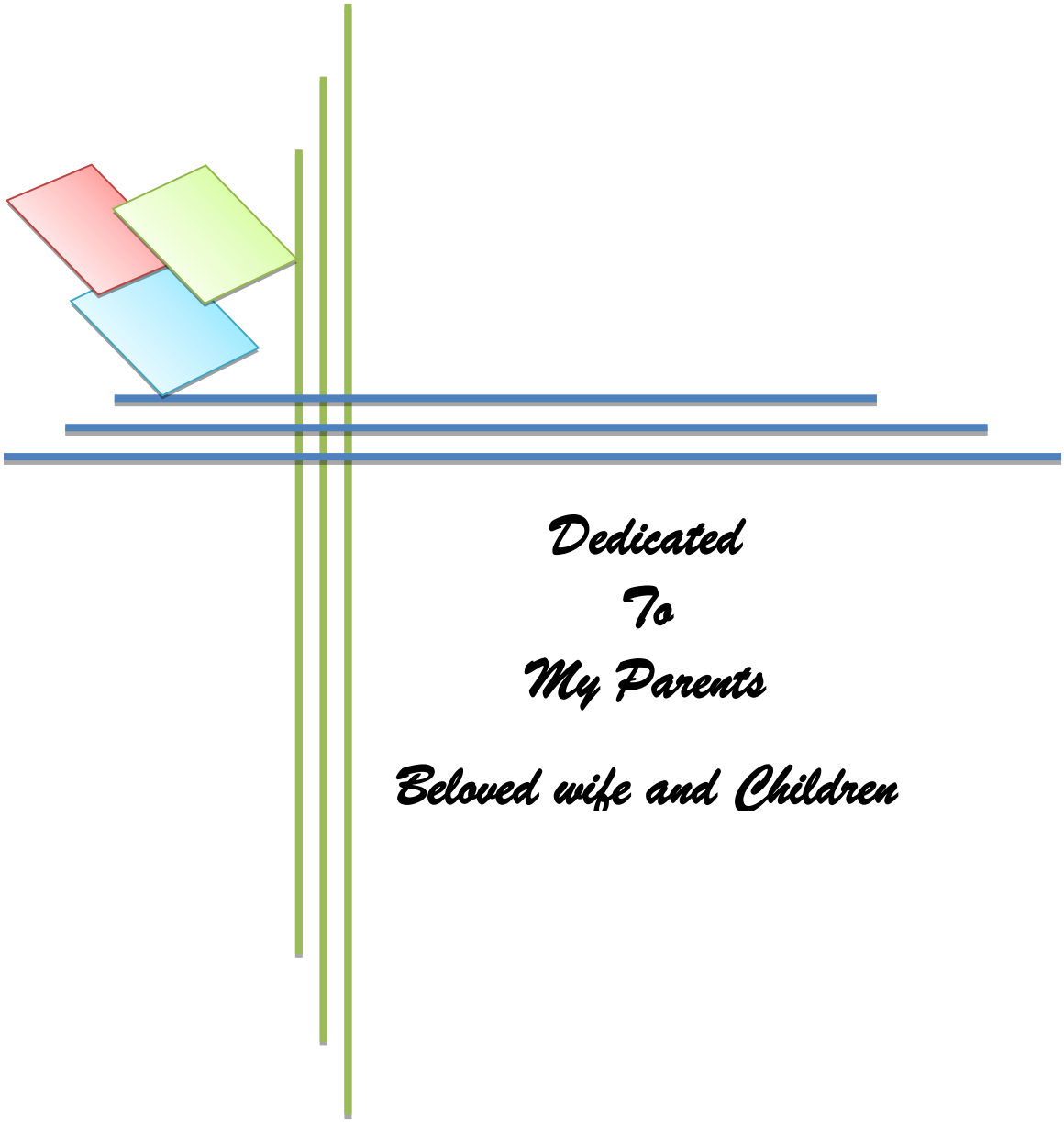
CERTIFICATE

This is to certify that thesis entitled "GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN F_1 AND F_2 POPULATIONS OF TOMATILLO (Physalis ixocarpa Brot./Physalis philadelphica Lam.) submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of ***DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by S.M. Ahsan-wz-zaman, Registration No: 17-08220 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 been acknowledged by him.

Dated: December, 2020
Place: Dhaka, Bangladesh

(Prof. Dr. NaheedZeba)
Supervisor



Dedicated

To

My Parents

Beloved wife and Children

SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviation	Full word	Abbreviation
Accession	Acc.	Incorporated	*Inc.*
Agriculture	*Agric.*	Information	*Inf.*
Agricultural	*Agril.*	International	*Intl.*
Agro-ecological zone	AEZ	Journal	*J.*
Analysis of variance	ANOVA	Kilogram	Kg
And others / Co-workers	*et al.*	Least Significant Difference	LSD
Applied	*Appl.*	Mid parent	MP
Archives	*Arch.*	Millimeter(s)	mm
Backcross	BC	Muriate of Potash	MOP
Bangladesh Bareau of Statistics	BBS	Negative logarithm of hydrogen ion concentration (-log $[H^+]$)	pH
Biology	*Biol.*		
Botany	*Bot.*	Non-significant	^{ns}
Better parent	BP	Number	No.
Breeding	*Breed.*	Percentage	%
Centimeter	cm	Phenotypic Coefficient of Variation	PCV
Coefficient of variation	CV		
Cross between two dissimilar parents	×	Principal component analysis	PCA
		Principal co-ordinate analysis	PCO
Critical Difference	CD	Proceedings	*Proc.*
Days After Sowing	DAS	Randomized Complete Block Design	RCBD
Degrees of Freedom	Df		
Degree Celsius	°C	Replication	*Rep.*
Ecology	*Ecol.*	Research	*Res.*
Economic	*Econ.*	Review	*Rev.*
Environment	*Environ.*	SCA variance	σ^2s
Etcetera	etc.	Science	*Sci.*
Experimental	*Expt.*	Serial	Sl.
First filial generation	F_1	Sher-e-Bangla Agricultural University	SAU
For Example	e.g.		
GCA variance	σ^2g	Society	*Soc.*
General	*Gen.*	Specific combining ability	SCA
Genetic advance	GA	That is	i.e.
General combining ability	GCA	The second generation of a cross between two dissimilar parents	F_2
Genetics	*Genet.*		
Genotypic Coefficient of Variation	GCV	Triple Super Phosphate	TSP
Gram	g	University	*Univ.*
Hectare	ha	Variety	*var.*
Heretability in broad sense	h^2b	Videlicet (namely)	*viz.*
Heretability in narrow sense	h^2n	Weight	wt.

ACKNOWLEDGEMENT

Alhamdulillah, all the praises and gratitude to the omniscient to almighty "Allah" the supreme ruler of the universe who enabled the author to pursue his higher study and to complete the research work as well as to submit the thesis for the degree of Doctor of Philosophy (Ph.D.) in Genetics and Plant Breeding from Sher-e-Bangla Agricultural University, Dhaka, Bangladesh.

The author expresses his deepest sense of gratitude, sincerest appreciation, profound thankfulness and indebtedness to his research Supervisor and Chairman of the Advisory Committee, Prof. Dr. Naheed Zeba, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for her boundless interest, scholastic guidance, valuable advices, co-operation, critically reviewing and all round help during the entire period of research work and in preparing the dissertation.

The author is highly obliged and expresses his heartfelt appreciation and gratitude to the other honorable members of the Advisory Committee, Prof. Dr. Md. Md. Sarowar Hossain and Prof. Dr. Jamilur Rahman, Department of Genetics and Plant Breeding, SAU, Dhaka and Prof. Dr. A.K.M. Ruhul Amin, Department of Agronomy, SAU, Dhaka for their valuable advices, suggestions, inspiration and cordial co- operation to complete the courses and the research work successful.

The author expresses his heartiest respect and indebtedness to Prof. Dr. Abdur Rahim, Chairman of the Department of Genetics and Plant Breeding. He is also thankful to all the honorable teachers and friendly staffs of the Department of Genetics and Plant Breeding, SAU, Dhaka for their teaching, sincere co-operation and inspiration throughout the period of the study.

A special thanks to his friends and family members, classmates Zubair & Nasrat, labmates AB Siddique & Nabila for their supports and inspirations throughout the study period. Finally, he is grateful to his spouse and daughters for their unconditional love and continuous support, immense patience and tolerance for bringing his dream to proper shape.

The Author

LIST OF CONTENTS

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF CONTENTS (CONT´D)

LIST OF TABLES

LIST OF TABLES (CONT'D)

LIST OF TABLES (CONT'D)

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

GENETIC ANALYSIS OF YIELD AND ITS COMPONENTS IN F_1 AND F_2 POPULATIONS OF TOMATILLO (*Physalis ixocarpa* Brot. / *Physalis philadelphica* Lam.)

By

S. M. AHSAN-WZ-ZAMAN

ABSTRACT

A tomatillo (*Physalis ixocarpa* Brot. /*Physalis philadelphica* Lam.) core collection consisting of five parental genotypes *viz*., SAU tomatillo 1 (G1), SAU tomatillo 2 (G2), PI003 (G3), PI004 (G4) and PI005 (G5) was explored for variation in plant growth, yield and fruit quality traits, in order to develop improved plants with desirable traits from subsequent tomatillo diallel crossing program. Twenty F_1 populations of tomatillo were derived from 5x5 diallel crosses to combine desirable genes from different parents and to produce pure-breeding progeny superior in many respects to the parental types. F_2 population was developed in order to select superior genotyes as the greatest genetic variability exists in the F_2 population and the most effective selection occurs there. The experiments were conducted at replicated plots following RCBD design in the central experimental field and central laboratory of Sher-e-Bangla Agricultural University, Dhaka during Oct/2017 to Mar/2020. Analysis of variance for agromorphogenic traits of five parental and twenty hybrids of tomatillo showed significant variation in yields and in quality traits. Maximum yield was found in parent G3 (740.67 g/plant), in F_1 population G1×G3 (1060.66 g/plant) and in F_2 population G1×G3 (1021.33 g/plant). Cross ability analysis of tomatillo showed excellent cross ability in G3, G1 and G4 and their crosses in three years. Estimation of heterosis, assessment of combining ability and gene actions for different characters were performed. Maximum standard heterosis was found in G1×G3 (19.35%) followed by G1×G2 (10.94) for yield/ha. These crosses deserve attention for their heterotic responses. The ANOVA of combining ability analysis showed highly significant results for most characters which suggested the presence of both additive and non-additive gene action for inheritance. The GCA effects revealed that the parents G1and G3 showed the best general combiner. The highest positive significant SCA effect was found in G3×G1 (11.51**) and the cross G1×G3 was the best specific combiner for yield per ha. Genetic analysis in F_1, F_2 populations revealed that both additive and non-additive genetic effects were important for different characters. Extent and direction of heterosis in F_1 varied greatly for different characters. Diallel analysis was performed using the Hayman's approach chiefly comprises the aspects, Hayman's ANOVA, Vr, Wr analysis with graphical representation and components of variation and genetic parameters. Vr-Wr graph suggested that partial dominance and/or over dominance gene actions were involved for all the characters in F_1. The ranks of parental dominance were: G5 > G4 > G1 > G2 > G3 in the increasing order for the trait yield. Magnitude of E for each character was much less compared to their respecting D and H1 suggesting the characters were influenced less by environment. The ratio of (H2/4H1) estimated the average frequency of positive and negative alleles in all the parents. The significant correlation was found in fruit pH, lycopene content (502) and fruit moisture content at genotypic level and in fruit moisture and lycopene content at phenotypic level. Based on the value of yield components, the highest selection score was found in G1×G3 (1065.57) having ranked 1 followed by G1×G2 (1032.15) with rank 2. The lowest ranked genotype was found in G2×G4 (701.66) with rank of 20 followed by G4×G2 (725.09) having ranked 19. The highest selection score was found in G1×G3 (18.719) having ranked 1 followed by G3×G1 (17.409) with rank 2 for quality traits. G1×G3 and G1×G2 could be recommended for further selection trial for higher yield towards variety development of tomatillo. Different gene actions underlying these traits provides valuable insight in the further selections and can be used to support breeding strategies for tomatillo crop improvement.

CHAPTER I
INTRODUCTION

Tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam. (2n = 2x = 24), known as Mexican husk tomato, belongs to Solanaceae family. It is popular as green or green-purple tomato, berry compote, miltomate or jam berry. The Spanish name translates to “little tomato". The unripe fruit is a bit tart, slightly sweet and sour with a hint of citrus and is the key ingredient for Mexican table chili sauces known as salsa verde (green sauce). Fully ripe fruits are eaten raw, like tomatoes or it can be dried like raisins. It is native to Mexico where different types and varieties are cultivated in the pre-columbian era, with significant variability in berry size, color and flavour (Singh *et al*., 2013). Now-a-days both cultivated and weedy annuals have been introduced and appreciated worldwide due to its wider adaptability. A staple of Mexican cuisine, they are eaten raw or cooked in a variety of dishes, particularly salsa verde. It looks as the "Foshka Begun" which appears to be a widespread plant in our nation. It can fill the husk and split it open by harvest when it reaches maturity. Gradually, the husk becomes brown. The husk's freshness and greenness are quality indicators. Tomatillo fruits resemble green tomatoes while they are in their husk, but they are compact, firm, and bright green inside. It’s inside is filled with a delicious flesh and small seeds. The primary culinary features of tomatillo fruit are its vibrant green and purple color and sour flavor. Tomatillo plant is herbaceous and indeterminate, sprawling and annual.

Tomatillos are a key ingredient in fresh and cooked Mexican and Central American green sauces. The green color and tart flavor are the main culinary contributions of the fruit. Purple and red-ripening cultivars often have a slight sweetness, unlike the green- and yellow-ripening cultivars, so generally are used in jams and preserves. About thirty years ago the crop began to be industrialized in Mexico and agro-industries are currently estimated to process 600 tons per year. Eighty percent of production is exported to the United States as whole tomatillos, without a calyx and canned. While the remain is used in the preparation of packaged sauces for the domestic market. In 2019, husk tomato production in Mexico was 834,274 ton, (Alafita-Vásquez *et al*., 2021). In Bangladesh, tomatillo is a very new crop. In 2013, Department of Genetics and Plant Breeding of Sher-e-Bangla

Agricultural University has brought it to Bangladesh and after multi-location yield trials, two tomatillo varieties were released as SAU tomatillo 1 and SAU tomatillo 2.

The fruits have tremendous nutritional and health benefits. It is rich in vitamin A, B, B2, C and polyphenols (Gonzalez-Mendoza *et al*., 2010; Sarangi *et al*., 1989: Brazanti and Monaresi 1980). Furthermore, recent scientific evidences pointed out the importance of health promoting compounds in husk tomato in relation to their high level of antioxidants including vitamin C and phenolic compounds. Many researchers also reported that ripe fruit have significant antioxidant properties and can be used as functional foods (Medina-Medrano *et al*., 2015, González-Mendoza *et al*., 2010). Tomatillo provide 32 Kcal of energy, 5.84 g of carbohydrates, 0.96 g of protein, 1.02 g of total fat, 1.02 g of dietary fiber, and 1.9 g of vitamins (folates, niacin, pyridoxine, thiamin, 114 IU of vitamin A, 11.7 mg of vitamin C,0.38 mg of vitamin E, and 1.850 mg of thiamin), K 10.1 mg), Sodium 0.1 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 mg, Zinc 0.2mg, Carotene-ß 63 mg, Carotene- 10 mg, and Lutein-zeaxanthin 467 mg (Yamaguchi, 1983).

Cultivation practices are common to most of the solanaceous plants. Its advantages include saving on seed, reduced weeding and the possibility of starting the cycle while there is still another crop on the ground as well as shortening the growing cycle.

Genetic improvement work in Mexico was aim to get plants with larger and firm fruits; higher yield, wide adaptation and resistance to viral diseases and powdery mildew. Heterosis and combining ability analysis was done for explorations and collect the better parent from both cultivated materials and wild plants found in cultivated fields as to consolidate the gene banks and contribute materials and information towards the genetic improvement program for this crop.

Development of tomatillo requires information on genetic variability, heritability, and genetic progress across various genotypes. Availability of natural and/or generated genetic variability is a prerequisite for any crop improvement and to develop superior cultivars as it provides a wide scope for the selection. The effectiveness of selection depends on the nature, extent, and magnitude of genetic variability present in the material and the degree of heritability. Selection of

genetically varied parental combinations, accurate classification of accessions, and intra- and inter-genus crossing all benefit from analysis of genetic variability, heritability, and genetic advancement of agro-morphogenic features. Genetic variability is the first step for a successful breeding program for any crop species and a successful survey of genetic variability is important before aiming to high yielding variety development. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al*., 1955). The co-relation co-efficient between yield components usually show a complex chain of interacting relationship. Path co-efficient analysis partitions the components of co-relation co-efficient into direct and indirect effects and visualizes the relationship in more meaningful way. In spite of genetic variability, current study aimed to determine correlation and path coefficients between twenty genotypes to establish selection criteria which might help to develop genotypes for high yielding.

Considering the prospect and above-mentioned aspects the present study was undertaken with following objectives:

1. To analyze the genetic variability in parental genotypes of tomatillo.
2. To know the cross-ability analysis of tomatillo genotypes.
3. To estimate the heterosis, combining ability and gene action in F_1 generations of tomatillo.
4. To determine the variability, direct and indirect relationship between yield and yield contributing characters and selection of superior genotypes in F_2 populations.
5. To determine the variability, direct and indirect relationship between nutritional characters and selection of superior genotypes in F_2 populations.

CHAPTER II
REVIEW OF LITERATURE

The tomatillo (*Physalis philadelphica* Lam. and *Physalis ixocarpa* Brot.), also known as the Mexican husk tomato, is a plant of the nightshade family bearing small, spherical and green or green-purple fruit of the same name (Morton, 1987). Tomatillos originated in Mexico and were cultivated in the pre-Columbian era (Plata, 1984). A staple of Mexican cuisine, they are eaten tomatillo as raw and cooked in a variety of dishes, particularly salsa verde.

The wild tomatillo and its related plants are found everywhere in the Americas except in the far north, with the highest diversity in Mexico. In 2017, scientists reported on their discovery and analysis of a fossil tomatillo found in the Patagonian region of Argentina, dated to 52 million years BP. The finding has pushed back the earliest appearance of the Solanaceae plant family of which the tomatillo is one genus (Wilf *et al.*, 2017). Tomatillos were domesticated in Mexico before the coming of Europeans, and played an important part in the culture of the Maya and the Aztecs, more important than the tomato. (Small, 2011). The specific name philadelphica dates from the 18th century (Small, 2011).

Tomatillo is adaptable to a wide range of soils light sandy, loamy and clay and requires well-drained soils. It could grow in semi-shade or no shade and dry or moist soil (El Sheikha, 2004). Physalis fruit and juice are nutritious, containing particularly high levels of niacin, carotenoids, and minerals (El Sheikha *et al*., 2008). Moreover, many medicinal properties have been attributed to Physalis. A decoction is used in the treatment of abscesses, cough, fevers or sore throat (Duke and Ayensu, 1985). A single plant may yield up to 0.5 kg fruits and carefully tended plants can provide 20–33 tons/hectare (Dremann, 1985). Fruits are longer lasting, can be stored in a sealed container and kept in a dry atmosphere for several months and possible to freeze as well (Coffey, 1993).

Tomatillo is a species native to Mexico and Central America and it is, for the time being, one of the most important vegetable crops in Mexico (Cantwell *et al*., 1992) ranking in the fourth place in planted area (47.472 ha) among commercially cultivated vegetables (Anonymous, 2011) introducing recently in Bangladesh may be promising.

2.1 Nomenclature, origin and distribution

The name tomatillo came from Nahuatl, tomatl is also known as husk tomato, Mexican ground cherry, large-flowered tomatillo, or Mexican husk tomato. Some of these names, however, can also refer to other species in the genus *Physalis* (Small, 2011). Other names are Mexican green tomato and miltomate. In Spanish, it is called tomate de cáscara (husk tomato), tomate de fresadilla (little strawberry tomato), tomatemilpero (field tomato), tomate verde (green tomato), tomatillo (Mexico;this term means "little tomato" elsewhere), miltomate (Mexico, Guatemala), frarolito(little lantern), or simply tomate (in which case the tomato is called jitomate from Nahuatl xitomatl) (Morton, 1987). The tomatillo genus name *Physalis* is from New Latin physalis, coined by Linnaeus from Ancient Greek which means “to puff up” or “to blow up”. There are many trades and common name of tomatillo like Winter cherry, Cape goose berry, Hogweed, Balloon cherry, Coqueret, Strawberry tomato, Cut leaf ground cherry, Wild tomato, Winter tomato, Winter cherry, Cow pops, Chinese lantern, Mullaca, Koropo, Camapu etc. Tomatillos are native to Central America and Mexico. The plant is grown mostly in the Mexican states of Hidalgo and Morelos, and in the highlands of Guatemala (Morton, 1987), where it is known as miltomate. In the United States, tomatillos have been cultivated since 1863, with one dubbed "jamberry" in 1945 and others with the names "Mayan husk tomato" and "jumbo husk tomato". Further distribution occurred in the Bahamas, Puerto Rico, Jamaica, and Florida. By the middle of the 20th century, the plant was further exported to India, Australia, South Africa, and Kenya (Morton, 1987).

2.2 Geographical distribution and habitat

About 120 species of *Physalis* (L.) are distributed worldwide. All of them *P. alkekengi* has an unknown center of origin and it is old world species originated from Asia. Other species viz. *P. angulata, P. peruviana and P. minima* are originated from tropical America (Deb, 1979). *P. peruviana* (L.) found most commonly in Brazil. There are six species of *Physalis* (L.) present in India, *viz: P. alkekengi* (L.); *P. angulata* (L.); *P. ixocarpa* Brot.; *P. longifolia* Nutt.; *P. peruviana* (L.) as cultivated species and *P. minima* (L.) as common weed (Deb, 1979). Various species of genus *Physalis* and their hybrids are now well established weeds that disturbed landscapes

and crops throughout the tropics, including Asia. (Vatsavaya *et al*., 2007). Tomatillos are grown as annuals throughout the Western Hemisphere and are generally eaten fried, boiled or steamed. Shorter life cycle of tomatillo has allowed it to be introduced in some other countries such as: Austria, France, Hungary, Italy, Poland, Russia, Spain, Turkey and United States (Abak *et al*., 1994; Cantwell *et al.,* 1992; Porcelli and Proto, 1991). Tomatillo fruits are surrounded by an inedible, paper-like husk formed from the calyx. When the fruit matures, it fills the husk and can split it open by harvest. The husk turns brown, and the fruit can be several colors when ripe, including yellow, red, green, or even purple. The Purple and red-ripening cultivars often have a slight sweetness, unlike the green and yellow ripening cultivars, and therefore more suitable for fruit-like uses like jams and preserves for uses.

2.3 Genetics of tomatillo

Tomatillos carry self-incompatible traits. The plant, i.e. the fertile hermaphrodite, is not able to produce zygotes after self-pollination occurs (Mulato-Brito, *et.al*., 2007). This limits the ability to improve tomatillo production regarding the seed quality and the production of varieties. Cytological variations of medicinal plants species caused by environmental stress, genetic recombination and mutation. *Physalis* (L.) is extensively studied by various researchers from India and other countries. The cytological analysis of first Indian species *viz., P. alkekengi* (L.) was done by various researchers world-wide and reported 2n=2x=24 (Badr *et al.,* 1997; Pogan *et al*., 1989; Kliphuis and Wieffering, 1979). The second Indian species *P. angulata* (L.) was cytologically well-studied and reported 2n=4x=48 (Pedrosa, 1999; Ganapathi *et al.,* 1991; Husaini and Iwo, 1990; Lydia and Rao, 1982). The third species *P. longifolia* reported to have chromosome count 2n=4x=48, whereas 2n=2x=24 was also reported for *P. longifolia* var. *longifolia* (Tuteja and Bhatt, 1984). The fourth Indian species*P. minima* (L.) was reported to have 2n=4x=48 and 2n=6x=72 chromosome numbers (Kumar and Sinha, 1989). The fifth Indian Species *P. peruviana* (L.) was reported tetraploid and hexaploid i.e. 2n=4x=48 and 2n=6x=72 (Panda and Rao, 1983). The sixth Indian species i.e. *P. ixocarpa* Brot. was cytologically examined and showed diploid (2n=2x=24) chromosome numbers (Quiros, 1984; Lydia and Rao, 1981; Rao, 1979). From the cytological data it is clear that the Indian species of the genus *Physalis* (L.) exhibit different (2x, 4x and 6x) ploidy levels.

2.4 Botany and Agronomy of tomatillo

The review of botany of tomatillo is described under the following subsections *viz*. morphology, classification, flower, fruit and yield.

2.4.1 Morphology

P. ixocarpa plant is an annual branched herb having weedy appearance and widely used. The flowers are yellow with purple markings. The fruit develops inside a green and purple bladder like calyx that looks like a small Chinese lantern hanging from the stem. (Kirtikar and Basu, 2008; Khare, 2007; Pandey, 2005; Parmar and Kaushal, 1982). Due to the high morphological variation and the abundance of wild populations, P. ixocarpa is considered as a species in a current domestication process (Tavares *et al*., 2015). Some authors consider that *P. ixocarpa* and *P. philadelphica* L. are synonymous names (Santiaguillo and Yáñez, 2009), whereas others suggest that they are separate taxonomic entities (Tavares *et al*., 2015; Lagos *et al*., 2005). Most varieties of tomatillo have been typified by their morphological and agronomical attributes (Osuna *et al*., 2015; Valerio *et al*., 2012). Several authors reported that *P. ixocarpa* is a species with a high genetic variability (Osuna *et al*., 2015; Santiaguillo *et al*., 2004). *P. philadelphica* grow up to 15 to 60 cm (5.9 to 23.6 in) and have few hairs on the stem. The leaves have acute and irregularly separated dents on the side (Montes and Aguirre, 1994). They are typically about one meter (3.3 ft) in height, and can be either compact and upright or prostrate with a wider, less dense canopy. The leaves are typically serrated and can be either smooth or pubescent.

2.4.2 Classification

The tomatillo is a member of the genus *Physalis*, erected by Carl Linnaeus in 1753. Jean-Baptiste de Lamarck described the tomatillo under the name *Physlis philadelphica* in 1786. Other species such as *P. aeuata* and *P. violacea* were described later. The tomatillo is also often classified as *P. ixocarpa* Brot. (Bukun, *et. al*., 2002). However, *P. philadelphica* is the most important species economically. (Simpson *et. al.*,1995) The nomenclature for *Physalis* changed since the 1950s. *P. philadelphica* was at one time classified as a variety of *P. ixocarpa*. Later, the classification of *P. ixocarpa* was revised under the species of *P. philadelphica*. Today,

the name *P. ixocarpa* is commonly used for the domestic plant and *P. philadelphica* for the wild one.

The self-compatibility gene is situated in the chromosomes of the tomatillo and is not inherited through cytoplasm. Only heterozygous plants can be self-compatible as the trait is controlled by a dominant gene. (Mulato-Brito, *et. al.,* 2007).Tomatillo can thus produce seeds through self-pollination due to the involvement of self-compatibility traits but the germination viability is different throughout the produced seeds. This suggests that not only incompatible pollen is involved but also inviability at the seedling stage. (Simpson *et. al*.,1995).

2.4.3 Flower

Flowers come in several colors, including white, light green, bright yellow, and sometimes purple. Flowers may or may not have purple spots toward the center of the corolla. The anthers are typically dark purple to pale blue. Tomatillo plants are highly self-incompatible, and two or more plants are needed for proper pollination. Thus, isolated tomatillo plants rarely set fruit. (Franklin-Tong and Vernonica , 2008).

2.4.4 Fruit

The tomatillo fruit is surrounded by an inedible, paper-like husk formed from the calyx. As the fruit matures, it fills the husk and can split it open by harvest time. The husk turns brown, and the fruit can be several colors when ripe, including yellow, green, or even purple. The freshness and greenness of the husk are quality criteria. The fruit is a berry (1.25– 2 cm wide), with smooth, waxy, orange-yellowish kernels. The part of the Physalis that can be use discomposed of husk(6%)and berry(94%).They are protected by papery husks with many minute seeds in a juicy pulp, which is sweet and tangy, resembling Chinese lanterns (Fouqué 1972). Now a day, Physalis is included in the priority list of many governments' horticulture and fruit export plan. It is relatively unknown in importing markets and remains an exotic fruit (El Sheikha *et al*., 2008). It is exported from several countries including Colombia, Egypt, Zimbabwe and South Africa, but Colombia stands out as one of the largest producers, consumers and exporters. In addition, no data about *Physalis* fruit juice are yet available. In this work we are reporting for the first time, on the chemical composition and some physicochemical parameters of *Physalis* fruit juice. The data

obtained will present here are an important indication of the potentially nutraceutical and economic potential of *Physalis* as a new source of fruit juices.

2.4.5 Yield

There is limited information about tomatillo production, even though tomatillos are distributed and grown worldwide as a home-grown garden plant. Tomatillos are mainly cultivated in outdoor fields in Mexico and Guatemala on a large scale. Smaller crops are planted in many parts of the United States. In Mexico, tomatillos are planted within a wide range of altitudes. (Diaz, *et.al*., 2015). Commercial tomatillo varieties grown in an open field experiment yielded 5.6-6.4 kg/m2 in New Hampshire, U.S.A. (Freyre and Loy, 2000); 1.1-1.9 kg per plant in Georgia, U.S.A. (Perez et al., 2005); 1.1-2.6 kg per plant in Mexico (Godina *et al*., 2013); and 1.8 kg plant in the European part of Russia (Mamedov, 2017). Naumova *et al*. (2018) also found similar yield in the south of West Siberia, Russia. They studied field-grown tomatillo yield and fruit properties and their relationship with soil chemistry and temperature, at five experimental sites. At each site, a micro plot experiment with two cultivars was conducted. Basic soil chemical properties and fruit pH and dry matter, total carbon, nitrogen, and ascorbic acid content were determined. Both cultivars grew and yielded very well, producing on average 70 fruits, 1.46 kg per plant, with 14 mg ascorbic acid per 100 g fresh weight and 9.0% dry matter. Tomatillo production in California was reported as ranging from 1.5 to 3.5 t/acre; i.e., 0.4-0.9 kg/m2, which is extremely low and even seems to be erroneous (Smith *et al.*, 1999). Somewhat higher, but still low, yields of 2.0-2.4 kg/m2 were reported for Florida (Maynard, 1993).

2.5 Diseases

Tomatillo is generally a very resistant type crop, as long as its climatic requirements are met. However, as with all crops, mass production brings with it exposure to pests and diseases. As of 2017, two diseases affecting tomatillo have been documented, namely tomato yellow leaf curl virus and turnip mosaic virus. Symptoms of tomato yellow leaf curl virus, including chlorotic margins and interveinal yellowing, were found in several tomato and tomatillo crops in Mexico and Guatemala in 2006 (Salati, *et al.*, 2010). After laboratory tests, the virus was confirmed. Symptomatic plants were associated with the presence of whiteflies, which were likely the cause for this outbreak. (Salati, *et al.*, 2010). Turnip mosaic virus was discovered in several

tomatillo crops in California in 2011, rendering 2% of commercially grown tomatillo plants unmarketable, with severe stunting and leaf distortion. (Liu, *et al*., 2011). The green peach aphid is a common pest in California, and since it readily transmits the turnip mosaic virus, this could be a threat to tomatillo production in California. (Liu, *et al*., 2011).

2.6 Soil and climate requirements

In general, tomatillo plants are tolerant to many different soil conditions. However, they do best in well-drained, sandy, fertile soil conditions with a pH between 5.5 and 7.3. (Masabni, 2016). Tomatillo plants are cold sensitive. They grow best at 25 to 32 °C (77 to 90 °F). Below 16 °C (61 °F), growth is very poor. Tomatillo plants prefer warm locations with full sun exposure.

2.7 Fertilization and field management

Tomatillo plants can reach heights of 1.5 to 2 meters (4.9 to 6.6 ft). Due to its rapid and branching growth it is recommended to stake them. Staking also facilitates later harvesting and prevents the fruit from touching the ground, which reduces damage to fruit and husk. Staking can also reduce disease, as well as slug damages. Fertilization is recommended at a moderate level. An application of 40–90 kg/ha (36–80 lb/acre) of phosphorus is common. Depending on soil type and irrigation, other nutrients and fertilizers (N/K) may be required. For non-commercial production, regular fertilization is recommended. Although tomatillo plants become more drought tolerant as they age, regular watering is required. Tomatillo plants require 25–38 mm (1.0–1.5 in) of water per week. Water can come either from rainfall or from irrigation. Irrigation frequency is dependent upon weather and the crop's growth stage, ranging from once or twice a week to daily during hot weather periods. (Smith and Cantwell, 1999). Weeds are a serious challenge in tomatillo production and especially important during the first few weeks. Plastic and organic mulches help to effectively control weeds. Applications of plastic mulches also help to restrict soil water evaporation and modifying microclimate, thereby affecting tomatillo growth and yield. (Diaz-Perez *et al*., 2015).

2.8 Harvest and postharvest treatment

Tomatillos are harvested when the fruits fill the calyx. This state is normally achieved 65 to 100 days after transplanting. Fruit production continues for 1 to 2 months or until first frost. Harvesting occurs regularly, typically every day, and is done by hand. A single plant produces 60 to 200 fruits within a single growing season, with an average yield of about 9 short tons per acre (20 t/ha). (Masabni, 2016). Tomatillos can be stored for up to three weeks in a cold and humid environment.

2.9 Uses

Tomatillos are a key ingredient in fresh and cooked Mexican and Central American green sauces. The green color and tart flavor are the main culinary contributions of the fruit. Purple and red-ripening cultivars often have a slight sweetness, unlike the green- and yellow-ripening cultivars, so generally are used in jams and preserves. Like their close relative the Cape gooseberry, tomatillos have a high pectin content. They keep even longer with the husks removed and the fruit refrigerated in sealed plastic bags. (Carter and Deane, 2008). They may also be frozen whole or sliced.

2.9.1 As food

The tomatillo can be harvested at different stages of its development. For salsa verde, it is harvested early, when the fruit is sour with a light flavor. For a sweeter taste, it can be picked later, when the fruit is seedier. (Johansen, 2017). In this stage, it could be suitable as a tomato substitute. Tomatillos have diverse uses in stews, soups, salads, curries, stirfries, baking, cooking with meats, marmalade, and desserts. (Morton, 1987). Tomatillos can also be dried to enhance the sweetness of the fruit in a way similar to dried cranberries, with a hint of tomato flavor. (Kindscher *et al*.,2012). The tomatillo flavor is used in fusion cuisines for blending flavors from Latin American dishes with those of Europe and North America. (McGorrin and Gimelfarb,1998).

2.9.2 Nutrition and medicinal value

Tomatillo found to have fantastic anti-bacterial and anti-cancer properties. It is rich in flavonoids which helps to protect from lung and oral cavity cancers (Hamm, 1985;

Quiros, 1984). On the other hand tomato also a worldwide popular vegetable and a good source of antioxidants and anticancer properties such as lycopene, vitamin C, phenolics and total soluble solids (% of brix) in human diet and has been linked with decreases risk of heart diseases, diabetes, prostate and various forms of cancer. Lycopene, a precursor of beta-carotene with well-known antioxidant activity and powerful health properties. Research for new anticancer drugs focuses more on the natural compounds such as physicochemical constituent from the regular human diet. Because of the lack of severe side effects yet efficiently can act on a wide range of receptors or molecular targets involved in carcinogenesis and cardiovascular diseases. In vivo, in vitro and clinical studies conducted in recent years have revealed an inverse association between the dietary intakes of lycopene with the risk of prostate cancer (PCa). L-Ascorbic acid (AsA), which is an essential nutrient component for human health and plant metabolism that plays key roles in diverse biological processes such as cell cycle, cell expansion, stress resistance, hormone synthesis, and signaling. Many scientists have studied quality character as well as anti-carcinogenic properties of tomato on human and many animals. Among them most relevant recent publications are reviewed below is good source of antioxidant phytochemicals known as Withanolides. Ixocarpalactone-A is one such Withanolides present in tomatillo.

2.9.2.1 Lycopene

Tomatillo has scanty amount of lycopene and it hardly found in tomatillo, tomatoes and various products derived from thermally processed tomatoes are major sources of lycopene, but apart from this micronutrient, other carotenoids such as â-carotene also are present in the fruit. They occur in tomato fruits and various tomato products in amounts of 2.62-629.00 (lycopene) and 0.23-2.83 mg/100 g (âcarotene). Standard methods for determining the carotenoid content require the extraction of the analyte as well as other cleanup step. Lycopene (LYC) is the red pigment and a major carotenoid in tomatoes. Lycopene's antioxidant capacity is roughly twice that of β-carotene. Numerous epidermiological and intervention studies have demonstrated that dietary intake of LYC-rich foods result in decreased incidence of certain cancers, including the prostate, lung, mouth, and colon cancer, coronary heart diseases, cataracts and possibly macular degeneration. Although the tomato is the richest source of lycopene among all fruits and vegetables, its concentration in the fruit of commercial cultivars is rather low, on average ranging from 30 to 60 μg lycopene/g fresh tomato tissue.

Using different traditional breeding techniques, Kinkade and Foolad (2013) has developed tomato breeding lines having fruit lycopene

Content from 100–200µg lycopene/g fresh fruit tissue. Lycopene is an important intermediate in the biosynthesis of many carotenoids, including beta carotene, responsible for yellow, orange or red pigmentation, photosynthesis, and photo-protection. Like all carotenoids, lycopene is a polyunsaturated hydrocarbon (an un-substituted alkene). Some of the previous reports on Lycopene experiment are discussed here (Datta *et al*., 2013; Dong *et al*., 2010; Alda *et al*., 2009; *Moigrădean et al*., 2007; Cucu and Loco, 2011).

Datta *et al*. (2013), observed lycopene may lower the incidence of prostate cancer. This study aimed to evaluate the tolerance and acceptance of three different amounts (4, 8, or 12 oz) of tomato juice (TJ) and their effect on serum lycopene during radiotherapy in 20 men with localized prostate cancer. A significant positive correlation between serum lycopene, weight, and body mass index, and a negative correlation between serum lycopene and prior nutritional supplement use was detected. Panthee (2013) uses 44 vintage tomato varieties and evaluated them. Pearson's correlation analysis indicated that estimated lycopene content was negatively correlated with the other physicochemical traits whereas vitamin C, TSS and TTA were positively correlated with each other. Dufera (2013) was conducted an experiment using twenty-one tomato germplasms. Higher genotypic and higher phenotypic coefficients variation values were recorded for lycopene content.

Mendelova *et al*. (2013) conducted a work to analyze the content of total carotenoids and lycopene in 8 varieties of tomato and to monitor dynamic changes after their different treatments (heating, drying). The experiment included following tomato varieties: Bambino F_1, Darina F_1, Diana F_1, Denar, Milica F_1, Orange F_1 Paulina F_1, Sejk F_1. They found that processing of tomato fruits into juices and dried slices positively affected the presence of carotenoids and lycopene. Zhu *et al*. (2004) studied that lycopene, with its acyclic structure and large array of conjugated double bonds carries many distinct biological and physicochemical properties. Lycopene is among the most efficient singlet oxygen quenchers of the natural carotenoids without pro-vitamin A activity. It acts as a natural antioxidant in human serum and other tissues to protect the oxidative damage of lipids, proteins, and DNA.

Elumalai *et al*., (2013) was conducted an experiment in human. Oxidative stress is recognized as one of the major contributors to the increased risk of cancer and lycopene being a potent antioxidant has been found to inhibit proliferation of several types of human cancer cells, including endometrial, prostate, breast, upper aero digestive tract and lung. Lycopene has tumor suppressor activity.

The lycopene content in fifteen varieties and three brands of tomato paste, three brands of ketchup and three brands of tomato hot sauce were determined by spectrophotometry and HPLC methods ranged from < 0.05 to 5.82 mg/100 g, and from 0.01 to 4.90 mg/100 g respectively (Bradbury *et al*., 2012). Dong *et al*. (2010) showed that the lycopene content is very significantly positively correlated with single inflorescence flower numbers, single inflorescence fruit numbers and soluble solids content, but very significantly negatively correlated with pedicel length and single fruit weight. He also reported that the lycopene content is significantly positively correlated with fruit shape index, but significantly negatively correlated with fruit firmness, flesh thickness, longitudinal diameter of fruit. Wright (2007) performed correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta -carotene, ascorbic acid and titratable acidity. Kumari *et al*. (2007) recorded data for total soluble solids, dry matter content, reducing sugars, titratable acidity, ascorbic acid, lycopene and found there were insignificant differences for acidity, early yield, total yield, and days to flowering.

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. They 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. Jones and scott, (1983) studied inheritance and characterization of anthocyanin fruit (Aft) in tomato, to estimate the genetic potential for increased levels of this important class of phytonutrients in tomato fruit. They concluded that fruit of accession LA 1996 contained predominantly petunidine, followed by malvidine and delphinidinin, while the levels of lycopene, β-carotene,

phytoene and phytofluene were similar to those of normal tomatoes and lower than those found in high pigmented tomatoes.

Davis *et al.*, (2003) evaluated 13 tomatoes (four different cultivars) and 38 tomato products. They used absorbance method (PAM) and had linear correlation coefficients with lycopene content determined by hexane extraction/spectrophotometry of R2=0.97 for fresh tomato, and 0.88 for tomato products. The fruits of 11 recent hybrids of processing tomato, grown under optimal conditions, were assessed for colour using Colorgard System 05 and for lycopene content examined by Siviero et al., (2000). Fresh DM regularly showed more mg lycopene/100 g than processed material.

2.9.2.2 Vitamin-C

As purple coloured tomatillo genotypes produce juice violet in color that's why possibility of having vitamin-C is very rare. On the other hand tomatillo genotypes which are greener and produce juice as like tomatoes do and show vitamin-C presence but very scanty amount. Tomatoes are excellent sources of vitamin C, with some varieties containing concentrations comparable to those found in oranges. Although all tomatoes contribute to our vitamin C intake, there are different amounts of vitamin C in different genotypes. For example, raw green tomatoes contain 23.4 milligrams, orange tomatoes contain 16 milligrams and yellow tomatoes contain 9 milligrams per 100 grams, which is slightly more than half of a large, 3-inch tomato. Sun-dried tomatoes are much richer in vitamin C, containing 39.2 milligrams per 100 grams. Crushed, canned tomatoes and tomato juice contain smaller amounts, respectively contributing 9.2 and 18.3 milligrams of vitamin C to our daily intake (Lee and Media, 2014).

Borguini *et al*. (2013) were analyzed tomatoes regarding ascorbic acid (Vit. C), lycopene content and antioxidant activity. Organic tomatoes presented higher content of ascorbic acid and total phenolics (641.39 and 4466.66 mg/100 g EAG on dry wt. basis) than did the conventional tomatoes (510.16 and 3477.50 mg/100 g EAG on dry wt. basis, respectively). There was no difference in lycopene concentrations between the organic and conventional.

Schwarz *et al*. (2013) evaluated ten tomato hybrids (Supera, Granadero, AP-529, AP-533, Katia, Laura, Fascinio, Tinto, Red Spring and Venus) for their quality, viz. soluble solids, ascorbic acid, lycopene and reducing sugars. The best performing hybrid for traits and for both segments was Granadero, but this hybrid showed low genotypic stability. So Venus and Tinto, despite lower yields, could be recommended because they presented good quality and stability.

Five tomato cultivars: four large-fruit (Rumba, Juhas, Kmicic, Gigant) and one cherry cultivar (Koralik) were selected for study by Hallmann *et al*. (2007). The organic tomato fruits contained more dry matter, total and reducing sugars, vitamin C, total flavones and beta-carotene, but less lycopene in comparison to conventionally grown tomatoes.

The study done by Schulzova *et al*. (2007) to investigate the effects of tomato cultivation systems on the content of both health promoting and of toxic components represented by carotenoids (lycopene, beta -carotene), vitamin C and glycol-alkaloids (alpha-tomatine, dehydrotomatine). The levels of biologically active compounds were shown to be strongly affected by the degree of fruit maturity.

Harer *et al.* (2002) grew 37 tomato genotypes in a field experiment. Correlation studies showed that genotypic correlation was higher than phenotypic correlation for all characters examined. Among them the ascorbic acid content had negative direct effects and association with fruit yield.

A study was conducted to test whether tomato fruits from a genotype with elevated levels of natural antioxidants produce seeds with a functionally greater total antioxidant capacity. The tomato genotype 'T4099', which produces elevated levels of lycopene and ascorbic acid, and the recurrent parent 'Flora-Dade' were grown in the field and greenhouse under standard agronomic practices. Ramirez (2005).

2.9.2.3 Brix (%)

Brix percentage is the sugar content of an aqueous solution. One percent Brix is 1 gram of sucrose in 100 grams of solution and represents the strength of the solution as percentage by mass. If the solution contains dissolved solids other than pure sucrose, then the % Brix only approximates the dissolved solid content. Various reports are available on variation of Brix % for different genotypes of tomatillo and tomato.

Nalla *et al*. (2014) done a field experiment using 27 tomato genotypes and reported fruit yield per plant (20.51), total soluble solids (17.38), and equatorial diameter (15.38) contributed high for divergence. For total fruit number, total soluble solids content, fruit firmness, length and pH, in a general way and for the majority of the genotypes, there were no statistical differences between the averages of the F_1 and F_2 generations. There was a significant ($p<0.01$) difference among genotypes and environments for all quality traits, Genotype x Environment interaction was significant ($p<0.01$) for all quality traits except for TSS found by Panthee et al., (2013). Narolia *et al*., (2012) found high estimates of genotypic coefficient of variation, heritability and genetic advance for acidity, total soluble solids, ascorbic acid content, and shelf life.

A study by Silva *et al.* (2012) evaluated the components of production and total soluble solids (Brix) of tomato cultivar Carolina. The fruits were harvested when they began the color change from green to red; on the occasion were evaluated content of soluble solids, number, weight, length and diameter. Petersen *et al*. (1998) found highest fruit yield (27.79 t/ha), total soluble solid content (6.11%), acidity (0.93%) and lycopene content (7.64 mg/100 g of juice). Seven tomato lines studied by Chen (2009) and found general heritability for vitamin C and total soluble solid content was high. Lines belonging to L. esculentum var. cerasiforme were better breeding materials in terms of vitamin C, organic acid and total soluble solid content.

Cheema *et al*., (2003) were studied on combining ability for 10 important characters and significant general (GCA) and specific combining ability (SCA) variances were observed for different characters except for total soluble solids indicating the importance of both additive and non-additive gene effects in the expression of these characters. Four commercial brands of tomato juices and ketchups were studied. Results showed that Brix is higher in ketchup (25-33 degrees Brix) than in tomato juices (4.8-5.5 degrees Brix). Pearson correlations showed statistically significant ($P<0.05$) correlations between Brix and HMF, lycopene, dry matter (negative correlation) and juice (negative); HMF and lycopene and dry matter (negative correlation); lycopene and dry matter (negative), pulp and juice; dry matter and pulp (negative) and juice; and pulp and juice (negative correlation).

Harer *et al*. (2002) were grown 37 tomato genotypes in a field experiment and correlation studies showed that genotypic correlation was higher than phenotypic correlation for all characters examined. Among them the total soluble solid content had positive but low direct effects and positive association with fruit yield.

The chemical contituents are concerned in the quality of tomato fruit in respect to color, texture, flavor, nutritive value, and wholesomeness. In general, high sugar contents, redness of color, and firm texture are associated with prominence of rich flavor. Biochemical changes as influenced by growth, maturation, and environment of tomato fruit are discussed.

Dhaliwal *et al*. (2002) conducted an experiment with twelve parents and their 66 F_1 hybrids to study the genetics of traits that are important for processing and bulk handling of tomatoes viz. TSS%, pericarp thickness and number of locules. The analysis of variance for combining ability exhibited the significance of both general combining ability and specific combining ability effects for all characters studied.

2.9.2.4 Fruit pH

Proximate composition and pH of tomatillo (*Physalis ixocarpa* Brot.) and Tomato (*Solanum lycopersicum* L.) grown in Sher-e Bangla Agricultural University, Dhaka were analyzed. Fruit's p^H differed significantly in all the genotypes ranging from 3.80 to 4.90. Tomatillo somewhat sour in taste at row condition that's why at row stage tomatillo content little bit higher pH then ripping stage. On the other hand tomato is also taste in sour at row condition but sweet at matured stage. As a result tomato has high pH rate at row stage and pH rate at ripping stage.

Moisture content varied from 77.67 to 95.00. Average kcalorie content was calculated to be about 31 kcals/100 g. The average pH of tomatillos was 3.76 (McKee, 1992; Ramos, 1991). Unlike tomatoes, they have a paper like husk which must be removed before consumption. Also unique to tomatillos is the waxy coat and sticky like substance noted on the surface.

2.9.2.5 Moisture percentage (%)

The most popular method of drying tomato is hot air drying due to its operation simplicity and relatively inexpensive technology (Akanbi *et al*. 2006). This technique employs flow of heated air stream (usual operational temperature range between 50 and 80 °C) to supply heat to the food and remove its moisture (Phongsomboon and Intipunya 2009). Tray drying (TD) is commonly used for drying of vegetables, and it was chosen because of its simplicity and low cost but time consuming. TD is also often used in R&D laboratories to simulate industrial tunnel or conveyor dryers (Nindo *et al*. 2003). In addition, determining the drying behavior by accurate mathematical models is important. Several mathematical models may be used to describe the drying process and help in its optimization, and assist in the effective design of dryers (Vega *et al*., 2007). Empirical equations frequently used to model the drying kinetics of food include: Newton, Page, Henderson–Pabis, Page modified, Logarithmic, Two-terms exponential, Thomson, Diffusion approach, Verma, Wang and Singh, Henderson–Pabis modified models and others (Meisami-asl *et al*., 2010; Vega *et al*., 2007). Recently, Diamante *et al*. (2010) proposed a new thin-layer drying model which gave the best curve fitting ability compared to the three widely used models, namely, Henderson–Pabis, Page and Logarithmic models, in kiwifruit and apricot.

The hot air convective drying characteristics of blanched tomatillo (*Physalis ixocarpa* Brot.) and tomato (Lycopersicon esculantum L.) slices have been investigated. Drying experiments were carried out at 70 °C into an automated oven and kept it going overnight. The effect of drying temperatures on the drying behavior of tomatillo and tomato slices was evaluated. All drying experiments had only falling rate period. The average effective diffusivity values varied from 77.67% to 95.00% with the average of 89.33%. In order to select a suitable form of the drying curve, six different thin layer drying models Diamante *et al*. (2010) were fitted to the experimental data. The goodness of fit tests indicated that the Logarithmic model gave the best fit to experimental results, which was closely followed by the Henderson–Pabis model. The influence of varied drying temperatures on quality attributes of tomatillo and tomato slices viz. Hunter color parameters, ascorbic acid, lycopene, titratable acidity, total sugars, reducing sugars and sugar/acid ratio of dried slices was also studied. Slices

dried at that temperature (70 °C) had high amount of total sugars, lycopene, sugar/acid ratio, Hunter L- and a-values.

So, the removal of moisture must be accomplished in a manner that will be least detrimental to the product quality. An understanding of the nutritional and colour changes of tomatillo and tomato slices during hot air drying is essential for any optimization study. The aim of this research was the study and modeling of the drying kinetics of mass transfer during the hot-air convective drying process of blanched tomatillo and tomato slices. The effect of drying temperatures on the quality attributes of the dried slices was also studied for determining the optimum drying temperature that might produce high-quality dried tomatillo and tomato slices. The chemical contituents are concerned in the quality of tomatillo and tomato fruit in respect to color, texture, flavor, nutritive value, and wholesomeness. In general, high sugar contents, redness of color, and firm texture are associated with prominence of rich flavor. Biochemical changes as influenced by growth, maturation, and environment of tomato fruit are observed.

2.10 Tomatillo taxonomy

To clarify the taxonomic classification of Physalis, Menzel (1951, 1957) and Waterfall (1967) made extensive cytologic and taxonomic studies of the genus. Menzel reduced P. *philadelphica* to synonymy under the variable P. *ixocarpa* Brot. a name that had to come to be widely used for the domesticated tomatillo (Hudson 1986). The only apparent difference between the two species was the length of the peduncle, with the peduncle of P. *ixocarpa* shorter than that of P. *philadelphica*. Waterfall (1958) accepted this nomenclature when studying the species of North Mexico, but he reversed himself when he analyzed Physalis spp. from Mexico and Central America (Waterfall 1967). He incorporated the small-flowered P. *ixocarpa* within the broader limits of P. *philadelphica*. Fernandes (1974) made a thorough investigation of this nomenclatural problem and concluded that P. ixocarpa is a distinct species, different from P. *philadelphica* based on previous cytological evidence, the distinctive sigma, and the small flowers of the type. Chromosome morphology has recently been used to understand the interspecific relationships in the genus. Gottschalk (1954) and Lydia and Rao (1981) studied the morphology of chromosomes during the pachytene stage with most important Physalis spp. and

demonstrated cytological differences between the species. Nevertheless, the taxonomic complexity of the genus is not yet clarified, especially between P. *ixocarpa* and P. *philadelphica.*

The modern worldwide accepted scientific name of tomatillo is *Physalis ixocarpa* Brot. The genus *Physalis*, established by Linneaus in 1753, contains about 100 species of annual and perennial herbs (Willis, 1966). The genus is characterized by the presence of pendant flowers and an inflated fruiting calyx which is closes the berry (Sullivan, 1984). Four species are cultivated in different parts of the world for their fruit: P. *peruviana* L. (cape gooseberry, uchuba) and P. *pruinosa* L. (ground cherry, husk tomato) are used as jam fruits; P. *alkekengi* L. (Chinese lantern) is used as an ornamental; and P. *ixocarpa* Brot. (tomatillo, tomate de cascara) is used as a vegetable or for sauces. Several species of *Physalis* are widespread in America as endemic weed species. Six important Physalis spp. are prevalent in the phyto-geographic region of Mesoamerica (Belize, Guatemala, Honduras, El Salvador, Nicaragua, Costa Rica, and Panama, and the Mexican states of Chiapas, Yucatan, and Quintana Roo: P. *angulata* L., P. *cordata* Mill., P. *gracilis* Miers, P. *ignota* Britt., P. *lagascae* R. and S., and P. *pubescens* L. (Gentry and D'Arcy, 1986). These *Physalis* spp. can be intercrossed, but incompatibility has been found (Quiros, 1984). The basic chromosome number of the genus is N=12 and most species are diploid; P. *peruviana* is a tetraploid (Menzel 1951).

Tomatillo has been known to botanists for nearly 400 years as P. philadelphica Lam. Francisco Hernandez in 1651 described two varieties from numerous plant types called tomate by the Aztecs. Botanists have suggested that the small-fruited miltomate is a wild-type plant, whereas, the tomatillo is a domesticated plant that derives from plants similar, if not identical, to miltomate (Hudson 1986). The specific boundaries in Physalis are poorly defined with some duplication of names and many changes in the nomenclature during the last 50 years. The complexity of the genus is caused mainly by the wide range of genetic variability present presumably resulting from interspecific hybridization (Menzel, 1957) and also by the ambiguity of the earlier taxonomic descriptions (Raja-Rao 1979). For example, P. *aequata* Jacq. and P. *capscicifolia* Rydb are considered synonymous with P. *ixocarpa.*

2. 11 Genetic variability

The fundamental key is to achieve the genetic improvement of a crop through a proper breeding programme 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, some researchers studied variation of various characters in tomatillo. 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 diversity 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).

Some of the previous related research reports of tomato are discussed here. Field experiment was carried out to study the genetic variation among twenty tomatillo accessions that helped in the reliable varietal selection programme for breeding. The study revealed that height of plant, fruit colour and fruit size show variability (Naz *et al.*, 2013). On the other hand by using nineteen exotic collections of tomato, Reddy *et al*. (2013) revealed considerable genetic variability for all the eighteen quantitative 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.

Mahesh *et al.* (2006) carried out an experiment to study genetic variability in 30 genotypes of tomato revealed significant difference for all the characters under study and observed a wide range of variation for plant height, number of branches per plant, fruit weight, fruit length, fruit diameter, number of locules per fruit, fruit set percentage, fruits per plant, fruit yield per plant, ascorbic acid content and total soluble solids. Again, Alam *et al*. (2012) suggested that Multivariate and biochemical analysis of genetic affinity among the tomato varieties are necessary before setting an y program for their improvement. They collected many tomato accessions to judge the BARI released varieties and the other commercially available varieties on the basis of their genomic information.

Singh *et al.* (2005) conducted 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. Shashikanth *et al*. (2010) carried out a field experiment to study the genetic variation among 30 tomato germplasm lines and observed that the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed that high genotypic variance was for most of the characters indicating a high contribution of the genetic component for the total variation.

Morphological trait measurements can provide a simple technique of quantifying genetic variation and simultaneously assessing genotype performance under relevant growing environments (Shuaib *et al*., 2007). Data recorded 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 evaluation of the Kenyan tomato germplasm by Agong (2001) showed a large and significant variation in the quantitative traits between the accessions. The average fresh and dry fruit weight varied notably among the accessions. Most of the landraces gave lower fresh and dry fruit yields than the market cultivars. Mohanty and Prusti (2001) showed considerable genetic variability 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. The fundamental key to achieve the genetic improvement of a crop through a proper breeding programme is to calculate the amount and nature of variation of plant characters in breeding population. The assessment helps breeder for improving the selection efficiency. Genotype is the genetic blueprint of an individual. Genotypic variation is variation in genotypes either between individuals of the same species or between different species that occurred during meiosis. There are three ways of variations which can occur genetically are with mutations, gene flow, and meiosis. Accurate knowledge between the genetic diversity and the relationships among preserved germplasm collections of any crop is essential and important for establishing, managing and ensuring long term success of appropriate crop improvement programs through breeding (Gwag *et al*., 2010). Study on genetic diversity and population structure of germplasm collections has been useful in

supporting conservation and genetic improvement strategies (Grandillo, 2014; Rao and Hodgkin, 2002).

In the breeding of fruit crops, to characterize the season, number of buds and of flowers, and fruit set are critical data to identify populations with promising traits (Parra *et al*., 2014). Determining the growth of reproductive structures that enables management of the fruit supply according to season and adaptation of production technologies available in the region (Antunes *et al*., 2008). Breeding will only be successful in a selection program if the genetic variability in the traits of interest is high. Variations in genetic make-up between different populations can contribute to the formation of a genotypic constitution of Physalis adapted to the particular soil and climatic conditions of regions with high temperatures in Bangladesh. The use of cultivars with genetic variability in the trait production peak contributes to the uninterrupted supply of the fruit and, consequently, increases sales and thus the farmers' income Segantini *et al*., (2014).

The experiment occurred of six *Physalis* populations, was performed by Trevisani *et al*. (2016) arranged in a randomized block design (RBD) to assess number of flower buds, number of flowers and number of fruits in 36, 43, 50, 57, 64 and 71 days after planting the seedlings in the field. They found significant effect of the population × time interaction, at 5% probability in analysis of variance. The morphological description of the population is the first step towards selection of superior parents (Singh *et al*., 2014). Again, Godina *et al.* (2013) evaluated yield and fruit quality in tomatillo autotetraploids (*Physalis ixocarpa*) and diploids under a completely randomized block design with four replications. They studied fruit yield, fruit weight, fruits per plant, equatorial and polar fruit diameter, total soluble fruit solids, fruit firmness, pH and Vitamin C content and they found equatorial diameter of fruit in diploids was 40.25 mm, the smaller diameter, 31.80 mm, while the wider was 46.50 mm for diploid; average polar diameter of fruits in diploids was 35.28 mm. The fruit equatorial diameter in autotetraploid was 40.45 mm. The polar diameter of autotetraploids showed an average of 31.44 mm and the values ranged from 30.32 to 32.34 mm. They also found diploids showed the following characteristics; fruit yield=1.809 kg plant-1; number of fruits per plant=56.2 while the autotetraploid presented fruit yield=1.688 kg plant-1, number of fruits per plant = 60.776. In the four diploid populations average fruit weight was 34.48 g/fruit with ranges from 6.16

g/fruit to 46.99 g/ fruit. In autotetraploids, the average fruit weight was 29.31 g/fruit with a range of 22.81 g/fruit to 34.99 g/fruit. As higher amount of biomass is produced the demand for nutrients is also higher, the plants are taller and need more days for flowering and harvest (Torres *et al.*, 2011); they also have a broader ecological tolerance, and larger cells (Cequea, 2000).

2.12 Heritability and genetic advance

Selection of promising plants on phenotypic characteristics is the most important task for all plant breeding practices. The effectiveness of selection for yield depends upon heritability. A character with high heritability gives better response to selection. Heritability and genetic advance are the most important parameters to judge the breeding potentiality of a population for future development through selection. Many researchers have studied heritability and genetic advance of yield and many yield contributing characters of tomato. The literatures very relevant to the present study are reviewed below:

Saleem *et al.* (2013) studied quantitative genetics of yield and some yield related traits. The highest estimates of genotypic and phenotypic coefficients of variability (GCV and PCV) were recorded for number of fruits per plant while fruit width was the most heritable trait. Buckseth et al. (2012) found high heritability with high genetic advance for number of fruits per plant, average fruit weight, yield per plant and pericarp thickness indicating that most likely the heritability is due to additive gene effects and selection may be effective. By Narolia *et al.* (2012) thirteen quantitative characters were studied in 55 genotypes of tomato. High heritability coupled with high genetic advance as per cent of mean was observed for all the characters except days to 50% flowering indicating the presence of additive gene action in the expression of these characters.

Shashikanth *et al*. (2011) observed the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed high genotypic variance for most of the characters indicating a high contribution of the genetic component for the total variation. Similarly, Ponnusviamy *et al.* (2010) evaluated 12 varieties of tomato to estimate heritability and reported that high heritability coupled with high genetic advance as percentage of mean for average fruit weight, indicating the control of such character by additive gene. He also recorded

that high heritability coupled with low genetic advance as percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components.

Nardar *et al.* (2007) evaluated 20 tomato genotypes and observed high heritability with high genotypic coefficient of variation and genetic gain for fruit weight and fruit yield, which could be improved by simple selection. Padda et al. (2007) observed that broad sense heritability was highest for number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%), reflecting the effectiveness of selection in the present germplasm of tomato improvement. Nandpuri *et al*. (1974) observed that heritability estimates were high for fruit size, plant 2 height and yield per plant in tomato. Expected genetic advance was also high for fruit size, yield and number of fruits per plant.

Dudi *et al.* (1983) reported that heritability and a genetic advance-were high for number of fruits per plant, individual fruit weight and yield by per plant. Mallik (1985) reported high genetic advance for plant height, number of fruits per plant, individual fruit weight and yield per plant but low heritability for yield per plant. Abedin and Khan (1986) also reported high values of heritability in broad sense and high genetic advance for plant height, number of fruits per plant and individual fruit weight. Again, Sonone *et al.* (1986) reported that heritability estimates for fruit number, plant height and individual fruit weight were high in tomato. He also reported that high genetic advance (>30%) was observed for fruit yield, plant height, individual fruit weight and number of fruits per plant. Estimates of high heritability and high genetic advance for number of fruits per plant, individual fruit weight and plant height indicated control by additive genetic effects.

Singh *et al.* (1988) evaluated 32 genotypes for agronomic characters and obtained high heritability values for yield per plant only. Singh and Singh (1980) reported high heritability for average fruit weight (91.08%), total fruits (85.04%) and days to first picking (80.97%).

Kasrawi and Amr (1990) reported that pH gave comparatively higher heritability estimates in a study of seven quality characters using F_2 populations.

Bai and Devi (1991) evaluated five varieties and nine hybrids of tomato. Heritability estimates of 90% were obtained for plant height, number of fruits per plant and individual fruit weight. Islam and Khan (1991) studied 12 tomato genotypes and reported that heritability values were high for most of the characters but moderate for days to first flowering, maturity and plant height. Again, Reddy and Reddy (1992) studied heritability and genetic advance in 139 tomato varieties. Heritability values for yield per plant, number of fruits per fruits per plant and average individual fruit weight were 97.99%, 95.96% and 98.46% respectively. Pujari *et al*. (1995) observed high heritability coupled with high genetic advance for number of fruits per plant, plant height and average fruit weight which indicated additive gene action.

Aditya and phir, (1995) reported high heritability (in broad sense) with high genetic advance in percentage of mean for number of fruits per plant, individual fruit weight and plant height. However, yield per plant showed moderate heritability and low genetic advance but highest genetic advance as percentage of mean under selection. In an another experiment, Mittal *et al.* (1996) estimated heritability and genetic advance in 27 genotypes of tomato. High heritability associated with high genetic advance were observed by them indicating the character, predominantly under the control of additive gene, could be improved through selection. Singh *et al*. (1997) estimated heritability and genetic advance in 23 genotypes of tomato. High values of heritability and genetic advance indicated that effective selection may be made for fruit weight and number of fruits per plant.

Phookan *et al*. (l998) observed high heritability and genetic advance in percentage of mean were 4 estimated for fruits per plant and average fruit weight suggesting their importance in selection for tomato improvement. Vikram and Kohli (1998) reported high heritability and genetic advance for mean fruit weight which suggested that improvement for this character should be fairly straight forward. Again, lslam *et al*. (1996) studied heritabiltiy and genetic advance in 26 diverse genotypes of tomato. High heritability and genetic advance was observed in number of fruits per plant, plant height, fruit yield and individual fruit weight.

Prasad and Mathura, (1999) estimated heritability in 75 exotic genotypes of tomato and reported very high heritability along with high genetic advance by fruit weight. Again, Brar *et al*. (2000) reported that the number of fruits per plant, total yield per

plant and marketable yield per plant had low to moderate estimates of heritability and genetic advance and number of marketable fruits per plant had high values of heritability and genetic advance. Nessa *et al*. (2000) reported high heritability for number fruits per plant, plant height and moderate heritability for yield per plant. Matin (2001) reported high degrees of heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit. Godekar et al. (1992) obtained high values for hetitability along with high genetic advance by fruit weight.

Mohanty (2001) evaluated 18 genotypes of tomato and revealed high heritability with moderate to high genetic gain for average fruit weight, number of fruits per plant and plant height. Mohanty (2003) observed that high heritability with high genotypic coefficient of variation was for fruit weight, plant height, number of fruits and number of branches per plant. Singh (2002) reported that heritability was high for all characters except days from fruit setting to red ripe stage and the highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits. Mohanty (2003) again, evaluated heritability in 18 tomato cultivars and observed that high heritability with high genotypic coefficient of variation for fruit weight, plant height, number of fruits and number of branches per plant.

Joshi *et al.* (2004) observed moderate heritability and moderate genetic gain for number of fruits per cluster, fruit length, fruit breadth, stem end scar size, number of locules per fruit, whole fruit firmness, ascorbic acid content and plant height indicating additive gene effects. Low heritability and low genetic gain was observed for pericarp thickness. Moderate heritability and low genetic gain for harvest duration suggests the presence of dominance and epistatic effects. High heritability combined with high genetic gain was observed for shelf life indicating additive gene action.

Shravan *et al.* (2004) estimated heritability and genetic advance in 30 tomato genotypes for the characters like number of primary branches per plant, plant height, number of fruits per plant, fruit yield per plant and average fruit weight. The average fruit weight showed high heritabilities that ranged from 89.10% to 96.50%. The rest of the characters showed moderate heritability and low genetic advance. Moderate heritability associated with moderate genetic advance for plant height of 37 tomato genotypes of tomato were reported by Arun et al. (2004). Singh *et al.* (2005) estimated heritability and showed that heritability estimates (in the broad sense) were

high for all the characters for November planting except for lycopene content. Mahesh et al. (2006) estimated heritability and expected genetic advance in 30 genotypes of tomato and observed that fruit weight, fruits per plant and plant height exhibited very high heritability values along with high genetic gain. It indicated the importance of considerable additive gene effects and therefore greater emphasis should be given on these characters while selecting the better genotypes in tomato.

Kumari *et al*. (2007) reported that the estimates of heritability were high for all the characteristics and genetic advance was high for plant height, moderate for total number of fruit bearing branches, weight per fruit and days to maturity, while the remaining characteristics had low values of genetic advance. Golani et al. (2007) evaluated 20 tomato genotypes and observed high heritability with high genotypic coefficient of variation and genetic gain for 10-fruit weight, number of locules per fruit and fruit yield, which could be improved by simple selection. Saeed et al. (2007) observed that broad sense heritability was highest for number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%), reflecting the effectiveness of selection in the present germplasm of tomato improvement.

Pandit *et al.* (2010) evaluated12 varieties of tomato to estimate heritability and reported that high heritability coupled with high genetic advance as percentage of mean for average fruit weight, indicating the control of such character by additive gene. He also recorded that high heritability coupled with low genetic advance as percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components.

Singh *et al.* (2006) estimated heritability for nineteen genotypes of tomato and observed high heritability for ascorbic acid content, average weight of fruits, number of leaves per plant, number of locules per fruit, number of fruits per plant, leaf area and dry matter content. High estimates of heritability with high genetic advance was recorded in case of number of leaves per plant, average weight of fruits, number of fruits per plant and plant height, whereas high heritability with low genetic advance was recorded for number of locules per fruit, dry matter content, pericarp thickness and yield per plant.

2.13 Correlation and path co-efficient analysis

The main benefits of correlation analysis are that it helps companies determine which variables they want to investigate further, and it allows for rapid hypothesis testing. The main type of correlation analysis use Pearson's r formula to identify the degree of the linear relationship between two variables. But, correlation does not say anything about the cause and effect relationship (Roy, 2000). Path coefficient analysis is a very important statistical tool that indicates which variables (causes) exert influence on other variables (effects), while recognizing the impacts of multi colinearity (Hailu *et al*., 2016; Akanda and Mundt, 1996).

2.13.1 Correlation among the characters

The Correlation between characters is estimate to evaluate the inter-relationships between the characters which will help the breeders to choose selection techniques. In most cases, correlation between yield and yield contributing characters was studied because yield is one of the main targets of most of the breeders. The yield contributing characters are also interrelated among themselves. So, association of characteristics with yield and among its components is important for planning effective selective breeding programme for maximization of yield. Such correlation studies may vary due to agro-climatological variations from year to year. If any component of yield has higher heritability than yield itself and there is positive correlation between these, then there may be some possibility to increase in the total yield by selecting that component. But, negative correlation co-efficient among yield components were generally observed indicating selection for any component might not bring improvement for yield. Many authors have studied correlation between yield and yield contributing characters of tomato. Some pertinent recent literatures are reviewed in this section.

Forty nine genotypes of tomato (*Solanum lycopersicum* L.) were evaluated for various quantitative and quality traits by Kumar *et al*. (2013).The character association analysis indicated that total numbers of fruits/plant were significantly and positively correlated with gross yield (g/plant), marketable yield (g/plant), number of marketable fruits/plant and plant height (cm). Mahapatra *et al*. (2013) found fruit yield had positive and significant correlation with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit

width, and average fruit weight. It was observed that with increase in plant height, there was corresponding increase in number of primary branches per plant, days to 50% flowering and number of flower clusters per plant.

According to Monamodi *et al.* (2013) there was a strong positive significant correlation between numbers of branches per plant with fruit number per plant. This was because the more the branch number in a plant, such plant will produce more fruits in a plant. The experiment carried out by Buckseth et al. (2012) consisting of 40 genotypes of tomato to study the correlation among different quantitative and qualitative traits in tomato genotypes. The study revealed highly significant differences among the genotypes for all the characters studied.

Weight were positively and significantly associated with yield per plant, while number of fruits per plant was associated negatively revealed by Rani *et al*. (2010). According to Ara *et al*. (2009) there was a strong positive significant correlation between numbers of trusses per plant with fruit number per plant. This was because the more the truss number in a plant, such plant will produce more fruits resulting in more fruit weight. This is supported by the observed strong positive association between fruit number per plant and fruit weight per plant. Wright (2007) performed correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant. Golani et al. (2007) observed that fruit weight had significant and positive correlation with fruit length at both levels.

Correlation cofficient analysis was studied for thirty diverse tomato genotypes and noticed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones and yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness (Kumar *et al*., 2011). Correlation analysis performed by Wagh et al. (2007) showed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta -carotene, ascorbic acid and titratable acidity. Kumar et al. (2006) performed correlation coefficient analysis of 30 tomato genotypes and observed that number of fruits per plant had significant and positive correlation with fruit yield per plant. Megha *et al*. (2006) studied correlation in exotic tomato cultivars

to determine the correlation of 26 tomato cultivars for number of flowers per cluster, flower clusters at first picking, number of fruits per cluster, weight per fruit, yield per plant and total yield. They observed that improvement in yield could be managed by selection for number of flowers per cluster, flower clusters at first picking, number of fruits per cluster and weight per fruit. Manivannan *et al.* (2005) carried out correlation coefficient analysis in cherry and observed that fruit yield was significantly and positively correlated with the number of leaves and fruit weight. Arun *et al*. (2003) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight and plant height.

Joshi *et al*. (2004) performed correlation analysis of 37 tomato genotypes and showed that yield per plant was positively and significantly correlated with average fruit weight, fruit length, plant height and harvest duration. The average fruit weight was positively correlated with fruit length, fruit breadth. However, fruit weight was negatively correlated with the number of fruits per plant, number of fruits per cluster and ascorbic acid content. Correlation coefficient analysis of 30 tomato genotypes was performed and observed that number of fruits per plant had significant and positive correlation with fruit yield per plant Kumar *et al*. (2004). Similarly, inter-relationships was studied in 92 tomato genotypes. Highly significant positive correlation was observed between the number of fruits per plant and yield and between plant height and number of fruits per plant while negative correlation was noticed between the number of primary branches per plant and number of fruits per plant (Singh *et al*., 2005). Correlation coefficient analysis carried out by Kumar *et al*. (2004) for thirty diverse tomato genotypes and observed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones. He also observed that yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness.

Mohanty (2003) studied correlation coefficient analysis of 18 tomato cultivars and reported that yield was significantly and positively correlated with number of fruits per plant and number of day to harvest, and significantly but negatively correlated with plant height, number of branches per plant and average fruit weight and the number of fruits per plant was inversely related to average fruit weight. He also reported that most early cultivars were small fruited and low yielders.

Harer *et al*. (2002) studied correlation of thirty-seven tomato genotypes and showed that the number of fruits per cluster and number of fruits per plant were significantly and positively correlated with fruit yield per plant, whereas the number of primary branches per plant, fruit weight had negative association with fruit yield. Again Mohanty and Prusti (2001) reported that the phenotypic and genotypic correlations of fruit yield were significant and positive with days to first harvest, number of branches and fruits/plant, significant and negative with plant height and average fruit weight and number of fruits per plant was inversely related with average fruit weight.

Correlation coefficient analysis was studied by Nesgea *et al*. (2002) in 13 tomato genotypes and revealed that plant height, number of branches per plant, plant spread, fresh plant weight, number of fruiting clusters, number of days to 50% flowering, number of fruits per cluster and number of fruits per plant should be considered for the enhancement of the yield of tomato. The negative correlation was observed between fruit weight and fruit number, plant height and fruit weight, fruit weight and fruit yield and plant height Padma et al. (2002). Susic *et al.* (2002) showed that a significant negative correlation was between mean fruit mass and number of fruits per plant and a significant positive correlation was found between fruit length and fruit width. Tiwari (2002) observed that the highest positive and significant association was between the yield and length of fruit. At the genotypic level, the highest positive association was observed between the yield and length of fruit.

Dhaliwal *et al*. (2002) studied genetic parameters and correlations concerning fruit weight, yield plant^{-1}. The correlation studies indicated that it would be possible to develop firm fruited - high yielding true breeding lines. Dhankar *et al*. (2001) reported the average fruit weight under normal condition showed the highest positive effect on yield, therefore selection for average fruit weight, number of fruits per plant and number of fruits per cluster is important for improvement of fruit yield. Kumar et al. (2004) reported that a significant positive genotypic correlation was found bet wean pericarp thickness and juice viscosity and between lycopene and ascorbic acid contents; and locule number was negatively correlated with pericarp thickness.

Matin *et al.* (2001) studied phenotypic and genotypic correlations of 13 qualitative and quantitative characters of 26 genotypes of tomato and found that individual fruit weight had significant positive correlations with plant height and yield per plant. He

also reported that number of fruits per plant also had significant positive correlations with fruit dry matter content and found significant negative correlations between number fruits per plant and individual fruit weight. Dry matter was negatively correlated with individual fruit weight. Information on yield correlations is derived from data on eight yield components recorded in eighteen genetically diverse genotypes by Sharma *et al*. (1993). It is concluded that when selected for high yield in tomato, the main emphasis should be placed on number of fruits/plant. Fruit diameter and average fruit weight are also important components.

Prasad *et al.* (1999) observed very high and significant positive correlation co-efficient were between yield and fruit weight. Das et al. (1998) studied correlation co-efficient in fruit characters of tomato. They observed significant positive correlation of fruit yield per plant with number of fruits per plant. In an another experiment, Aditya *et al.* (1995) studied phenotypic and genotypic correlation co-efficient to find out the associations between eight characters of 44 genotypes of tomato. He reported that yield of fruits per plant showed significant positive correlations with plant height and number of fruits per plant; and insignificant positive correlation with weight of individual fruit (phenotypically) and number of seeds per fruit. Naidu, (1993) studied correlation coefficient analysis in 13 tomato genotypes and revealed that plant height, number of branches per plant, plant spread, fresh plant weight, number of fruiting clusters, number of days to 50% flowering, number of fruits per cluster, and number of fruits per plant should be considered for the enhancement of the yield of tomato.

Correlation of 20 cultivars of tomato was studied and found that yield per plant was negatively correlated with number of fruits per plant but positively and significantly correlated with individual fruit weight and plant height (Abedin and Khan, 1986). Dudi and Kalloo (1982) investigated yield per plant and seven yield related characters in 40 lines of tomato and observed that yield per plant and fruits per plant are positively correlated with total yield at the phenotypic level.Mallik (1985) studied phenotypic and genotypic correlations in an experiment with 19 varieties of tomato and observed that individual fruit weight had positive significant correlations with plant height and yield.

2.13.2 Path co-efficient analysis for yield

The study of correlation does not provide an exact picture of relative importance of direct and indirect influence of each of the component character towards the desired character. So, this can be overcome by following path coefficient analysis technique by further partitioning the correlation coefficient into direct and indirect effects. Path co-efficient is a standard tool which measures the direct influence of one character upon another and permits the separation of correlation co-efficient into components of direct and indirect effects. Path co-efficient between yield and yield contributing characters provides an exact picture of the relative importance of direct and indirect influences of each other component characters on fruit yield. It also provides valuable additional information for improving fruit yield via selection for its yield components. Recent publications involving path co-efficient analysis between yield and components of yield relevant to the present study are reviewed in this section:

Meena and Bahadur (2015) studied the character association for tomato germplasm under open field condition. They evaluated nineteen indeterminate tomato germplasm to estimate the nature and magnitude of associations of different characters with fruit yield and among themselves. In order to obtain a clear picture of the interrelationship between fruit yield per plant and its components, direct and indirect effects were measured using path coefficient analysis. The character showed high direct effect on yield per plant indicated that direct selection for these traits might be effective and there is a possibility of improving yield per plant through selection based on no. of flowers per plant, fruits per plant and fruit weight. Low residual effect indicates that the characters used explained almost all variability towards yield. Monamodi *et al*. (2013) used six determinate tomatoes. Results obtained suggest that fruit number and single fruit weight are relevant components to use as selection criteria for improving tomato yield. Path coefficient analysis results showed that marketable fruit number and single fruit weight were directly related to yield. In a different study, Rani *et al*. (2010) conducted a field experiment to study path coefficient for yield components and quality traits in 23 hybrids of tomato and exhibited that fruit weight had the highest positive direct effect on yield per plant, while, fruit weight was also having high positive indirect effect on yield per plant. Golani *et al*. (2007) performed path analysis and confirmed that the 10-fruit weight had the highest positive direct effect. Dhankhar and Dhankhar (2006) reported that number of fruits per plant had the

maximum positive direct effect. Manivannan et. al. (2005) carried out path coefficient analysis in cherry tomato and showed that fruit weight had the highest direct effect on fruit yield. Mayavel *et al*. (2005) reported that number of branches per plant had the highest positive direct effect on fruit yield. Whereas, plant height, number of fruits per cluster and number of fruits per plants had negative direct effects on fruit yield.

Singh *et al*. (2005) reported that the genotypic and phenotypic path coefficient studies described that number of fruits per plant had the maximum positive effect on yield followed by average fruit weight. Regarding indirect effects, it was observed that number of fruits per plant exhibited positive indirect effect towards fruit yield via number of branches per plant, it was negative via plant height, days to 50 per cent flowering. Singh and Cheema (2006) have revealed that positive direct effect of number of fruits per plant on yield. It was also reported by Kumar et al. (2004). Its positive indirect effects through average fruit weight mainly contributed towards its strong association with yield. The findings were on consonance with Mohanty (2003). Singh *et al*. (2005) performed path analysis between yield and yield contributing characters of 92 tomato genotypes and reported that number of fruits per plant exerted the high positive direct effect on yield followed by average weight per fruit, number of primary branches per plant, plant height, days to 50% flowering and number of fruits per cluster. However, days to first fruit set, number of primary branches per plant, plant height, number of fruit clusters per plant. Arun *et al*. (2003) revealed that the number of fruits per plant is the most important yield contributing character followed by plant heighst through path co-efficient analysis. Mohanty (2003) conducted a field experiment to study path coefficient analysis of eighteen tomato cultivars and observed that the number of fruits per plant and average fruit weight had positive direct effects on the yield and negative indirect effects on each other. Bodunde (2002) carried out a field experiment on path coefficient analysis and observed that plant height and fruit diameter directly affected yield in tomato.

Harer *et al*. (2002) carried out a field experiment to study path analysis of thirty-seven tomato genotypes and reported that number of fruits per cluster, average fruit weight and number of fruits per plant had direct maximum effects on fruit yield. Mohanty (2003) performed path analysis and showed that the number of branches per plant and average fruit weight exerted high positive direct effect on yield and high positive indirect effect with each other. Padma *et al*. (2002) performed path analysis and

revealed that number of branches, fruit weight, fruit length and number of fruits per plant exhibited positive effect on yield per plant at the genotypic and phenotypic levels. Matin and Kuddus (2001) observed that the maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. He also reported that days to first flowering, plant height and number of seeds per fruit had negative direct effect on yield per plant. Verma and Sarnaik (2000) conducted an experiment to perform path analysis of yield components in thirty tomato genotypes and observed that total number of fruits per plant, average weight of fruit and number of branches per plant exhibited positive and high direct effects. Domini and Maya (1997) evaluated 18 tomato varieties for the relationship of six yield components to yield in two different seasons. They reported that fruit number per plant was the most important character having a direct effect on yield either in early sowing.

Kumar *et al*. (2004) performed path analysis of thirty diverse tomato genotypes and indicated that fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight. In another experiment conducted by Aditya *et al.* (1995), he revealed that plant height and number of fruits per plant had high positive direct effect on yield and on the other hand, weight of individual fruit had positive indirect effect on yield per plant. Supe and Kale (1992) studied path analysis of seven different characters of twelve indigenous varieties of tomato and observed that plant height had negative direct effect on yield per plant.

Gomez (1987) reported that days to first flowering has negative direct effect on yield of tomato. Gorbatenko and Gorbatenko (1985) carried out path co-efficient analysis of tomato and found that individual fruit weight had an appreciable direct effect on yield per plant. Dudi and Kalloo (1982) studied path analysis in tomato and reported highest direct effects of early yield per plant, fruit weight and fruits per plant. Islam and Khan (1991) observed that fruits per plant, average fruit weight, plant height and days to first flowering had positive direct effects on yield of tomato. Alam *et al*. (2012) studied path co-efficient in 19 cultivars of tomato and found that maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant.

2.14 Combining Ability

In quantitative genetics two types of combining ability-general and specific, are studied. The genetic values of parents are expressed in terms of combining ability. Sprague and Tatum (1942) introduced these two combining ability and defined as the term 'general combining ability' is used to designate the average performance of a line in hybrid combination and 'specific combining ability' is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved. General combining ability is due to genes, which are largely additive in their effects and specific combining ability is due to the genes with dominance or epistatic effect. Here, in this part, an attempt has been made to review those early studies on combining ability of tomato are directly related to the present investigation.

Panchal *et al.* (2016) carried out combining ability analysis in a field experiment through line × tester method using a set of 40 genotypes of tomato including seven females, four males, their 28 single F_1 hybrids and one standard check (Abhinav) for ten characters. Among the female parents, JTL-12-04, JTL-12-10 and JTL12-12 are identified as the best general combiners for fruit yield per plant. It also exhibited significant and desirable GCA effects for primary branches per plant, plant height, number of primary branches per plant, average fruit weight and some of its direct components. Among the testers, JT-3 and AT-3 exhibited significant and high positive GCA effects for fruit yield per plant and also other characters like, number of primary branches per plant, number of fruits per plant, first flowering node and other important traits. Parents, JTL-12-14 and GT-1 were proved to be poor general combiner's for majority of the traits under study. High GCA effects for such characters have been also been reported in tomato by Yadav *et al.* (2013), Angadi *et al*. (2012), Kumari and Sharma (2012), Shende *et al.* (2012), Souza *et al*. (2012) and Singh *et al.* (2011). None of the parents was best general combiner for all the traits indicating differences in genetic variability for different characters among the parents.

In the similar study, SCA effect in 13 hybrids was highly significant for fruit yield per plant. The good general combining parents when crossed do not always produce high SCA effects. In the same way, poor general combiner parents do not always produce exhibit lower SCA effects. Angadi *et al.* (2012), Kumari and Sharma, (2012), Shende

et al. (2012), Souza *et al*. (2012), Singh *et al*. (2011), Singh and Asati (2011), Singh *et al*. (2010) and Virupannavar *et al*. (2010) also reported positive and significant SCA effects for fruit yield per plant in tomatoes. Again, Chandrasekhar and Rao (1989) evaluated Kj progenies and parental genotypes mid reported significant variations of GCA and SCA. SCA effects were significant and 29 positive in 6 crosses for plant height fruit weight and yield. 'Pusa Early Dwarf' was the best general combiner.

Reddy *et al*. (2017) used forty hybrids generated from crossing ten lines with four testers for combining ability analysis in tomato. The general combining ability (GCA) and specific combining ability (SCA) were significant for all the characters, indicating the importance of both additive and non-additive genetic components. But it is found that there was predominance of non-additive genetic components for expression of different traits in the present set of materials. Amongst the lines, CO-3, Pant T-3 and Flawery were best general combiners for yield along with other traits, whereas among the testers H-24 and H86 were best general combiner for yield along with other traits. The most promising specific combiners for yield and other traits were Flawery × Sel-7, Fla-7171 × Azad T-5, GT-20 × Azad T-5, C0-3 × Sel-7, B-S-31-3 × H-24. Hence, the present study was carried out to obtain information on combining ability involved in expressing the different characters in tomato. High GCA effect of variety CO-3 was associated with its high GCA effect for primary branches per plant, fruits per plant, average fruit weight and yield per plant. The good combining ability of line T-3 was due to high fruits per cluster, fruits per plant and yield per plant. Among the female parents, H-24 and H-86 were the best general combiners for yield per plant along with high GCA for fruits per plant and average fruit weight. It was followed by for number of fruits per plant 'B-S-31-3', 'Sel-7' and 'Pant T-3', and for average fruit weight 'H-24', 'CO-3' and 'Punjab Upama' were good general combiners in desired directions. It is observed that a total of 16 crosses exhibited positive and significant SCA for yield per plant. The promising combinations for yield were 'Flawery × Sel-7' followed by 'Fla-7171 × Azad T-5' and 'GT20 × Azad T-5'. It is observed that majority of the crosses with high SCA for yields were involved with high/low or average/low combining parents. But very few crosses showing low/low general combiners showed high SCA. The cross combinations showing high negative SCA for days to flowering (earliness) were Pant T-3 × Sel-7, 'EC521087 × H-24', 'Flawery × H-86' and 'B-S-31-

3 × H-86'. For plant height, estimates of SCA are desirable and the good specific combiners were B-S-31-3 × Azad T-5, Flawery × Sel7, Fla-7171 × Azad T-5 and Kashi sharad × H-86.The cross combinations viz., 'GT-20 × H-86' and 'T-Local × H-86' were good specific combiners for primary branches per plant. The best specific combiners for flowers per cluster were Flawery × Azad T-5, Punjab Upama × H-24, Kashi sharad × Azad T-5 and T-Local × H-24.The cross combinations *viz.,* T-Local × H24, Kashi Sharad × Azad T-5 and Flawery × Azad T-5 showed higher SCA for fruits per cluster. For number of fruits per plant, the cross of Pant T-3 × H-24, Fla-7171 × Azad T-5, Punjab Upama ×H-86 and B-S-31-3 ×H-24 exhibited high specific combining ability for the trait. Cross GT-20 × Azad T-5 and Fla-7171 × H-86 showed high SCA for average fruit weight.

In a study with thirteen parental lines were crossed in line X tester fashion comprising 10 lines and 3 testers by Kumar *et al.* (2013). The analysis of components of genetic variance for yield components showed that the main part of genetic variance was due to additive effect. Estimation of general combining ability (GCA) for yield and earliness showed that Pant T-3 had the highest GCA for increasing yield and Punjab Upma had the highest GCA for both earliness and average fruit weight. Cross combination CO-3 X Azad T-5 exhibit significant specific combining ability (SCA) for the most of desirable traits among all cross combinations. An overall appraisal of gca effects revealed that among parents H24 emerged out as good general combiner for plant height, days to 50% flowering, fruits per cluster and total yield per plant whereas, line DT-2 traced out good general combiner for days to 50% flowering, average fruit weight and TSS and CO-3 for days to 50% flowering and total yield per plant. Among the parents Punjab Upma was found to be good general combiner for plant height, days to 50% flowering, and total yield per plant. Pant T-3 for days to 50% flowering and total yield per plant, whereas H-86 for plant height TSS, titratable acidity and lycopene. Selection -7 for number of fruits per plant, average fruit weight, fruits per cluster, ascorbic acid, titratable acidity and lycopene, while NDTVR-60 for days to 50% flowering, average fruit weight, TSS, titratable acidity and lycopene. Fla-7171 good general combiner for plant height, fruits per cluster and lycopene whereas, Kashi Amrit only for lycopene. Male parent Floradade for plant height and days to 50% flowering while Kashi Sharad good general combiner for average fruit weight, total yield per plant an lycopene as well as Azad T-5 for plant height, days to 50%

flowering, fruits per cluster, TSS and Lycopene. Significant SCA effects in favourable direction as observed in many crosses for Plant Height, Days of 50% flowering, No. of primary branches, No. of fruits per plant, Average fruit weight, Fruit per cluster, Total yield per plant, TSS, Ascorbic Acid, Titratable Acidity and Lycopene. This result getting support from the findings of Singh *et al.* (2010), Saleem *et al.* (2009), Hannan *et al.* (2007), Premalakshme *et al.* (2006), Duhan *et al.* (2005) and Dhaliwal *et al*. (2004).

In 2014, Bhavna *et al.* experimented on diallel analysis to study the combining ability in tomato for fourteen characters including fruit yield and its component characters and found that both additive and non-additive variances were significant for fruit yield and its related traits indicating their improvements in the expression of various traits. The magnitude of non-additive variance was higher for fruit yield and its contributing traits indicating predominant role of non-additive gene action in the inheritance of the traits. Similarly, Farzane *et al.* (2012) conducted a study on 10 × 10 diallel cross set of tomato including reciprocals to find out the combining ability for yield per plant (kg) and yield components (number of fruits per plant, individual fruit weight (g)) and locule number. Significant differences among genotypes were obtained for all of traits. The variances for general combining ability (GCA) and specific combining ability (SCA) were highly significant indicating the presence of additive as well as non-additive gene effects except the number of fruits per plant and relative magnitude of these variances indicated that additive gene effects were more prominent for all of the traits. The tomato genotype 'Mb3' proved to be the best general combiner for yield and number of fruits per plant.

Sharma (2014) found the most promising general combiners were PT-2009-02 for fruit yield per hectare, fruit yield per plant, average fruit weight, number of locules and pericarp thickness, S-816 for plant height, branches per plant and number of locules, PT-1 exhibited the highest general combining ability for days to first harvest and days to last harvest. PT-20 for plant height, fruit length and fruit width, PT-09-06 for number of seeds per gram and number of fruit per plant, S-06-1 for TSS at immature stage, turning stage and red ripe stage. Most promising hybrids exhibiting significant sca effects were, PT-19 x Punjab Chhuharafor fruit yield per hectare, fruit yield per plant and average fruit weight, PT-41 x Punjab Chhuhara for dwarfness and number of locules, PT-19 x PT-3 and PT-11 x PT-3 for earliness, PT-41 x Roma for

number of fruit per plant and tallness, PT-20 x Pumjab Chhuhara for fruit length ripe stage, fruit width for higher number of seeds per gram, PT-1 x Punjab Chhuhara for fruit width and PT-09-06 x Punjab Chhuhara for pericarp thickness. The combining ability analysis indicated the importance of both additive and non-additive gene action for different growth, yield and fruit quality characters.

Izge *et al.* (2012) performed combining ability studies for yield and yield components of tomato in a set of 6 lines and 2 testers during the 2009 and 2010 dry season under irrigation results showed that both general combining ability (GCA) and specific 20 combining ability (SCA) were influenced by the environment. Out of the 12 hybrids studied, 4 each were found to be good specific combiners for number of flower clusters and plant height, and 5 for number of fruits per plant over both the environment combined. Cherry × Hong Large and Cherry × Roma 'VF' were the best specific combiners for number of fruits per plant and incidentally having high number of trichome count. Souza *et al.* (2012), also studied the general combining ability (GCA), specific combining ability (SCA) in a complete diallel cross of fifteen genotypes (five parents and ten hybrids) tomato breeding lines for plant fruit yield, 'IAC-2' was the best parental line with the highest GCA followed by IAC-4 and IAC-1 lines. The hybrids IAC-1 × IAC-2, IAC-1 × IAC-4 and IAC-2 × IAC-4 showed the highest effects of SCA. From twenty-five varieties of tomato Peter *et al.* (2012) in the same way reported that the component characters locules per fruit and plant height were found to be important for the expression of genetic divergence.

In 1997 Chadha *et al.* reported the lines 'BWR-5 (HR)', 'LB79-5 (W)' and 'EC 129156' as good general combiners for marketable fruits per plant. They also found that four Fruits showed significant positive SCA effects and lines 'BT-1Q', 'BWR-5 (HR)' and 'EC 191540' as food general combiners for average fruit weight. Five F1 showed significant positive SCA effects for average fruit weight. Similarly, Vedyasagar *et al.* (1997) in a line (8) × tester (3) analysis observed superiority of 3 F1S to their respective better parents for fruit weight. Ghosh *et al.* (1996) from a 9 × 9 diallel cross and graphical analysis of tomato reported the partial dominance for days to first flowering, plant height, equatorial fruit diameter and polar fruit diameter, number of locules per fruit and yield per plant. From graphical analysis they reported the over dominance for total soluble solids (TSS). Dod *et al.* (1995) also studied combining ability of tomato in a 12 parent's diallel (excluding reciprocals) for number

of locules per fruit, TSS% and reported the importance of both additive and non-additive genetic components. They also found a predominant role for additive gene action. ‘AC238’, ‘Punjab Chhuhara’ and ‘Pusa Ruby’ were the best general combiners.

E-Mahdy *et al.* (1990) in a study of complete diallel set of 6 lines under heat stress reported that additive gene effect appeared more important than non-additive gene effects for early yield, fruit weight, TSS % and Zhou and Xu (1990) studied Soluble Solids Content (SSC) in fruits from 20 hybrid combinations from a 5 × 4 diallel without reciprocals and observed 74.15 % GCA and 25.85 % SCA variance.

In an experiment by Al-Daej (2014) the cross 1×4 proved the best for fruit length, diameter, firmness and weight; 1×7 for number of locales; 2×4 for TSS and the lowest fruit thickness over mid-parents. The variance values of general combining ability (GCA) were higher than the specific combining ability (SCA) for all the traits except the fruit thickness. While, additive and none additive components were similar in fruit thickness. Conclusion: The SCA effects showed that the cross 1×4 was the best in fruit weight, 1×6 in firmness, 2×3 in fruit diameter and weight, 2×5 in number of locales, 2×6 in fruit thickness and 2×7 in TSS. The magnitude of additive variance was more pronounced for all the seven characters of interest of fruit quality both when F = 0 and F = 1 except for fruit thickness. The presence of excess additive variance was confirmed by the study results for most of the investigated traits of tomato crop. The study findings indicated the improved lines and testers for histerosis analysis for cross pollination to obtain improved tomato high quality and high yielding cultivars. The cross 1×4 proved the best for fruit length, diameter, firmness and weight; 1×7 for number of locales; 2×4 for TSS and the lowest fruit thickness over mid-parents. The variance values of general combining ability (GCA) were higher than the specific combining ability (SCA) for all the traits except the fruit thickness. While, additive and none additive components were similar in fruit thickness. The SCA effects showed that the cross 1×4 was the best in fruit weight, 1×6 in firmness, 2×3 in fruit diameter and weight, 2×5 in number of locales, 2×6 in fruit thickness and 2×7 in TSS. The magnitude of additive variance was more pronounced for all the seven characters of interest of fruit quality both when F = 0 and F = 1 except for fruit thickness. The presence of excess additive variance was confirmed by the study results for most of the investigated traits of tomato crop. The study findings indicated the improved lines

and testers for histerosis analysis for cross pollination to obtain improved tomato high quality and high yielding cultivars.

2.15 Heterosis

When two pure or inbred lines are mated, the performance of F_1 may be superior or inferior to mid parental value. This superiority or inferiority over mean is called heterosis. The magnitude of heterosis varies upon accumulation of favorable dominant alleles of F_1 offspring. The more the parental populations differ from each other for useful dominant alleles, the higher will be the magnitude of heterosis. This relationship is proved by Falconer (1981) and his formula for heterosis is- Heterosis in $F_1 = dy^2$, Where, d = Magnitude of dominance, y = Difference between the parental population for allelic frequencies at the locus. Though tomato is a self fertilized crop where degree of heterosis was theoretically noticed that it has been attributed to the fact that tomato was basically a highly out crossing genus which was later evolved into a self fertilized one. Heterosis is estimated in three different ways- 1. Mid parent heterosis, 2. Better parent heterosis and 3. Standard heterosis.

Heterosis is defined as the superior performance of heterozygous hybrid individual over its homozygous parental inbred line. Hybrid often posses comparatively increased vigor than their parents (Sprague, 1983). In 1900, when Mendel's laws were rediscovered and drew the attention of the biological world on problems of heredity, led to introduce interest in hybrid vigor as one aspect of quantitative inheritance. Widespread understanding of heterosis was laid by Shull in 1908. He established that a variety was a complex mixture of genotypes. The variability among strains undergoing inbreeding, including loss of vigor, was a consequence of segregation and the eventual homozygosity of desired and deleterious alleles. He also revealed that when certain lines were combined, F_1 yields exceeded those of the parental varieties. The word heterosis was coined by Shull and first proposed in 1914. In 1876, Darwin reconsidered earlier literature and also his own experiments in several crop species. Most of these studies point out that the offspring arising from cross-fertilization were more vigorous than those obtained by selfing. He also decided that self-fertilization is 'harmful' (Allard, 1960).

A study on tomato was conducted by Bhatt *et al*. (2001) to find out the degree of heterosis for yield with two important quality characters, ascorbic acid and total

soluble solids. Significant differences among genotypes were noticed for all the three characters. Similarly, in 2001 Kurian and Peter conducted an experiment with tomato hybrids and the obtained F_1 hybrids showed highest significant heterobeltiosis for TSS and lycopene. The F_l hybrids usually performed better in fruit quality, i.e. uniform ripening, high lycopene and total solids. Premalakshme *et al.* (2005) presented a study for development of F_1 hybrids with high yield and quality in tomato through diallel crossing comprising six parents. The studies exposed remarkable heterosis over the better parent for earliness, plant height, and laterals per plant. In order of merit, the three best performing F_1 hybrids showed heterosis percentage of 14.43 and 13.90 for marketable fruit weight and fruit yield over the standard check, respectively.

From 20^{th} century heterosis began to utilize commercially in agriculture. Heterosis played a vital role in the breeding and development of crop hybrids, although the genetic basis of the phenomenon remained imprecise (Me Daniel, 1986; Rood *et al.*, 1988). Maybe Hayes and Jones in 1916 first suggested that hybrid vigor be exploited in vegetables (Hayes, 1952). However, the commercial exploitation of heterosis was first raised in 1930's. Nowadays, most of the world's sugar is produced by hybrid sugarcane or hybrid sugar beets. In Japan, F_1 hybrid eggplants were economically used before 1952. Hybrid rice is now being produced on an increasing area in China. In short, the economic importance of hybrid varieties can be grasped in Gardner's (1968) statement. Development and utilization of heterosis has been the most important practical accomplishment of genetics so far.

Heterosis effect was first introduced in tomatoes by Hedrick and Booth in 1907. Then, heterosis for yield and its component has been demonstrated by many researchers (Singh and Singh, 1993; Daskalof *et al*., 1967; Burdick, 1954).

In 2014, Sharma used thirty crosses were evolved in a line x tester mating design with 10 genotypes as female parents (lines) and 3 genotypes as male parents (testers). The hybrids, PT-11 x PT-3 and PT-20 x Punjab Chhuhara were most promising for earliness exhibiting highest negative heterosis. With respect to plant height, hybrids, PT-09-06 x PT-3 and PT-20 x Roma were most promising for tallness and dwarfness, respectively. Hybrid combination, PT-09-06 x PT-3 exhibited most promising results with respect to heterosis for fruit yield per plant and total fruit yield per hectare. Most promising hybrid for number of locules was PT-20 x Roma which exhibited negative

heterosis. The best hybrids with respect to heterosis were PT-2009-02 x PT-3 for average fruit weight, PT-09-06 x Punjab Chhuhara for number of fruits per plant, PT-1 x Punjab Chhuhara for number of seeds per gram, PT-20 x Punjab Chhuhara for pericarp thickness, PT-20 x Roma for number of locules, PT-20 x Punjab Chhuhara for pericarp thickness and fruit width, PT-09-06 x Punjab Chhuhara for fruit shape index, S-06-1 x Punjab Chhuhara for TSS at turning and red ripe stage.

Ahmad (2002) conducted a crosse 8 X 8 diallel set of tomato without reciprocal in May and July sowing and found highest heterobeltiotic effects in both the sowing in the hybrid TM051 X TM017 (-21.76% and -13.43% respectively). Again, heterosis was estimated for yield and yield related characters, plant height, days to 50% flowering, number of fruits per plant, average fruit weight, average fruit diameter, number of fruits per cluster and total yield per plant (Kumar *et al*., 1988). Vedyasagar *et al*. (1997) also studied a line (8) X tester (3) of tomatoes involving bacterial wilt (*Ralstonia Solanacearum*) resistant parents and observed that 12 F_1s each demonstrated superiority to their respective better parents for days to 50% (early) flowering. Again, significant differences among genotypes were noticed for all the traits such as, for fruit yield per plant, i.e. 29.95% over better parent and 32.36% over standard check. The hybrid also revealed significantly high percentage of positive heterosis over better and standard parent for number of fruits per cluster, average fruit weight but revealed negative heterosis for plant height and day to 50% flowering which are desirable traits. Heterosis over better parent and negative heterosis for days to flowering over the better parent in many of the hybrids vigor in their diallel progenies reported by Singh (1993) and Ahmed *et al*., (1988).

Saeed *et al.* (2014), used Line × Tester analysis to identify the potential parents and their hybrids from a set of 12 crosses derived from three lines used as females ‘LA-2661’, ‘LA-2662’ and ‘017899’ and four testers, including ‘BL-1078’, ‘BL-1079’, ‘CLN-2413’ and ‘CLN-2418-A’. Results showed that heterosis and heterobeltiosis in desired direction were recorded in two crosses viz. LA-2662 × CLN-2418A and LA-2662 × BL-1078. F1 hybrid LA-2662 × CLN-2418A proved to be the best cross in overall performance. Again Singh *et al.* (2014) studied the heterosis for yield components and yield per plant using 7 × 7 half diallel cross between bacterial wilt-resistant per tolerant genotypes and high yielding varieties. The heterosis over better parent (BP) was up to the extent of -38.14%, 42.04%,36.14, -5.70%, -5.65%, 26.32%,

63.44%, 4.83%, 16.50%, 38.88%, 62.70% and 45.89% was recorded for plant height, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, days to maturity, fruit set, fruit length, fruit width, number of locules per fruit, number of fruits per plant, fruit weight and fruit yield per plant, respectively. The extent of heterosis was not as high as we are also looking for resistant to the bacterial wilt disease. The crosses showing heterosis for fruit yield per plant were not heterotic for all the characters under study. The heterosis for yield was generally accompanied by heterosis for yield components. Five promising crosses viz., Arka Ahuti × LO-5973, Arka Vikas × TWC 4, Arka Ahuti × TWC-4, BRH-2 × LO-5973 and CAU-TS-9 × LO-5973 were identified for developing high-yielding F1 hybrids/varieties of tomato with many desirable traits.

Kumar *et al.* (1995a) researches on seven tomato lines, their 21 F_1s and three commercial hybrid standards and observed more heterosis over superior parents for early yield (41.6%). Jamwal *et al*. (1984) also crossed 10 foreign lines and 3 local testers and studied heterosis. In 2014 Shankar *et al*. studied heterosis for quality and yield characters in tomato. The study revealed that majority of the hybrids exhibited significant qualified heterosis, heterobeltiosis, standard heterosis in desired direction. The hybrids showed higher performance and also showed high standard heterosis. The crosses recorded high negative standard heterosis for earliness and days to 50 percent flowering. Negative heterosis was observed over mid and superior parent for marketable maturity (Kumari *et al*., 2010). Negative heterobeltiosis for this trait also reported by Singh and Sastry (2011), whereas, positive heterosis for this character had been reported by Hannan *et al*. (2007) and Mirshamssi *et al*. (2006). Negative heterobeltiosis and standard heterosis were seen for this trait (Kumar *et al*., 2009b).

Ahmad (2002) and Ahmed *et al.* (1988) reported highest heterosis over better parent in the cross TM026 X TM025 which were 32.24% and 26.90% respectively for May and July sowing. Mid-parent heterosis and better parent heterosis were observed for various quantitative characters in tomato Chattopadhya and Paul (2012). Obvious heterosis over better-parent was observed for fruit yield per plant (148.82%), fruiting clusters per plant (111.64%), number of fruits per plant (103.33%), fruit weight (62.79%) and plant height (50.57%). Kumar *et al.* (1995b) examined on seven tomato lines, their 21 F_1s and three saleable hybrids showed greatest heterosis (%) over superior parents for plant height. Heterosis of tomato in a 7X7 diallel set (without

reciprocal) and found maximum -45.40 per cent heterosis for plant height in the cross Japanese X Anobik over parental value studied by Bhuiyan (1982). Heterosis for plant height was also studied by Dod *et al*. (1992) from diallel cross.

Chattopadhyay and Paul (2012) a total of 25 entries consisting of 13 diversified genotypes of tomato along with their 12 F1 hybrids were evaluated during two consecutive rabi seasons which showed that Pronounced heterosis over better- parent was observed for number of locules per fruit, fruit length etc. Heterosis over mid parent and better parent, however, for most of the characters were in negative direction. Some of the parents having good potentiality for generating high cross combination for most of the quality traits under study were identified. Singh *et al.* (2012) in a complete 7 × 7 half diallel cross of tomato evaluate with parents for heterotic manifestation of yield and yield attributing characters. The crosses showing heterosis for yield per plant were not heterotic for all the characters under study. Five promising crosses viz., Ox-heart × Sutton Roma, Marglobe Supreme × Sutton Roma, Money Maker × Pusa Early Dwarf, Marglobe Supreme × Money Maker and Sutton Roma × Pusa Early Dwarf were identified for developing high yielding F1 hybrids/varieties of tomato with many desirable traits.

Souza *et al*. (2012) evaluated the yield and its components traits, *viz*., fruit yield per plant, fruit number per plant, average fruit weight, no. of cluster per plant, fruit number per cluster, fruit wall thickness and number of locules per fruit including some quality components, namely, total soluble solids, total titratable acidity, fruit length, fruit width, length to width ratio by studying heterosis in tomato. Again, Sharma and Sharma (2013) estimated the heterosis on the basis of mean performance and reported 43.67 percent heterosis over better parent for yield. The heterobeltiotic effect for number of fruits per cluster ranged from -34.39 to 33.0 percent. The fruit yield among the crosses varied from 764.33 to 1808.23 (g). Significant heterobeltiosis was observed in desirable direction for all the traits except days to first picking and total soluble solids. Maximum and significant heterosis in favorable direction was observed for yield, plant height, fruit number and fruits per cluster reported by Kumari and Sharma (2011). Heterosis was considerable in all hybrids. Resende *et al*. (2000) examined heterosis of tomato for number of fruits in 1^{st}, 2^{nd} and 3^{rd} trusses, found higher heterosis values in the hybrids than the standard cultivar Santa Clara for number of fruits per truss. Ninety-one F_1 crosses of tomato in a diallel set involving

13 percents (excluding reciprocals) to study heterosis for number of fruit/truss and found appreciable heterosis over best parental lines evaluated by Bhatt *et al*. (1999). Again, Hannan *et al*. (2007a) determined the heterosis in tomato for yield and yield component characters, *viz*., plant height at 60 days after transplantation, days to first flowering, number of flower per cluster, number of fruits per plant, fruit weight per plant, days to first fruit ripening. Gul *et al*. (2010) studied in tomato for degree of heterosis in yield and its five yield attributing components, *viz*., number of flowers per cluster, number of fruits set per cluster, fruit length, fruit width, fruit weight and fruit yield per plant. The degree of heterosis for plant height, fruit weight, bacterial wilt incidence and yield per plant were determined by Singh and Asati (2011). Ahmad (2002) found that highest heterosis over better parent in the cross TM041 X TM044 which were 159.70 and 181.36 percent respectively for May and July sowing.

Vedyasagar *et al*. (1997) studied in a line (8) X tester (3) analysis perceived better parents heterosis in 5 F_1s for marketable fruits/Plant. Similarly, Sekar (2001) observed that more than 10% heterosis over the best parent for the number of fruits per plant and yield per plant. In a study of line X tester analysis Dev *et al*. (1994) observed heterosis over the better parent 115.7% for the number of fruits per plant. Jamwal *et al*. (1984) crossed among 10 foreign lines and 3 local testers and observed that heterois for fruit number per plant. Bhuiyan (1982) also observed that maximum better parent heterosis (113.92 percent) for number of fruits per plant in the cross Fujuki X CL. 8d-0-7-l-0-0. In the same way, Chaudhury and Khanna (1972) reported that heterosis in 17 hybrids out of 28 hybrids for fruit number and with maximum increases over the better parent of 49.93% under high temperature growing environment.

Heterosis for the trait fruit weight was reported by many authors as Scott *et al*. (1986). Islam *et al*. (2012) studied the heterotic performance in F_1 generation of tomato. The hybrids showed that significant variation in heterosis. Chattopadhyay *et al*. (2012a) reported that mid-parent heterosis and better parent heterosis for various quantitative traits in tomato. Prominent heterosis over better-parent was observed for fruit yield per plant (148.82%), fruiting clusters per plant (111.64%), number of fruits per plant (103.33%), fruit weight (62.79%) and plant height (50.57%). Better parent heterosis for average fruit weight in the cross TM051 X TM017 reported by Ahmad (2002). Greatest heterosis over superior parents for average fruit weight (30.8% and 32.27%)

respectively, reported by Kumar *et al.* (1995a) and Kumar *et al.* (1995). A line (8) X tester (3) analysis observed superiority of 3 F_1S to their respective better parents for fruit weight (Vidyasager *et al*., 1997). Ahmed *et al*. (1988) also reported that heterosis over the better parent for fruit weight (Singh *et al.*, 1995). Heterosis for the trait fruit weight under high temperature environments was reported by Scott *et al.* (1986). Again, Alvarez (1985) studied that hybrid INCA 21X INCA 3 was superior to the better parent for average weight in summer. Maximum better parent heterosis (8.45 percent) for individual fruit weight in the cross Fujuki X World champion was observed by Bhuiyan (1982).

Heterosis over better parent for fruit size in few cases in tomato was reported by Scott *et al.* (1986). Highest better parent heterosis in the cross TM051 X TM025 (22.25 percent in May sowing and 2.87 percent in July sowing) for fruit length (Ahmad, 2002). A full diallel without backcrosses concerning seven parents recorded maximum heterosis for fruit length (4.62%) in the hybrid VI00 X 93/10 (Susie, 1998).Again, five new processing tomato lines as female parents to cultivars Meidong and Jiazhouzhiyong were crossed and perceived higher heterosis for fruit length (Wang *et al.*, 1998b). Singh *et al*. (1995) reported that heterosis in some crosses for length of fruit. Also Scott *et al*. (1986) and Chaudhury and Khanna (1972) reported that heterosis over better parent for fruit size in few cases in tomato. Evaluation trial of tomato hybrids in summer where also found that heterosis in equatorial diameter in the majority of cases (Alverez, 1985). Highest better parent heterosis in the cross TM051 X TM017 (22.65% in May sowing and 15.97% in July sowing) for fruit breadth (Ahmad, 2002). Susie (1998) studied on full diallel without backcrosses concerning seven parents and recorded maximum heterosis for fruit width (4.56%) in the hybrid D150 X NO-IO. Wang *et al*. (1998b) studied on using five lines and two cultivars observed that higher heterosis for fruit length. Chaudhruy and Khanna (1972) also reported that heterosis for fruit size, with maximum increases over the better parent of 6.82% (Chaudhury and Khanna, 1972). Heterosis for equatorial diameter in tomato was reported by Alvarez (1985).

Lower number of locules in oval and pear shaped variations like Roma and Italian Red Pear (Roy and Choudhary, 1972). The locule number ranged between 4 or 5 among F_1 hybrids like Mangla, Rupali and Vaishali (Sethi and Anand, 1986). Heterosis for locule number is also studied by Dod and Kale (1992), Ghosh *et al*.

(1997), Srivastava *et al*. (1998a), Premalakmhme *et al*. (2002), Anita *et al*. (2005) and Ahmed *et al*. (2011). Singh *et al*. (2005) and Kumar *et al*. (2009) reported that significant negative heterosis for number of locules per fruit. Heterosis using line x tester analysis between bacterial wilt (*Ralstonia solanaccarxm*) resistant/tolerant compliances (Sakthi, LE 214 and LE 206) and processing cultivars (HW 208F, St 64, Ohio 8129, Fresh Market 9 and TH 318) and identified heterotic hybrids for locule number (LE 206 X Ohio 8129 and LE214XSt 64) (Kurian and Peter, 2001). Sherif and Hussein (1992) also observed significant heterosis for fruit yield per plant, as reflected by differences in the highest yields of parents and F1 hybrids: 845.6 and 2084.7 g per plant for 'Yellow Pear' and Sweet 100 × Yellow Pear, respectively.

A trial comprising 15 hybrids and 8 parental lines was in conducted by Kumar *et al.* in 2012 and heterosis was estimated in fifteen single experimental cross hybrids, obtained by five parental lines namely H-24, DT-2, CO-3, Punjab Upma, Pant T-3 and three testers of tomato *viz*. Floradade, Kashi Sharad, Azad T-5 for yield and yield related traits; plant height, days to 50% flowering, number of fruits per plant, average fruit weight, fruit diameter, number of fruits per cluster and total yield per plant. Significant differences among genotypes were observed for all the traits. Positive and highly significant heterosis was found for number of fruits per plant 25.27%, 25.13% and 21.13% over better parent and 29.95%, 25.27% and 24.46% over standard parent and for total yield per plant 32.06%, 18.34%, 13.36% and 11.27% over better parent and 31.83%, 31.14%, 30.10% and 25.26% over standard check 'Azad T-5'. The hybrid also showed significantly high percentage of positive heterosis over better and standard parent for number of fruits per cluster, average fruit weight and the hybrids showed negative heterosis for plant height and day to 50% flowering which are desirable characters. Similarly, in an experiment conducted by Ramana *et al.* in 2011 ten parents (EC-165749, EC-157568, EC-164838, LE-56, LE-62, LE-64, LE-65, LE-66, LE-67 and LE-68) were crossed in diallele mating design (without reciprocals). The resultant 45 F1's were evaluated along with their parents and two standard checks (Siri and US-618) for six characters viz., plant height (cm), number of primary branches per plant, days to 50% flowering, number of fruits per cluster, average fruit weight (g) and fruit yield per plant (kg). Studies on heterosis revealed that majority of the hybrids exhibited relative heterosis, heterobeltiosis and standard heterosis in desirable direction. The potential crosses viz., LE-64 × LE-66, LE-56 x LE-68, EC-

157568 x LE-68 and EC-164838 x LE-66, exhibited high standard heterosis and high per se performance for fruit yield per plant, which offers scope for commercial exploitation through heterosis breeding.

Kumar *et al.* (2004) used six diverse parental lines of tomato were crossed in a 6 × 6 diallel mating design excluding reciprocals. The 15 F1 hybrids and two standard checks (HYB-Roop-666 and TS-15) along with their parents Top three cross combinations for fruit yield per plant as per their per se performance, ArkaAbha x Punjab Chhuhara, ArkaMeghali x Punjab Chhuhara, Punjab Chhuhara x Best of All came out to be expressing significantly positive standard heterosis. Most of the crosses manifested highly significant heterosis over bothchecks, for fruit length and Fruit breadth that reflect that hybrids have better chance of having bigger fruits in case of tomato. For average fruit weight, ArkaAbha x ArkaMeghali, ArkaMeghali x Punjab Chhuhara proved to be the best hybrids which has expressed significant positive results for all types of heterosis including over checks.Overall, hybrids have reported greater plant heights as compared to check and mid parents which indicate that heterosis can be exploited for further improving the plant heights.ArkaMeghali x Punjab Chhuhara found to be the best cross combination which have significant favourable heterosis, of all three types, for vitals yield attributing traits i.e. number of fruits per cluster and number of fruit clusters per plant. This study was same as the findings of Ahmed *et al*. (2011), Singh and Sastry (2011), Kumari and Sharma (2011), Kumari *et al*. (2010), Gul *et al*. (2010), Kumar *et al*. (2009), Singh *et al.* (2008), Rani and Veeraragavathatham (2008), Hannan *et al*. (2007a), Mirshamssi *et al*. (2006), Premalakshme *et al*. (2005), Anita *et al.* (2005), Singh *et al.* (2005a), Tiwri and Lal (2004), Thakur *et al.* (2004), Gunasekera and Parera (1999), Singh *et al.* (1995), Pujari and Kale (1994), Dev *et al.* (1994) and Ahmed *et al*. (1988).

CHAPTER III
MATERIALS AND METHODS

This chapter covers the detailed methodology used in the execution of the experiments. The experiments were conducted in four years for evaluation of different traits on different genotypes and on their cross combinations. The experiments were divided into three parts, *viz.*, Experiment 1 (Mean performance, genetic diversity and cross-ability analysis in tomatillo), Experiment 2 (Heterosis and combining ability analysis in tomatillo) and Experiment 3 (Genetic variability and character association in F_2 generation of tomatillo for quantitative and qualitative traits). The different steps of these experiments are described here chronologically in section 3.1, in 3.2 and in section 3.2 respectively.

3.1 Experiment 1: Mean performance, genetic variability and cross-ability analysis in tomatillo

A field experiment was conducted at central farm of Sher-e-Bangle Agricultural University, Sher-e-Bangla Nagar, Dhaka during the period from October 2017 to March 2018 to characterize collected materials based on various morphological traits and to identify potential genotypes. This section comprises a brief description of locations experimental site, planting materials, climate and soil, seed bed preparation, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data collection procedure, statistical and biochemical analysis procedure etc. which are presented as follows.

3.1.1 Experimental site

The experiments were carried out at the central experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh, during the period from October 2017 to March 2020. Location of the experimental site is 23°74' N latitude and 90°35' E longitude with an elevation of 8.6 meter from sea level in Agro-ecological zone of "Madhupur Tract" (AEZ-28). The experimental site is shown in the map of AEZ of Bangladesh in Appendix I.

3.1.2 Climate and soil

Experimental site was located in the subtropical climatic zone, set separated by plenty of sunshine and moderately low temperature prevails during October 2017 to March 2020 (Rabi season) which is suitable for tomatillo as well as tomato growing in Bangladesh. The soil was sandy loam in texture having pH 5.46 to 5.62. Weather information and physicochemical properties of the soil are presented in Appendix II and in Appendix III respectively.

3.1.3 Planting materials

Five genotypes of tomatillo which were originated from Mexico and seeds were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207 and Condor Seeds Production inc., Arizona, USA, which were used as the planting materials for the experiment. The name and source of collection of these genotypes are presented in Table 1.

Table1. Name and source of collection of the Tomatillo genotypes used in the Experiment 1

SL. No.	Genotype	Name/Accession No.	Source of collection
1	G1	SAU Tomatillo 1	Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University
2	G2	SAU Tomatillo 2	
3	G3	PI-003	
4	G4	PI-004	
5	G5	PI-005	Condor seed production Inc. USA.

3.1.4 Preparation of seed bed and seedlings raising

Seeds were sowing on 25th October, 2017 in the seedbed. Before that beds were prepared by well making of soil with decomposed manure. Before sowing, seeds were treated with Bavistin @ 1g/L for five minutes. Seedlings of all genotypes were raised in seedbeds in the central farm of Sher-e-Bangla Agricultural University, Dhaka-1207. Seeds were sown in rows spaced at 10 cm apart, beds were watered regularly to ensure maximum seedling growth. Seedlings were raised using regular nursery practices. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings became 30 days old then it was transplanted to the main field. Seedbed preparation and raising of seedlings were done in appropriate time with recommended operations and are shown in Plate 1A.

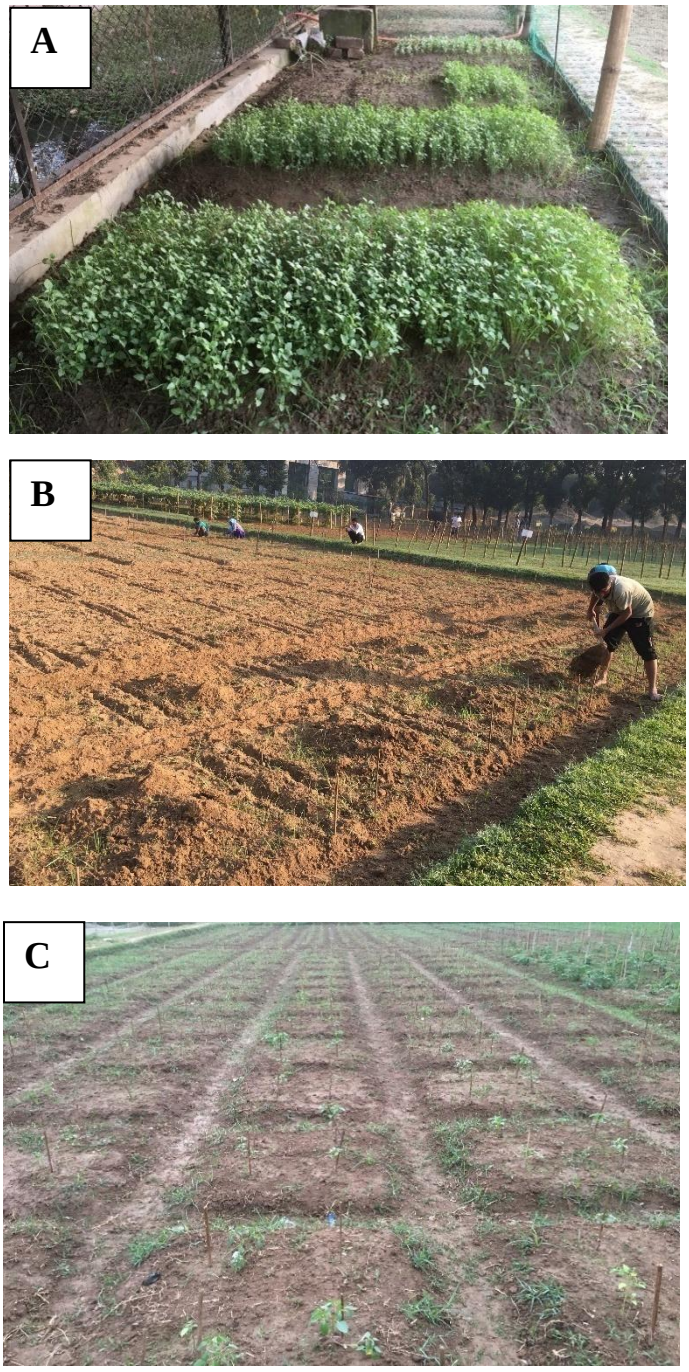


Plate 1. Different activities during raising of seedling, transplanting and land preparation. A. Raising of seedlings, B. land preparation and layout, C. Seedling transplanting

3.1.5 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth and provide good soil aeration. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. Some activities of land preparation is shown in Plate 1B.

3.1.6 Manure and fertilizer application

Generally, cow dung, Urea, TSP, and MOP fertilizers are required for tomatillo cultivation. Table 2 displays the rate of fertilizer application. The entire amount of cow dung was applied seven days before land preparation. Total TSP and half of MOP were applied at the time of final land preparation. Half of MOP and one third of urea were applied after 15 days of transplanting. Another one third of urea was applied after 30 days and remaining one third was applied after 40 days of transplanting.

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

SL. No.	Fertilizer/Manures	Dose (Quantity/ha)
1	Urea	550 kg
2	TSP	450 kg
3	MOP	250 kg
4	Cow Dung	10 ton

3.1.7 Design and layout of the experiment

The experiment was laid out in Randomized Complete Block Design (RCBD) with four replications. There were five genotypes and spacing was 60 cm × 40 cm. The field size was 400 m^2. All five genotypes were planted in each replication. The layout during land preparation is demonstrated in Plate 1B.

3.1.8 Transplanting of seedlings

When the seedlings become 30 days old, they were transplanted in the main field Plate 1C. Enough precautions were taken in pre- and post- transplanting stage of seedlings.

3.1.9 Intercultural operations

Necessary irrigation and intercultural operations were provided as and when required. Weeding was performed in all plots as and when required to keep plants free from weeds. Generally, the first and second weeding were done after 20 days and 40 days of transplanting respectively. Earthing up was done twice during the crop growing period. When plants were well established, stalking was done by bamboo stick between 20-30 days after transplanting to keep the plants erect. The plants were fastened loosely with the bamboo stick by jute string to keep them erect and prevent from lodging (Plate 2A). Tagging and labeling were done properly for each plant.

3.1.10 Harvesting and Processing

Fruits from various lines ripened gradually over a lengthy period of time and at different times. Harvesting lasted for roughly one and a half months. Mature fruits were harvested when the surrounding papery husk of the fruit turned from green to brown and begins to split. The fruit may bright green, purple, or yellow depending on the genotype. The fruits per plant were allowed to ripe and then seeds were collected and stored at 4^{o}C for future use. Harvesting was started from January and finished in March.

3.1.11 Data collection

Data were recorded on different yield and yield contributing, traits. A view of data collection in the field is presented in Plate 2B and in Plate 2C. Five plants in each replication of each genotype were selected randomly and were tagged. These tagged plants were used for recording of data in respect of the following parameters:

3.1.11.1 Plant height (cm)

It was measured in centimeter (cm) from the base to tip of the plant. Plant height of each plant at 65 days of mature stage was measured using meter scale and mean was calculated and recorded accordingly.

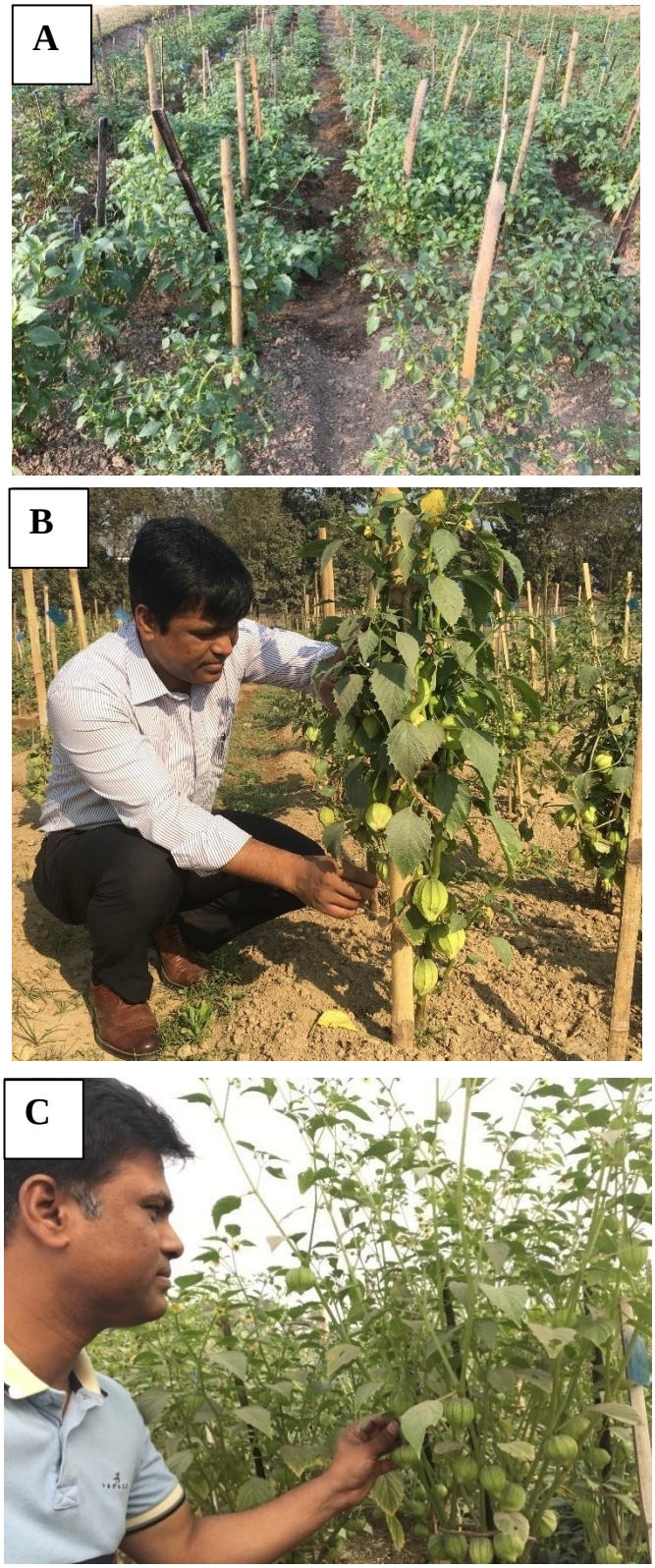


Plate 2. Different activities of intercultural operation and data collection. A. Stalking, B-C. Data collection

3.1.11.2 Number of branches per plant

Total number of branches arisen from the main stem was counted as the number of branches per plant.

3.1.11.3 Days to first flowering

The days to first flowering was counted from the date of tomatillo transplanting date to date of first flowering.

3.1.11.4 Days to 50% flowering

Days to 50% flowering were recorded from sowing date to the date of 50% flowering of every entry.

3.1.11.5 Number of fruits per plant

The total number of marketable fruits harvested from each plant was counted and recorded

3.1.11.6 Average fruit length (cm)

Fruit length was measured using Digital Caliper-515 (DC-515) in millimeter (mm). Later it was converted to centimeter (cm). Mean was calculated for each treatment and genotype.

3.1.11.7 Average fruit diameter (cm)

Fruit diameter were measured using Digital Caliper-515 (DC-515) in millimeter (mm). Later it was converted to centimeter (cm). Mean was calculated for each treatment and genotype

3.1.11.8 Leaf length (cm)

Three leaves length from each plant at mature stage was measured in cm using meter scale and mean was calculated.

3.1.11.9 Leaf width (cm)

Three leaves breadth from each plant at mature stage were measured in cm using meter scale and mean was calculated.

3.1.11.10 Leaf length × width (cm2)

Mean value of leaf length (cm) and width (cm) were multiplied and thus calculated leaf length × width in cm2.

3.1.11.11 Leaf area index

Leaf area index was measured after taking leaf length and leaf breadth and also by leaf area index meter.

3.1.11.12 Days to maturity

The days to maturity was counted from the date of tomatillo genotypes transplanting (DAT) to date of first harvesting in different genotypes in different plots.

3.1.11.13 Average fruit weight per plant (g)

Fruit weight was measured by electric precision balance. Average fruit weight per plant was recorded from randomly selecting five fruits per plant and mean value was calculated. Average fruit weight per plant was expressed in gram (g).

3.1.11.14 Number of seeds per fruit

All the seed extraction and drying were done from harvested fruits from representative tomatillo plants. Then number of seed per fruit was counted. Seeds were collected and preserved for future use/experiments.

3.1.11.15 Yield per plant (g)

Yield per plant was recorded from all harvests of each plant and expressed in gram (g) per plant.

3.1.11.16 Yield per plot (kg)

Total yield per plot was measured by multiplied with total number of plants per plot in kilogram (Kg).

3.1.11.17 Yield per hectare (ton)

Yield of plot converted into per hectare of yield and then was expressed in tons per hectare.

3.1.12 Development of F_1 hybrids

In first year collected materials of five parents were sown in the research Farm of SAU, maintaining line distance in the seed bed during rabi season in 2016. Normal agronomic practices were applied in the seed bed as well as in the main field after transplantation. At the flowering stage, hybridization was performed. From all parents both male and female were selected on the basis of more desirable morphological characters. Prior to making crosses both mature and over mature buds including already open flowers in inflorescence of female parents, male parts were remove carefully. Forceps were cleaned and dipped into alcohol after each touch to prevent contaminations.

3.1.12.1 Emasculation

Day before hybridization selected flowers were emasculated. Few mature unopened and little opened flower buds, which were supposed to open in the next day indicated by the yellowish color at the tip of the buds were selected for emasculation. By removing the sepals and petals with the help of a pair of the fine pointed forceps, emasculations were done. Anthers were removed very carefully with the fine forceps, so that the gynoecium was not injured. The flowers were then bagged.

3.1.12.2 Pollination

The next day of emasculation, at the very morning pollen from each genotype was collected. These pollens were then dusted on the stigmatic surface of the emasculated flowers reciprocally. After crossing, the pollinated flowers were bagged with clean paper envelops and clipped properly with proper labeling. Bags were removed after three to four days of pollinations and flowers allow to grow normally. After fruit setting the fruits were tagged carefully to ensure correct selection of crosses. The hybrid fruits were collected on proper maturation and F_1 seeds of each cross were collected separately. Seeds were properly dried and stored in a refrigerator at 4 ^{o}C till next season.

3.1.12.3 Cross combination

During hybridization, each genotype was once counted as female parent and then male parent respectively. Thus full diallel crosses were made (Table 3). To ensure

100% success in cross product same crossing was done several times in several flowers.

Table 3. Different cross combinations among five genotypes

Parents	**G1**	**G2**	**G3**	**G4**	**G5**
G1		G1 × G2	G1 × G3	G1 × G4	G1 × G5
G2	G2 × G1		G2 × G3	G2 × G4	G2 × G5
G3	G3 × G1	G3 × G2		G3 × G4	G3× G5
G4	G4 × G1	G4 × G2	G4 × G3		G4× G5
G5	G5 × G1	G5 × G2	G5 × G3	G4× G5	

3.1.13 Development of F_2

In second year to generate F_2 generations, F_1 plant from each cross was crossed at the flowering stage through hand emasculations and controlled pollinations. Paper bags were used to avoid contaminations. Pollinations to emasculated flower were repeated, if necessary for maximizing the seed setting.

3.1.14 Statistical analysis

Mean data of all characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all the characters under study using the mean values (Singh and Chaudhury, 1985). 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. All of these analyses were carried out in R software.

3.1.14.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955) using variability packages in R software.

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

3.1.14.2 Estimation of 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 % = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

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

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.1.14.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955) using Variability packages in R software.

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

3.1.14.4 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, $GA = K. h^2. \sigma_p$

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

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.1.14.5 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):

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

3.1.14.6 Estimation of genotypic and phenotypic correlation co-efficient

To calculate 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 using variability packages in R. 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

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

Where,

σ_{pxy} = Phenotypic covariance between the trait

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

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

3.1.14.7 Estimation of path co-efficient

Path co-efficient estimation was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield

and yield contributing characters were partitioned into direct and indirect effects on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3….and 113 on yield y, a set of simultaneous equations (twelve equations in this example) is required to be formulated as shown below:

$r_{1.y}= P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y}+ r_{1.9} P_{9.y} + r_{1.1}P_{10.y} + r_{1.11} P_{11.y} + r_{1.12} P_{12.y} + r_{1.13} P_{13.y}$

$r_{2.y}= r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y}+ r_{2.9} P_{9.y} + r_{2.10}P_{10.y} + r_{2.11} P_{11.y} + r_{2.12} P_{12.y}+ r_{2.13} P_{13.y}$

$r_{3.y}= r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y}+ r_{3.9} P_{9.y} + r_{3.10}P_{10.y} + r_{3.11} P_{11.y} + r_{3.12} P_{12.y} + r_{3.13} P_{13.y}$

$r_{4.y}= r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y}+ r_{4.9} P_{9.y} + r_{4.10}P_{10.y} + r_{4.11} P_{11.y} + r_{4.12} P_{12.y}+ r_{4.13} P_{13.y}$

$r_{5.y}= r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y}+ r_{5.9} P_{9.y} + r_{5.10}P_{10.y} + r_{5.11} P_{11.y} + r_{5.12} P_{12.y} + r_{5.13} P_{13.y}$

$r_{6.y}= r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y}+ r_{6.9} P_{9.y} + r_{6.10}P_{10.y} + r_{6.11} P_{11.y} + r_{6.12} P_{12.y}+ r_{6.13} P_{13.y}$

$r_{7.y}= r_{1.7} P1.y+ r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.y}+ r_{7.9} P_{9.y} + r_{7.10}P_{10.y} + r_{7.11} P_{11.y} + r_{7.12} P_{12.y}+ r_{7.13} P_{13.y}$

$r_{8.y}= r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y}+ r_{8.9} P_{9.y} + r_{8.10}P_{10.y} + r_{8.11} P_{11.y} + r_{8.12} P_{12.y} + + r_{8.13} P_{13.y}$

$r_{9.y}= r_{1.9} P_{1.y} + r_{2.9} P_{2.y} + r_{3.9} P_{3.y} + r_{4.9} P_{4.y} + r_{5.9} P_{5.y} + r_{6.9} P_{6.y} + r_{7.9} P_{7.y} + r_{8.9} P_{8.y} + P_{9.y} + r_{9.10}P_{10.y} + r_{9.11} P_{11.y} + r_{9.12} P_{12.y} + r_{9.13} P_{13.y}$

$r_{10.y} = r_{1.10} P_{1.y}+ r_{2.10} P_{2.y} + r_{3.10} P_{3.y} + r_{4.10} P_{4.y} + r_{5.10} P_{5.y} + r_{6.10} P_{6.y} + r_{7.10} P_{7.y} + r_{8.10} P_{8.y} + r_{9.10} P_{9.y} + P_{10.y} + r_{10.11} P_{11.y} + r_{10.12} P_{12.y}+ r_{10.13} P_{13.y}$

$r_{11.y} = r_{1.11} P_{1.y}+ r_{2.11} P_{2.y} + r_{3.11} P_{3.y} + r_{4.11} P_{4.y} + r_{5.11} P_{5.y} + r_{6.11} P_{6.y} + r_{7.11} P_{7.y} + r_{8.11} P_{8.y} + r_{9.11} P_{9.y} + r_{10.11} P_{10.y} + P_{11.y} + r_{11.12} P_{12.y} + r_{11.13} P_{13.y}+ r_{11.13} P_{13.y}$

$r_{12.y} = r_{1.12} P_{1.y}+ r_{2.12} P_{2.y} + r_{3.12} P_{3.y} + r_{4.12} P_{4.y} + r_{5.12} P_{5.y} + r_{6.12} P_{6.y} + r_{7.12} P_{7.y} + r_{8.12}$

$$P_{8.y} + r_{9.12} P_{9.y} + r_{10.12} P_{10.y} + r_{11.12} P_{11.y} + P_{12.y} + r_{12.13} P_{13.y}$$

$$r_{13.y} = r_{1.12} P_{1.y} + r_{2.12} P_{2.y} + r_{3.12} P_{3.y} + r_{4.12} P_{4.y} + r_{5.12} P_{5.y} + r_{6.12} P_{6.y} + r_{7.12} P_{7.y} + r_{8.12}$$

$$P_{8.y} + r_{9.12} P_{9.y} + r_{10.12} P_{10.y} + r_{11.12} P_{11.y} + P_{12.y} + r_{13.13} P_{13.y}$$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,….13)

1 = Plant Height

2 = leaf area

3 = No. of branches per plant

4 = Days to 1st flowering

5 = Days to 50% flowering

6 = Days to maturity

7 = Number of fruits per plant

8 = Fruit length (cm)

9 = Fruit diameter (cm)

10 = Individual fruit weight

11 = seeds per fruit

12 = Yield per plant

13 = yield per plot

14 = yield per ha

3.2 Experiment 2: Heterosis and combining ability analysis in tomatillo

Crosses from the experiment 1 was evaluated for heterosis and combining ability in this experiment. The different steps of this experiment *viz*., description of experimental site, climate and soil, seedbed preparation and seedling raising, land preparation, manure and fertilizer application, design and layout of experiment, transplanting of seedling, intercultural operations and harvesting and processing are

same as described in the sections, 3.1.1, 3.1.2, 3.1.4, 3.1.5, 3.1.6, 3.1.7, 3.1.8, 3.1.9 and 3.1.10 respectively.

3.2.1 Planting materials

Twenty genotypes of F_1 during the experiment 1 were used as planting materials for experiment 2 which are listed in the Table 4.

Table 4. List of the tomatillo genotypes used in Experiment 2

SL. NO.	Genotypes (F_1s)	SL. NO.	Genotypes (F_1s)
1	G1 × G2	**11**	G3 × G4
2	G1 × G3	**12**	G3 × G5
3	G1 × G4	**13**	G4 × G1
4	G1 × G5	**14**	G4 × G2
5	G2 × G1	**15**	G4 × G3
6	G2 × G3	**16**	G4 × G5
7	G2 × G4	**17**	G5 × G1
8	G2 × G5	**18**	G5 × G2
9	G3 × G1	**19**	G5 × G3
10	G3 × G2	**20**	G5 × G4

3.2.2 Data collection

Data were recorded on different yield and yield contributing, traits. Five plants in each replication of each genotype were selected randomly and were tagged. These tagged plants were used for recording of data same as described in the 3.1.11.1 to 3.1.11.17.

3.2.3 Statistical analysis

The following analysis were done for this experiment.

3.2.3.1 ANOVA

The objective of the experiment was to evaluate the performance of the hybrids and their parents, so data were recorded from all the genotypes and F_1 hybrids. To find out the variation among the different genotypes the collected data for various traits were

analyzed statistically using MSTAT-C program for F-test as it was a single factor experiment (Table 5). Coefficient of variation (CV%) was calculated as of Gomez and

Table 5. The general form of ANOVA for combining ability

Source of variation	d.f.	Sum of squares	Mean sum squares	F-test	Expected mean squares
GCA	$p-1$	Sg	Mg	MSg/MSe	σ_e^2+ (p+2)$\left\{\frac{1}{(p-1)}\right\}\sum Gi^2$
SCA	$p(p-1)/2$	Ss	Ms	MSs/MSe	σ_e^2+$\left\{\frac{2}{p(p-1)}\right\}\sum_i\sum_j S_{ij}^2 \quad i<j$
Error	$(r-1)(p-1)$	Se	Me		σ_e^2

Gomez (1984). From the ANOVA combining ability was estimated and heterosis was calculated from the mid values.

3.2.3.2 Statistical procedure used for combining ability analysis

In 1956, Griffing proposed four methods of analysis of combining ability depending on the materials used. Griffing has also considered Eisenhart's model I (fixed effect) and model II (random effect) in the analysis. In this study combining ability analysis were calculated as method 1 (including reciprocals) and Model-I. The mathematical model for the analysis was as follows

$Yij = m + gi + gj + Sij + 1/bc \sum\sum kleijkl$

Where, i, j=1, 2, ..., p

K=l, 2, ..., b

L=1, 2, ..., c

P = Number of parents

b = Number of blocks or replications

c = Number of observation in each plot

Yi = the mean of i^{th} x j^{th} genotype over K and L

m = the population mean

gj= The general combining ability (GCA) effect to i^{th} parent

gj = The GCA of j^{th} parent

sij = The SCA effect such that sij = sji

$1/bc \sum \sum kleijkl$ = the mean error effect

The restriction imposed: $\sum gi = 0$ and $\sum Sij + Sii = 0$

GCA = general combining ability

SCA = specific combining ability

p = Number of parents

r = Number of blocks or replications

Yi = Array total of the i^{th} parent

Yjj = Mean value of the i^{th} parent

Yg = Grand total of the p(p-l)/2 crosses and parental lines

Yij= Progeny mean values in the diallel table

Se = Sum of square due to error

$$Sg = \frac{1}{(P+2)}\left[\sum_i (Yi + Yii)^2 - \frac{4}{p} Y..^2\right]$$

$$Ss = \sum_i \sum_j Y_{ij}^2 \frac{1}{(p+2)} \sum (Yi + Yii)^2 + \frac{2}{(p+1)(p+2)} Y..^2$$

The GCA and SCA effects of each character were calculated as follows:

$$gi = \frac{1}{(p+2)}\left[\sum_i (Yi + Yii)^2 - \frac{2}{p} Y..^2\right]$$

$Sij = Yij - \frac{1}{(p+2)}\sum_i(\text{yi} + \text{yii} + \text{yj} + \text{yji}) + \frac{2}{(\text{p+1})(\text{p+2})}\text{Y..}$

The variance of GCA and SCA were,

$Var(gi) = \frac{(\text{P}-1)}{p(p+2)}\sigma_e^2$

$Var(Sij) = \frac{2(\text{P}-1)}{(\text{P}+1)(\text{P}+2)}\sigma_e^2 \ (i \neq j)$

Standard error (SE) of an estimate was calculated the square root of the variance of concerned estimate eg.

j Var (g;) and j Var (s.)

$\sqrt{Var(gi)}$ and $\sqrt{Var(Sij)}$

3.2.3.3 Estimation of heterosis

The amount of heterosis of the F_1 s was calculated using the following formula:

Heterosis over better parent (%) = $\frac{(\overline{F_1} - \overline{BP})}{\overline{BP}} \times 100$

Here,

$\overline{F_1}$= Mean of F_1 individuals

$\overline{BP}$= Mean of the better parent values

Heterosis over mid parent (%) = $\frac{(\overline{F_1} - \overline{MP})}{\overline{MP}} \times 100$

Here,

$\overline{F_1}$= Mean of F1 individuals

$\overline{MP}$= Mean of the mid parent values

CD (Critical Difference) values were used to test significance of heterotic effects.

Critical Differences (CD) = t × $\sqrt{\frac{2EMS}{r}}$

Here,

EMS= Error Mean Sum of square

r = No. of replication

t = Tabulated t value at error d.f.

CD values were compared with the values come from $(\overline{F_1} - \overline{BP})$and $(\overline{F_1} - \overline{MP})$to test significant effect of heterosis.

3.2.3.4 Diallel analysis using Hayman´s approach

Diallel analysis is the first step in most plant breeding programs aimed at improving yield and other related parameters. The diallel is defined as making all possible crosses in a group of genotypes. It is the most popular method used by breeders to obtain information on value of varieties as parents, and to assess the gene action in various characters (Pickett, 1993; Griffing, 1956). The two main approaches being followed for diallel analysis are: Hayman's approach and Griffing's approach. In the present study, the first approach was followed for the genetic analysis of diallel populations, subject to fulfill of certain assumptions (Hayman, 1954a) *viz.* diploid segregation, no reciprocal difference other than an environment, independent action of non-allelic genes, no multiple allelism, homozygous parents and genes independently distributed between the parents. The Hayman's approach chiefly comprises the aspects, Hayman's ANOVA, Vr, Wr analysis with graphical representation and components of variation and genetic parameters.

3.2.3.5 Hayman's ANOVA

An analysis of variance for the complete diallel table was given by Hayman (1954a), developing in one direction that of Yates (1947). Frequently, however, reciprocaldifferences are assumed absent, and only one of each pair of reciprocal crosses is raised. For such situation Morley Jones (1965) brought about some modification of Hayman's approach. In this modification using the same model as Hayman, the determination of the sums of squares corresponding to additive effects (a), and on the assumption of no epistasis to mean dominance (b1), to additional dominance effects that can be accounted for by genes having one allele present in only one line (b2) (the remaining n-1 lines being assumed to carry the same alternative allele) and to residual dominance effects (b3), is in essence a

straightforward application of fitting constants by least squares. Table 6. showed the skeletal outline of Hayman's ANOVA of diallel.

Table 6. General structure of Hayman´s ANOVA

Item	Df	Sum of squares	Mean squares
A	n-1	$\frac{1}{n+2}$ dev^2ur	Ma
b1	1	2	Mb1
b2	n-1	$\frac{1}{n^2 - 4}$ dev^2tr	Mb2
b3	n(n-3)/2	Total SS – (a ss + b_1 ss + b_2 ss)	Mb3
B	n(n-1)/2	b_1 ss + b_2 ss + b_3 ss	Mb
Error	(r-1)(t-1)	ESS	Me

Where,

a = Additive effects

b = Dominance effects

b1 = Mean dominance

b2 = Dominance deviation due to arrays

b3 = Residual dominance effects

dev2= Sum of square of deviations from the mean

ur = Xi. + Xii

tr = 2 (Xi. + Xii) – (n+2) Xii

3.2.3.6 Vr- Wr regression analysis

The regression coefficient was calculated by using the following formula

$$b = \frac{COV(Wr, Vr)}{Var(Vr)}$$

Where,

Vr = Variance of each array

Wr = Covariance between parents and their offsprings

Var (Vr) = Variance of Vr

Var (Wr) = Variance of Wr

Cov (Wr, Vr) = Covariance between Vr and Wr

Significant difference of 'b' from zero and unity was tested as follows:

Ho: b = 0

= (b – 0) / SE (b)

and

Ho: b = 1

= (1 – b) / SE (b)

These values were tested against tabulated values of 't' for (n-2) degrees of freedom. Vr, Wr analysis measures significant variation of the regression coefficient (b) from unity. If the regression coefficient does not significantly deviate from unity, then it proves the absence of non-allelic interaction

3.2.3.7 Vr_Wr graphs

Interpretation of diallel cross may be made by graphical presentations, which is generally known as Vr, Wr graph (Hayman 1954a, Jinks 1954). By calculating array variance (Vr) and parent-offspring covariances (Wr) and regression of Wr on Vr, it is possible to test the adequacy of the simple additive-dominance genetic model, to discern the relative proportion of dominant and recessive alleles present in the

common parents of each array and to find the average level of dominance. The Wri (covariance) values for each array were calculated by using the formula: Wri = (Vri x VOLO)½ By plotting Wr values against Vr values the external limits of the parabola were found. The regression line was drawn by plotting expected Wrei values against Vr values. The Wrei values were calculated by using the formula:

$$Wrei = Wr - b\,\overline{Vr} + b\,\overline{Vri}$$

Where,

$\overline{Wr}$ = Mean value of Wr

b= Regression coefficient

Vri = Individual array riance (Vr)

$\overline{Vr}$ = Mean value of Vr

The position of regression line on Vr, Wr graph provides information about the average degree of dominance. When the regression line passes through the origin, it indicates complete dominance (D = H1). When it passes above the origin cutting Wr axis, it shows partial dominance (D > H1). Whereas when it passes below the origin cutting the Wr – axis, it denotes the presence of over-dominance (D < H1).

The distribution of parents on the regression line also determines the presence of dominant and recessive genes. The parents having maximum dominant alleles show minimum values of Vr, Wr and also closer to the origin (0,0) and the parents having maximum number of recessive genes show maximum values of Vr, Wr and lie apart from the origin (0,0).

3.2.3.8 Components of variations and genetic parameters

The genetic and environmental components of variation along with allied or related genetic parameters in F_1 were calculated according to Hayman (1954b) and Jinks (1954). But in F_2 and backcross generations, these were calculated according to Jinks (1956) and Mather and Jinks (1971). In the present study it was as Table 7.

Table 7. Estimation of various components

D	VOLO – E
F	2 VOLO – 4 WOLO1 – 2 (n-2) E/n
H1	VOLO– 4WOLO1+ 4V1L1–(3n-2) E/n
H2	4 V1L1 – 4 VOL1 – 2E
h^2	4 (M L1 – MLO) 2 – 4 (n-1) E/n^2
E	{(Error SS + Rep.SS) / df}

Where,

D = Variation due to additive gene effect

H1 = Variation due to dominance gene effect

H2 = H1 [1 – (u – v)2] = Proportion of dominance variation that is due to positive and negative effects of gene. Here, u = proportion of positive genes and v = proportion of negative genes in the parents

h^2 = Dominance effect (as algebraic sum over all loci in heterozygous phase in all crosses

F = The mean of Fr over all arrays, where Fr is the covariance of additive and dominant effects in a single array

E = Expected environmental component of variance or error variance

VOLO = Variance of parents

V1L1 = Mean variance of the arrays

WOLO1 = Mean covariance between parents and the arrays

VOL1 = Variance of the means of arrays

(ML1–MLO)2 = Dominance relationship i.e. the difference between the mean of the parents and the mean of the n2 progenies.

3.3 Experiment 3. Genetic variability and character association in F_2 generations of tomatillo for quantitative and qualitative traits.

This experiment was carried out to estimate the variability analysis for morphological, and nutritional traits of F_2 generations of tomatillo obtained from F_1 generations. This study also includes the correlation, path coefficient and selection index analysis for F_2 genotypes. The experimental site and climate and soil was same as described in the section 3.1.1 and in the 3.1.2, respectively.

3.3.1 Planting materials

In second year to generate F_2 generations, F_1 genotypes were crossed with F_1 genotypes at the flowering stage through hand emasculations and controlled pollinations. Crossed and developed by crossing materials of F_1 generations. Paper bags were used to avoid contaminations. Pollinations to emasculated flower were repeated, if necessary for maximizing the seed setting. Standard agronomic and cultural practices were carried out for development of F_2 hybrids according to requirements of crops.

3.3.2 Activities of Experiment 3

Preparation of seed bed and seedlings raising, land preparation, manure and fertilizer applications, transplanting of seedlings, design and layout of the experiment, intercultural operations, harvesting and processing was done as described in the section of 3.1.4, 3.1.5, 3.1.6, 3.1.7, 3.1.8, 3.1.9 and 3.1.11

3.3.3 Data collection

Data were collected on agro-morphogenic traits and qualitative traits.

3.3.3.1 Agromorphogenic traits

Same as described in the section of 3.1.12.1.1-3.1.12.1.17.

3.3.3.2 Qualitative traits

Data were recorded on the basis of different nutritional traits using ripe fruits *viz*., Brix (%), Vitamin-C content (mg//100g) and Lycopene content (mg/100g).

3.3.3.2.1 Brix%

Brix percentages were measured by Portable Refractometer (ERMA, Tokyo, Japan) at room temperature. Single tomatillo fruit was blend and juice was collected to measure brix percentage.

3.3.3.2.2 Determination of Vitamin-C

Vitamin-C was measured by Oxidation Reduction Titration Method (Tee*et al*., 1988). Determination of vitamin C is shown in Plate 3. Dye preparation was required for

determination of Vitamin C. 260 mg 2, 6-dichloro indophenols with 210 mg sodium bicarbonate were mixed with one litter of distilled water. It was used in burette. 5% oxalic acid preparation was performed as 50 mg oxalic acid was mixed with one litter of distilled water and it was used for washing the fruit and for the preparation of fruit juice preparation. L-ascorbic acid was prepared as 10 mg of granular L-ascorbic acid was mixed with 100 ml oxalic acid solution. 5 ml was taken and volume was made up to 100 ml. from this solution, 5 ml was taken for titration against 2,6-dichloro indophenol from burette for 3 times and their mean was recorded as the required amount of dye for titrating L-ascorbic acid. Preparation of solution was done as single fruit was weighted and was blend with some drops of oxalic acid solution. It was filtered through whatman filter paper and the juice was collected. Volume was made up to 100 ml with oxalic acid. 5 ml was taken from that solution and titrated against dye solution. The required amount of dye was recorded for titrating solution. The amount of vitamin C was determined by following formula;

$$\text{Vitamin C} = \frac{0.5 \times dye\ required\ for\ tomato\ juice \times 100 \times 100}{dye\ required\ for\ L\text{-}ascorbic\ acid \times 5 \times weight\ of\ fruit}$$

3.3.3.2.3 Determination of Lycopene content

Absorption determination for lycopene content was estimated following the method of Alda*et al*. (2009) by using T60 UV-Visible Spectrophotometer. Lycopene in the tomatillo was extracted using hexane:ethanol:acetone (2:1:1) mixture. One gram juice of the each sample were homogenized with 25 ml of hexane:ethanol:acetone, which were then placed on the orbital shaker for 30 min., adding 10 ml distilled water and was continued agitation for another two min. The solution was then left to separate into distinct polar and non- polar layers. The absorbance was measured at 472 nm and 502 nm, using hexane as a blank. The lycopene concentration was calculated using its specific extinction coefficient (E 1%, 1cm) of 3450 in hexane at 472 nm and 3150 at 502 nm. The lycopene concentration was expressed as mg/100g product.

$$\text{At } \lambda = 502 \text{ nm: lycopene content (mg /100g)} = \frac{E}{3.15} \times \frac{20}{m}$$

Simillar formula was used to calculate At λ = 472nm: lycopene content (mg/100g).

Where,

m = the weight of the product (g)

E = extinction coefficient

3.3.3.2.4 Measuring of chlorophyll content

Leaf chlorophyll content was measured by using SPAD-502 plus portable chlorophyll meter. The chlorophyll content was measured at 60 DAT from 4 different portion of the leaf and then averaged for analysis.

3.3.3.2.5 Fruit PH

Sample of 5gm each of the fresh mesocarp were homogenous in 5ml of boil distill water and deionize water (pH 7) and the pH of the homogenate was measured with a pH meter.

3.3.3.2.6 Titratable acid content

Firstly 0.1 N NaOH solutions was prepared by taking 4 gm NaOH pellet into 1000 ml distilled water. It was used in burette. Single fruit was weighted and it was blended. Fruit juice was collected by passing it through whatman filter paper. Volume was made up to 50 ml by adding distilled water. Ten ml solution was taken and 2 drops of Phenolphthalein was added. It was titrated against 0.1 N NaOH and required amount of NaOH was recorded. Titrable acidity was determined by following formula;

$$\% \text{ Acidity} = \frac{titrate \times Normality\ of\ alkali \times vol.made\ up \times Equivalent\ wt.of\ acid \times 100}{Volume\ of\ sample\ taken \times weight\ of\ sample \times 1000}$$

3.3.3.2.7 Dry matter and moisture content in fruits

Wight of fresh fruit of each plant was taken. Fruit was pressed so that some moisture was released, and it was kept in hot air oven at 80°C for 48 hours. After 48 hours, dry weight of fruit was measured, and percentage of Moisture content was measured by following formula;

$$\%\text{Moisture Content} = \frac{\text{weight of freash fruit} - \text{Weight of oven dry fruit}}{\text{Weight of freash fruit}} \times 100$$

Dry Matter content was determined by following formula.

% Dry Matter Content= 100 - % Moisture content.

3.3.4 Statistical analysis

Mean data of all 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). 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. All of these analyses were carried out in R software.Estimation of genotypic and phenotypic variances, estimation of genotypic and phenotypic co-efficient of variation, estimation of heritability, estimation of genetic advance, estimation of genetic advance mean's percentage, estimation of genotypic and phenotypic correlation co-efficient, estimation of path co-efficient and estimation of selection index were performed as described in the section 3.1.15.1, 3.1.15.2, 3.1.15.3, 3.1.15.4, 3.1.15.5, 3.1.15.6, 3.1.15.7 and 3.1.15.11, respectively.

CHAPTER IV

RESULTS AND DISCUSSION

To achieve the objectives of the study three separate experiments were conducted. The results of the research works are presented, discussed and possible interpretations are given experiment wise with relevant heads and subheads as below.

4.1 Experiment 1. Genetic variability and cross-ability analysis in tomatillo (*Physalis ixocarpa* Brot. / *Physalis philadelphica* Lam.)

The experiment was conducted to perform the diversity analysis and cross-ability of different genotypes of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.) using morphological and yield contributing traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment 1. Among the morphological and yield contributing characters, plant height, number of branches per plant, leaf area index, days to first flowering, days to fifty percent flowering, days to maturity, number of fruits per plant, fruits length, fruit diameter, Individual fruit weight, seeds per fruits, yield per plant, yield per plot and yield per hectare were studied. The data pertaining to fourteen characters have been presented and statistically analyzed with the possible interpretations given under the following headings.

4.1.1 Genetic variability, heritability and genetic advance

Analysis of variance and mean performance of five tomatillo genotypes were presented in Appendix IV and Table 8 respectively. The analysis of variance indicated significantly higher amount of variability present among the genotypes for the characters studied *viz*., plant height, leaf area, days to 1st flowering, fruit length, fruit diameter, seeds per fruit, yield per plant, yield per plot and yield per hectare (Appendix IV). Therefore, there was a lot of scope for selection of the genotypes based on these traits.

Performance of the five tomatillo genotypes is described below for each character. The extent of variation among the genotypes in respect of fourteen characters was

studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV),

Table 8. Mean performance of five parental genotypes of tomatillo for fourteen morphological characters

Genotypes	Plant height (cm)	Leaf area	No. of branches/ plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length (mm)	Fruit diameter (mm)	Individual fruit weight (g)	Seeds / fruit	Yield/plant (g)	Yield/plot (kg)	Yield/ha (ton)
G1	90.11a	22.06a	10.93ab	33.40bc	50.62b	85.04a	30.10a	24.67b	30.25a	23.11a	382.67ab	708.00a	8.49a	58.97a
G2	86.22b	17.48b	10.80ab	30.93c	52.96ab	85.19a	28.20a	22.61bc	25.83b	20.65a	366.33bc	527.00b	6.32b	43.91b
G3	82.88c	19.18ab	11.27a	33.60ab	50.84b	83.30ab	28.03a	28.43a	33.15a	22.67a	395.33a	740.67a	8.89a	61.71a
G4	87.33b	16.70b	11.20ab	33.27bc	54.82a	82.33b	27.93a	20.09c	21.17c	23.08a	349.67c	424.67c	5.09c	35.32c
G5	83.37c	19.60ab	10.43b	36.08a	51.68b	85.16a	27.72a	22.42bc	25.40bc	22.48a	376.00abc	592.67b	7.11b	49.37b
Minimum	82.88	16.7	10.43	30.93	50.62	82.33	27.72	20.09	21.17	20.65	349.67	424.67	5.9	35.32
Maximum	90.11	22.06	11.27	36.08	54.82	85.19	30.1	28.43	33.15	23.11	395.33	740.67	8..87	61.71
Average	85.982	19.004	10.926	33.456	52.184	84.204	28.396	23.644	27.16	22.398	374	598.602	7.18	49.856
CV	1.42	8.29	3.94	3.39	3.10	1.66	4.47	6.98	8.29	6.99	3.85	5.96	5.96	5.97

Note : Genotypes means having the same letter are statistically identical and those having different letters are statistically different from each other.

heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) are presented in Table 9. The data were analyzed and possible interpretations are given here based on established scales. According to Deshmukh *et al.* (1986) PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Wide difference between PCV and GCV for the traits implies their susceptibility to environmental fluctuation, whereas narrow difference suggested their relative resistant to environmental alteration. Heritability is the percentage of phenotypic variance that is attributed to genetic variance. According to Singh (2009), heritability of a trait is considered as very high or high when the values is 80% or more and moderate when it ranged from 40-80% and when it is less than 40%, it is low. Therefore, the heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance and the genetic advance at percentage of mean. Deshmukh *et al.* (1986) classified genetic advance as percentage of mean as low (<10%), moderate (10-20%) and high (>20%).

4.1.1.1 Plant height

Analysis of variance showed statistically significant differences among the tomatillo genotypes in term of plant height at 1% level (Appendix IV). Highest plant height (90.11 cm) was observed in G1 followed by G2 (86.22 cm) and G4 (87.33 cm) (Table 8). Lowest plant highest was observed in G3 (82.88 cm) followed by G5 (83.37 cm). The mean value was 85.98 cm. Higher plant height indicated the more morphological growth and sometimes it enhanced the yield. The genotypic variance and phenotypic variance for this trait were 8.33 and 9.83, respectively (Table 9). The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait (Table 9). The phenotypic coefficient of variation and genotypic coefficient of variation of plant height was low (3.65 and 3.36 respectively) (Table 9). Phenotypic coefficient of variation was higher than the genotypic coefficient of variation suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV was very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. Plant height showed very high heritability (85%) and low in genetic advance (5.47) and genetic advance in

Table 9. Estimation of genetic parameters fourteen morphological characters of five tomatillo genotypes

Parameters	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Maximum	91.00	23.72	11.8	37	55.22	86.66	30.6	29.51	35.17	27.23	401.00	750	9.00	62.49
Minimum	82.65	15.73	10	28.6	48.27	80.29	25.00	18.80	18.92	19.82	321.00	414	4.96	34.44
GM	85.98	19.00	10.93	33.46	52.18	84.20	28.40	23.64	27.16	22.40	374.00	598.60	7.18	49.85
σ2g	8.33	3.51	0.05	2.74	2.14	1.08	0.40	8.87	19.84	0.21	227.33	16467.42	2.37	114.67
σ2e	1.49	2.48	0.18	1.77	2.61	1.95	1.61	2.73	5.07	2.45	206.83	1272.15	0.18	8.85
σ2p	9.83	5.99	0.24	4.51	4.76	3.03	2.01	11.60	24.91	2.66	434.16	17739.57	2.55	123.52
ECV	1.42	8.29	3.94	3.97	3.10	1.66	4.47	6.98	8.29	6.99	3.85	5.96	5.96	5.97
GCV	3.36	9.85	2.06	4.94	2.81	1.23	2.23	12.60	16.40	2.04	4.03	21.44	21.46	21.48
PCV	3.65	12.87	4.45	6.35	4.18	2.06	5.00	14.40	18.38	7.28	5.56	22.25	22.27	22.29
H^2B	0.85	0.59	0.21	0.61	0.45	9.35	0.20	0.76	0.80	0.08	0.52	0.93	0.93	0.93
GA	5.47	2.95	0.21	2.66	2.02	1.27	0.58	5.36	8.19	0.26	22.48	254.69	3.06	21.25
GA % (mean)	6.37	15.53	1.97	7.95	3.88	1.51	2.04	22.70	30.15	1.17	6.01	42.54	42.60	42.63
SEM	0.71	0.91	0.25	0.77	0.93	0.81	0.73	0.95	1.30	0.90	8.30	20.59	0.25	1.72
CD (5%)	2.30	2.96	0.81	2.50	3.04	2.63	2.39	3.11	4.24	2.94	27.08	67.16	0.81	5.60
CD (1%)	3.35	4.32	1.18	3.64	4.43	3.83	3.48	4.52	6.17	4.29	39.40	97.72	1.17	8.15

Here, GM= Grand mean; σ^2g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

percent of mean (6.37) (Table 9). High heritability coupled with low genetic advance indicated the presence of non-additive gene action. High heritability was due to the favorable influence of environment rather than the genotypes. So selection based on this trait would not be rewarding.

4.1.1.2 Leaf area

In leaf area index, analysis of variance showed significantly difference among the tomatillo genotypes at 5% level of significance (Appendix IV). The highest leaf area was found in G1 (22.06) followed by G5 (19.60) and G3 (19.18) and the lowest leaf area was observed in G4 (16.70) followed by G2 (17.48) (Table 8) with a mean of 19.00. The genotypic variance and phenotypic variance for this trait were 3.51 and 5.99 respectively (Table 9). The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait (Table 9). The phenotypic coefficient of variation and genotypic coefficient of variation of leaf area was low (12.87 and 9.85, respectively) (Table 9). Phenotypic coefficient of variation (12.87) was higher than the genotypic coefficient of variation (9.85) suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. Leaf area showed medium heritability (59%) and low in genetic advance (2.95) (Table 9). Moderate heritability coupled with medium genetic advance revealed this trait was heritable in next generation. Shashikanth *et al*. (2010) found low heritability and genetic advance for leaf area.

4.1.1.3 Number of branches / plants

Number of branches per plant showed non-significant differences among the five tomatillo genotypes (Appendix IV), where maximum number showed in G3 (11.27) followed by G4 (11.20), G1 (10.93) and G2 (10.80) and the lowest number of branches per plant was observed in G5 (10.43) genotype of tomatillo with a mean value of 10.93 (Table 8). The phenotypic variance (0.24) was higher than the genotypic variance (0.05). The genotypic co-efficient of variation and phenotypic co-

efficient of variation were 2.06 and 4.45, respectively (Table 9) indicating that the phenotypic expression of this trait was 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 low (21%), genetic advance (0.21%) and genetic advance in per cent of mean (1.97) were also low (Table 9), revealed that this trait was highly governed by environmental effects and selection would not be effective based on this trait.

4.1.1.4 Days to first flowering

Statistically significant variation was observed in days to first flowering of five tomatillo genotypes at 5% level of significant (Appendix IV). The average days to first flowering was recorded 33.46 days and its ranges from 30.93 days in G2 to 36.08 days in G5 (Table 8). The differences in days to first flowering might be due to genetically factors of the genotypes concerned. The genotypic variance and phenotypic variance for this trait were 2.74 and 4.51, respectively (Table 9). 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) (4.94) and phenotypic co-efficient of variation (PCV) (6.35) were more or less similar to each other, indicated presence of negligible variability in this trait (Table 9). 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 and Phir (1995) found in significant difference in days to first flowering. The heritability estimates for days to first flowering was high (61%) with low genetic advance (2.66) and genetic advance in percentage of mean (7.95%). 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.* (2013). Islam and Khan (1991) reported high heritability for days to first flowering.

4.1.1.5 Days to 50% flowering

Non-significant differences among the five tomatillo genotypes showed in days to 50% flowering (Appendix IV). The average fifty percent flowering ranges was

recorded from 54.82 days to 50.62 days. The earliest fifty percent flowering was recorded in G1 (50.62 days) followed by G3 (50.84 days), G5 (51.68 days), G2 (52.96) and G4 (54.82 days) genotypes respectively (Table 8). Different variety required different days to flowering initiation and 50% flowering. Mean value 33.46 days after transplanting (DAT) (Table 9). The genotypic variance and phenotypic variance for this trait were 2.14 and 4.76, respectively (Table 9). 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 character. Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low (2.81 and 4.18, respectively) (Table 9). 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 *et al.,* 2005 and Samadia *et al*., 2006). So, it can be referring that selection based upon phenotypic expression of this character wouldn't be productive for the improvement of tomatillo. The heritability was found 45% for this trait was medium with low genetic advance (2.02) and genetic advance in per cent of mean (3.88%), indicating this character was controlled by non-additive genes. Singh *et al.* (2014) and Kumar *et al.* (2004) support the finding.

4.1.1.6 Days to maturity

Days to maturity showed non-significant variation in different genotypes of tomatillo under the experiment (Appendix IV). The range of days to maturity was recorded from 82.33 days to 85.19 days. The earliest maturity was found in G4 (82.33 days) followed by G3 (83.30 days), G1 (85.04 days), G5 (85.16 days), and later maturity in G2 (85.19 days) genotype. The mean value was 84.20 (Table 8). The earlier maturity was more desirable than later maturity considering the duration of crops. The genotypic variance (1.08) was lower than phenotypic (3.03) variance. Genotypic co-efficient of variation (1.23) and phenotypic co-efficient of variation (2.06) were also close to each other (Table 9) suggesting environmental influence was minor on the expression of the genes controlling this parameter. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The results of Prashanth (2003) disagree with this result with high phenotypic

coefficient of variation. The heritability estimates for this trait was high (93%). In contrast genetic advance (1.27) and genetic advance in per cent of mean (1.51%) were found low, indicated that this trait was controlled by non-additive genes. High heritability was due to favorable environment rather than genetically effected, so the selection would not be recommended. Kumari *et al*. (2007), Islam and Khan (1991) was also found high heritability and moderately high genetic advance for days to maturity.

4.1.1.7 Number of fruits/plants

Also, number of fruits per plant showed the non-significant differences among five tomatillo genotypes. (Appendix IV). The highest number of fruits per plant was found in G1 (30.10)followed by G2 (28.20), G3 (28.03) and G4 (27.93) and the lowest number of fruits was recorded in G5 (27.72) genotype, respectively (Table 8). The mean value was 28.40 (Table 8). Higher number of fruits per plants indicated the higher yield in generally. Similar result was observed by Masabni (2016) a single plant produces 20 to 100 fruits within a single growing season. The difference between genotypic (0.40) and phenotypic (2.01) variances indicated high environmental influence (Table 9). The phenotypic coefficient of variation (5.00) and genotypic coefficient of variation (2.23) was low, which indicated presence of low variability among the genotypes (Table 9). Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi*et al*. (2004) supported the findings. The heritability estimates for this character was low (20%), genetic advance (0.58) and genetic advance in percent of mean (2.04%) were found low, indicated that this trait was governed by environmental effect and selection for this character would not be effective.

4.1.1.8 Fruit length (mm)

Fruit length exhibited significant variation at the level of 1% among the five tomatillo genotypes (Appendix IV). The highest fruit length was observed in G3 (28.43 mm) genotype and lowest fruit length was found in G4 (20.09 mm) genotype. The second highest fruit length was found in G1(24.67 mm) and third higher fruit length was recorded in G2 (22.61mm) then G5 (22.42mm) genotype, respectively. The mean value was 23.64 mm (Table 8). The genotypic variance was 8.87 which was low and phenotypic variance was 11.60 which was medium. Genotypic co-efficient of

variation (12.60) and phenotypic co-efficient variation (14.40) were close to each other (Table 9) indicating minor environmental influence on this character that would be effective for the improvement of this crop. Singh*et al*. (1997) showed that the phenotypic coefficient of variation was greater for this trait which was supported the present study. High heritability estimates (76%) with low genetic advance (5.36) and moderate genetic advance at percent of mean (22.70 %) (Table 9) indicated that effective selection may not be made for fruit length. The character was governed by non additive gene action. Moderate heritability and moderate genetic gain for this character was observed by Joshi *et al.* (2004).

4.1.1.9 Fruit diameter

Statistically significant variation was showed in fruit diameter of five tomatillo genotypes at the 1% level of significant (Appendix IV). Highest fruit diameter was found in G3 (33.15 mm) followed by G1 (30 .15 mm), G2 (25.83 mm), G5 (25.40 mm) and G4 (25.40 mm) in tomatillo with a mean value 27.16 mm (Table 8). The phenotypic variance was 24.91 which was high and genotypic variance was 19.84 which was medium. Genotypic co-efficient of variation (16.40) and phenotypic co-efficient variation (18.38) (Table 9) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement for the tomatillo crop. 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 (80%) with low genetic advance (8.19) over moderate percent of mean was 30.15% (Table 9), indicated that effective selection may not be made for fruit length. The character was governed by non additive gene action. High heritability coupled with low genetic gain for this character was observed by Pandit *et al*. (2010) in tomato.

4.1.1.10 Individual fruit weight

The average individual fruit weight showed non-significant differences among the five tomatillo genotypes (Appendix IV) and it's ranges from 23.11g to 20.65g with a mean of 22.40 g (Table 8). The highest fruit weight showed in genotype G1 and lowest fruit weight found in G2 genotype. Individual fruit weight was important factor which directly contributing to the yield and market potentiality. The genotypic

variance (0.21) and phenotypic variance (2.66) for individual fruit weight was low (Table 9). The genotypic co-efficient of variation and phenotypic co-efficient of variation were low (2.04 and 7.28, respectively), proved that environment had influence of the expression of this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Low GCV and PCV for average fruit weight were also noticed by Manivannan *et al*. (2005) and Singh *et al*. (2002). Heritability was observed 8%, which was very low associated with low genetic advance (0.26) in percent of mean (1.17%) (Table 9), indicating fruit weight was highly influenced by environment, therefore selection should not be supported. Pandit *et al.* (2010), Ara *et al.* (2009) and Singh *et al.* (2006) also experienced to the present findings.

4.1.1.11 Seeds /fruit

Seeds per fruit varied significantly different at 5% level of significant in all the five tomatillo genotypes (Appendix IV). The excellent number of seeds per fruit was found in G3 (395.33) genotype, followed by genotype G1 (382.67), G5 (376.00), G2 (366.33) and the lowest number of seeds per fruit was observed in genotype G4 (349.67) with a mean value of 374 (Table 8). The greater number of viable seeds per fruit was desirable for making successful further breeding program. Genotypic variance was found 277.33, on the other hand phenotypic variance was observed 434.16 which was very high. The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait (Table 9). The phenotypic coefficient of variation and genotypic coefficient of variation of seed per fruit was low (5.56 and 4.03 respectively) (Table 9). Phenotypic coefficient of variation (5.56) was higher than the genotypic coefficient of variation (4.03) suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. Seeds per fruit showed medium heritability (52%) and high in genetic advance (22.48) with percent mean genetic advance was 6.01% (Table 9). Medium heritability coupled with high genetic

advance indicated the presence of additive gene action. Medium heritability was due to the favorable influence of environment rather than the genotypes. so selection based on this raits will not be rewarding.

4.1.1.12 Yield per plant

Statistically significant differences were showed in five tomatillo genotypes for yield per plant in gram at 1% level of significant (Appendix IV). Yield per plant was varied from 740.67 g to 424.67g. The highest yield per plant was observed in G3 genotype (740.67 g) followed by G1 genotype (708.00 g), G5 genotype (592.67g), and G2 genotype (527.00 g). The lowest yield per plant was found in G4 genotype (424.67 g). (Table 8). The mean value of yield per plant was 598.60 g. Yield per plant directly affects the crop's final yield. The phenotypic variance (17739.57) found higher than genotypic variance (16467.42) (Table 9), suggested considerable influence of environment on the expression of the genes controlling this character. The phenotypic coefficient of variation and genotype coefficient of variation were 22.25 and 21.44, respectively for fruit yield per plant, which indicating that significant variation existed among different genotypes which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al.* (2005).

Estimation of very high heritability (93%) for fruit yield per plant with high genetic advance (254.69%) and high genetic advance of % mean (42.54%) (Table 9) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding program. High heritability and high genetic advance was also observed by Ara *et al.* (2009).

4.1.1.13 Yield per plot

Analysis of variance showed statistically significant differences among the tomatillo genotypes in term of yield per plot at 1% level (Appendix IV). The highest yield per plot was recorded in G3 genotype (8.89 kg), followed by G1 genotype (8.49 kg), G5 (7.11 kg) and G2 genotype (6.32 kg) and the lowest yield was found in G4 genotype (5.09 kg) with a mean value of 7.18 g on per plot basis. (Table 8). The yield per plot was an important factor directly contributing to final yield of crop. The phenotypic variance (2.55) found higher than genotypic variance (2.37) (Table 9), suggested

considerable influence of environment on the expression of the genes controlling this character.

The phenotypic coefficient of variation and genotype coefficient of variation were 22.27 and 21.46, respectively for yield per plot, which indicating that significant variation existed among five different genotypes of tomatillo, which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al*. (2005). Estimation of very high heritability (93%) for fruit yield per plot with low genetic advance (3.06) and high genetic advance of % mean (42.60%) (Table 9) revealed that this character was governed by non-additive gene action and selection will not be rewarded.

4.1.1.14 Yield/ha (Ton)

Final yield varied significantly (at 5% level) in different tomatillo genotypes under the present experimental studies (Appendix IV). Data revealed that the average yield ranged from 61.71 metric ton per hectare to 35.32 metric ton per hectare. The excellent highest (61.71 t/ha) yield was recorded in the genotype G3 which was followed by genotype G1 (58.97 t/ha), G5 genotype (49.37 t/ha) and G2 genotype (43.91 t/ha). The lowest yield was observed in genotype G4 (35.32 t/h). The mean value was 49.85 ton/ha. Yield is one of the main parameters for selection of crops. The higher yield indicated the potentiality of the future selection program of the genotype. Masabni, 2016, found similar results with an average yield of about 9 metric tons per acre (22.23 t/ha). The genotypic variance and phenotypic variance for this important parameter were 114.67 and 123.52, respectively (Table 9). 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 phenotypic coefficient of variation and genotypic coefficient of variation of yield was high (22.29 and 21.48, respectively) (Table 9). Phenotypic coefficient of variation (22.29) was higher than the genotypic coefficient of variation (21.48) suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Yield (t/h) showed very high heritability (93%) and high in genetic advance (21.25). Also observed high genetic advance of % mean (42.63%) (Table 2). Very high heritability coupled with high genetic advance indicated the presence of additive gene action. So, selection based on this trait will be effective and provides opportunity for selecting high valued genotypes for future breeding program. High heritability and high genetic advance were also observed by Ara *et al.* (2009).

4.1.2 Correlation Co-efficient

Determination of correlation co-efficient was provided the information how yield depends on different yield contributing characters. Correlation co-efficient studies along with path analysis provide a better understanding of the association of different characters with 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 tomatillo are given in Table 10 and Table 11.

4.1.2.1 Plant height

Plant height had non-significant negative correlation with yield (-0.16) at genotypic level and non-significant positive correlation (0.12) at phenotypic levels (Table 10 and Table 11), that was supported by Mohanty (2003). Plant height had also non-significant negative correlation with days to first flowering, number of fruits per plant, fruit length, fruit diameter, seeds per fruit, yield per plant, and yield per plot. It had

Table 10. Genotypic correlation coefficient among different pairs of morphological characters of five genotypes of tomatillo

Characters	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Plant height	1^{**}	0.29^{NS}	0.09^{NS}	-0.38^{NS}	0.11^{NS}	0.08^{NS}	-0.69^{NS}	-0.34^{NS}	-0.18^{NS}	0.39^{NS}	-0.40^{NS}	-0.16^{NS}	-0.16^{NS}	-0.16^{NS}
Leaf area		1^{**}	-0.69^{NS}	0.60^{NS}	-1.00^{NS}	0.66^{NS}	0.39^{NS}	0.64^{NS}	0.80^{NS}	0.62^{NS}	0.94^{*}	0.87^{NS}	0.87^{NS}	0.87^{NS}
No. of branches/plant			1^{**}	-0.36^{NS}	0.07^{NS}	$-.90^{NS}$	0.91^{NS}	0.56^{NS}	0.48^{NS}	0.73^{NS}	0.08^{NS}	0.07^{NS}	0.07^{NS}	0.07^{NS}
Days to 1st flowering				1^{**}	-0.26^{NS}	0.12^{NS}	-0.09^{NS}	-0.04^{NS}	0.06^{NS}	$.89^{NS}$	0.33^{NS}	0.28^{NS}	0.28^{NS}	0.28^{NS}
Days to 50% flowering					1^{**}	-0.79^{NS}	$-.92^{*}$	-0.90^{**}	$-.89^{*}$	-0.02^{NS}	$-.88^{NS}$	-0.90^{*}	-0.90*	$--90^{*}$
Days to maturity						1^{**}	-0.26^{NS}	-0.01^{NS}	0.26^{NS}	-0.87^{NS}	0.68^{NS}	0.34^{NS}	0.34^{NS}	0.34^{NS}
No. of fruits/plant							1^{**}	0.86^{NS}	0.87^{*}	0.90^{NS}	0.85^{*}	0.96^{**}	0.96^{**}	0.96^{**}
Fruit length								1^{**}	0.95^{*}	-0.11^{NS}	0.90^{*}	0.97^{**}	0.97^{**}	$0,97^{**}$
Fruit diameter									1^{**}	0.27^{NS}	0.89^{*}	0.90^{**}	0.90^{**}	0.90^{**}
Individual fruit weight										1^{**}	0.50^{NS}	0.39^{NS}	0.39^{NS}	0.39^{NS}
Seeds/ plant											1^{**}	0.92^{*}	0.92^{*}	0.92^{*}
Yield/ plant												1^{**}	1^{**}	1^{**}
Yield/plot													1^{**}	1^{**}
Yield/ha														1^{**}

Table 11. Phenotypic correlation coefficient among different pairs of morphological characters of five genotypes of tomatillo

Characters	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Plant height	1^{**}	0.28^{NS}	0.22^{NS}	-0.39^{NS}	0.16^{NS}	0.12^{NS}	-0.28^{NS}	-0.33^{NS}	-0.16^{NS}	0.15^{NS}	-0.27^{NS}	-0.12^{NS}	-0.12^{NS}	0.12^{NS}
Leaf area		1^{**}	0.08^{NS}	0.11^{NS}	-0.53^{*}	0.41^{NS}	-0.07^{NS}	0.32^{NS}	0.46^{NS}	0.37^{NS}	0.42^{NS}	0.71^{**}	0.71^{**}	9.71^{**}
No. of branches/plant			1^{**}	-0.45^{NS}	0.24^{NS}	-0.17^{NS}	0.06^{NS}	0.18^{NS}	0.05^{NS}	0.25^{NS}	-0.01^{NS}	0.09^{NS}	0.09^{NS}	0.09^{NS}
Days to 1st flowering				1^{**}	-0.35^{NS}	-0.07^{NS}	-0.07^{NS}	0.12^{NS}	-0.05^{NS}	0.35^{NS}	0.17^{NS}	0.14^{NS}	0.14^{NS}	0.14^{NS}
Days to 50% flowering					1^{**}	-0.30^{NS}	-0.12^{NS}	-0.60^{*}	-0.68^{**}	-0.22^{NS}	-0.60^{*}	-0.73^{**}	-0.73^{**}	-0.73^{**}
Days to maturity						1^{**}	-0.42^{NS}	0.13^{NS}	0.18^{NS}	0.04^{NS}	-0.01^{NS}	0.30^{NS}	0.30^{NS}	0.30^{NS}
No. of fruits/plant							1^{**}	0.48^{NS}	0.64^{*}	-0.23^{NS}	0.44^{NS}	0.49^{NS}	0.49^{NS}	9.49^{NS}
Fruit length								1^{**}	0.84^{**}	0.23^{NS}	0.75^{**}	0.83^{**}	0.83^{**}	0.83^{**}
Fruit diameter									1^{**}	0.04^{NS}	0.75^{**}	0.91^{**}	0.91^{**}	0.91^{**}
Individual fruit weight										1^{**}	0.01^{NS}	0.21^{NS}	0.21^{NS}	0.21^{NS}
Seeds/ plant											1^{**}	0.73^{**}	0.73^{**}	0.73^{**}
Yield/ plant												1^{**}	1^{**}	1^{**}
Yield/plot													1^{**}	1^{**}
Yield/ha														1^{**}

also non-significant positive correlation with leaf area, branches per plant, days to fifty percent flowering, days to maturity and individual fruit weight at both levels. However, it had strong negative correlation with number of fruits per plant (-0.69) at genotypic and days to first flowering (-0.39) at phenotypic level.

4.1.2.2 Leaf area

Leaf area had non-significant positive association with yield per ha (0.87) at genotypic level and significant positive relation (9.71) at phenotypic level (Table 10 and Table 11). Leaf area was also positive significant association with seeds per fruit (0.94*) and positive non-significant relation with days to first flowering, days to maturity, number of fruits per plant, fruit diameter, fruit length, individual fruit weight, yield per plant and yield per plot (Table 10). Also leaf are performed negative non-significant association with number of branches per plant and days to fifty percent flowering at genotypic level. Leaf area also showed highly positive significant association with yield per plant (0.71**) and yield per plot (0.71**) and positive non-significant association with number of branches per plant, days to first flowering, days to maturity, fruit length, fruit diameter, individual fruit weight and seeds per fruit at phenotypic level. It had also negative non-significant relation with days to fifty percent flowering and number of fruits per plant at phenotypic level (Table11). A positive correlation between number of clusters per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato.

4.1.2.3 Number of branches per plant

The number of branches per plant had positive non-significant correlation with yield per hectare, yield per plant and yield per plot at genotypic and phenotypic level (0.07 and 0.09 respectively). It had also positive non-significant relation with days to fifty percent flowering, number of fruits per plant, fruit length, fruit diameter, individual fruit weight at both the levels. The number of branches per plant had also negative non-significant association with days to first flowering (-0.36 and -0.45) and days to maturity (-0.90 and -0.17) at both genotypic and phenotypic levels (Table 10 and Table 11). Monamodi *et al*. (2013) found more branches 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). It had non-significant positive correlation with fruit diameter (0.48 and 0.05) at both levels. 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).

4.1.2.4 Days to first flowering

Days to first flowering had highly positive non-significant correlation with yield per hectare (0.28 and 0.14), yield per plot, yield per plant, seeds per fruit (0.33 and 0.17) and individual fruit weight (0.89 and 0.35) at genotypic and phenotypic level(Table 10 and Table 11) Patil and Bojappa (1993), Mayavel *et al.* (2005) and Samadia *et al.* (2006) observed positive correlations which support the present findings. This character also showed non-significant positive association with days to maturity (0.12) and fruit diameter (0.06) also negative non-significant relation with days to fifty percent flowering (-0.26), number of fruits per plant (-0.09) , fruit length (-0.04) at genotypic levels (Table 3). Days to first flowering also positively associated with fruit length (0.12) and negatively related with days to 50% flowering (-0.35), days to maturity (-0.07), number of fruits per plant (-0.07), and fruit diameter (-0.05) at phenotypic levels (Table 11).

4.1.2.5 Days to 50% flowering

Days to 50% flowering showed highly significant negative association with fruit yield per hactare (-0.90* and -0.73**), yield per plant and yield per plot at both genotypic and phenotypic levels (Table 10 and Table 11). The character revealed non-significant negative relation with days to maturity, individual fruit weight and seeds per fruit whereas significant negative association with number of fruits per plant (-0.92*), fruit length (-0.90**) and fruit diameter (-0.89*) at the genotypic levels. (Table 10).Days to 50% flowering also showed significant negative association with fruit length (-0.60*), fruit diameter (-0.68*) and seeds per fruit (-0.60*) whereas non-significant negative relation with days to maturity (-0.30), number of fruits per plant (-0.12) and individual fruit weight (-0.22) at phenotypic levels (Table 11). Non-significant association of this trait with yield indicated that the association was largely influenced by environment. Yield improvement can be achieved by selection for days to 50% flowering were reported by Wright *et al*. (2007).

4.1.2.6 Days to maturity

Days to maturity had non-significant positive correlation with yield per ha (0.34 and -0.30), yield per plant, yield per plot and fruit diameter (0.26 and 0.18) at genotypic and phenotypic levels (Table 10 and Table 11). It had also highly non-significant negative association with number of fruits per plant (0.26 and 0.42) at both genotypic and phenotypic levels (Table 10 and Table 11). Days to maturity showed non-significant negative relation with fruit length (-0.01) and individual fruit weight (-0.87) at genotypic level. This character also revealed non-significant positive relation with fruit length (0.13), fruit diameter (0.18) and individual fruit weight (0.04) and negative relation with seeds per fruit (-0.01) at phenotypic levels. (Table 11). Significant and positive correlation observed by Singh *et al.* (2002) and Mohanty (2003) between days to maturity and fruit yield per plant and this doesn't support the present findings.

4.1.2.7 Number of fruits per plant

The number of fruits per plant had highly significant and positive association with yield per hectare (0.96**) yield per plant (0.96**), yield per plot ((0.96**), seeds per fruit (0.85*) and fruit diameter (0.87*) also had non-significant positive relation with fruit length (0.86) and individual fruit weight (0.90) at genotypic levels (Table 10). Rani *et al.* (2010) reported that the number of fruits per plant was negatively associated with yield per plant which does not supportthis finding. The number of fruits per plant had also non-significant positive correlation with yield per hectare (0.49) yield per plant (0.49), yield per plot ((0.49), seeds per fruit (0.44) and fruit length (0.48) and negative relation with individual fruit weight (-0.23) and positive significant association with fruit diameter (0.64*) at phenotypic levels. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight.

4.1.2.8 Fruit length

Fruit length was highly significant positively correlated with fruit yield per ha (0.97** and 0.83**), yield per plant, yield per plot, seeds per fruit (0.90* and 0.75**) and fruit diameter (0.95* and 0.84**) at genotypic and phenotypic levels, respectively (Table 10 and Table 11). The character had non-significant positive correlation with

individual fruit weight (0.23) at phenotypic level (Table 11) and non-significant negative relation with individual fruit weight (-0.11) (Table 10).

4.1.2.9 Fruit diameter

Fruit diameter showed highly significant positive association with fruit yield per hectare (0.90** and 0.91**) yield per plant (0.90** and 0.91**), yield per plot (0.90** and 0.91**) and seeds per fruit (0.89* and 0.75**) at both genotypic and phenotypic level, respectively. Fruit diameter also had non-significant positive relation with individual fruit weight (0.27 and 0.04) at both genotypic and phenotypic levels (Table 10 and Table 11).

4.1.2.10 Individual fruit weight

Individual fruit weight showed non-significant and positive correlation with yield per hectare (0.39 and 0.21) yield per plant (0.39 and 0.21), yield per plot (0.39 and 0.21) and seeds per fruit (0.50 and 0.01) for both genotypic and phenotypic levels (Table 10 and Table 11). 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.

4.1.2.11 Seeds per plant

Seeds per plant had highly significant positive association with yield per ha (0.92* and 0. 73**), yield per plant (0.92* and 0. 73**) and yield per plot (0.92* and 0. 73**) at both genotypic and phenotypic levels. A positive correlation between number of seeds per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato.

4.1.2.12 Yield per plant

At genotypic level, yield per plant showed highly significant positive correlation with number of fruits per plant (0.96**), fruit length (0.97**), fruit diameter (0.90**), seeds per fruits, yield per plot (1**) and yield per ha (1**) (Table 10). Yield per plant showed negative significant correlation with days to 50% flowering (-0.90**). At

phenotypic level, yield per plant showed significant positive correlation with leaf area (0.71**), fruit length (0.83**), fruit diameter (0.91**), seeds per fruit (0.73**), yield per plot (1**) and yield per ha (1**). Yield per plant showed significant negative correlation with days to 50% flowering (-0.73**).

4.1.2.13 Yield per plot

At genotypic level, yield per plot showed highly significant positive correlation with number of fruits per plant (0.96**), fruit length (0.97**), fruit diameter (0.90**), seeds per fruits, yield per plant (1**) and yield per ha (1**) (Table 10). Yield per plot showed negative highly significant correlation with days to 50% flowering (-0.90**). At phenotypic level, yield per plot showed significant positive correlation with leaf area (0.71**), fruit length (0.83**), fruit diameter (0.91**), seeds per fruit (0.73**), yield per plant (1**) and yield per ha (1**). Yield per plot showed significant negative correlation with days to 50% flowering (-0.73**).

4.1.2.14 Yield per ha

At genotypic level, yield per ha showed highly significant positive correlation with number of fruits per plant (0.96**), fruit length (0.97**), fruit diameter (0.90**), seeds per fruits, yield per plant (1**) and yield per plot (1**) (Table 10). Yield per ha showed negative significant correlation with days to 50% flowering (-0.90**). At phenotypic level, yield per ha showed highly significant positive correlation with leaf area (0.71**), fruit length (0.83**), fruit diameter (0.91**), seeds per fruit (0.73**), yield per plant (1**) and yield per plot (1**). Yield per ha showed highly significant negative correlation with days to 50% flowering (-0.73**).

4.1.3 Path coefficient analysis

To get a clear picture of the inter–relationship between yield and other yield attributes, direct and indirect effects of yield contributing characters were worked out by using path analysis at genotypic level which also measured the relative importance of each component. Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on number of reproductive branches. Here yield per ha was considered as effect

(dependent variable) and plant height (cm), leaf area, number of branches per plant, days of first flowering, days to 50% flowering, days to maturity, fruits per plant, fruit length, fruit diameter, individual fruit weight, seeds per fruits, yield per plant and yield per plot were treated as causal (independent) variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of tomatillo in Table 12 and 13.

4.1.3.1 Plant height

In case of genotypic path coefficient analysis, plant height had positive direct effect on yield/ha (0.003) which was contributed to result non-significant negative genotypic correlation (-0.16) (Table 5). Plant height had positive indirect effect on leaf area (0.06), No. of branches/plant (0.002), days to maturity (0.01), seeds/fruit (0.002) and yield / plant (0.32). Plant height had negative indirect effect on days to first flowering (-0.02), days to 50% flowering (-0.01), no. of fruits/plant (-0.08), fruit length (-0.06), fruit diameter (-0.01), individual fruit weight (-0.003) and yield /plot (-0.38) (Table 12).

In case of phenotypic path coefficient, plant height had positive direct effect (0.002) on yield per ha which was contributed to result non-significant positive correlation with yield per ha (0.12) at phenotypic level (Table 13). Plant height had indirect positive effect on leaf area (0.04), number of branches per plant (0.008), days to maturity (0.008), seeds per fruit (0.001), yield per plot (0.02) and negative indirect effect on days to first flowering (-0.02), days to 50% flowering (-0.008), number of fruits per plant (0.03), fruit length (-0.03) , fruit diameter (-0.004), individual fruit weight (-0.002), yield per plant (-0.097) (Table 13).

4.1.3.2 Leaf area

Leaf area had positive direct effect on yield per ha (0.21) which contributed to non-significant positive genotypic correlation (0.87) (Table 12). Leaf area also had positive indirect effect on plant height (0.001), days to first flowering (0.04), days to 50% flowering (0.08), days to maturity (0.05), number of fruits per plant (0.04), fruit length (0.11), fruit diameter (0.04) and yield per plot (2.04). Leaf area had negative indirect effect on number of branches per plant (-0.02), individual fruit weight (-0.01), seeds per fruit (-0.01) and yield per plant (-1.71).

Table 12. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on yield/ha of tomatillo

Characters	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Genotypic correlation coefficient with yield/ha
Plant height	**0.003**	0.06	0.002	-0.02	-0.01	0.01	-0.08	-0.06	-0.01	-0.003	0.002	0.32	-0.38	-0.16^{NS}
Leaf area	0.001	**0.21**	-0.02	0.04	0.08	0.05	0.04	0.11	0.04	-0.01	-0.01	-1.71	2.04	0.87^{NS}
No. of branches/plant	0.000	-0.15	**0.03**	-0.02	-0.004	-0.15	0.22	0.09	0.03	-0.01	-0.0005	-0.14	0.16	0.07^{NS}
Days to 1st flowering	-0.001	0.13	-0.01	**0.06**	0.02	0.01	-0.01	-0.006	0.003	-0.012	-0.002	-0.55	0.66	0.28^{NS}
Days to 50% flowering	0.0004	-0.26	0.002	-0.02	**-0.07**	-0.06	-0.12	-0.17	-0.06	0.0001	0.008	2.32	-2.78	--90*
Days to maturity	0.0003	0.14	-0.07	0.007	0.05	**0.08**	-0.03	-0.001	0.013	0.017	-0.004	-0.67	0.80	0.34^{NS}
No. of fruits/plant	-0.003	0.08	0.07	-0.006	0.07	-0.02	**0.11**	0.26	0.06	-0.01	-0.007	-1.90	2.27	0.96**
Fruit length	-0.001	0.135	0.02	-0.002	0.07	-0.0005	0.17	**0.17**	0.07	0.001	-0.006	-1.92	2.29	0,97**
Fruit diameter	-0.0007	0.17	0.02	0.004	0.07	0.02	0.12	0.18	**0.05**	-0.002	-0.007	-1.98	2.36	0.90**
Individual fruit weight	0.001	0.13	0.02	0.08	0.001	-0.17	0.18	-0.02	0.01	**0.008**	-0.003	-0.78	0.92	0.39^{NS}
Seeds/ fruit	-0.001	0.20	0.003	0.02	0.09	0.05	0.13	0.19	0.06	-0.004	**-0.006**	-2.30	2.75	0.92*
Yield/ plant	-0.001	0.18	0.002	0.017	0.08	0.03	0.10	0.16	0.05	-0.003	-0.007	**-1.97**	2.35	1**
Yield/plot	-0.001	0.185	0.002	0.016	0.078	0.026	0.104	0.164	0.053	-0.003	-0.007	-1.97	**2.35**	1**

Table 13. Phenotypic path coefficient analysis showing the direct (bold) and indirect effect of different characters on n yield/ha of tomatillo

Characters	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Phenotypic correlation coefficient with yield/ha
Plant height	**0.002**	0.04	0.008	-0.02	-0.008	0.008	-0.03	-0.03	-0.004	-0.002	0.001	-0.097	0.02	0.12^{NS}
Leaf area	0.005	**0.14**	0.003	0.004	0.03	0.03	-0.009	0.03	0.01	-0.006	-0.001	0.598	-0.122	9.71^{**}
No. of branches/plant	0.003	0.011	**0.037**	-0.01	-0.02	-0.01	0.007	0.02	0.001	-0.004	0.0002	0.08	-0.02	0.09^{NS}
Days to 1st flowering	-0.0006	0.015	-0.016	**0.038**	0.018	-0.005	-0.008	0.011	-0.001	-0.005	-0.003	0.12	-0.02	0.14^{NS}
Days to 50% flowering	0.0003	-0.07	0.01	-0.01	**-0.05**	-0.02	-0.02	-0.06	-0.02	0.003	0.001	-0.62	0.13	-0.73^{**}
Days to maturity	0.0002	0.06	-0.007	-0.003	0.02	**0.07**	-0.05	0.01	0.005	-0.006	0.0003	0.25	-0.05	0.30^{NS}
No. of fruits/plant	-0.0004	-0.009	0.002	-0.003	0.006	-0.03	**0.013**	0.03	0.02	0.004	-0.009	0.411	-0.08	9.49^{NS}
Fruit length	-0.0005	0.04	0.007	0.005	0.03	0.009	0.06	**0.10**	0.02	-0.004	-0.002	0.70	-0.14	0.83^{**}
Fruit diameter	-0.0003	0.06	0.002	-0.001	0.03	0.012	0.08	0.08	**0.03**	0.0006	-0.002	0.77	-0.16	0.91^{**}
Individual fruit weight	0.002	0.05	0.009	0.01	0.01	0.003	0.03	0.02	0.001	**-0.015**	0.0002	0.17	-0.04	0.21^{NS}
Seeds/ fruit	-0.0004	0.06	-0.003	0.006	0.03	-0.001	0.06	0.07	0.02	0.0012	**-0.002**	0.62	-0.13	0.73^{**}
Yield/ plant	-0.0002	0.010	0.003	0.005	0.04	0.02	0.06	0.08	0.03	-0.003	-0.002	**0.85**	-0.17	1^{**}
Yield/plot	-0.0002	0.10	0.003	0.005	0.04	0.02	0.06	0.08	0.02	-0.003	-0.002	0.85	**-0.17**	1^{**}

In case of phenotypic path coefficient, leaf area had positive direct effect on yield per ha (0.14) which was contributed to result significant positive correlation (9.71) at phenotypic level (Table 13). It had positive indirect effect on plant height (0.005) number of branches per plant (0.003), days to first flowering (0.004), days to 50% flowering (0.03), days to maturity (0.03), fruit length (0.03), fruit diameter (0.01)), yield per plant (0.598) and negative indirect effect on number of fruits per plant (-0.009), individual fruit weight (-0.006), seeds per fruit (-0.001) and yield per plot (-0.122

4.1.3.3 No. of branches per plant

Number of branches per plant had positive direct effect on yield per ha (0.03) which contributed to non-significant positive genotypic correlation (0.07) (Table 12). It had positive indirect effect on plant height (0.00), number of fruit per plant (0.22), fruit length (00.9), fruit diameter (0.03) and yield per plot (0.16), and negative indirect effects on days to first flowering (-0.02), days to 50% flowering (-0.004), days to maturity (-0.15) and yield per plant (-0.14).

In case of phenotypic path coefficient, number of branches per plant showed direct positive effect on yield per ha (0.037) which was contributed to result positive no-significant correlation on yield (0.09) at phenotypic level (Table 13). Number of branches per plant had positive indirect effect on plant (0.003), leaf area (0.011), number of fruits per plant (0.007), fruit length (0.02), fruit diameter (0.001), seeds per fruit (0.0002), yield per plant (0.08) and negative indirect effect on days first flowering (-0.01) days to 50% flowering (-0.02), days to maturity (-0.01), individual fruit weight (-0.004) and yield per plot (-0.02).

4.1.3.4 Days to 1st flowering

Days to first flowering had positive direct effect (0.06) on yield per ha which contributed to positive non-significant genotypic correlation (0.28) (Table 12). Days to first flowering had positive indirect effect on leaf area (0.13), days to 50% flowering (0.02), days to maturity (0.01), fruit diameter (0.003) and yield per plot (0.66). It had negative indirect effects on plant height (- 0.001), number of branches per plant (-0.01), number of fruits per plant (-0.01), individual fruit weight (-0.012), seeds per fruit (-0.002) and yield per plot (-0.55). Days to 50% flowering had

negative direct effect on yield per ha (-0.07) which contributed to significant negative genotypic correlation (-0.90).

In case of phenotypic path coefficient, days to first flowering had direct positive effects on yield per ha (0.038) which was contributed to result non-significant positive effect of yield per ha at phenotypic level (Table 13). Days to first flowering had indirect positive effect on leaf area (0.015), days to 50% flowering (0.018), fruit length (0.011), yield per pant (0.12) and negative indirect effect on plant height (-0.0006), number of branches per plant (-0.016), days to maturity (-0.005), number of fruits per plant (-0.008), fruit diameter (-0.001), individual fruit weight (-0.005), seeds per fruit (-0.003) and yield per plot (-0.02).

4.1.3.5 Days to 50% flowering

Days to 50% flowering had positive indirect effect on plant height (0.0004), number of branches per plant (0.002), individual fruit weight (0.0001), seeds per fruit (0.008), yield per plant (2.32) and negative indirect effect on leaf area (-0.26), days to first flowering (-0.02), days to maturity (-0.06), number of fruits plant (-0.12), fruit length (-0.17), fruit diameter (-0.06), yield per plot (-2.78). Days to maturity had direct positive effect on yield per ha (0.08) with contributed to non-significant positive genotypic correlation (0.34) (Table 12).

In case of phenotypic path coefficient, days to 50 % flowering had negative direct effect (-0.05) on yield per ha which was contributed to result significant negative correlation (-0.73) at phenotypic level (Table 13). Days to 50% had indirect positive effect on plant height (0.0003), number of branches per plant (0.01), individual fruit weight (0.003), seeds per fruit (0.001), yield per plot (0.13) and negative indirect effect on leaf area (-0.07), days to first flowering (-0.01) , days to maturity (-0.02), number of fruits per plant ((-0.02), fruit length (-0.06), fruit diameter (-0.02), yield per plant (-0.62).

4.1.3.6 Days to maturity

Days to maturity had indirect positive effect on plant height (0.0003), leaf area (0.14), days to first flowering (0.007), days to 50% flowering (0.05), fruit diameter (0.013), individual fruit weight (0.017) and yield per plot (0.80). It had also negative indirect

effect on number of branches per plant (-0.07), number of fruits per plant (-0.03), fruit length (-0.001), seeds per fruits (-0.004) and yield per plant (-0.67).

In case of phenotypic path coefficient, days to maturity had direct positive effect (0.07) on yield per ha which was contributed to result non-significant positive correlation (0.30) at phenotypic level (Table 13). Days to maturity had indirect positive effect on plant height (0.0002), leaf area (0.06), days to 50% flowering (0.02), fruit length (0.01), fruit diameter (0.005), seeds per fruit (0.0003), yield per plant (0.25) and negative indirect effect on number of branches per plant (-0.007), days to first flowering (-0.003), number of fruits per plant (-0.05), individual fruit weight (-0.006) and yield per plot (-0.05).

4.1.3.7 No. of fruits per plant

Number of fruits per plant had positive direct effects on yield per ha (0.11) and it had also significant positive correlation (0.96) at genotypic level. Number of fruits per plant had positive indirect effect on leaf area (0.08), number of branches per plant (0.07), days to first flowering (0.07), fruits per plant (0.11), fruit length (0.26), fruit diameter (0.06), yield per plot (2.27) and negative indirect effect on plant height (-0.0003), days to first flowering (-0.006), days to maturity (-0.02), individual fruit weight (-0.001), yield per plant (-1.90) (Table 12).

In case of phenotypic path coefficient, number of fruits per had direct positive effect of yield per ha (0.013) which was contributed to result non-significant positive correlation (9.94) at phenotypic level. It had positive indirect effect on number of branches per plant (0.002), days to 50% flowering (0.006), fruit length (0.03), fruit diameter (0.02), individual fruit weight (0.004), yield per plant (0.411) and negative indirect effect on plant height (-0.0004), leaf area (-0.009), days to first flowering (-0.003), days to maturity (-0.03), seeds per fruit (-0.009), yield per plot (-0.08) (Table 13).

4.1.3.8 Fruit length

Fruit length showed positive direct effect on yield per ha (0.17) and significant positive correlations with yield per ha at genotypic level (0.97) (Table 12). Fruit length had indirect positive effect on leaf area (0.135), number of branches per plant

(0.02), days to 50% flowering, (0.07), number of fruits per plant, (0.17), fruit diameter (0.07), individual fruit weight (0.001), yield per plant (2.29) and negative indirect effect on plant height (-0.001), days to first flowering (-0.002), days to maturity (-0.0005), seeds per fruit (-0.006) and yield per plant (-1.92).

In case of phenotypic path coefficient, fruit length showed positive direct effect on yield per ha (0.10) which was contributed to result positive significant correlation on yield (0.83) at phenotypic level (Table 13). Fruit length had indirect positive effect on leaf area (0.04), number of branches per plant, (0.007), days to first flowering (0.005), days to 50% flowering (0.03), days to maturity (0.009), number of fruits per plant (0.06), fruit diameter (0.02), yield per plant (0.70) and negative indirect effect on plant height (-0.0005), individual fruit weight (-0.004), seeds per fruit (-0.002), yield per plot (-0.14).

4.1.3.9 Fruit diameter

Fruit diameter had positive direct effect on yield per ha (0.05) also significant positive correlation with yield (0.90) at genotypic level (Table 12). Fruit diameter had indirect positive effect on leaf area (0.17) number of branches per plant (0.02), days to first flowering (0.007), days to 50% flowering ()0.04, days to maturity (0.02), number of fruits per plant (0.12), fruit length (0.18), yield per plot (2.36), and also it had negative indirect effect on plant height (-0.0007), individual fruit weight (-0.002), seeds per fruit (-0.007) and yield per plant (-1.98).

In case of phenotypic path coefficient, Fruit diameter had positive direct effect on yield per ha (0.03) which was contributed to result positive significant correlation (0.91). Fruit diameter had also indirect positive effect on leaf area (0.06), number of branches per plant (0.002), days to 50% flowering (0.03), days to maturity (0.012),number of fruits per plant (0.08), fruit length (0.08), individual fruit weight (0.0006), yield per plant (0.77) and also had negative indirect effect on plant height (-0.0003), days to first flowering (-0.001), seeds per fruit (-0.002) and yield per plot (-0.16) (Table 13).

4.1.3.10 Individual fruit weight

Individual fruit weight had positive direct effect on yield per ha (0.008) and it had non-significant positive correlation on yield (0.39) at genotypic level (Table 12). Also individual fruit weight had indirect positive effect on plant height (0.0001), leaf area (0.13), number of branches per plant (0.02), days to first flowering (0.08), days to 50% flowering (0.001) , days to maturity (0.18), number of fruits per plant (0.18), fruit diameter (0.01), yield per plot (0.92) and negative indirect effect on days to maturity (-0.17), fruit length (-0.02) and yield per plant (-0.78) .

In case of phenotypic path coefficient, individual fruit weight had direct negative effect (-0.015) on yield per ha which was contributed to result non-significant positive correlation (0.21) at phenotypic level (Table 13). It had also positive indirect effect on plant height (0.0002), leaf area (0.05), number of branches per plant (0.009), days to first flowering (0.01), days to 50% flowering (0.01), days to maturity (0.003), number of fruits per plant (0.03), fruit length (0.02), fruit diameter (0.001), seeds per fruit (0.0002) and yield per plant (0.17) and negative indirect effect on yield per plot (-0.04).

4.1.3.11 Seeds per fruit

Seeds per fruit had direct negative effect on yield per ha (-0.006) and also significant positive correlation with yield (0.92) at genotypic level. (Table 12). It had also indirect positive effect on leaf area (0.20), number of branches per plant (0.003), days to first flowering (0.02), days to 50 % flowering (0.09), days to maturity (0.05), number of fruits per plant (0.13), fruit length (0.19), fruit diameter (0.06), yield per plot (2.75) and indirect negative effect on plant height (-0.001), individual fruit weight (-0.004), yield per plant (-2.30).

In case of phenotypic path coefficient, seeds per fruit had negative significant effect on yield per ha (-0.002), which leads to significant positive correlation with yield per ha (0.73) at phenotypic level (Table 13). It had indirect positive effect on leaf area (0.06), days to first flowering (0.006), days to 50% flowering (0.03), number of fruits per plant (0.06), fruit length (0.07), fruit diameter (0.02), individual fruit weight (0.0012), yield per plant (0.62), and negative indirect effect on plant height (-0.0004),

number of branches per plant (-0.003), days to maturity (-0.001) and yield per plot (-0.13).

4.1.3.12 Yield per plant

Yield per plant had negative direct effect of yield per ha (-1.97) which contributed to significant positive effects on yield (1) at genotypic level, yield per plant had positive indirect effect on leaf area (0.18), number of branches per plant (0.002), days to first flowering (0.017), days to 50 % flowering (0.08), days to maturity (0.03), number of fruits per plant (0.10), fruit length (0.16), fruit diameter (0.05), yield per plot (2.35) and indirect negative effect on plant height (-0.001), individual fruit weight (-0.003), seeds per fruit (-0.007) (Table 12).

In case of phenotypic path coefficient, yield per plant had direct positive effect (0.85) on yield per ha which was contributed to result significant positive correlation at phenotypic level. Yield per plant had positive indirect effect on leaf area (0.010), number of branches per plant (0.003), days to first flowering (0.005), days to 50% flowering (0.04), days to maturity (0.02), number of fruits per plant (0.06), fruit length (0.08), fruit diameter (0.03), and negative indirect effect on plant height (-0.0002), individual fruit weight (-0.003), seeds per fruit(-0.002) and yield per plot (-0.17) (Table 13).

4.1.3.13 Yield per plot

Yield per plot showed positive direct effect of yield per ha (2.35) which contributed to significant positive effects on yield at genotypic level, yield per plot had positive indirect effect on leaf area (0.185), number of branches per plant (0.002), days to first flowering (0.016), days to 50 % flowering (0.078), days to maturity (0.026) number of fruits per plant (0.104), fruit length (0.164), fruit diameter (0.053), and indirect negative effect on plant height (-0.001), individual fruit weight (-0.003), seeds per fruit (-0.007) and yield per plant (-1.97) (Table 12).

In case of phenotypic path coefficient, yield per plot had direct negative effect (-0.17) on yield per ha which was contributed to result significant positive correlation (1) at phenotypic level (Table 6). Yield per plot had positive indirect effect on leaf area (0.010), number of branches per plant (0.003), days to first flowering (0.005), days to

50% flowering (0.04), days to maturity (0.02), number of fruits per plant (0.06), fruit length (0.08), fruit diameter (0.02), yield per plant (0.62), and negative indirect effect on plant height (-0.0002), individual fruit weight (-0.003) and seeds per fruit (-0.002) (Table 13).

4.1.4 Cross ability analysis

Cross ability of different crosses of tomatillo genotypes based on their success rate in three years were recorded. Analysis of variance and mean performance of five tomatillo genotypes were presented in Appendix V and Table 14.

Year-1

Analysis of variance showed statistically significant differences among the crosses of tomatillo genotypes in Year-1, at 5% level (Appendix V). Highest success rate was observed in G4xG3 (76.66%) followed by G1 × G3 (73.33%), G2xG1 (73.33%), G2xG4 (73.33%) and G3xG2 (73.33%). Then next success crosses were G1xG2 (70%) and G4xG1 (70%). The lowest success rate was observed in cross G5xG5 (50%) followed by G3xG3 (53.33%) (Table 14).

Year-2

Analysis of variance showed non-significant positive variations among the crosses of tomatillo genotypes in Year-2 (Appendix V). Considering the mean performance of twenty crosses of tomatillo genotypes, highest success rate of different cross combinations was found in G4xG1 (71.66%) in crossing year-2, followed by G3xG2 (70%), G1xG3 (68.33%), G2xG4 (68.33%), G3xG1 (66.66%), G2xG3 (65%), G4xG3 (61.66%), G1xG2 (60%), G1xG4 (60%), G3xG5 (60%). The lowest success rate of crosses was found in G5xG4 (51.66%) and G5xG5 (51.66%) (Table 14).

Year-3

A positive significant variation was observed within crosses of tomatillo genotypes in Year -3 (Appendix V). On the basis of the mean performance of twenty five crosses of tomatillo genotypes, highest success rate in different cross combination were found in G1xG2 (68.33%), G3x G1 (68.33%) and G4xG1 (68.33%), in crossing year-3, followed by G1xG3 (66.66%), G4xG3 (66.66%), G2xG3 (65%). The lowest success rate of crosses in Year-3 was found in crosses G3xG5 (50.00%) (Table 14).

Table 14. Mean performance of cross success rate in different cross combination in tomatillo genotypes over three years

Crosses	% Success		
	Year 1	Year 2	Year 3
G1xG2	70.00 abc	60.00 abcdef	68.33 a
G1xG3	73.33 ab	68.33 abc	66.66 ab
G1x G4	66.66 abcd	60.00 abcdef	56.66 abcd
G1xG5	56.66 cde	55.00 def	55.00 bcd
G2xG1	73.33 ab	56.66 cdef	58.33 abcd
G2xG3	60.00 bcde	65.00 abcde	65.00 ab
G2xG4	73.33 ab	68.33 abc	56.66 abcd
G2xG5	53.33 de	55.00 def	55.00 bcd
G3x G1	66.66 abcd	66.66 abcd	68.33 a
G3xG2	73.33 ab	70.00 ab	63.33 abc
G3xG4	66.66 abcd	58.33 bcdef	56.66 abcd
G3xG5	60.00 bcde	60.00 abcdef	50.00 d
G4xG1	70.00 abc	71.66 a	68.33 a
G4xG2	66.66 abcd	58.33 bcdef	60.00 abcd
G4xG3	76.66 a	61.66 abcdef	66.66 ab
G4xG5	60.00 bcde	53.33 ef	51.66 cd
G5xG1	60.00 bcde	55.00 def	55.00 bcd
G5xG2	60.00 bcde	58.33 bcdef	55.00 bcd
G5xG3	56.66 cde	55.00 def	55.00 bcd
G5xG4	60.00 bcde	51.66 f	51.66 cd
CV	15.3	13.67	12.90
$LSD_{0.05}$	15.94	13.28	12.50

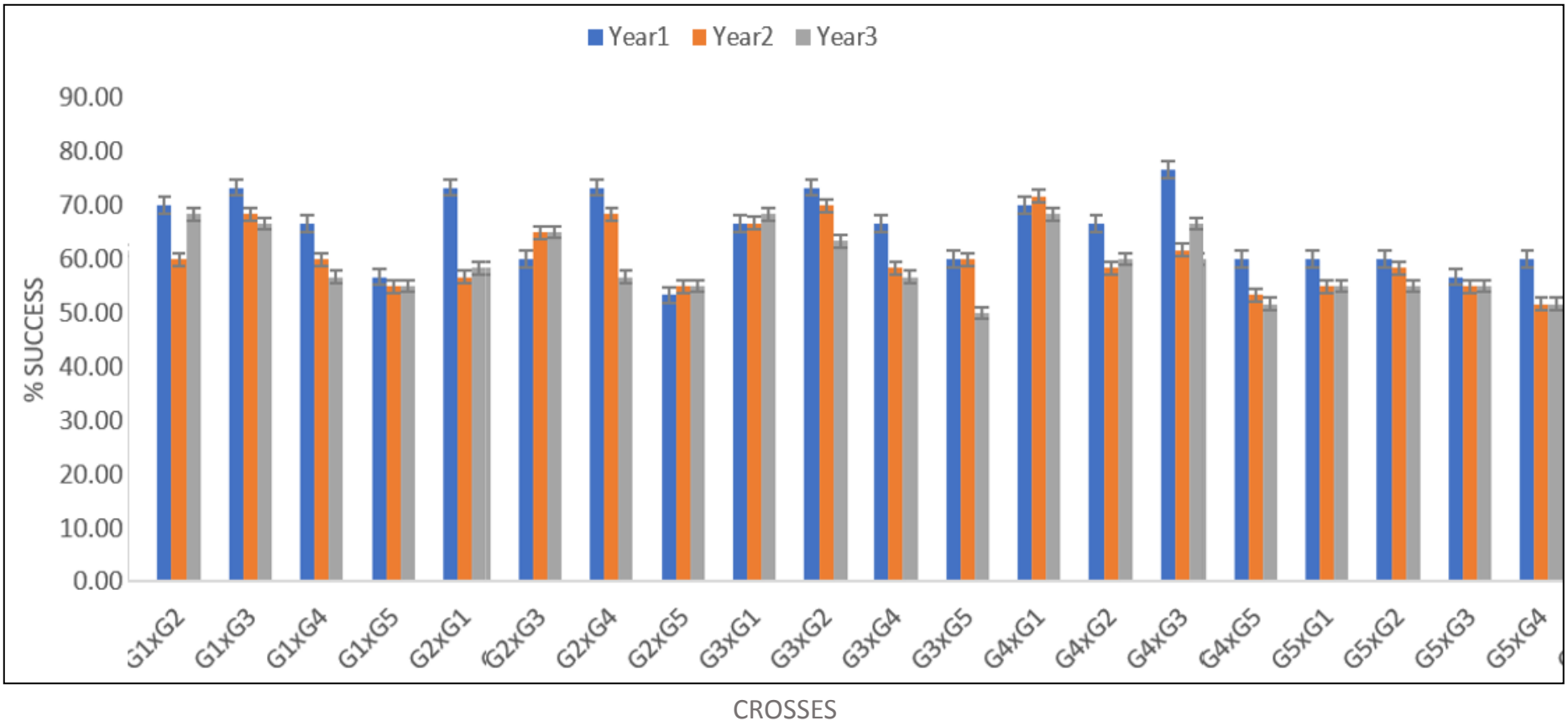


Figure 1. %Success in different combinations of tomatillo genotypes over the year

Experiment 2: Heterosis and combining ability analysis of F1 generation of tomatillo (*Physalis ixocarpa*Brot./*Physalis philadelphica* Lam.).

The present experiment was conducted to perform the full diallel analysis of five different parental genotypes and twenty crosses of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.) using agromorphogenic and yield contributing traits. The data pertaining to fifteen characters have been presented and statistically analyzed with the possible interpretations. The analysis of variance of the genotypes, mean performances of the parents and cross combinations, heterosis, combining ability variances, ration of GCA and SCA variances are presented in this experiment.

4.2.1 Mean performance and analysis of variance

Mean performance of 15 yield related agromorphogenic traits of parents and cross combinations are presented in Table 15. Significant genotypic variations were observed for all the characters under this studied (Appendix VI).

4.2.1.1 Germination %

For the germination%, the parents and cross combination showed a range of 76.33-88.33 with an average 81.76 (Table 15). Among the five parents, G3 showed the lowest (76.66) germination% where G4 showed the highest (83.33) germination %. Among the 20 cross combinations, G3×G1 showed the highest (88.33) germination %, and the lowest (76.33) germination% was observed in G2×G5.

4.2.1.2 Plant height (cm)

For the plant height the parents and cross combination showed a range of 80.10-91.87 with an average 84.25 (Table 15). Among the five parents G4 showed the highest (87.75) plant height where G5 showed the lowest (81.81) plant height. Among the 20 cross combinations G2×G1(91.87) showed the highest plant height, and the lowest plant height was observed in G2×G4 (80.10) (Table 15).

Table 15. Mean performance of five parents and twenty cross combinations for fifteen morphological characters of tomatillo

Genotypes	Germination %	Plant height (cm)	Leaf area index	No. of branches / plant	Days to first flowering
G1	79.00 defg	83.65 cdefg	24.76 ab	7.78 ab	28.22 abcde
G2	82.0 bcdefg	86.5 abcdefg	22.7 bcdefg	8.01 a	30.05 ab
G3	76.66 fg	82.663cdefg	22.6 bcdefg	7.93 ab	27.55 bcde
G4	83.33 abcde	87.75 abcd	21.213 efgh	7.71 ab	28.52 abcde
G5	80.00 defg	81.81 cdefg	21.14 efgh	7.64 ab	28.87 abcd
G1 × G2	84.33 abcd	81.59 cdefg	23.29 abcde	7.46 ab	29.46 abcd
G1 × G3	87.33 ab	86.67 abcdef	25.216 a	7.86 ab	24.83
G1 × G4	80.33 defg	80.27 fg	22.18 cdefgh	7.35 ab	28.25 abcde
G1 × G5	81.66 bcdefg	83.82 cdefg	23.66 abcd	7.41 ab	29.82abc
G2 × G1	79.00 defg	91.87 a	23.02 abcdef	6.93 ab	28.53 abcde
G2 × G3	82.33 bcdef	88.15 abc	21.82 cdefgh	7.8 ab	28.1 abcde
G2 × G4	84.00 abcd	80.1 g	19.91 h	6.43 b	30.32 a
G2 × G5	76.333 g	82.19 cdefg	21.42 defgh	7.21 ab	29.38 abcd
G3 × G1	88.33 a	80.44 efg	24 abc	7.61 ab	25.92 ef
G3 × G2	79.66 defg	91.61 ab	22.38 cdefg	6.77 ab	28.48 abcde
G3 × G4	83.00 abcde	85.22 bcdefg	20.77 fgh	7.31 ab	27.42 bcdef
G3 × G5	81.00 cdefg	85.78 abcdefg	21.65 defgh	7.483 ab	27.29 cdef
G4 × G1	78.00 efg	82.31 cdefg	20.64 gh	6.96 ab	28.61 abcd
G4 × G2	83.33 abcde	81.77 cdefg	20.62 gh	7.38 ab	29.46 abcd
G4 × G3	86.66 abc	87.25 abcd	22.71 bcdefg	7.62 ab	27.03 def
G4 × G5	82.66 abcde	81.42 defg	21.76 cdefgh	7.81 ab	28.79 abcd
G5 × G1	79.66 defg	81.72 cdefg	22.27 cdefg	7.67 ab	28.40 abcde
G5 × G2	82.00 bcdefg	82.98 cdefg	21.48 defgh	8.24 a	28.88 abcd
G5 × G3	79.66 defg	86.99 abcde	21.48 defgh	7.26 ab	27.51 bcde
G5 × G4	83.66 abcde	81.66 cdefg	21.28 efgh	7.34 ab	28.22abcde
CV	2.28	2.50	3.33	6.45	2.85
Average	81.76	84.25	22.16	7.48	28.31
Maximum	88.33	91.87	25.21	8.24	30.32
Minimum	76.33	80.10	19.91	6.43	24.83

Note : Genotypes means having the same letter are statistically identical and those having different letters are statistically different from each other.

Table 15. (CONT´D)

Genotypes	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length (mm)	Fruit dimeter (mm)
G1	49.77 a	80.31 defg	35.04 ab	32.1 abcd	32.76 abcd
G2	50.2 a	79.44 efg	31.81 cdefg	30.24 bcde	31.5 abcde
G3	48.18 ab	78.56 g	29.76 defg	29.6 cde	29.30 e
G4	50.04 a	79.92 efg	30.85 cdefg	28.96 e	29.15 e
G5	48.68 ab	78.73 fg	30.03 defg	30.42 bcde	29.59 de
G1 × G2	48.57 ab	80.64 bcdefg	35.05 ab	32.97 ab	33.32 abc
G1 × G3	45.79b	80.09 defg	35.67 a	34.31a	34.71 a
G1 × G4	49.13 ab	82.96 abcd	30.47cdefg	30.473 bcde	32.3 abcde
G1 × G5	48.87 ab	83.29abc	32.39 bcde	30.30 bcde	31.42 abcde
G2 × G1	49.43 a	83.51 ab	31.16 cdefg	29.98 bcde	33.11 abc
G2 × G3	48.23 ab	83.85 a	32.663 bcd	30.77 bcde	31.64 abcde
G2 × G4	50.04 a	81.57 abcdef	30.05 defg	28.75 e	30.21 cde
G2 × G5	49.38 a	79.91efg	30.48 cdefg	30.16 bcde	28.86 e
G3 × G1	45.87 b	83.96 a	33.12 abc	32.60abc	33.99 ab
G3 × G2	49.14 ab	81.50 abcdef	31.85 cdef	30.73 bcde	31.24 bcde
G3 × G4	49.13 ab	80.25 defg	31.27 cdefg	31.21 bcde	30.33 cde
G3 × G5	48.58 ab	79.44efg	29.36 fg	29.65cde	29.40 de
G4 × G1	49.66 a	83.66 a	30.60 cdefg	30.61 bcde	31.51 abcde
G4 × G2	50.49 a	82.08 abcde	29.49 efg	29.33 de	30.16 cde
G4 × G3	48.55 ab	80.59cdefg	30.91 cdefg	30.44 bcde	31.13 bcde
G4 × G5	48.95 ab	79.53 efg	29.26 fg	29.176 de	29.22 e
G5 × G1	48.98 ab	79.44efg	29.37 fg	29.90 cde	30.89 bcde
G5 × G2	48.56 ab	79.23 efg	29.00 fg	28.93 e	28.96 e
G5 × G3	48.15 ab	78.5 g	28.93 g	29.17 de	30.77 bcde
G5 × G4	49.18 ab	80.00 efg	29.97 defg	29.17 de	29.98 cde
CV	2.29	1.15	2.95	3.03	3.41
Average	48.86	80.84	31.14	30.40	31.02
Maximum	50.49	83.96	35.67	34.31	34.71
Minimum	45.79	78.50	28.93	28.75	28.86

Note : Genotypes means having the same letter are statistically identical and those having different letters are statistically different from each other.

Table 15. (CONT´D)

Genotypes	Individual fruit weight (g)	Seeds/fruit	Yield/plant (g)	Yield/plot (Kg)	Yield/ha (t)
G1	27.1 bc	395.33 abc	943.33 bc	11.05 abcd	78.12 bcd
G2	25.27cdef	399.33 abc	948 bc	11.24 abc	80.91bc
G3	25.87 cd	390 abcde	793.33 ef	9.52 cdef	66.09 efgh
G4	23.51 defghi	385.33 abcdef	769 efgh	9.2 defg	64.23 efghij
G5	22.59 fghi	391.66 abcde	721.66fghi	8.81 efg	61.44 fghij
G1 × G2	29.3 ab	380 bcdef	1017.33 ab	11.71 ab	86.66 ab
G1 × G3	30.20 a	408.66 a	1060.66 a	12.86 a	93.23 a
G1 × G4	23.44 defghi	365.33 defg	782.33 efg	8.97 efg	61.73 fghij
G1 × G5	27.22 bc	381.667 abcdef	905.33cd	11.06 abcd	65.21 efghi
G2 × G1	25.37 cde	371.33cdef	802.333 ef	9.42 cdef	65.43 efghi
G2 × G3	22.67fghi	363.66 efg	733 fghi	8.79 efg	61.05 fghij
G2 × G4	21.04 i	360.66 fg	622.66 j	7.47 g	61.33fghij
G2 × G5	23.21defghi	392.66abcd	690 ghij	8.16 fg	56.65 hij
G3 × G1	24.766 cdefg	404.66 ab	842.66 de	10.10 bcde	70.20 def
G3 × G2	21.58 hi	364 efg	718.33 fghij	8.44 efg	59.11 ghij
G3 × G4	22.73 efghi	379 bcdef	718.66 fghij	8.36 efg	59.75 ghij
G3 × G5	24.84 cdef	386 abcdef	761.66 efghi	9.16 efg	63.45 efghij
G4 × G1	22.076 ghi	381.66 abcdef	676.33 hij	8.16 fg	56.33 ij
G4 × G2	21.52 hi	339.66 g	669 ij	7.51 g	55.43 j
G4 × G3	24.05 defgh	374 cdef	812.33 def	9.67 cdef	71.87 cde
G4 × G5	22.64 fghi	388.66 abcdef	795.33 ef	9.4 cdef	66.79 efg
G5 × G1	24.84 cdef	394.66 abc	782 efg	9.33 defg	64.97 efghij
G5 × G2	23.85 defgh	381 abcdef	801.33 ef	9.65 cdef	67.04 efg
G5 × G3	25.62 cd	378 bcdef	783.33 efg	9.34 defg	64.84 efghij
G5 × G4	22.66 fghi	395.33 abc	780 efg	9.08 efg	63.98 efghij
CV	3.51	2.35	3.91	6.27	4.63
Average	24.32	382.09	797.20	9.46	66.63
Minimum	30.20	408.67	1060.7	12.86	93.23
Maximum	21.04	339.67	622.7	7.47	55.43

Note : Genotypes means having the same letter are statistically identical and those having different letters are statistically different from each other.

4.2.1.3 Leaf area index

For the leaf area, the parents and cross combination showed a range of 19.91-25.21 with an average 22.16 (Table 15). Among the five parental genotypes G1 showed the highest (24.76) leaf area index where the lowest leaf area index showed in G5 (21.14). Among the twenty cross combination G1×G3 (25.21) showed the highest leaf area and G2×G4 showed (19.91) the lowest leaf area index (Table 15).

4.2.1.4 Number of branches per plant

For the branches/plant, the parents and cross combination showed a range of 6.43-8.24 with an average 7.48 (Table 15). Among the five parents G2 showed the highest (8.01) number of branches per plant where the lowest number of branches per plant showed in G5 (7.64). Among the twenty-cross combination G5×G2 (8.24) showed the highest number of branches and G2×G4 showed (6.43) the lowest number of branches per plant (Table 15).

4.2.1.5 Days to first flowering

For the days to first flowering, the parents and cross combination showed a range of 24.83-30.32 with an average 28.31 (Table 15). Considering the mean performance, G3 (27.55) showed the earliest days to first flowering and G2 (30.05) showed the longest time for days to first flowering within five parents. Among the twenty crosses G1×G3 (24.83) showed the earliest days to first flowering and G2×G4 (30.32) performed longest days to first flowering (Table 15).

4.2.1.6 Days to 50% flowering

For the days to 50% flowering, the parents and cross combination showed a range of 45.79-50.49 with an average 48.86 (Table 15). Considering the mean performance, G3 (48.18) showed the earliest days to fifty % flowering and G2 (50.20) showed the longest time for days to fifty % flowering within five parents. Among the twenty crosses G1×G3 (45.79) showed the earliest days to first flowering and G4×G2 (50.49) showed longest days to fifty % flowering (Table 15).

4.2.1.7 Days to maturity

For the days to maturity, the parents and cross combination showed a range of 78.50-83.96 with an average 80.84 (Table 15). Among the five parents G3 showed the shortest (78.56) days to maturity where G1 (80.31) showed the longest average maturity days. Among the twenty-cross combination G3×G21 (83.96) showed longer days to maturity and G5×G3 (78.50) showed the shorter days to maturity from this study (Table 15).

4.2.1.8 Number of fruits per plant

For the number of fruits per plant, the parents and cross combination showed a range of 28.93-35.67 with an average 31.14 (Table 15). Among the five parents the lowest number of fruits per plant was found in G3 (29.76) and in G1 (35.04) was the highest number of fruits per plant. Among 20 cross combinations in G1×G3 (35.65) number of fruits per plant was the highest and in G5×G3 (28.93) it was observed the lowest (Table 15).

4.2.1.9 Fruit length (mm)

For the fruit length, the parents and cross combination showed a range of 28.75-34.31 with an average 30.40 (Table 15). Among the five parents the longest fruit was found in parent G1 (32.11) and in G4 (28.94) was found the shortest fruit length. Among 20 cross combinations in G1×G3 (34.31) was observed the highest fruit length and in G2×G4 (28.75) it was observed the lowest (Table 15).

4.2.1.10 Fruit diameter (mm)

For the fruit diameter, the parents and cross combination showed a range of 28.86-34.71 with an average 31.02 (Table 15). Among the five parents the lowest fruit diameter was found in G4 (29.15) and in G1 (32.76) was the highest fruit diameter. Among 20 cross combinations G1×G3 (34.71) was showed the highest fruit diameter and in G2×G5 (28.86) it was observed the lowest (Table 15).

4.2.1.11 Individual fruit weight (g)

For the individual fruit weight, the parents and cross combination showed a range of 21.04-30.20 with an average 24.32 (Table 15). Among the five parents the lowest individual fruit weight was found in G5 (22.59) and in G3 (25.87) was the highest individual fruit weight. Among 20 cross combinations in G1×G3 (30.20) highest individual fruit weight was found and in G2×G4 (21.04) it was observed the lowest (Table 15).

4.2.1.12 Seeds per fruits

For the seeds per fruits, the parents and cross combination showed a range of 339.67-408.67 with an average 382.09 (Table 15). Among the five parents the lowest number of seeds per fruit was found in G4 (385.33) and in G2 (399.33) was the highest number of seeds per fruits. Among 20 cross combinations in G1×G3 (408.66) number of seeds per fruit was the highest and in G4×G2 (339.66) it was observed the lowest (Table 15).

4.2.1.13 Yield per plant (g/plant)

For the yield per plant, the parents and cross combination showed a range of 622.7-1060.7 with an average 797.20 (Table 15). Among the five parents the highest number of yields per plant was found in G2 (948) and lowest yield per plant was found in G5 (721.66). Among 20 cross combinations in G1×G3 (1060.66) number of yields per plant was the highest and in G2×G4 (622.66) it was observed the lowest (Table 15).

4.2.1.14 Yield per plot (g)

For the yield per plot, the parents and cross combination showed a range of 7.47-12.86 with an average 9.46 (Table 15). Among the five parents the highest number of yield per plot was found in G2 (11.25) and lowest yield per plot was found in G5 (8.81). Among 20 cross combinations in G1×G3 (12.36) number of yield per plot was the highest and in G2×G4 (7.47) it was observed the lowest (Table 15).

4.2.1.14 Yield per ha (t)

For the yield per ha, the parents and cross combination showed a range of 55.43-93.23 with an average 66.63 (Table 20). Among the five parents the highest number of yield per plot was found in G2 (80.91) and lowest yield per plot was found in G5 (61.44). Among 20 cross combinations in G1×G3 (93.23) number of yield per plot was the highest and in G4×G2(55.43) it was observed the lowest (Table 15).

4.2.2 Heterosis analysis

Degree of heterosis is measured over a cultivated popular variety or hybrid variety is integrated for comparison during release of new hybrid variety. In this experiment G1 was included as check variety for better comparison of 15 yield contributing characters of the twenty experimental hybrids. Percent heterosis for different characters of the F_1 hybrids over respective mid, better and standard check parental values are shown in table 2. The percent of heterosis in crosses varied from character to character or from cross to cross.T he analysis of variance for genotypes i.e., parents and crosses showed significant difference for all the characters studied. The estimates of percent heterosis observed in F_1 generation over better parents and mid parents and standard heterosis are presented through Table 16.

4.2.2.1 Germination %

Among the twenty cross combinations 11 crosses showed positive heterobeltosis for germination % and 9 crosses showed negative heterobeltosis (Table 16). Heterosis for this character ranged from -6.91% to 11.81%. The highest negative heterosis was observed in G2×G5(-6.91%). The highest positive heterosis effect was observed in the cross G3×G1(11.81%) with mean 0.43%. Out of twenty crosses 16 showed positive heterosis over mid parent and 4 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from –5.76% to 13.49%. The highest significant positive heterosis was observed in the cross G3×G1 (13.49%). The highest negative heterosis was observed in the cross G2×G5 (-5.76%). Among twenty crosses two hybrids showed negative heterosis in standard check and eighteen crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G5 (-3.38 %) and maximum was found in G3×G1 (11.81%) with mean 3.99% (Table 16).

Table 16. Estimation of heterosis over better parent, heterosis over mid parent and standard heterosis for fifteen morphological characters of tweenty cross combinations of tomatillo genotypes

Crosses	Germination %			Plant height (cm)			Leaf area index			No. of branches/plant		
	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH
G1 × G2	2.85	4.76	6.75	-5.71	-4.11	-2.46	-5.96	-1.94	-5.96	-6.86	-5.49	-4.07
G1 × G3	10.55	12.21	10.55	3.61	4.23	3.61	1.82	6.46	1.82	-0.84	0.11	1.07
G1 × G4	-3.60	-1.03	1.69	-8.52	-6.33	-4.03	-10.44	-3.52	-10.44	-5.57	-5.16	-5.57
G1 × G5	2.08	2.73	3.38	0.20	1.31	0.20	-4.45	3.09	-4.45	-4.75	-3.87	-4.75
G2 × G1	-3.66	-1.86	0.00	6.16	7.97	9.83	-7.04	-3.06	-7.04	-13.51	-12.24	-10.92
G2 × G3	0.41	3.78	4.22	1.86	4.19	5.38	-4.02	-3.75	-11.90	-2.70	-2.19	0.21
G2 × G4	0.80	1.61	6.33	-8.72	-8.09	-4.24	-12.42	-9.39	-19.61	-19.79	-18.26	-17.39
G2 × G5	-6.91	-5.76	-3.38	-5.02	-2.36	-1.74	-5.78	-2.36	-13.51	-9.98	-7.81	-7.28
G3 × G1	11.81	13.49	11.81	-3.83	-3.26	-3.83	-3.10	1.32	-3.10	-4.08	-3.16	-2.23
G3 × G2	-2.85	0.42	0.84	5.87	8.30	9.52	-1.54	-1.26	-9.62	-15.51	-15.07	-12.98
G3 × G4	-0.40	3.75	5.06	-2.88	0.02	1.88	-8.12	-5.20	-16.14	-7.86	-6.58	-6.08
G3 × G5	1.25	3.40	2.53	3.78	4.31	2.55	-4.20	-0.99	-12.56	-5.67	-3.90	-3.85
G4 × G1	-6.40	-3.90	-1.27	-6.20	-3.95	-1.59	-16.64	-10.19	-16.64	-10.49	-10.11	-10.49
G4 × G2	0.00	0.81	5.49	-6.82	-6.17	-2.24	-9.28	-6.14	-16.73	-7.90	-6.14	-5.14
G4 × G3	4.00	8.33	9.70	-0.58	2.39	4.30	0.46	3.65	-8.30	-3.91	-2.58	-2.06
G4 × G5	-0.80	1.22	4.64	-7.22	-3.96	-2.66	2.61	2.79	-12.11	1.30	1.80	0.43
G5 × G1	-0.42	0.21	0.84	-2.30	-1.22	-2.30	-10.08	-2.98	-10.08	-1.41	-0.50	-1.41
G5 × G2	0.00	1.23	3.80	-4.10	-1.42	-0.79	-5.50	-2.07	-13.26	2.79	5.26	5.87
G5 × G3	-0.42	1.70	0.84	5.24	5.78	4.00	-4.98	-1.80	-13.27	-8.49	-6.76	-6.72
G5 × G4	0.40	2.45	5.91	-6.94	-3.69	-2.37	0.33	0.50	-14.06	-4.79	-4.32	-5.61
Minimum	-6.91	-5.76	-3.38	-8.72	-8.09	-4.24	-16.64	-10.19	-19.61	-19.79	-18.26	-17.39
Maximum	11.81	13.49	11.81	6.16	8.30	9.83	2.61	6.46	1.82	2.79	5.26	5.87
Mean	0.43	2.48	3.99	-2.11	-0.30	0.65	-5.42	-1.84	-10.85	-6.50	-5.35	-4.95

HBP= Heterosis over better parent; HMP= Heterosis over mid parent; SH= Standard heterosis.

Table 16. (CONT´D)

Crosses	Days to 1st flowering			Days to 50% flowering			Days to maturity			No. of fruits/plant		
	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH
G1 × G2	4.49	1.17	4.42	-2.42	-2.84	-2.43	1.51	0.95	0.41	0.15	4.92	0.15
G1 × G3	-9.86	-10.91	-12.00	-4.96	-6.51	-8.01	1.95	0.82	-0.27	1.92	10.16	1.92
G1 × G4	0.20	-0.36	0.13	-1.29	-1.55	-1.29	3.81	3.56	3.30	-12.92	-7.44	-12.92
G1 × G5	5.76	4.51	5.68	0.39	-0.73	-1.83	5.79	4.74	3.71	-7.45	-0.38	-7.45
G2 × G1	1.10	-2.07	1.11	-0.68	-1.10	-0.69	5.12	4.55	3.98	-11.09	-6.77	-10.97
G2 × G3	2.00	-2.43	-0.43	0.11	-1.94	-3.10	6.73	6.14	4.41	2.71	6.11	-6.68
G2 × G4	6.31	3.53	7.44	0.01	-0.15	0.53	2.68	2.37	1.56	-5.48	-4.05	-14.12
G2 × G5	1.77	-0.27	4.11	1.44	-0.12	-0.80	1.50	1.05	-0.50	-4.15	-1.41	-12.91
G3 × G1	-5.90	-7.04	-8.14	-4.80	-6.35	-7.85	6.86	5.69	4.54	-5.48	2.17	-5.35
G3 × G2	3.40	-1.09	0.94	1.99	-0.10	-1.28	3.74	3.16	1.48	0.10	3.38	-9.00
G3 × G4	-0.47	-2.19	-2.83	1.97	0.04	-1.30	2.14	1.27	-0.08	1.38	3.14	-10.64
G3 × G5	-0.94	-3.26	-3.30	0.82	0.31	-2.41	1.12	1.01	-1.09	-2.22	-1.84	-16.10
G4 × G1	1.37	0.84	1.38	-0.23	-0.49	-0.23	4.69	4.43	4.17	-12.68	-7.19	-12.56
G4 × G2	3.32	0.62	4.42	0.91	0.75	1.44	3.31	3.01	2.20	-7.29	-5.94	-15.72
G4 × G3	-1.88	-3.57	-4.21	0.77	-1.14	-2.46	2.58	1.71	0.35	0.04	1.91	-11.68
G4 × G5	0.95	0.33	2.02	0.57	-0.82	-1.65	1.01	0.26	-0.98	-5.29	-3.94	-16.38
G5 × G1	0.65	-0.49	0.66	0.63	-0.49	-1.59	0.91	-0.10	-1.08	-16.20	-9.70	-16.09
G5 × G2	0.06	-1.95	2.36	-0.25	-1.78	-2.45	0.64	0.19	-1.34	-8.83	-6.15	-17.12
G5 × G3	-0.13	-2.47	-2.50	-0.06	-0.57	-3.26	-0.08	-0.19	-2.26	-3.57	-3.19	-17.34
G5 × G4	-1.04	-1.64	0.01	1.03	-0.36	-1.21	1.61	0.85	-0.39	-2.85	-1.50	-14.37
Minimum	-9.86	-10.91	-12.00	-4.96	-6.51	-8.01	-0.08	-0.19	-2.26	-16.20	-9.70	-17.34
Maximum	6.31	4.51	7.44	1.99	0.75	1.44	6.86	6.14	4.54	2.71	10.16	1.92
Average	0.56	-1.44	0.06	-0.20	-1.30	-2.09	2.88	2.27	1.11	-4.96	-1.39	-11.27

HBP= Heterosis over better parent; HMP= Heterosis over mid parent; SH= Standard heterosis.

Table 16. (CONT´D)

Crosses	Fruit length			Fruit diameter			Individual fruit weight			Seeds/fruit		
	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH
G1 × G2	2.71	5.77	2.71	1.69	3.69	1.69	8.12	11.88	8.12	-4.84	-4.36	-4.84
G1 × G3	6.91	11.24	6.91	5.95	11.86	5.95	11.45	14.04	11.45	3.37	4.07	4.07
G1 × G4	-5.07	-0.20	-5.07	-1.42	4.33	-1.42	-13.49	-7.36	-13.49	-7.59	-6.40	-6.40
G1 × G5	-5.60	-3.06	-5.60	-4.10	0.78	-4.10	0.44	9.55	0.44	-3.46	-3.01	-3.01
G2 × G1	-6.60	-3.82	-6.60	1.05	3.04	1.05	-6.38	-3.17	-6.38	-7.01	-6.54	-6.54
G2 × G3	1.75	2.84	-4.14	0.46	4.08	-3.43	-12.36	-11.38	-16.33	-8.93	-7.85	-7.85
G2 × G4	-4.93	-2.88	-10.44	-4.08	-0.37	-7.79	-16.82	-13.78	-22.35	-9.68	-8.07	-8.07
G2 × G5	-0.83	-0.54	-6.02	-8.36	-5.50	-11.90	-8.23	-3.05	-14.33	-1.67	-0.72	-0.72
G3 × G1	1.58	5.69	1.58	3.75	9.54	3.75	-8.61	-6.54	-8.61	2.36	3.06	2.36
G3 × G2	1.63	2.72	-4.26	-0.81	2.77	-4.65	-16.68	-15.66	-20.37	-8.85	-7.77	-8.85
G3 × G4	5.45	6.59	-2.76	3.50	3.78	-7.44	-12.23	-7.99	-16.11	-2.82	-2.24	-2.24
G3 × G5	-2.52	-1.19	-7.62	-0.63	-0.14	-10.25	-4.08	2.46	-8.33	-1.45	-1.24	-1.45
G4 × G1	-4.64	0.25	-4.64	-3.81	1.80	-3.81	-18.54	-12.74	-18.54	-3.46	-2.22	-3.46
G4 × G2	-3.01	-0.92	-8.63	-4.24	-0.53	-7.95	-14.85	-11.75	-20.58	-14.94	-13.42	-14.94
G4 × G3	2.84	3.95	-5.17	6.26	6.54	-4.97	-7.04	-2.57	-11.25	-4.10	-3.53	-4.10
G4 × G5	-4.09	-1.74	-9.11	-1.26	-0.52	-10.82	-3.63	-1.74	-16.43	-0.77	0.04	-0.77
G5 × G1	-6.84	-4.34	-6.84	-5.73	-0.93	-5.73	-8.34	-0.04	-8.34	-0.17	0.30	-0.17
G5 × G2	-4.88	-4.59	-9.85	-8.05	-5.18	-11.61	-5.62	-0.34	-11.97	-4.59	-3.67	-4.59
G5 × G3	-4.10	-2.79	-9.12	3.98	4.49	-6.09	-0.95	5.73	-5.45	-3.49	-3.28	-3.28
G5 × G4	-4.10	-1.75	-9.12	1.33	2.09	-8.48	-3.60	-1.69	-16.36	0.94	1.76	1.76
Minimum	-6.84	-4.59	-10.44	-8.36	-5.50	-11.90	-18.54	-15.66	-22.35	-14.94	-13.42	-14.94
Maximum	6.91	11.24	6.91	6.26	11.86	5.95	11.45	14.04	11.45	3.37	4.07	4.07
Average	-1.72	0.56	-5.19	-0.73	2.28	-4.90	-7.07	-2.81	-10.76	-4.06	-3.25	-3.65

BP= Heterosis over better parent; HMP= Heterosis over mid parent; SH= Standard heterosis.

Table 16. (CONT´D)

Crosses	Yield/plant			Yield/plot			Yield/ha		
	HBP	HMP	SH	HBP	HMP	SH	HBP	HMP	SH
G1 × G2	7.31	7.58	7.84	4.21	5.08	5.97	7.10	8.99	10.94
G1 × G3	12.44	22.15	12.44	16.41	25.08	16.41	19.35	29.30	19.35
G1 × G4	-17.06	-8.62	-17.07	-18.79	-11.36	-18.79	-20.98	-13.27	-20.98
G1 × G5	-4.02	8.75	-4.03	0.06	11.36	0.06	-16.53	-6.55	-16.53
G2 × G1	-15.37	-15.16	-14.95	-16.16	-15.46	-14.75	-19.14	-17.71	-16.24
G2 × G3	-22.68	-15.81	-22.30	-21.77	-15.29	-20.45	-24.55	-16.94	-21.84
G2 × G4	-34.32	-27.47	-33.99	-33.54	-26.91	-32.42	-24.20	-15.49	-21.49
G2 × G5	-27.22	-17.35	-26.86	-27.40	-18.60	-26.18	-29.99	-20.42	-27.48
G3 × G1	-10.67	-2.94	-10.67	-8.56	-1.75	-8.56	-10.13	-2.64	-10.13
G3 × G2	-24.23	-17.48	-23.85	-24.88	-18.66	-23.61	-26.95	-19.58	-24.33
G3 × G4	-9.37	-7.98	-23.82	-12.18	-10.68	-24.37	-9.59	-8.30	-23.51
G3 × G5	-3.95	0.57	-19.26	-3.78	-0.05	-17.13	-3.98	-0.49	-18.77
G4 × G1	-28.30	-21.00	-28.30	-26.18	-19.42	-26.18	-27.89	-20.86	-27.89
G4 × G2	-29.43	-22.07	-29.08	-33.13	-26.45	-32.00	-31.49	-23.62	-29.04
G4 × G3	2.39	3.99	-13.89	1.65	3.38	-12.45	8.75	10.29	-8.00
G4 × G5	3.42	6.71	-15.69	2.17	4.39	-14.96	3.97	6.28	-14.50
G5 × G1	-17.10	-6.07	-17.10	-15.56	-6.02	-15.56	-16.82	-6.89	-16.82
G5 × G2	-15.47	-4.01	-15.05	-14.09	-3.67	-12.64	-17.15	-5.82	-14.18
G5 × G3	-1.26	3.41	-16.96	-1.89	1.91	-15.50	-1.90	1.68	-17.00
G5 × G4	1.43	4.65	-17.31	-1.30	0.83	-17.85	-0.39	1.82	-18.09
Minimum	-34.32	-27.47	-33.99	-33.54	-26.91	-32.42	-31.49	-23.62	-29.04
Maximum	12.44	22.15	12.44	16.41	25.08	16.41	19.35	29.30	19.35
Average	-11.67	-5.41	-16.50	-11.74	-6.11	-15.55	-12.13	-6.01	-15.83

BP= Heterosis over better parent; HMP= Heterosis over mid parent; SH= Standard heterosis

4.2.2.2 Plant height

Among the twenty cross combinations 7 crosses showed positive heterobeltosis for plant height and 13 crosses showed negative heterobeltosis (Table 16). The highest negative heterosis was observed in G2×G4 (-8.72%). The highest positive heterosis effect was observed in the cross G2×G1(6.16%) with mean -2.11% over the better parent.

Out of twenty crosses 9 showed positive heterosis over mid parent and 11 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from –8.09% to 8.30%. The highest significant positive heteros was observed in the cross G3×G2 (8.30%). The highest negative heterosis was observed in the cross G2×G4 (-8.09%) with mean -0.30% over mid parent.

Among twenty crosses 11 hybrids showed negative heterosis in standard check and 9 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-4.24 %) and maximum was found in G3×G1 (9.83%) with mean 0.65% (Table 16).

4.2.2.3 Leaf area index

Among the twenty cross combinations 4 crosses showed positive heterobeltosis for leaf area index and 16 crosses showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G4×G1 (-16.64%). The highest positive heterosis effect was observed in the cross G4×G5(2.61%) with mean -5.42% over the better parent.

Out of twenty crosses 6 showed positive heterosis over mid parent and 14 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from –10.19% to 6.46%. The highest positive heteros is was observed in the cross G1×G3 (6.46%). The highest negative heterosis was observed in the cross G4×G1 (-10.19%) with mean -1.84% over mid parent.

Among twenty crosses 19 hybrids showed negative heterosis in standard check and single crosses found positive heterosis. Minimum standard heterosis was found in

cross G2×G4 (-19.61%) and maximum was found in G1×G3 (1.82%) with mean -10.85% (Table 16).

4.2.2.4 Number of branches per plant

Among the twenty cross combinations 2 crosses showed positive heterosis over better parent for number of branches per plant and 18 crosses showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G2×G4 (-19.79%). The highest positive heterosis effect was observed in the cross G5×G2 (2.79%) with mean -6.50% over the better parent.

Out of twenty crosses 3 showed positive heterosis over mid parent and 17 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from –18.26% to 5.26%. The highest positive heteroses is was observed in the cross G5×G2 (5.26%). The highest negative heterosis was observed in the cross G2×G4 (-18.26%) with mean -5.35% over mid parent.

Among twenty crosses 16 hybrids showed negative heterosis in standard check and 4 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-17.39%) and maximum was found in G5×G2 (5.87%) with mean -4.95% (Table 16).

4.2.2.5 Days to first flowering

Among the twenty cross combinations 13 crosses showed positive heterosis over better parent for number of branches per plant and 7 crosses showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G1×G3(-9.86%). The highest positive heterosis effect was observed in the cross G2×G4 (6.31%) with mean (0.56%) over the better parent.

Out of twenty crosses 6 showed positive heterosis over mid parent and 14 of them showed negative heterosis. The maximum heterosis estimated 4.51% in G1×G5 and minimum heterosis was found -10.9%1 in G1×G3 with mean -1.44% over mid parent (Table 16).

Among twenty crosses 7 hybrids showed negative heterosis in standard check and 13 crosses found positive heterosis. Minimum standard heterosis was found in cross

G3×G1 (-12.00%) and maximum was found in G2×G4 (7.44%) with mean 0.06% (Table 16).

4.2.2.6 Days to fifty percent flowering

Among the twenty cross combinations 12 crosses showed positive heterosis over better parent for number of branches per plant and 8 crosses showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G1×G3 (-4.96%). The highest positive heterosis effect was observed in the cross G3×G2 (1.99%) with mean (-0.20%) over the better parent.

Out of twenty crosses 3 showed positive heterosis over mid parent and 17 of them showed negative heterosis. The maximum heterosis estimated 0.75% in G4×G2 and minimum heterosis was found -6.51% in G1×G3 with mean -1.30% over mid parent (Table 16).

Among twenty crosses 18 hybrids showed negative heterosis in standard check and 2 crosses found positive heterosis. Minimum standard heterosis was found in cross G1×G3 (-8.01%) and maximum was found in G4×G2 (1.44%) with mean -2.09% (Table 16).

4.2.2.7 Days to maturity

Among the twenty cross combinations 19 crosses showed positive heterosis over better parent for number of branches per plant and 1 cross showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G5×G3 (-0.08%). The highest positive heterosis effect was observed in the cross G3×G1(6.86%) with mean (2.88%) over the better parent.

Out of twenty crosses 18 showed positive heterosis over mid parent and 2 of them showed negative heterosis. The maximum heterosis estimated 6.14% in G2×G3 and minimum heterosis was found -0.19% in G5×G3 with mean 2.27% over mid parent (Table 16).

Among twenty crosses 9 hybrids showed negative heterosis in standard check and 11 crosses found positive heterosis. Minimum standard heterosis was found in cross

G5×G3 (-2.26%) and maximum was found in G3×G1 (4.54%) with mean 1.11% (Table 16).

4.2.2.8 Number of fruits/plants

Among the twenty cross combinations 6 crosses showed positive heterosis over better parent for number of branches per plant and 14 cross showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G5×G1(-16.20%). The highest positive heterosis effect was observed in the cross G2×G3(2.71%) with mean (-4.96%) over the better parent.

Out of twenty crosses 7 showed positive heterosis over mid parent and 13 of them showed negative heterosis. The maximum heterosis estimated 10.16% in G1×G3 and minimum heterosis was found -9.70% in G5×G1 with mean -1.39% over mid parent (Table 16). Among twenty crosses 18 hybrids showed negative heterosis in standard check and 2 crosses found positive heterosis. Minimum standard heterosis was found in cross G5×G3 (-17.34%) and maximum was found in G1×G3 (1.92%) with mean 11.27% (Table 16).

4.2.2.9 Fruit length

Among the twenty cross combinations 7 crosses showed positive heterosis over better parent for number of branches per plant and 13 cross showed negative heterosis over better parent (Table 16). The highest negative heterosis was observed in G5×G1 (-6.84%) and the highest positive heterosis effect was observed in the cross G1×G3 (6.91%) over the better parent with mean (-1.72%).

Over mid parent, out of twenty crosses 8 showed positive heterosis and 12 of them showed negative heterosis. The maximum heterosis estimated 11.24% in G1×G3 and minimum heterosis was found -4.59% in G5×G2 with mean 0.56% over mid parent (Table 16). Among twenty crosses 17 hybrids showed negative heterosis in standard check and 3 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-10.44%) and maximum was found in G1×G3 (6.91%) with mean -5.91% (Table 16).

4.2.2.10 Fruit diameter

Among the 20 cross combinations 9 crosses showed positive heterobeltosis for fruit diameter and 11 crosses showed negative heterosis (Table 16). Heterosis for this character ranged from -8.36% to 6.26%. The highest negative heterosis was observed in G2×G5 (-8.36%). The highest positive heterosis effect was observed in the cross G4×G3 (6.26%).

Thirteen crosses showed positive heterosis over mid parent and 7 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from-5.50% to 11.86%. The highest positive heterosis was observed in the cross G1×G3(11.86%). The highest significant negative heterosis was observed in the cross G2×G5 (-5.50%).

Among twenty crosses 16 hybrids showed negative heterosis in standard check and 4 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G5 (-11.90%) and maximum was found in G1×G3 (5.95%) with mean -4.90% (Table 16).

4.2.2.11 Individual fruit weight

Among the 20 cross combinations 3 crosses showed positive heterobeltosis for fruit diameter and 17 crosses showed negative heterobeltosis (Table 16). Heterosis for this character ranged from -18.54% to 11.45% with mean -7.07%. The highest negative heterosis was observed in G4×G1 (-18.54%). The highest positive heterosis effect was observed in the cross G1×G3 (11.45%).

Five crosses showed positive heterosis over mid parent and 15 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from -15.66% to 14.04% with mean -2.81%. The highest positive heterosis was observed in the cross G1×G3(14.04%). The highest significant negative heterosis was observed in the cross G3×G2 (-15.66%).

Among twenty crosses 17 hybrids showed negative heterosis in standard check and 3 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-22.35%) and maximum was found in G1×G3 (11.45%) with mean -10.76% (Table 16).

4.2.2.12 Seeds per fruit

Among the 20 cross combinations 3 crosses showed positive heterobeltosis for fruit diameter and 17 crosses showed negative heterobeltosis (Table 16). Heterosis for this character ranged from -14.94% to 3.37% with mean -4.06%. The highest negative heterosis was observed in G4×G2 (-14.94%). The highest positive heterosis effect was observed in the cross G1×G3 (3.37%).

Five crosses showed positive heterosis over mid parent and 15 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from -13.42% to 4.07% with mean -3.25%. The highest positive heterosis was observed in the cross G1×G3 (4.07%). The highest significant negative heterosis was observed in the cross G4×G2 (-13.42%).

Among twenty crosses 17 hybrids showed negative heterosis in standard check and 3 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-14.94%) and maximum was found in G1×G3 (4.07%) with mean -3.65% (Table 16).

4.2.2.13 Yield per plant

Among the 20 cross combinations 5 crosses showed positive heterobeltosis for fruit diameter and 15 crosses showed negative heterobeltosis (Table 16) for yield per plant. Heterosis for this character ranged from -34.32% to 12.44% with mean -11.67%. The highest negative heterosis was observed in G2×G4 (-34.32%). The highest positive heterosis effect was observed in the cross G1×G3 (12.44%).

Eight crosses showed positive heterosis over mid parent and 12 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from -27.47% to 22.15% with mean -5.41%. The highest positive heterosis was observed in the cross G1×G3 (22.15%). The highest significant negative heterosis was observed in the cross G2×G4 (-27.47%).

Among twenty crosses 18 hybrids showed negative heterosis in standard check and two crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-33.99%) and maximum was found in G1×G3 (12.44%) with mean -16.50% (Table 16).

4.2.2.14 Yield per plot

Among the 20 cross combinations 5 crosses showed positive heterobeltosis for fruit diameter and 15 crosses showed negative heterobeltosis (Table 16). Heterosis for this character ranged from -33.54% to 16.41% with mean -11.74%. The highest negative heterosis was observed in G2×G4 (-33.54%). The highest positive heterosis effect was observed in the cross G1×G3 (16.41%). Seven crosses showed positive heterosis over mid parent and 13 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from -26.91% to 25.08% with mean -6.11%. The highest positive heterosis was observed in the cross G1×G3 (25.08%). The highest significant negative heterosis was observed in the cross G2×G4 (-26.91%). Among 20 crosses 17 hybrids showed negative heterosis in standard check and 3 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-32.42%) and maximum was found in G1×G3 (16.41%) with mean -15.55% (Table 16).

4.2.2.15 Yield per hectare

Among the twenty cross combinations four crosses showed positive heterobeltosis for fruit diameter and 16 crosses showed negative heterobeltosis (Table 16) for yield per ha. Heterosis for this character ranged from -31.49% to 19.35% with mean -12.13%. The highest negative heterosis was observed in G4×G2 (-31.49%). The highest positive heterosis effect was observed in the cross G1×G3 (19.35%). Six crosses showed positive heterosis over mid parent and 14 of them showed negative heterosis (Table 16). The estimate of heterosis ranges from -23.62 % to 29.30 % with mean -6.01%. The highest positive heterosis was observed in the cross G1×G3 (29.30%). The highest significant negative heterosis was observed in the cross G4×G2 (-23.62%). Among 20 crosses 18 hybrids showed negative heterosis in standard check and 2 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-29.04%) and maximum standard heterosis was found in G1×G3 (19.35%) with mean -15.83% for yield per ha (Table 16).

4.2.3 Combining Ability

The analysis of variances for general combining ability (GCA) and specific combining ability (SCA) were found significant foremost of the traits studied (Table 17) indicating both additive and non-additive gene actions for the expression of these

Table 17. Analysis of variance (MS values) for GCA and SCA using the Griffings approach

Source of variances	Df	MS value							
		Germination %	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant
GCA	**4**	14.55**	6.41*	6.80**	0.07ns	6.09**	4.03**	6.29**	12.44**
SCA	**10**	12.58**	13.10**	0.85ns	0.18ns	0.95ns	1.21ns	2.77**	2.17**
Reciprocal	**10**	8.70**	4.73*	0.53ns	0.19ns	0.29ns	0.17ns	2.30**	1.74**
Error	**48**	1.48	1.16	0.18	0.08	0.22	0.42	0.29	0.28
σ2g		1.30	0.52	0.66	-0.0001	0.58	0.36	0.60	1.22
σ2s		11.09	14.03	0.66	0.10	0.73	0.79	2.49	1.88
σ2g/ σ2s		0.12	0.04	1.00	-0.001	0.80	0.45	0.24	0.64

Here,

** Significant at 1% level,

* Significant at 5% level; NS Non-significant. df = Degree of freedom.

Table 17. (CONT´D)

Sources of variances	Df	MS value						
		Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
GCA	**4**	6.04**	11.49**	15.97**	410.48**	25067**	3.65**	140.4**
SCA	**10**	1.34*	1.58ns	3.79**	351.64**	10174**	1.52**	84.44**
Reciprocal	**10**	0.74ns	0.24ns	2.83**	61.64ns	7221**	1.03**	65.67**
Error	**48**	0.28	0.37	0.25	26.82	324	0.12	3.17
σ2g		0.58	1.11	1.57	38.36	2474.33	13.73	13.73
σ2s		1.06	1.21	3.54	324.81	9850.35	81.27	81.27
σ2g/ σ2s		0.54	0.92	0.44	0.11	0.25	0.17	0.17

Here

** Significant at 1% level,

* Significant at 5% level; NS Non-significant. df = Degree of freedom.

traits. The general combining ability (GCA) variances foremost of the traits studied higher than the specific combining ability (SCA) variances indicating the predominance of the additive effect for these traits. The GCA component is predominantly a function of the additive genetic variance and GCA variances with each parent play's significant role in the choice of parents. A parent with higher positive significant GCA effects is considered as a good general combiner and the magnitude and direction of the significant effects for the five parents provide meaningful comparisons and would give indications to the future breeding program. The results of GCA effects for fifteen different characters were estimated and presented in Table 18. The SCA effects signify the role of non-additive gene action in the expression of the traits. It indicates the highly specific combining ability leading to highest performance of some specific cross combinations. That is why it is related to a particular cross. High GCA may arise not only in crosses involving high combiners but also in those involving low combiners. Thus, in practice, some of the low combiners should also be accommodated in hybridization program. The SCA effects of 20 F1 crosses for the same characters are presented in Table 19**.**

4.2.3.1 Germination %

The mean square (MS values) for GCA and SCA were positive significant for this trait which suggested the presence of both additive and non-additive gene action for this character (Table 22). Among the five parent studies the parent G3 (1.49**) showed highly significant positive GCA effects. On the other hand, G5(-1.23**) and G4 (-0.69*) showed the highly significant negative GCA effect and G1 showed non-significant negative effects. So the parent G3 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 7 crosses showed significant positive SCA effects. The highest positive significant effect was G3×G1 (3.11**) and the lowest positive significant effect was G1×G5 (0.39ns). Thus these 7 crosses were good specific combiner for plant height. The cross G3×G1 was the best specific combiner and 6 crosses showed significant negative SCA effects. The highest negative significant effect was G2×G1 (-5.14**) and the lowest negative significant effect was G1×G3 (-1.53*) (Table 19).

Table 18. General combing ability (GCA) effects of parents in a diallele cross of tomatillo

Parents	% Germination	Plant height	Leaf area index	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to fruit maturity	No. of fruits/plant
G1	-0.65ns	-0.09ns	1.22**	0.002ns	-0.289*	-0.28ns	0.98**	1.65**
G2	1.08**	-0.26ns	-0.22ns	-0.054ns	0.954**	0.56**	0.28ns	0.19ns
G3	1.49**	0.37ns	0.36**	0.077ns	-1.149**	-0.88**	-0.30*	0.19ns
G4	-0.69*	1.07**	-0.93**	-0.116ns	0.196ns	0.65**	0.21ns	-0.77**
G5	-1.23**	-1.09**	-0.43**	0.090ns	0.286*	-0.06ns	-1.16**	-1.26**

Here,

** Significant at 1% level,

* Significant at 5% level.

NS Non-significant.

df = Degrees of freedom.

Table 18. (CONT´D)

Parents	Fruit length	Fruit diameter	Individual fruit weight	Seeds/fruit	Yield/plant	Yield/plot	Yield/ha
G1	1.14**	1.65**	1.82**	5.77**	78.37**	0.91**	5.36**
G2	-0.19ns	0.03ns	-0.41**	-6.93**	-2.20ns	-0.10ns	0.82ns
G3	0.41**	0.16ns	0.50**	1.71ns	4.53ns	0.12ns	0.94ns
G4	-0.69**	-0.70**	-1.60**	-6.59**	-57.73**	-0.76**	-4.07**
G5	-0.67**	-1.15**	-0.31**	6.04**	-22.97**	-0.18**	-3.05**

Here

** Significant at 1% level,

* Significant at 5% level.

NS Non-significant.

df = Degrees of freedom.

Table 19. Specific combing ability (SCA) effects among the F1 generations in a diallele cross in tomatillo

F1 generation	Germination (%)	Plant height	Leaf area index	No. of branches/plant	Days to 1st flowering
G1 × G2	2.04**	0.26ns	-0.01ns	-0.23ns	0.01ns
G1 × G3	-1.53*	5.79**	0.86**	0.17ns	-1.50**
G1 × G4	-1.60*	-3.57**	-1.03**	-2.1ns	0.20ns
G1 × G5	0.39ns	0.09ns	0.01ns	-0.03ns	0.79**
G2 × G1	-5.14**	2.66**	0.13ns	0.26ns	0.46**
G2 × G3	3.05**	-0.87ns	-0.20ns	-0.21ns	0.11ns
G2 × G4	-3.70**	1.09ns	-0.74**	-0.40*	0.42ns
G2 × G5	-1.51*	-1.24ns	-0.05ns	0.20ns	-0.42ns
G3 × G1	3.11**	-0.50ns	0.60**	0.12ns	-0.54ns
G3 × G2	-1.73*	1.33ns	-0.28ns	0.51*	-0.19ns
G3 × G4	1.18ns	1.62*	0.14ns	0.02ns	-0.14ns
G3 × G5	1.87*	-0.70ns	-0.52*	-0.27ns	-0.05ns
G4 × G1	-1.02ns	1.17ns	0.76**	0.19ns	-0.17ns
G4 × G2	-0.83ns	0.33ns	-0.35ns	-0.47*	0.42ns
G4 × G3	-1.01ns	-1.83*	-0.97**	-0.15ns	0.19ns
G4 × G5	-0.77ns	1.42*	0.72**	0.12ns	-0.29ns
G5 × G1	1.04ns	1.00ns	0.69*	-0.13ns	0.70*
G5 × G2	-0.39ns	-2.83**	-0.03ns	-0.51*	0.24ns
G5 × G3	-0.60ns	0.66ns	0.08ns	0.11ns	-0.111ns
G5 × G4	-0.11ns	-0.50ns	0.24ns	0.23ns	0.23ns
Maximum	3.11	5.79	0.86	0.51	0.79
Minimum	-5.14	-3.75	-1.03	-0.51	-1.50
gca (j)	0.34	0.30	0.12	0.07	0.13
Sca(ii)	0.97	0.86	0.34	0.22	0.37
Sca(ij)	0.70	0.63	0.24	0.16	0.27
Reci(ij)	0.86	0.76	0.30	0.19	0.32

Table 19. (CONT´D)

F1 generation	Days to 50% flowering	Daus to maturity	No. of fruits/plant	Fruit length	Fruit diameter
G1 × G2	-0.14ns	-0.02ns	0.11ns	0.12ns	0.50ns
G1 × G3	-1.87**	0.51ns	1.41**	1.51**	1.51**
G1 × G4	0.15ns	1.28**	-1.48**	-0.30ns	-0.06ns
G1 × G5	0.40ns	0.70*	-0.65*	-0.76*	-0.37ns
G2 × G1	-0.43ns	-1.43**	1.94**	1.49**	0.10ns
G2 × G3	0.14ns	1.86**	0.72*	0.12ns	0.22ns
G2 × G4	0.18ns	0.49ns	-0.79*	-0.48ns	-0.15ns
G2 × G5	-0.39ns	-0.38ns	-0.33ns	0.01ns	-0.98**
G3 × G1	-0.03ns	-1.93**	1.27**	0.85*	0.36ns
G3 × G2	-0.45ns	1.17**	0.40ns	0.01ns	0.20ns
G3 × G4	0.20ns	-0.31ns	0.53ns	0.70*	0.25ns
G3 × G5	0.44ns	-0.40ns	-0.92**	-0.72*	0.05ns
G4 × G1	-0.26ns	-0.35ns	-0.06ns	-0.06ns	0.39ns
G4 × G2	-0.22ns	-1.25ns	0.28ns	-0.29ns	0.02ns
G4 × G3	0.29ns	-0.17ns	0.18ns	0.38ns	-0.40ns
G4 × G5	-0.39ns	-0.12ns	0.50ns	0.13ns	0.43ns
G5 × G1	-0.05ns	1.92**	1.51**	0.20ns	0.29ns
G5 × G2	0.41ns	0.34ns	0.73ns	0.61ns	-0.04ns
G5 × G3	0.21ns	0.47ns	0.21ns	0.24ns	-0.68ns
G5 × G4	-0.11ns	-0.23ns	-0.35ns	0.01ns	-0.38ns
Maximum	0.44	1.92	1.94	1.51	1.51
Minimum	-1.87	-1.93	-1.48	-0.76	-0.98
gca (j)	0.18	0.15	0.15	0.15	0.17
Sca(ii)	0.51	0.42	0.42	0.42	0.48
Sca(ij)	0.37	0.31	0.30	0.30	0.35
Reci(ij)	0.45	0.37	0.37	0.37	0.43

Table 19. (CONT´D)

F1 generation	Individual fruit weight	Seeds/fruit	Yield/plant	Yiled/plot	Yield/ha
G1 × G2	1.60**	-5.27ns	36.46**	0.28ns	3.22**
G1 × G3	0.84**	17.09**	71.56**	0.99**	8.78**
G1 × G4	-1.78**	-7.77*	-88.50**	-1.05**	-8.90**
G1 × G5	0.19ns	-5.74ns	-8.93ns	0.01ns	-3.85**
G2 × G1	1.96**	4.33ns	107.50**	1.14**	10.61**
G2 × G3	-2.28**	-13.04**	-73.86**	-0.86**	-8.30**
G2 × G4	-1.02**	-18.40**	-91.43**	-1.11**	-5.00**
G2 × G5	-0.06ns	5.62ns	-26.36*	-0.28ns	-2.55*
G3 × G1	2.71**	2.00ns	109.00**	1.38**	11.51**
G3 × G2	0.54ns	-0.16ns	7.33ns	0.18ns	0.97ns
G3 × G4	0.17ns	-0.70ns	21.50*	0.20ns	2.30*
G3 × G5	0.72*	-7.71*	-6.26ns	-0.15ns	-0.37ns
G4 × G1	0.68ns	-8.16*	53.00**	0.41ns	2.69*
G4 × G2	-0.24ns	10.50**	-23.16ns	-0.02ns	2.95**
G4 × G3	-0.65ns	2.50ns	-46.83**	-0.66**	-6.06**
G4 × G5	0.24ns	10.46**	71.16**	-0.76**	5.87**
G5 × G1	1.19**	-6.50ns	61.66**	0.72**	0.11ns
G5 × G2	-0.32ns	5.83ns	-55.66**	0.86**	-5.19**
G5 × G3	-0.39ns	4.00ns	-10.83ns	-0.75**	-0.69ns
G5 × G4	-0.01ns	-3.33ns	7.66ns	0.16ns	1.04ns
Maximum	2.71	17.09	109.00	1.38	11.51
Minimum	-2.28	-18.40	-91.43	-1.11	-8.90
gca (j)	0.13	1.46	5.09	0.35	0.50
Sca(ii)	0.39	4.14	14.40	1.40	1.42
Sca(ij)	0.28	3.02	10.40	1.04	1.03
Reci(ij)	0.34	3.66	12.73	0.46	1.25

4.2.3.2 Plant height

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G4 (1.07**) showed the significant positive GCA effects. On the other hand, G5 (-1.09**) showed the significant negative GCA effect. So the parent G4 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 4 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G1×G3 (5.79**) and the lowest positive significant effect was G4×G5 (1.42*). Thus these 4 crosses were good specific combiner for plant height. The cross G6×G3 was the best specific combiner and 3 crosses showed significant negative SCA effects. The highest negative significant effect was G1×G4 (-3.75**) and the lowest negative significant effect was G4×G3 (-1.83*).

4.2.3.3 Leaf area index

The mean square (MS values) for GCA was positive significant and SCA was positive non-significant for this character which suggested the presence of additive and absent non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (1.22**) and G3 (0.36*) showed the significant positive GCA effects.

On the other hand, G4(-0.93**) and G5 (-0.43**) showed the significant negative GCA effect, where G2 showed the non-significant GCA effects. So the parent G1 was the best general combiner for leaf area index (Table 18).

Among the 20 cross combinations 5 crosses showed significant positive SCA effects (Table 24). The highest positive significant effect was G1×G3 (0.86**) and the lowest positive significant effect was G3×G1 (0.60**). Thus these 5 crosses were good specific combiner for leaf area index. The cross G1×G3 was the best specific combiner and 3 crosses showed significant negative SCA effects. The highest negative significant effect was G1×G4 (-1.03**) and the lowest negative significant effect was G2×G4 (-0.74*) (Table 19).

4.2.3.4 Number of branches per plant

The mean square (MS values) for GCA and SCA were non-significant for this trait which suggested the absence of both additive and non-additive gene action for this character (Table 17). Among the five parents studies, the parent G1, G3 and G5 showed the non-significant positive and G2 and G4 showed non-significant negative GCA effects. The GCA value of G5 (0.090) was higher than G1 (0.002). On the other hand, no parents showed significant GCA effect (Table 18).

Among the 20 cross combinations the cross G3×G2 (0.51*) showed significant positive SCA effects (Table 19). Three crosses were found negative significant SCA effects. The highest negative significant effect was G5×G2 (-0.51*) and the lowest negative significant effect was G2×G4 (-0.40*) for the character days to first flowering.

4.2.3.5 Days to first flowering

The mean square (MS values) for GCA was positive significant and SCA was positive non-significant for this character which suggested the presence of additive and absent non-additive gene action for this character (Table 17).

Among the five parent studies the parent G2 (0.954**) and G5 (0.286*) showed the significant positive GCA effects. On the other hand, G3 (-1.149**) and G1 (-0.289*) showed the significant negative GCA effect, where G4 showed the non-significant GCA effects. So, the parent G2 was the best general combiner for days to first flowering (Table 18).

Among the twenty cross combinations 3 crosses showed significant positive SCA effects. The highest positive significant effect was G1×G5 (0.79**) and the lowest positive significant effect was G2×G1 (0.46**). Thus these 3 crosses were good specific combiner for Number of branches per plant. The cross G1×G5 was the best specific combiner. The cross G1×G4 (-1.50**) showed negative significant SCA effects for this character (Table 19).

4.2.3.6 Days to fifty percent flowering

The mean square (MS values) for GCA (4.03**) was positive significant and SCA (1.21ns) was positive non-significant for this character which suggested the presence of additive and absent non-additive gene action for this character (Table 17).

Among the five parent studied the parent G2 (0.56**) and G4 (0.65**) showed the significant positive GCA effects. On the other hand, G3 (-0.88**) showed the significant negative GCA effect, where G1 and G4 showed the non-significant GCA effects. So the parent G4 was the best general combiner for days to fifty percent flowering (Table 18).

Among the 20 cross combinations the cross G1×G3 (-1.87**) showed significant negative SCA effects. All other crosses were found negative significant SCA effects (Table 19) for the character days to fifty percent flowering.

4.2.3.7 Days to maturity

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (0.98**) showed the significant positive GCA effects. On the other hand, G5 (-1.16**) and G3 (-0.30*) showed the highly significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 4 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G5×G1 (1.92**) and the lowest positive significant effect was G3×G2 (1.17**). Thus these 4 crosses were good specific combiner for plant height. The cross G5×G1 was the best specific combiner and 2 crosses showed significant negative SCA effects. The highest negative significant effect was G3×G1 (-1.93**) and the lowest negative significant effect was G4×G1 (-1.432*).

4.2.3.8 Number of fruits per plant

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action

for this character (Table 17). Among the five parent studies the parent G1 (1.65**) showed the significant positive GCA effects. On the other hand, G5 (-1.26**) and G3 (-0.77**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 4 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G2×G1 (1.94**) and the lowest positive significant effect was G2×G3 (0.72*).Thus these 4 crosses were good specific combiner for number of fruits per plant. The cross G2×G1 was the best specific combiner. Four crosses showed significant negative SCA effects. The highest negative significant effect was G1×G4 (-1.48**) and the lowest negative significant effect was G1×G5 (-0.65*).

4.2.3.9 Fruit length

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (1.14**) and G3 (0.41*) showed the significant positive GCA effects. On the other hand, G4 (-0.69**) and G5 (-0.67**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 4 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G1×G3 (1.51**) and the lowest positive significant effect was G3×G4 (0.70*). Thus these 4 crosses were good specific combiner for number of fruits per plant. The cross G1×G3 was the best specific combiner. Two crosses showed significant negative SCA effects. The highest negative significant effect was G1×G5 (-0.76**) and the lowest negative significant effect was G3×G5 (-0.72*).

4.2.3.10 Fruit diameter

The mean square (MS values) for GCA (11.49**) was positive significant and SCA (1.58ns) was positive non-significant for this character which suggested the presence of additive and absent non-additive gene action for this character (Table 17).

Among the five parent studies the parent G1 (1.65**) showed the significant positive GCA effects. On the other hand, G4 (-0.70**) and G5 (-1.15**) showed the significant negative GCA effect, where G2 and G3 showed the non-significant GCA effects. So the parent G1 was the best general combiner for the character fruit diameter (Table 18).

Among the 20 cross combinations the cross G1×G3 (1.51**) showed significant positive and G2×G5 (-0.98**) showed significant negative SCA effects. All other crosses were found negative significant SCA effects (Table 19) for this character.

4.2.3.11 Individual fruit weight

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (1.82**) and G3 (0.50*) showed the significant positive GCA effects. On the other hand, G2 (-0.41*), G4 (-1.60**) and G5 (-0.31**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 6crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G3×G1 (2.71**) and the lowest positive significant effect was G3×G5 (0.72*). Thus these 6 crosses were good specific combiner for number of fruits per plant. The cross G3×G1 was the best specific combiner. Three crosses showed significant negative SCA effects. The highest negative significant effect was G2×G3 (-2.28**) and the lowest negative significant effect was G2×G4 (-1.02*).

4.2.3.12 Seeds per fruit

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (5.77**) and G5 (6.04**) showed the significant positive GCA effects. On the other hand, G2 (-6.93**) and G4 (-6.59**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18). Among the 20 cross combinations three crosses showed significant positive SCA effects (Table 19). The

highest positive significant effect was G1×G3 (17.09**) and the lower positive significant effect was found in G4×G5 (10.46**). Thus these 3 crosses were good specific combiner for these traits. The cross G1×G3 was the best specific combiner. Five crosses showed significant negative SCA effects. The highest negative significant effect was G2×G4 (-18.40**) and the lowest negative significant effect was G3×G5 (-7.71*).

4.2.3.13 Yield per plant

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (78.37**) showed the significant positive GCA effects. On the other hand, G4 (-57.73**) and G5 (-22.97**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18).

Among the 20 cross combinations 8 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G3×G1 (109.00**) and the lower positive significant effect was found in G3×G4 (21.50*). Thus these 8 crosses were good specific combiner for these traits. The cross G3×G1 was the best specific combiner. Six crosses showed significant negative SCA effects. The highest negative significant effect was G2×G4 (-91.43**) and the lowest negative significant effect was G2×G5 (-26.36*).

4.2.3.14 Yield per plot

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (0.91**) showed the significant positive GCA effects. On the other hand, G4 (-0.76**) and G5 (-0.18**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18). Among the 20 cross combinations 6 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G3×G1 (1.38**) and the lower positive significant effect was found in G5×G1 (0.72*). Thus these 8 crosses were good specific combiner for these traits. The cross G3×G1 was the best specific combiner. Six crosses showed

significant negative SCA effects. The highest negative significant effect was G2×G4 (-1.11**).

4.2.3.15 Yield per ha

The mean square (MS values) for GCA and SCA were positive significant for this character which suggested the presence of both additive and non-additive gene action for this character (Table 17). Among the five parent studies the parent G1 (5.36**) showed the significant positive GCA effects. On the other hand, G4 (-4.07**) and G5 (-3.05**) showed the significant negative GCA effect. So the parent G1 was the best general combiner for plant height (Table 18). Among the 20 cross combinations 8 crosses showed significant positive SCA effects (Table 19). The highest positive significant effect was G3×G1 (11.51**) and the lower positive significant effect was found in G3×G4 (2.30*). Thus these 8 crosses were good specific combiner for these traits. The cross G3×G1 was the best specific combiner. Seven crosses showed significant negative SCA effects. The highest negative significant effect was G1×G4 (-8.90**) and the lowest negative significant effect was G2×G5 (-2.55*).

4.2.4 Hayman´s approaches for gene action and genetic component

4.2.4.1 Hayman´s ANOVA

The results of the Hayman´s ANOVA for all the studied characters in F_1 generations are presented in Table 20. The additive genetic effects (a) were highly significant for all characters in F_1 except for the No. of branches/plant. The non-additive/dominance genetic effects (b) were highly significant for all characters in F_1. The significance value of a and b suggested that both additive and dominance components were involved in the inheritance of this characters. The magnitude of a was much lower than b which indicated the greater importance of dominance effect. In dispersion through the subcomponent of b, the average heterosis or mid parental deviation (b1) was non-significant for most of the characters except for germination%, fruit diameter, days to fruit maturity, individual fruit weight, seeds per fruit, yield per plant, yield per plot and yield per ha. The residual dominance effect (b3) accounted for the major proportion of the dominance effect (b) in the parents for all the characters studied. The mean dominance (b1) showed non-significant only for the leaf

Table 20. Hayman´s analysis of variance for fifteen morphological characters in diallele cross of tomatillo

Sources of variations	df	MS value							
		Germination %	Plant height	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	No. of fruits/plant	Fruit length	Fruit diameter
Repliation	2	5	1	0.16	1.8	0.6	0.9	2.4	3.0
Genotypes	24	28**	34**	0.51*	4.6**	3.7**	11.1**	5.6**	8.0**
Additive (a)	4	19**	44**	0.23^{NS}	18.3**	12.1**	37.3**	18.1**	34.5**
Dominance/Non-additive (b)	10	16775**	17802**	140.69**	2011.2**	5975.9**	2438.8**	2318.2**	2416.7**
mean dominance (b1)	1	46**	1^{NS}	2.11**	2.0^{NS}	4.9^{NS}	2.4^{NS}	0.3^{NS}	5.8*
Dominance due to array (b2)	4	37**	56**	0.31^{NS}	2.6**	2.6^{NS}	8.0**	5.9**	7.8**
Residual dominance effect (b3)	5	33511**	35559**	280.72**	4019.8**	11948.8**	4870.7**	4631.6**	826.0**
Maternal	4	12*	8^{NS}	0.53	0.7NS	0.6^{NS}	8.6**	2.6*	1.5NS
Reciprocal	6	24**	53**	0.96**	1.5*	0.7^{NS}	5.8**	3.2**	0.6NS
Error	48	3	4	0.23	0.7	1.3^{NS}	0.8	0.8	1.1

Table 20. (CONT´D)

Sources of variations	df	MS value						
		Leaf area index	Days ot fruit maturity	Individual fruit weight	Seeds/fruit	Yield/plant	Yield/plot	Yield/ha
Repliation	2	0.15	0	0.70	48	28	0.41	3.9
Genotypes	24	5.13**	9**	16.27**	722**	34279**	5.03**	257.9**
Additive (a)	4	20.41**	19**	47.93**	1231**	75205**	10.97**	421.4**
Non-additive (b)	10	1234.03**	16352**	1500.3**	366559**	1639543**	231.33**	11495.1**
mean dominance (b1)	1	2.04NS	39**	3.66**	1966**	26885**	4.76**	233.1**
Dominance due to array (b2)	4	1.80*	5**	12.04**	927**	32111**	5.44**	172.2**
Residual dominance effect (b3)	5	2466.2**	32693**	2989.96**	731983**	3248021**	457.36**	22805.8**
Maternal	4	2.58**	5**	19.73**	89NS	51781**	6.89**	346.8**
Reciprocal	6	1.85**	12**	5.05**	353**	13623**	2.32**	206.6**
Error	48	0.55	1	0.73	80	973	0.35	9.5

area index. Dominance due to array (b2) showed significant for all the characters except for the days to No. of branches/plant and days to 50% flowering.

4.2.4.2 Genetic components using Hayman´s approach

The components of genetic variations along with the derived genetic ratios for different morphological and yield contributing characters (Table 21) showed that the D (additive) and H (non-additive) components were significant for all the traits under studied except number of branches per plant suggesting the importance of both additive and dominance components for the inheritance of all traits in tomatillo. However, the magnitude of dominance was higher than the additive components for all the traits which indicated that dominance component had a predominant role in the inheritance of this traits. The H2 represents the dominance deviation due to relative frequency of positive and negative genes was significant for all the characters. The net dominance effect h2 expressed as the algebraic sum over all loci in the homozygous conditions in all the crosses, was highly significant for all the studied characters. This implied that substantial contribution dominance effects were due to the heterozygosity of the loci in all the characters. The result showed that characters including plant height, and fruit length possessed negative effects indicating the mean direction of dominance as well as important of excess of recessive genes in the expression of these traits. On the hand, the remaining characters exhibited the values in positive direction implying the mean direction as well as important of excess pf dominant genes in the expression of these traits.

The proportion of positive and negative effects as indicated by F value was highly significant for all the characters except for the number of branches per plant. The negative F value for number of branches per plant, days to first and fifty percent flowering, fruit diameter and days to fruit maturity exhibited a predominance of recessive alleles (Table 21). The remaining characters showed positive F value suggesting dominant alleles governing these characters.

The environmental component “E” exhibited highly significant values for all characters studied indicating the influence of environmental factors in the expression of those traits. However, the magnitude of E for each character was much less compared to their respecting D and H1 suggesting the characters were influenced less by environment.

Table 21. Genetic variance components and related statistics of fifteen characters of diallele analysis in tomatillo

Component of variations	Germination%	Plant height	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	No. of fruits/plant	Fruit length	Fruit diameter
E	1.18**	1.43**	0.07*	0.23*	0.41*	0.28**	0.30**	0.39**
D	5.58**	5.07**	-0.05NS	0.62**	0.38**	4.28**	1.07**	2.15**
F	9.01**	14.33**	-0.11*	-1.59**	-0.98*	5.29**	0.71**	-0.09**
H_1	35.88**	35.11**	0.44NS	3.84**	1.76**	14.41**	7.18**	6.34**
H_2	36.40**	31.70**	0.61**	9.46**	4.78**	21.37**	11.2**	14.65**
h^2	8.98**	-0.71**	0.40**	0.27**	0.78**	0.32**	-0.12*	0.99**
$(H1/D)^{1/2}$	2.54	2.63	2.97	2.49	2.15	1.83	2.59	1.72
$H_2/4H_1$	0.25	0.23	0.35	0.62	0.68	0.37	0.39	0.58
h^2/H_2	0.25	-0.02	0.66	0.03	0.16	0.01	-0.01	0.07

Here, D= Additive variance; H_1 = Dominance variance; H_2= Proportion of positive and negative genes in the parents; F= Relative frequency of dominant and recessive alleles in the parents; h2= Dominace effeect over all loci in heterozygous phase (heritability), E= Environmental variance; $(H1/D)^{1/2}$ =Mean degree of dominance; $H_2/4H_1$ =The proportion of dominant genes with positive and negative effects at all loci; h^2/H_2 =Total number of group of genes controlling the charactres with dominance effect.

Table 21. (CONT´D)

Component of variations	Leaf area index	Days ot fruit maturity	Individual fruit weight	Seeds/fruit	Yield/plant	Yield/plot	Yield/ha
E	0.17**	0.28**	0.24**	26.40**	311.6**	0.12**	3.09**
D	2.00**	0.28**	3.05**	1.82**	10548.7**	1.11**	73.55**
F	0.60**	-1.35**	1.07**	38.61**	11199.8**	1.27**	71.22**
H1	4.43**	9.44**	22.46**	776.5**	58091.1**	8.36**	455.26**
H2	9.84**	12.22**	37.02**	858.8**	81410.7**	11.53**	597.24**
h2	0.32**	8.18**	1.05**	402.5**	5536.10**	0.94**	47.74
(H1/D)0.5	1.49	5.81	2.71	20.66	2.35	2.74	2.49
H2/4H1	0.56	0.32	0.41	0.28	0.35	0.34	0.33
h2/H2	0.03	0.67	0.03	0.47	0.07	0.08	0.08

Here, D= Additive variance; H_1 = Dominance variance; H_2= Proportion of positive and negative genes in the parents; F= Relative frequency of dominant and recessive alleles in the parents; h2= Dominace effeect over all loci in heterozygous phase (heritability), E= Environmental variance; $(H1/D)^{1/2}$ =Mean degree of dominance; $H_2/4H_1$ =The proportion of dominant genes with positive and negative effects at all loci; h^2/H_2 =Total number of group of genes controlling the charactres with dominance effect.

The average degree of dominance as indicated by the $(H_1/D)^{0.5}$ was more than unity suggesting that over dominance was operating in the expression for most of the components of yield. The ratio of (H2/4H1) provides an estimate of the average frequency of positive and negative alleles in all the parents. The value of this ratio greater than 0.25 for all the characters except plant height suggested asymmetric distribution of alleles. The estimated number of effective factors (h^2/H_2) were less than the unity for all yield contributing characters. The proportion of genes or group of genes showing dominance was thus very less which could be owing to the predominant concealing effects of positive and negative effects of genes or to non-isodirectional distribution of polygenes.

4.2.4.3 Vr-Wr regression analysis

Vr-Wr graphs, the two-dimensional depiction made based on the parental variance (Vr) and parent offspring covariance (Wr) are presented in the Figure 2 to Figure 16. Hayman´s graphics approach to diallel analysis is based on monogenic additive model. The regression coefficient differs significantly from 0 and approaching to unity for all the traits studied suggesting that there was no epistasis for most of the traits indicated the validity of such type of analysis. Vr-Wr graphs for the fifteen characters are described below.

4.2.4.3.1 Germination %

The regression line intersected above the point of origin (0.14) suggesting the partial dominance gene action for controlling the trait (Figure 2). The distribution of array points indicated two parents (G4 and G5) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G2 and G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G5 > G2> G1>G3 in the increasing order.

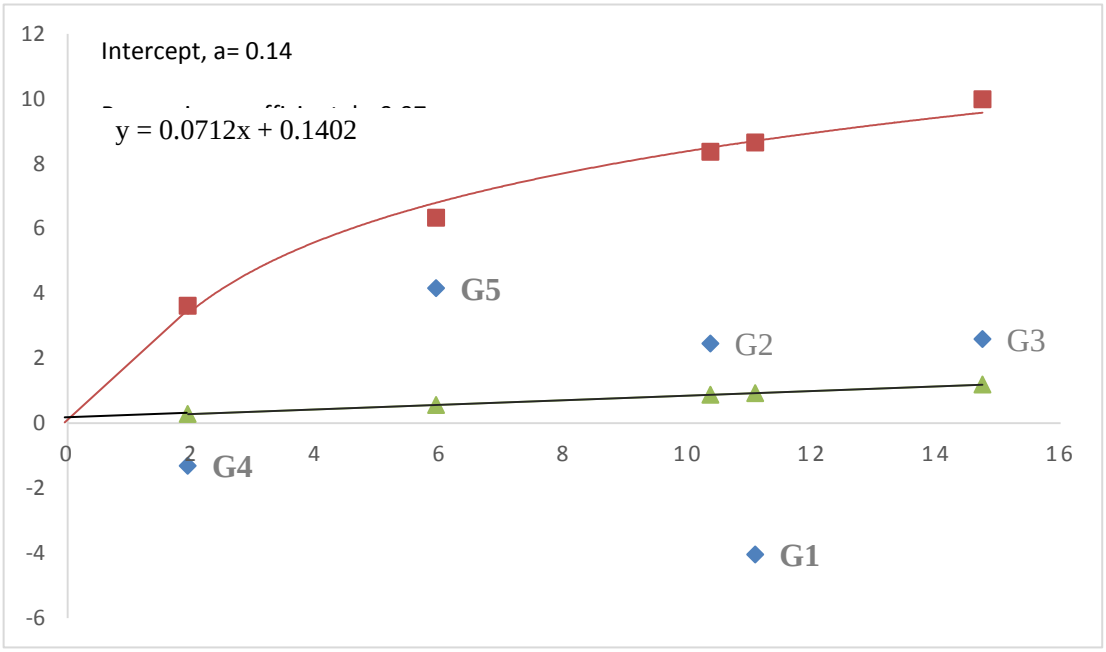


Figure 2. Vr-Wr graph for germination% in tomatillo

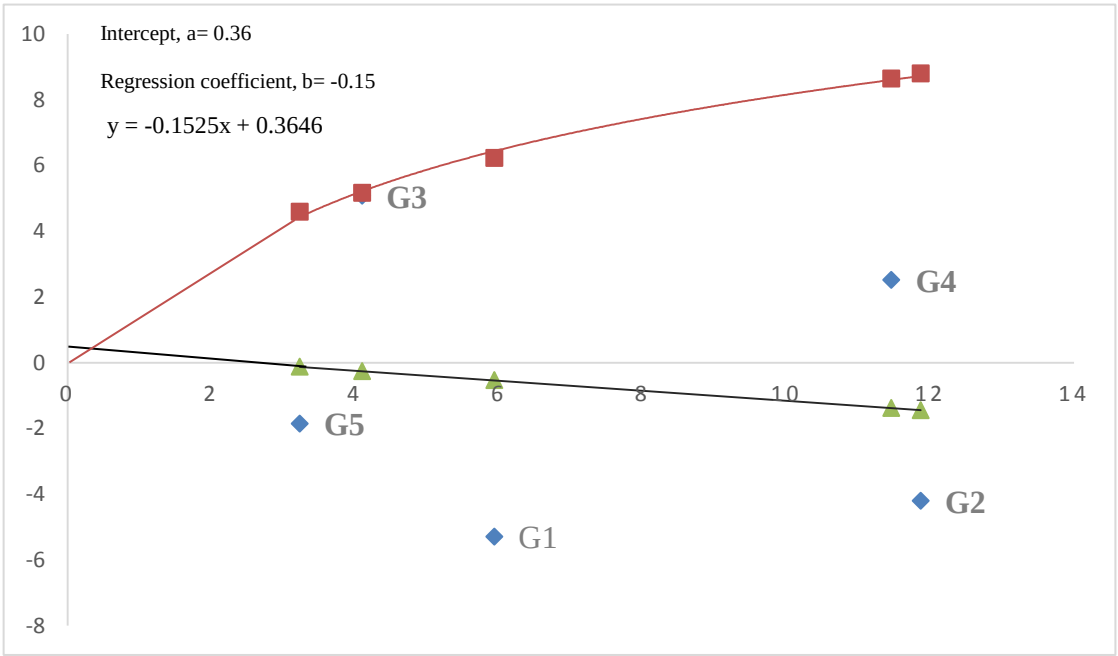


Figure 3. Vr-Wr graph for plant height in tomatillo

4.2.4.3.2 Plant height

The regression line intersected above the point of origin (0.36) suggesting the partial dominance gene action for controlling the trait (Figure 3). The distribution of array points indicated two parents (G5 and G3) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, G2 and G4 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G3 > G1> G4>G2 in the increasing order.

4.2.4.3.3 Number of branches per plant

The regression line intersected below the point of origin (-0.003) suggesting the over dominance gene action for controlling the trait (Figure 4). The distribution of array points indicated three parents (G1, G5 and G3) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G2 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G4) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G1 > G5 > G3> G4>G2 in the increasing order.

4.2.4.3.4 Days to first flowering

The regression line intersected above the point of origin (0.28) suggesting the partial dominance gene action for controlling the trait (Figure 5). The distribution of array points indicated three parents (G2, G5 and G4) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parents G1 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G3) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G2 > G5 > G4> G3>G1 in the increasing order.

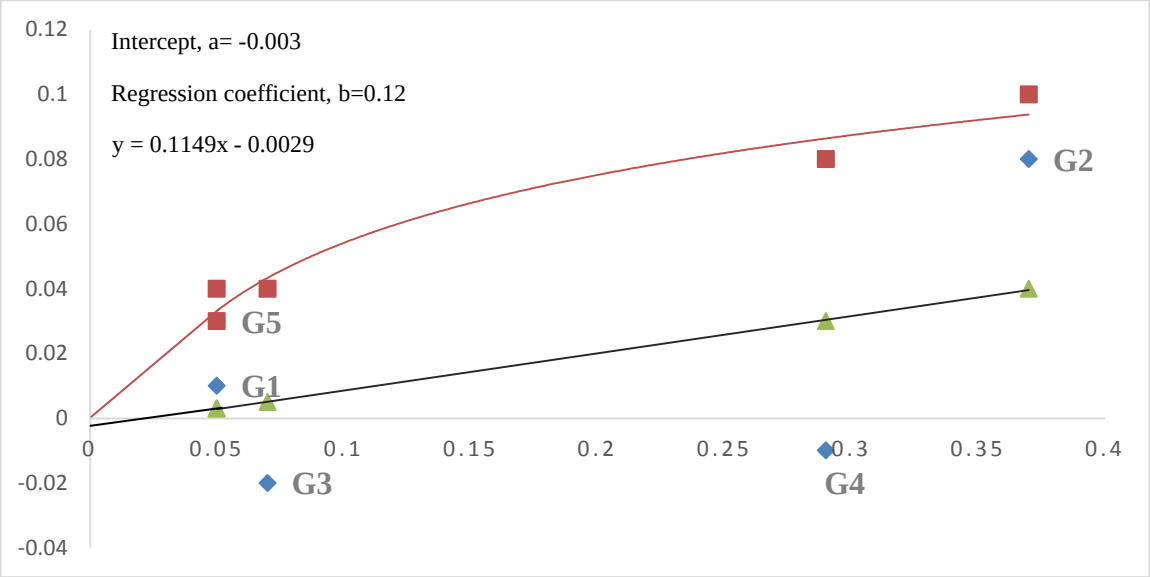


Figure 4. Vr-Wr graph for No. of branches/plant in tomatillo

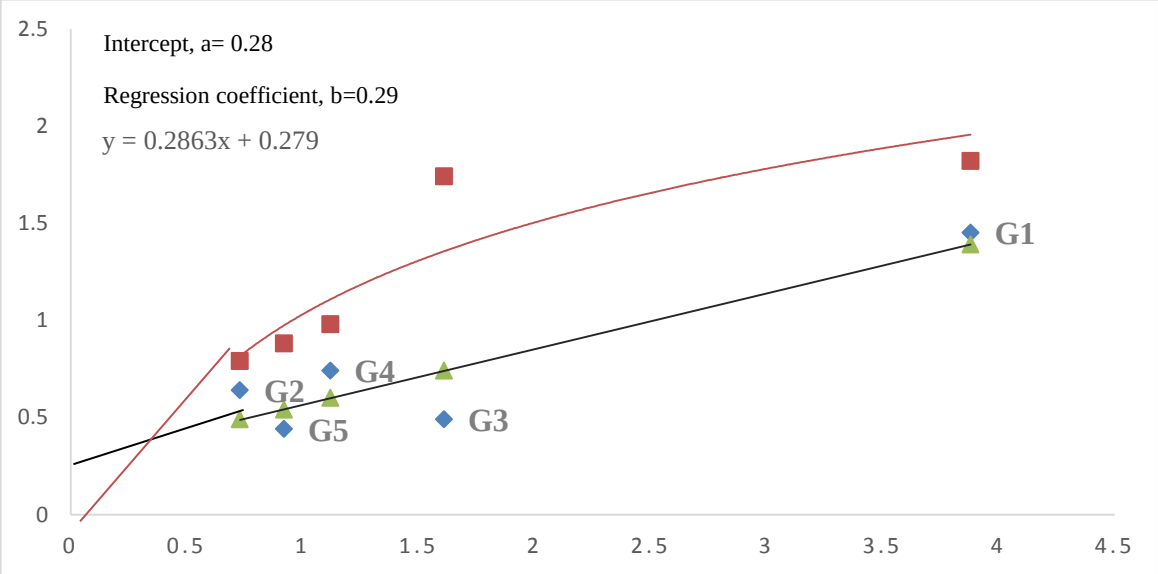


Figure 5. Vr-Wr graph for days to first flowering in tomatillo.

4.2.4.3.5 Days to 50% flowering

The regression line intersected above the point of origin (0.40) suggesting the partial dominance gene action for controlling the trait (Figure 6). The distribution of array points indicated three parents (G5, G4 and G2) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parents G1 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G3) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G4 > G2> G3>G1 in the increasing order.

4.2.4.3.6 Number of fruits per plant

The regression line intersected below the point of origin (-0.74) suggesting the over dominance gene action for controlling the trait (Figure 7). The distribution of array points indicated two parents (G4 and G5) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G2 and G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G5 > G2> G1>G3 in the increasing order.

4.2.4.3.7 Fruit length

The regression line intersected above the point of origin (0.32) suggesting the partial dominance gene action for controlling the trait (Figure 8). The distribution of array points indicated two parents (G5 and G4) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parents G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G2 and G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G4 > G2> G1>G3 in the increasing order.

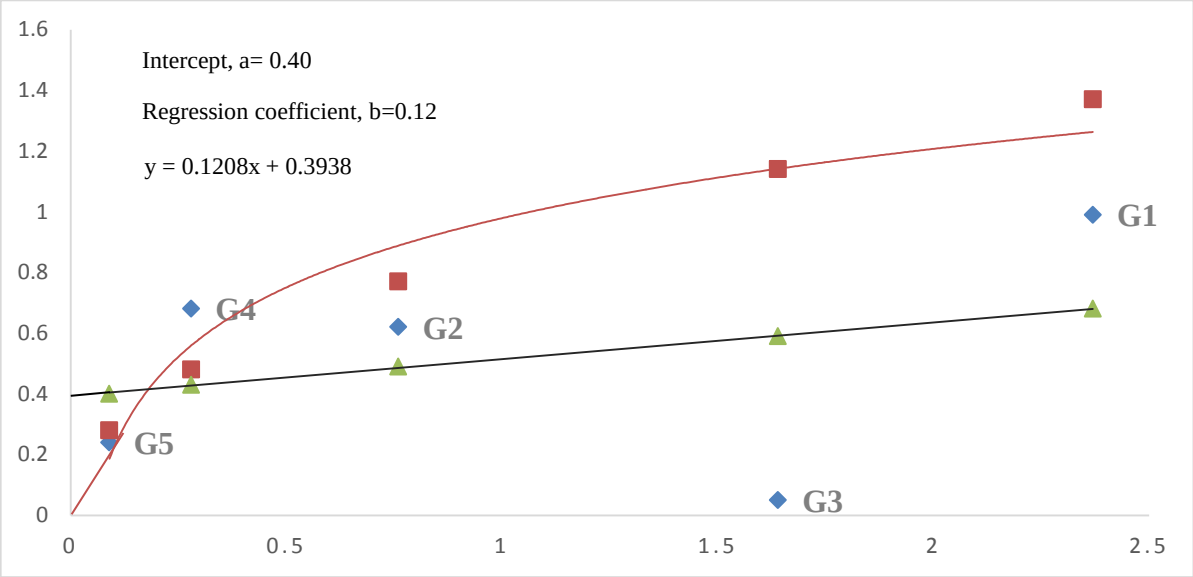


Figure 6. Vr-Wr graph for days to 50% flowering in tomatillo.

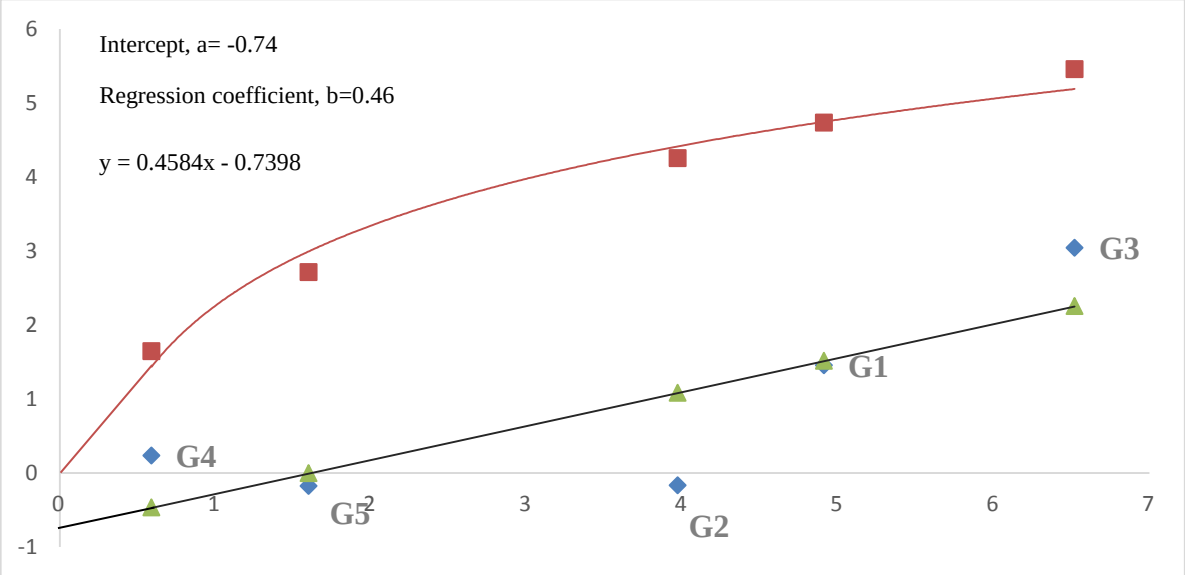


Figure 7. Vr-Wr graph for No. of fruits/plant in tomatillo.

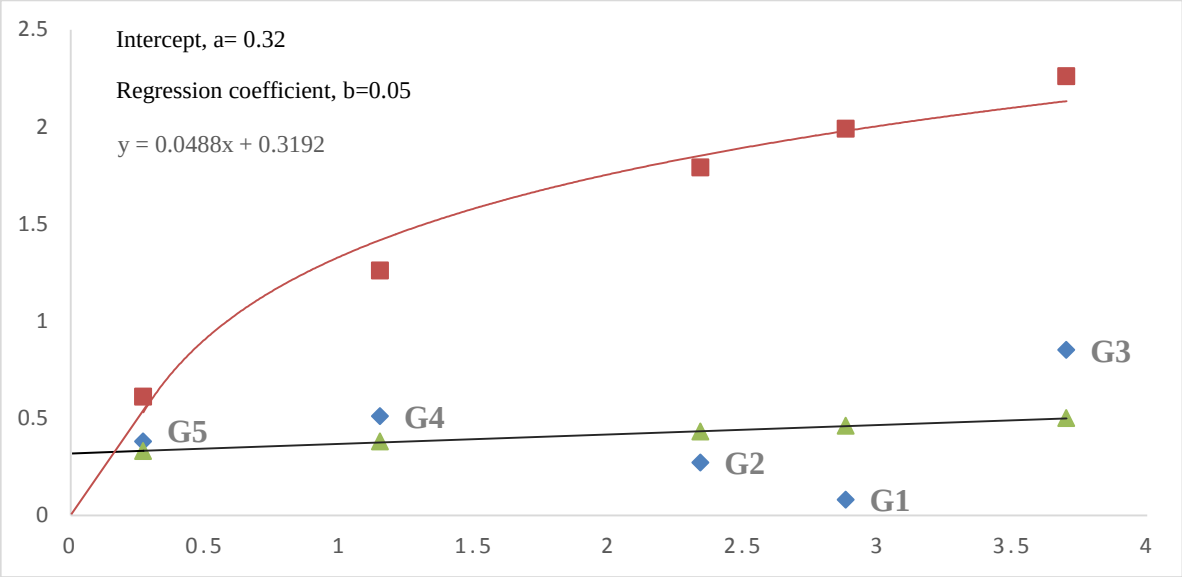


Figure 8. Vr-Wr graph for fruits length in tomatillo.

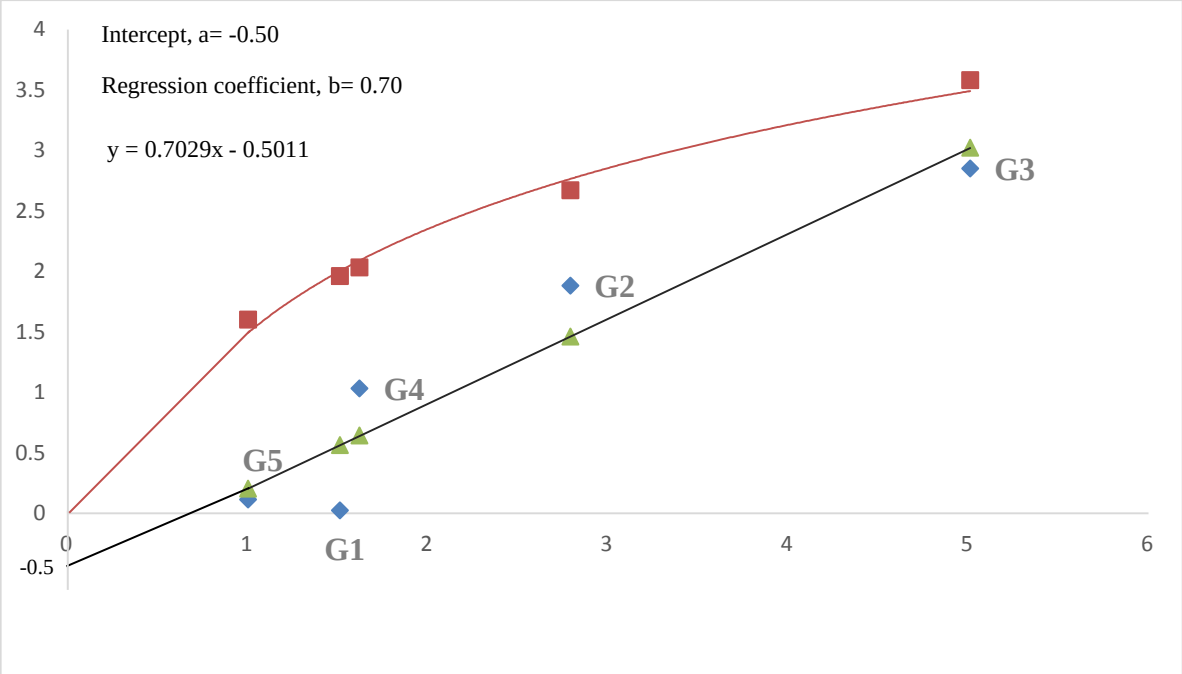


Figure 9. Vr-Wr graph for fruits diamter in tomatillo.

4.2.4.3.8 Fruit diameter

The regression line intersected below the point of origin (-0.50) suggesting the over dominance gene action for controlling the trait (Figure 9). The distribution of array points indicated three parents (G5, G1 and G4) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G2) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G1 > G4> G2>G3 in the increasing order.

4.2.4.3.9 Leaf area index

The regression line intersected below the point of origin (-0.48) suggesting the over dominance gene action for controlling the trait (Figure 10). The distribution of array points indicated two parents (G4 and G5) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G1 and G2) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G5 > G1> G2>G3 in the increasing order.

4.2.4.3.10 Days to fruit maturity

The regression line intersected below the point of origin (-0.55) suggesting the over dominance gene action for controlling the trait (Figure 11). The distribution of array points indicated two parents (G4 and G1) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G2 and G5) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G1 > G2> G5>G3 in the increasing order.

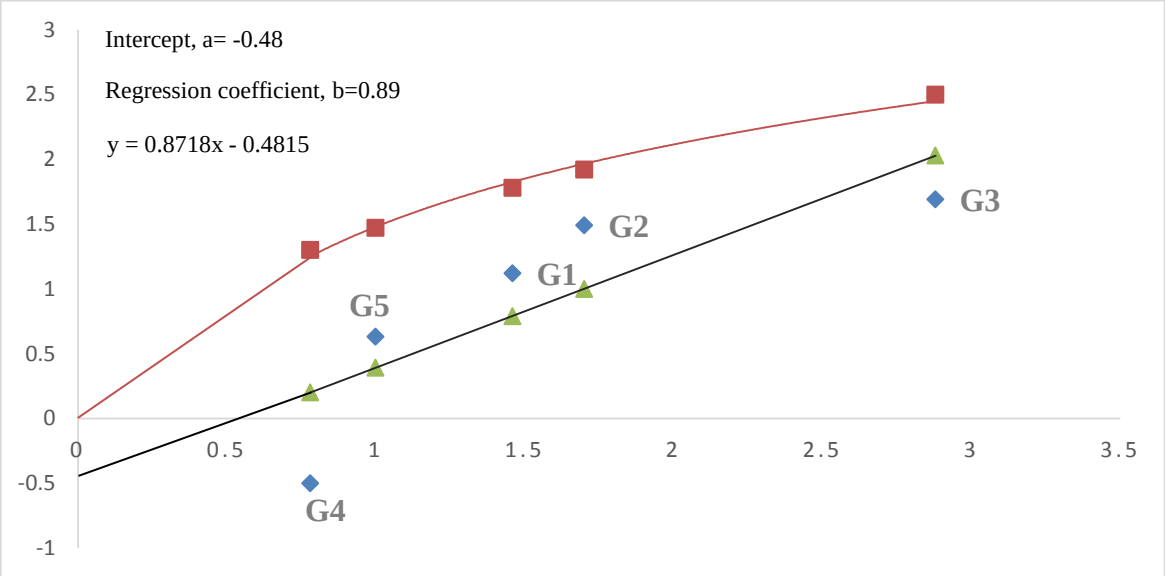


Figure 10. Vr-Wr graph for leaf area index in tomatillo.

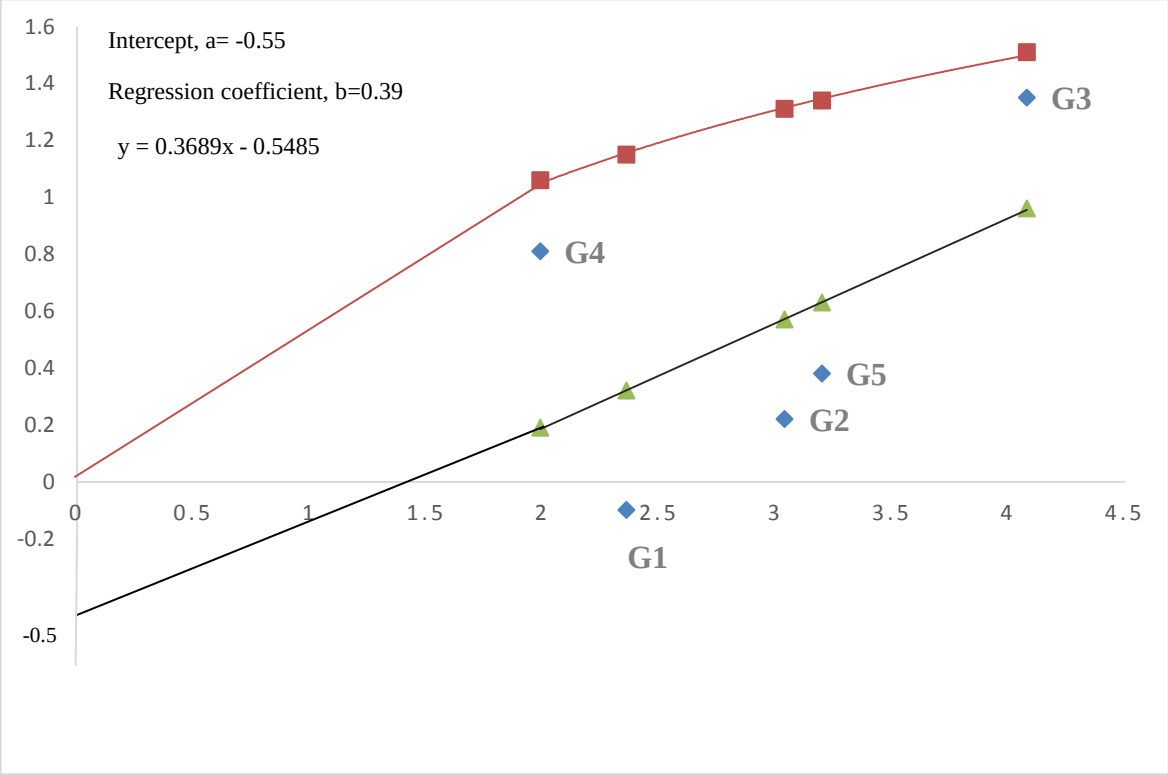


Figure 11. Vr-Wr graph for days to fruit maturity in tomatillo.

4.2.4.3.11 Individual fruit weight

The regression line intersected above the point of origin (0.48) suggesting the partial dominance gene action for controlling the trait (Figure 12). The distribution of array points indicated parents (G4) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parents (G2 and G3) felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the parents (G5 and G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G5 > G1> G3>G2 in the increasing order.

4.2.4.3.12 Seeds per fruit

The regression line intersected below the point of origin (-53.34) suggesting the over dominance gene action for controlling the trait (Figure 13). The distribution of array points indicated parents (G5) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G2 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the three parents (G4, G3 and G5) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G4 > G3> G1>G2 in the increasing order.

4.2.4.3.13 Yield per plant

The regression line intersected below the point of origin (-4693.43) suggesting the over dominance gene action for controlling the trait (Figure 14). The distribution of array points indicated three parents (G5, G4 and G1) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G2 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the three parents (G3) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G4 > G1> G3>G2 in the increasing order.

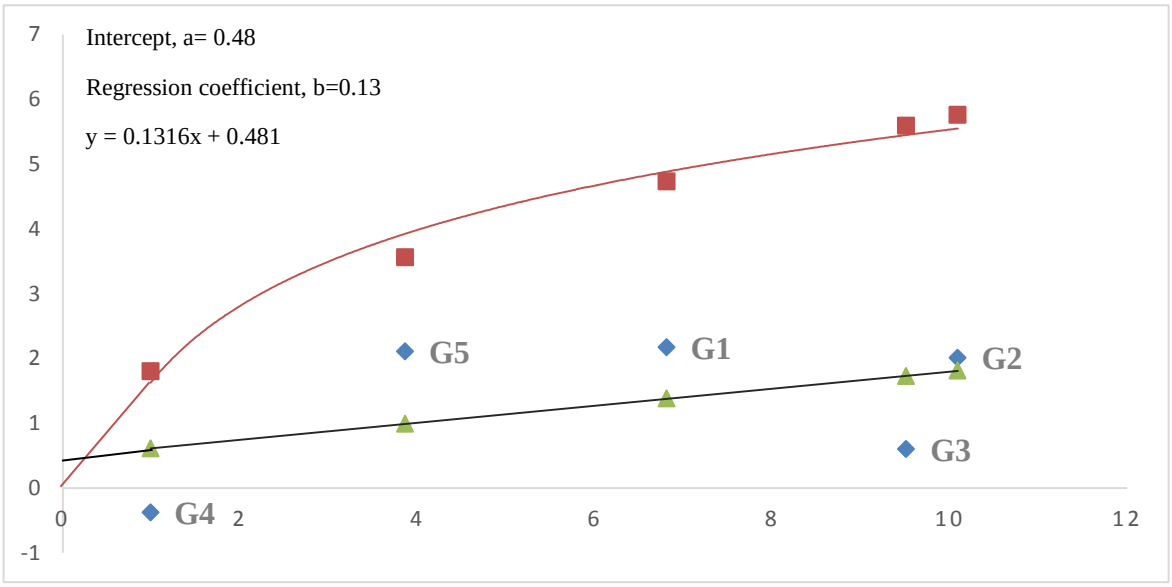


Figure 12. Vr-Wr graph for single fruit weight in tomatillo.

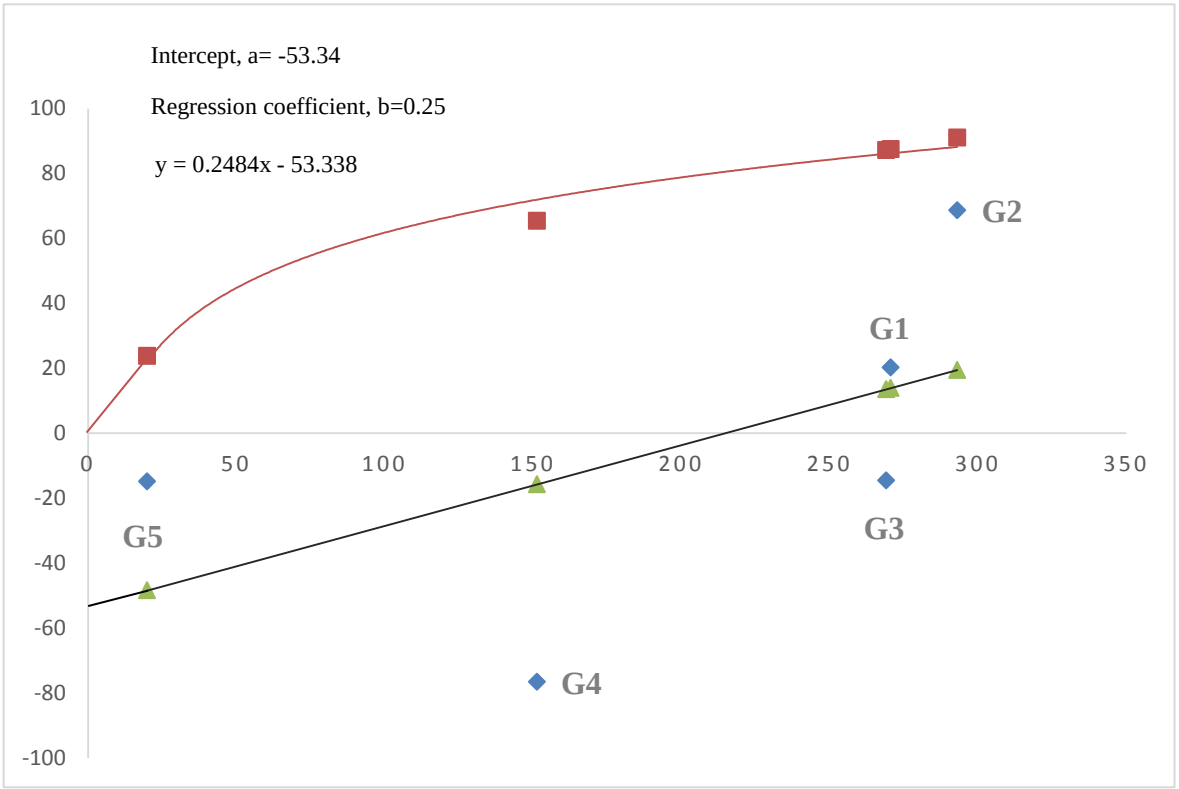


Figure 13. Vr-Wr graph for seeds per fruit in tomatillo.

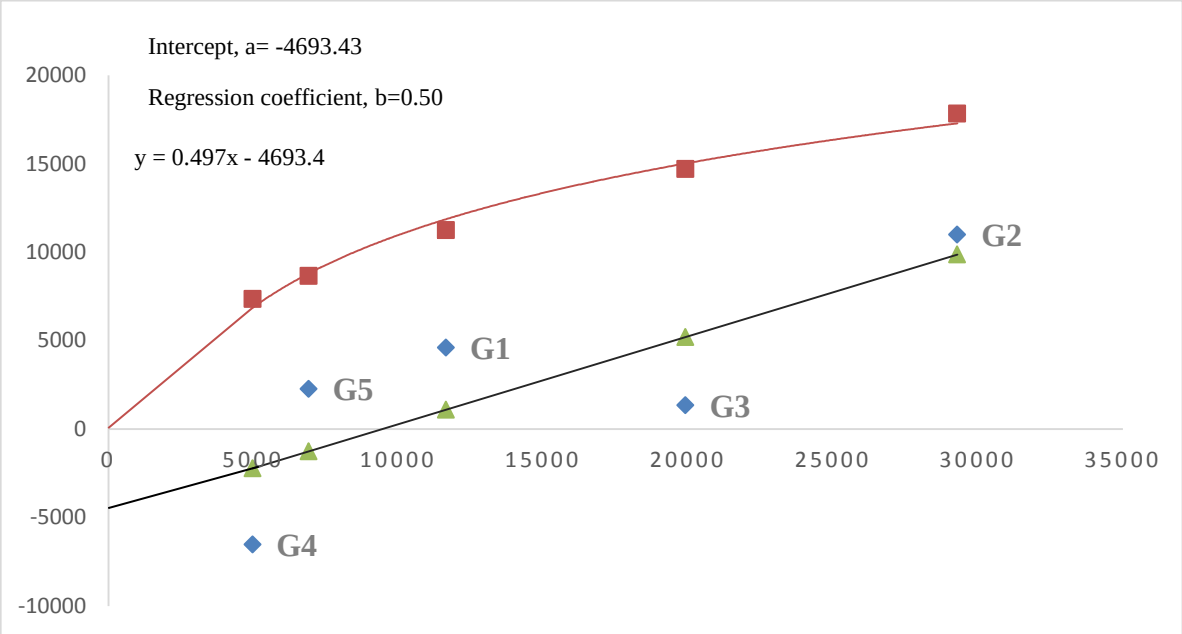


Figure 14. Vr-Wr graph for yield per plant in tomatillo.

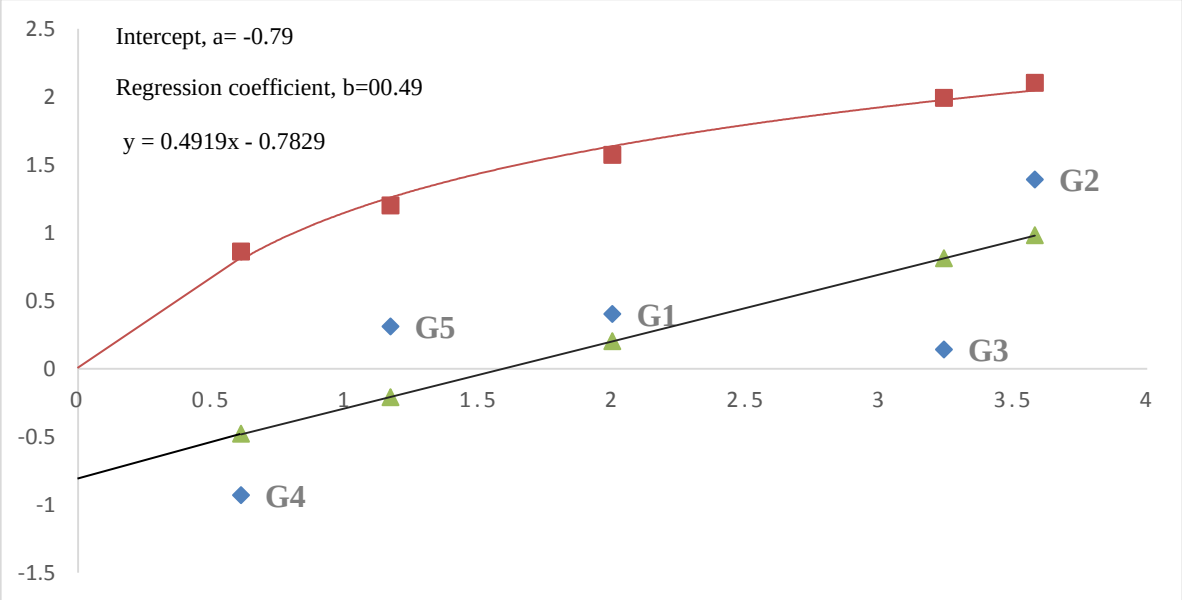


Figure 15. Vr-Wr graph for yield per plot in tomatillo.

4.2.4.3.14 Yield per plot

The regression line intersected below the point of origin (-0.79) on Wr axis, suggesting the over dominance gene action for controlling the trait (Figure 15). The distribution of array points indicated two parents (G4 and G5) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G2 and G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the three parents (G1) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G4 > G5 > G1> G3>G2 in the increasing order.

4.2.4.3.15 Yield per ha

The regression line intersected the Wr axis below the point of origin (-22.40) suggesting the over dominance gene action for controlling the trait (Figure 16). The distribution of array points indicated two parents (G5 and G4) contained the most dominant alleles as they felt closure to the point of origin. On the other hand, parent G3 felt far from the origin indicated that it possessed the maximum frequency of recessive alleles. Rest of the three parents (G1 and G2) felt at the intermediate from the origin which indicated the presence of less or more equal proportion of dominant and recessive genes. The ranks of parental dominance would be as follows: G5 > G4 > G1> G2>G3 in the increasing order.

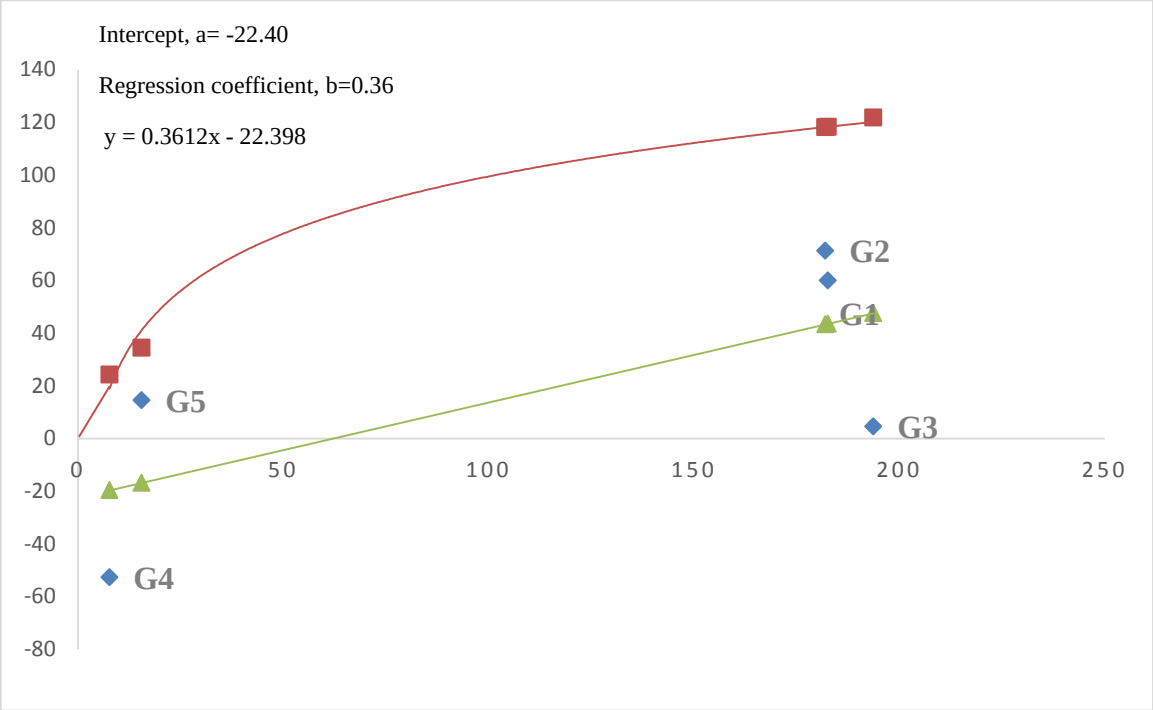


Figure 16. Vr-Wr graph for yield per ha in tomatillo.

4.3 Experiment 3a. Genetic variability, character association and selection index of morphological traits in twenty F_2 genotypes of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.)

The experiment was conducted to perform the diversity analysis and selection ranked of different genotypes of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.) using morphological and yield contributing traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment 3. Among the morphological and yield contributing characters, Plant height, Number of branches per plant, Leaf area index, days to first flowering, days to fifty percent flowering, days to maturity, number of fruits per plant, fruits length, fruit diameter, Individual fruit weight, seeds per fruits, yield per plant, yield per plot and Yield per hectare were studied. The data pertaining to fourteen characters have been presented and statistically analyzed with the possible interpretations given as below.

4.3.1 Mean performance analysis

Analysis of variance and mean performance of twenty F_2 tomatillo genotypes were presented in Appendix VII and Table 22. Highly significant variation among twenty F_2 tomatillo genotypes in terms of yield and yield contributing morphological fifteen parameters were recorded.

4.3.1.1 Germination %

Analysis of variance showed statistically significant differences among the twenty F2 tomatillo genotypes in term of germination percentage at 1% level (Appendix VII). The germination percentage ranged from 88.67 % to 77.00 %. Highest germination % (88.67) was observed in G1×G3 and lowest germination % was observed in G2×G5 (77.00) with average germination is 81.00% (Table 22).

4.3.1.2 Plant height

Analysis of variance showed statistically significant differences among twenty F2 tomatillo genotypes in term of plant height at 1% level (Appendix VII). Plant height ranged from 94.97 cm to 82.32 cm. Highest plant height (94.97 cm) was observed in G1×G3 and lowest plant highest was observed in G4×G1 (82.32 cm) with average plant height of 86.70 cm (Table 22).

Table 22. Mean performance of fifteen morphological traits of twenty F2 genotypes of tomatillo

Genotypes	Germination %	Plant height (cm)	Leaf area index	No. of branches/plant	Days to first flowering
G1 × G2	85.66 ab	90.28ab	23.29 abc	7.83 abcd	27.77 cde
G1 × G3	88.66 a	94.97 a	25.14 a	9.02 a	25.05 e
G1 × G4	82 abc	84.336 b	21.98 abc	6.91 bcd	27.70 cde
G1 × G5	81.66abc	88.99 ab	22.53 abc	7.63 abcd	28.17 bcde
G2 × G1	79.66bc	87.66 ab	22.29 abc	6.52 bcd	28.85 bcd
G2 × G3	80.66 abc	86.66 b	21.51 bc	7.2 abcd	29.93 abc
G2 × G4	81.33 abc	83.716 b	20.21 c	6.52 bcd	32.296 a
G2 × G5	77 c	83.756 b	22.85 abc	7.67 abcd	30.63 abc
G3 × G1	84.33 abc	86.65 b	24.24 ab	7.92 abcd	26.12 de
G3 × G2	81.66 abc	85.6 b	22.38 abc	6.40 cd	28.24 bcd
G3 × G4	83 abc	83.03 b	20.67 c	6.49 cd	27.81 cde
G3 × G5	78.66 bc	87.23 ab	22.24 abc	8.01 abcd	29.23 abcd
G4 × G1	77.33 c	82.32 b	21.14 bc	7.14 abcd	30.17 abc
G4 × G2	83 abc	82.51 b	21.02 bc	6.26 d	30.43 abc
G4 × G3	82.66 abc	88.14 ab	22.41 abc	6.53 bcd	29.29 abc
G4 × G5	77.33 c	85.21 b	21.346 bc	7.13 abcd	30.95 ab
G5 × G1	77.66 bc	86.68 b	21.16 bc	8.46 abc	29.13 bcd
G5 × G2	81 abc	88.38 ab	21.26 bc	7.31 abcd	29.99 abc
G5 × G3	79.33 bc	88.92 ab	21.286 bc	8.61 ab	29.03bcd
G5 × G4	77.33 c	88.87 ab	21.35 bc	7.42 abcd	30.11 abc
Average	81.00	86.70	22.02	7.35	29.05
Maximum	88.67	94.97	25.14	9.02	32.30
Minimum	77.00	82.32	20.21	6.26	25.05
CV	4.28	2.99	4.87	9.06	3.42

Table 22. (CONT´D)

Genotypes	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length (mm)	Fruit dimeter (mm)
G1 × G2	47.54 bcd	80.06 ab	34.46 ab	33.55 ab	35.83 a
G1 × G3	45.74 d	79.18 b	35.99 a	35.22 a	35.99 a
G1 × G4	50.07 ab	80.55 ab	31.89 bcd	31.33 bc	32.55 abc
G1 × G5	49.98 ab	81.21 ab	32.79 abcd	33.32 ab	31.79 bc
G2 × G1	49.21 abc	83.05 a	30.97 bcd	31.18 bc	31.85 bc
G2 × G3	49.75 ab	83.33 a	30.86 bcd	30.29 bc	31.16 bc
G2 × G4	50.66 a	81.88 ab	29.276 d	29.26 c	29.89 c
G2 × G5	50.30 ab	81.45 ab	30.716 bcd	30.72 bc	30.07 c
G3 × G1	46.28 cd	79.99 ab	33.44 abc	32.43 abc	33.99 ab
G3 × G2	50.11 ab	80.47 ab	30.67 bcd	31.22 bc	31.14 bc
G3 × G4	50.08 ab	81.19 ab	30.67 bcd	31.14 bc	30.67 bc
G3 × G5	50.17 ab	80.38 ab	31.21 bcd	31.55 bc	30.14 bc
G4 × G1	50.44 ab	82.80 a	30.15 cd	30.31 bc	31.35 bc
G4 × G2	50.59 ab	81.79 ab	29.353 d	29.41 c	30.46 bc
G4 × G3	48.55 abcd	82.07 ab	29.97 cd	30.42 bc	31.1 bc
G4 × G5	49.75 ab	81.6 ab	30.79 bcd	29.77 c	30.75 bc
G5 × G1	50.15 ab	80.25 ab	31.52 bcd	30.94 bc	29.73 c
G5 × G2	49.95 ab	80.58 ab	30.33 cd	31.23 bc	29.53 c
G5 × G3	50.37 ab	79.14 b	30.12 cd	30.31 bc	31.35 bc
G5 × G4	50.38 ab	80.57 ab	29.93 cd	29.89 c	30.65 bc
Average	49.51	81.08	31.26	31.18	31.50
Maximum	50.66	83.34	35.99	35.22	35.99
Minimum	45.75	79.14	29.28	29.26	29.53
CV	2.07	1.45	4.14	3.23	3.03

Table 22. (CONT´D)

Genotypes	Individual fruit weight (g)	Seeds/fruit	Yield/plant (g)	Yield/plot (Kg)	Yield/ha (t)
G1 × G2	30.69 ab	422 a	982 ab	11.78 ab	81.80 ab
G1 × G3	31.09 a	424 a	1021.33 a	12.25 a	85.10 a
G1 × G4	24.42 c	345.33 abc	712 cd	8.54 cd	59.32 cd
G1 × G5	24.13 c	413.66 a	826.66 bc	9.92 bc	68.87 bc
G2 × G1	24.88 c	375.66 abc	776.33 cd	9.33 cd	64.68 cd
G2 × G3	25.24 bc	342 abc	756.66 cd	9.08 cd	63.04 cd
G2 × G4	22.75 c	325.33 bc	623.33 d	7.48 d	51.93 d
G2 × G5	24.98 c	343 abc	787.33 cd	9.44 cd	65.58 cd
G3 × G1	24.66 c	420.33 a	835 abc	10.05 abc	69.57 abc
G3 × G2	22.61 c	363 abc	703.33 cd	8.44 cd	58.60 cd
G3 × G4	22.64 c	383.33 abc	688 cd	8.253 cd	57.32 cd
G3 × G5	24.51 c	342.66 abc	776.66 cd	9.32 cd	64.70 cd
G4 × G1	22.12 c	321 c	663 cd	7.95 cd	55.243 cd
G4 × G2	21.57 c	357.33 abc	631 d	7.57 d	52.57 d
G4 × G3	24.51 c	342.66 abc	776.66 cd	9.32 cd	64.71 cd
G4 × G5	23.62 c	394 abc	806 bcd	9.67 bcd	67.13 bcd
G5 × G1	23.28 c	406.33 ab	801.66 bcd	9.62 bcd	66.78 bcd
G5 × G2	22.65 c	403.66 abc	795.66 bcd	9.54 bcd	66.27 bcd
G5 × G3	22.65 c	385 abc	774.66 cd	9.29 cd	64.52 cd
G5 × G4	22.61 c	403 abc	802.66 bcd	9.63 bcd	66.85 bcd
Average	24.28	375.67	777.00	9.33	64.73
Minimum	31.10	424.00	1021.33	12.25	85.10
Maximum	21.58	321.00	623.33	7.48	51.94
CV	7.01	7.09	7.87	7.86	7.87

4.3.1.3 Leaf area

In leaf area index, analysis of variance showed significantly difference among the tomatillo genotypes at 1% level of significance. (Appendix VII). Leaf area ranged from 25.14 to 20.21. The highest leaf area index was found in G1×G3 (25.14) and the lowest leaf area was observed in G2×G4 (20.21) with average value is 22.02 (Table 22).

4.3.1.4 Number of branches / plants

For number of branches per plant, analysis of variance showed significantly difference among the twenty tomatillo genotypes at 1% level. (Appendix VII). Number of branches per plant ranged from 9.02 to 6.26. The highest number of branches per plant was found in G1×G3 (9.02) and the lowest leaf area was observed in G4×G2 (20.21) with average value is 7.35 (Table 22).

4.3.1.5 Days to first flowering

Statistically significant variation was observed in days to first flowering of twenty F2 tomatillo genotypes at 1% level of significant (Appendix VII). The average days to first flowering was recorded 29.05 days and its ranges from 32.30 days to 25.05 days. The highest days to first flowering observed in G2×G4 (32.30days) and the lowest days to first flowering was found in G1×G3 (25.05days) (Table 22). The differences in days to first flowering might be due to genetically factors of the genotypes concerned.

4.3.1.6 Days to fifty percent flowering

Different genotypes required different days to flowering initiation and 50% flowering. Statistically significant variation was observed in days to fifty percent flowering of twenty F2 tomatillo genotypes at 1% level of significant (Appendix VII). The average days to fifty percent flowering were recorded 49.51 days and its ranges from 50.66 days to 45.75 days. The highest days to fifty percent flowering was observed in G2×G4 (50.66 days) and the lowest days to first flowering was found in G1×G3 (45.75days) (Table 22). .

4.3.1.7 Days to maturity

Days to maturity showed positive significant variation in different F_2 genotypes of tomatillo under the experiment (Appendix VII). The range of days to maturity was recorded from 83.34 days to 79.14 days with average 81.08 days. The earliest maturity was found in G5×G3 (79.14 days) and later maturity was found in G2×G3 (83.34 days) genotype. (Table 22). The earlier maturity is more desirable than later maturity considering the duration of crops.

4.3.1.8 Number of fruits/plants

For number of branches per plant, analysis of variance showed significantly difference among the twenty tomatillo genotypes at 1% level (Appendix VII). Number of branches per plant ranged from 9.02 to 6.26. The highest number of branches per plant was found in G1×G3 (9.02) and the lowest leaf area was observed in G4×G2 (20.21) with average value was 7.35 (Table 22).

Higher number of fruits per plants indicated the higher yield in generally. Similar result was observed by Masabni, (2016) a single plant produces 20 to 100 fruits within a single growing season.

4.3.1.9 Fruit length (mm)

Fruit length exhibited significant variation at the level of 1% among the twenty F2 tomatillo genotypes (Appendix VII). The highest fruit length was observed in G1×G3 (35.22 mm) genotype and lowest fruit length was found in G2×G4 (29.26 mm) genotype with average value was 31.18 mm (Table 22).

4.3.1.10 Fruit diameter

Statistically significant variation was showed in fruit diameter of twenty F2 tomatillo genotypes at the 1% level of significant (Appendix VII). Highest fruit diameter was found in G1×G3 (35.99 mm) and lowest fruit diameter was found in G1×G3 (29.53mm) with average value of 31.50 mm in F_2 tomatillo genotypes (Table 22).

4.3.1.11 Individual fruit weight

Individual fruit weight is important factor which directly contributing to the yield potentiality. Statistically significant variation was showed in Individual fruit weightof twenty F_2 tomatillo genotypes at the 1% level of significant (Appendix VII). Highest Individual fruit weightwas found in G1×G3 (31.10 gm) and lowest individual fruit weightwas found in G4×G2 (21.58 gm) with average value of 24.28 gm in F_2 tomatillo genotypes (Table 22).

4.3.1.12 Seeds /fruit

Seeds per fruit is important factor which directly contributing to the yield potentiality. Statistically significant variation was showed in seeds/fruit of twenty F_2 tomatillo genotypes at the 1% level of significant (Appendix VII). Highest seeds per fruitwas found in G1×G3 (424) and lowest individual fruit weightwas found in G4×G1 (321) with average number of seeds per fruit 375.67 in F_2 tomatillo genotypes (Table 22). The greater number of viable seeds per fruit was desirable for making successful further breeding program.

4.3.1.13 Yield per plant

Statistically significant differences were showed in twenty F_2 tomatillo genotypes for yield per plant in gram at 1% level of significant (Appendix VII). Yield per plant was varied from 1021.33 gm to 623.33 gm. The highest yield per plant was observed in genotype G1×G3 (1021.33 gm) followed and the lowest yield per plant was found in genotype G2×G4 (623.33 gm) with average yield 777.00 gm per plant (Table 22). Yield per plant directly affects the crop's final yield.

4.3.1.14 Yield per plot

The yield per plot is an important factor directly contributing to final yield of crop. Statistically significant differences were showed in twenty F_2 tomatillo genotypes for yield per plot in kilogram at 1% level of significant (Appendix VII). Yield per plot was varied from 12.25 kg to 7.48 kg with average yield per plot was 9.33 kg. The highest yield per plant was observed in genotype G1×G3 (12.25 kg) followed and the lowest yield per plant was found in genotype G2×G4 (7.48 kg) (Table 22).

4.3.1.15 Yield/ha (Ton)

Yield is one of the main parameters for selection of crops. The higher yield indicated the potentiality of the future selection program of the genotype. Final Yield varied significantly (at 1% level) in twenty different F_2 tomatillo genotypes under the present experimental studies. (Appendix VII). Data revealed that the average yield ranged from 85.10 metric ton per hectare to 51.94 metric ton per hectare. The excellent highest (85.10 t/h) yield was recorded in the genotype G1×G3 (85.10 t) and the lowest yield was observed in genotype G2×G4 (51.94 t/h) (Table 22).

4.3.2 Genetic variability analysis

Performance of the twenty F_2 tomatillo genotypes is described below for each character. The extent of variation among the genotypes in respect of fifteen morphological characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 23.

4.3.2.1 Germination %

Maximum and minimum value for germination was 90.00 % and 75.00 % respectively with a grand mean of 81.00% The genotypic variance and phenotypic variance for this trait were 7.23 and 14.27 respectively (Table 23). Similar phenotypic and genotypic variance was observed in few experiments of tomatillo crops.

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 phenotypic coefficient of variation and genotypic coefficient of variation of germination % was low (4.66 and 3.32, respectively) (Table 23). Phenotypic coefficient of variation (4.66) was higher than the genotypic coefficient of variation (3.32) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Table 23. Estimation of genetic parameters of fifteen morphological characters of twenty F_2 tomatillo genotypes

Parameters	Germination%	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Maximum	90.00	97.85	25.45	9.75	33.33	52.45	85.15	38.13	38.01	37.85	32.11	442.00	1095.00	13.14	91.24
Minimum	75.00	79.88	19.69	5.45	25.01	45.23	77.75	27.71	28.33	28.99	20.99	241.00	590.00	7.08	49.16
GM	81.00	86.70	22.02	7.35	29.05	49.51	81.08	31.26	31.18	31.50	24.28	375.67	777.00	9.32	64.73
σ2e	7.04	6.73	1.15	0.44	0.99	1.05	1.38	1.67	1.01	0.91	2.90	709.08	3743.27	0.53	25.97
σ2g	7.23	7.18	1.07	0.48	2.50	1.62	0.93	2.39	1.87	3.03	5.29	931.67	8543.60	1.23	59.28
σ2p	14.27	13.91	2.21	0.93	3.49	2.66	2.31	4.06	2.88	3.94	8.19	1640.76	12286.87	1.76	85.25
ECV	3.28	2.99	4.87	9.06	3.42	2.07	1.45	4.14	3.23	3.03	7.01	7.09	7.87	7.86	7.87
GCV	3.32	3.09	4.69	9.45	5.44	2.57	1.19	4.95	4.38	5.53	9.47	8.13	11.90	11.90	11.89
PCV	4.66	4.30	6.76	13.09	6.43	3.30	1.87	6.45	5.44	6.30	11.78	10.78	14.27	14.26	14.26
H^2B	0.51	0.52	0.48	0.52	0.72	0.61	0.40	0.59	0.65	0.77	0.65	0.57	0.70	0.69	0.70
GA	3.94	3.96	1.48	1.03	2.76	2.04	1.26	2.44	2.26	3.15	3.81	47.38	158.78	1.90	13.23
GA % (mean)	4.87	4.57	6.70	14.05	9.50	4.12	1.56	7.82	7.26	9.99	15.68	12.61	20.43	20.45	20.43
SEM	1.53	1.50	0.62	0.38	0.57	0.59	0.68	0.75	0.58	0.55	0.98	15.37	35.32	0.42	2.94
CD (5%)	4.39	4.29	1.77	1.10	1.64	1.69	1.94	2.14	1.66	1.58	2.81	44.01	101.13	1.21	8.42
CD (1%)	5.88	5.74	2.37	1.48	2.20	2.26	2.60	2.86	2.23	2.11	3.77	58.96	135.46	1.62	11.28

Here, GM= Grand mean; σ^2g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

Germination % showed medium heritability (51%) and low in genetic advance (3.94) (Table 23). Medium to high heritability coupled with low genetic advance indicated the presence of non-additive gene action. High heritability was due to the favorable influence of environment rather than the genotypes. So selection based on this traits will not be rewarding.

4.3.2.2 Plant height

Maximum and minimum value for plant height was 97.85 cm and 79.88 cm, respectively with a grand mean of 86.70 cm. The genotypic variance and phenotypic variance for this trait were 7.18 and 13.91, respectively (Table 23). The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait (Table 28).

The phenotypic coefficient of variation and genotypic coefficient of variation of plant height was low (4.30 and 3.09, respectively) (Table 23). Phenotypic coefficient of variation (4.30) was higher than the genotypic coefficient of variation (3.09) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Plant height showed medium heritability (52%) and low in genetic advance (3.96) (Table 23). Medium to high heritability coupled with low genetic advance indicated the presence of non-additive gene action. High heritability was due to the favorable influence of environment rather than the genotypes. So, selection based on this trait will not be rewarding.

4.3.2.3 Leaf area index

Maximum value for leaf area index was 25.45 and minimum value for leaf area was 19.59 with a grand mean of 22.02 (Table 28).

The genotypic variance and phenotypic variance for this trait were 1.07 and 2.21 respectively (Table 23). 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 phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of leaf area was low (6.76 and 4.69 respectively) (Table 23). Phenotypic coefficient of variation (6.76) was higher than the genotypic coefficient of variation (4.69) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Leaf area showed medium heritability (48%) and low in genetic advance (1.48) (Table 23). Moderate heritability coupled with low genetic advance revealed this trait was heritable in next generation affected by environment rather than genetically. Thiyagu *et al.* (2013) found high heritability but Shashikanth *et al.* (2008) found low heritability and genetic advance for leaf area.

4.3.2.4 Number of branches per plant

Maximum Number of branches per plant in twenty F_2 tomatillo genotypes was 9.75 and the minimum was recorded 5.45 with grand mean 7.35 (Table 23). The phenotypic variance (0.93) was higher than the genotypic variance (0.48). 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 and phenotypic co-efficient of variation were 9.45 and 13.09, respectively (Table 23) indicating that the phenotypic expression of this trait was 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 low (52%), genetic advance was also low (1.03%) and genetic advance in per cent of mean (14.05) (Table 23) were found low, revealed that this trait was highly governed by environmental effects and selection will not be rewarded.

4.3.2.5 Days to first flowering

Days to first flowering performed maximum and minimum value was 33.33 days and 25.01 days respectively with a grand mean of 29.05 days (Table 23).

The genotypic variance and phenotypic variance for this trait were 2.50 and 3.49, respectively (Table 23). 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) (5.44) and phenotypic co-efficient of variation (PCV) (6.43) were more or less similar to each other, indicated presence of negligible variability in this trait. 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 high (72%) with low genetic advance (2.76) and genetic advance (2.76) and in percentage of mean of genetic advance was (9.50%). 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.

4.3.2.6 Days to 50% flowering

Maximum days found for days to 50% flowering was 52.45 and minimum was 45.23 with grand mean value 49.51 days after transplanting (DAT) (Table 23). The genotypic variance and phenotypic variance for this trait were 1.62 and 2.66, respectively (Table 23). The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. 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 character.

Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low (2.57 and 3.30, respectively) (Table 23). 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). So, it can be referring that selection based upon phenotypic expression of this character wouldn't be productive for the improvement of tomatillo.

The heritability was found 61% for this trait was high with low genetic advance (2.04) and genetic advance in per cent of mean (4.12%), indicating this character was controlled by non-additive genes. High heritability is due to favorable influence of environment rather than genetically influence. Singh *et al.* (2000) and Kumar *et al.* (2000) support the finding.

4.3.2.7 Days to maturity

Maximum days to maturity was found 85.15 DAT and the minimum was observed 77.75 DAT with grand mean value 81.08 (Table 23). The genotypic variance (0.93) was lower than phenotypic (2.31) variance with grand mean 81.08 days. The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait.

Genotypic co-efficient of variation (1.19) and phenotypic co-efficient of variation (1.87) were also close to each other (Table28). Suggesting environmental influence is minor on the expression of the genes controlling this parameter. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The results of Prashanth (2003) disagree with this result with high phenotypic coefficient of variation.

The heritability estimates for this trait were low (40%). In contrast genetic advance (1.26) and genetic advance in per cent of mean (1.56%) were found low, indicated that this trait was controlled by non-additive genes. High heritability is due to favorable environment rather than genetically effected, so the selection would not be recommended. Kumari *et al*. (2007), Islam and Khan (1991) were also found high heritability and moderately high genetic advance for days to maturity.

4.3.2.8 Number of fruits per plant

Observed the maximum number of fruits per plant was 38.13 and the minimum was recorded 27.71 with grand mean 31.26 (Table 23). The difference between genotypic (2.39) and phenotypic (4.06) variances indicated high environmental influence (Table 23).

The phenotypic coefficient of variation (6.45) and genotypic coefficient of variation (4.95) was low, which indicated presence of low variability among the genotypes (Table 23). Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi *et al*. (2003) supported the findings.

The heritability estimates for this character were low (59%), genetic advance (2.44) and genetic advance in percent of mean (7.82%) were found low, indicated that this trait was governed by environmental effect and selection for this character would not be effective.

4.3.2.9 Fruit Length

The maximum fruit length was recorded 38.01 and the minimum fruit length was recorded 28.33 mm. The grand mean of fruit length was noticed as 31.18 mm. (Table 23). The genotypic variance was 1.87 which was low and phenotypic variance was 2.88 which was also low.

Genotypic co-efficient of variation (4.38) and phenotypic co-efficient variation (5.44) were close to each other (Table 23), 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 greater for this trait which was supported the present study.

High heritability estimates (65%) with low genetic advance (2.26) over percent of mean (7.26%) (Table 23) indicate that effective selection may not be made for fruit length. The character was governed by non-additive gene action. Moderate heritability and moderate genetic gain for this character was observed by Joshi *et al.* (2004) which was not supporting these results.

4.3.2.10 Fruit Diameter

The grand mean of fruit diameter was recorded 31.50 mm with maximum 37.85 mm and minimum 28.99 mm (Table 23). The phenotypic variance was 3.94 which was low and genotypic variance was 3.03 which was also low.

Genotypic co-efficient of variation (5.53) and phenotypic co-efficient variation (3.03) (Table 23) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement for the tomatillo crop. 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 (77%) with low genetic advance (3.15) over moderate percent of mean was 9.99% (Table 28), indicated that effective selection may not be made for fruit length. The character was governed by non-additive gene action. High heritability coupled with low genetic gain for this character was observed by Pandit *et al*. (2010) in tomato.

4.3.2.11 Individual fruit weight

The maximum individual fruit weight was recorded 32.11g in and the minimum was recorded 20.99 g with grand mean value 24.28 g (Table 28). The genotypic variance (5.29) and phenotypic variance (8.19) for individual fruit weight was low (Table 23). The genotypic co-efficient of variation and phenotypic co-efficient of variation were low (9.47 and 11.78, respectively), proved that environment has little influence of the expression of this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Low GCV and PCV for average fruit weight were also noticed by Manivannan *et al*. (2005) and Singh *et al*. (2002).

Heritability was observed 65%, which was high associated with low genetic advance (3.81) in percent of mean (15.68%) (Table 23), indicating fruit weight was highly influenced by environment, therefore selection should not be supported. Pandit *et al.* (2010), Ara *et al.* (2009) and Singh *et al.* (2006) also experienced to the present findings.

4.3.2.12 Seeds per fruit

The maximum seeds per fruit were recorded 442 whereas minimum seeds per fruit were found 241 with grand mean 375.65 sees per fruit. (Table28). Genotypic variance was found 931.67, on the other hand phenotypic variance was observed 1640.76 which was very high. The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait (Table 23).

The phenotypic coefficient of variation and genotypic coefficient of variation of seed per fruit was low (10.78 and 8.13, respectively) (Table 23). Phenotypic coefficient of variation (10.78) was higher than the genotypic coefficient of variation (8.13) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. So, selection based upon phenotypic expression of this trait would not be effective for the improvement of the crop.

Seeds per fruit showed medium heritability (57%) and high in genetic advance (47.38) with percent mean genetic advance was 12.61% (Table 23). Medium heritability coupled with high genetic advance indicated the presence of additive gene action. Medium heritability is due to the favorable influence of environment rather than the genotypes. so, selection based on this traits will not be rewarding.

4.3.2.13 Yield per plant

Maximum fruit yield per plant was found 1095.00 g and the minimum was recorded 590.00 g with grand mean value 777.00 g (Table 23). The phenotypic variance (12286.87) found higher than genotypic variance (8543.60) (Table 23), suggested considerable influence of environment on the expression of the genes controlling this character.

The phenotypic coefficient of variation and genotype coefficient of variation were 14.27 and 11.90, respectively for fruit yield per plant, which indicating that variation exists among different genotypes which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al*. (2005).

Estimation of very high heritability (70%) for fruit yield per plant with high genetic advance (158.78) and high genetic advance of % mean (20.43%) (Table 28) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding program. High heritability and high genetic advance were also observed by Ara *et al.* (2009) and Anupam *et al.* (2002).

4.3.2.14 Yield per plot

Maximum yield per plot was found 13.14 kg and the minimum was observed 7.08 kg with grand mean value 9.32 kg (Table 23). The phenotypic variance (1.76) found little higher than genotypic variance (1.23) (Table 28), suggested considerable influence of environment on the expression of the genes controlling this character.

The phenotypic coefficient of variation and genotype coefficient of variation were 14.26 and11.90, respectively for yield per plot, which indicating that significant variation existed among twenty different F2 genotypes of tomatillo, which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al*. (2005).

Estimation of very high heritability (69%) for fruit yield per plant with low genetic advance (1,90) and high genetic advance of % mean (20.45%) (Table 23) revealed that this character was governed by non-additive gene action and selection will not be rewarded.

4.3.2.15 Yield per hectare

Maximum and minimum value for final yield was 91.24 t/h and 49.16 t/h respectively with a grand mean of 64.73 t/h (Table 23). The genotypic variance and phenotypic variance for this important parameter were 59.28 and 85.25, respectively (Table 23). 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 phenotypic coefficient of variation and genotypic coefficient of variation of yield was high (14.26 and 11.89, respectively) (Table 23). Phenotypic coefficient of variation (14.26) was higher than the genotypic coefficient of variation (11.89) suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the

differences between the PCV and GCV were very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop. Yield (t/h) showed high heritability (70%) and medium in genetic advance (13.23). Also observed high genetic advance of % mean (20.43%) (Table 23).

High heritability coupled with high genetic advance % indicated the presence of additive gene action. So, selection based on this trait will be effective and provides opportunity for selecting high valued genotypes for future breeding program. High heritability and high genetic advance were also observed by Ara *et al.* (2009) and Anupam *et al.* (2002).

4.3.3 Correlation Co-efficient

Determination of correlation co-efficient was provided the information how yield depends on different yield contributing characters. Correlation co-efficient studies along with path analysis provide a better understanding of the association of different characters with 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 F2 genotype of tomatillo are given in Table 24 and Table 25.

4.3.3.1 Germination %

Germination % had significant positive correlation with yield (0.50**) at genotypic level and significant positive correlation (0.35**) at phenotypic levels (Table 29 and

Table 24. Genotypic correlation coefficient among different pairs of morphological characters of twenty F2 generations of tomatillo

Characters	%Germination	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/ plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
%Germination	1 **	0.66**	0.88**	0.08NS	-0.80**	-0.92**	-0.40NS	0.82**	0.89**	0.91**	0.76**	0.43NS	0.50*	0.50*	0.50*
Plant height			0.73**	0.86**	-0.71**	-0.73**	-0.67**	0.82**	0.91**	0.74**	0.83**	0.80**	1**	1**	1.03**
Leaf area			1**	0.62**	-0.97**	-1**	-0.67**	1**	1**	0.98**	0.91**	0.64**	0.92**	0.92**	0.92**
No. of branches/plant				1**	-0.52*	-0.55*	-0.95**	0.77**	0.73**	0.48*	0.66**	0.78**	0.86**	0.86**	0.86**
Days to 1st flowering					1**	0.82**	0.62**	-1**	-1 **	-0.89**	-0.69**	-0.70**	-0.71**	-0.71**	-0.71**
Days to 50% flowering						1**	0.45*	-1**	-0.9**	-1**	-0.90**	-0.71**	-0.91**	-0.91**	-0.91**
Days to maturity							1**	-0.6**	-0.7**	-0.54*	-0.48*	-0.82 **	-0.71**	-0.71**	-0.71**
No. of fruits/plant								1**	1**	1**	1**	0.73**	0.93**	0.93**	0.93**
Fruit length									1**	0.85**	0.92**	0.70**	0.92**	0.92**	0.92**
Fruit diameter										1 **	0.95**	0.61**	0.80**	0.80**	0.80**
Individual fruit weight											1**	0.43NS	0.89**	0.89**	0.89**
Seeds/ plant												1**	0.84**	0.84**	0.84**
Yield/ plant													1**	1**	1**
Yield/plot														1**	1**
Yield/ha															1**

Table 25. Phenotypic correlation coefficient among different pairs of morphological characters of twenty F2 generations of tomatillo

Characters	%Germination	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/ plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
%Germination	1**	0.25*	0.35**	0.10^{NS}	-0.57**	-0.52**	-0.28*	0.48**	0.42**	0.53**	0.46**	0.31*	0.35**	0.35**	0.35**
Plant height		1**	0.54**	0.42**	-0.37**	-0.54**	-0.37**	0.50**	0.47**	0.40**	0.54**	0.49**	0.66**	0.66**	0.66**
Leaf area			1**	0.37**	-0.53**	-0.62**	-0.18^{NS}	0.53**	0.50**	0.57**	0.63**	0.26*	0.60**	0.60**	0.60**
No. of branches/plant				1**	-0.32*	-0.29*	-0.41**	0.43**	0.35**	0.28*	0.3*	0.25*	0.53**	0.53**	0.53**
Days to 1st flowering					1**	0.68**	0.48**	-0.6**	-0.6**	-0.5**	-0.43**	-0.41**	-0.45**	-0.4**	-0.4**
Days to 50% flowering						1**	0.28*	-0.57**	-0.56**	-0.63**	-0.61**	-0.37**	-0.56**	-0.57**	-0.56**
Days to maturity							1**	-0.38**	-0.24^{NS}	-0.21^{NS}	-0.12^{NS}	-0.39**	-0.31*	-0.31*	-0.31*
No. of fruits/plant								1**	0.73**	0.68**	0.65**	0.53**	0.72**	0.72**	0.72**
Fruit length									1**	0.70**	0.61**	0.51**	0.63**	0.63**	0.63**
Fruit diameter										1**	0.66**	0.33**	0.58**	0.59**	0.58**
Individual fruit weight											1**	0.37**	0.79**	0.79**	0.79**
Seeds/ plant												1**	0.60**	0.60**	0.6**
Yield/ plant													1**	0.99**	1**
Yield/plot														1**	0.99**
Yield/ha															1**

Table 25). Germination % had also significant positive correlation with Plant height (0.66), leaf area index (0.88), number of fruits per plant (0.82), fruit length, (0.89), fruit diameter (0.91), Individual fruit weight (0.76), yield per plant (0.50), and yield per plot (0.50). It had also negative significant correlation with days to first flowering (-0.80), days to fifty percent flowering (-0.92), at genotypic level. The same characters showed same both negative and positive significant at phenotypic level.

4.3.3.2 Plant height

Plant height had significant positive correlation with yield per ha at both the genotypic (1.00**) and phenotypic (0.66**) levels (Table 24 and Table 25), that was supported by Mohanty (2003). Plant height had also significant positive correlation with leaf area index, number of branches per plant, number of fruits per plant, individual fruit weight, fruit length, fruit diameter, seeds per fruit, yield per plant, and yield per plot at both the levels. It had also significant negative correlation with days to first flowering, days to fifty percent flowering, days to maturity at both levels.

4.3.3.3 Leaf area

Leaf area had highly significant positive association with yield per ha (0.92**) at genotypic level and significant positive relation (0.60**) at phenotypic level (Table 24 and Table 25). Leaf area was also positive significant association with number of branches per plant, number of fruits per plant, fruit length, fruit diameter, individual fruit weight, seeds per fruit, yield per plant, yield per plot and negative significant relation with days to first flowering, days to fifty percent flowering at both genotypic and phenotypic levels. A positive correlation between number of clusters per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato.

4.3.3.4 Number of branches per plant

The number of branches per plant had positive highly significant correlation with yield per hectare, yield per plant and yield per ha at genotypic and phenotypic level (0.86 ** and 0.53** respectively). It had also positive significant relation with number of fruits per plant, fruit length, fruit diameter, individual fruit weight, seeds per fruit, yield per plant, yield per plot at both the levels. The number of branches per

plant had also negative significant association with days to first flowering and days to maturity at both genotypic and phenotypic levels. (Table 24 and Table 25). 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). 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).

4.3.3.5 Days to first flowering

Days to first flowering had highly significant negative correlation with yield per hectare (G = -0.71** and P= - 0.40**), yield per plot, yield per plant, seeds per fruit, individual fruit weight, fruit length and fruit diameter at genotypic and phenotypic level (Table 24 and Table 25). Days to first flowering also positively associated with days to 50% flowering, days to maturity at both genotypic and phenotypic levels.

4.3.3.6 Days to 50% flowering

Days to 50% flowering showed highly significant negative association with fruit yield per hactare (G= -0.91** and P= -0.56**), number of fruits per plant, fruit length, fruit diameter, individual fruit weight, seeds per fruit, yield per plant and yield per plot at both genotypic and phenotypic levels (Table 24 and Table 25). Non-significant association of this trait with yield indicated that the association was largely influenced by environment. Yield improvement can be achieved by selection for days to 50% flowering were reported by Wright *et al*. (2007).

4.3.3.7 Days to maturity

Days to maturity had highly significant negative correlation with yield per ha (G= -0.71** and P= -0.31*), yield per plant , yield per plot and seeds per fruit at genotypic and phenotypic levels (Table 24 and Table 25). It had also highly significant positive association with number of fruits per plant at phenotypic level and negative significant at genotypic level. (Table 24 and Table 25). Days to maturity showed non-significant negative relation with fruit length (-0.24), fruit diameter (-0.21) and individual fruit weight (-0.12) at phenotypic level. Significant and positive correlation

observed by Singh *et al.* (2002) and Mohanty (2003) between days to maturity and fruit yield per plant and this doesn't support the present findings.

4.3.3.8 Number of fruits per plant

The number of fruits per plant had highly significant and positive association with yield per hectare (0.93**) yield per plant (0.93**), yield per plot ((0.93**), seeds per fruit (0.73**), individual fruit weight (1**) fruit diameter (1**) fruit length (1**) at genotypic levels. (Table 24). Rani *et al.* (2010) reported that the number of fruits per plant was associated with yield per plant which supported this finding.

The number of fruits per plant had also significant positive correlation with yield per hectare (0.72**) yield per plant (0.72**), yield per plot ((0.72**), seeds per fruit (0.53**) individual fruit weight (65**) and fruit length (0.73**) and fruit diameter (0.68**) at phenotypic levels. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight.

4.3.3.9 Fruit length

Fruit length was highly significant positively correlated with fruit yield per ha (0.92** and 0.63**), yield per plant, yield per plot, seeds per fruit (0.70** and 0.51**) and fruit diameter (0.85** and 0.70**) at genotypic and phenotypic levels respectively. (Table 24 and Table 25). The character showed all the positive significant correlation at both the level.

4.3.3.10 Fruit diameter

Fruit diameter showed highly significant positive association with fruit yield per hectare (0.80** and 0.58**) yield per plant (0.80** and 0.58**), yield per plot (0.90** and 0.58**) and seeds per fruit (0.61* and 0.33**) and individual fruit weight (0.95** and 0.66**) at both genotypic and phenotypic level respectively.

4.3.3.11 Individual fruit weight

Fruit weight showed highly significant and positive correlation with yield per hectare (0.89** and 0.79**) yield per plant (0.89** and 0.79**) yield per plot (0.89** and 0.79**) for both genotypic and phenotypic levels (Table 24 and Table 25).

Seeds per fruit showed non-significant positive relation (0.43^{NS}) at genotypic level and significant positive relation (0.37**) at phenotypic level. 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.

4.3.3.12 Seeds per plant

Seeds per plant had highly significant positive association with yield per ha (0.84** and 0. 60**), yield per plant (0.84** and 0. 60**) and yield per plot (0.84** and 0. 60**) at both genotypic and phenotypic levels. A positive correlation between number of seeds per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato.

4.3.3.13 Yield per plant

At genotypic level, yield per plant showed highly significant positive correlation with germination % (0.50*), plant height (1**), leaf area (0.92**), no. of branches per plant (0.86**), no. of fruits per plant (0.93**), fruit length (0.92**), fruit diameter (0.80**), individual fruit weight (0.89**), seeds per fruit (0.84**) , yield per plot (1**) and yield per ha (1**)(Table 29). At genotypic level, yield per plant showed significant negative correlation with days to first flowering (-71**). At phenotypic level, yield per plant showed significant positive correlation with germination % (0.35**), plant height (0.66**), leaf area (0.60**), no. of branches per plant (0.53), no. of fruits per plant (0.72**), fruit length (0.63**), fruit diameter (0.58**), individual fruit weight (0.79**), seeds per fruit (0.60**), yield per plot (0.99**), and yield per ha (1**) (Table 25). Yield per plant showed significant negative correlation with days to 1^{st} flowering (-0.45**), days to 50% flowering (-0.56**), days to maturity (-0.31**) (Table 25).

4.3.3.14 Yield per plot

At genotypic level, yield per plot showed highly significant positive correlation with germination % (0.50*), plant height (1**), leaf area (0.92**), no. of branches per plant (0.86**), no. of fruits per plant (0.93**), fruit length (0.92**), fruit diameter

(0.80**), individual fruit weight (0.89**), seeds per fruit (0.84**) , yield per plant (1**) and yield per ha (1**)(Table 29). At genotypic level, yield per plot showed significant negative correlation with days to first flowering (-71**). At phenotypic level, yield per plot showed significant positive correlation with germination % (0.35**), plant height (0.66**), leaf area (0.60**), no. of branches per plant (0.53), no. of fruits per plant (0.72**), fruit length (0.63**), fruit diameter (0.58**), individual fruit weight (0.79**), seeds per fruit (0.60**), yield per plant (0.99**), and yield per ha (1**) (Table 25). Yield per plot showed significant negative correlation with days to 1st flowering (-0.45**), days to 50% flowering (-0.56**), days to maturity (-0.31**) (Table 25).

4.3.3.15 Yield per ha

At genotypic level, yield per ha showed highly significant positive correlation with germination % (0.50*), plant height (1**), leaf area (0.92**), no. of branches per plant (0.86**), no. of fruits per plant (0.93**), fruit length (0.92**), fruit diameter (0.80**), individual fruit weight (0.89**), seeds per fruit (0.84**) , yield per plot (1**) and yield per plant (1**) (Table 24). At genotypic level, yield per ha showed significant negative correlation with days to first flowering (-71**). At phenotypic level, yield per plot showed significant positive correlation with germination % (0.35**), plant height (0.66**), leaf area (0.60**), no. of branches per plant (0.53), no. of fruits per plant (0.72**), fruit length (0.63**), fruit diameter (0.58**), individual fruit weight (0.79**), seeds per fruit (0.60**), yield per plot (0.99**), and yield per plant (1**) (Table 25). Yield per ha showed significant negative correlation with days to 1st flowering (-0.45**), days to 50% flowering (-0.56**), days to maturity (-0.31**) (Table 25).

4.3.4 Path coefficient analysis

The path coefficient analysis technique was developed by wright (1921) and demonstrated by Deway and Lu (1959) facilitates the partitioning of correlation coefficients into direct and indirect contribution of various characters on yield.

To get a clear picture of the inter–relationship between yield and other yield attributes, direct and indirect effects of yield contributing characters were worked out by using path analysis at genotypic level which also measured the relative importance

of each component. Here yield per ha was considered as effect (dependent variable) and plant height (cm), leaf area, number of branches per plant, days of first flowering, days 50% flowering, days to maturity, fruits per plant, fruit length, fruit diameter, individual fruit weight, seeds per fruits, yield per plant and yield per plot were treated as causal (independent) variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of tomatillo in Table 26. Path coefficient analysis revealed that yield/ha was directly influenced by plant height, leaf area, number of branches per plant, days of first flowering, days to maturity, fruits per plant, fruit length, fruit diameter, individual fruit weight, and yield per plot. Hence, selection for any of these independence characters leads to improving the genotypes for yield/ha. It might be concluded that improvement in yield/ha could be brought by selection these traits.

4.3.4.1 Germination %

Germination % had negative direct effect (-0.02) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.50*) where it showed positive indirect effect with plant height, leaf area index, number of branches per plant, days to first flowering, days to maturity, fruit diameter and yield per plant. It had also negative indirect effect on days to fifty % flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit. Singh *et al.* (2006) and Kumar *et al.* (2003) also observed fruits per plant had direct positive effects on fruit yield at the genotypic and phenotypic levels. Ara *et al.* (2009) also found similar results for this trait in tomato. Rani *et al.* (2010), Singh *et al.* (2006) and Manivannan *et al.* (2005) also reported positive direct effects of individual fruit weight on fruit yield in tomato.

4.3.4.2 Plant height

Plant height had positive direct effect (0.01) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (1**) where it showed positive indirect effect with leaf area index, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect number of branches per plant, days to fifty % flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

Table 26. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of fifteen characters of twenty F2 generations of tomatillo

Characters	Germination%	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/ plot	Genotypic correlation coefficient with yield/ha
Germination %	**-0.02**	0.00	0.03	0.00	0.01	-0.02	0.01	-0.03	-0.01	0.03	-0.02	-0.02	0.61	-0.07	0.50*
Plant height	-0.02	**0.01**	0.02	-0.04	0.01	-0.02	0.02	-0.03	-0.01	0.03	-0.02	-0.03	1.26	-0.15	1.03**
Leaf area	-0.02	0.00	**0.03**	-0.03	0.02	-0.02	0.02	-0.05	-0.01	0.04	-0.02	-0.02	1.12	-0.13	0.92**
No. of branches/plant	0.00	0.00	0.02	**-0.04**	0.01	-0.01	0.03	-0.03	-0.01	0.02	-0.02	-0.03	1.05	-0.12	0.86**
Days to 1st flowering	0.02	0.00	-0.03	0.02	**-0.02**	0.02	-0.02	0.04	0.01	-0.03	0.02	0.03	-0.87	0.10	-0.71**
Days to 50% flowering	0.02	0.00	-0.03	0.02	-0.01	**0.02**	-0.01	0.04	0.01	-0.04	0.02	0.03	-1.10	0.13	-0.91**
Days to maturity	0.01	0.00	-0.02	0.04	-0.01	0.01	**-0.03**	0.03	0.01	-0.02	0.01	0.03	-0.87	0.10	-0.71**
No. of fruits/plant	-0.02	0.00	0.04	-0.03	0.02	-0.02	0.02	**-0.04**	-0.01	0.04	-0.02	-0.03	1.14	-0.13	0.93**
Fruit length	-0.02	0.01	0.04	-0.03	0.02	-0.02	0.02	-0.05	**-0.01**	0.03	-0.02	-0.03	1.12	-0.13	0.92**
Fruit diameter	-0.02	0.00	0.03	-0.02	0.02	-0.02	0.02	-0.04	-0.01	**0.04**	-0.02	-0.02	0.98	-0.11	0.80**
Individual fruit weight	-0.02	0.00	0.03	-0.03	0.01	-0.02	0.01	-0.04	-0.01	0.04	**-0.02**	-0.02	1.08	-0.13	0.89**
Seeds/ plant	-0.01	0.00	0.02	-0.03	0.01	-0.01	0.03	-0.03	-0.01	0.02	-0.01	**-0.04**	1.03	-0.12	0.84**
Yield/ plant	-0.01	0.01	0.03	-0.04	0.01	-0.02	0.02	-0.04	-0.01	0.03	-0.02	-0.03	**1.21**	-0.14	1**
Yield/plot	-0.01	0.01	0.03	-0.04	0.01	-0.02	0.02	-0.04	-0.01	0.03	-0.02	-0.03	1.21	**-0.14**	1**

4.3.4.3 Leaf area index

Leaf area index had positive direct effect (0.03) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.92**) where it showed positive indirect effect with days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect effect on germination %, number of branches per plant, days to fifty % flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.4 Number of branches per plant

Number of branches per plant had negative direct effect (-0.04) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.86**) where it showed positive indirect effect with leaf area, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect on days to fifty % flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.5 Days to first flowering

Days to first flowering had negative direct effect (-0.02) on yield per ha (Table 26) which contributed to result significant negative genotypic correlation with yield per ha (-0.71**) where it showed positive indirect effect with germination % , number of branches per plan, days to fifty % flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit, and yield per plot. It had negative indirect on leaf area, days to maturity, fruit diameter and yield per plant.

4.3.4.6 Days to fifty % flowering

Days to fifty percent flowering had positive direct effect (0.02) on yield per ha (Table 26) which contributed to result significant negative genotypic correlation with yield per ha (-0.91**) where it showed positive indirect effect with germination % , number of branches per plan, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit, and yield per plot. It had negative indirect on leaf area index, days to maturity, fruit diameter and yield per plant.

4.3.4.7 Days to maturity

Days to maturity had negative direct effect (-0.03) on yield per ha (Table 26) which contributed to result significant negative genotypic correlation with yield per ha (-0.71**) where it showed positive indirect effect with germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit, and yield per plot. It had negative indirect on leaf area index, days to first flowering, fruit diameter and yield per plant.

4.3.4.8 Number of fruits per plant

Number of fruits per plant had negative direct effect (-0.04) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.93**) where it showed positive indirect effect with leaf area index, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.9 Fruit length

Fruit length had negative direct effect (-0.01) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.92**) where it showed positive indirect effect with plant height, leaf area index, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.10 Fruit diameter

Fruit diameter had positive direct effect (0.04) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.80**) where it showed positive indirect effect with leaf area index, days to first flowering, days to maturity and yield per plant. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number

of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.11 Individual fruit weight

Individual fruit weight had negative direct effect (-0.02) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.89**) where it showed positive indirect effect with leaf area index, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, seeds per fruit and yield per plot.

4.3.4.12 Seeds per fruit

Seeds per fruit had negative direct effect (-0.04) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (0.84**) where it showed positive indirect effect with leaf area index, days to first flowering, days to maturity fruit diameter and yield per plant. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight and yield per plot.

4.3.4.13 Yield per plant

Yield per plant had positive direct effect (1.21) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (1**) where it showed positive indirect effect with plant height, leaf area index, days to first flowering, days to maturity and fruit diameter. It had negative indirect on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot.

4.3.4.14 Yield per plot

Yield per plot had negative direct effect (-0.14) on yield per ha (Table 26) which contributed to result significant positive genotypic correlation with yield per ha (1**) where it showed positive indirect effect with plant height, leaf area index, days to first flowering, days to maturity, fruit diameter and yield per plant. It had negative indirect

on germination %, number of branches per plant, days to fifty percent flowering, number of fruits per plant, fruit length, individual fruit weight and seeds per fruit.

4.3.5 Selection index

Selection index with ranking the morphological characters and ranking the genotypes has been presented in Table 27 and Table 28. Based on the value presented in table 32, the most important characters were yield per plant (159.01) followed by no. of seeds per fruits (47.45), yield per ha (13.25) and plant height (3.97) (Table 27). The least important character for selection index was no. of branches per plant (1.03), days to maturity (1.26) and leaf area index (1.48). Based on the four high ranked characters, the total selection scores for each of the genotypes were estimated Table 33). The highest selection score was found in G1 × G3 (1065.57) having ranked 1 followed by G1 × G2 (1032.15) with rank 2. The lowest ranked genotype was found in G2 × G4 (701.66) with rank of 20followed by G4× G2 (725.09) having ranked 19) (Table 28).

Table 27. Ranking the morphological characters for selecting the better genotypes

Characters	b value	GA	Rank
Yield per plant	0.70	159.01	1
No. of seeds per fruit	0.57	47.45	2
Yield per ha	0.70	13.25	3
Plant height	0.52	3.97	4
% Germination	0.51	3.95	5
Fruit weight	0.65	3.81	6
Fruit diameter	0.77	3.15	7
Days to first flowering	0.72	2.76	8
No. of fruits per plant	0.59	2.45	9
Fruit length	0.65	2.27	10
Days to fifty % flowering	0.61	2.04	11
Yield per plot	0.70	1.91	12
Leaf area index	0.48	1.48	13
Days to maturity	0.40	1.26	14
No. of branches/plant	0.52	1.03	15

Table 28. Ranking the morphological characters for selecting the better genotypes

Genotypes	Selection Scores	Ranking
G1 × G2	1032.15	2
G1 × G3	1065.57	1
G1 × G4	780.62	17
G1 × G5	908.94	4
G2 × G1	848.43	10
G2 × G3	813.80	14
G2 × G4	701.66	20
G2 × G5	836.10	11
G3 × G1	917.85	3
G3 × G2	784.78	15
G3 × G4	783.40	16
G3 × G5	829.64	13
G4 × G1	728.55	18
G4 × G2	725.09	19
G4 × G3	830.12	12
G4 × G5	880.08	7
G5 × G1	884.60	5
G5 × G2	879.41	8
G5 × G3	853.12	9
G5 × G4	884.59	6

Experiment 3b. Genetic variability, character association and selection index of quality traits in twenty F_2 genotypes of tomatillo (*Physalis ixocarpa Brot./Physalis philadelphica* Lam.)

The experiment was conducted to perform the diversity analysis and selection ranked of different F_2 genotypes of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.) using quality traits. The data pertaining to nine quality characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.3.1 Mean performance analysis

Analysis of variance and mean performance of twenty F_2 tomatillo genotypes were presented in Appendix VIII and Table 29. Highly significant variation among twenty F_2 tomatillo genotypes in terms of quality matters of nine parameters were recorded.

4.3.1.1 Leaf chlorophyll content

Analysis of variance showed statistically significant differences among the twenty F2 tomatillo genotypes in term of leaf chlorophyll content at 1% level (Appendix VIII). The leaf chlorophyll content ranged from 83.88 to 77.58. Highest leaf chlorophyll content (83.88) was observed in G1×G3 and lowest leaf chlorophyll content was observed in G4×G1 (77.58) with average leaf chlorophyll content 79.61 (Table 29).

4.3.1.2 Brix percentage

Analysis of variance showed statistically significant differences among twenty F2 tomatillo genotypes in term of brix percentage at 1% level (Appendix VIII). Brix percentage ranged from 7.46 to 5.80. Highest brix percentage (7.46) was observed in G1×G3 and lowest brix percentage was observed in G5×G3 (5.80) with average plant height of 6.17 (Table 29).

4.3.1.3 Fruit pH

In fruit pH analysis of variance showed non-significantly difference among the twenty F_2 tomatillo genotypes (Appendix VIII). Fruit pH ranged from 4.42 to 3.84. The highest fruit pH index was found in G2×G5 (4.42) and the lowest fruit pH was observed in G1×G2 (3.84) with average value of 4.02 (Table 29).

Table 29. Mean performance of nine qualitative traits of twenty F2 genotypes oftomatillo

Genotypes	Leaf chlorophyll content	%Brix	Fruit pH	Vitamin C	Titratable acidity
G1 × G2	81.88 abc	6.39 bc	3.84	14.31	0.74
G1 × G3	83.87 a	7.46 a	3.95	20.08	0.75
G1 × G4	78.35 bc	6.00 c	4.09	18.93	0.69
G1 × G5	79.06 bc	6.14 bc	3.85	17.82	0.68
G2 × G1	78.33 bc	6.21 bc	4.13	14.27	0.59
G2 × G3	78.86 bc	6.04 c	3.94	15.30	0.75
G2 × G4	78.58 bc	6.18 bc	3.91	18.12	0.65
G2 × G5	80.40 abc	6.2 bc	4.42	18.70	0.71
G3 × G1	82.67 ab	7.11 ab	4.14	17.40	0.80
G3 × G2	79.32 abc	6.25 bc	4.06	15.72	0.80
G3 × G4	78.03 bc	5.81 c	4.06	15.92	0.68
G3 × G5	80.12 abc	5.92 c	4.05	19.45	0.72
G4 × G1	77.57 c	5.87 c	3.86	17.51	0.75
G4 × G2	78.48 bc	6.19 bc	4.01	17.10	0.79
G4 × G3	80.13 abc	5.91 c	3.90	16.40	0.78
G4 × G5	77.99 bc	5.86 c	3.94	18.01	0.76
G5 × G1	80.05 abc	6.063 c	4.18	17.29	0.74
G5 × G2	80.17 abc	6.03 c	3.86	16.95	0.81
G5 × G3	78.37 bc	5.79 c	4.23	16.09	0.77
G5 × G4	79.88 abc	5.99 c	3.97	16.95	0.76
Average	79.61	6.17	4.02	17.12	0.74
Maximum	83.88	7.46	4.42	20.08	0.81
Minimum	77.58	5.80	3.84	14.27	0.59
CV	1.92	5.29	5.84	11.92	16.44

Table 29. (CONT´D)

Genotypes	Lycopene content (472)	Lycopene content (502)	Fruit moisture content	Fruit dry matter content
G1 × G2	0.39	0.33	92.84	7.16
G1 × G3	0.33	0.27	92.97	7.03
G1 × G4	0.22	0.20	93.40	6.60
G1 × G5	0.18	0.21	93.95	5.95
G2 × G1	0.41	0.40	92.94	7.06
G2 × G3	0.49	0.44	92.66	7.39
G2 × G4	0.28	0.25	94.41	5.62
G2 × G5	0.26	0.23	93.48	6.54
G3 × G1	0.43	0.36	93.80	6.22
G3 × G2	0.35	0.33	93.28	6.72
G3 × G4	0.29	0.24	93.46	6.54
G3 × G5	0.39	0.38	93.07	7.09
G4 × G1	0.23	0.18	94.77	5.23
G4 × G2	0.36	0.27	92.76	7.24
G4 × G3	0.37	0.30	93.21	6.79
G4 × G5	0.45	0.39	93.32	6.58
G5 × G1	0.37	0.28	92.75	7.26
G5 × G2	0.33	0.38	93.66	6.16
G5 × G3	0.30	0.28	93.39	6.95
G5 × G4	0.42	0.41	93.25	6.50
Average	0.34	0.31	93.37	6.63
Maximum	0.49	0.44	94.77	7.39
Minimum	0.18	0.18	92.66	5.23
CV	46.04	52.98	1.60	20.41

4.3.1.4 Vitamin C

Statistically non-significant variation was observed in Vitamin C analysis among the twenty F2 tomatillo genotypes (Appendix VIII). Vitamin C ranged from 20.08 to 14.27. The highest Vitamin C was found in G1×G3 (20.08) and the lowest vitamin C was observed in G2×G1 (14.27) with average value of 17.12 (Table 29).

4.3.1.5 Titratable acidity

Statistically non-significant variation was observed in titratable acidity among the twenty F_2 tomatillo genotypes (Appendix VIII). Titratable acidity ranged from 0.81 to 0.59. The highest titratable acidity was found in G3×G1 (0.81) and the lowest titratable acidity was observed in G2×G1 (0.59) with average value of 0.74 (Table 29).

4.3.1.6 Lycopene content (472)

Statistically non-significant variation was observed in lycopene content (472) among the twenty F_2 tomatillo genotypes (Appendix VIII). Lycopene content (472) ranged from 0.49 to 0.18. The highest lycopene content (472) was found in G2×G3 (0.49) and the lowest lycopene content (472)was observed in G1×G5 (0.18) with average value of 0.34 (Table 29).

4.3.1.7 Lycopene content (502)

Statistically non-significant variation was observed in lycopene content (502) among the twenty F_2 tomatillo genotypes (Appendix VIII). Lycopene content (502) ranged from 0.44 to 0.18. The highest lycopene content (502) was found in G2×G3 (0.44) and the lowest lycopene content (502) was observed in G4×G1 (0.18) with average value of 0.31 (Table 29).

4.3.1.8 Fruit moisture content

Statistically non-significant variation was observed in fruit moisture content among the twenty F_2 tomatillo genotypes (Appendix VIII). Fruit moisture content ranged from 94.77 to 92.66. The highest fruit moisture content was found in G4×G1 (94.77)

and the lowest fruit moisture contentwas observed in G2×G3 (92.66) with average value of 93.37 (Table 29).

4.3.1.9 Fruit dry matter content

Statistically non-significant variation was observed in fruit dry matter content among the twenty F_2 tomatillo genotypes (Appendix VIII). Fruit dry matter content ranged from 7.39 to 5.23. The highest fruit dry matter content was found in G2×G3 (7.39) and the lowest fruit dry matter contentwas observed in G4×G1 (5.23) with average value of 6.63 (Table 29).

4.3.2 Genetic variability analysis

Performance of the twenty F_2 tomatillo genotypes is described below for each character. The extent of variation among the genotypes in respect of nine quality characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 30.

4.3.2.1 Leaf chlorophyll content

Maximum and minimum value for leaf chlorophyll content was 84.25 and 75.41 respectively with a grand mean value of 79.61. The genotypic variance and phenotypic variance for this trait were 1.94 and 4.27 respectively (Table 30). 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 phenotypic coefficient of variation and genotypic coefficient of variation of leaf chlorophyll content was low (2.59 and 1.75 respectively) (Table 30). Phenotypic coefficient of variation (2.59) was higher than the genotypic coefficient of variation (1.75) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV are very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Leaf chlorophyll content showed medium heritability (45%) and low in genetic advance (1.93) (Table 30). Medium heritability coupled with low genetic advance indicated the presence of non-additive gene action. Heritability is due to the favorable influence of environment rather than the genotypes. So selection based on this trait will not be rewarding.

4.3.2.2 Brix %

Maximum and minimum value for brix % was observed 7.59 and 5.15, respectively with a grand mean of 6.10. The genotypic variance and phenotypic variance for this trait were 0.13 and 0.24, respectively (Table 30). The phenotypic variance appeared to be high than the genotypic variance suggested influence of environment on the expression of genes controlling this trait.

The phenotypic coefficient of variation and genotypic coefficient of variation of plant height was low (8.00 and 6.01, respectively) (Table 30). Phenotypic coefficient of variation (8.00) was higher than the genotypic coefficient of variation (6.01) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this trait would be effective for the improvement of the crop.

Brix % showed medium heritability (56%) and low in genetic advance (0.56) (Table 35). Medium to high heritability coupled with low genetic advance indicated the presence of non-additive gene action. Medium to high heritability is due to the favorable influence of environment rather than the genotypes. So, selection based on this trait will not be rewarding.

4.3.2.3 Fruit pH

Maximum value for fruit pH was 4.85 and minimum value was 3.65 with a grand mean of 4.02 (Table 30). The genotypic variance and phenotypic variance for this trait were 0.004 and 0.05 respectively (Table 30). 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 phenotypic coefficient of variation

Table 30. Estimation of genetic parameters of nine qualitative characters of twenty F2 tomatillo genotypes

Parameters	Leaf chlorophyll content	%Brix	Fruit pH	Vitamin C	Titratable acidity	Lycopene content (472)	Lycopene content (502)	Fruit moisture content	Fruit dry matter content
Maximum	84.25	7.59	4.85	21.09	1.05	1.1	1.06	98.28	12.22
Minimum	75.41	5.15	3.65	10.32	0.33	0.02	0.09	87.78	1.72
GM	79.61	6.1	4.02	17.11	0.69	0.33	0.34	93.36	6.63
σ2e	2.32	0.10	0.05	4.16	0.001	0.01	0.001	0.001	0.001
σ2g	1.94	0.13	0.004	1.08	0.012	0.03	0.03	2.45	2.45
σ2p	4.27	0.24	0.05	5.24	0.013	0.04	0.031	2.451	2.451
ECV	1.91	5.28	5.8	11.91	1.23	1.05	4.3	0.04	0.03
GCV	1.75	6.01	1.61	6.08	15.74	53.705	57.38	1.67	23.61
PCV	2.59	8.00	6.05	13.38	15.74	53.70	57.38	1.679	23.61
H^2B	0.45	0.56	0.07	0.20	0.70	0.65	0.54	0.40	0.25
GA	1.93	0.57	0.03	0.97	0.22	0.36	0.40	3.22	3.22
GA % (mean)	2.43	9.30	0.88	5.70	32.43	110.63	118.21	3.45	48.65
SEM	0.88	0.18	0.13	1.17	0.20	0.11	0.12	0.06	0.06
CD (5%)	2.52	0.53	0.38	3.37	0.15	0.06	0.09	0.07	0.07
CD (1%)	3.37	0.72	0.51	4.51	0.22	0.14	0.12	0.11	0.11

Here, GM= Grand mean; σ^2g= Genotypic variance; σ2e= environmental variance; σ2p= phenotypic variance; GCV= genotypic coefficient of variation; ECV=Environmental coefficient of variation, PCV= Phenotypic coefficient of variation, GA= genetic advance; SEM=Standard error of mean, CD= Critical differences.

(PCV) and genotypic coefficient of variation (GCV) of fruit pH was low (6.05 and 1.61, respectively). Phenotypic coefficient of variation (6.76) was higher than the genotypic coefficient of variation (4.69) suggested that the appeared variation is not only due to the genotypes but also due to the favorable influences of environment. Fruit pH showed low heritability (7%) and low in genetic advance (0.03) (Table 30). Low heritability coupled with low genetic advance revealed this trait is heritable in next generation affected by environment rather than genetically. So, the selection will not be rewarded for this character. Thiyagu *et al.* (2013) found high heritability, but Shashikanth et al. (2008) found low heritability and low genetic advance in tomato.

4.3.2.4 Vitamin C

Maximum vitamin C among twenty F_2 tomatillo genotypes was 21.09 and the minimum was recorded 10.32 with grand mean 17.11 (Table 30). The phenotypic variance (5.24) was higher than the genotypic variance (1.08). 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 and phenotypic co-efficient of variation were 6.08 and 13.38, respectively (Table 30), higher phenotypic value 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 vitamin C.

The heritability estimates for this trait was low (20%), genetic advance was also low (0.97) and genetic advance in per cent of mean (5.70%) (Table 30) were found low, revealed that this trait was highly governed by environmental effects and selection will not be rewarded.

4.3.2.5 Titratable acidity

Titratable acidity performed maximum and minimum value was 1.05 days and 0.33 respectively with a grand mean of 0.69 (Table 30). The genotypic variance and phenotypic variance for this trait were 0.012 and 0.013 respectively (Table 30). The phenotypic variance appeared to be little high than the genotypic variance suggested influence of environment. on the expression of genes controlling this trait. The genotypic co-efficient of variation (GCV) (15.74) and phenotypic co-efficient of

variation (PCV) (15.74) were more or less like each other, indicated presence of negligible variability in this trait (Table 30). Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for titratable acidity were high (70%) with low genetic advance (0.22) and in percentage of mean of genetic advance was (32.43%). Thus, indicating this trait was mostly controlled by non-additive gene.

4.3.2.6 Lycopene content (472)

Maximum lycopene content was found 1.10 and minimum was 0.02 with grand mean value 0.33 lycopene content (Table 30). The genotypic variance and phenotypic variance for this trait were 0.03 and 0.04, respectively. The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low (53.705 and 53.70 respectively). The phenotypic variance appeared to be similar with the genotypic variance. The heritability was found 65% for this trait was high with low genetic advance (0.36) and genetic advance in per cent of mean (110.63%), indicating this character was controlled by non-additive genes. High heritability is due to favorable influence of environment rather than genetically influence. Singh *et al.* (2000) and Kumar *et al.* (2000) support the finding.

4.3.2.7 Lycopene content (502)

Maximum lycopene content (502) was found 1.06 and minimum was 0.09 with grand mean value 0.34 lycopene content (502) (Table 30). The genotypic variance and phenotypic variance for this trait were 0.03 and 0.031, respectively. The phenotypic variance appeared to be almost similar with the genotypic variance suggested considerable influence of genetically and environmental on the expression of genes controlling this trait. Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low (57.38 and 57.38, respectively) (Table 30). The phenotypic variance appeared to be similar with the genotypic variance. The heritability was found 54% for this trait was high with low genetic advance (0.40) and genetic advance in per cent of mean (118.21%), indicating this character was controlled by non-additive genes. High heritability is due to

favorable influence of environment rather than genetically influence. Singh *et al.* (2000) and Kumar *et al.* (2000) support the finding.

4.3.2.8 Fruit moisture content

The maximum fruit moisture content was recorded 98.28 and the minimum fruit length was recorded 87.78. The grand mean of fruit moisture content was noticed as 93.36. (Table 30). The genotypic variance was 2.45 which was low and phenotypic variance was 2.451 which was also low. Genotypic co-efficient of variation (1.67) and phenotypic co-efficient variation (1.679) were close to each other (Table 30), indicating minor environmental influence on this character that would be effective for the improvement of this crop. Low heritability estimates (40%) with low genetic advance (3.22) over percent of mean (3.45%) (Table 30) indicate that effective selection may not be made for fruit length. The character was governed by non-additive gene action. Moderate heritability and moderate genetic gain for this character was observed by Joshi *et al.* (2004) which was not supporting these results.

4.3.2.9 Fruit Dry matter content

The grand mean of fruit dry matter content was recorded 6.63 with maximum 12.22 and minimum 1.72 (Table 30). The phenotypic variance was 2.451 which was low and genotypic variance was 2.45 which was also low. Genotypic co-efficient of variation (23.61) and phenotypic co-efficient variation (23.61) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement for the tomatillo crop. Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character which does not support the present study. Low heritability estimated (25%) with low genetic advance (3.22) over moderate percent of mean was 48.65%, indicated that effective selection may not be made for fruit dry matter content. The character was highly governed by environment effects.

4.3.3 Correlation Co-efficient

Determination of correlation co-efficient was provided the information how dry matter depends on different quality characters. Correlation co-efficient studies along with path analysis provide a better understanding of the association of different

characters with dry matter content. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). Genotypic and phenotypic correlation coefficients among different pairs quality contributing characters for twenty F_2 genotypes of tomatillo are given in Table 31 and 32.

4.3.3.1 Leaf chlorophyll content

Leaf chlorophyll content had non-significant positive correlation with dry matter content (0.25) at genotypic level and non-significant positive correlation (0.17) at phenotypic levels (Table 31 and Table 32). Leaf chlorophyll content had also significant positive correlation with brix % (1.13 **), vitamin C (0.46*) at genotypic level, and significant positive (0.51**), correlation with brix % at phenotypic level. It had also positive non-significant correlation with lycopene content (472) at genotypic level and phenotypic level. It had also negative non-significant correlation with titratable acidity, lycopene content (502) and fruit moisture content at both the level.

4.3.3.2 Brix %

Brix % had non-significant positive correlation with dry matter content (0.24) at genotypic level and non-significant positive correlation (0.18) at phenotypic levels (Table 31 and Table 32). Brix % had also significant positive correlation with vitamin C (0.46*) at genotypic level. It had also positive non-significant correlation with fruit pH (0.07) and vitamin C (0.13) phenotypic level. It had also negative non-significant correlation with titratable acidity, both lycopene content and fruit moisture content at both genotypic and phenotypic level.

4.3.2.3 Fruit pH

Fruit pH had significant negative correlation with dry matter content (-0.53*) at genotypic level and non-significant negative correlation (-0.14) at phenotypic levels (Table 31 and Table 32). Fruit pH had also non-significant positive correlation with fruit moisture content (0.53*), at genotypic level. It had also positive non-significant correlation with vitamin C (0.28) and lycopene content (0.06) at genotypic level. It had also negative non-significant correlation with titratable acidity, lycopene content (502) at both genotypic and phenotypic level.

Table 31. Genotypic correlation coefficient among different pairs of nine qualitative characters of twenty F2 tomatillo genotypes

Characters	Leaf chlorophyll content	%Brix	Fruit pH	Vitamin C	Titratable acidity	Lycopene content (472)	Lycopene content (502)	Fruit moisture content	Fruit dry matter content
Leaf chlorophyll content	1 **	1.13**	-0.08 ^{NS}	0.46*	-0.02^{NS}	0.002 ^{NS}	-0.05 ^{NS}	-0.25 ^{NS}	0.25 ^{NS}
%Brix		1 **	-0.13^{NS}	0.46*	-0.25^{NS}	-0.07 ^{NS}	-0.10 ^{NS}	-0.24 ^{NS}	0.24 ^{NS}
Fruit pH			1 **	0.28^{NS}	-0.04^{NS}	0.06 ^{NS}	-0.15 ^{NS}	0.53 *	-0.53 *
Vitamin C				1 **	-0.27 ^{NS}	-0.16 ^{NS}	-0.15 ^{NS}	0.02 ^{NS}	-0.02 ^{NS}
Titratable acidity					1 **	0.26 ^{NS}	0.25 ^{NS}	-0.13 ^{NS}	0.13 ^{NS}
Lycopene content 472						1 **	0.91 **	-0.36 ^{NS}	0.36 ^{NS}
Lycopene content 502							1 **	-0.45 *	0.45 *
Fruit moisture								1 **	-1 **
Fruit dry matter									1 **

Table 32. Phenotypic correlation coefficient among different pairs of nine qualitative characters of twenty F2 tomatillo genotypes

Characters	Leaf chlorophyll content	%Brix	Fruit pH	Vitamin C	Titratable acidity	Lycopene content (472)	Lycopene content (502)	Fruit moisture content	Fruit dry matter content
Leaf chlorophyll content	1 **	0.51 **	0.04^{NS}	0.10 ^{NS}	-0.01 ^{NS}	0.001 ^{NS}	-0.04^{NS}	-0.17^{NS}	0.17^{NS}
%brix		1 **	0.07^{NS}	0.13 ^{NS}	-0.18 ^{NS}	-0.05 ^{NS}	-0.08^{NS}	-0.18^{NS}	0.18^{NS}
Fruit pH			1 **	0.05 ^{NS}	-0.01 ^{NS}	0.018 ^{NS}	-0.04 ^{NS}	0.14^{NS}	-0.14^{NS}
Vitamin C				1 **	-0.12 ^{NS}	-0.07 ^{NS}	-0.07^{NS}	0.01 ^{NS}	-0.01^{NS}
Titratable acidity					1 **	0.26 *	0.25*	-0.13^{NS}	0.13^{NS}
Lycopene content 472						1 **	0.91 **	-0.36 **	0.36**
Lycopene content 502							1 **	-0.45 **	0.45 **
Fruit moisture								1 **	-1 **
Fruit dry matter									1 **

4.3.3.4 Vitamin C

Vitamin C had non-significant negative correlation with dry matter content (-0.02) at genotypic level and non-significant negative correlation (-0.01) at phenotypic levels (Table 31 and Table 32). Vitamin C had also non-significant positive correlation with fruit moisture content (0.02 and 0.01) at genotypic and phenotypic level respectively. It had also negative non-significant correlation with titratable acidity, lycopene content at phenotypic level. It had also negative non-significant correlation with titratable acidity, lycopene content (472 and 502) at phenotypic level.

4.3.3.5 Titratable acidity

Titratable acidity had non-significant positive correlation with dry matter content (0.13) at genotypic level and non-significant positive correlation (0.13) at phenotypic levels (Table 31 and Table 32). Titratable acidity had also non-significant positive correlation with lycopene content at 472 and 502 absorbent at genotypic and significant positive correlation with phenotypic level. It had also negative non-significant correlation with fruit moisture content at genotypic and phenotypic level.

4.3.3.6 Lycopene content (472)

Lycopene content (472) had non-significant positive correlation with dry matter content (0.36) at genotypic level and significant positive correlation (0.36**) at phenotypic levels (Table 31 and Table 32). Lycopene content (472) had also significant positive correlation with lycopene content (502) (0.91**) at genotypic and phenotypic level. It had also negative significant correlation with fruit moisture content (0.36**) at genotypic and phenotypic level.

4.3.3.7 Lycopene content (502)

Lycopene content (502) had significant positive correlation with dry matter content (0.45*) at genotypic level and significant positive correlation (0.45**) at phenotypic levels (Table 31 and Table 32). Lycopene content (502) had also significant negative correlation with fruit moisture content (-0.45**) at genotypic and phenotypic level.

4.3.3.8 Fruit moisture content

Fruit moisture content had significant negative correlation with dry matter content (-1**) at genotypic level and significant negative correlation (-1**) at phenotypic levels (Table 31 and Table 32).

4.3.4 Path coefficient analysis

To get a clear picture of the inter–relationship between yield and other yield attributes, direct and indirect effects of yield contributing characters were worked out by using path analysis at genotypic level which also measured the relative importance of each component. Here dry matter content was considered as effect (dependent variable) and all other quality parameter were treated as causal (independent) variables. Path coefficient analysis was showed direct and indirect effects of different characters on dry matter content of tomatillo in Table 33.

4.3.4.1 Leaf chlorophyll content

Leaf chlorophyll content had negative direct effect (-0.11) on fruit dry matter content (Table 33) which contributed to result non-significant positive genotypic correlation with fruit dry matter content (0.25). It also showed positive indirect effect with brix %, lycopene content (472) and fruit moisture content. It had also negative indirect effect on fruit pH, vitamin C, tritatable acidity and lycopene content (502).

4.3.4.2 Brix %

Brix % had positive direct effect (0.68) on fruit dry matter content (Table 33) which contributed to result non-significant positive genotypic correlation with fruit dry matter content (0.24). It showed positive indirect effect with fruit moisture content. It had also negative indirect effect on leaf chlorophyll content, fruit pH, vitamin C, titratable acidity, lycopene content (472) and lycopene content (502).

4.3.4.3 Fruit pH

Fruit pH had positive direct effect (0.35) on fruit dry matter content (Table 33) which contributed to result significant negative genotypic correlation with fruit dry matter content (-0.53*). It also showed positive indirect effect with leaf chlorophyll content,

Table 33. Genotypic path coefficient analysis showing the direct (bold) and indirect effect of nine qualitative traits of twenty F2 generations of tomatillo

Characters	**Leaf chlorophyll content**	**%Brix**	**Fruit pH**	**Vitamin C**	**Titratable acidity**	**Lycopene content (472)**	**Lycopene content (502)**	**Fruit moisture content**	**Genotypic correlation with fruit dry matter**
Leaf chlorophyll content	**-0.11**	0.77	-0.03	-0.21	-0.48	-0.39	0.55	0.27	0.25 ^{NS}
%Brix	-0.13	**0.68**	-0.05	-0.21	-0.12	-0.07	-0.05	0.08	0.24 ^{NS}
Fruit pH	0.01	-0.09	**0.35**	-0.13	-0.02	0.12	0.05	0.54	-0.53 *
Vitamin C	-0.05	0.31	0.10	**-0.45**	-0.15	0.44	-0.48	-0.26	-0.02 ^{NS}
Titratable acidity	-0.08	0.12	0.01	-0.10	**0.68**	0.10	-0.79	-0.01	0.13 ^{NS}
Lycopene content 472	-0.09	0.10	-0.08	0.39	0.14	**0.51**	-0.93	0.39	0.36 ^{NS}
Lycopene content 502	-0.06	-0.03	0.01	0.20	0.49	0.42	**-1.10**	-0.11	0.45 *
Fruit moisture	0.04	-0.07	-0.25	-0.16	-0.01	0.26	0.16	**0.75**	-1 **

lycopene content (both absorbent) and fruit moisture content. It had also negative indirect effect on brix %, vitamin C and titratable acidity.

4.3.4.4 Vitamin C

Vitamin C had negative direct effect (-0.45) on fruit dry matter content (Table 33) which contributed to result non-significant negative genotypic correlation with fruit dry matter content (-0.02). It also showed positive indirect effect with brix %, Fruit pH and lycopene content (472). It had also negative indirect effect on leaf chlorophyll content, vitamin C and titratable acidity, lycopene content (502) and fruit moisture content.

4.3.4.5 Titratable acidity

Titratable acidity had positive direct effect (0.68) on fruit dry matter content (Table 33) which contributed to result non-significant positive genotypic correlation with fruit dry matter content (0.13). It also showed positive indirect effect with brix %, fruit pH and lycopene content 472. It had also negative indirect effect on leaf chlorophyll content, vitamin C, lycopene content (502) and fruit moisture content.

4.3.4.6 Lycopene content (472)

Lycopene content (472) had positive direct effect (0.51) on fruit dry matter content (Table 33) which contributed to result non-significant positive genotypic correlation with fruit dry matter content (0.36). It also showed positive indirect effect with brix %, vitamin C, titratable acidity and fruit moisture content. It had also negative indirect effect on leaf chlorophyll content, fruit pH and lycopene content (502).

4.3.4.7 Lycopene content (502)

Lycopene content (502) had negative direct effect (-1.10) on fruit dry matter content (Table 33) which contributed to result significant positive genotypic correlation with fruit dry matter content (0.45*). It also showed positive indirect effect with fruit pH, vitamin C, titratable acidity, and lycopene content (472). It had also negative indirect effect on leaf chlorophyll content, brix % and fruit moisture content.

4.3.4.8 Fruit moisture content

Fruit moisture content had positive direct effect (0.75) on fruit dry matter content (Table 33) which contributed to result significant negative genotypic correlation with fruit dry matter content (-1*). It also showed positive indirect effect with leaf chlorophyll content, lycopene content (472) and lycopene content (472). It had also negative indirect effect on brix % , fruit pH, vitamin C and titratable acidity.

4.3.5 Selection index

Selection index with ranking the morphological characters and ranking the genotypes has been presented in Table 34 and Table 35. Based on the value presented in table 39, the most important characters were leaf chlorophyll content (1.94) followed by vitamin C (0.98), moisture content (0.68) and % brix (0.58). The least important character for selection index was lycopene content (0.02) followed by titratable acidity (0.03).

Based on the first three high ranked characters, the total selection scores for each of the genotypes were estimated (Table 35). The highest selection score was found in G1×G3 (18.719) having ranked 1, followed by G3×G1 (17.409) with rank 2. The lowest ranked genotype was found in G4×G1 (14.893) with rank of 20 followed by G2 ×G1 (15.010) having ranked 19 (Table 35).

Table 34. Ranking the qualitative characters for selecting the better genotypes

Characters	b value	GA	Rank
Leaf chlorophyll content	0.46	1.94	1
Vitamin C	0.21	0.98	2
Moisture content	-0.25	0.68	3
%Brix	0.56	0.58	4
Dry matter	-0.18	0.47	5
Lycopene content (472)	-0.12	0.04	6
Fruit pH	0.07	0.04	7
Titratatble acidity	-0.14	0.03	8
Lycopene content (502)	-0.07	0.02	9

Table 35. Ranking the genotypes based on the selection scores

Genotypes	Selection Scores	Ranking
G1 × G2	16.643	5
G1 × G3	18.719	1
G1 × G4	15.884	10
G1 × G5	15.839	11
G2 × G1	15.010	19
G2 × G3	15.537	16
G2 × G4	15.566	14
G2 × G5	16.739	4
G3 × G1	17.409	2
G3 × G2	15.677	13
G3 × G4	15.095	18
G3 × G5	16.873	3
G4 × G1	14.893	20
G4 × G2	15.719	12
G4 × G3	16.198	8
G4 × G5	15.552	15
G5 × G1	16.470	6
G5 × G2	16.224	7
G5 × G3	15.299	17
G5 × G4	16.193	9

CHAPTER V
SUMMARY AND CONCLUSION

The present investigation comprised of four experiments conducted in three years during the period from 2017 to 2020. Among them three were field experiments and one was laboratory experiment with twenty populations of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.). The first field experiment was associated with variability assessment and the rest two field experiments were related to hybridization program. The researches were done to address the major issues, like: (i) assessment of genetic variability and cross ability in tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.) genotypes. (ii) determination of the heterosis and combining ability of parents and their crosses for yield and yield contributing characters by diallel analysis and (iii) To know the nature of association of traits, direct and indirect relation between yield and yield contributing characters (iv) Selection of superior genotypes in F_2 generation.

Genetic parameters were estimated among the morphological and yield contributing characters, plant height, number of branches per plant, leaf area index, days to first flowering, days to fifty percent flowering, days to maturity, number of fruits per plant, fruits length, fruit diameter, Individual fruit weight, seeds per fruits, yield per plant, yield per plot and yield per hectare were studied.

Significant differences were found among the tested materials for most of the characters. Univariate analysis was performed through mean, range, genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance, genetic advance in percentage of mean, standard error, F- ratio and coefficient of variation for fourteen quantitative characters.

Significant differences were observed among the genotypes for plant height. The highest plant height was observed in G1 (90.11cm) and the lowest was observed in G3 (82.88 cm). The phenotypic variance (9.83) was higher than genotypic variance (8.33). The phenotypic coefficient of variation (3.65) and the genotypic coefficient of variation (3.36) indicated presence of considerable variability among the genotypes.

The high heritability (85%) with considerable genetic advance (5.47) indicated the effectiveness for selection.

The maximum leaf area index was found in G1 (22.06 cm^2) and the minimum in G4 (16.70 cm^2) with significant differences. The phenotypic variance (5.99) was higher than genotypic variance (3.51) which indicated that the environment had a great influence for the expression of this trait. The phenotypic and genotypic coefficient of variation was 12.87 and 9.85, respectively. So the breeders should go for the high heritability for these traits to make improvement. Low heritability (59%) with considerable low genetic advance (2.95) indicated that this trait might be taken into consideration while selecting a suitable line. Number of branches per plant ranged from 11.27 in G3 to 10.43 in G5. The phenotypic variance (0.24) was considerably higher than genotypic variance (0.05) indicated environment had a great influence for the expression of no. of branches per plant. The existence of inherent variability among the genotype with possibility of high potential for selection were due to the moderate genotypic (2.06) and phenotypic coefficient of variation (4.45). Moderate heritability (21%) coupled with low genetic advance (0.21) in percentage of mean (1.97) exposed the action of both additive and non-additive gene effect on the expression of this character as well as scope of improvement through selection. Days to first flowering ranged from 36.08 days in G5 to 30.39 days in G2. The longest days to 50% flowering were observed in G4 (54.82 days) and the shortest was observed in G1 (50.62 days). The genotypic variance and phenotypic variance for this trait were 2.14 and 4.76, respectively. GCV and PCV were found low with medium heritability and low GA and per cent of mean (3.88%), indicating this character was controlled by non-additive genes. Days to first maturity ranged from G4 (82.33 days) to G3 (83.30 days). The genotypic variance (1.08) was lower than phenotypic (3.03) variance. Genotypic co-efficient of variation (1.23) and phenotypic co-efficient of variation (2.06) were also close to each other indicated less influence of environmental factors on expression of this character. Therefore, selection based on upon phenotypic expression of this character could be effective for the improvement of this crop. The heritability estimates for this trait was high (93%). In contrast genetic advance (1.27) and genetic advance in per cent of mean (1.51%) were found low, indicated that this trait was controlled by non-additive genes.

Number of fruits per plant ranged from G1 (30.10) to G5 (27.72). Maximum fruit length was found in G3 (28.23cm) and minimum was found in G4 (20.09cm). High heritability estimates (76%) with low genetic advance (5.36) over percent of mean (22.70%) indicated that effective selection may not be made. Maximum fruit diameter was found in G3 (33.15) and minimum was found in G4 (25.40cm). Genotypic co-efficient of variation (16.40) and phenotypic co-efficient variation (18.38) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement for the tomatillo crop. High heritability estimate (80%) with low genetic advance (8.19) over moderate percent of mean was 30.15%, indicated that effective selection may not be made for fruit length.Individual fruit weight ranges from G1 (23.11gm) to G2 (20.65gm). Number of seeds per fruit was found in G3 (395.33) with lowest in G4 (349.67). Genotypic variance was found 277.33, on the other hand phenotypic variance was observed 434.16 which was very high. Medium heritability(52%) coupled with high genetic advance(22.48) indicated the presence of additive gene action. Yield per plant was varied from 740.67 gm to 424.67gm found in G3 and G4, respectively. The phenotypic variance (17739.57) found higher than genotypic variance (16467.42), suggested considerable influence of environment on the expression of the genes controlling this character.Very high heritability (93%) for fruit yield per plant with high genetic advance (254.69%) and high genetic advance of % mean (42.54%) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding program.

The highest yield/ha was found in G3 (61.71 ton) and lowest yield was recorded in G4 (35.32 ton). The genotypic variance and phenotypic variance for this important parameter were 114.67 and 123.52 respectively. 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 phenotypic coefficient of variation and genotypic coefficient of variation of yield was high 22.29 and 21.48, respectively. Phenotypic coefficient of variation (22.29) was higher than the genotypic coefficient of variation (21.48) suggested that the appeared variation was not only due to the genotypes but also due to the favorable influences of environment. However, the differences between the PCV and GCV were very low which indicated that environmental influence was minor on the expression of the genes controlling this

trait. Very high heritability (93%) coupled with high genetic advance (21.25) indicated the presence of additive gene action. So, selection based on yield (t/h) will be effective and provides opportunity for selecting high valued genotypes for future breeding program.

Relationship between yield and yield contributing characters was studied through analysis of correlation between them. The significant positive correlation with yield /ha was found in number of fruits per plant, fruit length, fruit diameter, seeds per plant, yield per plant, yield per plot and negative significant relation with days to 50% flowering at genotypic and phenotypic level.

The path coefficient analysis was performed to determine the direct and indirect influence considering fourteen characters. It was revealed that plant height, leaf area index, number of branches per plant, days to first flowering, days to maturity, number of fruits per plant, fruit length, fruit diameter, individual fruit weight and yield per plot had the positive direct effect on yield per hectare whereas days to 50% flowering, seeds per fruit and yield per plant had negative direct effect on yield per yield /ha. The path coefficient studies indicated that plant height, leaf area index, number of branches per plant, days to first flowering, days to maturity, number of fruits per plant, fruit length, fruit diameter, individual fruit weight and yield per plot were the most important contributors to final yield/ha which could be taken in consideration for future hybridization program.

Cross ability analysis was showed significant in year 1, and non significant in year 2 and year 3. In year year1, highest success rate was observed in G4xG3 (76.66%) followed by G1×G3 (73.33%), G2xG1 (73.33%), G2xG4 (73.33%). In year 2, highest success rate of different cross combination were found in G4xG1 (71.66%) in crossing year-2, followed by G3xG2 (70%), G1xG3 (68.33%), G2xG4 (68.33%), G3xG1 (66.66%), and in crossing year-3, highest success rate of different cross combination were found in G1xG2 (68.33%), G3xG1 (68.33%) and G4xG1 (68.33%), followed by G1xG3 (66.66%), G4xG3 (66.66%) and G2xG3 (65%). The lowest success rate of crosses in Year-3 was found in crosses G3xG5 (50.00%).

The percent of heterosis varied from character to character or from cross to cross.The analysis of variance for genotypes i.e., parents and crosses showed significant difference for all the characters studied. For germination %, among the twenty cross

combinations 11 crosses showed positive heterobeltosis for germination % and 9 crosses showed negative heterobeltosis. The highest significant positive heterosis was observed in the cross G3×G1 (13.49%). The highest negative heterosis was observed in G2×G4 (-8.72%). Plant height showed highest positive heterosis effect was observed in the cross G2×G1 (6.16%). Seven crosses showed positive heterobeltosis for plant height and 13 crosses showed negative heterobeltosis. For leaf area index, among the twenty cross combinations 4 crosses showed positive heterobeltosis for leaf area index and 16 crosses showed negative heterosis over better parent. The highest positive and negative heterosis was observed in G4×G5 (2.61%) and G4×G1 (-16.64%), rspectively. The highest positively and negative heterosis was observed in G2×G4 (6.31%) and G1×G3 (-9.86%), respectively over the better parent. Among the twenty cross combinations 19 crosses showed positive heterosis over better parent for days to maturity and 1 cross showed negative heterosis over better parent. Among the twenty cross combinations four crosses showed positive heterobeltosis and 16 crosses showed negative heterobeltosis for yield per ha. Heterosis for this character ranged from -31.49% to 19.35% with mean -12.13%. The highest negative heterosis was observed in G4×G2 (-31.49%). The highest positive heterosis effect was observed in the cross G1×G3 (19.35%). Six crosses showed positive heterosis over mid parent and 14 of them showed negative heterosis. The highest significant negative heterosis was observed in the cross G4×G2 (-23.62%). Among 20 crosses 18 hybrids showed negative heterosis in standard check and 2 crosses found positive heterosis. Minimum standard heterosis was found in cross G2×G4 (-29.04%) and maximum standard heterosis was found in G1×G3 (19.35%) with mean -15.83% for yield per ha.

Mean squares due to general and specific combining ability were highly significant for most of the characters. These significant variations indicated that the additive and non-additive gene action played predominant role for the expression of these characters. The estimated components of SCA variance (σ2s) were higher than the GCA variance (σ2g) for all the traits, indicated predominance of non-additive gene action over the additive gene action in their inheritance.

The ratio of GCA and SCA variances were found less than unity for all of the characters except leaf area index which revealed predominance of non-additive (dominant) gene action over the additive gene action for those characters.

The GCA effects revealed the best general combiner was, for the trait germination % parent G3, for plant height parent G4, for leaf area index parent G1, for no. of branches per plant parent G5, for days to first flowering parent G2, for days to 50% flowering parent G4 , for days to maturity parent G1, for number of fruits per plant G1, for fruit length parent G1, for fruit diameter parent G1, for individual fruit weight parent G1, for seeds per fruit parent G5, for yield per plant parent G1, for yield per plot parent G1, for yield/ha parent G1. Parents with good GCA for a particular trait associated with large adaptability indicated additive type of gene action. Additive variance was fixable, and therefore, selection for these traits governed by additive variance was very effective.

The significant SCA effects were found for yield contributing traits. The highest positive significant effect was for G1×G3 (5.79**) and the lowest positive significant effect was G4×G5 (1.42*) for plant height. Out of 20 cross combinations 8 crosses showed significant positive SCA effects for yield per ha. The highest positive significant effect was G3×G1 (11.51**) and the lower positive significant effect was found in G3×G4 (2.30*). Thus these 8 crosses were good specific combiner for these traits. The cross G3×G1 was the best specific combiner. Seven crosses showed significant negative SCA effects. The highest negative significant effect was G1×G4 (-8.90**) and the lowest negative significant effect was G2×G5 (-2.55*).

The components of genetic variations along with the derived genetic ratios for different morphological and yield contributing characters showed that the D (additive) and H (non-additive) components were significant for all the traits under studied except number of branches per plant suggesting the importance of both additive and dominance components for the inheritance of all traits in tomatillo. The H2 represents the dominance deviation due to relative frequency of positive and negative genes were significant for all the characters. The net dominance effect h2 expressed as the algebraic sum over all loci in the homozygous conditions in all the crosses, was highly significant for all the studied characters. This implied that substantial contribution dominance effects were due to the heterozygosity of the loci in all the characters. The result showed that characters including plant height, and fruit length possessed negative effects indicating the mean direction of dominance as well as important of excess of recessive genes in the expression of these traits. On the hand, the remaining characters exhibited the values in positive direction implying the mean

direction as well as important of excess dominant genes in the expression of these traits. The environmental component "E" exhibited highly significant values for all characters studied indicating the influence of environmental factors in the expression of those traits. However, the magnitude of E for each character was much less compared to their respecting D and H1 suggesting the characters were influenced less by environment.

The average degree of dominance as indicated by the (H1/D) 0.5 was more than unity suggesting that over dominance was operating in the expression for most of the components of yield. The ratio of (H2/4H1) provides an estimate of the average frequency of positive and negative alleles in all the parents.

Relationship between yield and yield contributing characters was studied through analysis of correlation between them. The significant positive correlation with yield /ha was found with germination % (0.50*), Plant height (1.00*), leaf area index (0.92**), number of branches per plant (0.86**), number of fruits per plant (0.93**), fruit length(0.92**), fruit diameter (0.80**), individual fruit weight (0.89**) seeds per fruit (0.84**), yield per plant (1**), yield per plot (1**) and negative significant relation with days to first flowering (-0.71**), days to 50% flowering (-0. 91**), days to maturity (-0.71**) at genotypic level. At phenotypic level , significant positive correlation with yield /ha was found with germination % (0.35*), Plant height (0.66**), leaf area index (0.60**), number of branches per plant (0.53**), number of fruits per plant (0.72**), fruit length(0.63**), fruit diameter (0.58**), individual fruit weight (0.79**) seeds per fruit (0.60**), yield per plant (1**), yield per plot (0.99**) and negative significant relation with days to first flowering (-0.40**), days to 50% flowering (-0. 56**), days to maturity (-0.31**).

The path coefficient analysis was performed to determine the direct and indirect influence considering fourteen characters. It was revealed that plant height, leaf area index, days to 50% flowering, fruit diameter, yield per plant had the positive direct effect on yield per hectare whereas, germination %, number of branches per plant, days to first flowering, days to maturity, number of fruits per plant, fruit length, individual fruit weight, seeds per fruit and yield per plot had negative direct effect on yield per yield /ha. The path coefficient studies indicated that Plant height, leaf area index, days to 50% flowering, fruit diameter, yield per plant were the most important

contributors to final yield/ha which could be taken in consideration for future hybridization program.

Based on the value of morphological characters, selection index and ranked, the most important characters were yield per plant (159.01) followed by no. of seeds per fruits (47.45), yield per ha (13.25) and plant height (3.97). The least important character for selection index was no. of branches per plant (1.03), days to maturity (1.26) and leaf area index (1.48). The highest selection score was found in G1 × G3 (1065.57) having ranked 1 followed by G1 × G2 (1032.15) with rank 2. The lowest ranked genotype was found in G2 × G4 (701.66) with rank of 20 followed by G4× G2 (725.09) having ranked 19.

In terms of **quality matters** of nine parameters showed highly significant variation among twenty F2 tomatillo genotypes were recorded. Highest leaf chlorophyll content (83.88) was observed in G1×G3 and lowest leaf chlorophyll content was observed in G4×G1 (77.58). Highest brix percentage (7.46) was observed in G1×G3 and lowest brix percentage was observed in G5×G3 (5.80). The highest fruit pH index was found in G2×G5 (4.42) and the lowest fruit pH was observed in G1×G2 (3.84) with average value of 4.02. The highest Vitamin C was found in G1×G3 (20.08) and the lowest vitamin C was observed in G2×G1 (14.27). The highest titratable acidity was found in G3×G1 (0.81) and the lowest titratable acidity was observed in G2×G1 (0.59). The highest lycopene content (472) was found in G2×G3 (0.49) and the lowest lycopene content (472) was observed in G1×G5 (0.18). The highest lycopene content (502) was found in G2×G3 (0.44) and the lowest lycopene content (502)was observed in G4×G1 (0.18). The highest fruit moisture content was found in G4×G1 (94.77) and the lowest fruit moisture content was observed in G2×G3 (92.66) with average value of 93.37. The highest fruit dry matter content was found in G2×G3 (7.39) and the lowest fruit dry matter content was observed in G4×G1 (5.23) with average value of 6.63.

The extent of variation among the genotypes in respect of nine quality characters were 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) were recorded.

Relationship between fruit dry matter content and other quality parameter was studied through analysis of correlation between them. The significant correlation was found in fruit pH, lycopene content (502) and fruit moisture content at genotypic level and in lycopene content (472), lycopene content (502) and fruit moisture content at phenotypic level.

The path coefficient analysis was performed to determine the direct and indirect influence considering fourteen characters. It was revealed that % brix, fruit pH, titratable acidity, lycopene content (472), fruit moisture content had the positive direct effect on fruit dry matter content. Whereas, leaf chlorophyll content, vitamine C, lycopene content (502) had negative direct effect on fruit dry matter content.

Based on the selection value the most important characters were leaf chlorophyll content (1.94) followed by vitamin C (0.98), moisture content (0.68) and % Brix (0.58). The least important character for selection index was lycopene content (0.02) followed by titratable acidity (0.03). Based on the first three high ranked characters, the total selection scores for each of the genotypes were estimated. The highest selection score was found in G1×G3 (18.719) having ranked 1 followed by G3×G1 (17.409) with rank 2. The lowest ranked genotype was found in G4×G1 (14.893) with rank of 20 followed by G2×G1 (15.010) having ranked 19.

On the basis of the present studies, it can be concluded, based on characterization, evaluation and statistical analysis wide range of genetic diversity for morphological traits was observed among twenty genotypes of tomatillo (*Physalis ixocarpa* Brot./*Physalis philadelphica* Lam.). Combining ability study (F1) indicated that both additive and non-additive genetic components were important in the control of different morphological and yield related characters in which non-additive gene actions was predominant for most of the characters. The parent G1 was the best general combiner for leaf area index, days to maturity, number of fruits per plant, fruit length, fruit diameter, individual fruit weight, yield per plant, yield per plot and yield per ha. On the other hand, parents G3 was for germination %, parent G4 was for plant height, days to 50% flowering and parent G5 for number of branches per plant, seeds per fruit best general combiner.For genetic analysis, the cross G1 × G3 deserved attention for their heterotic response to plant height, individual fruit weight, seeds per fruit, yield per ha related characteristics.Genetic analysis in F1, F2 also showed that

both additive and non- additive gene actions were found to be important with predominance of additive gene action in the inheritance of all morphological traits.The Vr, Wr graph for good combiner parent G1 possessed an excess of recessive genes for related characteristics and had equal proportion of dominant and recessive genes for yield per ha in F1generations. Another good combiner parent G3 possessed equal proportion of dominant and recessive genes for morphological characteristic and exhibited abundant number of recessive genes for yield and yield contributing attributes in F1, indicated parents with recessive genes could be also contributed towards high yield/ha.Partial dominant or over-dominant gene action was involved for all the characters in all three generations. Parents with recessive genes could also be contributed towards high yield/ha.Among all crosses, the best crosses revealed by the SCA effects were if yield/ha is the most important selection criterion, G3×G1 was the best specific combiner. Highest selection score was found in G1 × G3 (18.719) having ranked 1.The ranks of parental dominance would be as follows: G5 > G4 > G1 > G2 > G3 in the increasing order for the trait yield per ha.

The following recommendations could be considered to develop and promote tomatillo (*Physalis ixocarpa*Brot./*Physalis philadelphica* Lam.). Findings of distinct grouping of genotypes could be an effective way and used for future research in developing improved varieties. It could be suggested for evaluating tomatillo genotypes with effective techniques like morphological as well as quality study to explore and measure the genetic diversity. More research might be done to support and precise the present findings of long-lasting tomatillo varieties. More hybridization program might be carried out to develop higher yielding tomatillo varieties.

REFERENCES

Abak, K., Güler, H.Y., Sari, N.Z.M. and Paksoy, M. (1994). Earliness and yield of *Physalis* (*P. ixocarpa* Brot. and *P. peruviana* L.) in greenhouse, low tunnel and open field. *Acta horticulturae*. **366**(37): 301-306.

Abedin, J. and Khan, S. H. (1986). Study of the morphogenetic divergence in tomato. *Bangladesh J. Agric. Res*. **11**(1): 39-47.

Aditya, P.M. and Phir, K. (1995). Studied on genetic variability in tomato. *Progr. Hort*. **32**(2): 172-182.

Agong, S.G., Schittenhelm, S. and Friedt, W. (2001). Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* L.) germplasm. *J. Food Technol. Africa*. **6**(1): 13-17.

Ahmad, S. (2002). Genetics of fruit set and related traits in tomato under hot-humid conditions. Ph.D. Thesis. BSMRAU. Gazipur, Bangladesh.

Ahmed, S., Quamruzzaman, A.K.M. and Uddin, M.N. (2011). Estimate of heterosis in tomato (*Solanum lycopersicum* L.). *Bangladesh J. Agric. Res.* **36**(3): 521-527.

Ahmed, S.U., Shaha, H.K. and Sharfuddin, A.F.M. (1988). Study of heterosis and correlation in tomato. *Thai J. Agric. Sci*. **21**(2): 117-123.

Akanbi, C.T., Adeyemi, R.S. and Ojo, A. (2006). Drying characteristics and sorption isotherm of tomato slices. *J. Food Eng*. **73**(2): 141-146.

Akanda, S.I. and Mundt, C.C. (1996) Path coefficient analysis of the effects of strip rust and cultivar mixtures on yield and yield components of winter wheat. *Theory Applied Genetics.* **92**: 666-672.

Alafita-Vásquez, G.. Hernández-Barrios, M., Teoba-Domínguez, S., Zulueta-Rodríguez, R.. Hernández-Montiel, L., Alemán-Chávez, I. and Lara-Capistrán, L. (2021). Economic profitability analysis of husk tomato (Physalis ixocarpa Brot. ex Hornem.) under different silicon dioxide concentrations. *Agro productividad.* https://doi.org/ 10.32854/agrop.v14i10.2002.

Alam, K.S., Ishrat, E., Zaman, M.Y. and Habib, M.A. (2012) Comparative karyotype and RAPD analysis for characterizing three varieties of (*Solanum lycopersicum* L.). *Bangladesh J. Bot.* **41**(2): 149-154.

Alda, L.M., Gogoasa, I., Bordean, D.M., Gergen, I., Alda, S., Moldovan, C. and Nita, L. (2009). Lycopene content of tomatoes and tomato products. *J. Agroalimentary Processes techonol*. **15**(4): 540-42.

Al-Daej, M.I. (2014). Line×tester analysis of heterosis and combining ability in tomato (*Lycopersicon esculentum* Mill.) fruit quality traits. *Pakistan J. Biol. Sci.* **21** (5): 224-231.

Allard, R. W. (1960). Principles of plant breeding. John Wiley and Song. Inc. New York, USA. pp. 1-485.

Alvarez, M. (1985). Evaluation of tomato hybrids in summer. Heterosis for Morphological characteristics and fruit weight. *Cultivars-Tropicals*. **7**(1): 37-45.

Angadi, A. and Dharmatti, P.R. (2012). Combining ability studies for processing quality traits in tomato (*Solanum lycopersicum* L.). *Res. J. Agric. Sci*. **3** (5): 1083-1085.

Anita, S., Gautam, J.P.S., Upadhyay, M. and Joshi, A. (2005). Heterosis for yield and quality characters in tomato. *Crop Res. Hissar*. **29**(2): 285-287.

Anonymous. (2011). www.faostat.fao.org, FAO Static Division. Rome, Italy.

Anonymous.(2015).http://www.biodiversitylibrary.org/page/358204#page/6/mode/1up and International Plant Name Index. (1753). Sp. Pl. 1:185.

Antunes, L.E.C., Gonçalves, E.D., Ristow, N.C., Carpenedo, S. and Trevisan, R. (2008). Fenologia, produção e qualidade de frutos de mirtilo. *Pesq. Agropec. Bras*. **43**: 1011-1015.

Ara, A.R., Narayan, N and Khan, S.H., (2009). Genetic variability and selection parameters for yield and quality attributes in tomato. *Indian J. Hort*. **66**: 73-78.

Arun, J., Kohil, U.K. and Joshi, A. (2003). Genetic divergence for quantitative and qualitative traits in tomato (*Lycopersicon esculentum* Mill.). *Indian J. Agric. Sci*. **73**(2): 110-113.

Badr, A., Khalifa, S., Aboel, I. and Abou, M. (1997). Chromosomal criteria and taxonomic relationships in the Solanaceae. *Cytologia*. **62**: 103-113.

Bai, N.R. and Devi, D.S. (1991). Study on genetic parameters in tomato hybrids. *Orissa J. Agric. Res.* **4**: 27-29.

Bhatt, R.P., Biswas, V.R. and Kumar, N. (2001). Heterosis, combining ability and genetics for vitamin C, total soluble solids and yield in tomato (*Lycopersicon esculentum*) at 1700m altitude. *J. Agri. Sci*. **137**(2): 71-75.

Bhatt, R.P., Biswas, V.R., Pandey, H.K., Verma, G.S. and Kumar, N. (1998). Heterosis for vitamin C in tomato (*Lycopersicon esculentum* Mill.). *Indian J. Agril. Sci.* **68**(3): 176-178.

Bhavna, M. and Patel, A.I., (2014). Combining ability study in tomato (*Lycopersicon esculentum* Mill.). *Trends Biosci.* **7**: 245-256.

Bhuiyan, M.S.R. (1982). Heterosis and Combining ability in tomato (*Lycopersicon esculentum* Mill.). MS Thesis, BAU, Mymensingh, Bangladesh.

Bodunde, J.G. (2002). Path co-efficient and correlation studies in tomato (*Lycopersicon esculentum* Mill.). *Moor J. Agric. Res*. **3**(2): 195-198.

Borguini, R.G. Bastos, D.H.M., Neto, J.M., Capasso, F.S. and Torres, E. (2013). Antioxidant potential of tomatoes cultivated in organic and conventional systems. *Brazilian Arch. Bio. Technol*. **56**(4): 521-529.

Bradbury, L.M.T., Shumskaya, M., Tzfadia, O., Wu, S.B., Kennelly, E.J. and Wurtzel, E.T. (2012). Lycopene cyclase paralog CruP protects against reactive oxygen species in oxygenic photosynthetic organisms. *Proc. Natl. Acad. Sci. USA:* **109**(27): 1888-1897.

Branzati, E.C. and Manaresi, L. (1980). L'alchechengi. *Frutticoltura*. **42**(59): 3-4.

Brar, G.S., Singh, S., Chima, D.S. and Dhariwal, M.S. (2000). Studies on variability, heritability, genetic advance for yield and components characters in tomato (*Lycopersicon esculentum* MilL). *J. Res. Punjab Agric. Univ*. **37** (3-4): 190-193.

Buckseth, T., Sharma, K.M. and Thakur, K.S. (2012). Genetic diversity and path analysis in tomato (*Solanum lycopersicum* L.). *Veg. Sci*. **39**(2): 221-223.

Bukun, B., Uygur, F., Nezihi, S., Turkmen, N. and Duzenli, A. (2002). A New Record for the Flora of Turkey: *Physalis philadelphica* Lam. var. maculata Waterf. (Solanaceae). *Turkish J. Botany*. **26**(5): 405-407.

Burdick, A. (1954). Genetics of Heterosis for earliness in the tomato. *Genetics*. **39**: 488- 505.

Burton, G.W. (1952). Quantitative interaction in grasses. **In**: Proc.6th Inter. Grassland Congr. **1**: 277-283.

Cantwell, M, Flores, M.J. and Trejo, G.A. (1992). Developmental changes and postharvest physiology of tomatillos fruits (*Physalis ixocarpa* L.). *Scientia Hort.* **50**: 59-70.

Carter, N and Deane, D. (2008). Tomatillo: a green sourpuss with a sweet side. Los Angeles Times. Retrieved 3 August 2009.

Cequea, A.C. (2000). Cytogenetic analysis of the artificial tetraploid *Lycopersicon esculentum* var cerasiforme. *Ciencia*. **8**(2): 119-126.

Chadha, S., Vidyasagar and Kumar, J. (1997). Combining ability and gene action studies in tomato involving important bacterial wilt resistant lines. *Himachal J. Agric. Res*. **23**(1 -2): 26-32.

Chandrasekhar, P. and Rao, M.R. (1989). Studies on combining ability of certain characters in tomato. *South Indian Hort.* **37**(1): 10-12.

Chattopadhyay, A. and Paul, A. (2012). Studies on heterosis in tomato (*Solanum lycopersicum* L.). *Intl. J. Bio-Res.* **3**(3): 278.

Chaudhury, R.C. and Khanna, K.R. (1972). Exploitation of heterosis in tomato yield and components. *South Indian Hort*. **20**: 59-65.

Cheema, D.S., Kumar, D. and Kaur. R. (2003). Diallel analysis for combining ability involving heat tolerant lines of tomato (*Lycopersicon esculentum* Mill). *Crop-Improvement.* **30**(1): 39-44.

Chen, J., Wang, H., Shen, H.L., Chai, M., Li, .J.S., Qi, M.F. and Yang, W.C. (2009). Genetic variation in tomato populations from four breeding programs revealed by single nucleotide polymorphism and simple sequence repeat markers. *Sci. Hort.* **122**: 6-16.

Coffey,T. (1993). The History and Folklore of North American Wild Flowers. Facts on File, New York, NY. ISBN 0-8160-2624-6

Comstock, R.E. and Robinson, H.F. (1952). Genetic Parameters their estimation and significance. Proc. of 6th Intl. Grassland Congr. **1**: 128-291.

Cucu, T. and Loco, J.V. (2011). Assessment of dietary intake of lycopene by the Belgian adult population. Wetenschappelijk Instituut Volksgezondheid and Institut Scientifique De Sante Publique. J. Wytsmanstraat 14, 1050 Brussels, Belgium.

Das, B., Hazarika, M.H. and Das, P.K. (1998). Genetic variability and correlation in fruit characters of tomato (*Lycopersicon esculantum* Mill.). *Ann. Agril. Res*. **19**(1): 77-80.

Daskalof, Yordanov, C.M. and Ognyanova, A. (1967). Heterosis in tomatoes. *Academy Press, Sofia*. p. 180.

Datta, M, Taylor, M.L. and Frizzell, B. (2013). Dietary and serum lycopene levels in prostate cancer patients undergoing intensity-modulated radiation therapy. *J. Medicinal-Food*. **16**(12): 1131-1137.

Davis, A.R., Fish, W.W. and Veazie, P. (2003). A rapid spectrophotometric method for analyzing lycopene content in tomato and tomato products. *Postharvest-Biol. Technol*. **28**(3): 425-430.

Deb, B. (1979). Solanaceae in India. **In**: The biology and taxonomy of solanaceae. J. Hawkes, R. Lester and A. Skelding, (eds.). Academicpress, London. pp: 3-48.

Deshmukh, S.N.N. , Basu, M.S. , Reddy, P.S. (1986). Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut. Indian J. Agric. Sci., 56 (1986), pp. 816-821

Dev, H., Rattan, R.S. and Thakur, M.C. (1994). Heterosis in tomato *(Lycopersicon esculentum* Mill.). *Hort. J.* **7**(2): 125-132.

Deway, D.R. and Lu, K.N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *J. Agron*. **51**: 515-518.

Dhaliwal, M.S., Singh, S., and Cheema, D.S. (2002). Estimating combining ability effects of the genetic male sterile lines of tomato for their use in hybrid breeding. *J. Genet. Breed*. **54**(3): 199-205.

Dhaliwal, M.S., Singh, S., Cheema, D.S. and Singh, P. (2004). Genetic analysis for important fruit characters of tomato by involving lines possessing male sterility genes. *Acta Hort*. **637**: 123-131.

Dhankar, S.K., Dhankar, B.S. and Sharma, N.K. (2001) Correlation and path analysis in tomato under normal and high temperature conditions. *Haryana J .Hort. Sci.* **30**(1-2): 89-92.

Dhankhar, S.K. and Dhankar, S.S. (2006). Variability, heritability, correlation and path coefficient studies in tomato. *Haryana J. Hort. Sci*. **35**(1&2): 179-181.

Diamante, L. M., Ihns, R., Savage, G.P. and Vanhanen, L. (2010). A new mathematical model for thin layer drying of fruits. *Intl. J. Food Sci Technol*. **45**: 1956-1962.

Diaz-Perez J., Phatak S.C., Giddings D., Bertrand D. and Mills H.A. (2015). Root zone temperature, plant growth and fruit yield of tomatillo as affected by plastic film mulch. *Hort. Sci*. **40**(5): 1312-1319.

Digby, P. Galway, N. and Lane, P. (1989). GENESTST 5: A Second Course. Oxford Science Publications, Oxford. p. 103-108.

Dod, V.N. and Kale, P.B. (1992). Heterosis for certain quality traits in tomato (*Lycopersicon esculentum* Mill.). *Crop Res.* **5**(2): 302-308.

Dod, V.N., Kale, P.B. and Wankhade, R.V. (1995). Combining ability for certain quality traits in tomato. *Crop Res. Hisar.* **9**(3): 407-412.

Domini, M.R. and Maya, C. (1997). Correlation and path coefficient estimates of different tomato seedlings stage. *Cult. Trop*. **18**(3): 63-65.

Dong, L., Shion, H., Davis, R.G., Terry-Penak, B., Castro-Perez, J., van Breemen, R. B. (2010). Collision cross-section determination and tandem mass spectrometric analysis of isomeric carotenoids using electrospray ion mobility time-of-flight mass spectrometry. *Anal. Chem*. **82**: 9014-9021.

Dremann, C.G. (1985). Ground cherries, husk tomatoes and tomatillos, Redwood City Seed Co., Redwood City, CA. USA.

Dudi, B.S. and Kalloo, G. (1982). Correlation and path analysis studies in tomato. *Haryana J. Hort. Sci***. 11**: 122-126.

Dudi, B.S., Dixit, J. and Partap, P.S. (1983). Components of variability, heritability and genetic advance studies in tomato (*Lycopersicum esculentum* Mil1.). *Haryana Agric.Univ. J. Res*. **13**: 135-139.

Dufera, J.T. (2013). Evaluation of agronomic performance and lycopene variation in Tomato (*Lycopersicon esculantum* Mill.) genotypes in Mizan, southwestern Ethiopia. *World App. Sci. J.* **27**(11): 1450-1454.

Duhan, D., Partap, P.S., Rana, M.K. and Dahiya, M.S. (2005). Heterosis study for quality characters in a line x tester set of tomato. *Haryana J. Hort. Sci*. **34:** 371-375.

Duke, J.A. and Ayensu, E.S. (1985). Medicinal plants of China. Reference publications Inc. MI. ISBN 0-917256-20-4.

EI-Mahdy, I., E-Metwally, G., EI-Fadly and Mazrouh, A.Y. (1990). Inheritance of yield and fruit setting quality of some tomato crosses grown under heat stress conditions in Egypt. *J. Agril. Res. Tanta Univ.* **16**(3): 517-526.

El Sheikha, A.F. (2004). Technological, chemical and microbiological studies on some packed foods. M.S. Thesis, Minufiya University, Egypt.

EL Sheikha, A.F., Zaki, Bakr, A.A., El Habashy, M.M. and Montet, D. (2008). Physico-chemical properties and biochemical composition of *Physalis* (*Physalis pubescens* L.) fruits. *Glob. Sci*. **2**: 124-130.

Elumalai, M, Karthika, B, Usha, V. (2013). Lycopene - role in cancer prevention. *Intl. J. Pharma. Bio-Sci.* **4**(3): 371-378.

Falconer, D.S. (1981). Introduction to Quantitative Genetics. Longman Inc. Ltd., New York. USA. p. 340.

Farzane, A., Nemati, H., Arouiee, H. and Kakhki, A.M. (2013). The estimate of heterosis and combining ability of some morphological characters in tomato transplants (*Lycopersicon esculentum* M.). *Intl. J. Farm Allied Sci.* **2**: 290-295.

Fernandes, R.B. (1974). Sur I'identification d'une espece de Physalis souspontanee au Portugal. *Bol. Soc. Brot.* **44**: 343-366.

Filippone, P.T. (2014). Tomato History - The history of tomatoes as food. Once considered poisonous. The tomato is now a favorite food. Home Cooking Expert.(http://homecooking.about.com/od/foodhistory/a/tomatohistory.htm.

Fouqué, A. (1972). Espèces fruitièresd'Amériquetropicale. *Fruits*. **27**(1): 62-72.

Freyre, R. and Loy, J.B. (2000). Evaluation and yield trials of tomatillo in New Hampshire. *Hort. Technol*. **10**: 373-377.

Ganapathi, A., Sudhakaran, S. and Kulothungan, S. (1991). The diploid taxon in Indian natural populations of *Physalis* L. and its taxonomic significance. *Cytologia*. **56**: 283-288.

Gentilcore, D. (2010). A history of the tomato in Italy Pomodoro. New York, NY: Columbia University Press, ISBN 023115206X.

Gentry, J.J., and Arcy, W.G. (1986). Solanaceae of Mesoamerica. **In**: Solanaceae biology and systematics. W.G. D'Arcy, (ed.). Columbia Univ. Press, New York, USA. pp. 2-26

Ghosh, P.K. Syamal, M.M. and Rath, S. (1997). Heterosis studies in tomato. *J. Maharasthra Agril. Univ.* **19**(1): 83-85.

Godekar, D.A., Dhanukshe, B.L. and Patil, F.B. (1992). Studies on variability, heritability and genetic advance in tomato. *J. Maharasthra Agric. Univ*. **17**: 305-306.

Godina, F.R., Torres, V.R., Pournabav, R.F., Mendoza, A.B., Piñero, J.L.H., Valdes, M.H.R. and Vázquez, M.A.A. (2013). Yield and fruit quality evaluation in husk tomato autotetraploids (*Physalis ixocarpa*) and diploids. *Australian J. Crop Sci*.**7**(7): 933-940.

Golani, I.J., Mehta, D.R., Purohit, V.L., Pandya, H.M. and Kanzariya, M.V. (2007). Genetic variability, correlation and path coefficient studies in tomato. *Indian J. Agril. Res*. **41**(2): 146-149.

Gomez, K.A. and Gomez, A.A. (1984). Statistical procedures for agricultural research (2nd ed.). John wiley and sons, NewYork. p. 680.

González-Mendoza, D., Grimaldo-Juárez, O., Soto-Ortiz, R., Escoboza-Garcia, F. and Hernández, J.F.S. (2010). Evaluation of total phenolics, anthocyanins and antioxidant capacity in purple tomatillo (*Physalis ixocarpa* Brot.) genotypes. *African J. Biotechnol*. **9**(32): 5173-5176.

Gorbatenko, E.M. and Gorbatenko, I.Y.U. (1985). Path analysis of economically usefull characters in tomato. *Tsitologiya Genetica*. **19**(3): 206-210.

Gottschalk, W. (1954). Die chromosomenstruktur der solanaceae unter berucksichtigung phylogenetischer fragestellungen. *Chromosoma*. **6**: 539-626.

Grandillo, S. (2014). Introgression libraries with wild relatives of crops. **In**: Genomics of plant genetic resources. Springer. pp. 87-122.

Griffing, B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian J. Biol. Sci*. **9**: 463-493.

Gul, R., Hidayat, U.R., Khalil, I.H., Shah, M.A. and Ghafoor, A. (2010). Heterosis for flower and fruit traits in tomato (*Lycopersicon escuantum* Mill). *African J. Biotecnol.* **9**(27): 4144-4151.

Gunasekera, D.M. and Parera, A.L.T. (1999). Production and genetic evalution of tomato hybrids using the diallel genetic design. *Tropical Agril. Res.* **11**: 123-133.

Gwag, J.G., Dixit, A., Park, Y.J., Ma, K.H., Kwon, S.J., Cho, G.T., Lee, G.A., Lee, S.Y., Kang, H.K. and Lee, S.H. (2010). Assessment of genetic diversity and population structure in mungbean. *Genes Genom*. **32**: 299-308.

Hailu, A. , Alamerew, S. , Nigussie, M, and Assefa, E. (2016). Correlation and Path Coefficient Analysis of Yield and Yield Associated Traits in Barley (*Hordeum vulgare* L.) Germplasm. *Adv. Crop Sci. Technol*. **4**(2): 2-7.

Hallmann, E, Rembiakowska, E. (2007). Comparison of the nutritive quality of tomato fruits from organic and conventional production in Poland. Improving-sustainability in organic and low input food production systems. Extended summary, Proc. 3rd Int. Congr. of the European Integrated Project Quality Low Input Food (QLIF). University of Hohenheim, Germany, March 20 – 23, 2007. 131-134.

Hamm, S.R. (1985). Profile: consumption and production of the U.S. vegetable industry. **In**: Proc. of analyzing the potential for alternative fruit and vegetable crop production seminar. E. Estes, (ed.). North Carolina Agr. Res. Serv and Tennessee Valley Authority. pp: 4-13.

Hannan, M.M., Ahmed, M.B., Razvy, R., Karim, R., Khatun, M., Haydar, A., Hossain, M. and Roy, U.K. (2007). Heterosis and correlation of yield and yield components in tomato (*Lycopersicon esculentum* Mill.). *American-Eurasian J. Sci. Res.* **2**(2): 146-150.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies on yield in segregating population of Korean Lespedeza. *Agron. J*. **48**: 268-272.

Harer, P.N., Lad, D.B. and Bhor, T.J. (2002). Correlation and path analysis studies in tomato. *J. Maharashtra Agric.Univ*. **27**(3): 302-303.

Hayes, H.K. (1952). Development of the heterosis concept. **In**: Heterosis. *J.W. Gowen, (ed.).* Iowa State College Press. Iowa, America.

Hayman, B.I. (1954a). The theory and analysis of diallel crosses. *Genetics*. **39**: 789-809.

Hudson, W.D. (1986). Relationships of domesticated and wild *Physalis philadelphica*. **In**: Solanaceae, Biology and Systematics. W.G. D'Arcy, (ed.). Columbia Univ. Press, New York. pp. 416-432.

Husaini, H. and Iwo, G. (1990). Cytomorphological studies in some weedy species of the family Solanaceae from Jos Plateau, Nigeria. *Feddes Report*. **101**: 41-47.

Islam, M.R., Ahmad, S. and Rahman, M.M. (2012). Heterosis and qualitative attributes in winter tomato (*Solanum lycopersicum* L.) hybrids. *Bangladesh J. Agril. Res.* **37**(1): 39-48.

Islam, M.S. and Khan, S. (1991). Variability and character association in tomato (*Lycopersicon esculentum* Mill). *Bangladesh J. Plant Breed. Genet*. **4**(1-2): 49-53.

Islam, P., Prakash, S. and Singh, A.K. (1996). Variability studies in tomato (*Lycopersicon esculentum* Mill). *Bangladesh J. Plant Breed. Genet*. **4**(1-2): 49-53.

Izge, A. U. and Garba, Y. M. (2012). Combining ability for fruit worm resistance in some commercially grown tomatoes in parts of north eastern Nigeria. *Int. J. Agric. Sci*., **2**(8): 240- 244.

Jamwal, R.S., Pattan, R.S. and Saini, S.S. (1984). Hybrid vigour and combining ability in tomato. *South Indian Hort*. **32**(2): 69-74.

Jinks, J.L. (1954). The analysis of continuous variation in a diallel crosses of *Nicotiana rustica* varieties. *Genetics*. **39**: 767-788.

Jinks, J.L. (1956). The F_2 and backcross generations from a set of diallel crosses. *Heredity.* **10**: 1-30.

Johansen, K. (2017). Tomatillos: Fruits with benefits. The Roanoke Times. Retrieved October.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 477-483.

Jones, R.A., Scott, S.J., (1983). Improvement of tomato flavor by genetically increasing sugar and acid contents. *Euphytica* **32**: 845-855.

Joshi, A., Vikram, A. and Thakur, M.C. (2004) Studies on genetic variability, correlation and path analysis for yield and physico- chemical traits in stomato (*Solanum lycopersicum* L.). *Progr. Hort*. **36**(1): 51-58.

Kasrawi, M. A. and Amr, A. S. (1990). Genotypic variation and correlation for quality characteristics in processing tomatoes. *J. Genet. Pl. Breed*. **44**: 85-99.

Khare, C.P. (2007). Indian medicinal plants: an illustrated dictionary. Springer (India) Pvt. Ltd. pp. 717-718.

Kindscher, K., Timmermann, B.N., Zhang, H., Gollapudi, R., Corbett, S., Samadi, A. and Cohen, M. (2012). Wild tomatillos (*Physalis* species) as food and medicine. *Planta Medica*. **78**(11): IL32.

Kinkade M.P. and Foolad, M.R. (2013). Validation and fine mapping of lyc12.1, a QTL for increaed tomato fruit lycopene content. *Theor. App. Genet*. **126**: 2163-2175.

Kirtikar, K. and Basu, B. (2008). Solanaceae (*Physalis*). **In**: Indian medicinal plants. **3**: 1766- 1767.

Kliphuis, E. and Wieffering, J. (1979). IOPB chromosome number reports LXIV. *Taxon.* **28**: 391-408.

Kumar, J. and Sinha, A. (1989). Influence of distributional pattern on the reproductive mechanism and recombination system of Solanaceous weeds. *Glimpses Cytogenet.* **2**: 62-67.

Kumar, M. and Dudi, B.S. (2011). Study of correlation for yield and quality characters in tomato (*Lycopersicon esculentum* Mill.). *Electronic J. Plant Breed*. **2**(3), 453-460.

Kumar, S. and Lal, G., (1988), Variability and correlation studies in tomato (*Lycopersicon esculentum* Mill.) under low temperature conditions. *Haryana J. Hort. Sci.* **17**: 261-264.

Kumar, S., Banerjee, M.K. and Pratap, P.S. (1995a). Studies on Heterosis for various characters in tomato. *Haryana J. Hort. Sci.* **24**(1): 54-60.

Kumar, S., Singh, T., Singh, B. and Singh, J.P. (2004). Studies on correlation coefficient and path analysis among the different characters including fruit

yield of tomato (*Lycopersicon esculentum* Mill.). *Plant Archives.* **4**(1): 191-193.

Kumar, V., Nandan, R., Srivastava, K., Sharma, S.K., Kumar, R. and Kuma, A. (2013). Genetic parameters and correlation study for yield and quality traits in tomato (*Solanum lycopersicum* L.). *Plant Archives*. **13**(1): 463-467.

Kumar, Y.K.H. Patil, S.S., Dharmatti, P.R., Byadagi, A.S., Kajjidoni, S.T. and Patil, R.H. (2009). Estimation of heterosis for tospovirus resistance in tomato. *Karnataka J. Agril. Sci.* **22**(5): 1073-1075.

Kumari, N., Srivastava, J.P., Shekhavat, A.K.S., Yadav, J.R. and Singh, B. (2007). Genetic variability and heritability of various traits in tomato (*Lycopersicon esculentum* Mill.). *Progr. Agric.* **7**(1-2): 80-83.

Kumari, N., Srivastava, J.P., Singh, B. and Deokaran. (2010). Heterotic expression for yield and its component in tomato (*Lycopersicon esculentum* Mill). *Ann. Hortic.* **3**(1): 98-101.

Kumari, S. and Sharma, M.K. (2011). Exploitation of heterosis for yield and its contributing traits in tomato (*Solanum lycopersicum* L.). *Intl. J. Farm Sci.* **1**(2): 45-55.

Kumari, S. and Sharma, M.K. (2012). Line × tester analysis to study combining ability effects in tomato (*Solanum lycopersicum* L.). *Veg. Sci*. **39**(1): 65-69.

Kurian, A., Peter, K.V. and Rajan, S. (2001). Heterosis for yield components and fruit characters in tomato. *J. Tropical Agric*. **39**(1): 5-8.

Lagos, T.C., Caetano, C.M., Vallejo, F.A., Muñoz, J.E., Criollo, H. and Olaya, C. (2005). Caracterización palinológica y viabilidad polínica de *Physalis peruviana* L. y *Physalis philadelphica* L am. *Agron. Colomb*. **23**: 55-61.

Lee, M. and Media, D. (2014). Do tomatoes have more vitamin C than oranges? (healthy eating.sfgate.com/tomatoes-vitamin-c-oranges-3711.html.

Liu, H.Y. Koike, S.T., Xu, D. and Li, R. (2011). First Report of Turnip mosaic virus in Tomatillo (*Physalis philadelphica*) in California. *Plant Disease.* **96**(2): 296.

Lush, J.L. (1943). Heritability of qualitative characters in farm animals. Proc. of 8th Cong. Genetics and Heriditasd Supplement. pp.356-375.

Lydia, G. and Rao, K. (1981). Spontaneous desynapsis in tomatillo (*Physalis ixocarpa* Brot.). *J. Cytol. Genet*. **16**: 197-201.

Lydia, G. and Rao, K. (1982). A new cytotype of *Physalis angulata* L. *Chromosome Information Service*. **32**: 3-4.

Mahalanobis, P.C. (1936). On the generalized distance in statistic. Proc. National acad. Sci. **2**: 79-85.

Mahapatra, A.S., Singh, A.K., Vani, V.M., Mishra, R., Kumar, H. and Rajkumar, B.V. (2013). Inter-relationship for various components and path coefficient analysis in tomato (*Lycopersicon esculentum* Mill). *Intl. J. Current Microbiology App. Sci.* **2**(9): 147-152.

Mahesh, D.K., Apte, Y.B. and Jadhav, B.B. (2006) Studies on genetic divergence in tomato (*Lycopersicon esculentum* Mill.). *Crop Res*. **32**(2): 401-402.

Mallik, A.K. (1985). Study on genetic parameters and character association of tomato. M.S. Thesis, BAU, Mymensingh.

Mamedov, M.I. and Engalychev, M.R. (2017). Morphological and reproductive features of *Physalis* spp. in temperate climate. *Veg. Crop. Russ.* **5**: 14-17.

Manivannan, K., Natarajan, J. and Irulappan, I. (2005). Correlation studies in tomato. *South Indian Hort*. **34**: 70-73.

Masabni, J. (2016). Easy gardening for Texas. Texas A and M University Press. ISBN 978-0972104975.

Mather, K. and Jinks, J.L. (1971). Biometrical genetics. 2nd Edition. Chapman and Hall, London.

Matin, K., and Kuddus, M. (2001). varietal resistance to bacterial wilt in tomato. *Plant Disease. Rep.* **60**: 120-123.

Mayavel, A., Balakrishnamurthy, G. and Natarajan, S. (2005). Variability and heritability studies in tomato hybrids. *South Indian Hort*. **53**(1-6): 262-266.

Maynard, D.N. (1993). Potential for commercial production of tomatillo in Florida. *Proc. Fla. State Hort. Soc.* **106**: 223-224.

McGorrin, R.J. and Gimelfarb, L. (1998). Comparison of flavor components in fresh and cooked tomatillo with red plum tomato. *Dev. Food Sci*. **40**: 295-313.

McKee, L.H. (1992) Personal communication. New Mexico State University, Las Cruces, New Mexico, USA.

Me Daniel, R.G. (1986). Biochemical and Physiological basis of heterosis. *Critical Rev. Plant Sci.* **4**(3): 227-246.

Medina Medrano, J.R., Almaraz Abarca, N., Gonzalez Elizondo, M.S., Uribe Soto, J.N., Gonzalez Valdez, L.S. and Herrera Arrieta, Y. (2015). Phenolic constituents and antioxidant properties of five wildspecies of *Physalis* (Solanaceae). *Bot. Studies*. **56**(1): 24.

Meena, O.P. and Bahadur, V (2015). Genetic associations analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicum* L.) germplasm under open field condition. *J. Agric. Sci.* **7**(3): 148-163.

Megha, U., Singh, J.P., Singh, A. and Joshi, A. (2006). Studies on genetic variability in tomato (*Solanum lycopersicum* L.). *Progr. Hort.* **3**(2): 463- 465.

Meisami-asl, E., Rafiee, S., Keyhani, A., Tabatabaeefar, A. (2010). Determination of suitable thin layer drying curve model for apple slices (variety-Golab). *POJ.* **3**(3): 103-108.

Mendelova, A, Fikselova, M, Mendel, L. (2013). Carotenoids and lycopene content in fresh and dried tomato fruits and tomato juice. Acta-Universitatis-Agriculturae-et-Silviculturae-Mendelianae-Brunensis. 61(5): 1329-1337.

Menzel, M.Y. (1951). The cytotaxonomy and genetics of *Physalis*. *Proc. American. Phil. Soc.* **95**: 132-183.

Menzel, M.Y. (1957). Cytotaxonomic studies of Florida coastal species of *Physalis*. *Yearbook American. Phil. Soc.* **1957**: 262-266.

Millar P.A., Williams J.C., Robinsen, H.F. and Comstock, R.E. (1958). Estimates of genotypic and environmental variance and covariance and their implication in selection. *Agron. J.* **50**: 126-131.

Miller, J.C. and Tanksley, S.D. (1990). RFLP analysis of phylogenetic relationships and genetic variation in the genus Lycopersicon. Theor. *Appl. Genet.* **80**: 437-448.

Mirshamssi, A., Farsi, M., Shahriari, F. and Nemati, H. (2006). Estimation of heterosis and combining ability for yield components and crossing method. *Agril. Sci. Technol.* **20**(3): 3-12.

Mittal, P. Prakash, S. and Singh, A.K. (1996). Variability studies in tomato (*Lycopersicon esculentum* Mill.) under sub-humid condition of Himachal pradesh. *South Ind. Hort*. **44**: 132-148.

Mohanty, B. K. (2003). Genetic variability, correlation and path coefficient studies in tomato. *Indian J. Agril. Res.* **37** (1): 68-71.

Mohanty, B.K., and Prusti, A.M. (2001). Analysis of genetic distance in tomato. *Res. Crops.* **2**(3): 382-385.

Moigrădean, D., Lăzureanu, A., Poiană, M.A., Gogoaşă, I., Hărmănescu, M. and Gergen, I. (2007). Sunlight influence of lycopene content in tomatoes varieties. *J. Agroalimentary Processes techonol*. 13(2): 369-72.

Monamodi, E.L., Lungu, D.M. and Fite, G.L. (2013). Analysis of fruit yield and its components in determinate tomato (Lycopersicon lycoperscicum) using correlation and path coefficient. *Bots. J. Agric. Appl. Sci*. **9**(1): 29-40.

Montes-Hernández, S. and Aguirre-Rivera, J.R. (1994). Neglected crops: 1492 from a different Perspective. **In**: Plant production and protection. J.E. Hernández-Bermejo and J. León, (eds.). Ser. 26. FAO, Rome. pp. 117-122

Morley Jones, R. (1965). Analysis of variance of the half diallel table. *Heredity*, **20**: 117-121.

Morton, J.F. (1987). Mexican husk tomato, *Physalis ixocarpa* Brot., *Physalis aequata* Jacq. **In**: Fruits of warm climates. J.F., Morton (ed.). Miami, Florida, USA. pp. 434-437.

Mulato-Brito, J., Peña-Lomelí, A., Sahagún-Castellanos, J., Villanueva-Verduzco, C. and López-Reynoso, J. (2007). Self-Compatibility inheritance in tomatillo (*Physalis Ixocarpa* Brot.). *Veg. Crops Res. Bulletin*. **67**(1): 17-24.

Naidu, D.Y. (1993). Study of segregating populations in tomato (*Solanum lycopersicum* L.). M.Sc. (Agril.) Thesis, UAS, Dharwad, India.

Nalla, M.K., Rana, M.K., Singh, S.J., Sinha, A.K., Reddy, P.K. and Mohapatra, P.P. (2014). Assessment of genetic diversity through D2 analysis in tomato (*Solanum lycopersicum* L.) *Intl. J. Innovation App. Studies*. **6**(3) 431-438.

Nandpuri, K.S., Singh, S. and Tarsem, L. (1974). Studies on the genetic variability and correlation of some economic characters in tomato. *J. Res. Punjab Agric. Univ*. **10**(3): 316-321.

Nardar, C.R., Muthukrishnan, C.R., Irulappan, I. and Shanmugusubramanian, A. (2007). Variability studies in tomato (*Solanum lycopersicum* L.). *South Indian Hort*. **28**: 123-127.

Narolia, R.K., Reddy, R.V., Sujatha, M. (2012). Genetic architecture of yield and quality in tomato (*Solanum lycopersicum*). *Agric. Sci. Digest*. **32**(4): 281-285.

Naumova, N., Nechaeva, T., Savenkov, O. and Fotev, Y. (2018). Yield and fruit properties of husk tomato (*Physalis phyladelphica*) cultivars grown in the open field in the South of West Siberia. *Horticulturae*. **5**(1): 19.

Naz, S., Zafrullah, A., Shahzadhi, K. and Munir, N. (2013). Assessment of genetic diversity within germplasm accessions in tomato using morphological and molecular markers. *J. Animal Plant Sci*. **23**(4): 1099-1106.

Nesgea, S., Krishnappa, K.S. and Raju, T.B. (2002). Correlation coefficient analysis in tomato. *Current Res. Univ. Agric. Sci*. **31**(7-8): 127-130.

Nessa, J., Rahman, L. and Alam, M.S. (2000). Comperative performance of ten genotypes of tomato in late planting. *Bangladesh J. Agric. Sci*. **27**(1): 121-124.

Nindo, C.I., Sun, T., Wang, S.W., Tang, J. and Powers, J.R. (2003;). Evaluation of drying technologies for retention of physical quality and antioxidants in asparagus (*Asparagus officinalis.* L.) *Lebensm-Wiss Technol*. **36**: 507-516.

Osuna, H.T.G., Escobedo, B.L., Torres, V.R., Benavides, M.A. and Godina, G.F.R. (2015). Germinación y micropropagación de tomate de cascara (*Physalis ixocarpa*) tetraploide. *Rev. Mexicana Ciencias Agríc*. **12**: 2301-2311.

Padda, D.S., Saibhi, M.S. and Singh, S. (2007). Genotypic and phenotypic variabilities and correlations in quality characters of tomato (*Solanum lycopersicum* L.). *Indian J. Agric. Sci*. **41**: 199-202.

Padma, E., Ravisankar, C. and Srinivasulu, R. (2002). Correlation and path coefficient studies in tomato (*Lycopersicon esculentum* Mill). *J. Res. ANGRAU.* **30**(4): 68-71.

Panchal, B.B., Patel, N.B., Patel, A.I., Tank, R.V. and Patel, H.B. (2016). Combining ability analysis for yield and its related traits in tomato (*Solanum lycopersicum* L.). *Adv. Life Sci*. **5**(1): 188-193.

Panda, R. and Rao, K. (1983). Spontaneous chromosome fragmentation in cape gooseberry (*Physalis peruviana* L.). *Cell Chromosome Res.* **6**: 9-10.

Pandey, C. (2005). Medicinal plants of Gujarat. Gujarat ecological educational and research foundation, Gujarat, India. p. 387.

Pandit, A., Rai, V. and Bal, S. (2010). Combining QTL mapping and transcriptome profiling of bulked RILs for identification of functional polymorphism for salt tolerance genes in rice (*Oryza sativa* L.). *Mol. Genet. Genomics.* **284**: 121-136.

Panthee, D.R., Labate, J.A., McGrath, M.T., Breksa, A.P. and Robertson, L.D. (2013). Genotype and environmental interaction for fruit quality traits in vintage tomato varieties. *Euphytica*. **193**(2): 169-182.

Parmar, C. and Kaushal, M. (1982). *Physalis minima*. **In**: Wild fruits. Kalyani Publishers; New Delhi, India. pp. 62-65

Parra, N.B., Pérez, J.O. and Fernández, J.H. (2014). Characterization and analysis of the genetic variability of sweet passion fruit (*Passiflora ligularis* Juss.) in Colombia using microsatellite markers. *Revista Brasileira de Fruticultura*. **36**: 586-597.

Pedrosa, A. (1999). Citogenetics of angiosperms collected in the state of Pernambuco-V. *Acta. Bot. Bras*. **13**(1): 49-60.

Peralta, I.E. and Spooner, D.M. (2001). Granule-bound starch synthase (GBSSI) gene phylogeny of wild tomatoes (*Solanum* L. section *Lycopersicon* (Mill.) Wettst. subsection *Lycopersicon*). *American. J. Bot*. **88**(10): 1888-1902.

Perez, J.C.D., Phatak, S.C., Giddings, D., Bertrand, D. and Mills, H.A. (2005).Root zone temperature, plant growth, and fruit yield of tomatillo asaffected by plastic film mulch. *Sci. Hort*. **40**: 1312-1319.

Peter, K.V. and Rai, B. (2012). Genetic divergence in tomato. *Indian J. Genet. Plant Breed.* **36**(3): 379-383.

Petersen, K.K., Willumsen, J. and Kaack, K. (1998). Composition and taste of tomatoes as affected by increased salinity and different salinity sources. *J. Hort. Sci.* **73**: 205-215.

Phongsomboon, P. and Intipunya, P. (2009). Comparative study on drying of osmotic treated carrot slices. *Asian J. Food Agro-Industry*. **2**(4): 448-456.

Phookan, D.B., Talukdar, P., Shadeque A. and chakravarty, B.K. (1998). Genetic variability and heritability in tomato (*Lycopersicon esculentum* Mill.) genotypes during summer season under plastic house condition. *Indian J. Agril Sci*. **68**(6): 304-306.

Pickett, A.A. (1993). Hybrid wheat – Results and Problems. Plant breeding 15. Berlin: Paul Parey Sc Publish. pp. 1-58.

Plata, E.M.de. (1984). Mexican Vegetarian Cooking. Inner Traditions/Bear. p. 17.

Pogan, E., Wcislo, H. and Jankun, A. (1989). Further studies in chromosome numbers of Polish angiosperms. *Acta biologica Cracoviensia.* **30**: 119-136.

Ponnusviamy, V. and Muthukrishnan, E.R. (2010). A study of inter and intra generation correlation coefficients in F2 and F3 generation of tomato. *South Indian Hort*. **25**: 39-43.

Porcelli, S. and Proto, M. (1991). *Physalis ixocarpa* Brot. -A new promising crop. *AGRIS*. **37**(6): 27-31.

Prasad, V.S.R. and Mathura, R. (1999). Genetic variability, components association and direct and indirect selection in some exotic tomato germplasm. *Indian J. Hort*. **56**(3): 262-266.

Prashanth, S.J. (2003). Genetic variability and divergence study in tomato (*Lycopersicon esculentum* Mill). M.S. (Agri.) Thesis, University of Agricultural Science, Dhanwad, India.

Premalakshme, V., Thangaraj, T., Veeraragavathatham, D. and Arumugam, T. (2005). Heterosis and combining ability in tomato (*Solanum lycopersicum* L.). *Veg. sci.* **32**(1): 47-50.

Premalakshme, V., Thangaraj, T., Veeraranathatham, D. and Arumagam, T. (2006). Heterosis and combining Ability analysis in tomato (*Solanum lycopersicom* Mill.). for yield and yield contributing traits. *Veg. Sci.* **33**(1): 5-9.

Pujari, C.V., Wagh, R.S. and Kale, P.N. (1995). Genetic variability and heritability in tomato. *J. Maharashtra Agric. Univ.* **20**(1): 15-17.

Quiros, F. (1984). Overview of the genetics and breeding of husk tomato. *Hort. Sci*. **19**: 872-874.

Raja-Rao, K.G. (1979). Morphology of the pachytene chromosomes of tomatillo (*Physalis ixocarpa* Brot.). *Indian Bot*. **2**: 209-213.

Ramirez, R.G., Bennett, A., McDonald, M.B. and Francis, D. (2005). Total antioxidant capacity of fruit and seeds from normal and enhanced lycopene tomato (*Lycopersicon esculentum* Mill.) genotypes. *Seed Tech*. **27**(1): 66-75.

Ramos D (1991) The safety of Chile salsas made with selected levels of tomatoes, vinegar and sugar using the water-bath canning process. M.S. Thesis, New Mexico State University, New Mexico, Mexico.

Rani, C.I., Muthuvel, I. and Veer, D. (2010). Correlation and path coefficient for yield components and quality traits in tomato (*Lycopersicon esculentum* Mill.). *Agric. Sci. Digest*. **30**(1): 11-14.

Rao, C.R. (1952). Advanced statistical methods in biometrics research, John Wiley and Sons, New York. pp. 357-369.

Rao, K. (1979). Morphology of the pachytene chromosomes of tomatillo (*Physalis ixocarpa* Brot.). *Indian J. Bot*. **2**: 209-213.

Rao, V.R. and Hodgkin, T. (2002). Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell Tissue Organ Cult*. **68**:1-19.

Reddy, B.R., Reddy, M.P., Begum, H. and Sunil, N. (2013). Genetic diversity studies in tomato (*Solanum lycopersicum* L.). *J. Agric. Vet. Sci*. **4**(4): 53-55.

Reddy, V.V.P. and Reddy, K.V. (1992). Studies in variability in tomato. *South Ind. Hort*. **40**: 257- 260.

Resende, L.V., Maluf, W.R., Resende, J.T.V., Gomes, L.A.A. (2000). Combining ability of oblong-fruit tomato breeding lines with different genetic controls and levels of tospovirus resistance. *Ciencia- e-Agrotecnologia.* **24**(3): 549-559.

Rood, S.B., Buzzel, R.I. and McDonald, M.D. (1988). Influence of temperature on heterosis in maize seedling growth. *Crop Sci*. **28**: 283-286.

Roy, D. (2000) Plant breeding analysis and exploitation of variation. Narosa Publishing House. New Delhi, India.

Roy, S.K. and Choudhury, B. (1972). Studies on Physiochemical characteristics of few varieties in relation to processing. *J. Food Sci. Technol.* **9**(3):151-153.

Saeed, A., Hasan, N., Shakeel, A., Saleem, M.F., Khan, N.H., Ziaf, K., Khan, R.A.M. and Saeed, N. (2014). Genetic analysis to find suitable parents for development of tomato hybrids. *Researcher.* **6**(6):77-82.

Saeed, A., Hayat, K., Khan, A.A., Iqbal, S. and Abbas, G. (2007). Assessment of genetic variability and heritability in *Lycopersicon esculentum* Mill. *Intl. J. Agric. Biol*. **9**(2): 375-377.

Salati, R., Shorey, M., Briggs, A., Calderon, J., Rojas, M.R., Chen, L.F. Gilbertson, R. L. and Palmieri, M. (2010). First Report of tomato yellow leaf curl virus infecting Tomato, Tomatillo, and Peppers in Guatemala. *Plant Disease*. **94** (4): 482.

Saleem, M.Y., Asghar, M., Ahsanul, M.H., Rafique, T., Kamran, A. and Khan, A. A. (2009). Genetic analysis to identify suitable parents for hybrid seed production in tomato (*Lycopersicon esculentum* Mill). *Pakistan J. Bot*. **41**(3): 1107-1116.

Saleem, M.Y., Iqbal, Q. and Asghar, M. (2013). Genetic variability, heritability, character association and path analysis in F1 hybrids of tomato. *Pakistan J. Agril. Sci*. **50**(4): 649-653.

Santiaguillo Hernandez, J.F. and Yáñez, S.B. (2009). Traditional use of *Physalis* species in México. *Revista de Geografía Agrícola*. **43**: 81-86.

Santiaguillo Hernandez, J.F., Santana, T.C. and Lomelí, A.P. (2004). Selection for fruit yield and quality from plant x plant crosses between husk tomato varieties. *Rev. Fitotec. Mex.* **27**(1): 85-91.

Sarangi, D, Sarkar, T.K., Roy, A.K., Jana, S.C., Chattopadhyay, T.K. (1989). Physio-chemical changes during growth of (*Physalis* sp.). *Progressive Hort*. **21**: 225-228.

Schulzova, V. and Hajslova, J. (2007). Biologically active compounds in tomatoes from various fertilisation systems. Intl. Congr. Eur. Integ. Project Quality. Uni. Hohenheim, Germany.144-147.

Schwarz, K. Resende, J.T., Preczenhak, A.P, Paula, J.T. Faria, M.V. and Dias, D.M. (2013). Agronomic performance and physico-chemical quality in tomato hybrids grown without guiding. *Hort. Brasileira*. **31**(3): 410-418.

Scott, J.W., Volin, R.B., Bryan, H.H. and Olson, S.M. (1986). Use of hybrids to develop heat tolerant tomato cultivars proceedings of the Florida State *Hort. Soc*. **99**: 311- 314.

Segantini, D.M., Leonel, S., Cunha, A.R.D., Ferraz, R.A. and Ripardo, A.K.S. (2014). Exigência térmica e produtividade da amoreira-preta em função das épocas de poda. *Rev. Bras. Fruticult*. **36**: 568-575.

Shankar, A., Reddy, R.V.S.K., Protap, M., Sujatha, M. (2013b). Combining ability and gene action studies for yield and yield contributing traits in tomato (*Solanum lycopersicum* L.). *Helix.* **6**: 431-435.

Sharma, S. A. (2014). Coaching learning: Perspectives on teaching and learning. Michigan Reading Journal 46(2), 57-74.

Sharma, D. and Sharma, H.R. **(**2013). Production and evaluation of tomato hybrids using diallel genetic design. *Indian J. Hort.* **70**(4): 531-537.

Sharma, S.K. and Rastogi, K.B. (1993). Evaluation of some tomato cultivars for seed production under mid hill condition of Himachal pradesh. *Annals. Agril. Res*. **14**(4): 494-496

Shashikanth, P., Das, K. and Mulal, K. (2010). Studies on tomato leaf curl virus. *Indian J. Virol.* **15**: 115-117.

Shashikanth, P., Das, K. and Mulal, K. (2010). Studies on tomato leaf curl virus. *Indian J. Virol*. **15**: 115-117.

Shende, V.D., Seth, T., Mukherjee, S. and Chattopadhyay, A. (2012). Breeding tomato (*Solanum lycopersicum*) for higher productivity and better processing qualities. *SABRAO J. Breed. Genet*. **44** (2): 302-321.

Sherif, T.H.I. and Hussein H.A. (1992). A genetic analysis of growth and yield characters in the tomato (*Lycopersicon esculentum* Mill.) under the heat stress of late summer in Upper Egypt. *Australian J. Agric. Sci*. **23**(2): 3-28.

Shravan, K., Biswash, C. and Mollik, P. (2004) Heterosis and inbreeding depression in tomato. *Utter Pradesh Indian J*. **60**: 139-144.

Shuaib, M., Alam, Z., Zahir, A., Waqar, A., Taufiq, A. and Ikhtiar, K. (2007). Characterization of wheat varieties by seed storage protein electrophoresis. *African. J. Biotechnol*. **6**: 497-500.

Shull, G.H. (1914). The genotype of maize. *America Nature*. **45**: 234.

Silva, P.F., Silva, A.C., Tavares, K.N. and Santos, D.P. (2012). Production and brix degrees' content of tomato irrigated with water of different saline concentrations. *Rev. Verde Agroe. Des. Sust*. **7**(4):85-89.

Simpson, J., Montes-Hernandez, S., Gutierrez-Campos, R. and Assad-Garcia, N. (1995). Herrera- Resources. Publication No. 7246

Singh, A.K. and Asati, B.S. (2011). Combining ability and heterosis studies in tomato under bacterial wilt condition. *Bangladesh J. Agric. Res*. **36**(2): 313-318.

Singh, B., Singh, S.K., Naresh, R.K., Singh, K.V., Bhatnagar, S.K. and Kumar, A. (2011). General combining ability analysis of yield and its contributing traits in tomato (*Solanum lycopersicum* L.). *Plant Archives*. **11**(1): 201- 204.

Singh, B.D. (2009). Plant Breeding principles and methods, Kalyani Publisher, New Delhi India.

Singh, D. (1993). Adaptive Significance of Female Physical Attractiveness: Role of Waist-to-Hip Ratio. Journal of Personality and Social Psychology, 65, 293-307.

Singh, D.B., Ahmed, N., Lal, S., Mirza, A., Sharma, O.C. and Pal, A.A. (2014). Variation in growth, production and quality attributes of *Physalis* species under temperate ecosystem. *Fruits*. 69: 31-40.

Singh, D.B., Ahmed, N., Mirza, A., Lal, S. and Pal, A.A. (2013). Introduction, characterisation and evaluation of husk tomato (*Physalis ixocarpa* Brot.) genotypes under temperate climate. *Indian J. Plant Genet. Resour*. **26**(3): 226-230.

Singh, D.N., Sahu, A. and Parida, A.K. (1997). Genetic variability and correlation studies in tomato (*Lycopersicon esculentum* Mill.). *Env. Ecol.* **15**(1) : 117-121.

Singh, J.K., Singh, J.P., Jain, S.K., Joshi, A. and Joshi, K. (2002). Studies on genetic variability and its importance in tomato (*Solanum lycopersicum* L.). *Progr. Hort*. **34**(1): 77-79.

Singh, J.P., Singh, A. and Joshi, A. (2005). Studies on genetic variability in tomato (*Lycopersicon esculentum* Mill.). *Progr. Hort*. **37**(2): 463-465.

Singh, P.K., Singh, B. and Pandey, S. (2006). Genetic variability and character association analysis in tomato. *Indian. J. Plant Genet. Resour*. 19(2): 196-199.

Singh, H. and Cheema, D.S. (2006). Correlation and path coefficient studies in tomato (*Lycopersicon esculentum* Mill.). *Haryana J. Hort. Sci*. **35**(1&2): 126-129.

Singh, R.K. and Choudhury, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci*. **12**(2): 151-156.

Singh, R.K. and Singh, V.K. (1993). Heterosis breeding in tomato (*Lycopersicon esculentum* Mill.). *Ann. Agric. Res.* **14**(4): 416-420.

Singh, R.R., Singh, J.P. and Singh, H.N. (1988). Genetic Divergence in tomato. *Indian J. Agric. Sci.* **50**(8): 591-594.

Singh, R. R. and Singh, H. N. (1980). Correlation Studies in tomato. Indian. J. Agric. Sci., 50(8):

Siviero, P., Spandei, L. and Zanotti, G. (2000). Valutazione del contenuto di licopene in ibridi di pomodoro da industria ëHPí (high pigment). *Inftore Agrario*. **12:** 83-87.

Small, E. (2011). Top 100 exotic food plants. CRC Press. pp. 117-20.

Smith, A.F. (1994). The Tomato in America: Early history, culture, and cookery. Columbia SC, USA: University of South Carolina Press.

Smith, R., Jimenez, M. and Cantwell, M. (1999). Tomatillo Production in California (Vegetable Production Series). Vegetable Research and Information Center, DANR (Division of Agriculture and Natural Resources). Publication No. 7246.

Sonone, A.H., More, D.C. and Thombre, M.V. (1986). Path analysis in tomato. *J. Maharashtra Agric. Univ*. **12**: 115-116.

Souza, L.M., Paterniani, M.E.A.G.Z., Melo, P.C.T. and Melo, A.M.T. (2012). Diallel cross among fresh market tomato inbreeding lines. *Hort. Brasileira*. **30**: 246-251.

Sprague, G.F. (1983). Heterosis in maize. Theory and practices. **In**: Heterosis, Reappraisal of Theory and practice. Monographs on Theoretical and Applied Genetics. R. Frannkel, (ed.). Springer-Verlag Berlin, Heidelberg, Germany.

Sprague, G.F. and Tatum, L.A. (1942) General vs Combining Ability in Single Crosses of Corn. Agronomy, 34, 923-932.

Srivastava, J.P., Singh, H., Srivastava, B.P. and Verma, H.P.S. (1998). Heterosis in relation to combining ability in tomato. *Vegetable. Sci*. **25**(1): 43-47.

Sullivan, J.R. (1984). Pollination biology of *Physalis viscosa* var. cinerascens (solanaceae*). American J. Bot*. **71**:815-820.

Supe, V.S. and Kale, P.B. (1992). Correlation and path analysis in tomato. *J. Maharashtra Agric. Univ*. **17**: 331-333.

Susic, Z., Pavlovic, N., Cvikic, D. and Rajicic, S.T. (2002). Studies of correlation between yield and fruit characteristics of (*Lycopersicon esculentum* Mill.) hybrids and their parental genotypes. *Acta Hort*. **579**: 163-166.

Tavares, P.Z., Ponce, O.V., Martínez, J.S. and Toledo, D.C. (2015). Diversity and genetic structure of the husk tomato (*Physalis philadelphica* L.) in Western Mexico. *Gen. Resour. Crop Evol*. **62**: 141-153.

Tee, E.S., Young, S.I., Ho, S.K. and Mizura, S.S. (1998). Determination of vitamin C in fresh fruits and vegetables using the dye-titration and micro-fluorometric methods. *Pertanika*. **11**(1): 39-44.

Tiwari, J.K. (2002). Correlation studies in tomato. *Haryana J. Hort. Sci*. **31**(1&2): 146-147.

Tiwari, A. and Lal, G. (2004). Studies on heterosis for quantitative and qualitative characters in tomato (*Lycopersicon esculentum* Mill.). *Progres. Hort.* **36**(1): 122-127.

Tiwari, J.K. (2002). Correlation studies in tomato. Haryana J. Hort. Sci. 31(1&2): 146-147.

Torres, V.R., Godina, F.R., Pournovab, R.F., Mendoza, A.B., Guzmán, G.H. and Valdes, M.H.R. (2011). Development of tomatillo (*Physalis ixocarpa* Brot.) autotetraploids and their chromosome and phenotypic characterization. *Breeding Sci*. **61**: 288-293.

Trevisani, N., Schmit, R., De Melo, R.C.D., Meirelles, C., Jefferson, L. and Guidolin, A.F. (2016). Growth Variation in Reproductive Structures of Physalis Populations Interciencia. Interciencia. 41(7): 470-475.

Tuteja, S. and Bhatt R. (1984). Chromosome number reports LXXXV. *Taxon*. **33**: 756-760

Valerio, J.J.P., Lomeli, A.L., Pérez, J.E.R., Aguilar, R.M., Brindis R.C. and Lira, N.M. (2012). Densidad y poda en tres variedades de tomate de cascara (*Physalis ixocarpa* Brot. ex Horm.) cultivada en invernadero. *Rev.Chapingo Serie. Hortic*. **18**: 325-332.

Vatsavaya, R., Reddy, C. and Rajarao, K. (2007). The myth of "minima" and "maxima," the species of *Physalis* in the Indian subcontinent. *Acta. Phytotaxonomica Sinica.* **45**(2): 239-245.

Vavilov, N.I. (1951). The origin, variation, immunity and breeding of cultivated plants. *Chronica Bot*. **13**: 361-366.

Vedyasagar, S., Chadha, S. and Kumar, J. (1997). Heterosis in bacterial wilt resistant tomato lines. *Himachal J. Agric. Res.* **23**(1-2): 40-44.

Vega, A., Fito, P., Andrés, A. and Lemus, R. (2007). Mathematical modeling of hot-air drying kinetics of red bell pepper (var. Lamuyo) *J. Food Eng*. **79**: 1460-1466.

Verma, S. K. and Sarnaik, D.A. (2000). Path analysis of yield components in tomato (*Lycopersicon esculentum* Mill). *J. App. Biol*. **10**(2): 136-138.

Vikram, A. and Kohli, U.K. (1998). Genetic variability, correlation and path analysis in tomato. *J. Hill. Sci.* **11**(1): 107-111.

Virupannavar, H., Dharmatti, P.R., Yashvant, K.H. and Ajjappa, Sogalad. (2010). Combining ability studies on bacterial wilt resistance in tomato for processing qualities and yield. *Asian J. Hort.* **5**(1): 111-113.

Wagh, R.S., Bharud, R.W., Patil, R.S. and Bhalekar, M.N. (2007). Correlation analysis of growth, yield and fruit quality components in tomato. *J. Mahar. Agric. Uni.* **32**(1): 29-31.

Wang, L., Wang, M., Shi, Y., Tian, S.P. and Yu, Q.H. (1998). Genetic and correlation studies on characters in processing tomato. *Adv. Hort.* **2**: 378-383.

Waterfall, U.T. (1958). A taxonomic study of the genus Physalis in North America north of Mexico. *Rhodora*. 60:107-114.

Waterfall, U.T. (1967). Physalis in Mexico, Central America, and the West Indies. *Rhodora*. **69**: 82-120.

Wilf, P., Carvalho, M.R., Gandolfo, M.A.; Cúneo, N. R. (2017). Eocene lantern fruits from Gondwanan Patagonia and the early origins of Solanaceae. *Science.* **355**(6320): 71-75.

Willis, J.C. (1966). A dictionary of the flowering plants and ferns. Cambridge Univ. Press, Cambridge, UK.

Wright, S. (2007). Correlation and causation. *J. Agric. Res*. **20:** 202-209.

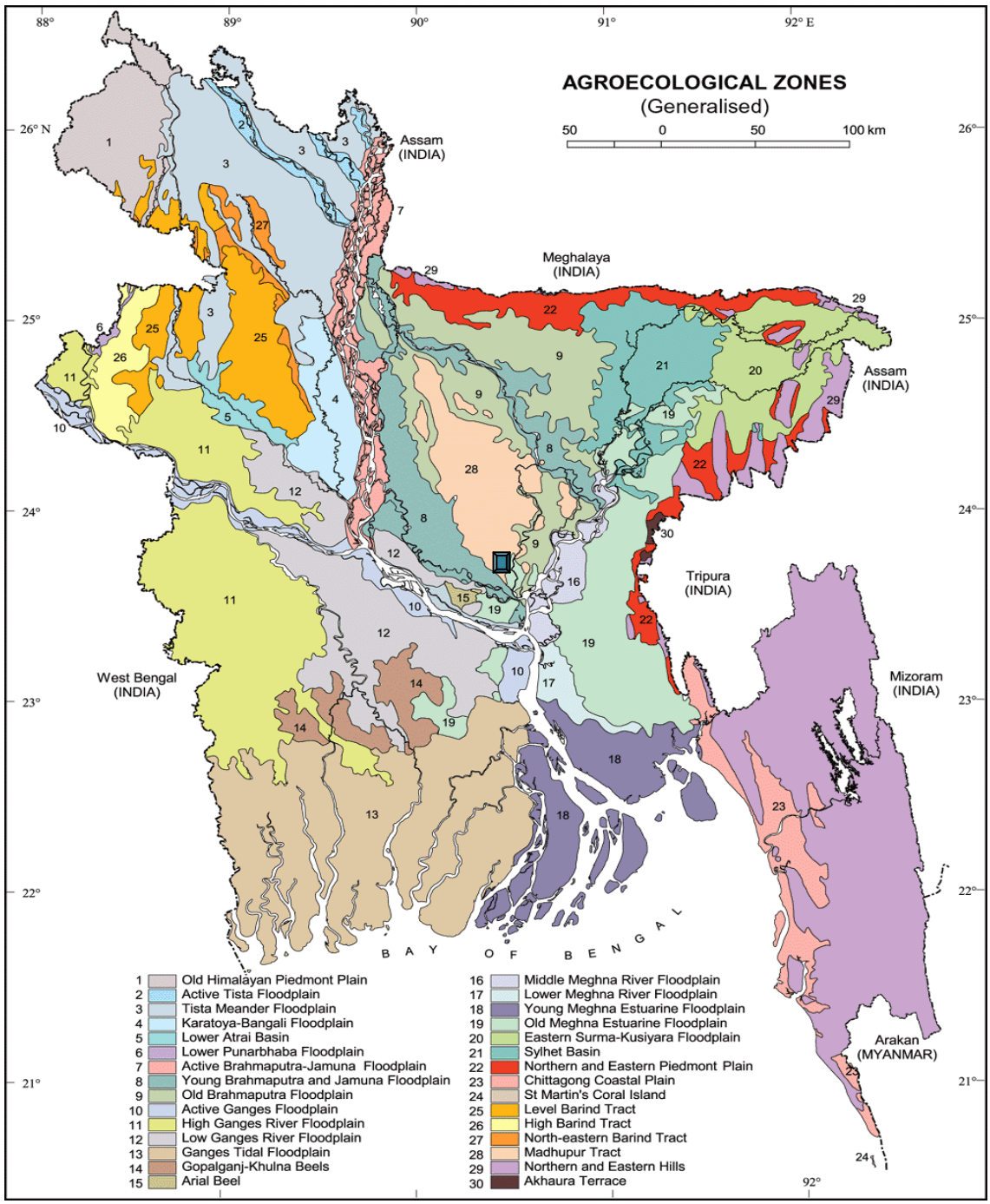
Yadav, M. S., D Valck, K., Hennig-Thurau, T. et al. (2013). Social-Commerce: A Contingency Framework for Assessing Marketing Potential. Journal of Interactive Marketing, 27, 311-323.

Yates, F. (1947). The analysis of data from all possible reciprocal between a set of parental lines. *Heredity*. **1**: 287-301.

Yi, S.S., Jatoi, S.A., Fujimura, T., Yamanaka, S. and Watanabe, K.N. (2008). Potential loss of unique genetic diversity in tomato landraces by genetic colonization of modern cultivars at a non-center of origin. *Plant Breed*. **127**: 189-196.

Zhu, H.S., Zhang, H., Mao, M.K., Li, H.T. and Wang, A.Y. (2004). The genetic diversity of Yunnan local varieties and wild species of tomato. *J. Yunnan Agric. Univ*. **19**: 373-377.

Appendix 1. Location of experimental plot



The experimental site under study

Appendix II. Average temperature, rainfall, relative humidity of the experimental site during Nov 2017-March 2018, Nov 2018-March 2019 and Nov 2019-March 2020

Month	Air temperature		Relative humidity (%)	Rainfall (mm)	Sunshine (h)
	Maximum	Minimum			
Nov, 2017	34.8	18.0	77	227	5.8
Dece, 2017	32.3	16.3	69	0	7.9
Jan, 2018	29.0	13.0	79	0	3.9
Feb, 2018	28.1	11.1	72	1	5.7
Mar,2018	32.5	22.4	24.0	75	50
Nov, 2018	33.8	18.0	76	225	5.8
Dece,2018	32.5	16.3	69	0	7.9
Jan, 2019	29.0	13.0	80	0	3.9
Feb, 2019	28.5	11.1	72	20	5.7
Mar,2019	32.5	21.9	24.0	75	50
Nov, 2019	35.8	18.0	78	220	5.8
Dece,2019	32.3	16.3	76	0	7.9
Jan, 2020	30.0	13.0	83	0	3.9
Feb, 2020	28.1	11.1	72	1	5.7
Mar,2020	33.5	24.0	76	25	5.5

Appendix III. Physical and chemical characteristics of initial soil (0-15 cm) of the experiment site

A. Physical composition of the soil

Soil separates	%
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix IV. Analysis of variance (ANOVA) for fourteen agromorphogenic traits of five parental genotypes of tomatillo

Sources of variances	df	MS Value												
		Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Genotypes	4	26.49**	12.99*	0.34NS	9.99*	9.05NS	5.18NS	2.81NS	29.34**	64.59**	3.07NS	888.8*	50674.4**	7.31**	352.88**
Replication	3	3.13	0.53	0.09	4.12	0.86	3.36	5.41	0.87	0.63	7.7	620.00	1849.4	0.27	12.99
Error	12	1.49	2.48	o.19	1.77	2.61	1.95	1.61	2.73	5.07	2.45	206.83	1272.2	0.18	8.85

** Significant at 1% level,

* Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

Appendix V. ANOVA for cross ability of different crosses of tomatillo genotypes based on their success rate in three years

SV	DF	MS		
		Year 1	Year 2	Year 3
Crosses	19	170.78*	106.33NS	93.75*
Replication	2	37.33	4.00	9.00
Error	38	94.28	65.46	57.96

Here, SV = Sources of Variation; DF = Degree of Freedom; MS = Mean Square.

*Significant at 5% level.

NS Non-significant.

Appendix VI. Analysis of variance (ANOVA) for fifteen morphological traits of F1tomatillo genotypes

Sources of variations	df	MS Value														
		Germination %	Plant height	Leaf area	No. of branches/plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Genotypes	19	28.13**	33.89**	5.13**	0.51*	4.60**	3.72**	9.49**	11.10**	5.62**	8.02**	16.27**	722.1**	34278.7**	5.03**	257.8**
Replication	2	4.84	1.17	0.15	0.16	1.84	0.63	0.40	0.93	2.45	2.96	0.70	48.17	28.0	0.41	3.94
Error	38	3.48	4.44	0.55	0.23	0.65	1.26	0.86	0.84	0.85	1.12	0.73	80.48	972.6	0.35	9.52

** Significant at 1% level,

* Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

Appendix VII. Analysis of variance (ANOVA) for fifteen morphological traits of twenty F2 genotypes of tomatillo

Sources of variances	df	MS Value														
		Germi-nation %	Plant height	Leaf area	No. of branches/ Plant	Days to 1st flowering	Days to 50% flowering	Days to maturity	No. of fruits/plant	Fruit length	Fruit diameter	Individual fruit weight	Seeds / fruit	Yield/plant	Yield/plot	Yield/ha
Replication	2	6.2	13.59	0.32	0.84	1.93	0.49	0.79	0.01	3.56	14.80	10.92	843.12	7037.1	1.04	48.57
Genotypes	19	28.73**	28.26**	4.34**	111.89**	8.49**	5.89**	4.17**	8.84**	6.61**	10.01**	18.77**	3504.11**	29374.1**	4.23**	203.81**
Error	38	7.04	6.73	1.15	0.44	0.99	1.04	1.37	1.67	1.01	0.91	2.89	709.09	3743.3	0.54	25.97

** Significant at 1% level,

* Significant at 5% level.
NS Non-significant.
df = Degree of freedom.

Appendix VIII. Analysis of variance (ANOVA) for nine qualitative traits of twenty F2 genotypes of tomatillo

Sources of variances	df	MS Value								
		Leaf chlorophyll content	Brix%	Fruit pH	Vitamin C	Titratable acidity	Lycopene content 472	Lycopene content 502	Fruit moisture content	Fruit dry matter
Replication	2	1.56	0.09	0.03	9.86	0.002	0.07	0.08	2.89	3.18
Genotypes	19	8.17**	0.52**	0.07^{NS}	7.41^{NS}	0.009^{NS}	0.02^{NS}	0.02^{NS}	0.91^{NS}	0.97^{NS}
Error	38	2.33	0.11	0.05	4.16	0.01	0.02	0.02	2.22	1.83
CV		1.92	5.29	5.84	11.92	16.44	46.04	52.98	1.60	20.41

** Significant at 1% level,

* Significant at 5% level.
NS Non-significant.
df = Degree of freedom.