GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF YIELD AND YIELD CONTRIBUTING CHARACTERS OF TOMATO (*Solanum lycopersicum* L.) GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled ***"GENETIC VARIABILITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF YIELD AND YIELD CONTRIBUTING CHARACTERS OF TOMATO (Solanum lycopersicum L.) GENOTYPES"*** *submitted to the faculty of Agriculture, Sher- e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING, embodies the result of a piece of bona fide research work carried out by* ***SUMON BEPARY, Registration No.: 15-06581*** *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.

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DEDICATED

TO MY

BELOVED PARENTS

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SOME COMMONLY USED ABREVIATIONS

FULLWORD	ABBREVIATION
Agro Ecological Zone	AEZ
Agricultural	Agril.
And others	*et al.*
Accessions	ACC
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Biological	Biol
Centimeter	cm
Co-efficient of Variation	CV
Genotypic Co-efficient of Variation	GCV
Phenotypic Co-efficient of Variation	PCV
Ecology	Ecol.
And	&
Et cetera	etc.
Environmental variance	δ^2e
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2g
Gram	gm
Heritability in broad sense	h^2b
Journal	J.

SOME COMMONLY USED ABREVIATIONS (CON'T)

FULLWORD	ABBREVIATION
Kilogram	kg
Meter	m
Mean Sum of Square	MSS
Muriate of Potash	MoP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2 p$
Randomized Complete Block Design	RCBD
Replication	Rep.
Research	Res.
Science	Sci.
Sher-e-Bangla Agricultural University	SAU
Triple super phosphate	TSP
Continue	cont.
Species	sp.
Standard Error	SE
Linnaeus	L.
At the rate	@
Bangladesh	BD
Degree Celsius	^{0}C
Degree of freedom	df
Millimeter	mm
Milliliter	ml
Hectare	ha
Decimal	dec.
First	1st
Second	2nd
Residuals	R
Temperature	temp.
Relative humidity	RH
Maximum	Max.
Minimum	Min.
Hour	hr
Weight	wt.
Serial number	Sl. No.
Cation Exchange Capacity	CEC
Department	Dept.

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By

SUMON BEPARY

ABSTRACT

Twenty-five genotypes of tomato (*Solanum lycopersicum* L.) were evaluated in a Complete Randomized Design (CRD) with three replications at the net house of Sher-e-Bangla Agricultural University, Dhaka to study the variability, correlation and path co-efficient analysis from October, 2021 to March, 2022 in Rabi season. The genotypes were found significantly variable for all the characters studied. Comparatively phenotypic variance was higher than the genotypic variance for all the characters. The high genotypic co-efficient of variation and phenotypic co-efficient of variation values were observed for yield per plant (kg). Maximum difference between phenotypic and genotypic co-efficient of variation were 30.31 and 13.82. Days to first flowering, days to first fruiting, no. of primary and secondary branches per plant, total number of fruits per cluster, skin diameter of fruit (mm), fruit pH, individual fruit wt. (g) and yield per plant (kg) showed high heritability along with genetic advance in percentage of mean, indicating high variability among these traits. The significant positive correlation with yield per plant (kg) was found in number of fruits per cluster, individual fruit weight (g). Both genotypic and phenotypic variance level indicated the importance of these traits in selection for increasing yield and were identified as yield attributing characters. Thus, selection can be relied upon these characters for the genetic improvement of yield for tomato (*Solanum lycopersicum* L.). According to path co-efficient analysis, number of primary branches per plant had the lowest positive direct effect and individual fruit weight (g) had the highest positive direct effect on yield. Days to first flowering, plant height (cm), number of secondary branches per plant, total number of fruits per cluster, individual fruit wt. (g) all had positive direct impact on yield per plant (kg), suggesting that direct selection based on these traits may be useful in the development of high yielding tomato genotypes. Considering genotypic variability and morphological characteristics of experimental tomato genotypes G5, G6, G7, G8, G13, G16, G18, G20 and G21 might be suggested as parents for future breeding program.

CHAPTER I

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is considered as one of the most economically remarkable vegetable crops and is grown all over the world. Due to its high nutritional value and various uses, tomato is the 2nd most consumed vegetable crop after potato in the world (Siddiqui *et al*., 2020). It is grown in a large scale during the winter season in Bangladesh. There is a production of 74,000 m tons of tomato in Bangladesh from 13,066 ha of land (Banglapedia, 2022). The production of tomato has a particular importance in tropical, subtropical and mild regions of the world, for both fresh and processing markets (Meena *et al.*, 2017). Tomato (2n=2x=24) belongs to the family Solanaceae and is native to Central and South America (Vavilov, 1951). The Genus *Lycopersicon* is derived from a Greek word meaning wolfs peach. There are nine species of this genus, among them only two are cultivated e.g., *Lycopersicon esculentum* (common tomato) and *Lycopersicon pimpinellifolium.* The ancestral species are believed to be native to the Pacific shore of South America. Despite the long period of time since tomato plants were introduced into the world, domestication schemes and routes are still largely controversial. But historical evidence says that the dissemination of tomato occurred eastwards and attributed to the conquerors of Mexico and Peru and their explorations (Blanca *et al*., 2012).

Nowadays, the need for conservation and characterization of genetic resources of tomatoes and its relatives has been increased. Since the early 1900s superior phenotypes have been selected with morphological markers (Foolad, 2007). On the other hand, genetic diversity between breeding genotypes can be estimated using DNA-based molecular markers, and many molecular markers have been used to study genetic variability in tomatoes (Kandel *et al*., 2019). In early days, tomato had a great adaptation and morphological variation.

Presently, tomatoes are consumed widely all over the world. It has been demonstrated that tomato is good for heart and other organs of human body and most effective natural source of antioxidants, lycopene. According to some research, the lycopene in cooked tomatoes can help to prevent prostate cancer and enhance the skin's defenses against damaging UV radiation (World Cancer Research Fund, 2007). Also it is a fruit with high nutritional value, including vitamin (31 mg per 100 g) and other vitamin, as well as minerals including calcium, phosphorus, and iron (Matin, *et al*., 1996). Lycopene provides a protective effect against the risk of ovarian cancers and help to reduce the risk of pancreatic cancer (Sharon, 2009).

The tomato is a model organism for genetic studies (Hay *et al*., 2004). Wild tomatoes exhibit a number of differences in morphological characters, mating system, and environmental existence. In adverse climatic conditions the plants survive by activating their physiological and metabolic defense systems and reach their peaks to adapt the sudden changes by structural modifications (Gong *et al*., 2009). Tomato fruits are important for dual-use (vegetable and fruit) products (Razifard *et al*., 2020). In recent days, farmers are cultivating tomato hybrids and some advanced lines throughout the year in Bangladesh. These varieties are more productive with high nutrient contents.

Most of the tomato varieties in Bangladesh are of inbred type which need to characterize and evaluate morphological variability as the selection of genotypes with desired traits result in variety development. Environmental conditions are continuously changing; under the pressure of arable land shortages, sustaining food production to feed increasing populations will be a challenge by 2050 (Hickey *et al.*, 2019). Tomato production has become more difficult specially in the face of global climate changes as a result the tomato domestication and selective breeding processes led to the reduction of genetic diversity in nowadays cultivated tomatoes (Lin *et al.,* 2014).

Genetic makeup of tomato makes possible means for plant breeders to create novel plant gene combinations and selection of crop varieties more suited to the needs of diverse agricultural systems (Glaszmann *et al*., 2010). Yield parameter of tomato is directed by different yield contributing characters which are largely influenced by environmental factors, as a result estimation of genetic heritability and genetic variability in respect of genetic advance are necessary for crop selection (Vaishya *et al*., 2017).

The cultivated tomato with higher yield and compact architectures but tends to be more vulnerable due to the attacks of physical as well as biological agents from the environment. Tomato production has become more difficult, especially in the face of global climate changes. Tomatoes are grown mainly in winter season in Bangladesh and farmers are interested to cultivate tomato commercially throughout the year. In recent years, BARI has developed three summer tomato varieties, but its area coverage is very limited. Research organization should take initiatives to disseminate these varieties to the farmers.

Tomato is considered as the most crucial vegetable crop for genetic studies due to broad genetic base and high genotypic and phenotypic diversity. The introduction of new tomato genotypes with higher yields are important source for human consumption and for the development of various industrial products throughout the world. The result of this study will facilitate the tomato breeders to harvest full potential of the HYVs, local cultivars and germplasms of tomato genotype and will support to design a suitable breeding program for the development of high yielding tomato genotypes.

The experiment has been conducted with the following objectives:

- To study the genetic variability and correlation of yield and yield contributing traits of tomato for checking variations of performance
- To evaluate the interrelationship among various yield contributing traits and
- To identify the high yielding tomato genotypes for future breeding program.

CHAPTER II

REVIEW OF LITERATURE

Tomato (*Solanum lycopersieum* L,) is a well-known vegetable crop with its wide range of adaptability, higher producing potentiality, and suitability for a variety of purposes in both the fresh and processed food industries. For the agricultural crops morphological characterization is a useful tool that can be used for future crop development programs. This research work has been done to study the genetic variability, correlation and path co-efficient analysis among different yield contributing parameters of the tomato. Many researchers in several institutions at home and abroad have already performed related studies. Some of the most relevant literatures are cited here.

2.1 Nomenclature, origin and distribution of tomato

Solanum lycopersicum L. is currently the established scientific name for most of the scientific community. From 1768 to 2005, the scientific term *Lycopersicon esculentum* Mill. was frequently used. Back to the original terminology used by Linnaeus in 1753 was the alteration that Spooner and his colleagues suggested in 2005 (Anonymous, 2014). The tomato was given the genus name *Solanum lycopersicum* by Linnaeus in 1753, and Philip Miller gave it the name *Lycopersicon esculentum* in 1768, according to the "International Plant Name Index" (Anonymous, 2014). The tomato (*Solanum lycopersicum* L.) is a self-pollinated species with a narrow genetic base. Since tomatoes were typically grown in protected surroundings in the European habitat, the introduction of the species from Mexico to Europe was critical in reducing genetic variability. This resulted in the conservation of a genotype only suited to autogamy, protecting the wild forms, which were at the time allogamous, from the influence of wind and insect pollinators (Foolad, 2007). It is native to western South America and Central America (Filippone, 2014). The tomato is a tropical plant that is grown all across the world, from the tropics to areas just a few degrees north of the Arctic Circle. The most likely place for tomato domestication is thought to be Mexico. The secondary centers of diversification are Spain and Italy (Gentilcore, 2010; Smith, 1994). It is adapted to a wide range of environmental condition.

2.2 Study of variability of yield and its components

2.2.1 Variability

Assessing the degree and kind of variation of plant traits in breeding populations is essential for achieving genetic improvement of a crop through an effective breeding program. It aids the breeder in increasing the effectiveness of selection. For this reason, numerous researchers looked at how different tomato traits varied. Any crop improvement program's success depends on the amount of genetic variability and the extent to which the desirable trait is heritable. Previous researchers have pointed out that the breeding material contains genetic variability (Naz *et al*., 2013; Reddy *et al*., 2013; Singh, 2009; Shuaib *et al*., 2007). In a field experiment, Naz *et al.* (2013) investigated the genetic diversity among 25 tomato accessions to assist in the development of a successful varietal selection program for breeding. All tomato accessions were evaluated using two parameters, morphological and molecular parameters. This study reveals variation in the plant's height, the color of the fruit, and the size of the fruit. On the other hand, Reddy *et al*. (2013) examined 19 exotic tomato collections and found significant genetic variability for all 18 quantitative features related to growth, earliness, yield, and quality.

The overall variation is represented by the fruit weight, plant height, and fruit production per plant. Measurements of morphological traits can offer a quick method for assessing genetic diversity. Additionally, it evaluates genotypic performance and traits in pertinent growing situations (Shuaib *et al*., 2007). Mahesha *et al*. (2006) determined the considerable variability for all the parameters under research and identified a broad range of variance for plant height, branch count per plant, fruit weight, length, and diameter, as well as fruit set percentage, fruits per plant, and fruit production per plant.

The tomato plant has a variety of germplasms that can be selected based on phenotypic traits like size, color, and taste. In a field experiment on 15 tomato advance generation breeding lines (Singh *et al*., 2005) examined the variation in total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content, and dry matter content to identify the genotypes' significant differences under normal circumstances.

2.2.1.1 Plant height (cm)

(Naz *et al*., 2013) conducted an experiment using 25 tomato germplasm to characterize the morphology by comparing the height of the plant, the length, shape, and arrangement of the leaves, as well as the size and shape of the fruit. This study found that plant height exhibits the most variety. The experiment by (Kumari *et al.,* 2007) showed the maximum genotypic co-efficient of variation for plant height. To assess the genetic diversity of 40 tomato cultivars, Joshi *et al*. (2004) conducted a field experiment. They reported that plant height had the highest heritability (78.82%).

In terms of plant height, Shravan *et al.* (2004) reported significant variation. Significant genotype x environment interaction for plant height has been found by Ravindra *et al*. (2003). In an experiment conducted by Hannan *et al*. (2007), the yield and yield component qualities of 45 single cross hybrid tomatoes derived from 10 tomato parental lines were evaluated for heterosis and character association. Plant height, days to first flowering, number of flowers per cluster, number of fruits per plant, fruit weight per plant, and days to first fruit ripening were the traits examined. They revealed positive high significant heterosis for FPP (72.9, 75.33 and 20.74), TFWPP (189, 172 and 187), NFPC (48.65, 44.14 and 37.86), over the mid parent, better parent, and standard parent heterosis, respectively, and a significantly high percentage of positive heterosis for NFPP, TFWPP, and NFC. They also discovered significant differences between genotypes for all the traits. They came to the conclusion that five hybrids had considerable beneficial heterobeltiosis for TFWPP, which was connected favorably with FPP, NFPC, and Plant height. They chose three single cross hybrids based on the way they performed heterotically.

In a study involving 23 tomato genotypes, Parthasarathy and Aswath (2002) found that there was a lot of variation among genotypes for 8 morphological features. Plant height, fruit number, and fruit size were the factors that contributed the most variation. In a field experiment, Singh *et al*. (2002) used 92 tomato genotypes to study genetic variability. They found that the analysis of variance revealed highly significant genetic variation for plant height, the number of days until the first fruit set, the number of fruit clusters per plant, the number of fruits per plant, the number of fruits per plant, the weight of the fruits per plant,

and the yield of the fruit. The features with sufficient variability may be taken into account in a tomato hybridization program to increase yield. Additionally, Matin and Kuddus (2001) noted that for plant height, phenotypic variance was generally higher than genotypic variance. Once more, they saw that the genotypic co-efficient of variance was less than the phenotypic co-efficient of variation, indicating that the environment may have an impact on how this attribute is expressed.

2.2.1.2 Number primary and secondary branches per plant

Upadhaya *et al*. (2005) analyzed 34 tomato genotypes and discovered a range of 2.33–7.0 branches per plant. He claimed that for this character, the PCV (35.93%) was higher than the GCV (24.72%). In a field experiment, Singh *et al*. (2005) used 30 tomato plants and five genotypes (DT39, RHR-33-1, ATL-16, DARL-13, and RT-JOB-21) that displayed a higher number of primary branches than the control. From BT-117-5-3-1, the maximum number of fruits per plant was determined. In DT-39, the fruit output was highest (1.84 kg/plant). In comparison to the control, the majority of the cultivars had fruits with higher total soluble solids content. In KS-60, the proportion of fruits with acidity was highest. At 7 days, NDT-111 experienced the greatest physiological weight reduction, while Plant T-3 experienced the least. The lycopene concentration of ATL-13 was the greatest (59.67 mg/100 g). Singh (2005), Mohanty (2003) and Upadhaya *et al*. (2001) observed in their study that GCV was slightly lower than PCV for number of branches per plant. In an experiment to investigate the genetic diversity of 30 tomato genotypes, Shravan *et al*. (2004) found a significant difference in the number of primary branches per plant between the genotypes. For the number of primary branches, Ravindra *et al*. (2003) discovered an incredible genotype x environment relationship. The genetic variability of 92 tomato genotypes was studied in a field experiment by Singh *et al*. (2002), who came to the conclusion that the analysis of variance revealed highly significant genetic variation for plant height, the number of days until the first fruit set, the number of fruit clusters per plant, the number of fruits per plant, the weight of the fruits per plant, and the fruit yield. The features with sufficient variability may be taken into account in a tomato hybridization program to increase yield.

2.2.1.3 Days to first flowering

In evaluating the combining ability of a 9x9 diallel hybrid, Farzaneh *et al.* (2013) shown earliness in the number of days to first flowering. Contrarily, Monamodi *et al.* (2013) had not discovered any appreciable variations in the number of days until the first flowering across tomato genotypes. Total soluble solids, dry matter content, Vitamin C, lycopene, p^H, days to flowering, days to maturity, individual fruit weight, fruit length, fruit diameter, total number of fruits per plant, plant height, early yield, and total yield were all measured by Kumari *et al.* (2007). They found that all of the characters between parents differed highly, with the exception of p^H, early yield, total yield, and days to flowering. Days to first flowering varied between 49.67 and 68.33 days for the 26 tomato genotypes, according to Matin *et al.* (2001). Additionally, he noted that there was a significant environmental influence on the number of days until the first flowering, with the phenotypic variance being significantly higher than the genotypic variance.

2.2.1.4 Number of clusters per plant

A study was carried out by Dufera (2013) using 21 tomato germplasm samples. Fruit clusters plant-1 has higher genotypic and phenotypic co-efficient of variation values than other traits, showing the possibility of improving these characters through selection and the existence of genotypic variability. The materials under examination showed a wide range of genetic variability for yield and yield components, with the largest genotypic co-efficient of variation being discovered for a number of clusters per plant, according to Singh *et al.*, (2006).

2.2.1.5 Number of fruits per cluster

Samadia *et al*. (2006) studied 14 tomato cultivars, and they discovered that the PCV and GCV values for this trait were quite similar. In contrast, Arun *et al*. (2003) investigated 37 tomato genotypes and found that given the number of fruits per cluster, the GCV was lower than the PCV. Aradhana and Singh (2003) noted a comparable outcome.

2.2.1.6 Average fruit weight (g)

In an experiment, Farzaneh *et al*. (2013) found significant variation due to general combining ability (GCA) and specific combining ability (SCA), which, in addition to the quantity of fruits produced per plant, highlighted the significance of additive and nonadditive types of gene action in the inheritance of all characters. In Utter Pradesh in India, Kumar *et al*. (2004) and Shravan *et al.* (2004) studied genetic diversity using 30 tomato genotypes and discovered a significant difference in the average fruit weight among the genotypes. In a field experiment, Mohanty *et al*. (2003) investigated the genetic diversity of 18 tomato cultivars and found that there were positive direct impacts on average fruit weight on yield and negative indirect effects on the number of fruits per plant. A field experiment was conducted by Singh *et al.* (2002) to investigate the genetic variability of fifteen heat-tolerant tomato varieties. For the average fruit weight, he demonstrated high phenotypic (PCV) and genetic (GCV) co-efficient of variation.

2.2.1.7 Fruit yield per plant (g)

In a research, Singh *et al*. (2006) found that the materials had a wide range of genetic diversity for yield, yield components, and biochemical characteristics. Additionally, he stated that the number of leaves per plant had the highest genotypic co-efficient of variation, followed by the number of clusters per plant. Significant differences were found in the yield per plant for the genotypes examined, according to Matin and Kuddus (2001). Additionally, he mentioned that there was a little environmental influence on this feature as the phenotypic variance was somewhat higher than the genotypic variance. In an experiment, Sachan (2001) employed certain tomato genotypes. He also stated that there were notable variations in yield per plant between genotypes. Thirty-two tomato genotypes were evaluated by Tiwari (2007) for their greater genotypic co-efficient of variation for average yield per plant. High levels of variation were evaluated and reported by Brar *et al*. (2000) for the average yield per plant among the 186 genotypes. In 139 tomato cultivars, Reddy (2013) noted significant variability in output per plant.

2.3 Correlation and path co-efficient analysis

2.3.1 Correlation co-efficient analysis between yield and yield contributing characters

Character correlation is an estimation of the inter-relationships between the characters that aids breeders in selecting selection methods. Since one of the main goals of the majority of breeders is yield, correlation studies between yield and features that contribute to yield have generally been conducted. The characters that contribute to the yield are also connected to one another. In order to create an efficient selective breeding program for yield maximization, it is crucial to consider the associations between traits and yield and among its components. Due to agro-climatological changes from one year to the next, these connection studies may differ. It may be possible to enhance the yield by selecting a component if it has a higher heritability than the yield itself and a positive association between the two. However, it was often found that there was a negative correlation co-efficient among the yield component parts, indicating that choosing one component over another might not boost yield. Numerous writers have investigated the relationship between tomato yield and traits that influence yield. This section reviews some recent literature that is relevant. 39 tomato genotypes (*Solanum lycopersicum* L.) were evaluated by Yadav *et al*. (2016) for a range of quantitative and qualitative properties.

The character association analysis revealed a substantial and positive correlation between the total number of fruits per plant and gross yield (g/plant), commercial yield (g/plant), the number of marketable fruits per plant, and plant height (cm). Mahapatra *et al*. (2013) discovered a positive and substantial association between fruit yield and plant height, primary branch count, flower cluster number, fruit number, fruit length, fruit breadth, and average fruit weight. The number of primary branches per plant, days to 50% flowering, and flower clusters per plant all increased in direct proportion to plant height. According to Monamadi *et al.* (2013), the number of branches per plant and the quantity of fruits per plant have a strong positive significant association. This was due to the fact that plants with more branches tend to bear more fruits overall. 40 tomato genotypes were used in an experiment by Buckseth *et al*. (2012) to examine the relationships between several quantitative and qualitative qualities in tomato genotypes. For all of the traits examined, the study found incredibly large variations in genotypes. According to Rani *et al*. (2010),

the yield per plant was favorably and significantly correlated with fruit weight, pericarp thickness, acidity, ascorbic acid, and lycopene, while the number of fruits per plant was adversely correlated. According to YaDong *et al*. (2010), soluble solids content, single inflorescence fruit number, and single inflorescence flower number are all strongly positively linked with lycopene concentration. The connection between pedicel length and single fruit weight, however, was extremely significant negative. Additionally, he stated that there is a substantial negative correlation between fruit firmness, fruit flesh thickness, and fruit longitudinal diameter and a significant positive correlation between lycopene concentration and fruit form index.

According to Ara *et al*. (2009), there was a strong positive significant relationship between the number of clusters per plant and the number of fruits per plant. This was due to the fact that a plant will produce more fruits, resulting in larger fruits, the more clusters there are in the plant. The identified high positive correlation between fruit number per plant and fruit weight per plant gives credence to this. According to Anitha *et al*. (2007), their corresponding genotypic correlations for oxalate and phenotypic values were lower than those for seediness, lycopene, TSS, and locule number. However, the content showed a significant positive correlation with seediness and a non-significant positive correlation with the other traits. Golani *et al.* (2007) reported a substantial and positive association between fruit weight and fruit length at both levels. When correlation co-efficient were analyzed in 30 different tomato genotypes, it was found that yield per plant was significantly and positively correlated with plant height, fruit number per plant, fruit shape index, and pericarp thickness. Correlation co-efficient at the genotypic level were generally higher than the corresponding phenotypic ones (Kumar *et al*., 2007).

Correlation research by Wagh *et al*. (2007) revealed that selection for 50% flowering, plant height, quantity of fruits per plant, and fruit quality traits like lycopene, beta-carotene, ascorbic acid, and titratable acidity can all be used to increase output. Wright (2007) conducted a correlation analysis and found that selecting for 50% flowering, plant height, and quantity of fruits per plant can boost yield. When Kumar *et al*. (2006) conducted correlation co-efficient research on 30 tomato genotypes, they found a substantial positive correlation between the number of fruits produced per plant and the plant's overall fruit

output. Megha *et al*. (2006) conducted a study to compare 26 tomato cultivars for the number of flowers per cluster, flower clusters at the time of first picking, number of fruits per cluster, weight of each fruit, yield per plant, and overall yield. They showed that selection for the quantity of flowers per cluster, or flower clusters initially, might control yield improvement. In 2005, Singh *et al.* conducted a correlation co-efficient analysis on 15 tomato breeding lines from the advance generation. Additionally, he noticed that the phenotypic co-efficient of variation were greater than the genotypic co-efficient of variation, showing that the genotypic effect is diminished when the environment is present. In an experiment with cherries to determine correlation co-efficient analysis, Manivannan *et al*. (2005) found that fruit yield was significantly and positively associated with the quantity of leaves and fruit weight.

According to Arun *et al.* (2004), the average fruit weight and plant height were positively and significantly connected with tomato yield per plant. Joshi *et al.* (2004) used 37 tomato genotypes for a correlation analysis, which revealed a significant and positive association between yield per plant and average fruit weight, fruit length, plant height, and harvest duration. Fruit length and fruit breadth were positively correlated with average fruit weight. However, there was a negative correlation between fruit weight and ascorbic acid concentration, number of fruits per plant, and number of fruits per cluster. When Kumar *et al*. (2004) performed a correlation co-efficient analysis on 30 tomato genotypes, it was found that there was a significant and positive link between the number of fruits per plant and the fruit yield per plant.

Using data from 18 tomato varieties, Mohanty (2003) examined the correlation co-efficient. Additionally, he stated that the yield was considerably and favorably connected with the quantity of fruits per plant and the number of days before harvest. However, the number of branches per plant, the average fruit weight, and the number of fruits per plant were all negatively linked with plant height. Additionally, he stated that the majority of early cultivars had small, low-yielding fruits. Genetic parameters and connections relating to fruit weight and yield per plant were examined by Dhaliwal *et al*. in 2002. The correlation tests suggested that real breeding lines with firm fruits and high yields may be developed. According to Mohanty (2002), there were significant phenotypic and genotypic

correlations between fruit yield and days until first harvest, number of branches, and fruits/plant. There were also significant and negative correlations between fruit yield and plant height and average fruit weight, and the ratio of fruits per plant to average fruit weight was inverse. Nesgea *et al*. (2002) conducted a correlation co-efficient analysis on 13 tomato genotypes and found that factors like plant height, number of branches per plant, spread, fresh plant weight, number of fruiting clusters, days to 50% flowering, number of fruits per cluster, and number of fruits per plant should all be taken into account when trying to increase tomato yield.

2.3.2 Path co-efficient analysis between yield and yield contributing characters

It becomes more challenging to identify the characteristics that actually influence the yield when more characters are included in the correlation analysis. The path analysis under such situation helps to determine the direct and indirect contribution of these traits towards the yield therefore, a good tool for understanding yield, with the exception of the relationships between yield and the qualities that contribute to yield. Additionally, it offers useful information for selecting fruits depending on their yield components to increase fruit production. This section reviews recent articles that analyze the path co-efficient between yield and yield components and are relevant to the current study.

Meena and Bahadur (2015) studied the character association for tomato germplasm grown in an open field. To determine the type and strength of connections between various features and fruit yield as well as among themselves, they assessed 19 indeterminate tomato germplasm samples. Using route co-efficient analysis, direct and indirect effects were assessed in order to get a comprehensive picture of how fruit output per plant and its constituent parts interact. There is a chance to increase yield per plant through selection based on the number of flowers per plant, the number of fruits per plant, and the weight of the fruits because the character had a high direct effect on yield per plant, suggesting that direct selection for these traits might be effective. Low residual effect means that the characters employed accounted for practically all yield-related variation. Six determinate tomatoes were examined by Monamodi *et al.* (2013). He said that the weight of a single fruit and the number of fruits is important factors to consider when making selections to

increase tomato yield. The number of marketable fruits and the weight of the fruit had favorable and significant direct effects on fruit yield. The findings of the path co-efficient study demonstrated a direct relationship between the yield and both the weight and number of marketable fruits. To study the path co-efficient of yield components and quality attributes in 23 tomato hybrids, Rani *et al.* (2010) conducted an experiment. He also demonstrated that fruit weight had both a high positive indirect effect and the largest positive direct effect on yield per plant, with fruit weight having both.

Following route analysis, Anitha *et al*. (2007) found that oxalates, acidity, ascorbic acid, and TSS had positive and significant direct effects on lycopene. Path analysis was examined by Golani *et al*. in 2007. He said that the weight of 10 fruits provided the greatest direct benefit. According to Dhankhar & Dhankhar (2006), the number of fruits produced per plant had the most direct positive impact. According to Mayavel *et al.* (2005), the number of branches per plant had the largest beneficial direct effect on fruit yield. Plant height, the quantity of fruits in each cluster, the number of fruits on each plant, and the number of locules in each fruit, on the other hand, all had a detrimental direct impact on fruit yield. In an experiment conducted by Singh (2005), it was shown that the average fruit weight was the factor that had the greatest positive impact on production, followed by the quantity of fruits per plant.

Regarding indirect effects, it was found that the number of fruits per plant had a positive indirect influence on fruit output via the number of branches per plant, however it had a negative indirect effect via the height of the plant and the number of days before 50% flowering. According to path co-efficient analysis by Arun *et al*., (2003), the number of fruits per plant was the contributing factor to yield the highest, followed by plant height. Thirty different tomato genotypes were used in an experiment by Kumar *et al*., (2003) to estimate path analysis. He claimed that, after average fruit weight, fruit number per plant had the greatest direct impact on output per plant. In order to examine route co-efficient analysis, Mohanty (2003) conducted a field experiment with 18 tomato cultivars. He found that the average fruit weight and number of fruits per plant had positive direct effects on the yield and negative indirect effects on each other. A field experiment was conducted by Harer *et al*., (2002) to explore the path analysis of 37 tomato genotypes. He found that the

number of fruits per cluster, the weight of an average fruit, and the number of fruits per plant all had the greatest direct impacts on fruit yield. Path analysis was carried out by Padma *et al*., (2002) according to this revelation, both genotypic and phenotypic factors had a favorable impact on the yield per plant, including the number of branches, fruit weight, fruit length, and fruit number per plant.

To estimate the path analysis for fruit quality features on fruit output, Bhushana *et al.*, (2001) used sixty genotypes of tomato. They found that all four variables (total soluble solids, ascorbic acid, pH, and titratable acidity) had weakly positive direct effects on fruit yield. According to Matin and Kuddus (2001), the weight of each fruit directly contributed the most to output, followed by the quantity of fruits harvested per plant. They also discovered that the number of seeds per fruit, the plant's height, and the days until the first flowering all directly impacted the yield per plant in a bad way. In an experiment, Verma and Sarnaik (2000) examined the yield components of thirty tomato genotypes. They claimed that the total number of fruits produced per plant, the average fruit weight, and the number of branches per plant all showed both favorable and significant direct benefits.

2.4 Biochemical analysis

The most widely grown vegetable crop nowadays is tomatoes. It is a significant source of antioxidants in the human diet, including vitamin C and total soluble solids (% of brix), and it has been associated with a lower risk of heart disease, diabetes, prostate cancer, and other cancer types. More attention is being paid to natural substances, such as physicochemical components found in a typical human diet, in current research for novel anticancer medicines. Because it has little side effects but effectively affects a variety of receptors or molecular targets implicated in the development of cancer and cardiovascular illnesses. The following list of recent publications includes the most relevant items:

2.4.1 Total Soluble Solids (% of Brix)

Brix percentage deals with the sugar content of an aqueous solution. One gram of sucrose in one hundred grams of solution equals one percent Brix, which measures the solution's strength as a proportion of its mass. The % of brix only provides an approximation of the

dissolved solid content if the solution contains dissolved solids other than pure sucrose. There are numerous publications on the variation in tomato genotype's % of Brix. Regarding the tomato fruit's color, texture, flavor, nutritious value, and wholesomeness, the chemical components are important. In general, the prominence of a rich flavor is linked to high sugar concentrations, red color, and firm texture. The biochemical alterations that result from tomato fruit growth, maturation, and environment are reviewed. In a field experiment with 27 tomato genotypes, Nalla *et al*. (2014) found that equatorial diameter (15.38), total soluble solids (17.38), and fruit production per plant (20.51) all contributed significantly to divergence. Hernandez *et al.* (2013) discovered no statistically significant variations between the averages of the F_1 and F_2 generations for total fruit number, total soluble solids content, fruit hardness, length, and p^H in general and for the majority of the genotypes. For all quality traits, there was a significant ($p^{0.01}$) difference between genotypes and environments. For all quality traits, with the exception of TSS discovered by Panthee *et al*. (2013), the genotype x environment interaction was significant (p0.01). For acidity, total soluble solids, ascorbic acid concentration, and shelf life, Narolia *et al*. (2012) discovered high values of genotypic co-efficient of variation, heritability, and genetic progress.

Research by Silva *et al*. (2012) assessed the Carolina tomato cultivar's production factors and total soluble solids (Brix). The fruits were picked as they started to turn red instead of green, and at that time, the soluble solids content, number, weight, length, and diameter were all measured. Chen *et al*. (2009) investigated seven tomato lines and showed that total soluble solid content and vitamin C heritability were both highly heritable traits. In terms of vitamin C content, organic acid content, and total soluble solid content, lines from L. esculentum var. cerasiforme were superior breeding materials. The highest fruit production (27.79 t/ha), total soluble solid content (6.11%), acidity (0.93%), and lycopene concentration (7.64 mg/100 g of juice) were found by Krishna and Allolli (2005). 37 tomato genotypes were grown in a field experiment by Harer *et al*. (2002), and correlation tests revealed that genotypic correlation was higher than phenotypic correlation for every trait considered. Among these, the total soluble solid content demonstrated a favorable correlation with fruit yield and positive indirect impacts with a low direct impact.

2.4.2 p^H

p^H and acid concentration are significant aspects of tomato quality and processing. According to several studies, a good sugar/acid ratio is essential for optimum tomato flavor. Processability depends on p^H, which must be lower than 4.4 to prevent issues with thermophilic organisms (Rice and Pederson, 1954). Longer processing durations are required for higher p^H values, which makes it more challenging to produce a high-quality product. Although a tomato's total acidity and p^H levels should be tightly correlated, there are situations when this relationship is still not ideal. The p^H and acidity are not always inversely connected and both values might be rather high in some kinds. According to (Louys and Meijaard, 2010) who discovered significant variation in the [H+]/titratable acidity (TA) ratio across 55 divergent accessions, the weak correlation between p^H and acidity is largely due to variations in the phosphorus content of the fruits. Since the TA is equal to the total of the TAs contributed by the buffers in the fruit, it should be possible to describe the link between TA and p^H using model systems. The p^H is likewise established by these buffers.

2.4.3 Lycopene Content (mg)

A significant carotenoid and the red pigment in tomatoes is lycopene (LYC). Numerous epidermiological and intervention studies have shown that eating foods high in LYC reduces the risk of developing various malignancies, such as prostate, lung, oral, and colon cancer, as well as coronary heart disorders, cataracts, and perhaps macular degeneration. Despite being the fruit and vegetable with the highest concentration of lycopene, the tomato, its content in the fruit of commercial cultivars is generally low, ranging from 30 to 60 micrograms lycopene/g fresh tomato tissue. Foolad recently (2007) created tomato breeding lines with fruit lycopene contents ranging from 100 to 200 micrograms lycopene/g fresh fruit tissue using several classical breeding approaches. Beta carotene, which is responsible for the yellow, orange, or red pigmentation, photosynthesis, and photo-protection of many carotenoids, such as lycopene, is one such key intermediary in the biosynthesis of carotenoids. Lycopene is a polyunsaturated hydrocarbon, just like all carotenoids (an un-substituted alkene).

Here, we address a few of the earlier publications on the lycopene experiment (Datta *et al*., 2013; Alda *et al*., 2009; Moigrädean *et al*., 2007; Cucu and Loco, 2011). Lycopene may reduce the occurrence of prostate cancer, according to Datta *et al*. (2013). This study examined how well 20 men with localized prostate cancer tolerated and accepted three different tomato juice doses (4, 8, or 12 oz) and their impact on serum lycopene levels after radiotherapy. Serum lycopene was found to have a strong positive connection with weight and body mass index and a weak negative link with prior dietary supplement consumption. Panthee (2013) tested 44 different vintage tomato varietals. According to Pearson's correlation analysis, vitamin C, TSS, and ITA were all favorably connected with one another, whereas estimated lycopene concentration was negatively correlated with the other physicochemical features. Twenty-one tomato germplasm samples were used in an experiment conducted by Dufera (2013). Lycopene content (mg) showed higher genotypic and phenotypic co-efficient of variation values.

According to Zhu *et al*. (2013) research, lycopene has a variety of unique biological and physicochemical features due to its acyclic structure and extensive array of conjugated double bonds. Lycopene is one of the natural carotenoids without pro-vitamin A activity that is most effective at quenching singlet oxygen. In human serum and other tissues, it functions as a natural antioxidant to prevent lipid, protein, and DNA oxidative damage. Lycopene, a powerful antioxidant, has been reported to suppress the proliferation of various types of human cancer cells, including endometrial, prostate, breast, upper aerodigestive tract, and lung. Data regarding total soluble solids, dry matter content, reducing sugars, titratable acidity, ascorbic acid, and lycopene were collected by Kumari *et al*. in 2007, and they discovered that changes in acidity, early yield, overall yield, and days to flowering were not significant.

CHAPTER III

MATERIALS AND METHOD

This part of the study contains the information involved to the research work that was done in the experiment. It bears a short illustration of the location of the experimental site, climatic condition, characteristics of soil, planting materials, preparation of seed bed, layout and design of the experiment, pot preparation, manuring and fertilizing, transplantation of seedlings, intercultural operations, harvesting, data recording procedure, and statistical analysis etc.

3.1 Experimental site

The experiment was conducted beside the net house of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207.

3.2 Experimental period

The experiment was conducted during the period from 16 October, 2021 to 15 March, 2022 (rabi season).

3.3 Geographical location

The research work was done 23°41' N latitude and 90°22' E longitude with an elevation of 8.6 meter from sea level (www.distancesfrom.com). The experimental place beside the net house belongs to AEZ-28 that is called Madhupur tract. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.4 Climate and soil condition

The organic carbon content was 0.82% and the p^H ranges from 5.47 to 5.63 with an analytical value of 5.55. The physical characteristics and chemical composition of the soil of experimental site were indicated in Appendix II. The experimental site was located in the subtropical climatic zone. The data on temperature, humidity and rainfall during the time of experiment were collected from the Bangladesh Meteorological Department, Agargaon, Dhaka and noted in Appendix III.

3.5 Design and layout of the experiment

The experiment was performed in Randomized Complete Block Design (RCBD) with three (3) replications. The tomato genotypes were distributed randomly within pots. Five plants were planted for each genotype in every replication.

3.6 Planting materials

Total 25 tomato genotypes were used for this research work. The genetically pure seeds of these genotypes were collected from Bangladesh Agricultural Research Institute (BARI), Department of Genetics and Plant Breeding of Sher-e-Bangla Agricultural University (SAU) and the local market of different districts of Bangladesh. The purity and germination percentage were tested as around 80 to 100. The experimental genotypes are presented in Table 1.

Table 1. List of genotypes with their collection of sources

SL. No.	Genotypes	Symbol	Collection Source
1	BARI Tomato 02	G1	BARI
2	BARI Tomato 03	G2	BARI
3	BARI Tomato 12	G3	BARI
4	BARI Tomato 14	G4	BARI
5	BARI Tomato 15	G5	BARI
6	BARI Tomato 16	G6	BARI
7	BARI Tomato 17	G7	BARI
8	BARI Tomato 18	G8	BARI
9	BARI Tomato 19	G9	BARI
10	Raja	G10	BARI
11	Roma VF	G11	BARI
12	F1 Hybrid*	G12	SAU
13	BD 7259	G13	BARI

Table 1. List of genotypes with their collection of sources (cont.)

14	BD 7306	G14	BARI
15	BD 7755	G15	BARI
16	BD 10122	G16	BARI
17	BD 10123	G17	BARI
18	BD 10124	G18	BARI
19	BD 10128	G19	BARI
20	BD 10949	G20	BARI
21	Bhondhu Beej	G21	LOCAL MARKET
22	T9B0001	G22	SAU
23	T9B0016	G23	SAU
24	T9B0026	G24	SAU
25	T9B0039	G25	SAU

*Note: F1 Hybrid (Crossing of BARI Tomato 11 x BARI Tomato 14)

3.7 Preparation of seedbed and seed sowing

Tomato seedlings were raised in seedbed of 3.0 m × 1.0 m size, located at Department of Genetics and Plant Breeding net house. The soil was well prepared by mixing with cow dung and urea, converted into fine structure and dried for seedbed. Seeds were sown on 16 October, 2021. Prior to sowing seeds were treated with fungicides. After sowing, seeds were covered with soil layer. Sevin powder was applied around the seedbeds to repel insects. Seeds sowing is showed in Plate 1.

3.8 Transferring of seedlings

The emergence of the seedlings takes place 4 to 7 days after sowing. Seedbeds were watered as needed and weeds were pulled as they appeared to ensure healthy and uniform seedlings. After 15 days of seed sowing, the seedlings were transferred into the polybags is represented in Plate 2.

Plate 1. Sowing of tomato seeds into the seedbeds

Plate 2. Transferring of seedlings into the polybags

3.9 Manure and fertilizers application

The well-pulverized soil had been dried in the sun. One third of urea, total TSP, half of the MoP, total Boric acid, Total Zinc, total Gypsum and well decomposed cow dung were applied before transplanting the seedlings to the pots. Remaining Urea and MoP were used at the time of 15 DAYS of transplanting and the time of first flowering. Fertilizer and manure doses are given in Table 2.

Table 2. Doses of fertilizer and manure

Sl. No.	Fertilizer/Manure	Dose/ha
1	Urea	8kg
2	TSP	6kg
3	MoP	4kg
4	Boric acid	500g
5	Zinc	500g
6	Gypsum	5kg
7	Cow dung	200kg

3.10 Pot preparation

The soil prepared for planting seedlings was totally free from weeds and stubbles. Pots were filled with prepared soil two days prior to transplantation. About 8 kg of soil were poured into each pot. The pot was 20 cm in height, 30 cm at the top and 20 cm at the bottom.

3.11 Transplanting of seedlings

The seedlings were transferred into the main plastic pot (one plant/pot) after 30 days of growth. After transplanting, the seedlings were frequently watered for few days so that the roots could establish a strong connection with the soil and stand upright. Picture of transplanting of seedlings into the plastic pots is represented in Plate 3.

Plate 3. Transplanting of seedlings: polythene bags to plastic pots

3.12 Intercultural operations

To get vigorous growth and proper development of the tomato plants several intercultural operations including weeding, irrigation, stalking, pruning etc. were done as per needed. Gap filling was carried out twice, once at 7 days and another at 14 days after transplanting (DAT). After establishment of seedlings, weeding was done in several times as per demand. Bamboo sticks and ropes were used to support the plants when the seedlings became large. To provide sufficient sunlight and lessen pest infestation certain lateral branches and foliage were pruned out. During the cropping period several pesticides were used about 7 times at 7 days interval in order to prevent the insect infestation. Watering in seedlings is showed in Plate 4.

3.13 Harvesting and processing

In this experiment, numerous tomato genotypes were used. As a result, the fruits of different genotypes matured sequentially at different dates, the harvest time was not the

same for all of the varieties, and it took around one and a half month. The harvesting process started in February and was finished in April. The harvesting of tomato is represented in Plate 5.

Plate 4. Watering of seedlings

Plate 5. Harvestable tomato genotypes at the experimental site

3.14 Data recording

Data were collected from each pot based on different yield and yield contributing parameters and qualitative traits.

3.15 Morphological traits

During the experiment, data for several physical parameters connected to yield and yield contributing characters were collected. These features are as follows:

3.15.1 Plant height (cm)

After harvesting each plant's ultimate height from each pot was measured using a centimeter scale.

3.15.2 Days to first flowering

From the date of sowing to the first flowering, the number of days was counted. Days to first flowering were calculated for each replication using the mean of three plants.

3.15.3 Days to 50% flowering

The number of days between the transplanting of the seedlings and the blooming of flowers in 50% of the plants for each genotype was recorded.

3.15.4 Days to first fruiting

From the date of transplanting tomato seedlings to the date of the first fruit setting, the number of days was counted.

3.15.5 Number of primary branches per plant

Number of primary branches per plant was counted from each of the selected plant during maturity stage. Mean value of three plants were considered as the number of branches per plant for each replication.

3.15.6 Number of secondary branches per plant

Number of secondary branches per plant was counted from each of the selected plant during maturity stage. Mean value of three plants were considered as the number of branches per plant for each replication.

3.15.7 Number of clusters per plant

The number of clusters per plant was counted at the harvesting time. The number of clusters per plant for each replication was calculated using a mean value of three plants.

3.15.8 Number of flowers per clusters

The number of flowers per cluster was recorded at the time of flowering. Mean value of three plants were considered as the number of flowers per clusters for each replication.

3.15.9 Skin diameter of fruit (mm)

Five fruits of each replication of every genotype were cut into equal part horizontally and their skin diameter was measured by using slide calipers (Plate 6-D). Mean value of five representative fruits skin diameter of each genotype was calculated and considered as skin diameter (mm) of the fruit.

3.15.10 Individual fruit weight (g)

An electronic precision balance was used to measure the weight of the fruit. Five fruits per plant were chosen at random and weighed to determine the average individual fruit wt. (g).

3.15.11 Yield per plant (kg)

Yield per plant was recorded from harvests of each plant and expressed in kilogram (kg).

3.16 Physiological traits

During the experiment, data for several physiological parameters connected to yield were collected. These features are as follows:

3.16.1 Brix percentage (%)

Brix percentages were estimated at room temperature using a portable refractive index measuring device (ERMA, Tokyo, Japan). Brix percentage (%) was calculated by extracting fruit juice from a single fruit of each genotype.

3.16.2 Fruit p^H

A single fruit from each genotype was blended to extract the juice, which was then used to measure fruit`s p^H (Plate 6-A) by using an electrode of p^H meter into the juice.

3.16.3 Lycopene content (mg)

Using a UV-visible spectrophotometer (Plate 6-C), lycopene concentration was determined Alda *et al*., (2009) technique of absorption determination. Using a mixture of hexane, ethanol, and acetone (2:1:1) (v/v), lycopene from the tomato was extracted. One ml of juice from each sample was mixed with 25 ml of hexane, ethanol, and acetone (Alda *et al*., 2009) before being shaken on an orbital shaker for 30 minutes. After that, 10 ml of distilled water was added, and the agitation was continued for an additional two minutes. Then the solution was allowed to form distinct polar and non-polar layers. Hexane was used as a blank to test the absorbance at 472 and 502 nm. The lycopene content was given as mg/100g of the product.

A) p^H meter

B) Brix meter

C) UV-Visible Spectrophotometer

D) Slide calipers

Plate 6. Some instruments used for biochemical analysis

3.17 Statistical analysis

To investigate the tomato genotype in relation to yield and yield contributing traits, the gathered data from 25 genotypes for various characters were statistically evaluated. By using the STATICTIX-10 computer software program, the analysis of variance (ANOVA), mean values for all the characters and the statistically significant difference between the treatment means were calculated.

3.17.1 Analysis of variance (ANOVA)

In order to evaluate the genetic variability, the analysis of variance (ANOVA) for each character was evaluated individually using mean data. Using the F test, the level of significance was estimated at 5% and 1%. The ANOVA model is presented as below:

Source of variation	**df**	**MSS**	**EMSS**	**F-Ratio**
Replication (r)	r-1	M1		M1/M3
Genotypes (g)	g-1	M2	$\delta e^2+\delta g^2$	M2/M3
Error (e)	(r-1) (g-1)	M3	δe^2	

Here,

r = Number of replications;
g = Number of genotypes;
df = degree of freedom;
MSS = Mean sum of square and
EMSS = Expected values of MSS

3.17.2 Estimation of variability parameters

Genotypic and phenotypic variations were calculated using the following formula from Johnson *et al.* (1955).

a) Genotypic variance,

$$\sigma_g^2 = \frac{\text{MSG}-\text{MSE}}{\text{r}}$$

Here,

MSG = Mean sum of square for genotypes;

MSE = Mean sum of square for error and

r = Number of replications.

b) Phenotypic variance,

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Here,

σ_p^2 = Phenotypic variance;

σ_g^2 = Genotypic variance and

σ_e^2 = Environmental variance = Mean square of error (MSE).

3.17.3 Estimation of genotypic and phenotypic co-efficient of variation

The following formula is used to determine the genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) for each character. Burton provided the formula in 1952.

$$\text{GCV} = \frac{\sigma_g \times 100}{\bar{x}}$$

$$\text{PCV} = \frac{\sigma_p \times 100}{\bar{x}}$$

Here,

GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{x}$ = Population Mean

Phenotypic and genotypic co-efficient of variation are classified as follows by Sivasubramanian and Madhavamenon (1973).

- Low (0-10%),
- Moderate (10-20%) and
- High (>20%)

3.17.4 Estimation of heritability

Singh and Chaudhary proposed the following formula to calculate broad sense heritability (1985).

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Here,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p= Phenotypic variance

3.17.5 Estimation of genetic advance

The formula provided by Allard (1960) was used to calculate the projected genetic advance for the various study of characters.

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Here,

GA = Genetic advance

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ_p = Phenotypic standard deviation

K= Standard selection differential which is 2.06 at 5% selection intensity.

3.17.6 Estimation of genetic advance in percentage of mean

Comstock and Robinson (1952) provided the following formula to estimate genetic advance as a percentage of the mean:

GA in percent of mean = $\frac{\text{GA}}{\text{Grand mean}} \times 100$

Johnson *et al.* (1955) suggested the following categories of genetic advance in percent of mean:

- Less than 10% as- Low
- 10-20% as -Moderate and
- More than 20% High

3.17.7 Correlation co-efficient analysis

The correlation co-efficient was calculated to determine the degree of association between various features and yield. The variance and covariance components were used to calculate the genotypic and phenotypic correlation co-efficient between fifteen characters, following the advice given by Al-Jibouri *et al.,* (1958).

$$r_g(xy) = \frac{Cov_g\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

$$r_p(xy) = \frac{Cov_p\ xy}{\sqrt{\sigma_x^2}.\sqrt{\sigma_y^2}}$$

Here,

rg(xy)- The genotypic correlation co-efficient;
rp(xy)- The phenotypic correlation co-efficient;
Cov_g & Cov_p are the genotypic and phenotypic covariance of x & y, respectively;
σ^2_g & σ^2_p and are the genotypic and phenotypic variance of x and y, respectively

The estimated value of "r" was compared with the table "r" value with n-2 degrees of freedom at a 5% and 1% level of significance, where "n" stands for the number of observational pairs. As a result, relevant statistical analysis was performed on the data from a variety of experimental goals in order to make defensible conclusions on the genetic divergence of brinjal genotypes.

3.17.8 Path co-efficient analysis

The method described by Dewey and Lu (1959), which was also cited by Singh and Chaudhary (1985), and Dabholkar (1992) involved doing Path co-efficient analysis using

Straight forward correlation values.

ryx1 = Pyx1 + Pyx2rx1x2 + Pyx3rx1x3

ryx2 = Pyx1rx1x2 + Pyx2 + Pyx3rx2x3

ryx3 = Pyx1rx1x3 + Pyx2rx2x3 + Pyx3

Assuming that x1, x2, and x3 all give y, a set of simultaneous equations (three equations in this example) must be stated as follows in order to evaluate the direct and indirect effects of the linked characters.

Here,

r denotes simple correlation co-efficient and P denotes path co-efficient.

P is in the above equations may be conveniently solved by arranging them in matrix form.

Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x1 on y;

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y; and

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

The residual effect (R) of the characters was determined by applying the following formula after determining their direct and indirect effects (Singh and Chaudhary, 1985).

$$P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$$

Here, $P_{RY}^2 = (R^2)$

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$

P_{iy} = Direct effect of the character on yield and

r_{iy} = Correlation of the character with yield.

Categories:

- Negligible (0.00 to 0.09);
- Low (0.10 to 0.19);
- Moderate (0.20 to 0.29);
- High (0.30 to 1.0) and
- Very High (>1.00)

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was undertaken to study the genetic variability of 25 tomato genotypes (*Solanum lycopersicum* L.). This study was also conducted to detect the phenotypic, genotypic and environmental variance; phenotypic and genotypic co-efficient of variation, heritability, genetic advance, genetic advance in percent of mean, correlation co-efficient and path co-efficient. It also carried out to estimate direct and indirect effects of yield contributing traits and identify the breeding values of different tomato genotypes in respect of genotypic effects and comparative performances. The data were recorded on the basis of different characters such as: plant height (cm), days to first flowering, days to first fruit setting, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of flowers per cluster, skin diameter of the fruit (mm), individual fruit weight (g), yield per plant (kg), brix percentage (%), fruit p^H and lycopene content (mg) of 25 tomato genotypes. Genetic variability was estimated among 25 genotypes of tomato which were replicated thrice. The data concerning to 13 yield and yield contributing characters were statistically analyzed and obtained results are described below under the following headings:

4.1 Genetic variability and mean performance of the genotypes

4.2 Heritability, genetic advance and genetic advance in percentage of mean

4.3 Correlation co-efficient analysis

4.4 Path co-efficient analysis

4.1 Genetic variability and mean performance of the genotypes

Any crop improvement program's success depends on the breeder's ability to precisely identify and aggregate the necessary genetic variability and to indirectly select for yield through highly heritable traits those are yield associated after minimizing the environmental component of phenotypic variation (Mather, 1949). In order to determine the estimation of heritability that aids the breeder in predicting the expected GA potentially by selection for a character, it is crucial to have prior knowledge of both phenotypic co-efficient variation

(PCV) and genotypic co-efficient variation (GCV). Analysis of variance for the experimental design pointed out significant differences for all the characters which indicated the presence of considerable genetic variation among the genotypes for all the traits in Table 3. Out of the thirteen traits studied, plant height, number of primary branches per plant, number of secondary branches per plant were considered as growth attributing characters. Days to first flowering and days to first fruit setting were considered as earliness attributes. Number of clusters per plant and number of flowers per cluster were regarded as reproductive traits. Skin diameter of the fruit (mm), individual fruit weight (g), yield per plant (kg), brix percentage (%), fruit p^H and lycopene content (mg) were the economic trait. The mean values of yield and yield contributing characters of all the genotypes are shown in Table 4. Data of some genetic parameters such as genotypic, phenotypic and environmental variance, phenotypic and genotypic co-efficient of variation is presented in Table 5 and the results of yield and yield contributing traits are presented below.

4.1.1 Days to first flowering

The shortest duration required for first flowering was in G16 which was 58 days. On the contrary, longest duration required for first flowering was noticed in G23 with 74 days. Mean value of days to first flowering in 25 genotypes of tomato was 68.60 (Table 4). The phenotypic variance (23.32) appeared to be higher than the genotypic variance (15.94) suggested considerable influence of environment on the expression of genes controlling this trait. The GCV and PCV were 5.80 and 7.02 respectively, which were more or less similar to each other that indicated presence of low variability in this trait in Table 5. Similar results were recorded by Bhuiyan *et al., (*2016); Singh *et al.,* (2002) for this character.

Table 3. Analysis of variance of 13 important characters of tomato genotypes

Source of variation	df	Mean sum of square												
		DFF	**DFFr**	**PH**	**NPB**	**NSB**	**TNC**	**NFC**	**SDF**	**p^H**	**LC**	**Br**	**IFW**	**YP**
Replications	2	2.77	1.49	33.61	0.52	0.28	0.33	0.08	0.16	0	2.45	0.11	31.72	0.02
Genotypes	24	55.19**	54.49**	543.34**	3.98**	1.59**	3.15**	0.52**	5.09**	0.14**	33.21**	0.26**	2975.2**	0.45**
Error	48	7.38	7.88	192.56	1.48	0.45	0.56	0.09	0.08	0.02	0.2	0.04	13.55	0.04
CV (%)		3.95	3.51	17.01	39.48	36.32	14.95	10.1	3.7	3.96	4.49	4.06	4.54	16.14

****** indicates 1% level of significant and df = Degree of freedom

DFF = Days to first flowering, DFFr = Days to first fruit setting, PH= Plant height (cm), NPBP= No. of primary branches per plant, NSBP= No. of secondary branches per plant, TNCP= Total number of clusters per plant, NFPC= No. of flowers per cluster, SDF = Skin diameter of the fruit (mm), pH= Fruit pH, LC= Lycopene content (mg), Br = Brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg)

Table 4. Mean performance of yield and yield contributing characters of tomato genotypes

Genotype	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	p^H	LC	Br	IFW	YP
G1	66.00 f-h	75.67 g-i	**54.67** h	3.00 c-e	1.33 de	4.67 d-g	3.40 b-d	9.50 b	3.33 d-i	17.77 b	5.10 c-e	86.33 g	1.35 cd
G2	71.00 a-e	83.00 a-e	87.33 b-f	3.67 bc	1.67 c-e	4.67 d-g	2.93 d-i	7.50 ef	3.40 c-g	11.50 z	5.13 b-e	88.33 fg	1.20 c-e
G3	70.33 a-f	81.33 a-f	77.00 c-h	2.67 c-e	2.00 c-e	5.67 b-d	2.93 d-i	7.93 e	3.43 b-f	12.57 d	5.10 c-e	105.67 d	1.77 ab
G4	74.33 a	84.00 a-d	87.00 b-f	1.33 e	1.00 e	4.33 e-g	2.87 e-i	**11.00** a	3.20 g-j	11.89 de	4.93 e-h	96.33 e	1.19 c-f
G5	71.33 a-d	82.33 a-e	81.67 b-g	2.67 c-e	1.67 c-e	7.00 a	3.63 ab	9.80 b	3.33 d-i	9.07 g	5.70 a	66.33 i-k	1.68 ab
G6	73.33 ab	84.67 a-c	69.00 d-h	2.33 c-e	1.33 de	4.67 d-g	**4.08** a	7.73 e	3.40 c-g	19.33 a	5.37 a-c	94.33 ef	1.79 ab
G7	74.00 a	84.33 a-c	78.33 b-g	2.00 c-e	1.67 c-e	4.67 d-g	2.17 k	7.20 fg	3.63 b	12.10 de	5.13 b-e	172.33 a	1.74 ab
G8	70.33 a-f	81.67 a-f	88.67 b-e	3.33 cd	2.67 bc	4.33 e-g	2.80 f-j	7.90 e	3.60 bc	10.30 f	5.13 b-e	163.67 b	1.96 a
G9	69.33 b-g	80.67 c-f	83.67 b-g	2.00 c-e	1.7 c-e	5.67 b-d	3.33 b-e	8.47 d	3.33 d-i	10.40 f	5.23 b-e	80.00 h	1.50 bc
G10	69.33 b-g	81.00 b-f	63.33 gh	2.67 c-e	1.67 c-e	4.33 e-g	2.83 f-j	7.50 ef	3.37 d-h	9.07 g	5.00 d-g	61.33 j-n	0.75 ij
G11	64.33 hi	76.00 g-i	67.33 e-h	2.67 c-e	1.67 c-e	5.00 def	2.53 i-k	9.00 c	3.10 j	7.40 hi	4.67 g-i	60.67 k-n	0.77 h-j
G12	67.66 c-h	79.67 d-g	65.67 f-h	2.33 c-e	1.67 c-e	3.00 h	3.17 b-g	7.83 e	3.13 ij	14.57 c	4.93 e-h	122.33 c	1.16 d-g
G13	67.00 d-h	79.67 d-g	**114.00** a	3.67 bc	1.67 c-e	7.33 a	2.93 d-i	6.47 h-j	3.37 d-h	7.60 hi	5.00 d-g	55.33 no	1.19 c-f
G14	60.66 ij	73.00 ij	87.67 b-f	3.00 c-e	2.33 cd	4.33 e-g	3.20 b-f	6.70 hi	3.17 h-j	7.43 hi	4.73 f-i	60.00 l-n	0.83 h-j
G15	66.66 e-h	78.67 e-g	68.33 e-h	2.33 c-e	1.33 de	5.33 c-e	2.70 g-j	6.43 h-j	3.33 d-i	7.43 hi	4.90 e-h	56.33 m-o	0.81 h-j
G16	58.00 j	**69.33** j	89.00 b-e	3.33 cd	2.00 c-e	4.67 d-g	3.07 c-h	6.33 i-k	3.50 b-e	7.33 hi	5.47 ab	64.67 j-l	0.92 e-j

Table 4. Mean performance of yield and yield contributing characters tomato genotypes (cont.)

Genotype	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	p^H	LC	Br	IFW	YP
G17	65.00 g-i	77.67 f-h	99.00 a-c	5.33 ab	2.67 bc	5.33 c-e	2.70 g-j	6.13 jk	3.30 e-j	8.00 h	5.00 d-g	56.67 m-o	0.81 h-j
G18	64.67 hi	75.33 g-i	97.67 a-c	5.67 a	4.00 a	6.33 a-c	2.63 h-k	6.77 g-i	3.23 f-j	7.30 hi	4.67 g-i	62.33 j-m	1.04 e-i
G19	71.33 a-d	81.67 a-f	78.33 b-g	3.67 bc	1.67 c-e	6.67 ab	3.00 d-i	6.40 h-j	3.53 b-d	7.33 hi	4.60 hi	53.67 o	1.07 d-h
G20	65.00 g-i	73.33 h-j	100.67 ab	6.00 a	3.67 ab	5.33 c-e	3.33 b-e	**5.93** k	3.13 ij	7.93 h	5.03 c-f	60.33 k-n	1.07 d-h
G21	68.33 c-h	79.67 d-g	69.33 d-h	3.00 c-e	1.33 de	5.00 d-f	3.50 bc	6.40 h-j	4.17 a	10.33 f	5.20 b-e	86.33 g	1.49 bc
G22	73.67 ab	**85.67** a	**91.67** a-d	3.33 cd	1.33 de	4.00 f-h	2.37 jk	6.10 jk	3.47 b-e	7.57 hi	5.03 c-f	63.33 j-l	0.61 j
G23	74.67 a	85.33 ab	78.67 b-g	3.00 c-e	1.33 de	4.33 e-g	2.73 f-j	6.47 h-j	3.33 d-i	7.20 i	4.67 g-i	72.00 i	0.85 h-j
G24	71.67 a-c	82.33 a-e	78.67 b-g	1.67 de	1.33 de	3.67 gh	3.33 b-e	6.83 gh	3.40 c-g	7.80 hi	4.40 i	71.00 i	0.85 g-j
G25	71.67 a-c	84.33 a-c	83.00 b-g	2.33 c-e	1.33 de	4.33 e-g	3.03 c-h	6.67 hi	3.43 b-f	7.83 hi	5.33 b-d	67.33 ij	0.88 f-j
Min.	58.00	69.33	54.67	1.33	1.00	3.00	2.17	5.93	3.10	7.20	4.40	53.67	0.61
Max.	74.67	85.67	114.00	6.00	4.00	7.33	4.08	11.00	4.17	19.33	5.70	172.33	1.96
Mean	**68.60**	79.83	81.79	3.12	1.89	5.00	3.02	7.48	3.40	10.14	5.02	83.44	1.18
SE	2.22	2.29	11.33	0.99	0.55	0.61	0.25	0.22	0.11	0.36	0.17	3.01	0.15
$LSD_{0.05}$	4.46	4.61	22.78	2.00	1.10	1.22	0.50	0.45	0.22	0.73	0.33	6.04	0.31

DFF = Days to first flowering, DFFr = Days to first fruit setting, PH= Plant height (cm), NPB= No. of primary branches per plant, NSB= No. of secondary branches per plant, TNC= Total number of clusters per plant, NFC= No. of flowers per cluster, SDF = Skin diameter of the fruit (mm), p^H= Fruit p^H, LC= Lycopene content (mg), Br = Brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg). SE= Standard error, LSD=Least Significant Difference

Table 5. Estimation of genetic parameters of tomato genotypes

Parameters	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	pH	LC	Br	IFW	YP
σ_g^2	15.94	15.53	116.93	0.83	0.38	0.87	0.14	1.67	0.04	11.01	0.07	987.23	0.14
σ_p^2	23.32	23.42	309.49	2.31	0.83	1.42	0.24	1.75	0.06	11.20	0.11	1000.78	0.17
σ_e^2	7.38	7.88	192.56	1.48	0.45	0.56	0.09	0.08	0.02	0.20	0.04	13.55	0.04
GCV	**5.80**	4.93	13.25	29.65	33.50	18.66	12.60	17.47	5.90	33.56	5.34	38.75	31.82
PCV	**7.02**	6.05	21.56	49.37	49.41	23.91	16.15	17.86	7.10	33.86	6.71	39.02	35.68

DFF = Days to first flowering, DFFr = Days to first fruit setting, PH= Plant height (cm), NPB= No. of primary branches per plant, NSB= No. of secondary branches per plant, TNC= Total number of clusters per plant, NFC= No. of flowers per cluster, SDF = Skin diameter of the fruit (mm), p^H= Fruit p^H, LC= Lycopene content (mg), Br = Brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg), σ_g^2 = Genotypic variance, σ_p^2= Phenotypic variance, σ_e^2 = Environmental variance, GCV= Genotypic Co-efficient of variation, PCV =Phenotypic Co-efficient of variation

4.1.2 Days to first fruit setting

The first fruit setting was observed in G16 with 69.33 days. On the other hand, maximum duration was recorded in G22 with 85.67 days. Mean performance of days to first fruit setting was 79.83 days (Table 4). The phenotypic variance (23.42) appeared to be higher than the genotypic variance (15.53) suggested considerable influence of environment on the expression of genes controlling this trait. The GCV and PCV were 4.93 and 6.05 respectively, were more or less similar to each other that indicated presence of low variability in this trait (Table 5).

4.1.3 Plant height (cm)

The genotype G1 had the shortest plants (54.67 cm) and the genotype G13 had the tallest plants (114 cm). Mean performance of plant height was 81.79 cm (Table 4) & (Figure 1). The genotypic and phenotypic variance was observed as 116.93 and 309.49, respectively with large environmental influence (Table 5). The phenotypic co- efficient of variation (21.56 %) and genotypic co-efficient of variation (13.25 %) were moderate for plant height (Table 5).

4.1.4 Number of primary branches per plant

The grand mean number of primary branches per plant was found to 3.12 and ranged from 6.00 to 1.33. The maximum number of primary branches (6.00) was recorded in the genotype G20 and the minimum number of primary branches (1.33) was recorded in the G4. The phenotypic variance (2.31) appeared to be higher than the genotypic variance (0.83) suggested considerable influence of environment on the expression of genes controlling this trait. The GCV and PCV were 29.65 and 49.37, respectively (Table 5).

4.1.5 Number of secondary branches per plant

The grand mean number of secondary branches per plant was recorded 1.89. It ranged from 4.0 to 1.0 (Table 4). The maximum number of secondary branches (4.0) was recorded in the genotype G18 and the minimum (1.0) was recorded in G4. The mean performance of no. of secondary branches per plant was 1.89 (Table 4). The phenotypic variance (0.83) appeared to be higher than the genotypic variance (0.38) indicating minor environmental influence on this character.

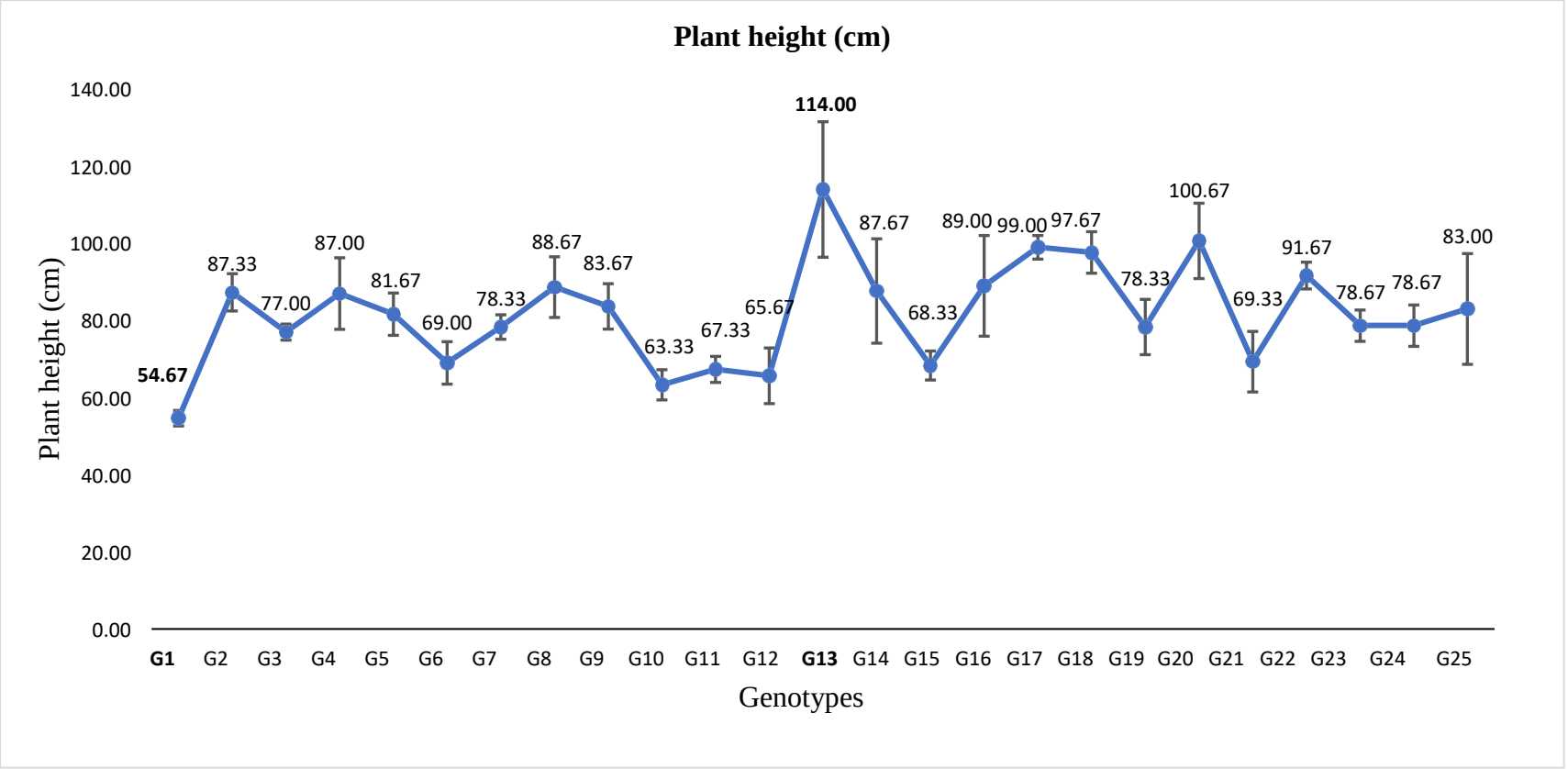

Figure 1. Mean performance of plant height (cm) in tomato genotypes

4.1.6 Number of clusters per plant

Significant differences were observed among the genotypes for number of clusters per plant which ranged from 7.33 (G13) to 3.0 in (G12) with mean value of 5.0 (Table 4). Mean performance of number of clusters per plant among the genotypes of tomato is represented in (Figure 2) through line graph. The cluster of tomato fruit is showed in (Plate 7). The genotypic variance and phenotypic variance for this trait were 0.87 and 1.42 respectively, indicating that environment had moderate influence for the expression of this trait (Table 5). Phenotypic and genotypic co-efficient of variation were moderate but the phenotypic variance appeared higher than the genotypic variance. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 18.66 % and 23.91%, respectively, which indicated presence of high variability among the genotypes (Table 5).

Plate 7. An individual plant with number of clusters of fruit

4.1.7 Number of flowers per cluster

The phenotypic variance (0.14) appeared to be higher than the genotypic variance (0.24) indicating minor environmental influence on this character. The GCV and PCV were moderate with 12.60 and 16.15 percent, respectively (Table 5).

4.1.8 Skin diameter of fruit (mm)

The variance due to skin diameter showed that the genotypes differed significantly and ranged from 11 mm in G4 to 5.93 mm in G20 with mean value 7.48 (Table 4). The genotypic variance and phenotypic variance for this trait were 1.67 and 1.75, respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (17.47) and PCV (17.86) were more or less similar to each other, indicated presence of high variability in this trait (Table 5).

4.1.9 Fruit p^H

The mean value of tomato p^H was 3.40 with a range of 4.17 (G21) to 3.10 (G11) (Table 4) with very low phenotypic and genotypic variance (0.04 and 0.06, respectively) (Table 5). Genotypic co-efficient of variation (5.90%) and phenotypic co-efficient variation (7.1 %) (Table 5) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato.

4.1.10 Lycopene Content (mg)

The lycopene content of fruit was ranged from 19.33 (Max. in G6) to 7.20 (Min. in G23) with mean value of 10.14 (Table 4). The phenotypic variance (11.01) appeared to be higher than the genotypic variance (11.20) indicating minor environmental influence on this character. The GCV (33.56) and PCV (33.86) were more or less similar to each other, indicated presence of high variability in this trait (Table 5).

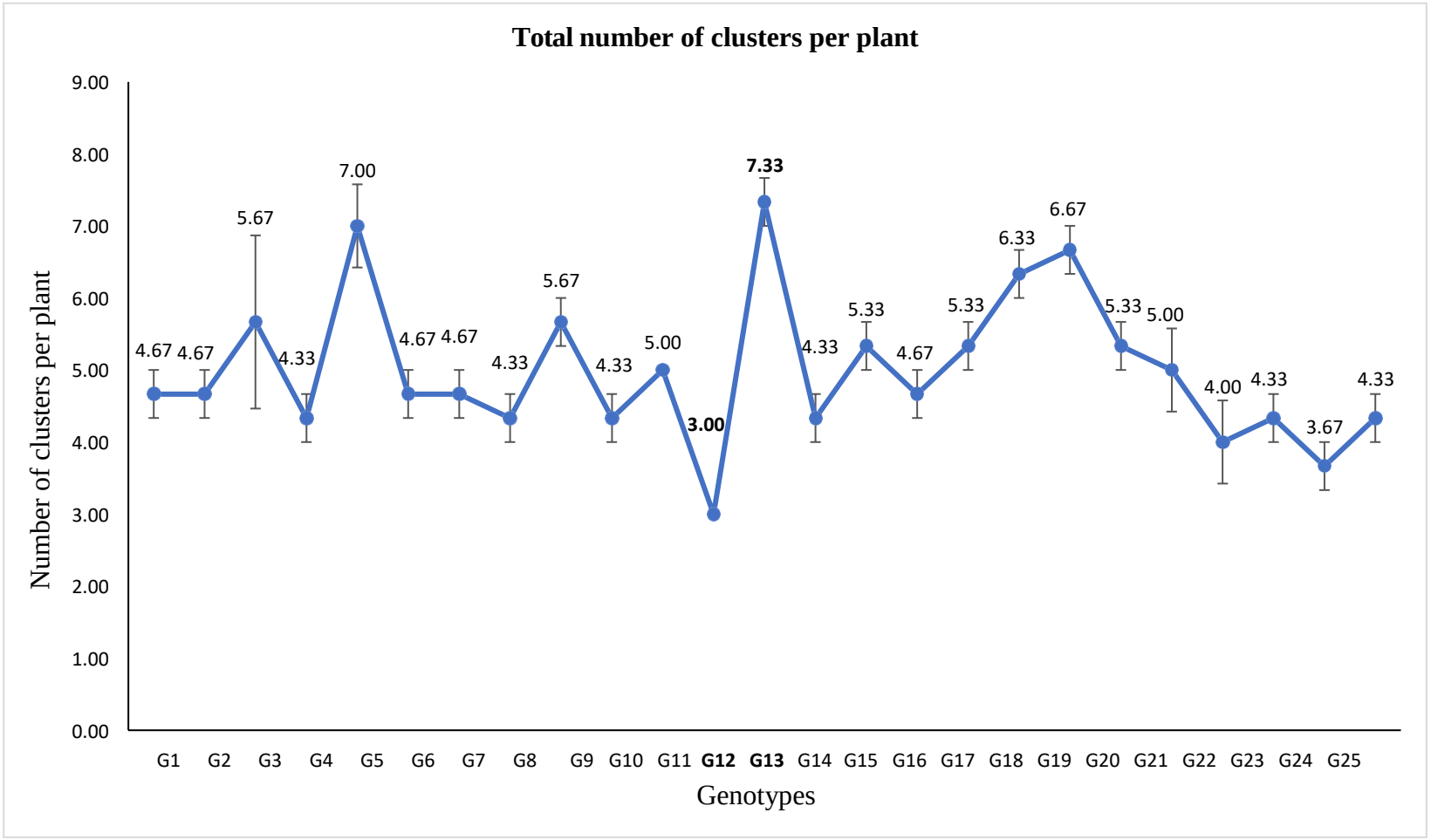

Figure 2. Mean performance of number of clusters per plant in tomato genotypes

4.1.11 Brix percentage (%)

Percentage of brix is primarily a measure of the Total Soluble Solid (TSS) content in tomato. Highly significant variations were observed among the tested genotypes for the character brix percentage (Table 3). The mean value of Brix percent was 5.02 with a range of 5.70% (G5) to 4.40% (G24) with very low phenotypic and genotypic variance (0.07 and 0.11 respectively) in (Table 5). The GCV (5.34%) and PCV (6.71 %) (Table 5) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato.

4.1.12 Individual fruit weight (g)

The maximum fruit weight was recorded (172.33g) in G7 and minimum was recorded (53.67g) in G19 with mean value of 83.44 (Table 4). The genotypic variance (987.23) and phenotypic variance (1000.78) for fruit weight was high (Table 5). The genotypic co-efficient of variation (38.75 %) and phenotypic co-efficient of variation (39.02 %) were high and close to each other, proved that environment has little influence on the expression of this character (Table 4). Therefore, selection based upon this character would be effective for the improvement of this crop. High GCV and PCV for average fruit weight were also noticed by Manivannan *et al*., (2005) and Singh *et al*., (2002). Individual fruit wt. of tomato showed in Plate 8.

Plate 8. Measuring individual fruit weight (g) by an electric weight balance

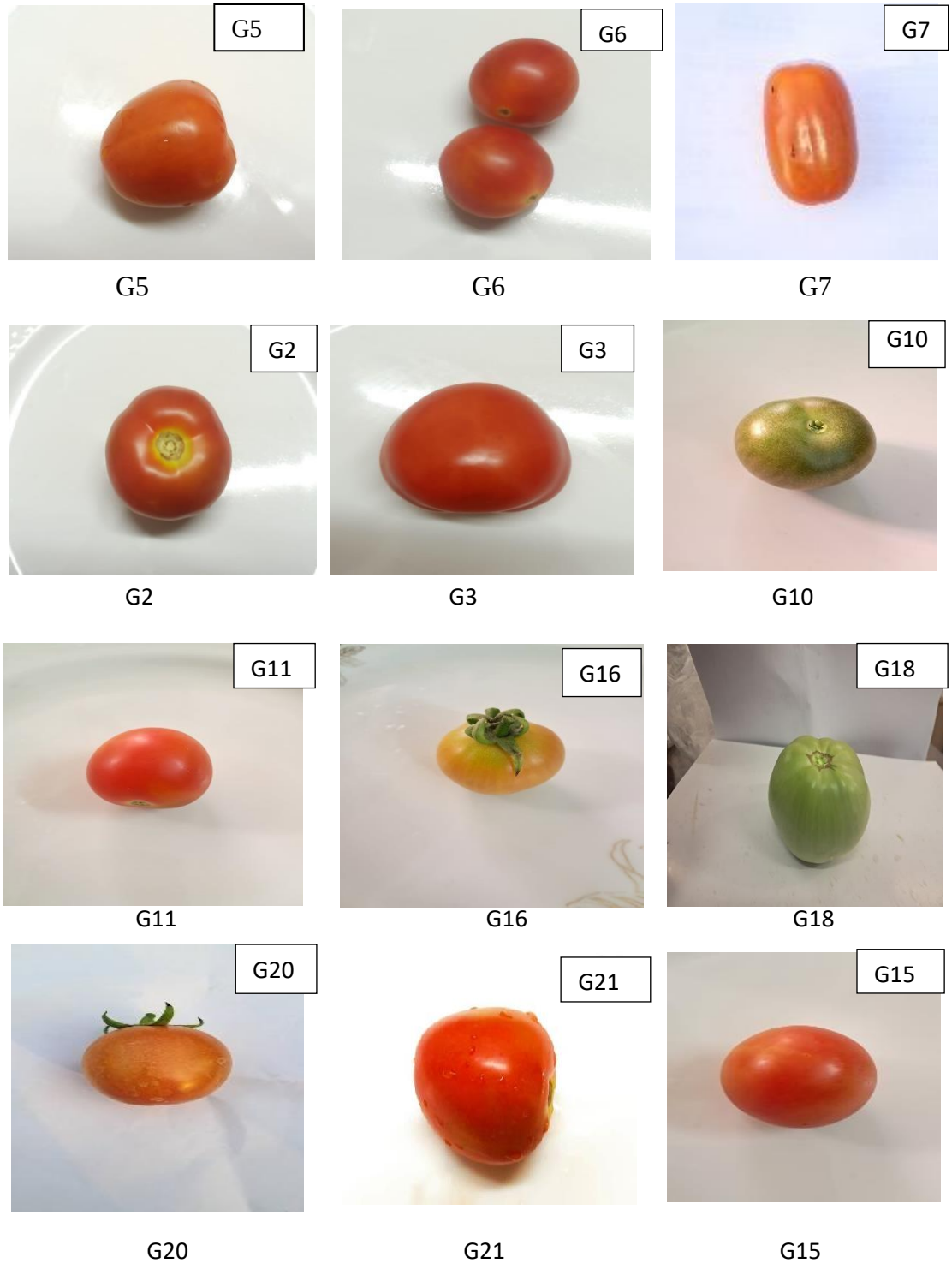

Plate 9. Individual fruit of different tomato genotypes

4.1.13 Yield per plant (kg)

Highest fruit yield per plant was found (1.96 kg) in G8 and the lowest was recorded (0.61 kg) in G22 with mean value of 1.18 (Table 4). The phenotypic co-efficient of variation and genotype co-efficient of variation were 35.68 % and 31.82%, respectively for fruit yield per plant, which indicating that significant variation exists among different genotypes which made the trait effective for selection (Table 5).

4.2 Heritability, genetic advance and genetic advance in percentage of mean

The co-efficient of variation does not permit the full opportunity for heritable variation. It can be discerned with greater degree of accuracy when heritability in association with genetic advance is discussed. Hence, heritability and genetic advance are essential parameters to study the scope of improvement in various characters via selection. Heritability, genetic advance and genetic advance in percent of means for yield and yield contributing characters of 25 genotypes are presented in (Table 5) and also figured through line graph (Figure 3).

4.2.1 Days to first flowering

High heritability (68.33%) in association with low genetic advance (6.80) was noted for this character rendering them unfit for improvement through simple selection due to prevalence of non-additive gene action. Lower value of genetic advance in percent of mean (9.88) was also recorded (Figure 3).

4.2.2 Days to first fruit setting

High heritability of 66.34% with low genetic advance (6.61) was noted for the character and the value of genetic advance in percent of mean was lower (8.26) in (Figure 3). High heritability having low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective.

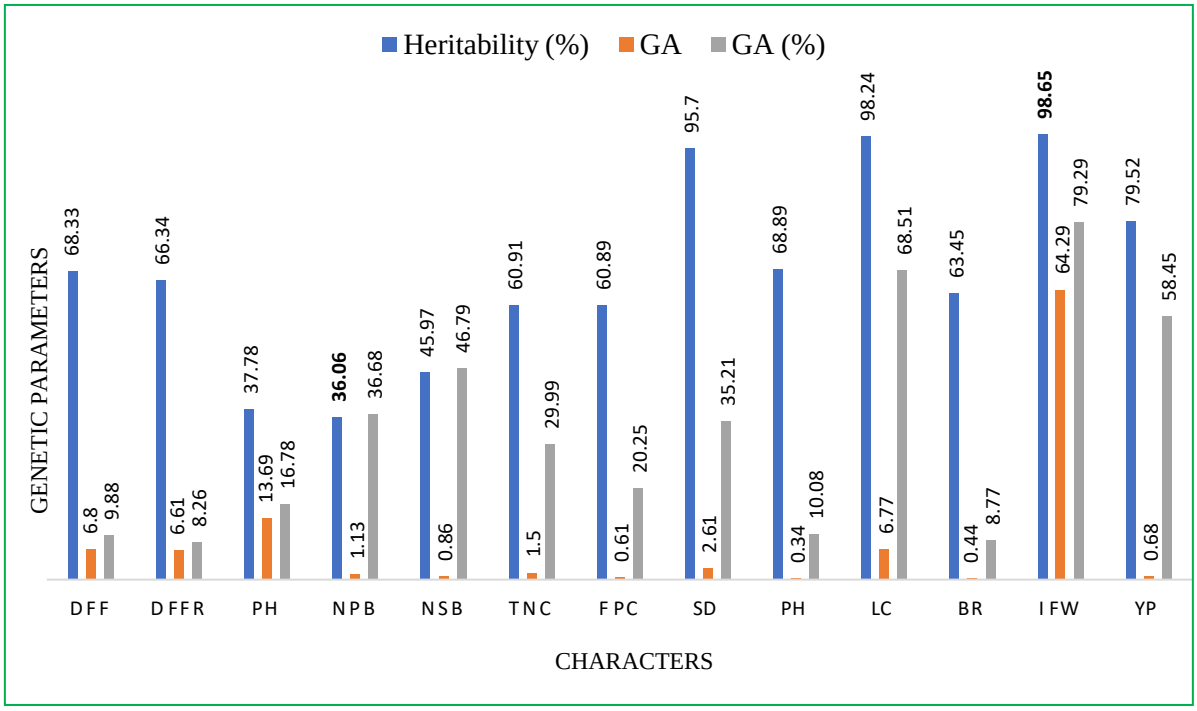

Figure 3. Heritability (%), genetic advance and genetic advance in percent of means for yield and yield contributing characters of tomato

DFF = Days to first flowering, DFFr = Days to first fruit setting, PH= Plant height (cm), NPB= No. of primary branches per plant, NSB= No. of secondary branches per plant, TNC= Total number of clusters per plant, FPC= No. of flowers per cluster, SD = Skin diameter of the fruit (mm), p^H= Fruit p^H, LC= Lycopene content (mg), BR = Brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg); GA= Genetic advance, GA (%) = Genetic advance in percentage of mean

4.2.3 Plant height (cm)

Low heritability 37.78% along with moderate genetic advance (13.69) in (Figure 3) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait, whereas genetic advance in percent mean was recorded moderate (16.78) in (Figure 3).

4.2.4 Number of primary branches per plant

Lowest heritability 36.06 % along with low genetic advance (1.13) indicating the presence of non-additive gene action which was responsible for the ineffectiveness of the selection for this trait. Higher value of genetic advance in percent of mean (36.68) was also recorded (Figure 3).

4.2.5 Number of secondary branches per plant

High heritability of 45.97% with low genetic advance (0.86) was noted for the character and the value of genetic advance in percent of mean was high (46.79) (Figure 3). High heritability with high genetic advance in percent of mean suggested the prevalence of additive gene action. So, improvement through selection might be so effective.

4.2.6 Number of clusters per plant

High heritability of 60.91% with low genetic advance was noted for the character number of clusters per plant and the value of genetic advance (%) of mean was high (29.99) in (Figure 3). So, improvement through selection might be effective. The clusters per plant is showed in Plate 10.

Plate 10. The number of clusters of fruit per plant

4.2.7 Number of flowers per cluster

High heritability 60.89 % along with low genetic advance (0.61) indicating the presence of

non-additive gene action which was responsible for the ineffectiveness of the selection for this trait whereas genetic advance in percent mean was recorded moderate (20.25) in (Figure 3).

4.2.8 Skin diameter of fruit (mm)

The heritability for skin diameter were high (95.70%) with low genetic advance (2.61%) and genetic advance in percentage of mean was high (35.21%) in (Figure 3). That indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which was in accordance with the findings of (Saeed *et al.*, 2007) high heritability for skin diameter were reported (Plate 11).

Plate 11. T.S. section of tomato fruit for measuring skin diameter (mm)

4.2.9 Fruit p^H

High heritability 68.89% with low genetic advance (0.34) indicating the presence of non-additive gene action and so selection was not so effective for the improvement of the crop. Low value of genetic advance in percentage of mean was recorded (10.08) for this trait (Figure 3).

4.2.10 Lycopene Content (mg)

High heritability of 98.24% was noted for the character number of clusters per plant and the value of genetic advance (%) of mean was high (68.51) in (Figure 3). High heritability with high genetic advance in percent of mean suggested the prevalence of additive gene action.

4.2.11 Brix percentage (%)

High heritability of 63.45% with low genetic advance (0.44) was noted for the character and the value of genetic advance in percent of mean was lower (8.77) in (Figure 3). High heritability having low genetic advance suggested the prevalence of non- additive gene action and so, improvement through selection might not be so effective.

4.2.12 Individual fruit weight (g)

High heritability of 98.65% with high genetic advance (64.29) was noted for the character and the value of genetic advance in percent of mean was also high (79.29) in (Figure 3). High heritability with high genetic advance indicated the presence of additive gene action. So, improvement through selection might be so useful.

4.2.13 Yield per plant (kg)

High heritability of 79.52% with low genetic advance (0.68) was noted for the character number of clusters per plant and the value of genetic advancein percent of mean was high (58.45) in (Figure 3). High heritability with high genetic advance in percent of mean suggested the prevalence of additive gene action.

4.3 Correlation co-efficient analysis

Correlation co-efficient is a numerical measure of some type of interrelation to detect the direction and strength of relationship between the relative movements of two or more variables. The values of correlation co-efficient ranges between -1.0 and +1.0. A correlation of -1.0 exhibits a perfect negative correlation, whereas a correlation of +1.0 exhibits a perfect positive correlation between the traits. A correlation of 0.0 exhibits no relationship between the movements of the two variables.

Yield being a target character is governed by polygene and highly influenced by the environment. So, selection based on only yield itself is ineffectual. When selection is done for any character which is highly correlated with yield, it may affect other correlated characters simultaneously. Therefore, knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection vis-à-vis provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Both genotypic and phenotypic correlation co-efficient of different characters of tomato are presented in Table 7 and Table 8. It was conspicuous that genotypic correlation co-efficient were higher than their analogous phenotypic ones suggested that these traits were strongly correlated genetically and the phenotypic expression of these traits was less influenced by the environment. Similar result was found by (Pankaj *et al.*, 2002). In many cases, phenotypic correlation co-efficient was higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation performed in the same direction and finally maximized their expression at phenotypic level.

4.3.1 Days to first flowering

Days to first flowering exhibited highly significant and positive correlation with days to first fruit setting (r_g = 0.986, r_p =0.949), lycopene content (mg) (r_g = 0.293, r_p =0.229), individual fruit weight (g) (r_g = 0.399, r_p =0.324) and yield per plant (kg) (r_g = 0.329, r_p =0.282) at genotypic and phenotypic level respectively. Days to first flowering also exhibited highly significant and positive correlation with skin diameter of fruit (mm) (r_g = 0.252) and fruit p^H (r_g = 0.290) at genotypic level. It means a possible increase in days to first fruit setting, lycopene content (mg), individual fruit weight (g) and yield per plant (kg) by increasing days to first flowering. It exhibited highly significant and negative correlation with number of primary branches per plant (r_g = -0.621, r_p = -0.274) and number of secondary branches per plant (r_g = -0.582, r_p = -0.396) at genotypic and phenotypic level. Which indicated a possible increase in number of primary branches per plant and number

of secondary branches per plant by decreasing days to first flowering. It also showed insignificant and positive correlation with skin diameter of fruit (mm) (r_p = 0.214), fruit p^H (r_p = 0.159) at phenotypic level and brix percentage (%) (r_g =0.044) at genotypic level. It also showed insignificant and negative correlation with number of clusters per plant (r_g = -181, r_p = -0.062) and number of flowers per cluster (r_g = -0.029, r_p = -0.084) at genotypic and phenotypic level. It also showed insignificant and negative correlation with brix percentage (%) (r_p = -0.396 at phenotypic level. Insignificant association of these traits revealed that the combination between these traits was largely influenced by environmental factors. (Table 6 and 7).

4.3.2 Days to first fruit setting

Days to first fruit setting showed highly significant and positive correlation with individual fruit weight (g) (r_g = 0.360, r_p = 0.290) and yield per plant (kg) (r_g = 0.269, r_p = 0.227) at both genotypic and phenotypic level. It also showed highly significant and positive correlation with fruit p^H (r_g = 0.302), and lycopene content (%) (r_g = 0.246) at genotypic level. It stated that a possible increase in individual fruit weight (g), yield per plant (kg), fruit p^H and lycopene content (mg) increase the days to first fruit setting. Days to first fruit setting showed highly significant and negative correlation with number of primary branches per plant (r_g = -0.697, r_p = -0.270) and number of secondary branches per plant (r_g = -0.679, r_p = -0.411) at both genotypic and phenotypic level.

It means possible increase in number of primary branches per plant and number of secondary branches per plant decreases the days to first fruit setting. It showed insignificant and positive correlation with skin diameter of fruit (mm) (r_g = 0.182, r_p = 0.161) at both genotypic and phenotypic level, fruit p^H (r_p = 0.185), lycopene content (mg) (%) (r_p = 0.181) at phenotypic level and brix percentage (%) (r_g = 0.096) at genotypic level. It showed insignificant and negative correlation with plant height (cm) (r_g = -0.208, r_p = -0.062), number of clusters per plant (r_g = -0.186, r_p = -0.089), number of flowers per clusters (r_g = -0.082, r_p = -0.101) at both genotypic and phenotypic level, and brix percentage (%) (r_p = 0.005) at phenotypic level insignificant association of these traits revealed that the combination between these traits was largely influenced by environmental factors (Table 6 and 7).

Table 6. Genotypic correlation co-efficient among yield and yield contributing characters of tomato

Trait	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	p^H	LC	Br	IFW	YP
DFF	1												
DFFr	**0.986****	1											
PH	-0.226*	-0.208ns	1										
NPBP	-0.621**	-0.697**	0.676**	1									
NSBP	-0.582**	-0.679**	0.672**	1.032**	1								
TNCP	-0.181ns	-0.186ns	0.488**	0.593**	0.451**	1							
NFPC	-0.029ns	-0.082ns	-0.245*	-0.228*	-0.170ns	0.176ns	1						
SDF	0.252*	0.182ns	-0.470**	-0.658**	-0.375**	-0.003ns	0.195ns	1					
p^H	0.290*	0.302**	-0.113ns	-0.161ns	-0.317**	0.058ns	0.063ns	-0.285*	1				
LC	0.293**	0.246*	-0.639**	-0.413**	-0.340**	-0.290*	0.506**	0.493**	0.071ns	1			
Br	0.044ns	0.096ns	-0.005ns	-0.153ns	-0.152ns	0.170ns	0.434**	0.246*	0.406**	0.370**	1		
IFW	0.399**	**0.360****	-0.250*	-0.408**	-0.070ns	-0.392**	-0.158ns	0.286*	0.316**	0.528**	**0.236***	1	
YP	0.329**	**0.269***	-0.162ns	-0.228*	0.063ns	0.142ns	0.392**	0.425**	0.416**	0.638**	0.571**	**0.738****	1

DFF = Days to first flowering, DFFr = Days to first fruit setting, PH= Plant height (cm), NPB= No. of primary branches per plant, NSB= No. of secondary branches per plant, TNC= Total number of clusters per plant, NFC= No. of flowers per cluster, SDF = Skin diameter of the fruit (mm), p^H= Fruit p^H, LC= Lycopene content (mg), Br = Brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg); Genetic advance in percentage of mean, ns= non-significant

Table 7. Phenotypic correlation co-efficient among yield and yield contributing characters tomato

Trait	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	p^H	LC	Br	IFW	YP
DFF	1												
DFFr	**0.949****	1											
PH	-0.092ns	-0.062ns	1										
NPBP	-0.274*	-0.270*	0.470**	1									
NSBP	-0.396**	-0.411**	0.388**	0.665**	1								
TNCP	-0.062ns	-0.089ns	0.331**	0.189ns	0.093ns	1							
NFPC	-0.084ns	-0.101ns	-0.204ns	-0.023ns	-0.071ns	-0.062ns	1						
SDF	0.214ns	0.161ns	-0.253*	-0.342**	-0.252*	-0.037ns	0.199ns	1					
p^H	0.159ns	0.185ns	-0.154ns	-0.103ns	-0.191ns	0.010ns	0.076ns	-0.242*	1				
LC	0.229*	0.181ns	-0.386**	-0.246*	-0.218ns	-0.221ns	0.402**	0.482**	0.046ns	1			
Br	-0.000ns	-0.005ns	0.012ns	-0.039ns	-0.082ns	0.140ns	0.281*	0.199ns	0.124ns	0.307**	1		
IFW	0.324**	**0.290***	-0.147ns	-0.257*	-0.042ns	-0.306**	-0.135ns	0.271*	0.272*	0.517**	**0.170ns**	1	
YP	0.282*	**0.227***	-0.053ns	-0.172ns	-0.063ns	0.318**	0.304**	0.364**	0.305**	0.571**	0.429**	**0.659****	1

DFF= Days to 1st flowering, DFFr= days to first fruit setting, PH= plant height (cm), NPB= no. of primary branches per plant, NSB= no. of secondary branches per plant, TNC= total number of cluster per plant, NFC= number of flower per cluster, SDF = Skin diameter of the fruit (mm), p^H= fruit p^H, LC= lycopene content, Br= brix (%), IFW= individual fruit weight (g), YP= yield per plant (kg), GA= Genetic advance, GA (%)= Genetic advance in percentage of mean, ns= non-significant

4.3.3 Plant height (cm)

Plant height (cm) showed highly significant and positive correlation with number of primary branches per plant (r_g = 0.676, r_p = 0.470), number of secondary branches per plant (r_g = 0.672, r_p = 0.388) and number of clusters per plant (r_g = 0.488, r_p = 0.331) at both genotypic and phenotypic level. It stated that a possible increase in number of primary branches per plant, number of secondary branches per plant and number of clusters per plant increases the plant height (cm). It showed insignificant and positive correlation with brix percentage (%) (r_p = 0.012) at phenotypic level.

Plant height (cm) showed significant and negative correlation with skin diameter of fruit (mm) (r_g = -0.470, r_p = -0.253), lycopene content (mg) (%) (r_g = -0.639, r_p = -0.386) at both genotypic and phenotypic level and number of flowers per clusters (r_g = -0.228) individual fruit weight (g) (r_g = -0.250) at genotypic level. It stated that skin diameter of fruit (mm), lycopene content (%), number of flowers per cluster and individual fruit weight (g) had a very little association with plant height. Plant height (cm) exhibited insignificant and negative correlation with fruit p^H (r_g = -0.113, r_p = -0.154) and yield per plant (kg) (r_g = -0.162, r_p = -0.053) at both genotypic and phenotypic level. And exhibited insignificant and negative correlation with number of flowers per cluster (r_p = -0.204) at genotypic level, brix percentage (%) (r_g = -0.005) and individual fruit weight (g) (r_p = -0.147) at phenotypic level. It stated that a possible increase in number of flowers per cluster, brix percentage (%) and individual fruit weight (g) decreases plant height (cm) (Table 6 and 7).

4.3.4 Number of primary branches per plant

Number of primary branches per plant showed highly significant and positive correlation with number of secondary branches per plant (r_g = 1.032, r_p = 0.665) at both genotypic and phenotypic level and number of clusters per plant (r_g = 0.593) at genotypic level stated that a possible increase in number of secondary branches per plant and number of clusters per plant increases the number of primary branches per plant. It showed insignificant and positive correlation with number of clusters per plant (r_p = 0.189) at phenotypic level. Number of primary branches per plant showed highly significant and negative correlation with skin diameter of fruit (mm) (r_g = -0.658, r_p = -0.342), lycopene content (mg) (r_g = -0.413, r_p = -0.246) and individual fruit weight (g) (r_g = -0.408, r_p = -0.257) at both genotypic

and phenotypic level. It also showed significant and negative correlation with number of flowers per cluster (r_g = -0.228) and yield per plant (kg) (r_g = -0.228) at genotypic level. It stated that number of flowers per cluster and yield per plant (kg) had a very little association with number of primary branches per plant. Number of primary branches per plant exhibited insignificant and negative correlation with fruit p^H (r_g = -0.161, r_p = -0.103) and brix percentage (%) (r_g = -0.153, r_p = -0.039) at both genotypic and phenotypic level and number of flowers per clusters (r_p = -0.023) and yield per plant (kg) (r_p = -0.172) at phenotypic level (Table 6 and 7).

4.3.5 Number of secondary branches per plant

Number of secondary branches per plant showed highly significant and positive correlation with number of clusters per plant (r_g = 0.451) at genotypic level stated that a possible increase in number of clusters per plant increases the number of secondary branches per plant. Number of secondary branches per plant showed insignificant and positive correlation with number of clusters per plant (r_p = 0.318) at phenotypic level and yield per plant (kg) (r_g = 0.063) at genotypic level. It showed significant and negative correlation with skin diameter of fruit (mm) (r_g = -0.375, r_p = -0.252) at both genotypic and phenotypic level. It also showed significant and negative correlation with fruit p^H (r_g = -0.317) and lycopene content (%) (r_g = -0.340) at genotypic level. It stated that fruit p^H and lycopene content (mg) had a very little association with number of secondary branches per plant. Number of secondary branches per plant showed insignificant and negative correlation with number of flowers per cluster (r_g = -0.170, r_p = -0.071), brix percentage (%) (r_g = -0.152, r_p = -0.082) and individual fruit weight (g) (r_g = -0.070, r_p = -0.042) at both genotypic and phenotypic level. Also exhibited insignificant and negative correlation with fruit p^H (r_p = -0.191) and yield per plant (kg) (r_p = -0.063) at phenotypic level stated that a possible increase in fruit p^H and yield per plant (kg) decreases number of secondary branches per plant (Table 6 and 7).

4.3.6 Number of clusters per plant

Number of clusters per plant showed highly significant and positive correlation with yield per plant (kg) (r_p = 0.318) at phenotypic level stated that a possible increase in yield per plant (kg) increases the number of clusters per plant. Number of clusters per plant showed

insignificant and positive correlation with plant height (cm) (r_g = 0.058, r_p = 0.010) and brix percentage (%) (r_g = 0.170, r_p = 0.140) at both genotypic and phenotypic level. It also exhibited insignificant and positive correlation with number of flowers per cluster (r_g = 0.170) and yield per plant (kg) (r_g = 0.142) at genotypic level stated that it had a very little association with number of clusters per plant. It showed significant and negative correlation with individual fruit weight (g) (r_g = -0.392, r_p = -0.306) at both genotypic and phenotypic level. It also showed significant and negative correlation with lycopene content (mg) (r_g = -0.290) at genotypic level. Number of clusters per plant showed insignificant and negative correlation with skin diameter of fruit (mm) (r_g = -0.003, r_p = -0.037) at both genotypic and phenotypic level. Also exhibited insignificant and negative correlation with flower per clusters (r_p = -0.062) and lycopene content (%) (r_p = -0.221) at phenotypic level (Table 6 and 7).

4.3.7 Number of flowers per cluster

Number of flowers per cluster exhibited highly significant and positive correlation with lycopene content (mg) (r_g = 0.506, r_p = 0.402), brix percentage (%) (r_g = 0.434, r_p = 0.281) and yield per plant (kg) (r_g = 0.392, r_p = 0.304) at both genotypic and phenotypic level. It indicates a possible increase in lycopene content (mg), brix percentage (%) and yield per plant (kg) increases the number of flowers per clusters. It showed insignificant and positive correlation with skin diameter of fruit (mm) (r_g = 0.195, r_p = 0.199) and fruit p^H (r_g = 0.063, r_p = 0.076) at both genotypic and phenotypic level stated that it had a very little association with number of flowers per clusters. It showed insignificant and negative correlation with individual fruit weight (g) (r_g = -0.158, r_p = -0.135) at both genotypic and phenotypic level stated that a possible increase in individual fruit weight (g) decreases number of flowers per clusters (Table 7 and 8).

4.3.8 Skin diameter of fruit (mm)

Skin diameter of fruit (mm) exhibited highly significant and positive correlation with lycopene content (mg) (r_g = 0.493, r_p = 0.482), individual fruit weight (g) (r_g = 0.286, r_p = 0.271) and yield per plant (kg) (r_g = 0.425, r_p = 0.364) at both genotypic and phenotypic level. It also exhibited highly significant and positive correlation with brix percentage (%) (r_g = 0.264) at genotypic level. It indicates a possible increase in lycopene content (mg),

brix percentage (%), individual fruit weight (g) and yield per plant (kg) increases the skin diameter of fruit (mm). It also exhibited highly significant and positive correlation with brix percentage (%) (r_g = 0.264) at genotypic level. Skin diameter of fruit (mm) exhibited highly significant and negative correlation with plant height (cm) (r_g = -0.285, r_p = -0.242) at both genotypic and phenotypic level stated that a possible increase in plant height (cm) decreases the skin diameter of fruit (mm) in Table 6 and Table 7.

4.3.9 Fruit p^H

Fruit p^H exhibited highly significant and positive correlation with individual fruit weight (g) (r_g = 0.316, r_p = 0.272) and yield per plant (kg) (r_g = 0.416, r_p = 0.305) at both genotypic and phenotypic level. It also exhibited highly significant and positive correlation with brix percentage (%) (r_g = 0.406) at genotypic level. It indicates that increase in brix percentage (%), individual fruit weight (g) and yield per plant (kg) increases the fruit p^H. It also showed insignificant and positive correlation with lycopene content (mg) (r_g = 0.071, r_p = 0.046) at both genotypic and phenotypic level and brix percentage (%) (r_p = 0.124) at phenotypic level stated that it had a very little association with fruit p^H in (Table 6 and 7).

4.3.10 Lycopene Content (mg)

Lycopene content (mg) exhibited highly significant and positive correlation with brix percentage (%) (r_g = 0.370, r_p = 0.307), individual fruit weight (g) (r_g = 0.528, r_p = 0.517) and yield per plant (kg) (r_g = 0.638, r_p = 0.571) at both genotypic and phenotypic level. It indicates a possible increase in brix percentage (%), individual fruit weight (g) and yield per plant (kg) increases the lycopene content (mg) in (Table 6 and 7).

4.3.11 Brix percentage (%)

Brix percentage (%) exhibited highly significant and positive correlation with yield per plant (kg) (r_g = 0.571, r_p = 0.429) at both genotypic and phenotypic level. It also exhibited highly significant and positive correlation with individual fruit weight (g) (r_g = 0.236) at genotypic level. It indicates a possible increase in individual fruit weight (g) and yield per plant (kg) increases the brix percentage (%). It also showed insignificant but positive correlation with individual fruit weight (g) (r_p=0.170) at phenotypic level stated that it had a very little association with brix percentage (%) (Table 6 and 7).

4.3.12 Individual fruit weight (g)

Individual fruit weight (g) exhibited highly significant and positive correlation with yield per plant (kg) ($r_g = 0.738$, $r_p = 0.659$) at both genotypic and phenotypic level indicating that an increase in individual fruit weight (g) tends to increase yield per plant (kg) showed in (Table 6 and 7).

4.4 Path co-efficient analysis

Simple correlation cannot reveal complex correlations between the many attributes associated to the dependent variable. The linear relationship between variables is shown by correlation co-efficient. However, when the direct relationship between the variables is necessary, merely describing these associations is insufficient. In order to assess the direct or indirect impacts of yield-contributing features on fruit yield per plant and estimate the relative importance of each component on fruit yield per plant, it was indicated that path co-efficient analysis is the most popular statistical method. Fruit yield per plant is considered as dependent (resultant) variable and its attributes as independent variables (causal) such as days to first flowering, days to first fruit setting, plant height, number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of flowers per clusters, skin diameter of fruit (mm), fruit p^H, lycopene content (mg), brix percentage (%) and individual fruit weight (g). Path co-efficient analysis for estimating direct and indirect effects of yield contributing characters on fruit yield per plant of 25 tomato genotypes are presented in (Table 8).

4.4.1 Days to first flowering

Path co-efficient analysis revealed that days to first flowering had positive direct effect (0.808) on yield per plant. The trait showed positive indirect effect on yield per plant via days to first fruit setting (0.797), skin diameter of fruit (mm) (0.204), fruit p^H (0.235), lycopene content (mg) (0.237), brix percentage (%) (0.036) and individual fruit weight (g) (0.322) followed by negative indirect effect via plant height (cm) (-0.183), number of primary branches per plant (-0.502), number of secondary branches per plant (-0.470), number of clusters per plant (-0.146), number of flower per clusters (-0.023). Finally, the trait showed highly significant positive genotypic correlation with the yield per plant(kg).

4.4.2 Days to first fruit setting

Days to first fruit setting showed negligible negative direct effect (-0.784) towards yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.163), number of primary branches per plant (0.547), number of secondary branches per plant (0.532), number of clusters per plant (0.146), number of flowers per clusters (0.064). The trait showed negative indirect effect on yield per plant via days to first flowering (-0.774), skin diameter of fruit (mm) (-0.143), fruit p^H (-0.237), lycopene content (mg) (-0.193), brix percentage (%) (-0.076) and individual fruit weight (g) (-0.282). Finally, the trait showed significant positive genotypic correlation with yield per plant (kg) (0.269) which was highly significant in Table 8.

4.4.3 Plant height (cm)

Plant height exhibited negative direct effect (-0.057) on yield per plant. The trait showed positive indirect effect on yield per plant via days to first flowering (0.013), days to first fruit setting (0.012), number of flowers per cluster (0.014), skin diameter of fruit (mm) (0.027), fruit p^H (0.006), lycopene content (mg) (0.037), brix percentage (%) (0.000) and individual fruit weight (g) (0.014). The trait showed negative indirect effect on yield per plant via number of primary branches per plant (-0.039), number of secondary branches per plant (-0.039) and number of clusters per plant (-0.028). The trait had insignificant negative genotypic association with yield per plant (kg) (-0.162) showed in Table 8.

Table 8. Partitioning of genotypic correlations into direct and indirect effects of important characters by path co-efficient analysis

Character	DFF	DFFr	PH	NPB	NSB	TNC	NFC	SDF	p^H	LC	Br	IFW	Genotypic correlation with YP
DFF	**0.808**	-0.774	0.013	-0.044	0.068	-0.079	-0.010	-0.007	-0.012	-0.016	0.009	0.373	0.329**
DFFr	0.797	**-0.784**	0.012	-0.049	0.080	-0.081	-0.029	-0.005	-0.013	-0.013	0.019	0.336	0.269*
PH	-0.183	0.163	**-0.057**	0.048	-0.079	0.214	-0.086	0.014	0.005	0.034	-0.001	-0.234	-0.162ns
NPB	-0.502	0.547	-0.039	**0.070**	-0.121	0.260	-0.080	0.019	0.007	0.022	-0.031	-0.381	-0.228*
NSB	-0.470	0.532	-0.039	0.073	**-0.117**	0.198	-0.060	0.011	0.013	0.018	-0.030	-0.066	0.063ns
TNC	-0.146	0.146	-0.028	0.042	-0.053	**0.438**	0.062	0.000	-0.002	0.016	0.034	-0.366	0.142ns
NFC	-0.023	0.064	0.014	-0.016	0.020	0.077	**0.352**	-0.006	-0.003	-0.027	0.087	-0.147	0.392**
SDF	0.204	-0.143	0.027	-0.046	0.044	-0.001	0.069	**-0.029**	0.012	-0.027	0.049	0.267	0.425**
p^H	0.235	-0.237	0.006	-0.011	0.037	0.025	0.022	0.008	**-0.041**	-0.004	0.081	0.295	0.416**
LC	0.237	-0.193	0.037	-0.029	0.040	-0.127	0.178	-0.014	-0.003	**-0.054**	0.074	0.493	0.638**
Br	0.036	-0.076	0.000	-0.011	0.018	0.074	0.153	-0.007	-0.017	-0.020	**0.200**	0.221	0.571**
IFW	0.322	-0.282	0.014	-0.029	0.008	-0.171	-0.055	-0.008	-0.013	-0.028	0.047	**0.934**	0.738**

Bold figures indicate direct effects.

DFF= Days to first flowering, DFFr= Days to first fruit setting, PH= Plant height (cm), NPB= no. of primary branches per plant, NSB= No. of secondary branches per plant, TNC= Total number of cluster per plant, NFC= Number of flower per cluster, SDF= Skin diameter of the fruit (mm), p^H= fruit p^H, LC= lycopene content (mg), Br= brix (%), IFW= Individual fruit weight (g), YP= Yield per plant (kg), GA= Genetic advance, GA (%)= Genetic advance in percentage of mean, ns= non-significant

4.4.4 Number of primary branches per plant

Number of primary branches per plant showed negative direct effect (-0.117) towards yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.048), no. of secondary branches per plant (0.073) and total number of clusters per plant (0.042). The trait showed negative indirect effect on yield per plant via days to first flowering (-0.044), days to first fruit setting (-0.049), number of flowers per cluster (-0.016), skin diameter of fruit (mm) (-0.046), fruit p^H (-0.011), lycopene content (mg) (-0.029), brix percentage (%) (-0.011) and individual fruit weight (g) (-0.029). The trait had significant negative genotypic association with yield per plant (kg) (-0.228) showed in Table 8.

4.4.5 Number of secondary branches per plant

Number of secondary branches per plant showed positive direct effect (0.070) towards yield per plant. The trait showed positive indirect effect on yield per plant via days to first flowering (0.068), days to first fruit setting (0.080), number of flowers per clusters (0.020), skin diameter of fruit (mm) (0.044), fruit p^H (0.037), lycopene content (mg) (0.040), brix percentage (%) (0.018), and individual fruit weight (g) (0.008). The trait showed negative indirect effect on yield per plant via plant height (cm) (-0.079), number of primary branches per plant (-0.121) and number of clusters per plant (-0.053). The trait had insignificant positive genotypic association with yield per plant (kg) (0.063) represented in Table 8.

4.4.6 Number of clusters per plant

Path co-efficient analysis revealed that number of clusters per plant had positive direct effect (0.438) on yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.214), no. of primary branches per plant (0.260), no. of secondary branches per plant (0.198), number of flower per clusters (0.077), fruit p^H (0.025), and brix percentage (%) (0.074) followed by negative indirect effect via days to first flowering (-0.079), days to first fruit setting (-0.081), skin diameter of fruit (mm) (-0.001), lycopene content (mg) (-0.127) and individual fruit weight (g) (-0.171). Finally, the trait showed highly insignificant positive genotypic correlation with yield (kg) per plant (0.142) in Table 8.

4.4.7 Number of flowers per cluster

Number of flowers per clusters showed positive direct effect (0.352) towards yield per plant. The trait showed positive indirect effect on yield per plant via number of clusters per plant (0.062), skin diameter of fruit (mm) (0.069), fruit p^H (0.022), lycopene content (mg) (0.178) and brix percentage (%) (0.153). The trait showed negative indirect effect on yield per plant via days to first flowering (-0.010), days to first fruit setting (-0.029), plant height (cm) (-0.086), no. of primary branches per plant (-0.080), no. of secondary branches per plant (-0.060) and individual fruit weight (g) (-0.055). The trait had significant positive genotypic association with yield per plant (kg) (0.392) showed in Table 8.

4.4.8 Skin diameter of fruit (mm)

Skin diameter of fruit (mm) exhibited negative direct effect (-0.029) on yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.014), number of primary branches per plant (0.019), number. of secondary branches per plant (0.011), total number of clusters per plant (0.000) and fruit p^H (0.008). The trait showed negative indirect effect on yield per plant via days to 1st flowering (-0.007), days to first fruit setting (-0.005), number of flowers per cluster (-0.006), lycopene content (mg) (-0.014), brix percentage (%) (-0.007) and individual fruit weight (g) (-0.008). The trait had significant positive genotypic association with yield per plant (kg) (0.425) reported in Table 8.

4.4.9 Fruit p^H

Fruit p^H exhibited negative direct effect (-0.041) on yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.005), number of primary branches per plant (0.007), number of secondary branches per plant (0.013) and skin diameter of fruit (mm) (0.012). The trait showed negative indirect effect on yield per plant via days to first flowering (-0.012), days to first fruit setting (-0.013), total number of clusters per plant (-0.002), number of flowers per cluster (-0.003), lycopene content (mg) (-0.003), brix percentage (%) (-0.017) and individual fruit weight (g) showed in (-0.013).

4.4.10 Lycopene Content (mg)

Lycopene content exhibited negative direct effect (-0.054) on yield per plant. The trait showed positive indirect effect on yield per plant via plant height (cm) (0.034), number of

primary branches per plant (0.022), number of secondary branches per plant (0.018) and total number of clusters per plant (0.016). The trait had significant positive genotypic association with yield per plant (kg) (0.638) showed in Table 8.

4.4.11 Brix percentage (%)

Brix percentage (%) exhibited positive direct effect (0.200) on yield per plant. The trait showed positive indirect effect on yield per plant via days to first flowering (0.009), days to first fruit setting (0.019), total number of clusters per plant (0.034), number of flowers per cluster (0.087), skin diameter of fruit (mm) (0.049), fruit p^H (0.081), lycopene content (mg) (0.074), and individual fruit weight (g) (0.047). The trait showed negative indirect effect on yield per plant via plant height (cm) (-0.001), number of primary branches per plant (-0.031) and number of secondary branches per plant (-0.030). The trait had significant positive genotypic association with yield per plant (kg) (0.571) in Table 8.

4.4.12 Individual fruit weight (g)

Individual fruit weight (g) exhibited positive direct effect (0.934) on yield per plant. The trait showed positive indirect effect on yield per plant via days to 1st flowering (0.373), days to first fruit setting (0.336), skin diameter of fruit (mm) (0.267), fruit p^H (0.295), lycopene content (mg) (0.493), and brix percentage (%) (0.221). The trait showed negative indirect effect on yield per plant via plant height (cm) (-0.234), number of primary branches per plant (-0.381) and number of secondary branches per plant (-0. 066), total number of clusters per plant (-0.366) and number of flowers per cluster (-0.147). The trait had significant positive genotypic association with yield per plant (kg) (0. 738) represented in Table 8.

4.4.13 Residual effect

The residual effect (R) of path co-efficient analysis was (0.02) which reported that the traits under study contributed 98% for the fruit yield per plant. It could be said that there were some other factors those contributed 2% to the fruit yield per plant and that were not included in the present study. The significant effect on fruit yield per plant (kg) showed in Table 8.

CHAPTER V

SUMMARY AND CONCLUSION

At the experimental farm of Sher-e- Bangla Agricultural University in Dhaka, experiment using twenty-five genotypes of tomato was conducted to ascertain the genetic variability, correlation, and path co-efficient for yield and its contributing attributes during October, 2021 to March, 2022. A Complete Randomized Design (CRD) with three replications was used to set up the experiment in the pots beside the net house. For the majority of the analyzed characters' the studied genotypes were found to have a high level of variation. According to the mean performance the minimum duration required for first flowering was found in G16 (58 DAS) and maximum duration was noticed in G23 (74.67 DAS). The minimum duration required for first fruit setting was found in G16 with 69.33 DAS and maximum duration was recorded in G23 (85.67 DAS). The maximum plant height (cm) was observed in G13 (114 cm) and minimum was G1 (54.67 cm). The maximum number of primary branches (6.00) was recorded in the genotype G20 and the minimum number (1.33) was recorded in G4. The maximum number of secondary branches was recorded in the genotype G18 (4.0) and the minimum was recorded in G4 (1.0). The minimum number of clusters per plant was found in G12 (3.0) and maximum was G13 (7.33). The minimum value for number of flowers per cluster was found in G7 with 2.17 and the maximum was noticed in G6 (4.08). The minimum value for skin diameter (mm) was found in G20 (5.93 mm) and the maximum was noticed in G6 (11 mm). The minimum value of tomato p^H was 3.10 (G11) and maximum value was 4.17 (G21). The minimum value for lycopene content (mg) was 7.20 in G23 and the maximum was 19.33 in G6. The minimum value of tomato brix percentage was 4.40% in G24 and the maximum was 5.70% in G5. The maximum fruit weight (g) was recorded (172.33g) in G7 and minimum was recorded (53.67g) in G19. Fruit yield per plant (kg) was found 1.96 kg in G8 which is highest and the lowest was recorded (0.61 kg) in G22. For all the characters under study, the phenotypic variance was higher than the corresponding genotypic variance, indicating a greater influence of the environment on these characters' expression. Characters like, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, lycopene content (mg), individual fruit wt. (g) and yield per plant (kg) exhibited

high genotypic and phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the characters. Maximum difference between phenotypic and genotypic co-efficient of variation were 49.37and 29.65, respectively for the character seed thickness (cm) was mostly determined by the environmental condition. Highest phenotypic co-efficient of variation (49.37) was found in number of primary branches per plant and genotypic co-efficient of variation (38.75) was found in individual fruit weight (kg). High heritability associated with high genetic advance and genetic advance in percentage of mean was found in individual fruit weight (g) which indicated that additive gene expression on this character. Total number of clusters per plant, number of flowers per cluster, skin diameter of the fruit (mm), lycopene content (mg) and yield per plant (kg) showed high heritability with low genetic advance and high genetic advance in percentage of mean that might be due to the action of additive and non-additive genes. High heritability with low genetic advance and low genetic advance in percentage of mean were found in days to 1st flowering, days to first fruit setting, fruit p^H and brix percentage (%). Moderate heritability with low genetic advance and high genetic advance in percentage of mean were found in plant height (cm), number of primary branches per plant and number of secondary branches per plant. Assessments of character association indicating that fruit yield per plant had highest significant positive correlation with days to first flowering, followed by days to first fruit setting, total number of cluster per plant, number of flower per cluster, skin diameter of the fruit (mm), fruit p^H, lycopene content (mg), brix percentage (%) and individual fruit weight (g) in both genotypic and phenotypic level indicating the importance of these trait in selection for increasing yield and were identified as yield attributing characters. Thus, selection can be effective upon these characters for the genetic improvement of yield of tomato. Path analysis showed that highest positive direct effect was found in the trait individual fruit weight (kg) (0.934) and the lowest positive direct effect was in the trait number of primary branches per plant (0.070) or yield. Days to first flowering total, number of clusters per plant, number of flowers per cluster and brix percentage (%) showed positive direct effect on fruit yield per plant (kg) indicating that direct selection based on these traits may be effective in evolving high yielding varieties of tomato. On the other hand, negative direct effect was found by days to first fruit setting, plant height (cm), number of secondary branches per plant, skin

diameter of the fruit (mm), fruit p^H and lycopene content (mg). Selection may be practiced among genotypes based on their yield and yield contributing characters. Based on the objectives, the genotypes such as G16 for early flowering and fruit setting, G6 for lycopene content (mg), number of flowers per cluster and skin diameter (mm), G13 for plant height (cm) and number of clusters per plant, G20 for number of primary branches, G18 for number of secondary branches was, G21 for fruit p^H, G5 for brix %, G7 for maximum individual fruit weight (g) and G8 for higher fruit yield (kg) per plant. Therefore, it may be decided that the genotypes G5, G6, G7, G8, G13, G18, G20 and G21 might be used in future breeding programs.

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http://www.banglapaedia.com
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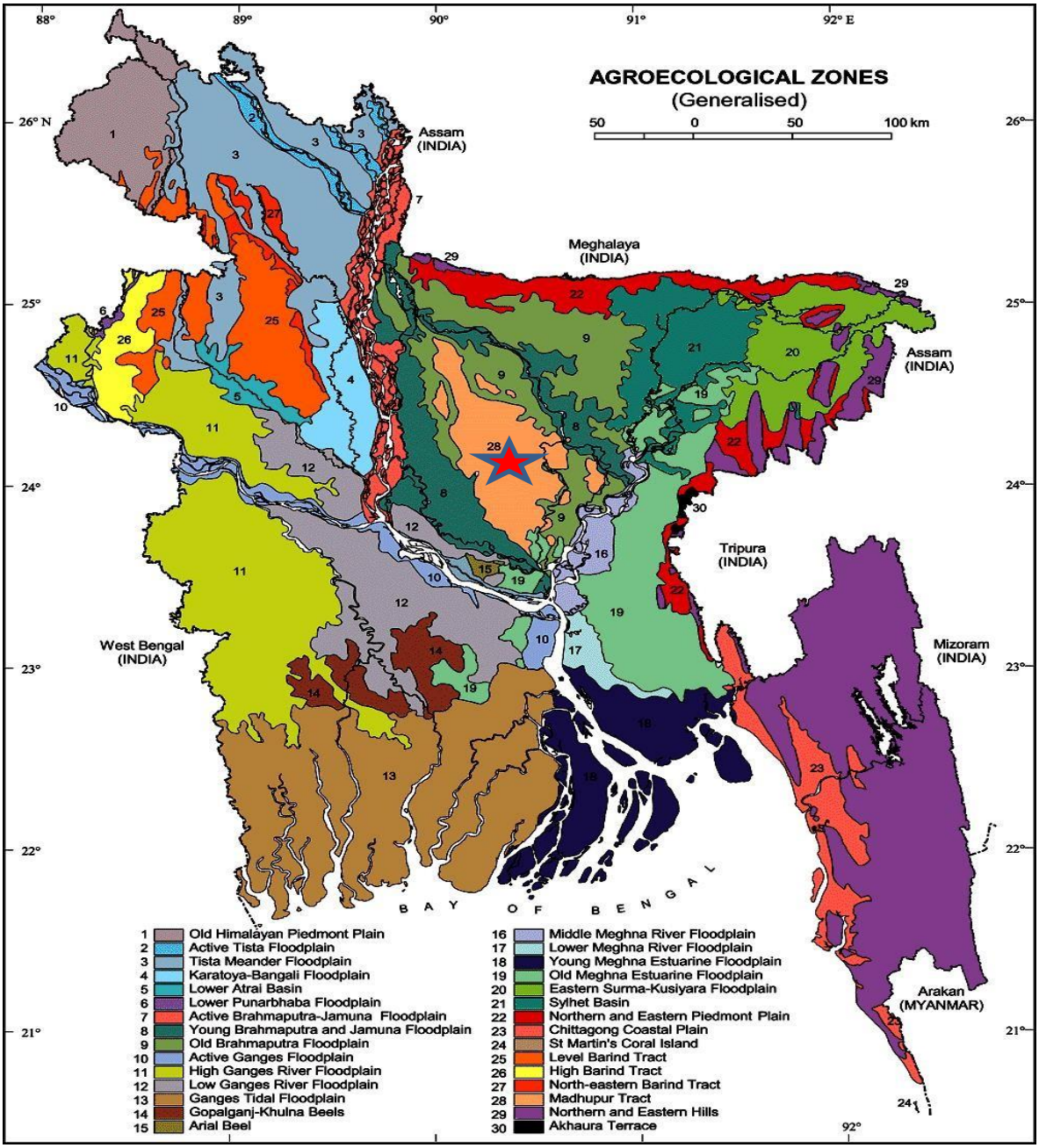
APPENDICES

Appendix I. Map showing the experimental site under the study



Source: Bangladesh Agro-Meteorological Information Service (BAMIS)

Legend is showing the research site

Appendix II: Physical and chemical characteristics of initial soil depth of the experimental site belongs to the soil beside the net house

A. Physical composition of the soil:

Soil separates	**Percentage (%)**	**Methods**
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Textural class	Clay loam	Do

Source: www.sau.edu.bd

B. Chemical composition of the soil:

SL No.	**Soil characteristics**	**Analytical data**	**Methods**
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total P (ppm)	840.00	Olsen and Sommers, 1982
4	Total S (ppm)	225.00	Bardsley and Lanester, 1965
5	Available P (kg/ha)	69.00	Olsen and Dean, 1965
6	Available N (kg/ha)	54.00	Bremner, 1965
7	Available S (ppm)	16.00	Hunter, 1984
8	Exchangeable K (kg/ha)	89.50	Pratt, 1965
9	CEC (Cation Exchange Capacity)	11.23	Chapman, 1965
10	p^H (1:2.5 soil to water)	5.55	Jackson, 1958

Source: www.sau.edu.bd

Appendix III: Monthly average temperature, average relative humidity and total rainfall and total sunshine of the experimental site during the period from October, 2021 to March, 2022.

Month	**Air temperature (° C)**		**Relative humidity (%)**	**Total rainfall (mm)**	**Sunshine (hr)**
	Minimum	**Maximum**			
November, 2021	20.5	29.2	73	34.4	7.3
December, 2021	17	26.4	73	12.8	7.4
January, 2022	15.3	26	71	7.7	7.6
February, 2022	17.4	29.8	64	28.9	7.5
March, 2022	21.3	34	62	65.8	10.1

Source: Bangladesh Meteorological Department (BMD), Agargaon, Dhaka-1207