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GENERATION MEAN ANALYSIS OF TWO POPULATIONS OF TOMATO (*Solanum lycopersicum* L.) FOR YIELD AND YIELD COMPONENTS

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B.Sc. (HONS) CROP SCIENCE (NJALA UNIVERSITY, SIERRA LEONE)

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GENERATION MEAN ANALYSIS OF TWO POPULATIONS OF TOMATO

(*Solanum lycopersicum* L.) FOR YIELD AND YIELD COMPONENTS

A THESIS SUBMITTED TO THE DEPARTMENT OF CROP AND SOIL SCIENCES, FACULTY OF AGRICULTURE, KNUST, KUMASI, IN PARTIAL FULFILMENT OF THE REQUIRMENT FOR THE AWARD OF MPHIL AGRONOMY

(PLANT BREEDING)

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BSc. (HONS) CROP SCIENCE (NJALA UNIVERSITY, SIERRA LEONE)

SEPTEMBER, 2015

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DECLARATION

I hereby declare that this work is a direct result of my field research undertaken and are supported by cited references in relation to other previous and similar work performed which have been duly acknowledged. This thesis has not been presented anywhere for another degree.

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DEDICATION

I dedicate this work to my parents Alhaji Moiwa Kanneh and Mrs Massa Sheriff Kanneh (late), may Allah grant them Heaven. This thesis is also dedicated to the entire Kanneh and Sheriff families. This is in acknowledgement of their numerous financial sacrifices, prayers and moral support to ensure the realization of my academic achievements.

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ABSRTACT

Owing to the limited availability of high yielding cultivars that are suitable for different purposes, the yield of tomato in Ghana falls between 7.5 and 10 tones/ha which is far below the world‟s average yield 45-50 tones/ha. Therefore, identification of superior plant and fruit types for further improvement in yield is necessary. Hence, two separate experiments designated as genotype (F) and genotype (G) were conducted at the Horticulture Division, Council for Scientific and Industrial Research (CSIR)-Crops Research Institute (CRI) Kwadaso, Kumasi, Ghana to evaluate early generations of interspecific crosses of tomato (*Solanum lycopersicum* L.) genotypes for yield using a Randomized Complete Block Design with three replications under field conditions. Data were collected on growth parameters and yield components, including plant height, stem girth, days to flowering, days to maturity, fruit weights, number of fruits per plant, fruit length, fruit diameter, fruit flesh thickness, brix, total fruit weight per genotype, marketable fruits and nonmarketable fruits per plant. Heritability was estimated on the above traits. Results from the study showed that total marketable fruits was higher for „BC_2F_1‟, „F_2‟, „F_1‟, P_2 (213)‟, and „P_2 (042)‟ than the rest of the genotypes, whereas P_1 (083), P_1 (097), BC_1F_1 had the lowest for total marketable yield. Considering yield and yield components, F_2 was found to be better than the rest of the genotypes for most of the characters for genotype (F), while P_2 (213) produced higher yield than segregating population for genotypes (G) and F1 was found to be the poorest performer for almost all parameters for genotypes (F) and (G). Fruit flesh thickness, fruit length, fruit diameter and number of nonmarketable showed high broad sense heritability. Number of marketable fruits, total fruit weight, number of fruit per plant, brix, days to flowering, days to maturity, fruit flesh thickness, fruit weight per plant and stem girth showed high heritability.

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LIST OF ABBREVIATION

AVRDC	Asian Vegetable Research and Development Center
BC	Backcross
CRI	Crops Research Institute
CSIR	Council of Scientific and Industrial Research
DNA	Deoxyribonucleic acid
FAO	Food and Agricultural Organization
GCA	General Combining Ability
IFPRI	International Food Policy Research Institute
KAFACI	Korea Africa Food and Agricultural Cooperative Initiative
LSD	Least significant difference
MOFA	Ministry of Food and Agriculture
MSSD	Modified Single Seed Descent
NARP	National Agricultural Research Project (NARP).
NMKTFPP	Number of marketable fruits per plant
NNMKTFPP	Number of non-marketable fruits per plant
QTL	Quantitative Trait Loci
RCBD	Randomized complete block design
RFLP	Restriction Fragment Length Polymorphism
SCA	Specific Combining Ability
TMKTFW	Total marketable fruit weight
TS	Total sugar
TSS	Total solid soluble

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TYLCV	Tomato yellow leave curl virus
UNESCO	United Nations Educational, Scientific and Cultural Organization
USA	United States of America
USDA	United States Department of Agriculture
VA	Variance Additive
V_{AD}	Additive and Dominance variance
VB_1	Backcross 1 variance
VB_2	Backcross 2 variance
VD	Dominance variance
VE	Environmental variance
VF_1	Filial 1 variance
VF_2	Filial 2 variance
VG	Genetic variance
V_{GE}	Genetic and Environmental variance
VI	Epistasis variance
VP	Phenotypic variance

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CHAPTER ONE

1.0 INTRODUCTION

1.1 Background of the study

Tomato (*Solanum lycopersicum* L*)* is an edible fruiting plant often grouped as vegetable (Godia, 2014). Tomato comes from the *Solanaceae* family (Youdeowei, 2004). This family also comprises other species, such as tobacco, peppers, eggplant and potato. Tomatoes originated in South America but they are currently found all over the world (Hokche *et al.*, 2008). The Portuguese introduced tomato into the West African sub-region between the 16th and 17th century (Osei *et al*., 2013). It is an important vegetable crop widely cultivated for human consumption and second to potato in the world. The vegetable growers can grow tomato on a small scale in the home garden, where a few plants yield fruits for the whole family and a commercial scale as a cash crop (Mylavarapu and Kennelley, 2002).

The edible fruit of the tomato plant has a series of usages in different forms. The crop is nutritious and contain high amount of dietary source of vitamins A, B, C, E and nicotinic acid (Osei, 2010; Godia, 2014). In 2008, approximately 130,000,000 t fresh fruit of tomato were produced (FAO, 2010). In Ghana, it is consumed as fresh fruit, salads, soup, stew and often used in other dishes. Its cultivation provides source of employment to many and continue to play a key horticultural role in the country in terms of reducing poverty and food insecurity (Osei *et al*., 2014).

The recent Global production of fresh fruit tomato is about 100 million tons cultivated on 3.7 million hectares (Godia, 2014). In Ghana, the average yield on farm is between 7.5-10t/ha (Godia, 2014) which is far below the potential yield of 45-50

Mt/ha. Several soil types can be used for tomato production. According to Boatright and Mckissick (2004), well-drained, deep, medium textured sandy loamy fertile soils are good for optimal tomato production.

According to (Robinson and Kovalli, 2010), tomatoes sector in Ghana is unable to achieve its potential, like other countries in relation to production and processing aspects. This is largely due to its inability to improving the livelihood of tomato farmers through increase in production of tomatoes and the commodity chain. Thus, because of production seasonality, high perishability, poor market access, and competition from imports, some farmers are unable to sell their tomatoes; these are left to rot in their fields (IFPRI, 2013).

Regardless of government efforts that include the establishment of a number of tomatoes processing factories, tomatoes of the right quality and quantity for commercial agro-processing are not being grown. Many farmers plant local varieties, characteristically low yielding, susceptible to pest and diseases, poor shelf life, high water content, many seeds, poor colour, and low brix against the increasing demand at local and international levels (Elizabeth and Shashi, 2010). In order to overcome this, the development of high yielding tomato genotypes through hybridization to identify and evaluate those genotypes with good horticultural characteristics and make recommendations for their inclusion into breeding programme for further yield improvement cannot be overemphasized. This study, therefore, sought to create genetic variations and assess the early generations of two tomato genotypes for yield and yield components in Ghana. Moreover, crop improvement programmes require that desired traits are heritable which direct or aid the breeder to determine at what stage of the breeding programme meaningful selections are to be practiced. Generation mean analysis undoubtedly offers one of the numerous methods available in research for the estimation of genetic transfer from parents to segregating populations. Heritability

estimate is important in achieving this because it shows how much variation in a phenotypic trait in a population is due to genetic variation among individuals in that population Wray and Visscher (2008). This facilitates the selection process in crop improvement by alerting the breeder about the progress made. Utilization of result obtained from the study increases research findings and or understanding of the genetic variability existing within the breeding populations for wider geographical use. This may lead to possible development and release of high yielding cultivars. Identification of variability among tomato accessions is useful to upkeep, utilize and acquire germplasm resources (Mwirigi *et al*., 2009). Additionally, effective study and assessment of tomato genotypes is of great significance for current and future agronomic and genetic improvement of the crop. Moreover, if an improvement programme is to be carried out, evaluation of genotypes is imperative to understand the genetic background and the breeding value of the available genotypes (Agong, 2001)

The main objective of this study was to evaluate and identify two populations of tomato for yield and yield components and identify superior plant and fruit types of F_2 population for further improvement in yield using generation mean analysis.

The specific objectives were to:

i. determine the potential of F_1, F_2, BC_1F_1 and BC_2F_1 over the parents for yield and yield components, and ii. estimate heritability of some important quantitative traits.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and domestication of tomato

The tomato *(Solanum lycopersicum* L.*)* is the edible, often red fruit generally known as a tomato plant. The *Solanum lycopersicum* is believed to have come from the ancestor of cultivated tomato *Solanum lycopersicum cerasiforme*, centered on its wide existence in Central America and the presence of a condense style extent in the flower (Cox, 2000). Current genomic inquiries indicated that the plants famous as „cerasiforme" are a combination of wild and cultivated tomatoes rather than being „ancestral" to the cultivated tomatoes (Nesbitt and Tanksley, 2002). The inherent variance present in the wild species has been studied for specific characters and is being conquered in tomato breeding (Walter, 1967; Rick and Chetelat, 1995; Larry and Joanne, 2007).

Tomato species are believed to have originated in South America Andes (Bai and Lindhout 2011). They are now found all over the world (Hokche *et al*., 2008). It is also believed that tomato was brought to Mexico, cultivated and cultured there by 500 BC (Jan Cashman, 2011). However, the imaginative place of domestication and the initial proceedings of cultivating tomato remain vague (Peralta and Spooner, 2007). It is thought that the first cultivated tomato was small and yellow (Jan Cashman, 2011). Columbus and/or Cortez are certainly thought to had carried tomatoes to Europe and the Spanish explorers took them throughout the world (Jan Cashman, 2011). The crop was introduced in Italy and Britain in the 1548s and 1590s respectively (David and Gentilcore, 2010; Smith, 1994).

In North America, the first reference to tomatoes cultivation dated 1710 (Smith, 1994). Introduced from the Caribbean to North America in the mid-18th century, they were

grown on farms as decorative plants than as food because tomatoes were considered as noxious plants (Smith, 1994). In the Middle East and North Africa, John Barker, British consul in Aleppo around 1799 to 1825, made tomato known to farming.

Generally, tomato was introduced into Africa and in particular in the West African sub-region and in Ghana as well by the Portuguese between the 16th and 17th century (Norman, 1992: Osei *et al*., 2013). It is an essential vegetable crop extensively cultivated for human consumption and second to potato in the world (Naan DanJain, 2012). Since the introduction of the crop, it has become an integral component of the sub region dietary. In Ghana, tomato is a key vegetable produce largely cultivated, and currently the number one vegetable consumed (Schippers, 2000; Osei *et al.*, 2010). The fruit contains high levels of vitamins A, B, C and E, and nicotinic acid (Davies and Hobson, 1981; AVRDC, 2004). Its cultivation offers a source of engagement to numerous people in the country (Osei *et al*., 2010). Although, the crop is grown in all the agro-ecological zones of Ghana, it is extensively cultivated in the Ofinso North, Bolgatanga and Ada districts of Ghana (Norman, 1992; Osei *et al*., 2010). Since the introduction of the crop in Ghana, farmers have made local selections resulting in the production of several land races (Osei *et al*., 2013). Additionally, the crop has undergone some research to improve its adaptability. Varieties especially, hybrids from elsewhere are continually introduced for cultivation in Ghana.

2.2 Economic importance of tomato

Tomato is one of the most common but core vegetables all over the world (FAO, 2011; Naan DanJain, 2012). Globally, it is one of the most cultivated vegetables in most regions of the world, next in importance to potatoes in several nations (Ojo *et al.*, 2009) with Asia and Africa accounting for about 79 percent of the overall tomato area, with around 65 percent of world productivity (FAO, 2008). According to USDA (2005), tomato in the United States of America (USA) is the third most economically important

vegetable (with a total farm value of $2.062 billion) following potato ($2.564 billion) and lettuce ($2.064 billion). The total harvested area for tomato in the U.S. in 2013 was projected to be 430,000 ha (130,000 ha fresh market and 300,000 ha processing tomatoes) with an aggregate farm value of about $3.00 billion ($1.6 billion fresh market and $1.4 billion processing) (USDA, 2013). Additionally, in the USA, Pennsylvania is considered the highest cultivator of process and fresh market tomatoes (USDA, 2013). The distinguishing reddish colouration of ripe tomato fruits and related products is principally accounted for the Lycopene pigment (Shi and LeMaguer, 2000). According to Shi and Le-Maguer (2000), because of their genetic and physical characteristics the crop as a natural antioxidant and its impact has attracted attention. Tomatoes and tomato products are the main source of lycopene related compounds, and source of carotenoids that are important in the human diet (Willcox *et al*., 2003). Products from tomato are a superior source of alpha-tocopherol and vitamin C (USDA, 2004). In adding to their micronutrient benefits in our diets, tomatoes also comprise valued phytochemicals, with carotenoids and polyphenols
(USDA, 2004).

The fruits are mostly eaten fresh in salads or prepared in sauces, soup and meat or fish dishes. Tomato fruits can be processed into purées, juices and ketchup. They are economically important product when canned and dried (Shankara *et al*., 2005). It is an exceptional source of diverse vitamins like A, C and minerals like Calcium, Potassium, phosphorus, magnesium and Fe, carotenoids, flavonoids and phenolic for human diet (Horneburg and Myers, 2012; Dhaliwal *et al*., 2003; USDA, 2009). According to Hossain *et al*. (2004), tomato has a rich source of lycopene antioxidant that moderates the threat of prostate cancer Moreover, according to Kaushik *et al*. (2011), tomato has therapeutic values and is used for blood decontamination and cure of gastrointestinal diseases. Besides tomato nutritive and medicinal values, the crop is

known as an excellence produce for both indigenous and foreign markets and provides a way out of poverty for smallholder growers living in emerging nations (Tewodros and Asfaw, 2013). Therefore, tomato is considered as the vegetable of the mainly underprivileged grassroots (Adepetu, 2005). In Italy, tomatoes were cultured mainly as ornamentals after their arrival (David and Gentilcore, 2010). But in Africa, Nigeria is rated second major producer of tomato in Africa and the 13th largest in the world, producing 1.701 million tons of tomatoes each year an average of 25-30 tons per hectare (FAO, 2010). In Ethiopia, the plant is grown in several major producing regions of the country. Eaten in many homes (fresh) and as a market commodity in many areas of the country and is promising to improve the incomes and livelihoods of thousands small farmers in Ethiopia and diversifying and increasing agricultural exchange earnings from the export of Ethiopia (CSA, 2006 and Lemma, 2001).

In Ghana, tomato is a very important and popular vegetable crop and its cultivation is a key economic activity for low-income farmers (Horna *et al*., 2006). Every Ghanaian household eats tomato almost every day (Osei *et al*., 2010). Furthermore, tomato is consumed in large amounts as flavouring in stews and soups, and in uncooked state in pepper sauces and sometimes in salads. They can also be processed by factories into secondary merchandises such as tomato paste, tomato puree and ketchup (Osei *et al*., 2010). Ghana accounted for tomato export of 4,368 metric tonnes of tomatoes valued at $ 427,000 (FAO, 2005). However, the industry is performing below its potential (Robinson and Kolavalli, 2010)

2.3 Genetic diversity in tomato

Improving yield and superiority in self-pollinated crops like tomato is usually attained through selection of genotypes with needed trait combinations present in nature or by hybridization. The success of hybridization programme hinges on the choice and

selection of suitable parental of diverse origin. Shah *et al*. (2015) reported that without genetic diversity it becomes difficult for a population to adapt to environmental changes generating a fixed population.

According to Kurlovich and Rep'ev (2000), this has led to the establishment of institutional germplasm banks for saving current genetic diversity, sustaining and assessing it, following the pioneer work of Nikolai Vavilov (1887-1943). This was followed by Charles Rick (1915-2002) who devoted his time to unearth, assemble and designate exotic tomato germplasm (Tanksley and Khush, 2002). This has resulted to a stockpiled in excess of 83,000 tomato accessions in seed banks in the world, superceding other plant species collected with respect to tomatoes (FAO, 2010). The key assemblage centers include: In USA, the Tomato Genetic Resources Center in California (TGRC), and the USDA2 collection (www.ars.usda.gov), the World Vegetable Center in Taiwan and various Europeans assemblages (Bauchet and Causse, 2012). Tomatoes have a vast genomic diversity of the wild, particularly within the self-incompatible varieties such as *S. chilense* and *S. peruvianum* (Tellier,

Laurent *et al*. 2011) compared with the cultivated tomatoes which are genetically poor (Bai and Lindhout, 2007). Additionally, it is estimated that the genomes of tomato cultivars contain less than five per cent of the inherent difference of their desolate families (Miller and Tanksley, 1990). According to Larry and Joanne (2007), the inherited differences existing in the desolate types has been studied intensively for precise characters currently exploited in tomato propagation. Molecular marker studies discovered that more genomic differences be detected inside a particular accession of the self-incompatible kinds than in all accessions of any of the selfcompatible species (Bauchet and Causse, 2012). Moreover, the DNA technologies used to visualize diversity in the cultivated tomato and polymorphisms within the cultivated tomato

gene pool have been known, even via sensitive molecular markers (Tam *et al.*, 2005). Sherifova *et al*. (2013) examined the genetic diversity of the local tomato genotypes. They also suggested that tomato accessions within the same environment have the propensity to be grouped together, but accessions from diverse areas could be narrowly associated irrespective of their physical locations. This proposes that collection of parental genotypes for propagation ought not to be centred on geographical derivation only because this is not always an accurate indicator of genetic diversity (Keneni *et al*., 2005; Zvingila *et al*., 2005; Gashaw *et al*., 2007; Celka *et al*., 2010). Albrecht *et al*. (2010) compared genetic diversity of 14 *S. lycopersicoides* Albrecht *et al*. (2010) and seven *S. sitiens* Albrecht *et al*. (2010) populations based on geographical origin using a common set of markers and concluded that the selected *S. chilense* population was genetically more diverse than the average *S. lycopersicoides* population. Corrado *et al*. (2013) used 214 genotypes to evaluate genetic diversity; the finding indicated that adaptation and selection have led to a genomic name in cultivated landraces and that the subpopulation structure of existing diversities is shaped by focussed breeding and mainly of new origin. In Africa, genetic diversity in tomato production is evidence and is a subject of research for breeding high yielding tomato varieties**.** Asgedom *et al*. (2010) subjected 25 farmers‟ varieties from Eritrea, two from South Africa and two from Zaire to genetic diversity analysis assumed to be maintained by self-pollination for several years, the results clearly confirmed that there was a high genetic diversity among the Eritrean varieties compared with the samples from the Centre for Genetic Resources of The Netherlands (CGN) suggesting genetic contamination among the Eritrean genotypes.

Meaning Eritrean farmers‟ varieties are genetically contaminated and are common phenomenon in many crops in Africa (Hirpa *et al*., 2010).

In Ghana, several research work has been conducted to determine the genetic diversity in cultivated tomatoes which could however, lead to the exploitation of desired characters, enhance research findings and/or understanding of the genetic diversity existing for breeding (Osei *et al*., 2014). The CSIR-Crops Research Institute assembled large tomato germplasm in 1995 under National Agricultural Research Project (NARP). Due to unreliable storage conditions, large amount of tomato germplasm stored at the CSIR-Plant Genetic Resource Research Institute lost their viability. To restore this, another germplasm collection was carried out in 2012 under Korea Africa Food and Agricultural Cooperative Initiative (KAFACI) as a first start for tomato breeding programme in Ghana. Since then, the CSIR-Crops Research Institute has successfully evaluated and developed a number of tomato lines that could lead to the releases of new varieties (M. K. Osei, Personal communication. According to Osei *et al*. (2014), accessions had diversity in majority of the traits measured representing presence of a high degree of morphological polymorphism among the evaluated accessions especially those from Ghana which was attributed to segregation and perhaps mutation followed by intensive selection by isolated human communities in diverse environments. The results indicated the presence of diverse morphotypes at the individual genotype level pointing to ample possibilities of obtaining desirable trait combinations in specific cultivars. Therefore, evaluating genetic variability in tomato is crucial in catching up the increasing diverse demands of farmers, researchers and consumers of tomato.

2.4 Tomato varieties in Ghana

Tomato occupies an integral component of the vegetables sector in Ghana and plays nutritive, medicinal and economics role in the country. In Ghana, the common cultivated varieties of tomato are the cherry, plum (Roma), and the shared table varieties (Jansen and Shock, 2009). According to MOFA (2008), cultivated tomato varieties in

Ghana include Roma VF, Pectomech VF, Tropimech, Rio Grande, Cac J, Wosowoso, and Laurano 70. Different tomato varieties are grown in different areas and under varied environments in the country. Moreover, Robinson and Kolavalli (2010) described the Pectomech variety as being ideal for processing, preferred by users and commanding the best price over other varieties. However, on the other hand, Relf *et al*. (2009) classify tomatoes according to their fruit appearances and colour of their fruit such as the cherry tomatoes, beefsteak type tomatoes, paste tomatoes and winter storage tomatoes. Adubofour *et al*. (2010) quoted two varieties of tomato grown in Ghana as the Bolga and Ashanti. According to Robinson and Kolavalli (2010), two varieties Power Rano and Pectomech are varieties that are grown widely in Brong Ahafo under rainfed conditions, and suitable for processing that is grown widely in the Upper East and in Burkina Faso as well respectively. Key local open pollinated varieties that farmers wash and recycle are Rasta, Power Rano, and Wosowoso, with Power Rano often being preferred due to its high tolerance and/or resistance to diseases. Typically local varieties have plants that grow vigorously; fruits that are often spherical with crevices; have a low total soluble content; high water content; and are acidic with a "biting" taste. Because they are open-pollinated, a range of varieties have emerged over time from uncontrolled crossing (Robinson and Kolavalli, 2010). Improved varieties include Pectomech, Heinz, and Nimagent F1 (Asuming-Brempong and Boakye, 2008). They have been the most important driver of yield improvements in the sector, mostly under irrigated conditions. However improved varieties can also do well under rainfed conditions (Dorward *et al.*, 2009).

2.5 Breeding tomato through hybridization

Plant breeding is the art and science of altering the characters of plants that result from modification of traits to desired characteristics (Sleper and Poehlman, 1995). Plant

breeding can be accomplished using diverse means ranging from simple selection of plants with desired traits for breeding, to more complex molecular techniques. Hybridization on the other hand generally results in increased variability in the population after segregation with the potential of obtaining new and enriched plant types (Allard, 2015). The appropriate variability and desirable traits which the breeder seeks may be absent from the introduced or collected materials. The breeder, therefore, has to create his own variability by crossing two or more lines or varieties. For a successful hybridization programme, the hybridization system must be well determined according to the breeding objectives and the genetic basis for its choice understood, the best parents for the particular trait must be used, the number of F1 seed must be sufficient for a particular cross, and the hybridization technique must be appropriate. Hybridization is followed by generation of selections before lines are put into observational and replicated yield trials (Ahmad, 2005). Hybrid tomato plants combine two different varieties of tomato plant to produce a cultivated variety with beneficial traits from both its parents (Opeña *et al*., 2001). According to Shankara *et al*. (2005), hybridized tomato cultivars have many benefits compared to openpollinated varieties. Hybrid tomatoes generally produce higher yields and usually complete physiological processes earlier and are more homogeneous (Shankara *et al*., 2005). Furthermore, most tomato cultivars from crosses have superior fruit quality, resistance to disease and with a specific growth habit and have economic traits to make them viable at commercial level (Shankara *et al*., 2005). Amaefula *et al*. (

2014) researched on Hybrid Vigor and Genetic Control of Some Quantitative Traits of Tomato (*Solanum lycopersicum* L.) and concluded that high level of epistasis controlled some of the quantitative traits and hybridization shown by the result was effective in developing new tomato cultivars with positive heterotic effects in fruit yield. According to Amaefula *et al*. (2014), the extent of heterosis was dependent on the addition of

favorable dominant alleles in the F1 population. The increased yield was attributed to high yielding parents selected for hybridization and in conformity with the findings of Shankara *et al.* (2005). Nemati *et al*. (2010) assessed 80 F1 crosses and their parental (8 male sterile and 10 fertile lines) for average weight and quantity of fruits per plant in Moscow and observed high values for these traits due to combined effects of high general (GCA) and specific combining abilities (SCA). Fruit weight and number of fruit per plant were controlled by dominant polygenes and recessive polygenes respectively. Moreover, demand for hybrid seeds of tomato is increasing and have the potential to open a new market for researchers, seed companies and growers VKoundinya and Kumar (2014). Hartman and St. Clair (1998) conducted research on two inbred backcross populations of tomato using the method of Bliss (1982) to evaluate fruit quality and other horticultural traits. They observed significant variation among Inbred lines for the amount of fruit damage by beet armyworm and tomato fruitworm, the result indicated that, BC_1 accounted for greater variance in fruit damage than BC_2 populations signifying alleles introgression from the *L. pennellii* donor parent LA 716, contributed greatly to reduced fruit damage by beet armyworm and tomato fruitworm in a no-choice field assay. The efficient handling of the segregated progenies for the desired results, certain breeding methods and selection procedures are employed (Teerawat, 2010). In summary, tomato hybrid breeding provides research protection, a decrease in time for selection of desired traits, and methodology for the utilization of genes, which require heterozygosity for their usage in increasing production systems (Banga and Banga, 1998). Several breeding methods are available to plant breeders for germplasm improvement, such as the pedigree method, bulk method, single seed descent, backcross method, and recurrent selection (NDSU, 2012)

2.5.1 Pedigree method

In pedigree method, individual plants are selected from F2 and the subsequent generation and their progenies are tested. During the entire operation, a record of the entire parent‟s offspring relationship is kept, is known as pedigree record. The selection of individual plant is continued until the progenies show no segregation. At this stage, selection is done among the progenies, because there would be no genetic variation within progenies.

Additionally, pedigree may be defined as a description of the ancestors of an individual and it generally goes back to some distant ancestors. Thus, it describes the parents grandparents, great grandparents so on of an individual Osei *et al.* (2014)

Furthermore, pedigree is a plant breeding technique that is used to create entirely new varieties of plants that combine the best qualities of selected existing varieties. The technique is restricted to self-pollinating species where parents are selected and are artificially crossed. The main objective of pedigree method is to isolate superior, recombinant, homozygous lines from F2 generation onwards until genetic purity is reached (Osei *et al*., 2014). It is the most extensively used method to handle segregating generations from crosses. Park *et al*. (2004) evaluated 74 tomato cultivars from California to ascertain their distinctive identifications and pedigree status using seven primer combinations. The result of the study revealed that all 74 tomato cultivars originated from California and shared at least some germplasm in their pedigrees likely as a result of their relatedness among the cultivars. They concluded that inherited variant in selected germplasm groups is provided not only by the original parents, but also by de novo generation of variation, which can include uneven passage over, DNA methylation, single-allele changes, and element transpositions (Rasmusson and Phillips, 1997).

Similarly, in South Africa, Biljon *et al*. (2010) investigated the potential of SSR as genetic markers in five classes of the *Solanum nigrum* complicated found in South Africa as well as their progeny. The result indicated close link between entries, attesting complex in the *S. nigrum* as a group of plants very closely interrelated, yet the parentages and their progeny could be visibly eminent as reported by Dehmer and Hammer (2004) that tomatoes are closely related crop. However, they were able to determine the pedigree between the parents and their progeny of the evaluated tomato species.

In general, characters in tomato can be upgraded concurrently through pedigree selection. Several programmes combine backcross and pedigree selection and desired genes are transferred in the first generations by backcross, followed by selection for other traits by pedigree selection (Razdan and Mattoo, 2006). Selection is performed at the F2 generation onward until genetic purity is reached (Osei *et al.*, 2014)

According to Osei *et al.* (2014), pedigree method provides maximum opportunity to the breeder that is well suited for characters that are simply inherited. It allows transgressive segregants to be easily identified through records while information about inheritance is precisely obtained. However, the drawbacks of pedigree method accounts for prolong time in the maintenance of pedigree record, largely dependent on skill of the breeder and selection for yield in F_2 and F_3 is ineffective.

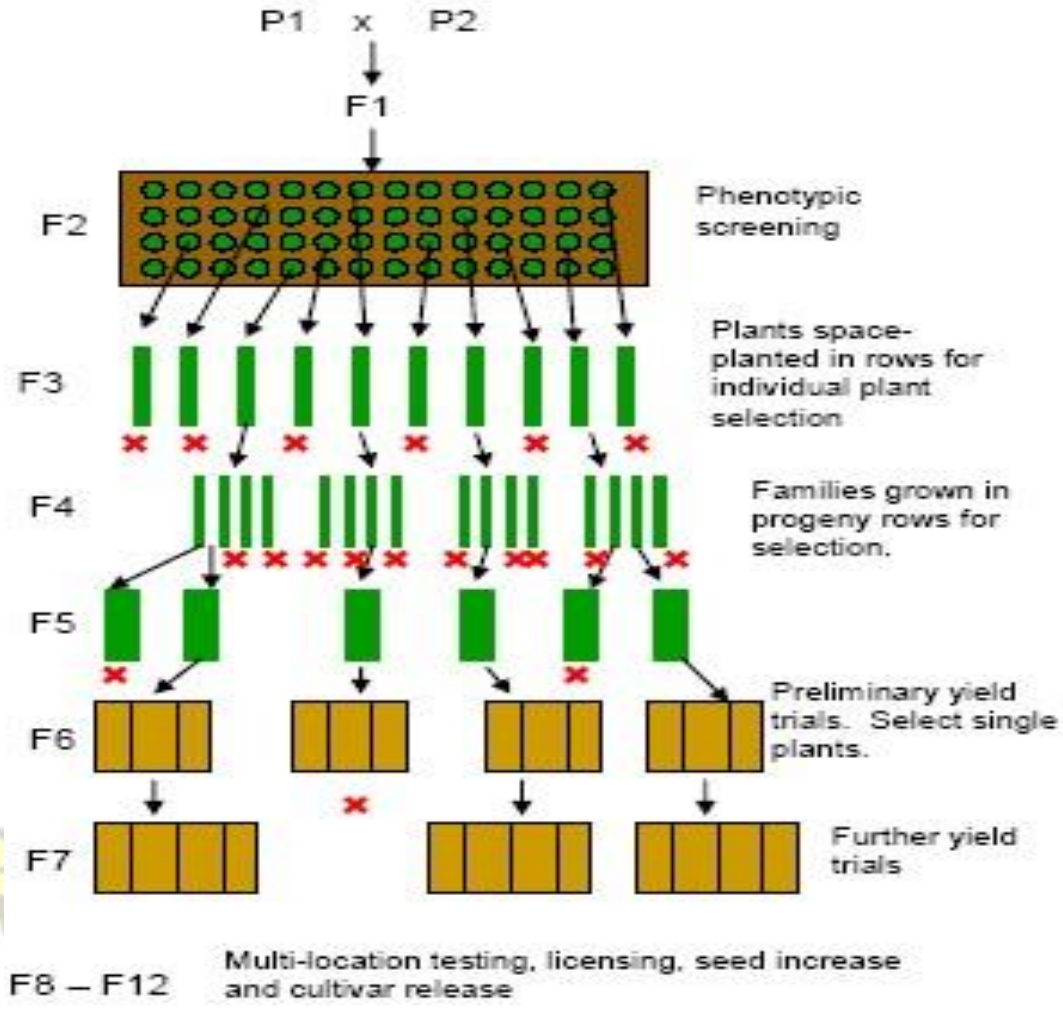

Figure 2.1 Schematic presentation of pedigree method in tomato production

Compared with the backcross, a more genetically diverse germplasm base is developed, but the time required to release a variety is much longer. In a pedigree method, recombination and segregation among the unselected genes permits the development of unique genotypes and phenotypes. The backcross and pedigree methods are forms of inbreeding that ultimately result in the development of pure lines (Barker *et al.*, 1989).

2.5.2 Single-seed descent

The single-seed descent breeding method provides the opportunity for advancing genotypes, potentially reducing the time for inbred line development that separates the inbreeding phase from the selection phase (Osei *et al.*, 2014). Modified single seed

descent is a single seed descent procedure that bulks two or three seeds from each plant during harvest. Bulking two or more seeds for the modified single-seed descent (MSSD) method helps avoid loss of F2 plant lineages due to seed unavailability or crop failure (Jumbo *et al*., 2011). Single-seed descent is based on the principle of equal fecundity. Two parents are mated to produce an F2 base population, but only one offspring is derived from each F2 individual and carried · forward to the F3 generation. Likewise, a single progeny from each F3 is contributed to the F4, and so on. Thus, in all future generations of inbreeding, every individual traces back to a single and different F2 progenitor (Brim, 1966; Empig and Fehr, 1971).

However, advancing random lines without selection for adaptation or other highly heritable traits may reduce the efficiency of this procedure, particularly with exotic germplasm. Selection is done at F6 generation after which the selected progeny are tested in replication trials and recommended for release as new varieties (Osei *et al.*, 2014).)

2.5.3 Backcrossing method

Backcross and introgression are valuable tools for genomic enhancement in breeding programmes. It is also useful to classify the genomic organizational design of measurable characters because it segregates a gene, or chromosomal region, in a diverse genetic family (the genetic background of the recurrent parent). In fact, it is one of the limited dependable techniques to certify the additive result in a quantitative trait locus (QTL). In addition, backcrossing could be used prior to, or in conjunction with, QTL detection to increase the precision of QTL mapping (Hospital, 2005).

Backcrossing is an important breeding method use in exploiting crops possessing many traits of potential interest to tomato breeders, including environmental stress tolerance,

resistances to disease and pests, and certain fruit quality characteristics (Chetelat *et al.*, 2006).

Brouwer *et al*. (2004), screened and mapped thirty-five interspecific F1 tomato hybrids, derived by crossing E × H and using H as the male parent, using detachedleaflet assays to identify the Quantitative trait loci (QTLs) for resistance to *Phytophthora infestans* (late blight) in tomato. They confirmed an aggregate of 15 and 18 QTLs in the BC-E and BC-H populations, respectively and concluded that genetic control of resistance to P. *infestans* contributed by L. *hirsutum* LA2099-MD1 was influenced quantitatively, genetically and ecologically and relationship map was drawn for each BC population with RFLPs.

Pilowsky and Cohen (1990) used backcrossing method between wild *Lycopersicon peruvianum* and cultivated tomato (L. *esculentum*) to induce tolerance in tomato against tomato yellow leaf curl virus (TYLCV) to which the cultivated tomato was susceptible. The segregated progenies were evaluated and confirmed tolerance to TYLCV suggesting that backcrossing is a reliable tool for incorporating desired traits into a deficient plants.

Frimpong and Safo-Kantanka (2006) used two primary gene pools of wild and cultivated tomato to increase productivity of tomato through interspecific crosses. They reported that all F1 hybrids from the backcross showed vigorous growth in all the vegetative data and recorded high fruit yield compared to parents. This was attributed to alleles added by the wild Cherry during backcrossing (Frimpong and Safo-Kantanka, 2006). Agble (1974) observed that cherry tomato could be used for enhancement of other tomato varieties.

Similarly, White (2010) employed backcrossing programme to improve the water use efficiency of tomatoes via increased ABA biosynthesis in the absence of water stress using ten wild species closely related to tomato. The results indicated the introgression of *S. galapagense* and the *S. neorickii NCED1* alleles (*SgNCED1* and *SnNCED1* into the cultivated research findings and confirmed the reliability of the method in transferring genes from donor parent to enrich deficient plant.

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2.5.4 Heritability estimates of some quantitative traits in tomato

Heritability can be defined as the percentage of observed variances on a characteristic among individuals of a population that are owing to genetic differences. Heritability is an important concept in quantitative genetics, particularly in selective plant breeding and behaviour genetics. It can be measured by estimating the relative contributions of genetic and non-genetic differences to the total phenotypic variation in a population. Heritability is important in plant breeding because it is used in estimating physiological traits in recombinant inbred lines in tomato (Flowers *at el.*, 2005). It has broad applications across a range of disciplines, from evolutionary biology, agriculture and to human medicine (Wray and Visscher, 2008)

Factors such as genetics, environment and random chance can all add to the difference between individuals in their visible characteristics (Raj and Oudenaarden, 2008). In developing an effective breeding approach for a crop, adequate understanding of the manner of inheritance of measureable characters is very critical. Heritability of a trait aids the plant breeder in expecting the behaviour of the successive generations for making desired variety. The higher the heritability, the simpler the selection process and greater the response to selection (Larik *et al*., 1999)

The estimation of genetic parameters, particularly in initial generations, is very valuable for directing the selection process in breeding programmes. According to Kaushik *et al.*

(2011), heritability estimates are the better indicators of heritable proportion of variation; high heritability indicates the efficacy of selection centred on phenotype. Nevertheless, this does not generally mean a high genetic gain for a specific character (Swarup and Chougule, 1962).

The accomplishment of plant breeding for any character requires, as a rule, that it be heritable and also the presence of variant in the population under selection (Cruz and Carneiro, 2003). Consequently, heritability is a very significant component for the breeder, permitting the approximation of the heritable portion of phenotypic variant, the estimation of genetic advancement and the selection procedures applied (Reis *et al*. 2002). Costa *et al*. (2007) estimated broad and narrow sense heritability in 57 F2 and F3 families derived from 6 two-way crosses of soybean and concluded that broad and narrow sense heritability coefficients, frequently were closer, which they attributed to the genetic variance that was probably due to additive nature supported by the high CVg/CVe ratio obtained. Similarly, Philip and Miklas (2007) used marker-assisted selection for quantitative trait loci (QTL) to confer partial resistance could facilitate breeding for resistance to Sclerotinia white mold in dry bean. The result indicated reduction in disease severity among BC_3 $F_{4:6}$ lines in the field assays.

Basically, two specific types of heritability can be estimated, broad sense and narrow

$H_b^2 = \frac{V_G}{V_P}$ captures the proportion of sense heritability. Broad-sense heritability $H_b^2 = \frac{V_G}{V_P}$ phenotypic variation due to genetic values that may include effects due to dominance (V_A), captures only that and epistasis. Conversely, narrow-sense heritability ($h_b^2 = \frac{V_A}{V_P}$) proportion of genetic variation that is due to additive genetic values (AV). The H^2_b and h^2_n can be estimated using the variance of the parents, F_1, F_2 and backcross generations to estimate V_P, V_E, V_G, V_A, V_D and V_{AD} variances.

$V_G = V_A + V_D + V_I$

$V_P = V_G + V_E + V_{GE} = (V_A + V_D + V_I) + V_E + V_{GE}$ (Allard, 1960; Warner, 1952)

Where

V_G = Genetic variance V_P=Phenotypic variance

V_A= Additive variance V_E=Environmental variance

V_D= Dominance variance $V_{AD=}$ Additive and Dominance variance

V_I= Epistasis variance $V_{GE=}$ Genetic and Environmental variance

The heritability percentage in broad sense (h^2_b) can be calculated as the ratio of the total genetic variance to the phenotype variance and the formulae as suggested by (Johnson *et al*., 1955).

$$h^2_b = \frac{V_G}{V_P}$$

Where, h^2_b = Heritability estimates in broad sense

V_G = Genotypic variance V_P

= Phenotypic variance

Similarly,

$V_P = V_{F2}$

$V_E = (V_{P1} + V_{P2} + V_{F1})/3$

$V_G = V_{F2} - V_E$

$V_A = 2(V_{F2}) - V_{B1} - V_{B2}$

$V_D = V_{B1} + V_{B2} - V_{F2} - V_E$ (Allard, 1960; Warner, 1952)

Where,

V_{B1} = Backcross 1 variance

V_{B2} =Backcross 2 variance

V_{F1} = Filial 1 variance

V_{F2} = Filial 2 variance

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2.6 Crop protection

Plant breeders are increasingly introducing varieties that are resistant or offer partial resistance to a range of diseases such as Verticillium wilt, *Septoria*, *Fusarium*, *Alternaria*, *Stemphylium* and the Tobacco mosaic virus as well as nematodes. Growers can minimize the impact of diseases such as blight by using appropriate fungicide programmes. Integrated Crop Management techniques that keep the foliage dry, and dew free, will help minimize the outbreaks of diseases such as Blight (http://www.yara.us/agriculture). Sterilization of soils, hot water treatment of seed and appropriate use of bactericides will minimize bacterial canker and bacterial spot. Insect pests such as whitefly, thrips and red spider mite are more difficult to control as a result of increasingly widespread resistance to pesticides. In soil-grown crops, weed control is essential to reduce competition for moisture and nutrients.

2.6.1 Biotic and abiotic stresses of tomato

Ecological stress conditions (drought, heat, salinity, cold) and/or pathogen infection (nematodes, viruses, fungi,) can have a devastating effect on plant growth and yield under field conditions (Suzuki *et al.*, 2014), which inhibits the plants from attaining their complete genetic potential for growth and reproduction (Bray *et al.*, 2000; Rockstrom and Falkenmark, 2000). Biotic stress affects economic decisions as well as practical ecosystem nutrient cycling (Robert *et al.*, 2001) and reduced yield of the

cultivated crop or affect the quality of the harvested products (Karim and Sazzad, 2007). According to Godia (2014), although plants protect themselves from attack by a great variety of pests and pathogens, including fungi, bacteria, viruses, nematodes, and herbivorous insects, many abiotic stress disorders are revealed to deteriorate the defensive mechanism of plants and improved their susceptibility to pathogen infection (Amtmann *et al*., 2008; Goel *et al*., 2008; Mittler and Blumwald, 2010; Atkinson and Urwin, 2012). Major prospective crops being cultivated in the fields are likely to be opened to a greater range and number of abiotic and biotic conditions, as well as their combination. Hence, it is now a major focus of agricultural research, because biotic stress accounts for massive economic losses in crop production (Mittler and Blumwald, 2010)

2.6.2 Nematodes

Nematodes are microscopic, eel-like roundworms parasites of almost every species of animal, including humans, and plant and cause enormous social and economic damage. There are many different species of root-feeding nematodes; the most destructive ones to crops (vegetables, fruit trees, and ornamentals) are the root-knot nematodes, *Meloidogyne incognita* species. They spread easily, from one agricultural field to another through soil on tools and boots or on infested plants and are difficult to control (Perry *et al.*, 2010). Tomato is considered as the most susceptible host for root-knot nematodes (Bem *et al*., 2014). Usually, they cause distinctive swellings (galls) on the roots of affected plants. Globally root-knot nematodes cause approximately 5% in economic crops loss (Sasser and Carter, 1985). According to Nicol *et al*. (2011), the tropical and sub-tropical climates, crop production losses attributable to nematodes were estimated at 14.6% compared with 8.8% in developed countries.

In Ghana, plant parasitic nematodes cause as much as 55% crop loss in vegetables (Haougui *et al*., 2008). According to Djibey (2012) tomato total yield loss can arise when the crop is grown on severely infested soils. Nematodes are one of the main limitations to tomato production in many parts of the country (Djibey, 2012). However, for effective, efficient and sustainable tomato production, crop rotation at least three years with non-host crops, use of transplants and nursery stock certified free of root knot nematode, planting disease and nematode resilient tomato varieties are particularly vital in controlling root knot-nematodes and when limited agricultural land is available (Djibey, 2012).

2.6.2 Viruses

According to Roossinck (2011), viruses are Small obligate intracellular parasites containing an RNA or DNA genome surrounded by a protective, virus-coded protein coat. Virus diseases transmitted by an insect vector whitefly (*Bemisia tabaci*) Gressel, (2004) from the family *Geminiviridae and Closteroviridae* and order *Hemiptera*, constitute a major biotic constraint to tomato production in developing countries including those of Sub-Saharan Africa (SSA). Tomato yellow leaf curl virus (TYLCV) causes the most destructive disease of tomato, resulting in significant economic yield losses from 90-100% (Glick, 2009; Osei *et al.*, 2010).

TYLCV remains the limiting factor for tomato production, both in the field and in protected screen houses (Lapidot *et al*., 2001). Viruses of the family *Geminiviridae* cause mostly leaf curl, small round leaflets, shortened internodes, marginal yellowing flower abscission, and reduced yield (Czosnek and Laterrot, 1997) whereas those of the *Closteroviridae* induce infectious chlorosis (Wisler *et al*., 1998).

According to Ssekyewa (2006), TYLCV is general in the tropics; it has been reported from South Africa, Senegal, Tanzania, Malawi, Zambia, Zimbabwe, Nigeria, Ivory

Coast, Egypt and Sudan (Yassin *et al*., 1982; AVRDC, 1993, 1998; Czosneck *et al*.1990; Nakhla *et al*., 1993; Nono-Womdim *et al*., 1994; Chiang *et al*., 1996). It is also widely spread in the South East Asia and East Asia, the Americas and the Mediterranean (Green and Kallo, 1994; Chiang *et al*., 1996; Polston and Anderson, 1997; Czosnek and Laterrot, 1997). Tomato yellow leaf curl viruses are amongst major viruses whose prevalence and spread are influenced by presence of the whitefly vector (*Bemisia tabaci*) as well as weather conditions within the agro-ecosystem and of damaging threats to tomato production. According to Godia (2014), tomato spotted wilt virus (TSWV) adds substantially to yield and fruit quality fall owing to the presence of necrotic or chlorotic spots on fruits. In Ghana during the dry season, local production of tomato is not able to meet the domestic demand because of disease and other production constraints such as fungal, viral, bacterial and nematode diseases and therefore, tomatoes are imported mainly from Burkina Faso (Sasser *et al*., 1983).

2.6.3 Fungi

Fungi are among the causative agents of infectious diseases of crop plants and significantly cause annual crop yield losses. Fungal pathogens of plants are of serious economic factor, attracting the attention of farmers, plant breeders, and scientists alike due to their devastating and epidemiological consequences on crop plants (Knogge, 1996). Fungi navigate the plant's outer structural walls, the cuticle and the epidermal cell wall to gain entrance into the plant. Early blight caused by *Alternaria solani* (Kemmitt, 2013) is the most damaging infection of tomatoes in the tropical and subtropical regions (Pandey *et al*., 2006). Each 1% rise in intensity of the disease has the potential to reduce yield by 1.36%, and complete crop failure can occur when the disease is most severe (Pandey *et al*., 2006). Yield losses of up to 79% have been reported in the USA, of which 20-40% is due to seedling losses (Collar rot) in the field

(Chaerani and Voorrips, 2006). Among other tomato diseases, fungal diseases reduce the yield significantly. The most important fungal disease is the late blight (Jett, 2002). The tomato late blight disease is often caused by seedborne fungus *Phytophthora infestans*, which is a difficult disease to manage and causes significant reduction in yield (Jett, 2002). This disease influences the overall health and final crop stand economic losses (Bissdorf, 2005; Pandey *et al*., 2006).

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2.6.4 Bacteria wilt

Bacterial wilt (southern bacterial wilt) is a disease caused by soil borne bacterium, *Ralstonia solanacearum* Denny, (2006) that lives in the soil and attacks plants in the Solanaceae (tomato, peppers, potatoes, and eggplant). Through the plant‟s root or stem, most often where plants have been cut, injured or weakened by transplanting, cultivation, insects, or other diseases. The disease cause 25% economic yield losses on tomato (El-Alwany, 2014). According to AVRDC (2004), high temperatures (30–35°C) and high soil moisture favour disease development. High soil moisture increases the survival of the pathogen, its rate of infection and development, and its spread through the soil. However, to date, there is no chemical treatment available; the disease can be managed by avoiding physical damage to roots and stems, control root-knot nematodes, which are known to weaken tomato roots and allow bacteria access to plants. Preventive measures includes, crop rotation, use of resistant varieties, removal and destruction of affected plants, plant tomatoes in well-drained soil with a balanced pH and space plants generously AVRDC (2004).

2.7 Abiotic factors

Plants have evolved to live in environments where they are exposed to different stress factors in combination (Nicky and Urwin, 2012)**.** Being fixed, they have developed specific mechanisms that allow them to detect precise environmental changes and

respond to complex stress conditions to minimize damage while conserving valuable resources for growth and reproduction. However, several crop plants are cultivated in environments that are suboptimal, which inhibits the plants from achieving their fully inherited potential for growth and reproduction (Bray *et al.*, 2000; Rockstrom and Falkenmark, 2000)**.** Crop plants are damaged by non-infectious factors, causing problems that can collectively be called "abiotic diseases" (disorders). Unfavourable soil properties, fertility imbalances, moisture extremes, temperature extremes, chemical toxicity, physical injuries, and other problems are examples of abiotic disorders that can reduce plant health and even kill plants (Kennelly *et al*., 2012). Abiotic disorders predispose plants to biotic stresses such as diseases (Kennelly *et al.*,
2012). The yield difference can sometimes be largely accounted for by unfavourable environmental conditions, which, when creating potentially damaging physiological changes within plants, often referred to as stresses (Shao *et al*., 2008).

According to Abdelmageed and Gruda (2009), high temperature negatively affects plant growth and survival, which affect crop yield. Furthermore, Morejon (2013) stated that up to 70% of global agriculture crop production is affected by environmental constraints (abiotic stress) and only 3.5% of the worldwide land area is not adversely affected by any ecological factors during a cropping cycle (FAOSTAT, 2006). Abiotic stress factors such as heat, cold, drought, salinity, and nutrient stress have a huge impact on world agriculture, and it has been proposed that they decrease average yields by >50% for most key crop plants (Wang *et al*., 2003).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Study area

The study was carried out at the Horticulture Division, Council for Scientific and Industrial Research (CSIR)-Crops Research Institute (CRI) Kwadaso, Kumasi. Two experiments (designated by genotypes F and G) were conducted during the major and minor rainy seasons from May 2014 to July 2015. The research field falls within the semi-deciduous rain forest zone and is characterized by a bimodal rainfall pattern, from April to July and September to December, with an average annual rainfall of 1500 mm. The soil is Ferric Acrisol (FAO/UNESCO legend, 1986). Total rainfall and mean sunshine recorded for CSIR – CRI, Kwadaso during period of the experiment was 531.1mm and 30.4h respectively. Maximum and minimum mean temperatures were however, 32.7˚C and 22.7˚C respectively. Kwadaso station lies between latitude 06, 42˚ North and longitude 001, 4˚ West.

3.2 Generation of F1 and F2 genotypes

In 2012, CSIR-CRI generated 14 different F1 genotypes. Selections of their parents were purposefully based on specific horticultural traits such as plant height, fruit shape, fruit size, and resistance to virus (Table 3.1). Out of the 14 F1 genotypes developed by CSIR-CRI; two were used for this study. These include; P2 (042 ♀) and P1 (083 ♂) used as female and male respectively for genotype (F) and P2 (213 ♀) and P1 (097 ♂) also used as female and male respectively for genotype (G) as illustrated in figure 3.1. The F1 seeds were nursed on April 10th, 2014 and transplanted to the field three weeks thereafter. They were space-planted (100 cm x 50 cm) alongside their parents so that each F1 plant produces enough seed for F2 generation. The size of the plot was

324 m^2 (18 m x 18 m). At maturity, fruits from each F1 genotype were harvested separately, as well as their parents. Their seeds were extracted to produce F_2 seeds.

In the F_2 generation, Seeds extracted from F_1 and their parents were nursed on the 1st August, 2014 and transplanted on the 1st September, 2014. Large population (182) of F_2 plants was space-planted at 60 cm x 50 cm to facilitate the identification of superior plant types for selection. The parents for each genotype were planted in proximity to the genotype as a check and for comparison with the performance of the progenies. At F2 maturity, for each genotype (F and G), five breeding lines were selected for field evaluation together with their parents based on good horticultural characters of interest. These selected plants had their seeds extracted separately.

Table 3.1 Tomato accessions, desirable traits, names and sources

ACCESSION	DESIRABLE TRAIT	NAME	SOURCE
P1 (083)	Many fruits (small fruit sizes)	6(A)	SARI
P2 (042)	Big fruit size and fewer fruits	Local tomato	Virus resistant
P1 (097)	Fruit size (medium) and early maturing.	Local tomato	Binduri (Upper East)
P2 (213)	Big fruit size and late maturing	AVTO 0102	AVRDC

P1 (♀) X P2 (042 ♂) (083

F_1 (F)

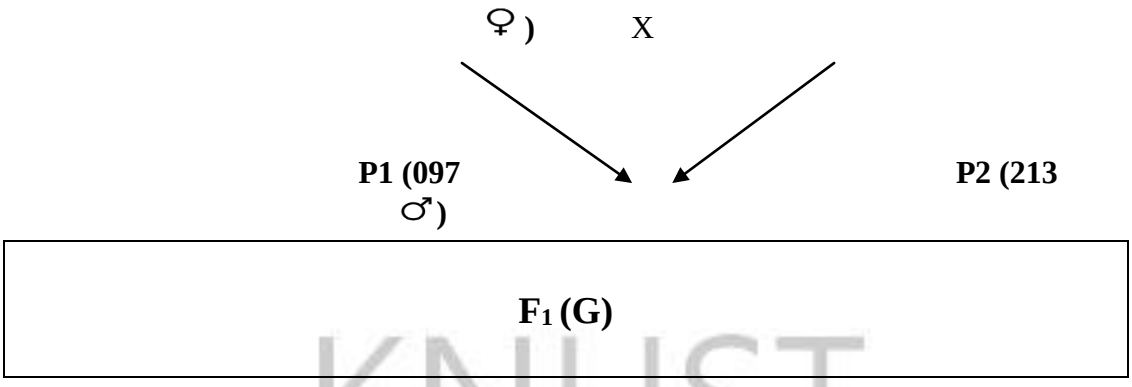

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Figure 3.1 Schematic presentation of crosses P1 (083 ♀) x P2 (042 ♂), P1 (097 ♀) and P2 (213 ♂) to generate F_1 hybrids (F and G) respectively (CSIR-CRI 2012/2013)

3.2.1 Generation of BC_1F_1 and BC_2F_1 population.

Seeds of F_1S, F_1 (G) and F_1 (F) and their recurrent parents for generating backcrosses were nursed on the 10th August, 2014 and transplanted into pots on the 9th September, 2014. To generate BC_2F_1, seeds were nursed on the 28th November, 2014 and transplanted into pots on the 24th December, 2014. Eight seedlings were arranged in pots of two rows placed beside the recurrent parents to facilitate crosses. They were space-planted at 100 cm and 50 cm between rows and within rows. BC_1F_1 crosses involved F1 genotypes (F and G) and their respective recurrent parents viz.; F_1 (G♀) x P1 (097♂), F_2 (G ♀) x P2 (213♂), F_1 (F ♀) x P1 (083♂) and F_1 (F ♀) x P2 (042♂). The crosses were carried out from September to October 2014, in the morning between 7:00 and 8:00 am while for BC_2F_1; crosses were done in early February, 2015 in the late afternoon daily.

Emasculation of female parents was done manually prior to anthesis and paper sole tapes to avoid contamination from foreign pollen covered their pistils. The female stigma was pollinated immediately by using the freshly collected pollens from the male

parent. Between crosses, pointed forceps were sterilized in alcohol using 100% mentholated spirit. This was done to prevent contamination of the pollen between the successive crosses. Figure 3.2 shows illustrations of backcrosses.

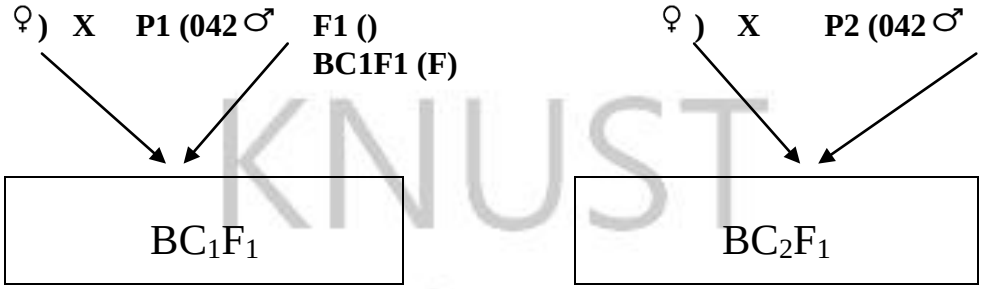

Figure 3.2 Schematic illustration of crosses

Flower buds ready for emasculation showed pale yellow colouration. They were opened using sterilized sharp-pointed forceps as described by Opena *et al*. (2001). Prior and during crosses, all recommended agronomic practices (weeding, fertilizer application, staking, insect control and pruning to induce flowering) were observed to enhance success of crosses. YaraMila Winner (150 kg ha^{-1}) and YaraLiva Nitrabor (50 kg ha^{-1}) were used as basal fertilizer at transplanting and fruit ripening and Krista K 50 kg ha^{-1} in five applications, started before flowering and every two weeks during the crosses. Victory (Metalaxyl 80g/Kg and Mancozeb 640g/Kg) at 50 g mixed in 15 Liters of water) used as foliar spray for the control of fungus diseases, 20 g Golan (Acetamiprid 200g/l against white fly, Acetamiprid 20%SP) at vegetative stage, 50ml Deltapaz + 35ml Rim-On and alternated with Deltapaz with 50ml Karate + RimOn after one week at flowering stage and at fruiting stage 50ml of Karate. Knapsack sprayer was used for application.

The flowers of the female plants were carefully emasculated (anthers removed) to locate unopened flowers (Fig 3.3). The anther cones were removed by pinching between thumb and forefinger, gently rock side to side to pull straight off the side of the anther cone with tweezers. To expose the stigma of the female flowers, the base of the flower

was held at the pedicel and pull straight out to eliminate the possibility of damaging the pistillate parts.

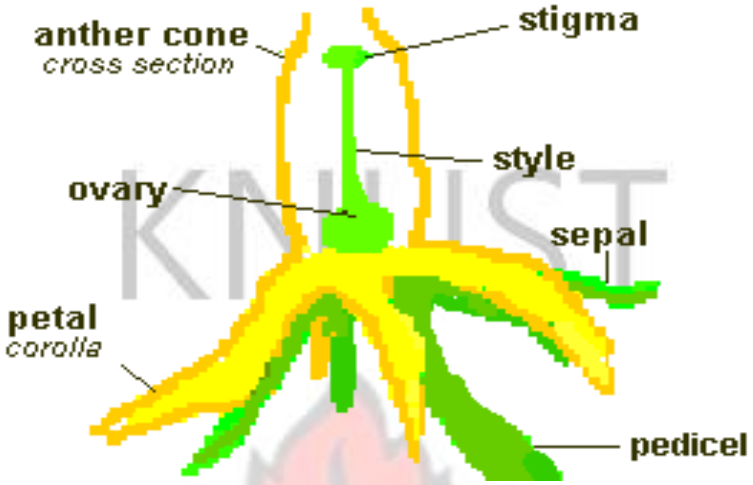

Figure 3.3 Illustration of female flowers ready for pollination

(http://www.kdcomm.net/~tomato/Tomato/xingtom.html Accessed 13th July, 2015)

Plate 3.1 A cross between BC_1 and recurrent parent

The pedicel, the sepals and the pistillate parts were left intact. Pollen was collected from the anther cones of opened or partially opened flowers from the parent (male) plant in a small glass vial for crossing. The flower was tapped to facilitate release of the pollen. Pollen was applied to the emasculated flower by holding the emasculated flower

in one hand; apply the pollen to the stigma of the mother plant (female) surface. The pollen was applied sufficiently to cover the entire stigma. The stigma was dipped onto a slide containing pollen by the fingers and covered with paper tape to protect it from adverse environmental conditions, so as to allow for fertilization and fruits setting. At the end of each crossing, pollinating tags were used to label crossed plants to distinguish them from other flowers on the same or nearby inflorescences. Closely located flowers were removed immediately after crossing to prevent them from shedding pollen onto the newly pollinated stigma.

Plate 3.2 Fruit of BC_1F_1

3.3 Evaluation of tomato genotypes (parents, F_1, F_2, BC_1F_1 and BC_2F_1)

A field experiment was conducted during the major season on the 14th June 2015 to evaluate the tomato genotypes (Parents, F_1, F_2 BC_1 and BC_2) for yield and yield components. The experiment consisted of two different F1 genotypes designated as genotypes (F) and (G.)

3.3.1 Experimental design

Seeds of F_1, F_2, BC_1F_1, BC_2F_1 and the parents of each genotype were planted on the 15th April, 2015 on a raised bed treated with the fungicide; Victory (Metalaxyl 80g/Kg Mancozeb 640g/Kg) at 50 g mixed in 15 Liters of water) and organic manure (poultry at 2 t ha^{-1}) added. Seedlings were transplanted on 15th May, 2015 on a plot size of 476 m^2 (28 m x 17 m) in a randomized complete block design (RCBD) with three replications for each experiment. Each replicate constituted 55 plants of parents and F_1S, 143 F_2, 77 BC_1 and BC_2 plants. Spacing of 60 cm between rows and 50 cm within rows respectively at a density of a single plant per stand was used. Data were taken on 30 plants for parents and F_{1S}, 120 F_2, 60 BC_1 and BC_2. Table 3.2 shows treatments used in the experiments. Standard agronomic practices such as weed control, fertilizer application which includes YaraMila Winner (150 kg ha^{-1}) at transplanting and fruit ripening, YaraLiva Nitrabor (50 kg ha^{-1}) at transplanting, 125 kg ha^{-1} before flowering and 75 kg ha^{-1} at fruit ripening and Krista K 50 kg ha^{-1}in 5 applications, starts before flowering and every 2 weeks to reach a total quantity of

250kg ha^{-1}. Spraying of fungicides which includes Victory (Metalaxyl 80g/Kg

Mancozeb 640g/Kg) 50 g plus 15 liters water, and alternated with50 g Triamagol plus 15 liters water were done after one week at vegetative stage. 300 ml TopCop (Tri Basic Copper Sulfate 8.4% and Sulfur, as elemental 50%) plus 15 liters water was also alternated with 60 g Funguran plus 15 liters water after one week at the flowering stage. The insecticides were used as follow: 20 g Golan (Acetamiprid 200g/L, Acetamiprid 20%SP) at vegetative stage, 50 ml Deltapaz (Deltamethrin) + 35 ml Rim-On (Noraluran) and alternated with Deltapaz with 50 ml Karate (Chloropyriphos

Ethyl) + Rim-On after one week at flowering stage and at fruiting stage 50 ml of Karate.

Soil samples from the experimental sites were collected from six different locations of the planting field at a depth of 0-15 cm for laboratory analysis at the Soil Analysis Division of CSIR-CRI, Kwadaso. Table 3.3 shows the result of the soil analysis.

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Table 3.2 Treatments for field evaluation

Treatment	Genotype (F)	Genotype (G)
T1	P_1 (083 ♂)	(097 ♂)
T2	P_2 (042 ♀)	P2 (213 ♀)
T3	F_1	F_1
T4	F_2	F_2
T5	BC_1	BC_1
T6	BC_2	BC_2

Table 3.3 Physio–chemical properties of the top soil (0 – 15 cm depth) of the experimental field

Properties	Soil depth (0 – 15 cm)
pH (1:1H_2O)	6.54
Percent organic carbon	0.78
Percent total nitrogen	0.14
Percent organic matter	1.34
Exchangeable cations (me/100g)	
Ca	5.07

Mg	1.6
K	0.14
Na	0.08
Available P (ppm)	92.48
Particle size distribution	
Percent sand	64.52
Percent clay	16.02
Percent silt	19.46
Soil texture	Sandy Loam

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3.4 Data collected and Analysis

Data were taken on plant height (cm), stem girth (cm), days to 100% flowering. Days to maturity was recorded from the day seedlings were transplanted onto the field. Others included; fruit weight (FW), locule number (LN) fruit flesh thickness (FFT), number of fruits per plant, fruit length, fruit diameter, TSS (ºBrix), marketable and non-marketable fruits. Data recorded were subjected to Analysis of Variance (ANOVA) using the Genstat (12th edition) statistical package. Least Significance Difference at 5% was used to separate the treatment means. The means and variances obtained were used to estimate genetic parameter such as broad sense and narrow sense heritability.

3.4.1 Heritability of 14 characters in the broad sense

Broad sense heritability (h^2_b) of 14 characters of tomato was estimated using the methodology of Allard (1960). $H^2_b = (V_{F2} – V_E) / V_{F2}$: Where;

- H^2_b= Broad sense heritability
- $V_E = (V_{P1}+V_{P2}+V_{F1})/3$
- V_E = Error variance

- V_{F2} = Variance of F2 family
- V_{P1} = Variance of parent 1
- V_{P2} = Variance of parent 2
- V_{F1} = Variance of F1 family

3.4.2 Narrow sense heritability

Narrow sense heritability (h^2_n) was computed according to the method of (Halloran *et al*., 1979) as follows:

$h^2_n = [2V_{F2} – V_{BC1} – V_{BCP2}] / V_{F2}$, where: V_{F2}, V_{BCP1} and V_{BCP2} are the variances of the F_2, P_1 (083) / F_1 and P2 (042) / F_1 for genotype (F) and F_2, P_1 (097) / F_1 and P_2 (213) / F_1 genotype (G) respectively.

CHAPTER FOUR

4.0 RESULTS

4.1 Agronomic characteristics of six tomato genotypes (F)

Mean range, variance and standard deviation (SD) of plant height and stem girth for six tomato genotypes (F) are presented in Table 4.1. Plant height at 100% flowering ranged from 92.17 to 95.12 cm. Mean for F_2 (93.54cm) genotype was the highest which exceeded parental limits and was significantly ($P<0.05$) different from all the other genotypes. BC_2F_1 (78.45 cm) recorded the shortest plant height at 100% flowering. The range of variation and variance in F_2 was higher than the parents, F_1, BC_1F_1 and BC_2F1. In addition, stem girth varied from 9.5 cm to 11.36 cm. The maximum and minimum mean performance for stem girth were recorded in BC_2F_1 (10.31 cm) and P_1 083 (7.69 cm) respectively. The mean of F_1 and BC_1F_1 were within the limit of parent two but exceed that of parent one.

Table 4.1 Mean, Range, Variance and Standard Deviation (SD) of plant height and stem girth for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
Plant height (cm)	P1 (083)	85.59	85.00-88.12	1.51	1.23
	P2 (042)	82.59	81.23-84.11	2.09	1.45
	F_1	86.43	85.00-88.12	1.48	1.22
	F_2	93.54	92.17-95.12	3.21	1.79
	BC_1F_1	79.83	78.32-81.41	2.39	1.55
	BC_2F_1	78.45	77.00-80.14	3.51	1.87
	Lsd (P<0.05)	**0.18**			
	CV (%)	**0.10**			
Stem girth (cm)	P1 (083)	7.69	7.10-8.12	0.28	0.53
	P2 (042)	9.40	8.00-10.92	2.14	1.46
	F_1	7.83	7.22-8.39	0.35	0.59
	F_2	9.81	8.63-11.29	2.83	1.68
	BC_1F_1	8.63	7.01-9.74	2.25	1.50
	BC_2F_1	10.31	9.50-11.36	1.96	1.40
	Lsd (P<0.05)	**1.61**			
	CV (%)	**9.90**			

Mean, range, variance and standard deviation (SD) of days to flowering and days maturity for six tomato genotypes (F) are presented in Table 4.2.

Number of days to 100% flowering ranged from 28.00 to 30.00 with a maximum and minimum mean of 29.00 and 23.00 for BC_2F_1 and F_1 respectively. Mean for F_2, BC_1F_1 and BC_2F_1 were all outside the parental limits except F_1 mean which falls within the parental limits. The range of variation and variance in BC_2F_1 was higher than that of parent two but lower than that of parent one. In terms of days to maturity, there were significant differences among genotypes. Days to maturity varied from 56.00 to 64.00 days. F_2 (63.00) had the longest days to maturity while parent one (58.67) had the shortest days to maturity. The range of variation and variance in parent one was higher than in all of the other genotypes.

Table 4.2 Mean, Range, Variance and Standard Deviation (SD) of days to flowering and days to maturity for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
Days to flowering	P1 (083)	24.67	23.00-27.00	4.33	2.08
	P2 (042)	26.67	26.00-28.00	1.33	1.16
	F_1	23.00	22.00-24.00	1.00	1.00
	F_2	28.33	27.00-29.00	3.33	1.82
	BC_1F_1	27.67	27.00-29.00	2.49	1.58
	BC_2F_1	29.00	28.00-30.00	3.84	1.96
	Lsd (P<0.05)	**2.47**			
	CV (%)	**5.10**			
Days to maturity	P1 (083)	58.67	56.00-62.00	6.33	2.52
	P2 (042)	59.00	57.00-61.00	1.46	1.20
	F_1	60.67	60.00-61.00	0.33	0.57
	F_2	63.00	61.00-64.00	3.68	1.92
	BC_1F_1	60.33	59.00-62.00	3.33	1.82
	BC_2F_1	62.33	61.00-63.00	3.53	1.88
	Lsd (P<0.05)	**3.48**			
	CV (%)	**3.20**			

4.2 The yield and yield components of six tomato genotypes (F)

Table 4.3 displays mean, range, variance and standard deviation (SD) of fruit weight per plant and number of fruits per plant for six tomato genotypes (F). The average fruit

weight per plant varied from 24.06 g to 33.31 g. The mean maximum and minimum fruit weight was recorded by parent two (32.82 g) and F_2 (26.71 g) respectively. In addition, BC_1F_1 and BC_2F_1 had their range of variation and variances higher than that of their corresponding parents. There were significant differences among genotypes for that trait. There were variations among genotypes with respect to number of fruit per plant ranging from 19.00 to 32.00. The maximum and minimum number of fruit per plant was recorded by P_2 (29.00) and BC_1F_1 (22.33) respectively. The result showed that F_1 had higher range of variation and variance than the rest of the tomato genotypes.

Table 4.3 Mean, Range, Variance and Standard Deviation (SD) of fruit weight per plant and number of fruit per plant for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
Fruit weight/plant (g)	P1 (083)	27.81	26.73-28.80	2.01	1.42
	P2 (042)	32.82	32.00-33.31	0.51	0.71
	F_1	28.12	24.06-30.54	8.51	2.92
	F_2	26.71	24.73-29.00	4.62	2.15
	BC_1F_1	29.40	28.00-31.31	2.94	1.71
	BC_2F_1	28.12	24.19-31.00	8.41	2.90
	Lsd (P<0.05)	**4.63**			
	CV (%)	**8.80**			
Number of fruits/plant	P1 (083)	27.00	26.00-28.00	1.00	1.00
	P2 (042)	29.00	27.00-32.00	5.00	2.23
	F_1	26.33	23.00-31.00	12.33	3.51
	F_2	27.33	24.00-31.00	10.33	3.21
	BC_1F_1	22.33	19.00-25.00	9.53	3.09
	BC_2F_1	27.67	25.00-31.00	9.83	3.14
	Lsd (P<0.05)	**4.56**			
	CV (%)	**9.40**			

Mean, range, variance and standard deviation (SD) of total marketable fruit weight and number of marketable fruit per plant for six tomato genotypes (F) are presented in Table 4.4. Total marketable fruit weight varied among tomato genotypes and ranged from 3.46 kg to 6.31 kg. The maximum and minimum of total marketable fruit weights were recorded by BC_2F_1 (5.85 kg) and P1 (4.24 kg) respectively. Conversely,

the range of variation and variance in P_2 were higher than P_1, F_2, BC_1F_1 and BC_2F_1 respectively. Number of marketable fruit per plant varied from 14.00 to 26.00. The highest and lowest number of marketable fruit per plant was recorded by P_2 (22.33) and BC_1F_1 (17.00). Besides, the range of variation and variance in F_1 was higher than recurrent parents, F_2, BC_1F_1 and BC_2F_1 respectively.

Table 4.4 Mean, Range, Variance and Standard Deviation (SD) of total marketable fruit weight and number of fruit per plant for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
TMKTFW (kg)	P1 (083)	4.24	4.11-4.45	0.03	0.17
	P2 (042)	5.01	4.23-5.45	0.46	0.68
	F_1	5.36	3.46-6.86	0.04	0.20
	F_2	5.36	4.79-5.67	0.24	0.49
	BC_1F_1	4.43	4.15-4.61	0.06	0.24
	BC_2F_1	5.85	5.13-6.31	0.40	0.63
	Lsd (P<0.05)	**0.86**			
	CV (%)	**10.10**			
NMKTFPP	P1 (083)	20.00	19.00-21.00	3.00	1.73
	P2 (042)	22.33	20.00-25.00	6.33	2.52
	F_1	19.33	16.00-24.00	17.00	4.12
	F_2	22.00	18.00-26.00	16.00	4.00
	BC_1F_1	17.00	14.00-19.00	11.74	3.43
	BC_2F_1	22.00	19.00-26.00	13.61	3.69
	Lsd (P<0.05)	**4.57**			
	CV (%)	**12.30**			

TMKTFW – Total marketable fruits weight, NMKTFPP – Number of marketable fruit per plant

Mean, range, variance and standard deviation (SD) of non-marketable and fruit length for six tomato genotypes (F) are shown in Table 4.5. The non-marketable fruit per plant varied among tomato genotypes ranging from 5.00 to 8.00. The maximum and minimum values were recorded by P_1 and F_1 on one hand and on the other hand F_2 and BC_1F_1 respectively. P_1 had the highest range of variation and variance over BC_2F_1, BC_1F_1, F_2, P_2 and F_1 respectively.

The fruit length among tomato genotypes varied significantly from 25.31 cm to 38.43 cm. F_2 (36.53 cm) had the longest fruit length and P_1 recorded the shortest fruit length (25.96 cm). However, the range of variation and variance in F_2 was higher than recurrent parents, F_1, BC_1F_1 and BC_2F_1 respectively.

Table 4.5 Mean, Range, Variance and Standard Deviation (SD) of nonmarketable fruit and fruit length for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
NNMKTFPP	P1 (083)	7.00	6.00-8.00	1.00	1.00
	P2 (042)	6.67	6.00-7.00	0.33	0.57
	F_1	7.00	7.00-7.00	0.00	0.00
	F_2	5.33	5.00-6.00	0.33	0.57
	BC_1F_1	5.33	5.00-6.00	0.06	0.24
	BC_2F_1	5.67	5.00-6.00	0.04	0.20
	Lsd (P<0.05)	**1.19**			
	CV (%)	**10.70**			
Fruit length (cm)	P1 (083)	25.96	25.31-27.13	1.03	1.01
	P2 (042)	27.66	26.19-29.62	3.12	1.77
	F_1	32.01	27.81-33.15	1.58	1.26
	F_2	36.53	35.16-38.43	3.88	1.97
	BC_1F_1	31.88	28.17-32.00	2.78	1.67
	BC_2F_1	29.77	30.25-33.15	3.81	1.95
	Lsd (P<0.05)	**2.46**			
	CV (%)	**4.50**			

NNMKTFPP – Number nonmarketable fruits per plant

Mean, range, variance and standard deviation (SD) of Fruit diameter and fruit flesh thickness for six tomato genotypes (F) are indicated in Table 4.6. Fruit diameter varied from 35.21 to 38.41cm. It was significantly larger in F_2 genotype (42.18cm) than the other genotypes and BC_2F_1 (28.72cm) recorded the smallest fruit diameter. The range of variation and variance in F_2 was higher than recurrent parents, BC_2F_1, F_1, and BC_1F_1 respectively.

The fruit flesh thickness of the tomato genotypes varied from 2.87 to 3.7 mm and the variation was significant. The maximum and minimum mean values were (3.74mm) and (2.87mm) accounted for by BC_2F_1 and P1 respectively. However, the range of variation and variance in F_2 was higher than recurrent parents, F_1, BC_2F_1, and BC_1F_1 respectively.

Table 4.6 Mean, Range, Variance and Standard Deviation (SD) of fruit diameter and fruit flesh thickness for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
Fruit diameter (mm)	P1 (083)	35.88	35.17-39-15	1.32	1.15
	P2 (042)	37.94	36.62-39.21	1.68	1.30
	F_1	28.72	26.33-30.31	2.27	1.51
	F_2	42.18	35.21-43.41	3.11	1.76
	BC_1F_1	34.82	32.17-35.01	2.89	1.70
	BC_2F_1	36.71	35.07-38.64	1.79	1.34
	Lsd (P<0.05)	**2.79**			
	CV (%)	**4.30**			
Fruit flesh thickness (mm)	P1 (083)	2.87	2.51-3.10	0.10	0.32
	P2 (042)	3.50	3.40-3.60	0.01	0.10
	F_1	2.93	2.80-3.10	0.02	0.14
	F_2	3.40	3.30-4.0	0.11	0.33
	BC_1F_1	3.23	3.40-4.12	0.10	0.32
	BC_2F_1	3.74	3.14-4.50	0.06	0.24
	Lsd (P<0.05)	**0.53**			
	CV (%)	**8.70**			

The Mean, range, variance and standard deviation (SD) of locule number and brix of six tomato genotypes (F) are indicated in Table 4.7. The locule number varied from 3.00 to 6.00. The maximum and minimum mean values were 5.65 and 3.84 recorded by P_2 and BC_1F_1 respectively. However, F_2 and BC_1F_1 recorded the same values for the range of variation and variances with respect to locule number.

Brix varied from 2.11 to 7. 31. The highest and lowest was between 5.51 and 3.44 recorded by F_2 and F_1 respectively. The range of variation and variance in BC_2F_1 was higher than recurrent parents, BC_1F_1, and F_1 respectively.

Table 4.7 Mean, Range, Variance and Standard Deviation (SD) of locule number and brix for six tomato genotypes (F)

Character	Genotype	Mean	Range	Variance	SD.
Locule Number	P1 (083)	5.00	4.00-6.00	0.39	0.62
	P2 (042)	5.65	5.40-6.00	0.10	0.32
	F_1	4.77	4.00-5.31	0.27	0.52
	F_2	4.84	4.0-5.51	0.59	0.77
	BC_1F_1	3.84	3.00-4.50	0.59	0.77
	BC_2F_1	4.03	3.56-4.52	0.43	0.66
	Lsd (P<0.05)	**1.30**			
	CV (%)	**15.30**			
Brix (°C)	P1 (083)	4.19	2.86-5.86	2.33	1.53
	P2 (042)	3.96	2.91-5.42	1.71	1.31
	F_1	3.44	2.11-5.11	2.33	1.53
	F_2	5.51	4.09-7.31	2.70	1.64
	BC_1F_1	3.85	2.62-5.43	2.16	1.47
	BC_2F_1	4.43	3.17-6.11	2.84	1.69
	Lsd (P<0.05)	**0.22**			
	CV (%)	**2.90**			

4. 3 Heritability estimate of broad sense (h^2_b) and narrow sense (h^2_n) for 14 characters of tomato genotypes (F)

Broad sense heritability **(h^2_b)** and narrow sense heritability **(h^2_n)** have been presented in Table 4.8. The magnitude of heritability is classified as high (>50), moderate (2049) and low (~ 0-19). Broad sense heritability estimate was high **(>50)** for plant height, fruit diameter, stem girth, fruit flesh thickness and locule number. Stem girth at 100% flowering recorded the highest heritability for broad sense (67 %) and a narrow sense of (51 %). This was followed by fruit flesh thickness with an estimated broad sense heritability of (64 %) and narrow sense of (55 %). Fruit diameter and locule number had the same broad sense heritability estimate (57 %) but varied in narrow sense 50%

and 27% respectively. Plant height at 100% flowering had a broad sense heritability estimate of (52 %) with a corresponding value of (16 %) for narrow sense.

Fruit length, number of fruit per plant, number of marketable fruits per plant, days to flowering, days to maturity, total marketable fruit weight, individual fruit weight and brix recorded moderate broad sense heritability (20-49 %). Furthermore, number of non-marketable fruit per plant had the lowest (~ 0 %) heritability.

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Table 4.8 Heritability estimate of broad sense (h^2_b) and narrow sense (h^2_n) for 13 characters of six tomato genotype (F)

Characters	Heritability	
	Broad Sense (h^2_b)	Narrow Sense (h^2_n)
Plant height at 100% flowering	52.00	16.00
Fruit weight per plant (cm)	20.00	19.00
Brix (%)	22.00	14.00
Days to flowering	33.00	9.00
Days to maturity	26.00	13.00
Fruit diameter (cm)	57.00	50.00
Fruit length (cm)	49.00	30.00
Fruit flesh thickness (mm)	64.00	55.00
Stem girth at 100% flowering (cm)	67.00	51.00

Number of fruit per plant	41.00	13.00
Locule number	57.00	27.00
Number of marketable fruits	45.00	42.00
Total marketable fruit weight (kg)	25.00	8.00

4.4 Agronomic characteristics of six tomato genotypes (G).

Mean, range, variance and standard deviation (SD) of plant height and stem girth for six tomato genotypes (G) are indicated in Table 4.9. Plant height at 100% flowering varied from 85.21 to 93.21. The maximum and minimum plant height were recorded by F_2 (95.25cm) and BC_2F_1 (87.25cm) respectively. The range of variation and variance in BC_2F_1 was higher than the corresponding parents, BC_1F_1, F_1 and F_2.

Similarly, stem girth at 100% flowering exhibited high variation among genotypes and ranged from 7.34 to 13.00. The largest stem girth was recorded by P1 (11.67) and the smallest recorded by BC_2F_1 and P_2 (9.16) simultaneously. The range of variation and variance in F_2 was higher than the parents, BC_2F_1, BC_1F_1 and F_1.

Table 4.9 Mean, Range, Variance and Standard Deviation (SD) of plant height and stem girth for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
Plant height (cm)	P1 (097)	90.73	89.00-92.00	2.40	1.55
	P2 (213)	90.49	89.12-93.12	3.18	1.78
	F_1	85.93	86.41-90.24	2.01	1.42
	F_2	95.25	89.23-96.21	3.42	1.85
	BC_1F_1	90.60	86.00-91.14	1.19	1.09
	BC_2F_1	87.25	85.21-89.16	3.91	1.98
	Lsd (P<0.05)	**3.14**			
	CV (%)	**1.90**			
Stem girth (cm)	P1 (097)	11.67	11.00-13.00	1.34	1.16

P2 (213)	9.16	8.75-9.72	0.26	0.51
F_1	10.29	8.99-12.00	2.38	1.54
F_2	11.21	10.27-13.00	2.40	1.55
BC_1F_1	9.16	7.34-10.30	2.55	1.60
BC_2F_1	9.36	8.14-10.01	1.45	1.20
Lsd (P<0.05)	**2.57**			
CV (%)	**14.00**			

Mean, range, variance and standard deviation (SD) of plant height and stem girth for six tomato genotypes (G) are indicated in Table 4.10. Days to 100% flowering ranged from 25.00 to 32.00cm. The maximum and minimum mean of 30.67 and 27.00cm for BC_1F_1 and P_1 respectively. Mean for F_2, BC_1F_1 and BC_2F_1 were all within the parental limits. The range of variation and variance in F_2 was higher than parents, BC_1F_1, BC_2F_1 and F_1.

With respects to days to maturity, the mean performance was greatly varied from 55.00 to 68.00 days. P_2 (68.00) had the longest days to maturity while P_1 (58.67) recorded the shortest days to maturity. The range of variation and variance in F_2 was higher than the parents, F_1, BC_2F_1 and BC_1F_1.

Table 4.10 Mean, Range, Variance and Standard Deviation (SD) of days to flowering and days to maturity for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
Days to flowering	P1 (097)	27.00	26.25-28.00	1.00	1.00
	P2 (213)	30.00	28.00-31.00	3.00	1.73
	F_1	27.33	25.00-29.00	4.33	2.08
	F_2	29.47	27.00-31.00	5.65	2.38
	BC_1F_1	30.67	29.00-32.00	3.97	1.99
	BC_2F_1	29.67	28.00-31.00	4.86	2.20
	Lsd (P<0.05)	**3.31**			

	CV (%)	**6.30**			
Days to maturity	P1 (097)	57.33	55.00-60.00	3.33	2.82
	P2 (213)	66.67	65.00-68.00	2.33	1.53
	F_1	60.00	59.00-61.00	1.45	1.20
	F_2	60.67	59.00-63.00	5.33	2.31
	BC_1F_1	61.33	60.00-63.00	4.33	2.08
	BC_2F_1	60.33	59.00-62.00	3.77	1.94
	Lsd (P<0.05)	**3.18**			
	CV (%)	**2.90**			

4.5 The yield and yield components of six tomato genotypes (G)

Mean, range, variance and standard deviation (SD) of fruit weight per plant and number of fruits per plant for six tomato genotypes (G) are presented in Table 4.11. The average fruit weight per plant was greatly varied from 33.15 to 65.17g. The mean maximum and minimum fruit weight was recorded by parent two (63.37g) and P_1 (35.12 g) respectively. Additionally, F_2 had range of variation and variance higher than that of the corresponding parents, F_1, BC_1F_1 and BC_2F_1. There were significant differences among genotypes for that trait.

There were variations among genotypes with respect to number of fruit per plant ranging from 34.00 to 45.00. The maximum and minimum number of fruit per plant was accounted for by P_2 (41.00) and BC_1F_1 (28.67) respectively. The result showed that P_1 had higher range of variation and variance than P2, BC_2F_1, BC_1F_1, F_1 and F_2.

Table 4.11 Mean, Range, Variance and Standard Deviation (SD) of fruit weight per plant and number of fruit per plant for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
Fruit weight/plant (g)	P1 (097)	35.12	33.15-37.21	4.13	2.03
	P2 (213)	63.37	61.28-65.17	3.85	1.96
	F_1	39.66	37.74-41.81	4.18	2.04

	F_2	47. 29	44.56-50.00	7.42	2.72
	BC_1F_1	36.33	36.18-40.11	5.88	2.42
	BC_2F_1	43.00	39.10-45.38	6.59	2.57
	Lsd (P<0.05)	**4.19**			
	CV (%)	**4.90**			
Number of fruits/plant	P1 (097)	39.33	36.00-45.00	13.51	3.68
	P2 (213)	41.00	40.00-42.00	1.00	1.00
	F_1	37.00	34.00-41.00	8.56	2.93
	F_2	40.33	37.00-43.00	9.86	3.14
	BC_1F_1	28.67	27.21-30.18	5.14	2.27
	BC_2F_1	36.33	41.00-45.00	3.11	1.76
	Lsd (P<0.05)	**5.75**			
	CV (%)	**8.00**			

Mean, range, variance and standard deviation (St Dev) of total marketable fruit weight and number of marketable fruit per plant for six tomato genotypes (F) are presented in Table 4.12. Total marketable fruit weight varied among tomato genotypes and ranged from 3.40 kg to 11.45 kg. The maximum and minimum of total marketable fruit weights were recorded by P2 (9.42 kg) and P1 (4.77 kg) respectively. Conversely, the range of variation and variance in BC1F1 were higher than Parents, BC2F1, F1 and F2 respectively.

Number of marketable fruit per plant varied from 25.00 to 38.00. The highest and lowest number of marketable fruit per plant was recorded by BC2F1 (37.00) and BC1F1 (29.00). Besides, the range of variation and variance in F2 was higher than recurrent parents, F1, BC1F1 and BC2F1 respectively.

Table 4.12 Mean, Range, Variance and Standard Deviation (SD) of total marketable fruit weight and number of marketable fruit per plant for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
TMKTFW (kg)	P1 (097)	4.77	3.40-6.41	3.32	1.82

	P2 (213)	9.42	7.25-11.45	3.21	1.76
	F_1	5.55	3.61-7.42	3.33	1.82
	F_2	7.44	5.51-9.48	3.91	1.98
	BC_1F_1	5.35	3.49-7.23	4.69	2.17
	BC_2F_1	8.53	6.73-10.23	2.57	1.60
	Lsd (P<0.05)	**3.71**			
	CV (%)	**29.80**			
NMKTFPP	P1 (097)	32.00	29.00-36.00	0.33	0.57
	P2 (213)	36.33	36.00-37.00	0.33	0.57
	F_1	32.33	28.00-37.00	1.33	1.15
	F_2	35.33	32.00-37.00	2.60	1.61
	BC_1F_1	29.33	25.00-34.00	1.33	1.15
	BC_2F_1	37.00	36.00-38.00	2.33	1.53
	Lsd (P<0.05)	**5.35**			
	CV (%)	**8.70**			

TMKTFW – Total marketable fruit weight, NMKTFPP – Number of marketable fruits per plant and NNMKTFPP – Number nonmarketable fruits per plant.

Mean range, variance and standard deviation (SD) of non-marketable and fruit length for six tomato genotypes (F) are shown in Table 4.13. The non-marketable fruit per plant varied among tomato genotypes ranging from 3.00 to 9.00. The maximum and minimum values were recorded by P_1 (7.33) while F_1 and P_2 (4.67) recorded the same value respectively. F_2 had the highest range of variation and variance parents, BC_2F_1, F_1, and BC_1F_1, respectively.

The fruit length among tomato genotypes was significantly varied from 26.00 cm to 38.00 cm. F_2 (36.22cm) had the longest fruit length and F_1 recorded the shortest fruit length (28.0 cm). However, the range of variation and variance in BC_1F_1 was higher than recurrent parents, F_1, BC_2F_1 and F_2 respectively.

Table 4.13 Mean, Range, Variance and Standard Deviation (SD) of number of non-marketable fruit per plant and fruit length for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD
NNMKTFPP	P1 (097)	7.33	6.00-9.00	0.33	0.57
	P2 (213)	4.67	4.00-5.00	0.33	0.57
	F_1	4.67	3.00-6.00	1.33	1.15
	F_2	5.00	4.00-6.00	2.00	1.41
	BC_1F_1	7.00	6.00-8.00	0.83	0.91
	BC_2F_1	6.00	5.00-7.00	1.57	1.25
	Lsd (P<0.05)	**2.19**			
	CV (%)	**21.10**			
Fruit length (cm)	P1 (097)	32.80	31.50-34.41	2.94	1.71
	P2 (213)	33.89	32.89-35.77	2.67	1.63
	F_1	28.00	27.00-29.00	1.00	1.00
	F_2	36.22	34.00-38.00	5.48	2.34
	BC_1F_1	29.33	26.00-31.00	8.33	2.89
	BC_2F_1	34.00	33.00-35.00	1.00	1.00
	Lsd (P<0.05)	**3.50**			
	CV (%)	**6.00**			

NNMKTFPP – Number of nonmarketable fruits per plant

Mean range, variance and standard deviation (SD) of Fruit diameter and fruit flesh thickness for six tomato genotypes (F) are indicated in Table 4.14. Fruit diameter was varied greatly among tomato genotypes and ranged from 34.41 to 46.00cm. The largest and smallest fruit diameter was observed in P_2 (44.40cm) and BC_1F_1 (35.66cm) respectively. The range of variation and variance in BC_1F_1 was higher than parents, F_1, BC_2F_1, and F_2 respectively.

The fruit flesh thickness of the tomato genotypes was varied from 2.15 to 5.21mm and the variation was significant. The maximum and minimum mean values were (4.44mm) and (2.99 mm) accounted for by F_2 and BC_1F_1 respectively. However, the range of variation and variance in F_2 was higher than parents, F_1, BC_2F_1, and BC_1F_1 respectively.

Table 4.14 Mean, Range, Variance and Standard Deviation (SD) of fruit diameter and fruit flesh thickness for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
Fruit diameter (cm)	P1 (097)	35.24	34.41-37.85	0.55	0.74
	P2 (213)	44.40	43.21-46.00	2.07	1.44

	F_1	37.61	36.71-38.12	0.62	0.78
	F_2	42.81	41.42-45.00	3.69	1.92
	BC_1F_1	35.66	34.21-38.24	4.03	2.01
	BC_2F_1	40.95	39.19-43.00	2.69	1.64
	Lsd (P<0.05)	**3.08**			
	CV (%)	**4.30**			
Fruit flesh thickness (mm)	P1 (097)	3.28	2.15-3.90	0.97	0.98
	P2 (213)	3.71	3.31-4.30	0.27	0.52
	F_1	3.07	2.51-3.41	0.24	0.49
	F_2	4.44	4.00-5.21	1.45	1.20
	BC_1F_1	2.99	2.41-3.57	1.33	1.15
	BC_2F_1	3.63	3.34-4.13	0.79	0.89
	Lsd (P<0.05)	**1.24**			
	CV (%)	**19.40**			

Mean, range, variance and standard deviation (SD) of locule number and brix of six tomato genotypes (G) are shown in Table 4.15. The locule number varied from 3.00 to 4.87.00. The maximum and minimum mean values were 4.46 and 3.23 recorded by F_2 and P_2 respectively. However, P_1 recorded values for the range of variation and variances with respect to locule number than the rest of the genotypes.

Brix was greatly varied from 2.43 to 5. 40 %. The highest and lowest was between 4.53 and 2.97% recorded by P_2 and F_1 respectively. The range of variation and variance in F_2 was higher than parents, F_1, BC_2F_1 and BC_1F_1, respectively.

Table 4.15 Mean, Range, Variance and Standard Deviation (SD) of locule number and brix for six tomato genotypes (G)

Character	Genotype	Mean	Range	Variance	SD.
Locule number	P1 (097)	3.93	3.31-4.47	0.34	0.58
	P2 (213)	3.23	3.13-3.42	0.12	0.34
	F_1	3.32	3.00-3.80	0.18	0.42
	F_2	4.46	4.00-4.87	0.29	0.54
	BC_1F_1	3.37	3.00-4.00	0.10	0.31
	BC_2F_1	3.42	3.00-3.65	0.14	0.37
	Lsd (P<0.05)	**0.77**			
	CV (%)	**11.70**			
Brix (%)	P1 (097)	4.24	4.00-4.61	0.11	0.33

P2 (213)	4.53	3.78-5.40	0.68	0.82
F_1	2.97	2.43-3.86	0.63	0.79
F_2	3.82	3.11-4.55	1.52	1.23
BC_1F_1	3.79	3.33-4.61	1.25	1.11
BC_2F_1	3.19	2.73-3.42	0.86	0.93
Lsd (P<0.05)	**0.93**			
CV (%)	**13.70**			

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4.5.1 Heritability estimate of broad sense (h^2_b) and narrow sense (h^2_n) for 14 characters of six tomato genotypes (G)

Table 4.16 shows broad sense heritability (h^2_b) and narrow sense heritability (h^2_n) for 14 characters. The magnitude of heritability is classified as high (>50), moderate (2049) and low (~ 0-19). Broad sense heritability estimate was high (>50) for plant height, fruit diameter, brix, fruit flesh thickness, days to flowering, days to maturity, fruit length, number of marketable fruit per plant, and number of non-marketable fruit per plant. Fruit flesh thickness recorded the highest heritability for broad sense (96.53%) and a narrow sense of (53%). Number of marketable fruit per plant followed this with an estimated broad sense heritability of (75%) and narrow sense of (59%). Furthermore, plant height at 100% flowering had an estimated heritability of broad sense of (72%) and narrow sense (53%). Fruit diameters had broad sense heritability estimated as (70%) and narrow sense of (18%). Brix recorded a broad sense heritability of (69 %) and narrow sense (61%). This was closely followed by number of non-marketable fruit per plant which recorded broad sense heritability of (67%) and narrow sense of (8%). Fruit length recorded broad sense and narrow sense heritability as (60%) and (30 %) respectively. Days to maturity and days to 100% flowering recorded broad sense heritability as (56 %) and (51%), narrow sense (48%) and (41%) respectively.

Average fruit weight per plant, locule number, stem girth at 100% flowering and number of fruit per plant exhibited moderate broad sense heritability (20-49%). Additionally, number of total marketable fruit weight had the lowest (~ 0 – 19%) heritability.

Table 4.16 Heritability estimate of broad sense (h^2_b) and narrow sense (h^2_n) for 14 characters of six tomato genotypes (G)

Characters	Heritability	
	Broad Sense (h^2_b %)	Narrow Sense (h^2_n %)
Plant height at 100% flowering	72.00	53.00
Fruit weight per plant (cm)	45.00	32.00
Brix (%)	69.00	61.00
Days to flowering	51.00	43.00
Days to maturity	56.00	48.00
Fruit diameter (cm)	70.00	18.00
Fruit flesh thickness (mm)	96.00	53.00
Fruit length (cm)	60.00	30.00
Stem girth at 100% flowering (cm)	45.00	33.00
Number of fruit per plant	22.00	16.00
Locule number	28.00	17.00

Number of marketable fruits/plant	75.00	59.00
Number of non-marketable fruits/plant	67.00	8.00
Total marketable fruit weight (kg)	15.00	14.00

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CHAPTER FIVE

5.0 DISCUSSION

5.1 Agronomic Traits of Tomato genotypes (F & G)

Agronomic characters of six tomato genotypes (F) showed significant differences in plant height, stem girth, days to 100% flowering and days to maturity. Similarly tomato genotypes (G) with characters such as plant height and days to maturity indicated significant differences. These may be due to differences in genetic and environmental conditions such as temperature, rainfall, and soil nutrients. The result is in agreement with findings of (Blay et al., 1999; Gongolee *et al.*, 2015) who reported that different genotypes perform in a different way in the same environment. Variations in the climatic conditions especially the soil nutrient status during the experiments may have substantially contributed to the differences observed in the performance of the genotypes. Understanding the performance of genotypes for breeding purpose, assortment efficiency and prediction of their performances is essential. Furthermore,

Ibrahim *et al*. (2000) and Sajjan *et al*. (2002) reported that genetic constitution of crop varieties influence growth characters such as plant height. It is also similar to the findings of Iken and Anusa (2004) who stated that growth and yield differences of crop varieties might be attributed to right choice of suitable agroecological zone.

One of the major sites for storage of food material from photosynthesis is plant stem girth. Bigger stem girth is considered to be useful in relation to drought resistance because of it extra capacity to store food material, which is advantageous during moisture stress situation. Translocation of food from stem to economic part is important in crop productions in which thicker stem girth with more number of conducting tissues (xylem and phloem) plays vital role. Variations observed in stem girth among the genotypes may be attributed to genetic differences for conducting tissues (xylem and phloem). The genotype with the highest stem girth had better conducting tissues as a result, better capacity to store food material. These results were in conformity to the findings of Manoj and Uday (2006) who reported on the significance of stem girth in crop production especially during moisture stress situations. Conversely, the finding does not agree with what was reported by Gongolee *et at*. (2015) who reported higher values than what was obtained from this study.

Days to flowering are an important component in tomato production because it is a transition for the initiation of reproductive stage in the life cycle of the plant. It also indicates earliness to maturity. Variations observed in the number of days to 100% flowering may be attributed to differences in genetic constitution between the two genotypes (F and G) which strongly influenced development and growth of plants. The finding is in line with Sinnadurai (1992) who stated that flowering in tomato usually starts 50 to 65 days after sowing.

The wider variations observed in days to maturity among tomato genotypes may be attributed to genetic differences and the environmental conditions prevailing at the

experimental site that might have influenced the differences in fruit maturity of some of the genotypes which affected the growth and development of tomato genotypes. This could be responsible for differences in the number of days to harvesting. This is in harmony with Farai *et al*. (2015) who made similar observation in the differences of days to maturity in their study of hybrid indeterminate tomato and ascribed it to the genetic factors of the hybrids and the environmental conditions. It must be noted that earliness in any plant genotype is envisaged as important parameter for rainy and offseason production of tomato. This determines the adaptability of a variety to a particular environment and to some extent, incidence of pests and diseases.

5.2 Yield components and yield of tomato genotypes (F & G)

The yield components of cultivated tomato fruits are most important from production point of view. The variation in the number of fruits per plant observed among the evaluated genotypes maybe attributed to the differences in ability to produce and retained higher number of flowers that developed into fruit. The genotype which had the least number of fruits per plant perhaps may have had about 50% of its flowers dried up and fell off or formed tiny fruits which shriveled up and fell off without further development. Flowers of genotypes with high numbers of fruits successfully developed in more fruits possibly because of better genetic components. The result is in agreement with the findings of Adelana (1975) and Olaniyi *et al*. (2010) who reported that only 50% of flowers produced developed into fruits, thus sink size (genetically controlled) influences fruit production in tomato. It may also be attributed to better genetic structure and higher potentials to transport photosynthetic materials towards economic yield as reported by Clark *et al*. (1997) and Zaki *et al.* (1999). Furthermore, the results is in agreement with what had been reported by several other authors (Khokhar *et al*., 2001; Eshteshabul *et al*., 2010; Turhan *et al*., 2011; Abrar *et al*., 2011; Falak *et al*., 2011) that the mean number of fruits per plant lay between 4.46 and 98.30. Agong *et al*. (2001)

showed a value between 9.70 and 158.90 while Lemma (2002) showed a range between 26 and 62.

The yield obtained from the findings varied among genotypes among the two populations. This perhaps, may be ascribed to possibility of possession of higher stomata conductance, better partitioning of photosynthetic materials towards economic yield, better genetic structure from recurrent parents and higher potential to transport photosynthetic materials within plants. The result is analogous to the findings of Costa and Campos (1990), Gardner *et al*. (1990) and Zaki *et al*. (1999) who attributed the yield differences in crop cultivars with special reference to tomato plants, to stomata conductance value and differences in partitioning of photosynthetic materials towards economic yield. It is also in accord with the findings of Clark *et al*. (1997) who attributed the differences in yield and its components between crop genotypes to variations in genetic structure, mineral concentration and potentials to transport photosynthetic materials within plants.

Average fruit weight per plant is one of the most important components in tomato breeding that directly affect and determine the overall yield of tomato variety which is an ultimate aim of plant breeders. The variations observed among tomato genotypes for average fruit weight per plant may be attributed to genetic differences mainly related to sink strength through cell division that influence the capacity for photosynthetic storage. Cell number is a determinant factor of fruit sink strength, usually determined during the early stages of tomato fruit development (Joubes *et al*., 1999). Additionally, higher number of fruit set, large fruit size and higher retention of matured fruits/plant because of genotypic combination in the development of fruit size and weight. According to Cong *et al*. (2002), large-fruit alleles of *fw2.2* are related with a greater mitotic index (especially in cortical tissue) throughout the cell division stage just after

anthesis. The result is in agreement with Sultana (2013) who reported that variation in individual fruit weight among tomato genotypes studied.

Furthermore, the findings are in agreement with several authors including Mangal and Jasim (1987) in plastic house, Papadopoulos and Ormrod (1991) in green house, Munshi and Kumar (2000) under greenhouse conditions and Choudhury and Bhuyan (1992) in shade house. The findings further revealed that genotype G is a better combiner than genotype F for this trait. The finding is conformity with Wang *et al*. (1998) who conducted an experiment with five tomato cultivars following diallel cross to analyze the combining ability and the results from the variance analysis showed general combining ability (GCA) and specific combining ability (SCA) were highly significant for individual fruit weight. However, the result obtained for genotype F for average fruit weight is inconsistent with what were reported by Meena and Bahadur (2015).

The observed variations in total soluble solids (TSS/°Brix) among genotypes (F and G) may be ascribed to differences in genetic makeup that might have influenced the performance of these genotypes for the trait. The variations in this study are in conformity to those found by (Durvesh and Singh; 2006Dar *et al*., 2012), who reported that quality attributes like total soluble solids of the fruit ranged from 4.0 to 5.0%. Additionally, Rodica *et al*. (2008) reported that total sugar (TS) content and acidity are the most important characteristics of tomatoes taste. High sugars are required for best flavor (Kader, 1986). The results also agree with Petro-Turza (1987) who studied total sugar content of ripe tomato and reported content to be between 1.7 and 4.7%. However, Campos *et al*. (2006) and Kader *et al*. (1987) have reported minimum value of soluble solid to be around 4.5%, which is considered low for industrial tomatoes. Which means BC_2F_1 can be further improved in brix content for industrial utilization.

The variations in fruit flesh thickness among genotypes (F) could be ascribed to fruit firmness and possibly genetic differential for the trait. The result is in line with Durvesh and Singh 2006; Dar e*t al*., 2012. Additionally, Dhaliwal *et al*. (1999) and Roopa *et al*. (2001) attributed FFT to gene actions which may contribute to long fruit shelf-life. Prolonged fruit shelf-life is an essential component in tomato breeding as it allows for appreciable storage period without considerable loss of value.

The differences in locule number among genotypes (G) may be related to the fact that progenies may not have genes responsible for locule number or if they do, may be recessive which is expressed in the differences in individual fruit weights. The finding conforms to (Durvesh and Singh, 2006; Dar *et al*., 2012) who observed considerable variations in tomato genotypes with respect to locule number.

In addition, the finding is in agreement with Barrero and Tanksley (2004) who reported that fruit size and weight are strongly dependent on the final number of locule. In general, fewer LN results to small fruit sizes and less fruit weight while more LN results to large fruit sizes and hence much heavier fruits. The gene, *fas* is a strong determinant of LN in fruit, and most large-fruited tomatoes carry the *fas* allele, which is associated with high locule number (Barrero and Tanksley, 2004). Most domesticated large fruit-bearing varieties of tomato carry both *fas* and *lc* mutations, suggesting that limited genetic variation governs locule number in domesticated tomatoes than most wild Solanaceae species of tomato (Munos *et al*., 2011)

Similarly, considerable variability observed in fruit length and fruit diameter perhaps is as a result of combination of factors such as fruit shape, (spherical, elongated, flat or pear-like), plant health and ability of plant to take up and utilizes available moisture (water), nutrients and possibly gene actions. The findings is in agreement with (Atherton and Rudich, 1986; Regassa *et al*., 2012). Furthermore, Lippmann and Tanksley (2001) suggested that increase locule number can increase fruit size by as

much as 50%. Thus, the increase in locule number is an important step in the development of larger tomato fruits.

5.3 Yield and Yield Contributing Attributes

The observed variations among genotypes for marketable and nonmarketable fruits could be attributed to the number of flowers set, developed into fruits and retained by the plants onto harvest for marketable fruits and in the other hand nonmarketable fruits could be associated with cracks, damage by diseases and pest, sunburn, moisture shortage and deformed fruits. It may also be attributed to size and weight of fruit. Similar noticeable differences in fruit yield of tomato varieties were reported by Mishra and Lal (1998) and Rida *et al*. (2002). The trend observed in the results indicates that the higher yield may not necessarily depend on the number of fruits but weight of marketable fruits per plant strongly influence yield, as well as earliness to maturity.

5.4 Estimates of heritability in the broad sense genotypes (F) and (G)

Heritability is used for predicting the progress from selection. Broad sense heritability indicate the ratio of total genetic variance to the total phenotypic variance where as in narrow sense, heritability is the ratio of additive genetic variance to the phenotypic variance. The magnitude of heritability is classified as high (>50), moderate (20-49) and low (~ 0-19). Heritability in broad sense is a parameter of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression. The results obtained from the study revealed higher magnitude of broad sense heritability percentage (>50 %) for plant height, fruit diameter, stem girth, locule number and fruit flesh thickness for genotype F while on the other hand, genotype G recorded higher magnitude of broad sense heritability percentage (>50 %) for plant height, brix, days to flowering, days to maturity, fruit diameter, fruit flesh thickness number of marketable and nonmarketable fruits. Additionally, the magnitude of broad sense heritability for plant height, fruit diameter

and fruit flesh thickness was higher in genotype G than genotype F indicating that genotype G phenotype was better correlated to the genotype than genotype F and that the influence of environmental conditions was relatively lower in genotype G than genotype F for these traits. However, genotype F had high broad sense heritability for stem girth and locule number as opposed to genotype G. The variations observed between genotypes G and F for broad sense heritability for the aforementioned traits could be attributed to genetic differences between the different populations suggesting that these characters are under additive gene effects as such selection based on phenotypic expression could be relied upon as reliable indices for selection and higher responses of these trait could be expected from selection because there is major role of genetic constitution in the expression of these characters for both genotypes. It also indicates differences between the two populations with respect to general combining ability (GCA) and specific combining ability (SCA) of which genotype G is superior to genotype F. The results showed that additive gene actions govern the expression of characters, that is, plant height, fruit diameter, fruit flesh thickness, fruit length, stem girth, locule number, brix, days to flowering, days to maturity, number of marketable fruits and number of nonmarketable fruits, which additionally proposed that meaningful phenotypic selection could be done at an early stage of the breeding programme. The results are in agreement with Bahmankar *et al*. (2014) who reported high broad sense heritability for plant height, days to maturity and days to flowering. The findings from the study further conform with earlier reports by Haydar *et al*. (2007) and Mohamed *et al*.

(2012) for plant height and days to flowering in different genotypes of tomato; Kumar (2010) for days to flowering, fruit diameter, TSS (brix). Mehta and Asati (2008) also estimated high broad sense heritability for plant height and TSS. Additionally, Kumar *et al*. (2013) found high broad sense heritability for plant height and fruit diameter while

Islam *et al*. (2012) recorded high broad sense for days to flowering; Osekita and Ademiluyi (2014) also found high heritability in broad sense for days to flowering and plant height which were ascribed to additive gene actions.

Moderate heritability values (20-49) were observed in the following; fruit weight, brix, days to flowering, days to maturity, fruit length, number of fruit per plant and total marketable fruit weight for genotype F while genotypes G had moderate heritability for average fruit weight per plant, locule number, number of fruit per plant and stem girth respectively. This indicates that the phenotypes are not correlated to the genotypes and environmental factors had strong influence on these traits at the time of the experiment. This means that selection is ineffective to fix superior lines at the early stage of the breeding programme in the segregating generations. This is in agreement with what was reported by Bhateria *et al*. (2006), Mohamed *et al*. (2012, Boakye *et al*. (2013) and Sharanappa and Mogali (2014), and) who reported moderate broad sense heritability for average fruit weight per plant. However, this result does not conform to Saeed *et al.* (2007) and Đorđević *et al*. (2010) who reported high broad sense heritability values for fruit weight per plant. Perhaps, this might accounts for one of the several factors influencing the inability of most breeders to effectively combine desired traits. However, two or more cycles of recurrent selection through pedigree breeding could help to overcome this problem before effective and or useful superior lines can be selected for further improvement.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATION

6.1 CONCLUSION

For the development of potential plant material of *Solanum lycopersicum* L. through selection and breeding, availability of variation in the desired characters is imperative for vegetable breeder.

Result from this study showed that genotype (G) was a better performer than genotype (F) in terms of marketable yield and fruit weight per plant. Therefore, the following genotypes or lines were selected for further improvement in yield: BC_2F_1 (F), F_2 (F), P_2 (213) and BC_2F_1 for genotype (G). The observed variation would be helpful for the development of desired plant material in tomato. However, a
continuous study for the genetic basis of variation is essential.

The following lines for genotype (F) were identified and selected in view of their superior yields F2 (G) R8P4 (6), F2 (G) R3P8 (6), F2 (G) R3P9 (4), BC2F1 (F) R2P1, BC2F1 (F) R2P2 and BC2F1 (F) R5P1.

F1, F2 and BC2F1 genotypes (F) provided or showed high competitive potential over parental lines.

Heritability estimate were high for plant height, brix, days to flowering, days to maturity, fruit diameter, fruit flesh thickness, fruit length, number of marketable fruit per plant, locule number and stem girth. This indicates that the phenotype is highly correlated to the genotype and that there was limited contribution of environmental conditions for these traits. Additionally, this study has set roll for further improvement through backcrosses and pedigree selections to develop inbred lines and subsequent hybrid varieties.

6.2 RECOMMENDATIONS

- Further development is needed to obtain pure lines or inbred lines.
- Based on the above findings, it is recommended that genotypes such as F_2 (G) R8P4 (6), F_2 (G) R3P8 (6), F_2 (G) R3P9 (4), BC_2F_1 (F) R2P1, BC_2F_1 (F) R2P2 and BC_2F_1 (F) R5P1 should be incorporated into tomato breeding for improvement for yield.
- Future work should incorporate disease aspect using molecular analysis for TYLCV and other diseases for screening.

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APPENDICE GENOTYPES (F)

Appendix 1. Summary ANOVA for plant height at 100% flowering of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	F-value	F-prob.
Treatment	5	445.96	89.19	8802.95	<.001
Error	10	0.10	0.01		
Total	15	446.06	89.20		
Lsd	**0.18**				
CV (%)	**0.1**				

Appendix 2. Summary of ANOVA for stem girth at 100% flowering of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	F-value	F-prob.
Genotype	5	17.23	3.44	4.40	0.022
Error	10	7.83	0.78		
Total	15	25.06	4.22		
Lsd	**61**				
CV (%)	**9.9**				

Appendix 3. Summary of ANOVA for average fruit weight per plant of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	68.42	13.68	2.11	0.147
Error	10	64.83	6.48		
Total	15	133.25	20.16		
Lsd	**4.63**				
CV (%)	**2.54**				

Appendix 4. Summary of ANOVA for Brix of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	7.56	1.51	97.80	<.001
Error	10	0.15	0.01		
Total	15	7.71	1.52		
Lsd	**0.22**				
CV (%)	**2.9**				

Appendix 5. Summary of ANOVA for Days to 100% flowering of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	79.77	15.95	8.60	0.002
Error	10	18.55	1.85		
Total	15	98.32	17.80		
Lsd	**47**				
CV (%)	**5.1**				

Appendix 6. Summary of ANOVA for Days to maturity of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	45.33	9.06	2.47	0.105
Error	10	36.66	3.66		
Total	15	81.99	12.72		
Lsd	**3.48**				
CV (%)	**3.2**				

Appendix 7. Summary of ANOVA for Fruit diameter of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	2.51	0.50	5.89	0.009
Error	10	0.85	0.08		
Total	15	3.36	0.58		
Lsd	**53**				
CV (%)	**8.7**				

Appendix 8. Summary of ANOVA for Fruit flesh thickness of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	2.51	0.50	5.89	0.009
Error	10	0.85	0.08		
Total	15	3.36	0.58		
Lsd	**0.53**				
CV (%)	**8.7**				

Appendix 9. Summary of ANOVA for Fruit length of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	208.75	41.75	22.77	<.001
Error	10	18.33	1.83		
Total	15	227.08	43,58		
Lsd	**2.46**				
CV (%)	**4.5**				

Appendix 10. Summary of ANOVA for number of fruits per plant of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	77.61	15.52	2.47	0.105
Error	10	62.88	6.28		
Total	15	140.49	21.80		
Lsd	**4.56**				
CV (%)	**2.50**				

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Appendix 11. Summary of ANOVA for Locule number of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	6.62	1.32	2.58	0.095
Error	10	5.13	0.51		
Total	15	11.75	1.83		
Lsd	**1.30**				
CV (%)	**15.3**				

Appendix 12. Summary of ANOVA number of marketable fruit per plant of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	65.11	13.02	2.06	0.155
Error	10	63.22	6.32		
Total	15	128.33	19.34		
Lsd	**4.57**				
CV (%)	**12.3**				

Appendix 13. Summary of ANOVA number of unmarketable fruits per plant of the genotypes (F)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.

Genotype	5	9.83	1.96	4.54	0.020
Error	10	4.33	0.43		
Total	15	14.16	2.39		
Lsd	**1.19**				
CV (%)	**10.7**				

Appendix 14. Summary of ANOVA Total marketable fruits (kg) of the genotypes (F)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**Fvalue**	**F-prob.**
Genotype	5	9.87	1.97	8.65	0.002
Error	10	2.28	0.22		
Total	15	12.15	2.19		
Lsd	**0.86**				
CV (%)	**10.1**				

Appendix 15. Summary ANOVA for plant height at 100% flowering of the genotypes (G)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**F-value**	**F-prob.**
Treatment	5	64.40	12.88	4.30	0.024
Error	10	29.94	2.99		
Total	15	94.34	15.87		
Lsd	**3.14**				
CV (%)	**1.9**				

Appendix 16. Summary of ANOVA for average fruit weight per plant of the genotypes (G)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**Fvalue**	**F-prob.**
Genotype	5	1878.62	375.72	70.55	<.001

Error	10	53.25	5.32
Total	15	1931.87	381.04
Lsd	**4.19**		
CV (%)	**4.9**		

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Appendix 17. Summary of ANOVA for Brix of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	5.31	1.06	3.99	0.030
Error	10	2.66	0.26		
Total	15	7.97	1.32		
Lsd	**0.93**				
CV (%)	**13.7**				

Appendix 18. Summary of ANOVA for Days to 100% flowering of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	33.64	6.72	2.03	0.160
Error	10	33.22	3.32		
Total	15				
Lsd	**3.31**				
CV (%)	**6.3**				

Appendix 19. Summary of ANOVA for Days to maturity of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	141.61	28.32	9.27	0.002
Error	10	30.55	3.05		

Total	15				
Lsd	**3.18**				
CV (%)	**2.9**				

Appendix 20. Summary of ANOVA for Fruit diameter of the genotypes (G)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**Fvalue**	**F-prob.**
Genotype	5	220.66	44.13	15.31	<.001
Error	10	28.83	2.88		
Total	15				
Lsd	**08**				
CV (%)	**4.3**				

Appendix 21. Summary of ANOVA for Fruit flesh thickness of the genotypes (G)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**Fvalue**	**F-prob.**
Genotype	5	4.27	0.85	1.83	0.194
Error	10	4.67	0.46		
Total	15	8.94	1.31		
Lsd	**1.24**				
CV (%)	**19.4**				

Appendix 22. Summary of ANOVA for Fruit length of the genotypes (G)

Source of variation	**d.f**	**Sum of Squares**	**Mean Squares**	**Fvalue**	**F-prob.**
Genotype	5	144.91	28.98	7.81	0.003
Error	10	37.10	3.71		
Total	15	182.01	32.69		
Lsd	**3.50**				
CV (%)	**6.0**				

Appendix 23. Summary of ANOVA for number of fruits per plant of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	88.44	17.69	1.76	0.208
Error	10	100.22	10.02		
Total	15	188.66	27.71		
Lsd	**5.75**				
CV (%)	**8.0**				

Appendix 24. Summary of ANOVA for Locule number of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	3.43	0.68	3.82	0.034
Error	10	1.80	0.18		
Total	15	5.23	0.86		
Lsd	**0.77**				
CV (%)	**11.7**				

Appendix 25. Summary of ANOVA number of marketable fruit per plant of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	132.94	26.58	3.07	0.062
Error	10	86.55	8.65		
Total	15	219.49	35.23		
Lsd	**5.35**				
CV (%)	**8.7**				

Appendix 26. Summary of ANOVA number of unmarketable fruits per plant of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	18.94	3.78	2.60	0.093
Error	10	14.55	1.45		
Total	15	33.49	5.21		
Lsd	**2.19**				
CV (%)	**21.1**				

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Appendix 27. Summary of ANOVA Total marketable fruits (kg) of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	Fvalue	F-prob.
Genotype	5	54.08	10.81	2.59	0.094
Error	10	41.70	4.17		
Total	15	95.78	15.98		
Lsd	**3.71**				
CV (%)	**29.8**				

Appendix 28. Summary ANOVA for Stem girth at 100% flowering of the genotypes (G)

Source of variation	d.f	Sum of Squares	Mean Squares	F-value	F-prob.
Treatment	5	18.10	3.62	1.81	0.19
Error	10	20.02	2.00		
Total		38.12	5.62		

	15
Lsd	**2.57**
CV (%)	**14.0**

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