STUDIES ON GENETIC VARIABILITY IN AGRONOMIC AND FRUIT QUALITY TRAITS AMONG SOME TOMATO (*SOLANUM LYCOPERSICUM* L.) GENOTYPES

BY

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DECLARATION

I, Ochar Kingsley, hereby declare that except for the references to other people's work which have been duly cited, this thesis is the result of my original findings and that this thesis has neither in part nor in whole been presented for a degree in Ghana or elsewhere.

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ABSTRACT

In the present study, a total of twenty (20) tomato genotypes were evaluated simultaneously under greenhouse and field conditions in order to determine genetic variability present in the agronomic and fruit quality traits. The experiments were laid out in a Randomized Complete Block Design (RCBD) with three (3) replications. Both individual and combined analyses of variance were employed. The individual analysis of variance showed a significant ($P < 0.01$) variability among the genotypes for almost all characters studied. The components of variance estimated on individual location basis indicated a moderate to high GCV, high broad sense heritability as well as high genetic gain for almost all traits. However, stem diameter, pH and gallic acid recorded low estimated GCV under greenhouse conditions while plant height, stem diameter, chlorophyll content, number of days to 50 % flowering, fruit set percentage, number of days to fruit maturity and pH recorded lower estimates for GCV under field conditions. The combined analysis of variance (ANOVA) showed significant ($P < 0.01$) difference among the genotypes, locations and their interactions. The component of variance based on a two-factor analysis of variance revealed considerable effect of location and Genotype x Location interaction on the expression of traits especially, fruit phytochemical composition traits. Relative performance of the genotypes differed with location. Among the genotypes evaluated, MONGAL F1, PLATINUM F1, NKANSAH HT, WOSOWOSO, ROMA and SUMO F1 displayed superior performance for fruit yield across all locations. Large variation was observed among the genotypes for all fruit quality traits studied. Genotypes produced under greenhouse conditions recorded higher amounts of flavonoid composition while phenolic acids content were higher among field-produced tomato genotypes. Number of trusses per plant, number of fruits per plant as well as total fruit weight per plant showed a positive significant association with fruit yield under both greenhouse and field conditions. Consistency of correlation across the two locations was observed. However the correlation coefficients differed due to the effects of G x L interaction.

DEDICATION

I dedicate this research work to the Almighty God and the entire members of my family

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LIST OF ABBREVIATIONS

AA	Antioxidant activity
ANOVA	Analysis of Variance
ASC	Ascorbic acid content
CARO	Carotene content
CAT	Catechin content
CC	Chlorophyll Content
CV (%)	Coefficient of variation expressed as percentage
DAT	Days after Transplanting
df	Degree of freedom
DFM	Number of days to fruit maturity
DNA	Deoxyribonucleic acid
DPPH	diphenyl-2-picrylhydrazyl
ECV	Environmental coefficient of variability
EGA	Expected genetic advance
EMS	Expectation of means
FAO	Food and Agricultural Organization
FAOSTAT	Food and Agriculture Organization Statistical Databases

FD	Fruit diameter
FF	Fruit firmness
FL	Fruit length
FOHCREC	Forest and Horticultural Crops Research Centre
FPF	Number of days to 50 % flowering
FPFS	Number of days to 50 % fruiting
FPP	Number of fruits per plant
FPT	Number of flowers per truss
FSI	Fruit shape index
FSP	Percentage fruit set
FW	Fresh Weight
FWP	Total fruit weight per plant
GA	Gallic acid
GAM	Genetic advance as percentage of mean
GCV	Genotypic coefficient of variability
G X L	Genotype-by-location interaction
GEN	Genestein content
HES	Hesperetin content
h^2_b	Broad Sense Heritability

IC_{50}	Inhibition Coefficient at 50 %
KAE	Kaempferol content
k	Selection differential
LOC	Number of locules
LSD	Least Significant Difference
LYC	Lycopene
MA	Malic acid content
MS	Mean square
MYR	Myricetin content
n.d.	No date
N.P.K	Nitrogen, Phosphorus and Potassium
NaOH	Sodium hydroxide
NFF	Number of days to first flowering
NFPT	Number of fruits per truss
NFS	Number of days to fruit set
NL	Number of leaves
NPB	Number of primary branches per plant
PCV	Phenotypic coefficient of variability
PHT	Plant height

PTK	Pericarp thickness
QUE	Quercetin content
RCBD	Randomized Complete Block Design
RA	Rosmarinic acid content
ROS	Reactive Oxygen Species
RUT	Rutin content
SFW	Single fruit weight
SD	Stem diameter
SSD	Single Seed Decent
t/ha	tonnes per hectare
TA	Titrable acidity
TPP	Number of truss per plant
TSS	Total Soluble Solids content
TSS/TA	Flavour indicator (ratio of TSS to TA)
UNESCO	United Nations Educational Scientific and Cultural Organization
VA	Vanillic acid content
WHO	World Health Organization
YPP	Fruit Yield per plant

λ	Wave length
σ^2_E	Environmental variance
σ^2_G	Genotypic variance
σ^2_{GL}	Genotype x environment interaction variance
σ^2_L	Location variance
σ^2_P	phenotypic variance

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CHAPTER ONE

1.0 INTRODUCTION

Tomato *(Solanum lycopersicum* L., 2n = 24) is one of the most widely produced, consumed and processed vegetable crops (Tekeoka *et al.*, 2001, Rukshar *et al.*, 2012). Epidemiological and medical research reports reveal an association between the consumption of tomato and its products with a reduction in certain chronic and degenerative diseases such as those related to the cardiovascular system, certain types of cancer as well as ageing conditions (Harrigan *et al.*, 2007; Tambo and Gbemu, 2010). The medicinal and health benefits associated with tomato are mainly attributed to the antioxidant function of important compounds present in the fruits. It is therefore crucial to monitor the quality components of tomato since consumers and processors currently show preference for specific quality traits of the fruits (Radzevicius *et al.*, 2013). Development of tomato cultivars that combine high yielding potential with improved nutritional and quality traits could be essential in the quest to meet the needs of tomato growers, fresh tomato consumers as well as the processing industry (Radzevicius *et al.*, 2013).

Several studies have indicated that the tomato crop is adaptable to different climatic conditions and diverse cropping systems (Van der Hoeven *et al.*, 2002; Shankara *et al.*, 2005; Hossain *et al.*, 2010). This characteristic of the crop enables it to be transferred or introduced from one geographical location to another (Kader and Rolle, 2004). In Ghana, wide range of tomato genetic resources are under cultivation on both small and large scale commercial production systems (Blay *et al.*, 1999). This represents very rich source of genetic materials that can be evaluated, exploited and utilized in tomato improvement programmes (Lecomte *et a.l*, 2003). Yet knowledge is limited in terms of tomato genetic resources in Ghana that are endowed with better fruit quality traits particularly their antioxidant content. This makes genetic variability study in the crop very essential.

Agro-morphological evaluation is an essential technique that has been extensively used by many researchers to determine variability in crop genetic resources. The method is simple, fast and cost effective (Hoogendijk and Williams, 2001). However, the expressions of quantitative traits are reported to be associated with the masking effects of several interrelated environmental factors (Panthee *et al.*, 2012; Nour *et al.*, 2013). Consequently, a particular genotype of a crop is subjected to performing differently across different environments or locations irrespective of its inherent genetic potential. It is thus very significant that the genetic assessment of a crop is carried out over different locations or environments (Nwosu *et al.*, 2014).

Over the years, open field tomato production systems have been the main system of production practiced especially in the less developed regions of the world. Currently, tomato fruits are produced year round to satisfy the rising consumer and processors' demand in greenhouse production systems. Enhancing increase in tomato farmers' incomes, reduction in poverty level as well as ensuring food security necessitates development of tomato cultivars with better performance for yield trait under different growing conditions. Considering the nutritional significance of tomato, and the need to satisfy the rising consumers' and processors' demand in terms of quantity and quality, it is important to develop cultivars with desirable quality traits as well as high yields (Willcox *et al.*, 2003). Knowledge about genetic variability in tomato in terms of its agronomic and fruit quality components is indispensable for achieving the important breeding objective of improvement in yield and fruit quality traits of tomato (Emami, *et al.*, 2013; Osekita and Ademiluyi (2014). This study was therefore carried out to evaluate twenty tomato genotypes for genetic variability in their agronomic and fruit quality traits under greenhouse and field conditions so as to identify better performing ones for incorporation into crop improvement programmes.

OBJECTIVE

The main purpose of the study was to identify genetic variability in tomato genotypes that will form the basis for development of cultivars with high yielding ability and desirable quality traits. The specific objectives of the study were to;

1. Determine genetic variability among the genotypes based on selected agronomic and fruit quality traits.
2. Select promising tomato genotypes for incorporation into future breeding programmes.
3. Determine the genetic and environmental effects on the studied traits
4. Estimate the heritability and genetic gain of the studied traits
5. Determine the association among the selected agronomic and fruit quality traits

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin, domestication and distribution of tomato

Tomato (*Solanum lycopersicum* L.) is reported to have originated from the Andean regions of Western and Southern America (Peralta and Spooner, 2007) though other hypotheses suggest Mexico instead (Bai and Lindhaut, 2007). While the early history of tomato domestication is reported to be unclear, Peru is suggested as the most probable centre of diversity of tomato wild relatives whereas Mexico is the original centre of domestication (Larry and Joanne, 2007). Currently, wild tomato genotypes are still found growing in their centres of origin and domestication. Genetic variability studies meant to develop desirable traits in the cultivated tomato's wild relative, *Solanum lycopersicum var cerasiforme* to be incorporated into tomato breeding programmes have been carried out (Larry and Joanne, 2007). New tomato species are continuously being identified and preserved in various gene banks (Peralta *et al.*, (2005).

Domestication of tomato in its centre of origin occurred and remained there until its introduction to Europe around the 15th C where domestication continued over the 18th and 19th centuries (Sims, 1980). Tomato is adaptable to a wide range of environments and agro-ecological zones; hence it is found cultivated throughout the world as one of the most important vegetable crops. The introduction of tomato in West Africa is reported to have occurred around the 16th and 17th centuries (Norman, 1992). It is extensively cultivated in Eastern, Central and West Africa especially in Ghana and Nigeria (De Lannoy, 2001).

2.2 Botany of tomato

2.2.1 Vegetative description

Tomato (*Solanum lycopersicum* L.), a member of the *Solanaceae* family (Peralter and Spooner, 2007) is a short-term duration perennial herb but usually grown as an annual vegetable crop. The crop is dicotyledonous with a tap root system which can grow to a length

of about 50 cm with characteristic dense lateral and adventitious roots (Akinfasoye, 2011). The glandular stem of the plant can grow to about 2 to 4 m high (Shankara *et al.*, 2005). Its compound leaves consist of ovate to oblong leaflets spirally arranged along the hairy weak wooden stem by the petiole (Yeboah, 2011). Tomato plants are usually classified as determinate, semi-determinate or indeterminate based on their growth habits. The determinate types discontinue growing further at about 1.5 m high following the formation of flower cluster at the terminal growing point. Unlike the indeterminate types, determinate tomatoes are generally self-supporting and require no staking. Their cultivation is less labour-intensive, making them highly popular for commercial cultivation. The indeterminate types in contrast continue to grow after flowering though growth may cease when cultivated under tropical conditions or due to diseases and pests attacks (Shankara *et al.*, 2005).

2.2.2 Reproductive description

The cultivated tomato (*Solanum lycopersicum* L.) plant is an autogamous species (flowers are self- pollinated) though cross-pollination may occur (Agong *et al.*, 2001, Shankara *et al.*, 2005). The plant produces a cluster of inflorescence with an average of 6 to 12 bisexual flowers whose petals are coloured yellow. The 6 stamens and anthers are bright yellow and surround the style with an elongated sterile tip. The ovary is superior with 2-9 locules. The fruit is fleshy and variable in shape, length and diameter. The immature fruits change from green to yellow, orange or red at ripe stage. The brightly coloured edible fruits are larger among the cultivated types compared to the wild species. Fruits of the determinate types are known to be fast ripening compared to the indeterminate ones. The slower rate in ripening together with the high leaf to fruit ratio improves the taste of indeterminate types.

2.3 Nutritional and health benefits of tomato

Tomato fruits are valued all over the world by consumers and processors due to the presence of many important nutritional components like vitamins, minerals and antioxidant

constituents reported to play essential role in human health (Reddy *et al.*, 2013). It is a rich source of vitamin C, lycopene, beta-carotene, folate, potassium, flavonoids and vitamins (Willcox *et al.*, 2003). The chemical constituents such as β-carotene, potassium and vitamins (A, and C) are significant determinants of nutritional quality of tomato. The fruits are also major sources of micronutrients, minerals, and oxalic acids (ascorbic, citric, malic and fumeric). Report by Borguini and Da Silva Torres (2009) revealed a number of vital nutritional components in tomato fruits such as minerals, vitamins (vitamin C, E, B6, folic acid, niacin), potassium and trace elements.

Several epidemiological and medical reports have indicated a high rate of the occurrence of chronic and degenerative diseases throughout the world and that phytochemical compositions in fruits and vegetables are associated with reduced risk of many of such chronic and degenerative diseases. Report by WHO (2003) indicated that diet containing important phytochemical components could help reduce or avoid about 90% Type II diabetes, 80% cardiovascular-related conditions as well as 1/3 of certain types of cancer. Consumption of fruits and vegetables and their associated nutritional and several other metabolite compositions in reducing the risk associated with those disease conditions have currently received research attention. The tomato fruit is an excellent source of organic acids and other important metabolites such as carotenoids, lycopene, phenolics acids and flavonoids which possess antioxidant properties (Mertenz-Talcott *et al.*, 2003). Abdul-Hammed *et al.*, (2009) suggested a need for consumption of fruits and vegetables due to the rising rate of chronic diseases including obesity, diabetes, different kinds of cancer and heart-related diseases. Flavonoids for instance are important components of the tomato fruit reported to be associated with reduction in cancer-related diseases by inhibiting the excretion of certain molecules from cancerous cells (Yu and Sacco, 2005). Also, Hounsome *et al.* (2008) indicated the role of antioxidant composition of tomato in protecting the human cell from

oxidants responsible for several human cancerous conditions known to occur in the stomach, oesophagus, lung, pharynx, endometrium, pancreas and colon.

2.4 Agronomic and morphological evaluation of tomato

Agronomic and morphological evaluation involves identification and recording of visible characters of plants including height, leaf type, leaf colour, hairiness and floral features (Godia, 2014; Nwosu *et al.*, 2014). The use of morphological data is one of the most important methods in estimating genetic variability in a crop. The method is simple, less costly and concise and thus used as diagnostic tool in evaluating the performance of different genotypes under specific growing environments (Hoogendijk and Williams, 2001). Osei *et al.* (2014) reported that morphological approach to genetic variability studies involves growing sample plants in an environment and taking visual score of their agro-morphological characters. Such characters are good markers that can be used to assess genetic variability existing in the crop and to further facilitate systematic crop improvement programmes aimed at understanding their adaptability to diverse environments. Agro-morphological evaluation in a crop gives direction to the choice of parents in hybridization breeding. Descriptors developed by the IBPGR are used as guide during such data recordings (Ibitoye *et al.*, 2009).

Characterization and evaluation of plants in the most precise, quick and reliable manner is highly essential in crop improvement programmes. Genetic variability and genotype performance evaluation are easy to be conducted in the required growing conditions of a crop through the use of morphological data (Nwosu *et al.*, (2014). Blay *et al*. (1999) carried out an experiment on morphological and agronomic characterization of some tomato (*Lycopersicum esculentum*) germplasm in Ghana. The results of the study showed an existence of variability among several traits including plant height, fruit set, number of fruits per plant, fruit weight, number of locules per fruit and fruit yield. Fruit set percentage was low due to the sensitivity of genotypes to heat stress.

2.5 Quality characteristics of tomato

Generally, consumers and processors of tomato show preference for specific tomato fruit quality traits and hence tomato growers are obliged to produce specific varieties in order to successfully compete in the markets**.** While such traits like appearance, firmness and flavour influence fresh market demands, total soluble solids content, pH and firmness determine the quality of tomato in the processing industry. This phenomenon also calls for the evaluation of available cultivars and the development of new tomato varieties which are consumer focused (Lecomte *et al.*, 2003). Quality parameters of tomato are determined by a number of physical and chemical traits of the fruits **(**Aoun *et al.*, 2013). Fruit flavour, sweetness, taste, texture, firmness and nutritional properties are vital determinants of fruit quality that influence consumers of fresh tomato (Carli *et al.*, 2009; Rocha *et al.*, 2012). Most of these traits are in turn dictated by several other components which are themselves quality determinant traits. These quality components include acidity, sugars, total soluble solids content, ascorbic acid, lycopene, β-carotene, flavonoids, and phenolic acids. The level of production and thus the concentration of these compounds in fruits are not only influenced by genetic factors but also the crop's surrounding environment as well as genotype-by-environment interaction effects (Chattopadhyay *et al.*, 2013). These factors therefore bring about significant variability among different tomato genotypes and could be exploited for further genetic improvement of the crop (Rocha *et al.*, 2012).

Currently, tomato research attention has in addition to improvement in yield and resistance to biotic and abiotic stresses, incorporated fruit quality component traits. Efforts are therefore directed at developing tomato varieties with improved antioxidant composition in order to fulfill their medicinal and epidemiological significance (Harrigan *et al.*, 2007).

2.6 Antioxidants activity on free radicals

Antioxidants represent a valuable group of compounds which when in human body at lower concentrations are capable of inhibiting and counteracting the oxidative species and their associated damaging effects on the body cells and tissues (Shiow, 2003). Since oxidative processes of free radicals result in various chronic and degenerative diseases in humans, it can be inferred that by their counteracting activity, antioxidant compounds are involved in the prevention of chronic and degenerative diseases. Such chronic and degenerative diseases according to medical research reports include cardiovascular diseases, certain type of cancers, arthritis, neurological diseases, fibrosis, ageing and several others (Bachir *et al.*, 2014).

It is reported that several enzymes within the human body are involved in the free radical scavenging function. However, plant antioxidant (phytochemical or chemo-protective compounds) commonly obtained in human diet represent an important and more abundant source. Some of the most frequently reported phytochemical compounds with antioxidant roles include vitamins (ascorbic acid), carotenoids (β-carotene and lycopene), phenolic compounds (phenolic acids and flavonoids) as well as some mineral elements especially trace elements (Nour *et al.*, 2013). Contrast to the animal cell where antioxidant production is limited, the plant cell produces a broad range of these antioxidant compounds whose concentration and antioxidant capacity vary among different fruits and edible plant parts.

In a study by Bachir *et al.* (2014), fruits are endowed with a wide range of antioxidant compounds capable of neutralizing the oxidative damage arising from free radical accumulation and consequently lower the risks of chronic and degenerative diseases. The total composition of antioxidant compounds in tomato is reported to be highly influenced by genetic factors and to some extent by environmental factors (Nour *et al.*, 2013).

2.7 Some antioxidant compounds in tomato

2.7.1 Ascorbic acid

Tomato (*Solanum lycopersicum* L.) is an important source of ascorbic acid with a property of scavenging the free radicals that may potentially cause several chronic and degenerative diseases in humans (Sablani *et al.*, 2006). Clinical and epidemiological research therefore suggest a 100–120 mg/L daily intake of ascorbic acid so as to help avoid the risk associated with cardiovascular, stroke and cancer among the growing human population (Abdul-Fatawu, 2013). The relative concentration of ascorbic acid like many other antioxidant compounds is reported to vary among different genotypes due to genetic and environmental influence (Peng *et al.*, 2008; Adalid *et al.*, 2010). Singh *et al*. (2014) evaluated tomato hybrids for growth, yield and quality performance and recorded an ascorbic acid content range of 12.65–15.63 mg/100 g. According to this author, high ascorbic acid content in tomato fruits improves upon the quality of the fruits and thus required as an important determinant of the suitability of a genotype for processing. Variability in ascorbic acid content has been reported in earlier studies by Radzevicius (2013) who found ascorbic acid range of 8.20 to 16.20 mg/100 g and Aoun *et al*. (2013) who recorded ascorbic acid a range of 6.01 to 12.94 mg/100 g. Ascorbic acid content has been reported to be higher in fruits produced under field conditions due to high light intensity as compared with greenhouse cultivation environment characterized by being shady. Lower light intensity reduces the synthesis of sugar which is a substrate for ascorbic acid biosynthesis, hence reduced ascorbic acid content (Lee and Kader, 2000).

2.7.2 Carotenoids

Tomato is an important source of many carotenoid compounds chiefly among which are β – carotene and lycopene. The concentration of carotenoid compounds in tomato is greatly determined by the genotype or cultivar of the plant (Kuti and Konuru, 2005). Other factors reported to have influence on the amount of carotenoids in plants include the growing

environment of the plant such as climatic, fertilizer and soil conditions. Different tomato cultivars have been reported to be variable in lycopene content from 13, 48, 49 and 45 mg/100 g (Ilic *et al.*, 2014).

Lycopene is the most abundant micronutrient among the entire carotenoid component in tomato fruits and it is formed during the ripening stage of the tomato fruit. Ibitoye *et al.* (2009) indicated that lycopene concentration in fresh tomato is responsible for the deep red colour variation among different tomato genotypes and it is known to be directly correlated with fruit ripeness and increasing pH. This compound accounts for almost 80 to 90 % of the overall carotenoid content of the tomato fruit higher than beta-carotene content (5-10%)

Both β-carotene and lycopene play essential health promoting roles due to their antioxidant capacity. They reduce the occurrence of many chronic and degenerative diseases (like cardiovascular, diabetes and certain cancer related conditions by neutralizing the effects of oxidative damage to cells (Tepic *et al.*, 2006). A study conducted by Capanoglu *et al.* (2010) revealed that almost 85 % of lycopene requirement in the human body is sourced from tomato and besides being the most abundant of all carotenoids compounds, it is the most effective antioxidant in neutralizing free radicals and by far, the most stable to changes during processing. Humans and other animals are unable to synthesize lycopene and hence depend on diets that contain lycopene (Tapier *et al.*, 2004).

A study by Kuti and Konuru (2005) who evaluated the effects of genotype and cultivation environment on lycopene content in red-ripe tomatoes, a significant variability among the studied tomato genotypes was reported and that both environment and cultivar factors influence lycopene content in tomato fruits.

The concentration of lycopene in tomato fruits has been reported to differ as a result of genotype factor and growing environmental conditions (light and temperature). Also

lycopene concentration is reported to be higher in fruit skin (approximately 37 %). This has been indicated to be 3-6 times higher than the entire pulp content. Whereas the outer pericarp is known to contain high amount of lycopene and carotenoids, the proportion of carotenoids is higher in the locules (Toor and Savage, 2005)

2.8 Phenolic compounds

Phenolic compounds are essential for plant growth, reproduction and development. They also play a role in plant pigmentation, as protective agents against ultraviolet light, act as anti-feedants and anti-pathogen, pesticides and as structural material for plant stability (Msaada *et al.* (2014). Their essential function as antioxidant compounds as well as their inhibitory effects on oxidative stress and some harmful enzyme systems make phenolic compounds an attractive area by most researchers. Many important phenolic compounds are known to exist and are diverse in chemical structure irrespective of the common presence of hydroxyl group. Phenolic acids and flavonoids represent different categories of phenolic compounds which form essential component of plants by virtue of their antioxidant activity (Jaffel *et al.*, 2011). Phenolic acids are regarded as strong antioxidant compounds capable of scavenging all oxidative molecules (free radicals) through their unique hydroxyl groups (Sroka and Cicowski, 2003). Important compounds of phenolic acid group include gallic acid, vanillic acid, rosmarinic acid, salicylic, etc. They are extensively distributed in plant species and play important function in human body as antibacterial, antiviral, anti-inflammatory and as antioxidant compounds (Klem *et al.*, 2000)

Flavonoids are a group of poly-phenolic compounds formed as secondary plant metabolites and are reported to be the largest and most studied category of plant phenols that occur by nature. These compounds possess anti carcinogenic, anti-inflammatory, anti-allergic and anti-mutagenic properties (Tokusoglu *et al.*, 2003). Flavonols are a category of flavonoids predominant in almost all plants and thus form a component of human diet. The composition

of flavonols in plants is influenced by both environment (temperature, soil, light nutrition and pathogen) and genotype specific factors (Tokusoglu *et al*., 2003). Some of the most common flavonols include quercetin, kaemferol, myricetin, catechin, hesperitin, rutin, isorhamatin and genestein.

Among the flavonols, quercetin and kaemferol are the most abundant in fruits with quercetin being highly potent in defending the human body against reactive oxygen species (Martinez-Valverde *et al*., 2002). Lee and Kader (2000) mentioned that ascorbic acid and quercetin concentrations in tomato are known to increase with exposure to sun light. Riadh *et al.* (2009) evaluated lycopene content of advanced breeding lines of tomato for their bioactive compounds and antioxidant activity. Significant differences were observed among the genotypes for all studied characters (agronomic, total carotenoids, lycopene, total phenolics, flavonoids, ascorbic acid as well as their antioxidant activities).

Bachir *et al.* (2014) conducted a study on antioxidant activity of eight tomato (*Solanum lycopersicum* L.) varieties and recorded significant difference among the genotypes for lycopene (which varied between 3.90 to 7.70 mg/100 g), phenolic compounds (with a range of 20.6 to 49.55 mg/100 g). Generally, the concentration of phytochemical compounds has been found to be higher in fruits produced under field conditions than that of the greenhouse. Tomato fruits produced under field condition tend to receive higher amount of light and thus associated with high phenolic content. Light increases phenolic compounds biosynthesis by increasing enzymatic reactions (Caliman *et al*., 2010). High environmental conditions including temperature, relative humidity, light intensity and rainfall increases the expression of rutin and thus increase its content in fruits. Higher amounts of rutin in fruits has also been reported to have no negative effects on certain fruit quality traits like carotenoids, vitamin C, pH, fruit taste, colour or TSS.

2.9 Tomato improvement

Since the early period of tomato domestication and its subsequent introduction across various regions of the world, several attempts have been made to enhance improvement in the available genotypes of the crop (Deery, 2012). According to Shende *et al.* (2012), the use of exotic tomato genetic materials and incorporation of economically essential novel genes into existing tomato genetic resource has resulted to success in tomato improvement programmes. The existence of over 83 300 tomato accessions in the gene banks globally is an indication of a great variability in the crop and this provides an essential tool with which breeders work (FAO, 2010). Deery (2012) assumed that tomato improvement programmes have been so much focused on morphological traits to enhance increased yield. Similarly, Maul *et al.* (2000) reported that breeding work has over the years centered on developing varieties which show disease resistance, response to fertilization and higher nutrient content.

Today, tomato breeding objective has been geared towards developing varieties which are adaptable to growth constraints, disease and pest resistance, fruit productivity and more importantly, quality attributes (Albrecht *et al.*, 2010). Several reports confirm the current rising global population and its parallel consumption rate of vegetable crops which necessitates monitoring of nutritional constituents of horticultural crops including tomato. Carli, *et al.* (2009) therefore suggest the need to develop tomato genotypes that meet consumers' preferred fruit quality traits by considering sensory attributes of tomato as a key breeding objective irrespective of the difficulties reported to be involved in their assessment. Improvement of quality traits of vegetable crops like tomato with known health promoting implications of their micro-phytonutrients has therefore gained research focus in recent years. It has been hypothesized that tomatoes, both cultivated and wild species alike possess important agronomic and physicochemical (quality) characters that can be exploited in tomato improvement programmes (Firas *et al.* 2012; Panthee, 2012). The success in tomato

improvement programmes, either conventional, molecular or tissue culture techniques very much depend on knowledge about the nature and magnitude of genetic variability in agronomic and consumer desired quality attributes of the crop. Equally significant is an understanding of the individual and collective roles of environment and genotype factors in causing variability in crop performance (Mutumpike, 2013).

According to Shende *et al.* (2012), improvement programmes in tomato has over the years relied on such breeding methods as pedigree, hybridization and backcrossing among parents of desirable traits. Such breeding programmes have led to the development of improved hybrid varieties with better yield and resistance to certain pathogens. There have also been value addition to important agronomic characters including higher fruit setting, earliness, uniformity in fruit ripening, adaptation, firmness and long shelf life (Kalloo and Banerjee, 2000; Hazra and Chattopadhyay, 2009; Shende *et al.*, 2012).

In recent times important tomato breeding systems combine conventional and nonconventional methods (molecular or biotechnological tools).Whereas the conventional breeding methods involving hybridization are postulated to be a prolonged breeding strategy with limited success rate (Pessarakli and Dris, 2004), the molecular-based techniques are fast with high rate of success. Breeding work in tomato started with selection and progressed through hybridization to molecular techniques. As a result of the growing consumption of fresh tomato fruits and its related products all over the world, efforts are now being made to develop tomato varieties with improved yield and quality traits including high antioxidant composition by employing both conventional and biotechnological means (Romer *et al.*, 2000).

2.10 Evaluation of tomato characters for genetic variability

Genetic variability in a given trait is an important requirement for successful breeding programmes to be conducted (Bello *et al.*, 2012). Genetic constitution of any organism or

species is composed of the heritable or additive variance, the surrounding environment made up of non-heritable components and the interaction between these two factors. These factors further determine the phenotypic character of an organism. Variability in the phenotypic value is therefore the result of variations due to the genotypic values and deviations arising from the environment whose relative proportions control the genetic distinctiveness of a population (Pradip, 2013). Partitioning the phenotypic value into its components becomes significant in variability studies as it aids in quantifying genotypic parameters including heritability, co-heritability, genetic gain and genotypic correlation. This further gives an idea as to whether selection for any specific trait in cultivar development will be transmitted to the successive generation or not (Jagatpati *et al.*, 2013; Pradip, 2013).

Estimation of genotypic coefficient of variation (GCV) gives a true suggestion of the magnitude of genetic variation in a studied population (Mohamed *et al.*, 2012; Vinod *et al.*, 2013). The values of phenotypic and genotypic coefficient of variability can be categorized as high (>20 %), moderate (10 -20) or low (< 10 %) (Reddy *et al.*, 2013). Higher values of phenotypic variance and phenotypic coefficient of variability than the corresponding genotypic component is an indication of the relative role of environment on the expression of characters (Ullah *et al.*, 2011).

A study conducted by Nwosu *et al.* (2014) revealed very small differences in values between PCV and GCV in several traits including days to 1st flowering, days to 50 % flowering, days to fruit ripening, fruit length, fruit per inflorescence, fruit diameter, fruit weight and number of days to fruit maturity. The study thus indicated a lower environmental influence on the expression of the traits, hence the possibility of selecting those traits for further improvement programmes. On the other hand, wider differences in values were recorded between PCV and GCV for some traits including plant height, number of branches per plant, number of fruits per plant and fruit yield. This suggested a greater imposition of environment than genotypic

factors on the expression of such traits. Similarly, Osekita and Ademiluyi (2014) recorded a wide difference between phenotypic and genotypic coefficient of variability (PCV and GCV) for some traits including number of fruits per plant, number of clusters per plant, and number of locules per plant.

Mohamed *et al.* (2012) studied heritability and genetic variability for different plants and fruit characters of 30 tomato genotypes and reported significant variability in the studied genotypes for all characters that were scored. High genetic variance as well as phenotypic and genotypic coefficient of variation was observed in fruit weight**.** The results implied a higher magnitude of variability among the studied traits. However, lowest values were recorded for number of fruits per plant (0.17 and 0.39) and days to 50 % flowering (0.0552 and 0.0885). Genotypic coefficient of variation was high for most characters suggesting a higher contribution of genetic component to total variation.

In order to measure genetic variability in tomato for yield and resistance to bacterial wilt disease**,** Pradeepkumar *et al.* (2001) estimated genetic variability, heritability and genetic advance for some agronomic and fruit morphological characters. Higher values of genotypic coefficient of variation were recorded for all the characters studied (plant height, number of days to fruit maturity, number of fruits per plant, pericarp thickness, number of locules, total soluble solids, average fruit weight and fruit yield) which suggests an existence of genetic variation among the genotypes.

Reddy *et al.* (2013) observed a wide range of variability for all studied characters. Higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for most characters including number of clusters per plant, number of fruits per plant, fruit weight and yield, as well as fruit acidity. Number of primary branches per plant, ascorbic acid and TSS were higher (>20 %) for PCV but moderate values were recorded for GCV. Also, moderate PCV and GCV were recorded for plant height, number of

flowers per cluster, number of fruits per cluster and fruit length. However, characters such as number of days to 50 % flowering, days to 50 % fruit set and days to fruit maturity had both lower PCV and GCV. Although, values for PCV were higher than their corresponding GCV, differences observed between the PCV and that of the GCV were smaller indicating high genetic control in the expression of the studied traits.

Vinod *et al*. (2013) studied genetic parameters and correlation for yield and quality traits in tomato (*Solanum lycopersicum* L.) and observed moderate to low values of the genetic parameters estimated in most traits. The phenotypic variance and coefficients of variability were greater than their genotypic counterparts for all traits studied. Higher values of phenotypic and genotypic variances were recorded for plant height, average fruit weight and number of fruits per plant establishing a greater contribution of genetic constitution to total variation.

Shushay *et al.* (2013) evaluated 36 tomato genotypes for genetic variability and association of characters in tomato (*Solanum lycopersicum* L.) and reported highly significant variation among the genotypes for all traits studied. Generally the phenotypic variances and coefficient of variations were higher than the corresponding genotypic values. Genotypic and phenotypic coefficient of variation estimated were higher (>20 %) for most traits including number of matured fruits per plant, fruit set percentage, total yield per hectare, number of fruit clusters per plant, average weight of fruits per plant and single fruit weight per plant. This indicated the potential for improvement of the traits via selection. Number of primary branches per plant, fruit polar diameter, fruit equatorial diameter, number of days to flowering, days to 50 % flowering and total soluble solids recorded medium values (10–20 %) for phenotypic and genotypic coefficient of variation. Also, the difference in value between PCV and GCV was found to be high for number of primary branches per plant, number of fruits per cluster, average weight of fruits per plant and single fruit weight per plant. This suggests that the

expression of the traits were affected by environmental factors. Nonetheless, differences in value between PCV and GCV were observed to be narrow for total soluble solids, number of matured fruits per plant, fruit set percentage, and fruit equatorial diameter suggesting a negligible effect of environment on the expression of the traits.

2.11 The concept of heritability and genetic advance

Heritability indicates the proportion of the total variability that exists among species as a result of genetic factors whereas genetic advance measures the degree of genetic gain. Heritability estimated along with genetic gain gives a good indication of the gene action involved in the inheritance of a character. Jagatpati *et al.* (2013) stated that the extent of heritability estimated for different parameters is dictated by the genotypic make up of the genetic materials and this is required for choosing breeding strategies. Heritability of a trait has been categorized as high, medium (moderate) and low when the values estimated are > 60 %, 30 – 60 % and < 30 % respectively (Reddy *et al.*, 2013).

Similarly, values of genetic gain (expressed as genetic advance as percentage of mean) has been classified as high (>20 %), moderate (10 – 20 %) and low (<10 %) (Reddy *et al.*, 2013). A trait with very high heritability value (≥80 %) suggests a close correspondence between the genotype and the phenotype. This permits easy selection for the trait as the effects of environment on the expression of the traits is minimal (Shushay *et al.*, 2013)

Variation in a particular trait resulting from genotypic features is best determined by estimating heritability. Estimate of heritability enables a breeder to determine the phenotypic variability of a trait coming from the contribution of inherent genetic factors. Heritability has a predictive role and expresses the reliability of the phenotypic value. Whereas high values of heritability and genetic advance for a trait gives an idea about the possibility of selection in

early generations of the character, low values of heritability indicate limited scope of selection of characters for genetic improvement (Ullah, 2010).

Higher heritability value along with higher genetic advance gives a better indication of additive gene action for a trait and consequently allows effective selection in early generations (Atnafua, 2013; Farshadfar and Esterghari, 2014) using simple methods like pure line, mass selection, bulk or SSD (Reddy *et al.*, 2013). Similar reports have been made by Manju and Sreelathakumary (2002) that higher values of heritability suggest existence of fixable additive factors which can be improved upon by effective selection. For selection to be effectively done, heritability must accompany genetic advance. High heritability value accompanied by low genetic advance suggests the presence of non-additive gene action. On the other hand, higher values of GCV, heritability and genetic advance are better indication for selection of traits for improvement programmes.

Riaz *et al.* (2013) reported that higher estimate of genetic advance is an indication that additive genes control the character hence the character can be improved upon through selection. However, a high value of heritability along with low genetic gain suggests that non additive gene action controls the expression of the trait and such a phenomenon does not permit simple selection methods. Rather, improvement of such traits could be amenable to hybrid development or heterosis breeding procedures involving the development of transgressive segregants (Reddy *et al.*, 2013).

Anshuman *et al.* (2013) stated that information obtained about heritability along with genetic advance provides a better scope of selection. Genotypic coefficient of variability which indicates all the genotypic variability transmitted from parents to successive generation is manifested in heritability estimated. An environmental effect on a character is known to be higher when the estimated broad sense heritability is lower. Estimation of heritability alone does not give any indication regarding the amount of gain or improvement that will result

from selection of individual genotypes. Understanding heritability in broad sense along with genetic advance is therefore valuable to arrive at a better conclusion (Ajmal *et al.*, 2009).

Shushay *et al*. (2013) recorded very high heritability values (> 80 %) in tomato genotypes along with high genetic gain (> 20 %) for most traits studied suggesting a minimal influence of environment on their expression. For instance, number of mature fruits per plant, fruit set percentage, number of days to fruit maturity, total fruit yield, number of days to 50 % fruiting, number of locules per fruit, plant height, number of flowers per plant and total soluble solids recorded very high heritability estimates. Mehta and Asati (2008) observed high broad sense heritability estimates for plant height, number of fruits per cluster, fruit weight per plant, total fruit yield, number of locules as well as total soluble solids content.

Nwosu *et al*. (2014) evaluated 19 tomato genotypes for genetic variability and correlation and recorded higher values for heritability and genetic advance for most characters studied including days to 50 % flowering, fruits per plant, fruit length and diameter, as well as fruit weight. It could be inferred therefore that the inherent genetic effects on the phenotypic expression of such traits are basically additive and consequently, a greater and effective selection response for those characters is possible (Farshadfar and Estehghari, 2014).

High broad sense heritability values were estimated for most characters (plant height, average fruit weight, number of branches per plant and number of days to 50 % flowering) in a study conducted by Mohamed *et al.* (2012) giving an indication that the characters were influenced by additive gene action valuable for making selection decisions. In the study, Plant height recorded the highest heritability value (97%). Osekita *et al.* (2014) recorded different magnitudes of heritability ranging from low, moderate and high. Heritability was lowest for number of cluster per plant (2.60) and highest for number of days to 50 % flowering. Fruit shape index, plant height, average fruit weight and pericarp thickness also recorded higher heritability values (> 60 %).

Pradeepkumar *et al.* (2001) observed higher values of heritability along with high genetic advance for all parameters studied in an experiment that evaluated some tomato genotypes for variability in yield and bacterial wilt resistance. The results indicated that environmental factors played a lesser significant role in the expression of the traits. The higher value estimated for genetic advance also implied that additive gene action was higher. Effective selection of the traits for further crop improvement programmes is therefore possible.

In a study that evaluated 19 tomato genotypes for variability, Reddy *et al.* **(**2013) observed high values of heritability (> 60 %) along with high genetic advance (> 20 %) for most of the characters including plant height, cluster number per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, yield per plant, ascorbic acid, TA and TSS. Number of primary branches per plant, days to fruit maturity, and fruit width recorded moderate values of heritability (30-60 %). The results suggest higher contribution of additive gene action than environmental factors to the expression of the traits, hence a potential for selection of the traits for further improvement. Whereas number of days to 50 % flowering, days to first fruit set and fruit width recorded moderate (10-20 %) values of genetic gain, days to fruit maturity (first and last harvests) had low genetic gain (< 10 %).

A study by Hadhayatullah *et al.* (2008) revealed high heritability estimated for plant height, number of fruits per plant, fruit weight per plant, fruit length and diameter, single fruit weight pericarp thickness, number of locules and total soluble solids in tomatoes.

2.12 Genotype x Environment Interaction in Variability Studies

Environmental factors coupled with the genotype of a plant are responsible for the existence of variability in the performance of a crop. The consequences associated with interaction between genotype and environment may pose difficulties in deciding on better performing genotypes in terms of desirable characters for any given environment (Mutumpike, 2013). For a homogeneous environment where genotype-by-environment interaction is absent, a top

performing genotype will definitely perform well irrespective of location. On the other hand, as a result of the existence of genotype-by-environment interaction, the performance of a given genotype will vary across different environments.

Understanding the magnitude of genotype, environment and their interactive effects is essential requirement for establishing the possibility of developing desirable cultivars with high environmental stability or for specific environments. Apart from this, Genotype -by-environment interaction studies to discover variation among genotypes is required in selecting new and best cultivars with respect to their desirable quality traits (Rosello *et al.*, 2011).

The growing interest of consumers and processors for quality tomato fruits has been recognized and thus tomato breeders are making efforts to develop varieties with both improved yield and quality traits such as improvement in the content of carotenoids, lycopene, ascorbic acid, TSS, TA and many other antioxidant components in recent times (Causse *et al.*, 2002). Knowledge about differences in performance of different varieties under different growing environments is valuable to any crop improvement programme by facilitating the identification of optimal location for future breeding.

Similarly, Panthee *et al.* (2012) reported that in addition to inherent genetic factors which bring about variability among crop genotypes, the growing environment or location (including climatic, soil and cultural management conditions) have significant impact on a crop's performance. As a result, the performance of a genotype may not necessarily be the same across diverse environments. This phenomenon is reported to be due to the interaction between the genotype and the environment and requires adequate understanding in order to plan developing cultivars that are adapted to or perform well across multi environments. This is valuable in selection that targets variables including lycopene, ascorbic acid, soluble solids and TA (Panthee *et al.*, 2012).

Panthee *et al.* (2012) determined the magnitude of genotype x environment interactions affecting tomato fruit quality in three locations and reported significant variability among the tomato genotypes involved as well as the location and their interaction. The study further revealed a higher environmental effect on lycopene contents but least affected titrable acidity. The study also indicated that no location-specific pattern of performance was noticed among the genotypes thus proofing the existence of genotype x environment interaction.

Rosello *et al.* (2011) reported a significant influence of environment on the expression of phenotypic traits of tomato and a higher genotypic along with a considerable amount of GXE interaction variation in a study that evaluated genotype, environment and their interaction on carotenoids and ascorbic acid accumulation in tomato germplasm. Results also indicated that phenotypic expression of traits was significantly influenced by environmental impacts.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Location

Two experiments were conducted simultaneously under field and greenhouse growing conditions at the University of Ghana Forest and Horticultural Crops Research Centre (FOHCREC), Okumaning-Kade in the Eastern Region of Ghana between November, 2014 and March, 2015. FOHCREC-Kade is in the Kwaebibrim District and forms part of the forest agro-ecological zone of Ghana (Ofosu-Budu, 2003; Nkansah *et al.*, 2007). Geographically, the study area is located between latitude 6^0, 0854'N and longitude 0^0, 5400'W at about 114 m above sea level. The soils of the area are predominantly Haplic Acrisol (FAO/UNESCO, 1990). The mean annual rainfall ranges between 1200 mm-1300 mm and has a bimodal rainfall pattern of two peaks that occurs around June to July and September to October. It has a mean annual temperature of 25-38 ^{0}C (Ofosu-Budu, 2003).

3.2 Genetic Materials

A total of 20 tomato genotypes were evaluated for their genetic variability in agronomic and fruit quality traits. The source of the genetic materials, type and growth habits are shown in Table 3.1.

3.3 Nursery and Nursery Management Practices

Seedlings of all the twenty (20) tomato genotypes were first produced under greenhouse conditions. Plastic seed trays consisting of 98 cells filled with carbonated rice husk (biochar) as growth medium was used to raise seedlings. Prior to seed sowing, the seed trays and the growth medium were sterilized using sodium hypochlorite solution in order to control microbial and fungal infection. Daily watering of seedlings (early morning and late afternoon) was carried out following germination using watering can.

Table 3. 1 Tomato genotypes used in the study

GENETIC MATERIAL	SOURCE	GROWTH HABIT
WOSOWOSO	UNIVERSITY OF GHANA	INDETERMINATE
NKANSAH HT	FOHCREC	DETERMINATE
PECTOMECH	AGRISEED COMPANY LTD	DETERMINATE
ROMA	AGRISEED COMPANY LTD	DETERMINATE
ROMA VF	AGRISEED COMPANY LTD	DETERMINATE
BUFFALO	AGRISEED COMPANY LTD	DETERMINATE
11-172	FOHCREC	INDETERMINATE
L11	FOHCREC	INDETERMINATE
NS 504	FOHCREC	DETERMINATE
#20880	FOHCREC	INDETERMINATE
SHAKTIMAN	FOHCREC	INDETERMINATE
HEINZ-1370	AGRISEED COMPANY LTD	DETERMINAT
CHERRY	AGRISEED COMPANY LTD	DETERMINATE
MONGAL F1	AGRISEED COMPANY LTD	DETERMINATE
NIRVANA F1	DIZENGOFF GHANA LTD	SEMI-DETERMINATE
INLAY F1	AGRISEED COMPANY LTD	INDETERMINATE
PLATINUM F1	AGRISEED COMPANY LTD	DETERMINATE
THORGAL F1	AGRISEED COMPANY LTD	DETERMINATE
COBBRA F1	AGRISEED COMPANY LTD	DETERMINATE
SUMO F1	AGRISEED COMPANY LTD	DETERMINATE

When seedlings were 7 days old, the fungicide, Mancozep 80 WP (Mancozeb dithiocarbonate) at 10 g per litre of water was sprayed on seedlings to control fungal infection especially damping off. This was repeated at days 12 and 17 before healthy and uniform

seedlings were transferred to the experimental sites at day 21. The chemical fertilizer, N.P.K. (19:19:19) at the rate of 70-90 g/15 L was applied at weekly intervals to provide nutrients to the seedlings.

3.4 Experimental Design and Field Layout

The 20 tomato genotypes were arranged in a Randomized Complete Block Design (RCBD) with three replications. The seedlings were transplanted in a spacing of 30 cm x 40 cm in both field and greenhouse experimental locations. In the field experiment, each genotype was transplanted in four rows of five plants while under greenhouse conditions, seedlings were transplanted in two drip rows of five plants each. Data were collected from 6 tagged plants in the middle rows. The climatic conditions (mean monthly temperature, relative humidity, and rainfall (for field experiment only) prevalent in the two experimental sites were recorded (Tables 3.2 and 3.3).

Table 3. 2 Climatic data in the greenhouse environment

	Temperature (^{0}C)		Relative humidity (%)	
Month	Maximum	Minimum	Maximum	Minimum
November, 2014	40.70	16.70	79.89	31.23
December, 2014	39.26	16.70	81.20	34.23
January, 2015	40.65	16.68	88.40	33.25
February, 2015	40.34	16.71	82.30	34.24

SOURCE: FOHCREC

Table 3. 3 Climatic data at the field experimental location

Month	Temperature (^{0}C)		Relative humidity (%)		Rainfall
	Maximum	Minimum	Maximum	Minimum	(mm)
November, 2014	34.40	23.51	94.98	39.52	0.47
December, 2024	34.57	22.79	99.11	45.15	1.90
January, 2015	34.57	22.54	98.64	46.19	2.11
February, 2015	34.80	22.60	99.43	47.75	0.70

SOURCE: FOHCREC

3.5 Preparation of Experimental Sites

3.5.1 Field experiment

A site previously cultivated to cucumber was cleared and burnt. A composite soil sample taken from 15 locations in the field at 0-20 cm depth was analyzed for physical and chemical properties using standard laboratory procedures. Soil analysis was carried out in the laboratory of the Department of Soil Science, University of Ghana, Legon. The samples were adequately mixed, air dried, ground and sieved on a 2.0 mm mesh before analysis. Table 3.4 shows the physical and chemical properties of the soil at the field experimental site. The experimental field was tilled thoroughly before lining and pegging of the field was carried out.

Table 3. 4 Physicochemical properties of soil at the field experimental location

S/N	Property	Value
1	Texture	Sandy clay loam
2	Sand 9%)	52.1
3	Silt (%)	25.9
4	Clay (%)	22.0
5	pH	6.3
6	Total nitrogen (%)	0.6
7	Available phosphorus (mg/kg)	7.74
8	Available potassium (cmol/kg)	0.6
9	Organic carbon	2.26
10	Electrical conductivity (ds/m)	0.73

3.5.2. Greenhouse experiment

Beds which have previously been used to cultivate tomato was removed and replaced with fresh soil medium. A composite soil sample was analysed for physical and chemical composition (Table 3.5). Crops were planted on raised beds of approximately 21.5 m length, 0.3 m width and 0.2 m high. The greenhouse area was 24 m x 10 m and consisted of a total of 7 beds each of which was made up of 2 rows. The entire greenhouse environment was sterilized by hot water treatment and sprayed with insecticide (cydim super) both within and outside the surroundings.

3.6 Transplanting

Three weeks after seed sowing, uniform and healthy seedlings of each genotype were transplanted in the experimental sites. Transplanted seedlings had an average height of 10-13 cm with 5-6 leaves. Prior to transplanting, seedlings were well watered before removal from the nursery to the field. In each case, watering was carried out immediately after transplanting in order to avoid stress.

Table 3. 5 Physicochemical properties of soil in the greenhouse environment

S/N	Property	Value
1	Texture	Sandy clay loam
2	Sand 9%)	41.45
3	Silt (%)	29.92
4	Clay (%)	27.10
5	pH	5.10
6	Total nitrogen (%)	0.13
7	Available phosphorus (mg/kg)	10.18
8	Available potassium (cmol/kg)	0.54
9	Organic carbon	1.53
10	Electrical conductivity (ds/m)	0.61

3.7 Agronomic Practice

Daily watering of transplanted seedlings was carried out throughout the experiment early morning and late afternoon. Immediately after transplanting, crop starter solution was applied to seedlings at the rate of 60-150 ml/15 L to enable seedlings overcome transplanting shock. The N.P.K. fertilizer (19:19:19) was applied in solution to each transplanted seedling at two weeks after transplanting at the rate of 70-90 g/15 L of water and repeated every 2 weeks as a vegetative booster. Sulphate of ammonia was also applied at the rate of 125 kg /ha in split doses during the reproductive growth stage of the crop. Also, multi K (80 %) was applied to crops at the rate of 150-200 g/15 L of water once every two weeks as fertigation at flowering and fruiting stages of the crops according to the manufacturers instruction. A fruit set enhancer was sprayed on the plants at the rate of 100-150 ml/15 L of water during flowering and fruit formation stages of the crop following the manufacturer's instruction.

Cydim super (an insecticide) was sprayed on crops at the rate of 35 ml/15 L of water at weekly interval to control various kinds of insects in both the field and the greenhouse

experimental locations. Cuprofix 30 (fungicide and bactericide) at the rate of 40-60 g/15 L of water was also sprayed on crops at pre-harvest interval of 10-14 days to control fungal and bacterial infection.

Weeds were regularly removed with hoe as and when necessary and lower yellowish leaves pruned just after data on number of leaves at the reproductive stage had been scored. Tomato plants were provided with support in the form of trellis in both experiments. Fruits were harvested by hand picking when they had reached their physiological maturity (fully ripe) stage. Harvesting was done 3 times at an interval of 5 days until fruits of all varieties had been picked.

3.8 Data Collection

3.8.1 Agronomic traits

Mean plant height (PHT): This was determined as the mean perpendicular height (cm) of six tagged plants measured from the soil level to the tip of the shoot at reproductive stage (30 DAT) of the crop using a meter rule.

Mean stem diameter (SD): This was determined as the mean diameter (cm) of six tagged plants measured at about 10 cm from the base of the plant using Vernier caliper at reproductive stage (30 DAT) of the crop.

Mean number of leaves per plant (NL): This was determined as the mean number of leaves of six tagged plants counted at reproductive (30 DAT) growth stage of the crop.

Mean chlorophyll content (CC): Chlorophyll content (nm) was determined on six tagged plants at reproductive stage of the plant growth (30 DAT) using the chlorophyll meter and the mean value determined

Mean number of primary branches per plant (NPB): The number of primary branches of six tagged plants was counted at the end of the growing season and the mean number of branches per plant determined.

Mean number of days to first flowering (NFF): This was determined by counting the number of days from transplanting to first flower emergence of each genotype per replication

Mean number of days to 50 % flowering (FPF): This was determined by counting the number of days from transplanting until 50 % of the tagged plants per genotype had flowered.

Mean number of days to fruit set (NFS): This was determined by counting the number of days from transplanting to first fruit appearance.

Mean number of days to 50 % fruit set (FPFS): This was determined by counting the number of days from transplanting until 50 % of tagged plants per plot had fruited.

Mean number of days to fruit maturity (DFM): This was determined by counting the number of days from transplanting until 50 % of the tagged plants had at least one fruit ripened (at breaker stage)

Mean number of trusses per plant (TPP): The number of trusses per plant was counted on tagged plants and the mean number of trusses per plant determined

Mean number of flowers per truss (FPT): The number of flowers per truss was counted for 10 trusses on each of the tagged plants and the mean number determined

Mean number of fruits per truss (NFPT): The number of fruits per truss was counted for each of the six tagged plants and the mean number per truss determined

Mean fruit set percentage (FSP): Fruit set percentage was determined by dividing the number of fruits by the number of flowers per cluster and the mean computed and expressed in percentage.

Mean number of fruits per plant (FPP): Number of fruits per plant was determined by counting the number of harvested fruits from each of the six recorded plants and the mean number determined.

Mean single fruit weight per plant (SFW): Single fruit weight was determined as total weight (g) of fruits harvested from tagged plants divided by the total number of fruits harvested from tagged plants

Mean fruit weight per plant (FWP): Mean fruit weight (g) per plant was determined by weighing the harvested fruits from the six tagged plants using an electronic balance and the mean determined

Mean fruit yield per plant (YPP): The mean fruit weight for each of the six record plants was used to calculate yield per hectare and converted to yield in tonnes per hectare (t/ha)

3.8.2 Fruit physical and quality traits

Fruit samples per genotype were collected separately from the experiments conducted under each of the greenhouse and field conditions during the peak period of harvest when the fruits were fully ripe and were in their mature stage. Composite samples of 10 fruits were taken from the selected tagged plants from all the three (3) replications to determine fruit physical and quality characters. Fruit physical characters were scored shortly after harvest while composite samples of fruits per genotype from replications were carried to the laboratory for chemical trait analysis.

Tomato fruit physical characteristics

Mean fruit length (FL): Fruit length (cm) was recorded at harvest from ten fruits per genotype, from the stem end (pedicel attachment) to the blossom end (apex) using Vernier caliper and the mean determined.

Mean fruit diameter (FD): Fruit diameter (cm) was recorded at harvest from ten fruits at the largest diameter of cross-sectional fruits to one decimal place using Vernier caliper and the mean determined.

Mean fruit shape index (FSI): This was determined by dividing the mean polar diameter (fruit length) value by the mean equatorial diameter (fruit diameter) value of the fruit.

Mean pericarp thickness (PTK): This was determined by making a transverse cut through 10 randomly selected fruits per each genotype and the thickness of the pericarp measured using Vernier caliper at four cardinal points and their mean determined.

Mean number of locules (LOC): This was determined by counting the number of locules from 10 randomly dissected fruits of each genotype per replication and their mean determined.

Mean fruit firmness (FF): This was determined shortly after harvest using a hand held penetrometer (HANNA Instruments; model GY-3 of higher precision). Readings (kg/cm^2) were recorded on 3 fruits per genotype per replication and the mean value determined.

Tomato fruit quality characteristics

Mean fruit dry matter content (total solids): Dry matter content of fruits (g) was determined by drying 5 g of fresh fruits in an oven set at 70 ^{0}C to a constant weight.

Determination of pH and total soluble solids (TSS)

Sample preparation

Ten fruits per genotype per replication were selected separately from each experimental location. The fruits were thoroughly washed with distilled water; cut open and macerated using a blender (DOUBLE-M German Superior quality multifunctional blender DM-106 A). Macerated samples were then used to determine each of the fruit quality traits.

Determination of pH

Sample juice extracted from blended fruits per each genotype per location was poured into separate beakers. A digital pH meter (JENWAY 3520) was then used for the pH readings. The readings were taken in triplicates and the average for each replication determined.

Determination of total soluble solids content (TSS)

The total soluble solids content was determined by placing a thin film of blended tomato sample on a DIGITAL BENCH MODEL refractometer (HANNA Instruments HI 96801 0-85) and the total soluble solids content scored in % ^{0}Brix units (percentage solids). In each case, measurements were taken in triplicates for each sample by recording the readings on the prism scale. Before each sample test was carried out, the prism plate was cleaned with distilled water and wiped dry with soft tissue. The activity was done in triplicates per genotype per replication and the mean value of the total soluble solids content computed.

Determination of acidity and malic acid content

Acidity of tomato samples was determined by diluting 3 ml of the extracted fruit juice with 10 ml distilled water. The resulting mixture was then titrated against 0.1 M NaOH using phenolphthalein indicator until the content of the conical flask changed from colourless to a

stable pink**.** Titration was carried out in triplicates for each genotype and the mean of the titre values determined. Total acidity content (expressed as citric acid concentration) and malic acid content were calculated according to the procedure of Hawkins (n.d.) as indicated below:

$$Titrable\ acidity\ (mg/ml\ citric\ acid) = \frac{Titre\ x\ acid\ \ factor\ \ (0.0064)\ x\ 100\ x\ 10}{10\ (ml\ \ juice\ )}$$

source: Hawkins (n.d.)

$$Malic\ acid\ content\ (mg/ml) = \frac{Titre\ x\ acid\ \ factor\ \ (0.0067)\ x\ 100\ x\ 10}{10\ (ml\ \ juice\ )}$$ *source:* Hawkins (n.d.)

Determination of flavour indicator (TSS/TA)

Flavour indicator (TSS/TA) was determined by dividing sugar concentration (% ^{0}Brix) value by the value of the citric acid concentration (g/L) according to the equation provided below:

$$TSS/TA\ ratio = \frac{Brix\ \ value}{Citric\ \ acid\ \ (ml/L)}$$

Determination of ascorbic acid content

Standardization of the iodine solution

Samples of solid ascorbic acid (0.05 g) were weighed in triplicate and placed in 3 separately labeled conical flasks. A volume of 30 ml distilled water and 5 drops of starch solution were added to the content of each of the flasks. A clean burette was filled with 50 ml iodine solution and titrated against ascorbic acid solution. The initial and the final volume readings from the burette were recorded. The procedure was repeated for the other two ascorbic acid solutions.

Preparation of sample

Fruit samples of 100 g were cut into pieces topped up with 50 ml of distilled water and blended. A volume of 10 ml of distilled water was added to the sample and then strained through Whatman filter paper. The filtrate was then collected in a beaker and later poured into a graduated measuring cylinder and made up to 100 ml with distilled water.

Titration of fruit juice

Twenty milliliters (20 ml) of each sample solution was measured into a conical flask and topped up with 25 ml of distilled water followed by 1 ml of starch indicator solution. The sample was then titrated against the standardized iodine solution until a permanent dark blue-black colour was formed due to the starch-iodine complex.

Determination of amount of ascorbic acid in the sample

Determination of ascorbic acid content in the sample was carried out according to the procedure of Kartz (2013).

Step 1 Concentration (M) of Iodine solution (M_{Iodine})

$$M(iodine) = mass\ (ascorbic\ acid)\ x\ \left[\frac{1\ mole\ (ascorbic\ acid)}{176.12\ g\ (ascorbic\ acid)}\right] x \frac{1000\ ml/L}{volume\ of\ iodine(ml)}$$

Source: Kartz, 2013

Step 2 Concentration of ascorbic acid in the tomato fruit sample (mg) ($Mg_{ascorbic\ acid}$)

$$Mg\ (ascorbic\ acid) = M\ (iodine\ solution)\ x\ [ml\ (iodine\ solution]\ x\ 176.12\ g/mole]$$

Source: Kartz, 2013

Determination of carotene and lycopene content

The β-carotene and lycopene contents were determined separately according to the method used by Kipandula *et al.* (2014). An amount of 5 ml of 70 % methanol was added to 5 g of

sample tomato extract and thoroughly shaken for a minute. The content of the resulting mixture was filtered through Whatman No. 4 filter paper. The absorbance of the filtrates were then measured at wave length (λ) = 453, 505 and 663 nm using a spectrophotometer. β-carotene and lycopene contents were then calculated according to the following equations:

β-Carotene (mg/100 ml) = *0.216 A663 - 0.304 A505 + 0.452 A453*

Lycopene (mg/100 ml) = *-0.0458 A663 + 0.372 A505 - 0.0806 A453*

Determination of phenolic acid content

The composition of phenolic compounds in the methanolic extracts of tomato samples was determined according to the Folin-Ciocalteau spectrophotometric process (Harbone, 1973). Distilled water (1200 µl) and aqueous sodium carbonate solution (450 µl) were added to each sample (150 µl, 10 mg/ml). The Folin-Ciocalteau reagent (100 µl) was then added to the mixture and vortexed. The content was made to stand for 1 hr 30 min after which absorbance were read at the respective wave lengths for each phenolic acid compound using UV/visible spectrophotometer (SpectraMax plus 384, United States). The concentration of the individual phenolic acid compounds was determined according to their standard curves of linear equations (Table 3.6).

Table 3. 6 Phenolic acid compounds and their standard curves

Phenolic aid compounds	Standard curve
Gallic acid (mg/100 ml)	Y = 0.0871x - 0.102
Vanillic acid (mg/100 ml)	Y = 0.053x + 0.012
Rosmarinic acid (mg/100 ml)	Y = 0.069x + 0.022

Determination of flavonoid content

The modified aluminium chloride colorimetric procedure of Barros *et al*. (2007) was used for the determination of flavonoid content in the tomato samples. Sample extract (100 µl, 100 mg/ml) was added to 500 µl of distilled water and sodium nitrite, $NaNO_2$ (5%, 30 µl). The resulting mixture was made to stand for 5 minutes after which a solution of aluminium chloride $AlCl_3$. H_2O (10 %, 30 µl) was added to the mixture. Again the mixture was allowed to stand for 6 minutes after which sodium hydroxide, NaOH (1 M, 200 µl) and 110 µl distilled water were added to the solution and vortexed. Measurements of absorbance of solution was made at various wave length (SpectraMax plus 384, Unitd States). The concentration of individual flavonoid compounds was calculated according to their respective standard curves and the results expressed as mg/ml of the extract (Table 3.7).

Table 3.7 Flavonoid compounds and their standard curves

Flavonoid compound	Wave length (nm)	Standard curves
Rutin (mg/100 ml)	425	Y = 0.010x + 0.223
Quercetin (mg/100 ml)	415	Y = 0.015x + 0.246
Catechin (mg/100 ml)	276	Y = 0.011x + 0.0154
Hesperitin (mg/100 ml)	350	Y = 0.0067x + 0.466
Kaemferrol (mg/100 ml)	368	Y = 0.028x + 0.435
Myricetin (mg/100 ml)	266	Y = 0.025x + 0.226
Genestein (mg/100 ml)	260	Y = 0.021x + 0.190

Determination of antioxidant activities

An amount of 5 µl of DPPH solution was added to 100 µl of methanolic sample extracts. An amount of 1 ml of methanolic extract was added to 0.002 % DPPH prepared solution The same amount of the sample extract was added to the standard solution to be tested separately. The resulting mixtures were allowed to stand in the dark for 20 min after which optical

density was measured at 517 nm using spectrophotometer against methanol. Percentage inhibition was calculated from the optical density record values according to the formula as given below:

Percentage inhibition of DPPH activity = (A – B/A) x 100

where A = optical density of the blank and B = optical density of sample. Analysis was carried out in triplicates and the results expressed in mean values.

3.9 Statistical Analysis of Data

Data collected under field and greenhouse growing conditions were analyzed for variances. Both individual and combined analyses of variance were performed. The Fisher's Least Significant Difference, LSD was used to separate means that differed significantly based on parameters gathered following the procedure described by Gomez and Gomez 1984). GENSTAT statistical software (12th edition) was used for the data analysis. The variance component format was employed in the computation of variances, coefficient of variability, heritability and genetic advance.

3.9.1 Estimation of variance components

3.9.1.1 Individual analysis of variance

Variances of each trait were estimated separately for field and greenhouse data based on the RCBD analysis of variance following the format in Table 3.8 (Usman, 2013). The genotypic, environmental and phenotypic variances were computed from mean squares as per the methods suggested by Farshadfar and Estehghari (2014) (Table 3.9). Broad sense heritability (h^2_b) was estimated for all the key traits following the method adopted by (Farshadfar and Estehghari, 2014) (Table 3.9).

Table 3. 8 Format for individual analysis of variance

Source of variation	df	MS	EMS	F-test
Replication	r-1	MS_R	$\sigma^2_E + g\sigma^2_R$	
Genotype	g-1	MS_G	$\sigma^2_E + r\sigma^2_G$	MS_G/MS_E
Error	(r-1) (g-1)	MS_E	σ^2_E	
Total	gr-1			

Where df = degree of freedom; MS = mean square; EMS = expected mean square; MSR = mean square due to replication; MSG = mean square due to genotypes; MSE = mean square of error; σ^2_G, σ^2_R *and* σ^2_E *are variances due to genotype, replication and Error respectively; r = Number of replications; g = number of genotypes.*
Source: Usman (2013)

Table 3. 9 Estimation of variances and broad sense heritability on individual location basis

Genotypic parameter	Symbol	Determination method
Environmental variance	σ^2_E	MS_E
Genotypic variance	σ^2_G	$(MS_G - MS_E)/r$
Phenotypic variance	σ^2_P	$\sigma^2_p = \sigma^2_G + \sigma_E{}^2$
Broad sense heritability	h^2_b	σ^2_G / σ^2_P

Source: Farshadfar and Estehghari (2014)

3.9.1.2 Combined analysis of variance

A two-factor analysis of variance (ANOVA) was performed for the combined data scored on all traits from the two experiments (greenhouse and open field) following the procedure described by Ntawuruhunga and Dixon (2010) (Table 3.10) for the randomized complete block design (RCBD). Fisher's Least Significant Difference (LSD) was used for the mean comparison. Based on the model used, Replication (R) and Location (L) were treated as random effect whereas genotype (G) was treated as fixed effect. The linear additive model used was;

$Y_{ijk} = \mu + G_i + L_j + (G \times L)_{ij} + R_{j(k)} + E_{ijk}$ where,

Y_{ijk} is the observation on the *ith* genotype in the *jth* location in the *kth* replication, μ is the general mean, *Gi* is the fixed effect of the *jth* genotype, *Lj* is the effect of the *jth* location, $(G \times L)_{ij}$ is the interaction of the *jth* genotype with *jth* location, $Rk_{(j)}$ is the effect of *kth* randomized block within the *jth* location and E_{ijk} is the experimental error associated within the *ijkth* observation.

Table 3. 10 Format for a two-factor (combined) analysis of variance

Source of variation	df	MS	EMS	F-test
Replication (R)	r-1	MS_R		
Replication (Location)	r(l-1)	$MS_{R(L)}$		
Location (L)	l-1	MS_L	$\sigma^2_E + r\sigma^2_{GL} + rg\,\sigma^2_L$	MS_L/MS_{GE}
Genotype (G)	g-1	MS_G	$\sigma^2_E + r\sigma^2_{GL} + rl\,\sigma^2_G$	MS_G/MS_E
Genotype x Location (G x L)	(g-1) (l-1)	MS_{GE}	$\sigma^2_E + r\,\sigma^2_{GL}$	MS_{GE}/MS_E
Residual	(gl-1) (r-1)	MS_E	σ^2_E	
Total	glr-1			

Where df = degree of freedom; MS = Mean square; EMS = expected mean square; MS_R = Mean square due to replication; MS_L = Mean square due to location; MS_G = Mean square due to Genotype; MS_{GL}= Mean square due to genotype x location; MS_E = Error mean square; σ^2_L = Location variance, σ^2_{GL} = Genotype by location variance, σ^2_E = Error variance, r = Number of replications, l = Number of locations and g = Number of genotypes.
Source: Ntawuruhunga and Dixon (2010)

3.9.1.3 Estimation of variances and heritability for combined data

The estimation of variance components for genotype, phenotype, environment (locations), and genotype x location interaction as well as heritability (h^2_b) were carried out following the two-factor analysis of variance method as adopted by (Usman, 2013) (Table 3.11).

Table 3. 11 Estimation of variance and broad sense heritability on combined location basis

Genotypic parameter	Symbol	Determination method
Environmental variance	σ^2_E	MS_E
Location variance	σ^2_L	$(MS_L - MS_{GL})/ rg$
Genotypic variance	σ^2_G	$(MS_G - MS_{GL})/rl$
G x L interaction variance	σ^2_{GL}	$(MS_{GL}- MS_E)/r$
Phenotypic variance	σ^2_P	$\sigma^2_G + (\sigma^2_{GE}/l) + (\sigma^2_E/rl)$
Broad sense heritability	h^2_b	$\sigma^2_{G/} \sigma^2_P$

Source: Usman (2013)

3.9.1.4 Estimation of coefficient of variability

Genotypic (GCV), Environmental (ECV) and phenotypic coefficient of variation (PCV) were computed according to the formulae adopted by Jalal and Ahmad (2011) and Farshadfar and Estehghari (2014) and categorized as high (> 20 %), moderate (10 – 20 %) and low < 10 %) following the procedure adopted by Reddy *et al*. (2013) **(**Table 3.12)

Estimation of expected genetic advance and genetic advance as percentage of mean

The expected genetic advance (EGA) for selection intensity (k) at 5% (2.06) and the genetic advance as percentage of mean (GAM) were estimated according to the procedure of Jalal and Ahmad (2011) adopted from Johnson *et al*. (1955) (Table 3.12).

Table 3. 12 Methods for computing coefficient of variability and genetic gain (EGA & GAM)

Genotypic parameter	Symbol	Determination method
Genotypic coefficient of variability	GCV %	$(\sqrt{\sigma^2_G}/GM)*100$
Phenotypic coefficient of variability	PCV %	$(\sqrt{\sigma^2_P}/GM)*100$
Environmental coefficient of variability	ECV %	$(\sqrt{\sigma^2_E}/GM)*100$
Expected genetic advance	EGA	$k * \sqrt{\sigma^2_P} * h^2_b$
Genetic advance as percentage of mean	GAM	$(EGA/GM)* 100$

3.9.4 Correlation coefficient estimation

The Pearson's correlation coefficient was used to establish the association between selected agronomic and fruit quality characters of the tomato genotypes.

CHAPTER FOUR

4.0 RESULTS

4.1 Mean performance of tomato genotypes for agronomic traits across locations

4.1.1 Mean plant height (cm) (PHT)

The mean values for plant height at flowering for the 20 tomato genotypes are presented in Table 4.1. The lowest mean plant height of 98.22 cm under greenhouse conditions was recorded by genotype HEINZ-1370 while the highest mean value of 158.83 cm was recorded by genotype L11. Under field conditions, the lowest mean value of 41.06 cm was recorded by genotype NKANSAH HT while the highest mean value of 61.33 cm was recorded by genotype MONGAL F1. The genotype HEINZ-1370 recorded the lowest mean plant height of 71.34 cm across the two locations while the highest mean value of 105.39 cm was recorded by genotype L11. Based on the combined analysis of variance, the effects of genotype, location and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 11).

4.1.2 Mean stem diameter per plant (cm) (SD)

The mean values for stem diameter are presented in Table 4.1. The lowest mean stem diameter value of 6.58 cm under greenhouse conditions was recorded by NIRVANA F1 while the highest mean value of 8.70 cm was recorded by SUMO F1. Under field conditions, the lowest mean value of 6.86cm was recorded by genotype 11 – 172 while the highest mean value of 10.25 cm was recorded by SUMO F1. Across the two locations, the lowest mean stem diameter value of 7.09 cm was recorded by genotype 11-172 while the highest mean value of 9.48 cm was recorded by genotype SUMO F1. Significant ($P< 0.01$) differences were observed among the 20 genotypes for stem diameter based on the combined analysis of

variance. The effects of location and genotype x location interaction were also significantly (P< 0.01) different (Appendix 11).

4.1.3 Mean number of leaves per plant (NL)

The mean values for number of leaves per tomato plant are presented in Table 4.1. The lowest mean value of 23 under greenhouse conditions was recorded by genotype HEINZ-1370 while the highest mean value of 61 was recorded by the genotype WOSOWOSO. Under field conditions, the lowest mean value of 30 was recorded by genotype THORGAL F1 while the highest mean value of 67 was recorded by genotype NKANSAH HT. Across the two locations, the lowest mean value of 28 was recorded by genotype THORGAL F1 while the highest mean value of 57 was recorded by genotype NKANSAH HT. From the combined analysis of variance, significant differences were observed among the 20 tomato genotypes for the trait. The effects of location and genotype x location interaction were significantly (P< 0.01) different (Appendix 11).

4.1.4 Mean chlorophyll content (nm) (CC)

The mean values for chlorophyll content per tomato plant among the genotypes evaluated are presented in Table 4.2. The lowest mean chlorophyll content of 22.97 nm under greenhouse conditions was recorded by genotype ROMA VF while the highest mean value of 44.74 nm was recorded by genotype #20880. Under field conditions, the lowest mean value of 30.97 nm was recorded by genotype CHERRY while the highest mean value of 48.91 nm was recorded by the genotype NKANSAH HT. Across the two locations, the lowest mean value of 27.96 nm was recorded by genotype CHERRY while the highest mean value of 41.44 nm was recorded by genotype NIRVANA F1. Significant (P< 0.01) differences were observed among the 20 genotypes for chlorophyll content. The combined analysis of variance showed that effects of location and genotype x location interaction were significantly (P< 0.01) different (Appendix 11).

Table 4. 1 Mean Plant height, Stem diameter and Number of leaves per plant

Genotype	Plant height (cm)			Stem diameter (cm)			Number of leaves		
	Green house	Open field	pooled mean	Green house	Open field	pooled mean	Green house	Open field	pooled mean
PECTOMECH	115.86	48.38	82.12	6.80	7.89	7.35	25.00	37.00	31.00
PLATINUMF1	144.50	47.11	95.81	7.19	7.64	7.42	34.00	46.00	40.00
NS 504	143.50	54.39	98.95	7.86	8.33	8.10	31.00	33.00	32.00
NKANSAH HT	102.94	41.06	72.00	7.08	8.08	7.58	47.00	67.00	57.00
CHERRY	134.55	49.44	92.00	7.66	7.89	7.78	54.00	54.00	54.00
11-172	139.89	57.22	98.56	7.31	6.86	7.09	33.00	39.00	36.00
ROMA	124.83	48.00	86.42	8.42	8.20	8.31	33.00	47.00	40.00
L11	158.83	51.95	105.39	6.86	7.58	7.22	32.00	40.00	36.00
HEINZ-1370	98.22	44.46	71.34	7.75	10.14	8.95	23.00	43.00	33.00
NIRVANA F1	128.72	52.33	90.53	6.58	8.36	7.47	30.00	42.00	36.00
BUFFALO	141.70	51.41	96.56	7.28	8.05	7.67	36.00	48.00	42.00
INLAY F1	139.22	51.60	95.41	7.40	8.68	8.04	33.00	39.00	36.00
MONGAL F1	130.74	61.33	96.04	7.34	9.28	8.31	43.00	65.00	54.00
#20880	111.87	49.39	80.63	7.18	9.03	8.11	28.00	44.00	36.00
SUMO F1	128.33	45.89	87.11	8.70	10.25	9.48	38.00	42.00	40.00
ROMA VF	109.11	42.48	75.80	8.41	8.42	8.42	35.00	43.00	39.00
SHAKTIMAN	131.78	49.20	90.49	7.32	7.47	7.40	28.00	38.00	33.00
THORGAL F1	124.11	51.78	87.95	7.39	8.42	7.91	26.00	30.00	28.00
COBBRA F1	127.83	50.00	88.92	7.50	7.86	7.68	33.00	33.00	33.00
WOSOWOSO	133.50	49.50	91.50	7.47	8.58	8.03	61.00	45.00	53.00
MEAN	128.24	49.85	89.17	7.48	8.35	7.91	35.00	44.00	40.00
$LSD_{(0.05)}$	1.95	3.51	2.01	0.40	1.36	0.73	1.26	5.81	2.99

4.1.5 Mean number of primary branches per plant (NPB)

The mean values for number of primary branches per plant among the tomato genotypes evaluated are presented in Table 4.2. The lowest mean value of 2 under greenhouse conditions was recorded by genotype SHAKTIMAN while the highest mean value of 6 was recorded by genotype CHERRY. Under field conditions, the lowest mean value was 3 and this was recorded by the 8 genotype while the highest mean value of 5was recorded by genotype CHERRY. Across the two locations, the highest mean value of 6 was recorded by genotype CHERRY while the lowest value of 3 was recorded by 5 genotype. Significant differences were observed among the genotypes based on the combined analysis of variance. The effects of location and genotype x location interaction were also significantly ($P< 0.01$) different (Appendix 11).

4.1.6 Mean root length per plant (cm) (RTL)

The mean values for root length per tomato plant among the genotypes evaluated are presented (Table 4.2). The lowest mean root length of 15.00 cm under greenhouse conditions was recorded by genotype THORGAL F1 while the highest mean root length of 32.00 cm was recorded by genotype COBBRA F1. Under field conditions, the lowest mean root length was 12.00 and was recorded by the genotype CHERRY while the highest mean value of 27.00 was recorded by genotype SUMO F1. The genotype CHERRY recorded the lowest mean root length of 16.00 cm across the two locations while the highest mean value of 25 cm was recorded by genotype ROMA VF. Combined analysis of variance showed significant ($P< 0.01$) genotype, location and genotype x location effects (Appendix 11).

Table 4. 2 Mean Chlorophyll content, Number of primary branches per plant and Root length

Genotype	Chlorophyll content (nm)			Number of primary branches			Root length (cm)		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Mean
PECTOMECH	25.33	40.02	32.68	3.00	3.00	3.00	20.00	19.00	19.50
PLATINUMF1	32.12	44.12	38.12	3.00	4.00	4.00	16.67	22.00	19.33
NS 504	26.28	39.89	33.09	3.00	4.00	4.00	24.00	16.00	20.00
NKANSAH HT	23.68	48.91	36.30	3.00	4.00	4.00	24.67	15.00	19.83
CHERRY	24.95	30.97	27.96	6.00	5.00	6.00	20.00	12.00	16.00
11-172	32.22	42.53	37.38	3.00	3.00	3.00	22.67	15.00	18.83
ROMA	37.61	38.16	37.89	3.00	4.00	4.00	21.33	20.00	20.67
L11	34.20	40.20	37.20	4.00	4.00	4.00	17.00	25.67	21.33
HEINZ-1370	40.01	37.16	38.59	4.00	3.00	4.00	22.00	15.00	18.50
NIRVANA F1	37.87	45.00	41.44	4.00	3.00	4.00	16.33	22.00	19.17
BUFFALO	26.71	38.15	32.43	3.00	3.00	3.00	17.33	25.00	21.17
INLAY F1	28.46	41.28	34.87	3.00	4.00	4.00	21.00	21.00	21.00
MONGAL F1	32.26	40.04	36.15	4.00	4.00	4.00	20.67	18.00	19.33
#20880	44.74	34.77	39.76	3.00	4.00	4.00	21.53	26.00	23.77
SUMO F1	32.74	39.85	36.30	3.00	4.00	4.00	21.00	27.00	24.00
ROMA VF	22.97	36.44	29.71	3.00	4.00	4.00	31.00	19.00	25.00
SHAKTIMAN	32.26	43.03	37.65	2.00	3.00	3.00	17.33	19.00	18.17
THORGAL F1	28.48	41.39	34.94	3.00	3.00	3.00	15.00	18.00	16.50
COBBRA F1	31.01	37.26	34.14	4.00	3.00	4.00	32.00	15.00	23.50
WOSOWOSO	28.41	41.39	34.90	4.00	5.00	5.00	24.67	20.33	22.50
MEAN	31.12	40.03	35.57	3.00	4.00	4.00	21.31	19.50	20.40
$LSD_{(0.05)}$	1.72	3.26	1.89	0.40	0.65	0.38	1.48	1.70	1.10

4.1.7 Mean number of days to 1st flowering (NFF)

The mean values for number of days to 1st flowering among the tomato genotypes are presented in Table 4.3. The lowest mean value of 15 days under greenhouse conditions was recorded by genotype NKANSAH HT, CHERRY, MONGAL F1, ROMA VF, THORGAL F1 and WOSOWOSO while the highest mean value of 20 was recorded by genotypes PECTOMECH, NIRVANA F1 and #20880. Under field conditions, the lowest mean value of 12 days was recorded by NKANSAH HT while the highest mean value of 24 days was

recorded by the genotype 11- 172. Tomato genotypes NKANSAH HT, CHERRY, MONGAL F1 and WOSOWOSO recorded the lowest mean value of 14 days across the two locations while the highest mean value of 22 days was recorded by the genotype 11-172. From the combined analysis of variance, the effects of genotype, location and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 11).

4.1.8 Mean number of days to 50 % flowering (FPF)

The mean values for number of days to 50 % flowering for all the 20 tomato genotypes are presented in Table 4.3. The lowest mean value of 18 days under greenhouse conditions was recorded by genotype NKANSAH HT, CHERRY, MONGAL F1 and COBBRA F1 while the highest mean value of 29 days was recorded by genotype PECTOMECH. Under field conditions, the lowest mean value of 21 days was recorded by genotypes NKANSAH HT and CHERRY while the highest mean value of 29 days was recorded by the genotype ROMA VF. The genotype NKANSAH HT and CHERRY recorded the lowest mean value of 20 days across the two locations while the highest mean value of 27 was recorded by the genotype PECTOMECH. The effects of genotype, location and genotype x location interaction were significantly ($P < 0.01$) different based on the combined analysis of variance (Appendix 11).

4.1.9 Mean number of days to 1st fruit set (NFS)

The mean values for number of days to 1st fruit set among tomato genotypes evaluated are presented in Table 4.3. The lowest mean number of days to 1st fruit set was 26 days under the greenhouse conditions and this was recorded by genotype NKANSAH HT while the highest mean value of 48 days was recorded by genotype INLAY F1. Under field conditions, the lowest mean value of 26 days was recorded by genotype NKANSAH HT while the longest mean number of days to 1st fruit set was 42 days and was recorded by genotype #20880. Across the two locations, the lowest mean value of 26 days was recorded by genotype NKANSAH HT while the highest mean value of 44 days was recorded by genotype #20880.

The effects of genotype, location and genotype x location interaction were significantly ($P < 0.01$) different based on the combined analysis of variance (Appendix 11).

4.1.10 Mean number of days to 50 % fruit set (FPFS)

The mean values for number of days to 50 % fruit set are presented in Table 4.4. The lowest mean value of 28 days under greenhouse conditions was recorded by genotype NKANSAH HT while the highest mean value of 56 days was recorded by genotype SUMO F1. Under field conditions, the lowest mean value of 36 days was recorded by genotype NKANSAH HT while the highest mean value of 52 days was recorded by genotype HEINZ-1370. Across the two locations, the lowest mean value of 29 days was recorded by genotype WOSOWOSO while the highest mean value of 52 days was recorded by the genotype L11. Combined analysis of variance showed significant ($P < 0.01$) genotype, location and genotype x location effects.

4.1.11 Mean percentage fruit set (FSP)

The mean values for percentage fruit set among the tomato genotypes evaluated are presented in Table 4.4. The lowest mean percentage fruit set of 38.56 % under greenhouse conditions was recorded by genotype #20880 while the highest mean percentage value of 85 % was recorded by genotype PLATINUM F1. Under field conditions, the lowest mean percentage fruit set of 47.58 % was recorded by genotype NIRVANA F1 while the highest mean percentage value of 65.39 % was recorded by genotype CHERRY. Across the two locations, the lowest mean value of 47.29 % was recorded by genotype NS 504 while the highest mean value of 72.93 % was recorded by genotype PLATINUM F1. The combined analysis of variance showed significant ($P < 0.01$) genotype and genotype x location effects (Appendix 12). Also, the effect of location was significantly ($P < 0.05$) different.

Table 4. 3 Mean Number of days to 1st flowering, 50 % flowering and Number of days to 1st fruit set

Genotype	Number of days to 1st Flowering			Number of days to 50 % flowering			Number of days to 1st fruit set		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	20.00	14.00	17.00	29.00	25.00	27.00	36.00	40.00	38.00
PLATINUMF1	16.00	17.00	17.00	19.00	25.00	22.00	35.00	35.00	35.00
NS 504	19.00	22.00	21.00	23.00	27.00	25.00	41.00	37.00	39.00
NKANSAH HT	15.00	12.00	14.00	18.00	21.00	20.00	26.00	26.00	26.00
CHERRY	15.00	13.00	14.00	18.00	21.00	20.00	36.00	36.00	36.00
11-172	19.00	24.00	22.00	23.00	27.00	25.00	45.00	35.00	40.00
ROMA	17.00	13.00	15.00	20.00	23.00	22.00	41.00	39.00	40.00
L11	16.00	17.00	17.00	20.00	23.00	22.00	41.00	39.00	40.00
HEINZ-1370	18.00	17.00	18.00	19.00	27.00	23.00	41.00	41.00	41.00
NIRVANA F1	20.00	18.00	19.00	23.00	27.00	25.00	46.00	40.00	43.00
BUFFALO	19.00	14.00	17.00	23.00	27.00	25.00	45.00	33.00	39.00
INLAY F1	17.00	14.00	16.00	19.00	23.00	21.00	48.00	32.00	40.00
MONGAL F1	15.00	13.00	14.00	18.00	26.00	22.00	30.00	34.00	32.00
#20880	20.00	13.00	17.00	23.00	27.00	25.00	46.00	42.00	44.00
SUMO F1	18.00	16.00	17.00	22.00	26.00	24.00	40.00	40.00	40.00
ROMA VF	15.00	17.00	16.00	25.00	29.00	27.00	37.00	41.00	39.00
SHAKTIMAN	16.00	16.00	16.00	20.00	26.00	23.00	42.00	40.00	41.00
THORGAL F1	15.00	14.00	15.00	19.00	27.00	23.00	37.00	37.00	37.00
COBBRA F1	17.00	17.00	17.00	18.00	24.00	21.00	29.00	35.00	32.00
WOSOWOSO	15.00	13.00	14.00	22.00	22.00	22.00	28.00	27.00	27.00
MEAN	17.00	16.00	17.00	21.00	25.00	23.00	39.00	37.00	38.00
$LSD_{(0.05)}$	0.68	0.94	0.62	0.92	1.26	0.78	1.00	2.31	1.22

4.1.12 Mean number of days to fruit maturity (DFM)

The mean number of days to fruit maturity among the tomato genotypes evaluated has been presented in Table 4.4. The tomato genotype NKANSAH HT recorded the least number of

days to fruit maturity under each of the greenhouse and field conditions with mean values of 55 and 56 days respectively. The highest mean value of 77 days to fruit maturity under greenhouse conditions was recorded by the genotype 11–172 whereas genotype 11-172 recorded the maximum value of 78 days under field conditions. Across the two locations, the least mean value of 56 days was recorded by the genotype NKANSAH HT while the highest mean value of 75 days was recorded by the genotypes L11 and NIRVANA F1. Combined analysis of variance showed significant ($P < 0.05$) difference between locations. The effects of genotype and genotype x location interaction were also significantly ($P < 0.01$) different (Appendix 12).

4.1.13 Mean number of trusses per plant (TPP)

The mean values for number of trusses per plant among the tomato genotypes are shown in Table 4.5. The lowest mean number of trusses recorded was 6.00 under greenhouse conditions and this was recorded by genotype #20880 while the highest mean value of 21.00 was recorded by genotypes NKANSAH HT and MONGAL F1. The lowest mean value of 10.00 under field conditions was recorded by #20880 while the highest mean value of 33 was recorded by genotype NKANSAH HT. Across the two locations, the lowest mean value of 8.00 was recorded by genotype #20880 while the highest mean value of 27.00 was recorded by genotype NKANSAH HT. Significant ($P< 0.01$) differences were observed among all genotypes evaluated for the trait. The effects of location and genotype x location interaction were also significantly ($P< 0.01$) different (Appendix 12).

4.1.14 Mean number of flowers per truss (FPT)

The mean values for number of flowers per trusses per tomato plant are presented in Table 4.5. The lowest mean value of 4 under greenhouse conditions was recorded by genotype L11, INLAY F1 and SHAKTIMAN while the highest mean value of 7 was recorded by genotype NKANSAH HT, CHERRY, #20880, COBBRA F1 and WOSOWOSO.

Table 4. 4 Mean Number of days to 50 % fruit set, Percentage fruit set and Number of days to fruit maturity

Genotype	Number of days to 50 % fruit set			Fruit set percentage (%)			Number of days to fruit maturity		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	54.00	46.00	50.00	50.93	55.11	53.02	63.00	63.00	63.00
PLATINUMF1	44.00	42.00	43.00	85.46	60.39	72.93	62.00	65.00	63.50
NS 504	49.00	51.00	50.00	43.04	51.54	47.29	62.00	66.00	64.00
NKANSAH HT	28.00	36.00	32.00	69.43	54.76	62.10	55.00	56.00	56.00
CHERRY	39.00	43.00	41.00	73.86	65.39	69.63	62.00	64.00	63.00
11-172	54.00	44.00	49.00	52.47	53.32	52.90	77.00	71.00	74.00
ROMA	42.00	48.00	45.00	48.61	54.44	51.53	60.00	66.00	63.00
L11	54.00	50.00	52.00	68.75	53.94	60.85	72.00	78.00	75.00
HEINZ-1370	48.00	52.00	50.00	49.55	51.10	50.33	70.00	71.00	71.00
NIRVANA F1	50.00	48.00	49.00	47.93	47.58	47.76	75.00	74.00	75.00
BUFFALO	48.00	44.00	46.00	54.55	54.87	54.71	68.00	67.00	68.00
INLAY F1	54.00	46.00	50.00	60.95	56.55	58.75	71.00	63.00	67.00
MONGAL F1	35.00	39.00	37.00	64.45	54.65	59.55	57.00	63.00	60.00
#20880	54.00	44.00	49.00	38.56	62.59	50.58	73.00	74.00	74.00
SUMO F1	56.00	46.00	51.00	67.52	57.87	62.70	73.00	69.00	71.00
ROMA VF	47.00	47.00	47.00	50.47	60.21	55.39	64.00	65.00	65.00
SHAKTIMAN	44.00	50.00	47.00	69.94	51.61	60.78	63.00	70.00	67.00
THORGAL F1	42.00	44.00	43.00	43.65	54.97	49.31	60.00	58.00	59.00
COBBRA F1	41.00	41.00	41.00	60.16	51.79	55.98	58.00	58.00	58.00
WOSOWOSO	29.00	29.00	29.00	42.85	56.16	49.51	57.00	57.00	57.00
MEAN	46.00	45.00	45.00	57.16	55.39	56.28	65.00	66.00	65.00
$LSD_{(0.05)}$	1.16	3.50	1.79	12.38	5.89	6.67	0.95	2.23	1.18

Under field conditions, the lowest mean value of 5 was recorded by the genotype #20880, MONGAL F1 and WOSOWOSO while the highest mean value of 9 was recorded by genotype NKANSAH HT. Across the two locations, the lowest mean value of 5 was recorded by genotype L11, INLAY F1, SUMO F1 and SHAKTIMAN while the highest mean value of 8±0.27 was recorded by genotype NKANSAH HT. The effects of genotype, location and genotype x location interaction were significantly (P< 0.01) different (Appendix 12).

4.1.15 Mean number of fruits per truss (NFPT)

The mean values for number of fruits per truss among the tomato genotypes evaluated have been presented in Table 4.5. The lowest mean value of 3.00 under greenhouse conditions was recorded by 13 genotypes while the highest mean value of 5.00 was recorded by genotype NKANSAH HT, CHERRY and COBBRA F1. Under field conditions, the lowest mean value of 2.00 was recorded by genotype ROMA while the highest mean value of 5.00 was recorded by NKANSAH HT and CHERRY Across the two locations, the lowest mean value of 3.00 was recorded by 14 genotypes while the highest mean value of 5.00 was recorded by genotype NKANSAH HT and CHERRY. Based on the combined analysis of variance, significant (P < 0.05) difference was observed among the genotypes, locations and genotype x location interaction effects (Appendix 12).

4.1.16 Mean number of fruits per plant (FPP)

The mean values for number of fruits per tomato plant are shown in Table 4.6. The lowest mean value of 3.00 was recorded by genotype L11 under greenhouse conditions while the highest mean value of 31.00 was recorded by genotype CHERRY. Under field conditions, the lowest mean value of 5.00 was recorded by genotype L11 and THORGAL F1 while the highest mean value of 35 was recorded by genotype CHERRY.

Table 4. 5 Mean Number of trusses per plant, Number of flowers per truss and Number of fruits per truss

Genotype	Number of trusses per plant			Number of flowers per truss			Number of fruits per truss		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	8.00	12.00	10.00	6.00	6.00	6.00	3.00	3.00	3.00
PLATINUMF1	14.00	16.00	15.00	5.00	7.00	6.00	4.00	4.00	4.00
NS 504	13.00	15.00	14.00	5.00	7.00	6.00	3.00	3.00	3.00
NKANSAH HT	21.00	33.00	27.00	7.00	9.00	8.00	5.00	5.00	5.00
CHERRY	18.00	32.00	25.00	7.00	7.00	7.00	5.00	5.00	5.00
11-172	9.00	17.00	13.00	6.00	8.00	7.00	4.00	4.00	4.00
ROMA	11.00	17.00	14.00	5.00	7.00	6.00	4.00	2.00	3.00
L11	13.00	11.00	12.00	4.00	6.00	5.00	3.00	3.00	3.00
HEINZ-1370	13.00	13.00	13.00	6.00	6.00	6.00	3.00	3.00	3.00
NIRVANA F1	16.00	12.00	14.00	5.00	7.00	6.00	3.00	3.00	3.00
BUFFALO	12.00	12.00	12.00	6.00	8.00	7.00	3.00	3.00	3.00
INLAY F1	14.00	12.00	13.00	4.00	6.00	5.00	3.00	3.00	3.00
MONGAL F1	21.00	29.00	25.00	5.00	7.00	6.00	4.00	4.00	4.00
#20880	6.00	10.00	8.00	7.00	5.00	6.00	3.00	3.00	3.00
SUMO F1	14.00	14.00	14.00	5.00	5.00	5.00	3.00	3.00	3.00
ROMA VF	11.00	19.00	15.00	5.00	7.00	6.00	3.00	3.00	3.00
SHAKTIMAN	7.00	11.00	9.00	4.00	6.00	5.00	3.00	3.00	3.00
THORGAL F1	15.00	13.00	14.00	6.00	6.00	6.00	3.00	3.00	3.00
COBBRA F1	13.00	15.00	14.00	7.00	7.00	7.00	5.00	3.00	4.00
WOSOWOSO	15.00	15.00	15.00	7.00	5.00	6.00	3.00	3.00	3.00
MEAN	13.00	16.00	15.00	6.00	7.00	6.00	4.00	3.00	3.00
$LSD_{(0.05)}$	1.55	1.72	1.13	0.70	0.70	0.58	0.52	0.79	0.46

Across the two locations, the lowest mean value of 4.00 was recorded by genotype L11 while the highest mean value of 33.00 was recorded by genotype CHERRY. Significant (P< 0.01) differences were observed among the genotypes evaluated based on the combined analysis of variance. The effects of location and genotype x location interaction were also significantly (P< 0.01) different (Appendix 12).

4.1.17 Mean single fruit weight per plant (g) (SFW)

The mean values for single fruit weight per tomato plant are presented in Table 4. 7. The lowest mean value for single fruit weight per plant was recorded by genotype CHERRY under each of the greenhouse and field conditions with values 20.70 g and 17.70 g respectively. The highest mean value for single fruit weight per plant under greenhouse and field conditions was recorded by genotype SUMO F1 with values 127.74 and 96.89 respectively. Across the two locations, the lowest mean value of 19.20 was recorded by genotype CHERRY while the highest mean value of 112.32 was recorded by the genotype SUMO F1. Combined analysis of variance showed significant (P< 0.01) genotype, location and genotype x location interaction effects (Appendix 12).

4.1.18 Mean total fruit weight (g) per plant (FWP)

The mean values of total fruit weight per plant are presented in Table 4.7. The lowest mean value of 150.33 g under the greenhouse conditions was recorded by genotype L11 while the highest mean value of 1492.72 was recorded by genotype PLATINUM F1. Under field conditions, the lowest mean value of 242.08 g was recorded by genotype NS 504 while the highest mean value of 1472 g was recorded by genotype MONGAL F1. Across the two locations, the lowest mean value of 217.99 g was recorded by the genotype L11 while the highest mean value of 1475.12 was recorded by the genotype PLATINUM F1. Significant (P< 0.01) differences were observed among the 20 genotypes. The effects of location and genotype x location interaction were significantly (P< 0.01) different (Appendix 12).

Table 4. 6 Mean Number of fruits per plant (FPP)

Genotype	Number of fruits per plant		
	Greenhouse	Open field	Pooled Mean
PECTOMECH	5.00	17.00	11.00
PLATINUMF1	19.00	21.00	20.00
NS 504	9.00	11.00	10.00
NKANSAH HT	27.00	33.00	30.00
CHERRY	31.00	35.00	33.00
11-172	7.00	9.00	8.00
ROMA	8.00	12.00	10.00
L11	3.00	5.00	4.00
HEINZ-1370	5.00	7.00	6.00
NIRVANA F1	4.00	8.00	6.00
BUFFALO	12.00	16.00	14.00
INLAY F1	9.00	11.00	10.00
MONGAL F1	19.00	21.00	20.00
#20880	4.00	6.00	5.00
SUMO F1	7.00	7.00	7.00
ROMA VF	6.00	12.00	9.00
SHAKTIMAN	4.00	10.00	7.00
THORGAL F1	5.00	5.00	5.00
COBBRA F1	20.00	10.00	15.00
WOSOWOSO	7.00	9.00	8.00
MEAN	11.00	13.00	12.00
$LSD_{(0.05)}$	0.69	1.39	0.76

4.1.19 Mean fruit yield per plant (t/ha) (YPP)

The mean values for fruit yield among tomato genotypes are presented in Table 4.7. The lowest mean fruit yield of 12.54 t/ha under greenhouse conditions was recorded by genotype L11 while the highest mean value of 124.68 t/ha was recorded by genotype MONGAL F1. Under the field conditions, the lowest mean fruit yield of 23.80 t/ha was recorded by

genotype L11 while the highest mean fruit yield of 122.69 t/ha was recorded by genotype MONGAL F1. Across the two locations, the lowest mean value of 18.17 t/ha was recorded by genotype L11 while the highest mean value of 123.69 t/ha was recorded by genotype MONGAL F1. Significant ($P< 0.01$) differences were observed among the 20 tomato genotypes evaluated. The effects of location and genotype x location interaction were also significantly ($P< 0.01$) different (Appendix 13).

4.2 Mean performance of tomato for fruit physical and quality traits across locations

4.2.1 Mean tomato fruit length per plant (cm) (FL)

The mean value for fruit length of the tomato genotypes evaluated has been presented in Table 4.8. The lowest mean value of 2.96 cm under greenhouse conditions was recorded by genotype CHERRY while the highest mean value of 5.64 cm was recorded by genotype 11-172. Under field conditions, the lowest mean tomato fruit length of 2.91 cm was recorded by genotype CHERRY while the highest mean fruit length of 7.05 cm was recorded by genotype ROMA VF. Across the two locations, the lowest mean fruit length of 2.94 cm was recorded by genotype CHERRY while the highest mean value of 6.24 cm was recorded by genotype ROMA VF. Combined analysis of variance showed significant ($P< 0.01$) genotype, location and Genotype x Location interaction effects (Appendix 13).

Table 4. 7 Mean Single fruit weight per plant, Total fruit weight per plant, and Fruit yield per plant

	Single fruit weight per plant (g)			Total fruit weight per plant (g)			Fruit yield per plant (t/ha)		
Genotype	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	58.72	37.53	48.13	276.67	607.11	441.89	23.05	50.70	36.88
PLATINUMF1	81.59	71.82	76.71	1492.72	1457.51	1475.12	124.40	121.45	122.93
NS 504	90.54	39.63	65.09	759.95	242.08	592.02	63.34	35.34	49.34
NKANSAH HT	42.75	34.95	38.85	1156.65	1160.05	1158.35	96.38	96.67	96.53
CHERRY	20.70	17.7	19.20	603.16	601.78	602.47	50.28	50.14	50.21
11-172	56.06	55.56	55.81	356.98	503.95	430.47	29.74	41.99	35.87
ROMA	73.04	64.50	68.77	600.05	773.32	686.69	50.01	64.44	57.23
L11	59.80	58.24	59.02	150.33	285.65	217.99	12.54	23.80	18.17
HEINZ-1370	104.4	84.73	94.57	524.77	506.75	515.76	43.73	42.24	42.99
NIRVANA	57.85	57.4	57.63	212.36	483.22	347.79	17.69	40.30	29.00
BUFFALO	51.93	45.62	48.78	583.99	709.32	646.66	48.63	59.12	53.88
INLAY F1	59.33	42.11	50.72	502.23	406.75	454.49	41.85	33.89	37.87
MONGAL F1	79.73	76.06	77.90	999.42	1472.36	1235.89	124.68	122.69	123.69
#20880	73.69	52.51	63.10	187.53	299.45	243.49	15.62	24.95	20.29
SUMO F1	127.74	96.89	112.32	922.49	650.15	786.32	76.87	54.18	65.53
ROMA VF	56.71	62.22	59.47	358.30	721.67	539.99	29.85	60.14	45.00
SHAKTIMAN	50.81	39.29	45.05	178.78	386.02	282.40	14.90	32.17	23.54
THORGAL F1	57.57	65.27	61.42	265.78	342.51	304.15	22.10	28.54	25.32
COBBRA F1	53.36	57.69	55.53	1062.56	597.34	829.95	88.55	49.78	69.17
WOSOWOSO	122.01	96.60	109.31	932.72	824.50	878.61	77.73	68.71	73.22
MEAN	68.90	57.80	63.37	606.40	660.70	633.50	52.60	55.10	53.80
$LSD_{(0.05)}$	5.48	3.36	3.14	49.50	61.70	162.10	3.56	5.15	3.05

4.2.2 Mean fruit diameter (cm) (FD)

The mean values for tomato fruit diameter are presented in Table 4.8. The lowest mean fruit diameter of 3.05 cm under greenhouse conditions was recorded by genotype CHERRY while the highest mean value of 7.18 cm was recorded by genotype WOSOWOSO. Under field conditions, the lowest mean value of 2.80 cm was recorded by genotype CHERRY while the highest mean fruit diameter of 6.79 cm was recorded by genotype WOSOWOSO. Across the two locations, the lowest mean fruit diameter of 2.93 cm was recorded by genotype CHERRY while the highest mean value of 6.99 cm was recorded by the genotype WOSOWOSO. Significant ($P< 0.01$) differences were observed among the 20 genotypes based on the combined analysis of variance. Also, the effects of location and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 13).

4.2.3 Mean fruit shape index of tomato (SI)

The mean values for fruit shape index of all the tomato genotypes evaluated are presented in Table 4.8. The smallest tomato fruit shape index of 0.57 under greenhouse conditions was recorded by the genotype WOSOWOSO while the largest mean fruit shape index of 1.15 was recorded by genotype PLATINUM F1. Under field conditions, the smallest mean fruit shape index of 0.57 was recorded by genotype WOSOWOSO while the highest mean value of 1.66 was recorded by genotype ROMA VF. The genotype WOSOWOSO recorded the lowest mean value of 0.57 across the two locations while the highest mean value of 1.29 cm was recorded by genotype 11-172. Based on the combined analysis of variance, significant ($P < 0.01$) differences were observed among the tomato genotypes. The effects of location and genotype x location interaction were also significantly ($P< 0.01$) different (Appendix 13).

Table 4. 8 Mean Fruit length, Fruit diameter and Fruit shape index

Genotype	Fruit length (cm)			Fruit diameter (cm)			Fruit shape index		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	4.37	5.56	4.97	4.57	4.94	4.76	0.94	1.12	1.03
PLATINUMF1	4.49	4.76	4.63	3.94	4.74	4.34	1.15	1.00	1.08
NS 504	4.28	4.67	4.48	4.90	5.18	5.04	0.88	0.90	0.89
NKANSAH HT	3.95	3.98	3.97	3.72	3.46	3.59	1.07	1.16	1.12
CHERRY	2.96	2.91	2.94	3.05	2.80	2.93	0.98	1.07	1.03
11-172	5.64	5.28	5.46	4.32	4.16	4.24	1.3	1.28	1.29
ROMA	5.57	5.04	5.31	5.56	4.39	4.98	1.00	1.17	1.09
L11	5.03	4.94	4.99	5.36	5.66	5.51	0.99	0.86	0.93
HEINZ-1370	5.16	4.79	4.98	5.88	6.11	6.00	0.89	0.79	0.84
NIRVANA	3.92	5.04	4.48	3.74	4.10	3.92	1.06	1.25	1.16
BUFFALO	5.50	6.08	5.79	4.81	4.47	4.64	1.14	1.38	1.26
INLAY F1	5.09	5.5	5.30	6.03	5.06	5.55	0.85	1.04	0.95
MONGAL F1	4.3	4.49	4.40	6.82	6.07	6.45	0.64	0.74	0.69
#20880	5.16	5.04	5.10	6.03	5.77	5.90	0.86	0.91	0.89
SUMO F1	4.67	4.70	4.69	6.74	6.24	6.50	0.70	0.76	0.73
ROMA VF	5.43	7.05	6.24	6.08	4.21	5.15	0.89	1.66	1.28
SHAKTIMAN	3.92	5.21	4.57	3.68	4.43	4.06	1.01	1.2	1.11
THORGAL F1	4.48	4.55	4.52	4.23	5.31	4.77	1.07	0.86	0.97
COBBRA F1	5.01	3.64	4.33	4.72	3.97	4.35	1.06	0.93	1.00
WOSOWOSO	4.09	4.04	4.07	7.18	6.79	6.99	0.57	0.57	0.57
MEAN	4.65	4.86	4.76	5.07	4.89	4.98	0.95	1.03	0.99
$LSD_{(0.05)}$	0.25	0.52	0.29	0.37	0.52	0.32	0.12	0.10	0.07

4.2.4 Mean number of locules per fruit (LOC)

The mean values recorded for number of locules per fruit have been presented in Table 4.9.

The lowest mean number of locules was 2.00 under greenhouse conditions and this was

recorded by 7 tomato genotypes while the highest mean value of 8.00 locules was recorded by genotype WOSOWOSO. Under field conditions, the smallest mean number of locules recorded was 2 and it was recorded by 8 genotypes while the highest mean value of 8.00 was recorded by genotype WOSOWOSO. Across the two locations, the lowest mean value of 2.00 was recorded by 7 genotypes while the highest mean value of 8.00 was recorded by genotype WOSOWOSO**.** Based on the combined analysis of variance, differences observed among the 20 tomato genotypes were significantly ($P < 0.01$) different. The effects of location and genotype x location interaction were not significant ($P < 0.05$) (Appendix 13).

4.2.5 Mean fruit pericarp thickness (mm) (PTK)

The mean values for fruit pericarp thickness recorded in the study are presented in Table 4.9. The smallest mean value of 3.00 mm under greenhouse conditions was recorded by the genotype CHERRY while the maximum mean value of 6.19 mm was recorded by the genotype COBBRA F1. Under field conditions, the lowest mean pericarp thickness of 2.71 mm was recorded by genotype CHERRY while the highest mean pericarp thickness of 6.01 mm was recorded by the genotype ROMA VF. The genotype CHERRY recorded the lowest mean pericarp thickness of 2.86 mm across the two locations while the highest mean value of 5.51 mm was recorded by genotype PLATINUM F1 .The combined analysis of variance showed significant ($P < 0.01$) genotype, location and genotype x location interaction effects (Appendix 13).

4.2.6 Mean fruit firmness (kg/cm^2) (FF)

The mean values for fruit firmness among the tomato genotypes evaluated are presented in Table 4.9. The lowest mean value of 2.87 kg/cm^2 under greenhouse conditions was recorded by genotype MONGAL F1 while the highest mean value of 5.13 kg/ cm^2 was recorded genotype 11-172. Under field conditions, the lowest mean value of 2.40 kg/cm^2 was recorded by genotype MONGAL F1 while the highest mean value of 3.73 kg/cm^2 was recorded by

ROMA VF. Tomato genotype MONGAL F1 recorded the lowest mean value of 2.64 kg/cm^2 across the two locations while the highest mean value of 4.27 kg/cm^2 was recorded by the genotype 11-172. Significant (P< 0.01) difference was observed among the 20 genotypes based on the combined analysis of variance (Appendix 13). The effects of location and genotype x location interaction were also significantly (P< 0.01) different.

4.3.5 Mean fruit pH value of tomato (pH)

The mean pH values of the tomato genotypes are presented in Table 4.10. The lowest mean pH value of 3.90 under greenhouse conditions was recorded by genotype WOSOWOSO while the highest mean value of 5.11 was recorded by genotype #20880. Under field conditions, the lowest mean value of 4.22 was recorded by the tomato genotype 11 - 172 while the highest mean value of 4.52 was recorded by seven tomato genotypes (PLATINUM F1, CHERRY, L11, BUFFALO, #20880, SHAKTIMAN, and WOSOWOSO). Across the two locations, the lowest mean value of 4.09 was recorded by NKANSAH HT while the highest mean value of 4.81 was recorded by the genotype #20880. Significant (P< 0.01) differences were observed among the 20 genotypes. The effects of location and genotype x location interaction were also significantly (P< 0.01) different (Appendix 14).

4.3.6 Mean fruit dry matter content of tomato (g) (FDM)

The mean values showing fruit dry matter content of tomato are presented in Table 4.10. The lowest mean value for dry matter content of 0.22 g under greenhouse conditions was recorded by genotype ROMA while the highest mean dry matter content of 0.65 g was recorded by the genotype ROMA VF. Under field conditions, the lowest mean dry matter content of tomato was 0.27 g and was recorded by MONGAL F1, SHAKTIMAN and WOSOWOSO while the highest mean value of 0.49 g was recorded by ROMA VF.

Table 4. 9 Mean Number of locules, Fruit pericarp thickness and Fruit firmness

	Number of locules			Fruit pericarp thickness (mm)			Fruit firmness (kg/cm^2)		
Genotype	Green house	Open field	Poole Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	2.00	2.00	2.00	5.72	3.42	4.57	3.40	3.37	3.39
PLATINUMF1	2.00	2.00	2.00	5.80	5.22	5.51	3.50	2.83	3.17
NS 504	3.00	3.00	3.00	4.00	5.16	4.58	3.90	2.80	3.35
NKANSAH HT	3.00	3.00	3.00	4.58	3.42	4.00	4.63	3.50	4.07
CHERRY	2.00	2.00	2.00	3.00	2.71	2.86	3.63	3.23	3.43
11-172	2.00	2.00	2.00	3.75	3.80	3.78	5.13	3.40	4.27
ROMA	3.00	5.00	4.00	5.80	3.75	4.78	5.07	3.27	4.17
L11	3.00	3.00	3.00	3.99	4.25	4.12	3.85	3.13	3.49
HEINZ-1370	4.00	4.00	4.00	5.16	5.10	5.13	3.63	3.67	3.65
NIRVANA	2.00	2.00	2.00	4.21	4.00	4.11	3.90	3.57	3.74
BUFFALO	4.00	4.00	4.00	4.72	5.69	5.21	3.67	3.57	3.62
INLAY F1	3.00	3.00	3.00	4.45	4.53	4.59	4.10	3.47	3.79
MONGAL F1	5.00	5.00	5.00	5.04	4.99	5.02	2.87	2.40	2.64
#20880	5.00	5.00	5.00	5.10	4.89	5.00	3.77	3.43	3.60
SUMO F1	7.00	7.00	7.00	4.56	4.44	4.50	4.50	3.33	3.92
ROMA VF	2.00	2.00	2.00	4.96	6.01	5.49	3.33	3.73	3.53
SHAKTIMAN	4.00	2.00	3.00	4.08	3.47	3.78	4.43	2.43	3.43
THORGAL F1	5.00	5.00	5.00	4.00	3.94	3.97	3,23	2.50	2.87
COBBRA F1	2.00	2.00	2.00	6.19	3.00	4.60	3.70	3.37	3.54
WOSOWOSO	8.00	8.00	8.00	4.03	4.08	4.06	3.70	2.50	3.10
MEAN	3.55	3.55	3.55	4.66	4.29	4.48	3.90	3.18	3.54
$LSD_{(0.05)}$	0.02	1.51	1.13	0.52	1.01	0.57	0.61	0.51	0.39

The genotype ROMA recorded the lowest mean value of 0.29 g across the two locations while the highest mean value of 0.57 g was recorded by ROMA VF. From the combined analysis of variance, Significant (P< 0.01) differences were observed among the 20 genotypes. The effects of location and genotype x location interaction were also significantly (P< 0.01) different (Appendix 13).

4.3.7 Mean total soluble solids content (^{0}Brix) (TSS)

The mean total soluble solids content of tomato fruits are presented in Table 4.10. The lowest mean total soluble solids content of 2.26 ^{0}Brix under greenhouse conditions was recorded by ROMA while the highest mean value of 6.58 ^{0}Brix was recorded by ROMA VF. Under field conditions, the lowest mean total soluble solids content of 2.58 ^{0}Brix was recorded by genotype SHAKTIMAN while the highest mean value of 6.98 ^{0}Brix was recorded by genotype WOSOWOSO. Across the two locations, the lowest mean value of 2.66 ^{0}Brix was recorded by genotype ROMA while the highest mean value of 6.26 ^{0}Brix was recorded by genotype WOSOWOSO. Significant (P< 0.01) differences were observed among the tomato genotypes evaluated. The effects of genotype and genotype x location interaction were significantly (P< 0.01) different (Appendix 14).

4.3.8 Mean acidity content (mg/100 ml) (TA)

The mean value for acidity content of tomato fruits are presented in Table 4.11. The lowest mean acidity content of 0.19 mg/100 ml under greenhouse conditions was recorded by ROMA and MONGAL F1 while the highest mean value of 0.44 mg/100 ml was recorded by HEINZ-1370 and ROMA VF. Under field conditions, the lowest mean value of 0.32 mg/100 ml was recorded by genotype SHAKTIMAN while the highest acidity content of 0.66 mg/100 ml was recorded by genotype WOSOWOSO. Across the two locations, the lowest mean value of 0.27 mg/100 ml was recorded by genotype MONGAL F1 while the highest mean value of 0.54 was recorded by WOSOWOSO. Significant (P< 0.01) differences were

observed among the 20 genotypes. Also, the effects of location and genotype x location interaction were significantly (P< 0.01) different (Appendix 14).

Table 4. 10 Mean pH value, Fruit dry matter content and Total soluble solids content

Genotype	pH			Fruit dry matter content (g)			Total soluble solids (^{0}Brix)		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	4.04	4.31	4.18	0.38	0.38	0.38	3.85	3.91	3.88
PLATINUMF1	4.24	4.52	4.38	0.35	0.35	0.35	3.64	3.45	3.55
NS 504	4.13	4.23	4.18	0.36	0.32	0.34	3.62	2.63	3.13
NKANSAH HT	3.92	4.27	4.09	0.41	0.39	0.40	3.95	4.33	4.14
CHERRY	4.57	4.52	4.54	0.43	0.36	0.40	4.41	4.50	4.46
11-172	4.67	4.22	4.44	0.51	0.38	0.45	5.28	6.64	5.86
ROMA	4.23	4.30	4.26	0.22	0.36	0.29	2.26	3.05	2.66
L11	4.87	4.52	4.70	0.44	0.35	0.40	4.33	5.17	4.75
HEINZ-1370	4.34	4.23	4.29	0.50	0.41	0.46	5.18	3.90	4.54
NIRVANA	4.08	4.30	4.19	0.52	0.36	0.44	5.30	2.74	4.02
BUFFALO	4.20	4.52	4.36	0.43	0.39	0.41	4.39	3.15	3.77
INLAY F1	4.13	4.24	4.19	0.51	0.38	0.45	5.22	3.79	4.51
MONGAL F1	4.66	4.30	4.48	0.36	0.27	0.32	3.78	4.12	3.95
#20880	5.11	4.52	4.81	0.32	0.38	0.35	3.16	4.23	3.70
SUMO F1	4.32	4.23	4.28	0.33	0.37	0.35	3.40	3.44	3.42
ROMA VF	4.29	4.30	4.29	0.65	0.49	0.57	6.58	4.22	5.40
SHAKTIMAN	4.12	4.52	4.32	0.55	0.27	0.41	5.55	2.58	4.07
THORGAL F1	4.20	4.23	4.22	0.63	0.28	0.46	6.44	3.93	5.19
COBBRA F1	4.07	4.30	4.18	0.29	0.38	0.34	2.93	3.23	3.08
WOSOWOSO	3.90	4.52	4.21	0.55	0.27	0.41	5.54	6.98	6.26
MEAN	4.30	4.36	4.33	0.44	0.36	0.40	4.44	4.00	4.22
$LSD_{(0.05)}$	0.03	0.03	0.02	0.04	0.07	0.04	0.29	0.2	0.19

4.3.9 Mean flavour index (TSS/TA)

The mean values for flavour index (TSS/TA) of tomato fruits are presented in Table 4.11. The lowest flavour index (TSS/TA) of 9.61 under greenhouse conditions was recorded by PECTOMECH while the highest mean value of 19.49 mg/100ml was recorded by genotype L11. Under field conditions, the lowest mean flavour index (TSS/TA) of 6.76 was recorded by genotype NS 504 while the highest flavour index (TSS/TA) of 14.40 was recorded by genotype 11 - 172. The genotype PLATINUM F1 recorded the lowest mean value of 9.39 across the two locations while the highest mean value of 15.67 as recorded by genotype MONGAL F1. The combined analysis of variance showed significant ($P< 0.01$) differences among the 20 genotypes. Also, the effects of genotype and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 14).

4.3.10 Mean malic acid content (mg/100 ml) (MA)

The mean value for malic acid contents of the tomato fruits are presented in Table 4.11. Under greenhouse conditions, the lowest mean value of 0.22 mg/100 ml was recorded by MONGAL F1 while the highest mean value of 0.48 mg/100 ml was recorded by HEINZ-1370. Under field conditions, the lowest mean value of 0.34 mg/100 ml was recorded by SHAKTIMAN while the highest mean value of 0.69 mg/100 ml was recorded by the genotype WOSOWOSO. Across the two locations, the lowest mean value of 0.29 mg/100 ml was recorded by MONGAL F1 while the highest mean value of 0.57 mg/100ml was recorded by the genotype WOSOWOSO. Significant ($P < 0.01$) differences among the genotypes and locations for malic acid content were observed based on the combined analysis of variance (Appendix 13). Also, Genotype x Location interaction effects was significantly ($P < 0.01$) different.

Table 4. 11 Mean Titrable acidity, TSS/TA and Malic acid content of tomato fruits

Genotype	Titrable acidity (mg/100 ml)			Flavour index (TSS/TA)			Malic acid content (mg/100 ml)		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled mean	Green house	Open field	Pooled mean
PECTOMECH	0.42	0.36	0.39	9.61	10.89	10.25	0.45	0.37	0.41
PLATINUMF1	0.36	0.45	0.41	10.31	8.46	9.39	0.35	0.44	0.40
NS 504	0.28	0.43	0.36	12.12	6.76	9.44	0.33	0.46	0.40
NKANSAH HT	0.28	0.44	0.36	13.24	9.55	11.40	0.36	0.48	0.42
CHERRY	0.27	0.47	0.37	16.15	9.76	12.96	0.28	0.48	0.38
11-172	0.34	0.47	0.41	15.78	14.40	15.09	0.36	0.47	0.42
ROMA	0.19	0.36	0.28	11.49	8.89	10.19	0.23	0.36	0.30
L11	0.26	0.46	0.36	19.49	10.81	15.15	0.23	0.52	0.38
HEINZ-1370	0.44	0.36	0.40	11.66	10.64	11.15	0.48	0.38	0.43
NIRVANA	0.39	0.34	0.37	13.00	8.24	10.62	0.41	0.36	0.39
BUFFALO	0.27	0.36	0.32	15.59	8.75	12.17	0.30	0.35	0.33
INLAY F1	0.38	0.33	0.36	13.91	11.38	12.65	0.37	0.39	0.38
MONGAL F1	0.19	0.34	0.27	19.27	12.06	15.67	0.22	0.35	0.29
#20880	0.24	0.36	0.30	12.75	11.79	12.27	0.26	0.38	0.32
SUMO F1	0.28	0.43	0.36	12.07	8.58	10.33	0.30	0.42	0.36
ROMA VF	0.44	0.39	0.42	16.07	10.74	13.41	0.43	0.41	0.42
SHAKTIMAN	0.36	0.32	0.34	15.48	7.97	11.73	0.38	0.34	0.36
THORGAL F1	0.37	0.42	0.40	17.55	9.41	13.48	0.38	0.44	0.41
COBBRA F1	0.23	0.34	0.29	12.73	9.47	11.10	0.24	0.36	0.30
WOSOWOSO	0.42	0.66	0.54	13.26	10.62	11.94	0.44	0.69	0.57
MEAN	0.32	0.40	0.36	14.08	9.96	12.02	0.34	0.42	0.38
$LSD_{(0.05)}$	0.03	0.03	0.02	0.80	0.62	0.54	0.03	0.04	0.03

4.3 Mean performance of tomato for phytochemical composition across locations

4.4.1 Mean β-Carotene content in tomato fruit (mg/100 ml) (β -CARO)

The mean value for β-Carotene content of tomato fruits are presented in Table 4.12. The tomato genotype ROMA VF recorded the lowest value for β-Carotene content under greenhouse conditions with a mean value of 7.31 mg/100 ml while the highest mean value of 34.39 mg/100 ml was recorded by NIRVANA F1. Under field conditions, the lowest mean value for β-Carotene content of 13.31 was recorded by PECTOMECH while the highest mean β-carotene content of 33.79 mg/100ml was recorded by genotype 11–172. Across the two locations, the lowest mean value of 13.60 was recorded by ROMA VF while the highest mean value of 30.38 mg/100 ml was recorded by the genotype 11-172. The combined analysis of variance showed significant ($P < 0.01$) genotype, location and genotype x location interaction effects (Appendix 14).

4.4.2 Mean lycopene content in tomato fruit (mg/100 ml) (LYC)

The mean value for lycopene content in tomato fruit are shown in Table 4.12. The lowest mean value of 7.50 mg/100 ml under greenhouse conditions was recorded by THORGAL F1 while the highest mean lycopene content of 30.74 mg/100 ml was recorded by NIRNANA F1. Under field conditions, the lowest mean lycopene content of 6.56 mg/100 ml was recorded by genotype PECTOMECH while the highest mean value of 25.79 mg/100 ml was recorded by genotype 11–172. The genotype THORGAL F1 recorded the lowest mean value of 8.83 mg/100 ml across the two locations while the highest mean value of 26.50 was recorded by the genotype NIRVANA F1. Significant ($P < 0.01$) differences were observed among the genotypes and locations based on the combined analysis of variance (Appendix 14). Also, Genotype x Location interaction effects was significantly ($P < 0.01$) different.

4.4.3 Mean ascorbic acid content in tomato fruit (mg/100 ml) (ASC)

The mean value for ascorbic acid content in tomato fruits are presented in Table 4.12. The tomato genotype INLAY F1 recorded the lowest ascorbic acid content of 6.11 mg/100 ml under greenhouse conditions while the highest mean value of 17.39 mg/100 ml was recorded by CHERRY. Under field conditions, the lowest mean value of 5.33 mg/100 ml was recorded by L11/while the highest mean value of 12.94 mg/100 ml was recorded by genotype ROMA. The genotype INLAY F1 recorded the lowest mean value of 7.11 mg/100 ml across the two locations while the highest mean value of 13.98 mg/100 ml was recorded by genotype CHERRY. Significant ($P < 0.01$) differences were observed among the genotypes and locations based on the combined analysis of variance (Appendix 14). Also, Genotype x Location interaction effects was significantly ($P < 0.01$) different.

4.4.4 Mean gallic acid content in tomato fruit (mg/100 ml) (GA)

The mean value for gallic acid content in tomato fruit has been presented in Table 4.13. The lowest mean gallic acid content of 1.50 mg/100 ml under greenhouse conditions was recorded by COBBRA F1 while the highest mean value of 1.77 mg/100 ml was recorded by genotype NIRVANA F1. Under field conditions, the lowest mean value of 1.49 mg/100 ml was recorded by genotype L11 while the highest mean gallic acid content of 2.72 mg/100 ml was recorded by PLATINUM F1. Across the two locations, the lowest mean value of 1.54 mg/100 ml was recorded by the genotype NKANSAH HT while the highest mean value of 2.18 mg/100 ml was recorded by PLATINUM F1. Significant ($P< 0.01$) differences were observed among the 20 genotypes. Also, the effects of location and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 14).

Table 4. 12 Mean β-Carotene, Lycopene and Ascorbic acid contents of tomato fruits

Genotype	β-Carotene content (mg/100 ml)			Lycopene content (mg/100 ml)			Ascorbic acid content (mg/100 ml)		
	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	29.19	13.31	21.25	22.12	6.56	14.34	12.89	8.92	10.91
PLATINUMF1	14.75	24.70	19.73	11.45	19.23	15.34	13.72	10.72	12.22
NS 504	8.13	27.02	17.58	8.36	10.03	13.70	11.72	8.50	10.11
NKANSAH HT	21.19	25.16	23.18	12.84	13.12	12.98	13.89	12.17	13.03
CHERRY	16.72	26.46	21.59	14.76	19.28	17.02	17.39	10.56	13.98
11-172	26.97	33.79	30.38	22.31	25.79	24.05	14.28	11.06	12.67
ROMA	23.07	25.92	24.50	13.55	17.02	15.29	8.33	12.94	10.64
L11	18.95	21.50	20.23	19.50	12.48	15.99	9.72	5.33	7.53
HEINZ-1370	13.29	31.03	22.16	11.04	24.99	18.02	8.42	11.11	9.77
NIRVANA F1	34.39	26.18	30.29	30.74	22.25	26.50	12.56	9.28	10.92
BUFFALO	13.23	19.32	16.28	10.75	13.63	12.19	10.11	9.82	9.97
INLAY F1	10.66	28.28	19.47	19.50	12.48	15.99	6.11	8.11	7.11
MONGAL F1	19.68	15.33	17.51	12.55	9.86	11.21	15.39	5.83	10.61
#20880	17.74	18.39	18.07	15.29	13.46	14.38	12.67	12.05	12.36
SUMO F1	13.50	29.85	21.68	12.15	20.01	16.08	14.00	9.94	11.97
ROMA VF	7.31	19.89	13.60	11.29	13.53	12.41	8.33	8.00	8.17
SHAKTIMAN	33.71	22.28	28.00	28.52	18.74	23.63	8.39	12.06	10.23
THORGAL F1	17.13	21.96	19.55	7.50	10.15	8.83	13.11	7.89	10.50
COBBRA F1	27.59	20.69	21.14	23.86	7.65	15.76	11.11	6.83	8.97
WOSOWOSO	30.50	15.91	23.21	16.40	8.99	12.70	12.50	7.11	9.81
MEAN	19.89	23.35	21.62	16.22	15.41	15.82	11.73	9.41	10.57
$LSD_{(0.05)}$	0.82	4.95	2.44	0.70	1.23	0.69	4.58	0.76	2.28

4.4.5 Mean rosmarinic acid content in tomato fruit (mg/100 ml) (RA)

The mean values for rosmarinic acid content in tomato fruit are present in Table 4.13. The lowest mean value of 0.66 mg/100 ml under greenhouse conditions was recorded by PECTOMECH while the highest mean value of 1.08 mg/100 ml was recorded by genotype NIRVANA F1. Under field conditions, the lowest mean value of 0.72 mg/100 ml was recorded by genotype L11 while the highest mean value of 2.28 mg/100 ml was recorded by PLATINUM F1. Across the two locations, the lowest mean value of 0.70 mg/100ml was recorded by the PECTOMECH while the highest mean value of 1.59 mg/100ml was recorded by PLATINUM F1. Significant ($P< 0.01$) differences were observed among the 20 genotypes based on the combined analysis of variance. The effects of location and genotype x location interaction were also significantly ($P< 0.01$) different (Appendix 14).

4.4.6 Mean vanillic acid content in tomato ((mg/100 ml) (VA)

The mean values for vanillic acid content in tomato fruits have been presented in Table 4.13. The lowest mean value of 0.57 mg/100ml under greenhouse conditions was recorded by genotype NKANSAH HT while the highest mean vanillic acid content of 1.22 mg/100ml was recorded by the genotype NIRVANA F1. Under field conditions, the lowest mean value of 0.75 mg/100 ml was recorded by genotype L11 while the highest mean value of 2.78 mg/100 ml was recorded by PLATINUM F1. Across the two locations, the lowest mean value of 0.83 mg/100 ml was recorded by NKANAH HT while the highest mean value of 1.88 mg/100 ml was recorded by PLATINUM F1. Significant ($P< 0.01$) differences were observed among the 20 genotypes. The effects of genotype and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 14).

Table 4. 13 Mean Gallic, Rosmarinic and Vanilic acids content of tomato fruits

Genotype	Gallic acid (mg/100 ml)			Rosmarinic acid (mg/100 ml)			Vanillic acid (mg/100 ml)		
	Green house	Open field	Pooled mean	Green house	Open field	Pooled mean	Green hose	Open field	Pooled mean
PECTOMECH	1.61	1.66	1.64	0.66	0.73	0.70	0.79	0.88	0.84
PLATINUMF1	1.63	2.72	2.18	0.90	2.28	1.59	0.98	2.78	1.88
NS 504	1.53	1.64	1.59	0.78	0.92	0.85	0.82	1.00	0.91
NKANSAH HT	1.38	1.70	1.54	0.58	0.98	0.78	0.57	1.09	0.83
CHERRY	1.53	1.66	1.60	0.78	0.94	0.86	0.82	1.04	0.93
11-172	1.60	1.79	1.70	0.86	1.11	0.99	0.93	1.25	1.09
ROMA	1.55	1.71	1.63	0.80	1.00	0.90	0.86	1.12	0.99
L11	1.64	1.49	1.57	0.91	0.72	0.82	1.00	0.75	0.88
HEINZ-1370	1.53	1.67	1.60	0.78	0.95	0.87	0.82	1.05	0.94
NIRVANA F1	1.77	1.59	1.68	1.08	0.84	0.96	1.22	0.91	1.07
BUFFALO	1.72	1.72	1.72	1.01	1.01	1.01	1.13	1.13	1.13
INLAY F1	1.57	1.65	1.61	0.82	0.92	0.87	0.88	1.01	0.95
MONGAL F1	1.54	1.65	1.60	0.79	0.92	0.86	0.84	1.01	0.93
#20880	1.56	1.55	1.56	0.81	0.80	0.81	0.87	0.86	0.87
SUMO F1	1.57	2.33	1.95	0.82	1.78	1.30	0.87	2.13	1.50
ROMA VF	1.53	1.71	1.62	0.77	1.00	0.89	0.82	1.11	0.97
SHAKTIMAN	1.66	1.75	1.71	0.93	1.05	0.99	1.03	1.17	1.10
THORGAL F1	1.65	1.66	1.66	0.93	0.93	0.93	1.02	1.03	1.03
COBBRA F1	1.50	1.65	1.58	0.73	0.93	0.83	0.76	1.02	0.89
WOSOWOSO	1.54	1.60	1.57	0.79	0.86	0.83	0.84	0.93	0.89
MEAN	1.58	1.75	1.66	0.83	1.03	0.93	0.89	1.16	1.03
$LSD_{(0.05)}$	0.04	0.45	0.11	0.15	0.59	0.15	0.12	0.75	0.19

4.4.7 Mean catechin content in tomato fruit (mg/100 ml) (CAT)

The mean values for catechin content in tomato fruits have been presented in Table 4.14. The lowest mean value of 54.66 mg/100 ml under greenhouse conditions was recorded by INLAY F1 while the highest mean catechin content of 190.22 mg/100 ml was recorded by THORGAL F1. Under field conditions, the lowest mean value of 42.03 mg/100 ml was recorded by genotype MONGAL F1 while the highest mean value of 311.02 mg/100 ml was recorded by WOSOWOSO. Across the two locations, the lowest mean value of 53.04 mg/100 ml was recorded by genotype INLAY F1 while the highest mean value of 192.84 mg/100 ml was recorded by WOSOWOSO. Significant ($P< 0.01$) differences were observed among the 20 genotypes. Also, the effects of genotype and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 15).

4.4.8 Mean genestein content in tomato (mg/100 ml) (GEN)

The mean value for genestein content in tomato fruits has been presented in Table 4.14. The lowest mean genestein content of 35.40 mg/100 ml under greenhouse conditions was recorded by ROMA VF while the highest mean value of 112.77 mg/100 ml was recorded by genotype NIRVANA F. Under field conditions the lowest mean value of 23.70 mg/100 ml was recorded by ROMA VF while the highest mean genestein content of 164.56 mg/100 ml was recorded by WOSOWOSO. Across the two locations, the lowest mean value of 29.55 mg/100ml was recorded by genotype ROMA VF while the highest mean value of 102.66 mg/100 ml was recorded by genotype WOSOWOSO. Combined analysis of variance showed significant ($P< 0.01$) differences among the 20 genotypes evaluated. Also, the effects of genotype and genotype x location interaction were significantly ($P< 0.01$) different (Appendix 15).

4.4.9 Mean hesperetin content in tomato fruit (mg/100 ml) (HES)

The mean hesperetin content in tomato fruit among the genotypes are presented in Table 4.14. The genotype INLAY F1 recorded the lowest mean value of 26.78 mg/100 ml under greenhouse conditions while the highest mean value of 273.63 mg/100 ml was recorded by THORGAL F1. Under field conditions, the lowest mean hesperetin content of 18.44 mg/100 ml was recorded by NIRVANA F1 while the highest mean value of 495.11 mg/100 ml was recorded by WOSOWOSO. The genotype INLAY F1 recorded the lowest mean hesperetin content of 22.98 mg/100 ml across the two locations while the highest mean value of 278.45 mg/100 ml was recorded by WOAOWOAO. Based on the combined analysis of variance, significant (P< 0.01) genotype, location and genotype x location interaction effects was observed (Appendix 15).

4.4.10 Mean kaempferol content in tomato fruit (mg/100 ml) (KAE)

The mean value for kaempferol content in tomato fruits are presented in Table 4.15. The lowest mean kaempferol content of 9.46 mg/100 ml under greenhouse conditions was recorded by INLAY F1 while the highest mean value of 68.48 mg/100 ml was recorded by the genotype NIRVANA F1. Under field conditions, the lowest mean value of 1.75 mg/100 ml was recorded by the genotype ROMA VF while the highest mean Kaempferol content of 120.07 mg/100 ml was recorded by WOSOWOSO. Across the two locations, the lowest mean value of 6.04 mg/100ml was recorded by genotype ROMA VF while the highest mean value of 67.21 mg/100 ml was recorded by WOSOWOSO. Significant (P < 0.01) differences among the genotypes and locations for kaempferol content were recorded based on the combined analysis of variance. The effects of location and Genotype x Location interaction were also significantly (P < 0.01) different (Appendix 15).

Table 4. 14 Mean Catechin, Genestein and Hesperetin content of tomato genotypes

	Catechin (mg/100 ml)			Genestein (mg/100 ml)			Hesperetin (mg/100 ml)		
Genotype	Green house	Open field	Pooled mean	Green house	Open field	Pooled mean	Green house	Open field	Pooled mean
PECTOMECH	104.44	63.68	84.06	56.35	34.98	45.67	116.39	41.59	78.99
PLATINUM F1	74.65	70.53	72.59	40.81	38.57	39.69	61.96	54.18	58.07
NS 504	161.93	43.49	102.71	86.46	24.49	55.48	221.77	44.37	113.07
NKANSAH HT	189.50	111.53	150.52	101	60.04	80.52	272.33	129.37	200.85
CHERRY	154.15	113.84	134.00	82.39	61.27	71.83	207.51	133.63	170.57
11-172	110.62	185.36	147.99	59.58	98.75	79.17	127.70	264.73	196.22
ROMA	113.54	75.83	94.69	61.11	41.37	51.24	133.07	64.00	98.54
L11	92.43	60.11	76.27	50.05	33.03	41.54	90.70	35.11	62.91
HEINZ-1370	160.72	64.18	112.45	85.83	35.21	60.52	219.50	42.33	130.92
NIRVANA F1	65.78	51.02	58.40	112.77	28.36	70.57	44.38	18.44	31.41
BUFFALO	65.77	75.36	70.57	48.36	55.04	51.70	45.11	65.29	55.20
INLAY F1	54.66	51.42	53.04	56.41	28.57	42.49	26.78	19.18	22.98
MONGAL F1	104.66	42.03	73.35	56.46	30.64	43.55	116.77	30.08	59.93
#20880	69.74	62.84	66.29	50.39	34.56	42.48	85.53	40.11	62.82
SUMO F1	80.43	260.11	170.27	57.74	137.9	97.82	74.59	401.77	238.18
ROMA VF	64.45	42.13	53.29	35.4	23.70	29.55	43.07	33.48	23.28
SHAKTIMAN	112.58	81.73	97.16	60.61	39.37	49.99	131.3	63.63	97.47
THORGAL F1	190.22	54.16	122.19	101.28	57.94	79.61	273.63	21.96	147.80
COBBRA F1	69.21	78.30	73.76	37.89	42.65	40.27	51.78	68.44	60.11
WOSOWOSO	74.66	311.02	192.84	40.75	164.56	102.66	61.78	495.11	278.45
MEAN	105.71	94.93	100.32	64.08	53.55	58.82	120.28	103.34	109.39
$LSD_{(0.05)}$	3.70	6.64	3.75	5.12	2.36	2.78	23.83	7.08	12.11

4.4.11 Mean myricetin content in tomato fruits (mg/100 ml) (MYR)

The mean value for myricetin content in tomato fruits have been presented in Table 4.15. The lowest mean value of 19.93 mg/100 ml under greenhouse condition was recorded by ROMA

VF while the highest mean value of 85.07 mg/100 ml was recorded by NIRVANA F1. Under field conditions, the lowest mean myricetin content of 10.11 mg/100ml was recorded by ROMA VF while the highest mean value of 128.43 mg/100 ml was recorded by genotype WOSOWOSO. The genotype ROMA VF recorded the lowest mean value of 15.02 mg/100 ml across the two locations while the highest mean value of 76.43 mg/100 ml was recorded by WOSOWOSO. Significant (P< 0.01) differences were observed among the 20 genotypes. Also, the effects of location and Genotype x Location interaction were significantly (P< 0.01) different (Appendix 15).

4.4.12 Mean rutin content in tomato fruit (mg/100 ml) (RUT)

The mean value for rutin content in tomato fruit are presented in Table 4.15. The lowest mean value of 44.37 mg/100 ml under greenhouse conditions was recorded by INLAY F1 while the highest mean value of 188.48 mg/100 ml was recorded by THORGAL F1. Under field conditions, the lowest mean value of 23.47 mg/100 ml was recorded by genotype MONGAL F1 while the highest rutin content of 321.37 mg/100 ml was recorded by the tomato genotype WOSOWOSO. Across the two locations, the lowest mean value of 37.86 mg/100 ml was recorded by genotype ROMA VF while the highest mean value of 191.37 mg/100 ml was recorded by WOSOWOSO. Significant (P< 0.01) differences were observed among the 20 genotypes. Also, the effects of location and genotype x location interaction were significantly (P< 0.01) different (Appendix 15).

4.4.13 Mean quercetin content in tomato fruit (mg/100 ml) (QUE)

The mean quercetin content in tomato fruit among the genotypes evaluated have been presented in Table 4.16. The lowest mean value of 29.04 mg/100 ml under the greenhouse condition was recorded by INLAY F1 while the highest mean value of 124.12 mg/100 ml was recorded by the genotype THORGALF1.

Table 4. 15 Mean Kaempferol, Myricetin and Rutin contents of tomato genotypes

	Kaempferol (mg/100 ml)			Myricetin (mg/100 ml)			Rutin (mg/100 ml)		
Genotype	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	26.04	11.22	18.63	37.53	19.58	28.555	94.13	49.25	71.69
PLATINUM F1	14.45	14.18	14.32	24.45	22.59	23.52	61.48	56.91	59.20
NS 504	48.63	2.29	25.46	62.8	10.61	36.705	157.36	27.05	92.21
NKANSAH HT	59.46	32.29	45.88	74.96	40.65	57.805	187.70	101.92	144.81
CHERRY	45.56	33.31	39.44	59.38	41.66	50.52	148.81	104.48	126.65
11-172	28.75	64.78	46.77	40.23	73.17	56.7	100.92	183.14	142.03
ROMA	29.62	16.60	23.11	41.54	24.96	33.25	104.14	62.70	83.42
L11	22.64	9.66	16.15	32.24	18.04	25.14	87.59	45.37	66.48
HEINZ-1370	48.15	11.40	29.78	62.29	19.77	41.03	156.03	49.70	102.87
NIRVANA F1	68.48	5.66	37.07	85.07	14.02	49.545	79.60	35.37	57.49
BUFFALO	13.33	16.11	14.72	30.83	36.47	33.65	54.03	64.87	59.45
INLAY F1	9.46	5.84	7.65	37.62	14.2	25.91	44.37	35.81	40.09
MONGAL F1	26.13	4.22	15.18	37.59	15.93	26.76	94.36	23.47	58.92
#20880	11.57	10.86	11.22	32.5	19.22	25.86	54.95	48.37	51.66
SUMO F1	17.09	97.66	57.38	38.7	106.02	72.36	67.06	265.36	166.21
ROMA VF	10.33	1.75	6.04	19.93	10.11	15.02	50.14	25.58	37.86
SHAKTIMAN	29.24	15.18	22.21	41.11	23.54	32.325	103.08	59.14	81.11
THORGAL F1	59.74	7.18	33.46	75.27	15.54	45.405	188.48	37.48	112.98
COBBRA F1	12.20	17.67	14.94	22.03	26.03	24.03	55.37	65.37	60.37
WOSOWOSO	14.35	120.07	67.21	24.43	128.43	76.43	61.37	321.37	191.37
MEAN	29.76	24.90	27.33	44.025	34.03	39.0	97.55	83.14	90.34
$LSD_{(0.05)}$	13.32	2.36	6.71	3.32	1.86	1.87	8.14	4.17	4.45

Under field conditions, the lowest mean value of 15.36 mg/100 ml was recorded by genotype MONGAL F1 while the highest quercetin content of 212.71 mg/100 ml was recorded by the genotype WOSOWOSO. Across the two locations, the lowest mean value of 23.71 mg/100 ml was recorded by ROMA VF while the highest mean value of 126.05 was recorded by

genotype WOSOWOSO. Significant (P< 0.01) differences were observed among the 20 tomato genotypes. Also, the effects of location and Genotype x Location interaction were significantly (P< 0.01) different (Appendix 15).

4.4.14 Mean antioxidant activity (mg/100 ml) (AA)

The mean values for antioxidant activity in tomato among all the genotypes evaluated are presented in Table 4.16. The lowest mean IC_{50} value of 1.96 mg/100 ml under greenhouse conditions was recorded by SHAKTIMAN while the highest mean value of 5.61 mg/100 ml was recorded by PECTOMECH. Under field conditions, the lowest mean IC_{50} value of 0.92 mg/100 ml was recorded by genotype WOSOWOSO while the highest value of 10.28 mg/100 ml was recorded by #20880. The genotype WOSOWOSO recorded the lowest mean value of 1.58 mg/100 ml across the two locations while the highest mean value of 6.53 mg/100 ml was recorded by genotype #20880. Combined analysis of variance showed significant (P< 0.01) genotype, location and Genotype x Location interaction effects (Appendix 15).

Table 4. 16 Mean Quercetin content and Antioxidant activity

	Quercetin content (mg/100 ml)			Antioxidant activity (mg/100 ml)		
Genotype	Green house	Open field	Pooled Mean	Green house	Open field	Pooled Mean
PECTOMECH	61.22	31.30	46.26	5.61	3.39	4.50
PLATINUM F1	39.45	36.34	37.90	5.31	2.87	4.09
NS 504	103.50	16.40	59.95	3.17	1.73	2.45
NKANSAH HT	123.60	66.41	95.01	3.10	2.19	2.65
CHERRY	97.67	68.12	82.90	2.67	4.21	3.44
11-172	65.74	120.56	93.15	3.64	6.72	5.18
ROMA	67.89	40.26	54.08	3.50	2.83	3.17
L11	52.41	28.70	40.56	4.91	3.25	4.08
HEINZ-1370	102.48	31.60	67.04	3.68	7.86	5.77
NIRVANA F1	73.75	22.04	47.90	2.11	9.29	5.70
BUFFALO	36.61	42.78	39.70	2.01	2.71	2.36
INLAY F1	28.04	22.34	25.19	2.60	3.69	3.15
MONGAL F1	61.38	15.36	38.37	3.47	4.99	4.23
#20880	36.21	30.71	33.46	2.78	10.28	6.53
SUMO F1	43.17	175.38	109.28	4.10	2.48	3.29
ROMA VF	31.89	15.53	23.71	2.90	5.57	4.24
SHAKTIMAN	67.18	36.79	51.99	1.96	2.98	2.47
THORGAL F1	124.12	23.45	73.79	3.61	2.63	3.12
COBBRA F1	35.38	42.04	38.71	3.91	4.24	4.08
WOSOWOSO	39.38	212.71	126.05	2.24	0.92	1.58
Mean	64.55	53.94	59.25	3.36	4.24	3.80
$LSD_{(0.05)}$	5.48	3.05	3.14	0.31	0.42	0.26

4.4 Variance components, heritability and genetic gain of tomato characters

4.4.1Variance components of tomato traits studied under greenhouse conditions

The components of variance were estimated for all traits scored under greenhouse conditions (Tables 4.17-4.19). With the exception of stem girth, pH and gallic acid content which recorded low values (<10 %) for genotypic and phenotypic coefficient of variation (GCV and PCV), all the other studied traits had moderate (10–20 %) to high (>20%) estimates. Number of fruits per plant recorded the highest estimated value of GCV and PCV (74.24 and 74.34 respectively) whereas gallic acid had the least estimated values of the same genotypic parameter (5.04 and 5.27 respectively). Generally, the PCV estimated were higher than the

corresponding GCV for all the agronomic and quality characters evaluated indicating the relative role of environment on the expression of the traits. However, the ratio of the GCV to PCV was near unity for almost all the characters studied.

4.4.2 Heritability of tomato traits studied under greenhouse conditions

The estimate of broad sense heritability for tomato characters studied under greenhouse conditions are presented in Tables 4.17–4.19. High estimate of broad sense heritability (> 60 %) was recorded for most of the studied traits. The lowest broad sense heritability value of 42 % was recorded by the trait ascorbic acid. Traits including number of fruits per plant, number of locules per fruit, pH, β-carotene, lycopene and catechin recorded the highest estimated broad sense heritability value of 100 %.

4.4.3 Genetic gain (GAM) of tomato traits studied under greenhouse conditions

The estimated genetic gain expressed as genetic advance as percentage of mean (GAM) of all tomato characters scored under greenhouse conditions is presented in Table 4.17–4.19. Genetic gain was high (> 20 %) for almost all the studied traits. However, gallic acid recorded low (< 10 %) estimated value while stem diameter, pH and rosmarinic acids recorded moderate (10 – 20 %) values. Number of fruits per plant recorded the highest value (152.73) for estimated GAM.

4.4.4 Variance components of tomato traits studied under field conditions

The results of the estimated genotypic parameters for tomato traits gathered from the open field experimental location are presented in Tables 4.20 – Table 4.22. The magnitude of variability for most characters ranged from moderate to high as showed by the moderate (10 – 220 %) and high (> 20 %) estimated values for both GCV and PCV. However, chlorophyll content, number of days to 50 % flowering, fruit set percentage, number of days to fruit maturity and pH recorded low estimates (<10%) of both GCV and PCV. However, number of

days to 50 % flowering, percentage fruit set, number of days to fruit maturity and pH recorded low estimates (<10%) of both GCV and PCV. Also, plant height and stem girth recorded low (< 10 %) values of GCV. Higher values of GCV and PCV were observed in most of the quality parameters. The highest estimated values of GCV and PCV (100.01and 100.07 respectively) were recorded by quercetin (an antioxidant trait) while the lowest values (2.952.and 98 respectively) was recorded by the trait pH. Generally, the estimated PCV values were higher than their corresponding GCV values. The ratio of GCV to PCV was close to unity for almost all traits suggesting the dominant role of genetic factors in the phenotypic expression of the traits.

Table 4. 17 Estimate of variances, heritability and genetic advance for 16 vegetative and reproductive characters under greenhouse conditions

Character	GM	Variance component					Heritability & genetic gain			
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV	ECV	H^2_b (%)	EGA	GAM
Pant height (cm)	128.24	225.81	227.19	1.38	11.72	11.75	0.92	99	30.86	24.07
Stem girth (cm)	7.48	0.28	0.34	0.06	7.03	7.76	3.27	82.	0.98	13.13
Number of leaves	35.00	89.84	90.42	0.58	27.08	27.17	2.18	99	19.46	55.61
Chlorophyll content	31.12	30.63	32.37	1.74	17.79	18.28	4.24	95	11.25	35.64
Number of primary branches	3.00	0.56	0.62	0.06	24.94	26.25	8.16	90	1.47	48.84
Root length per plant	21.31	19.76	20.58	0.82	20.86	21.29	4.25	96	8.97	42.11
Number of days to 1st flowering	17.00	3.64	3.81	0.17	11.23	11.49	2.43	96	3.84	22.61
Number of days to 50 % flowering	21.00	9.11	9.42	0.31	14.38	14.62	2.65	97	6.12	29.12
Number of days to first fruit set	38.00	43.21	43.57	0.36	17.37	17.37	1.58	99	13.49	35.49
Number of days to 50 % fruit set	46.00	69.50	69.99	0.49	18.12	18.19	1.52	99	17.11	37.20
Percentage fruit set	57.16	137.70	193.77	56.07	20.53	24.35	13.10	71	20.38	35.65
Number of days to fruit maturity	65.00	46.64	46.97	0.33	10.51	10.54	0.88	99	14.02	21.57
Number of truss per plant	13.00	14.72	15.60	0.88	29.51	30.38	7.22	94	7.68	59.06
Number of flowers per truss	6.00	0.94	1.12	0.18	16.19	17.66	7.07	84	1.83	30.56
Number of fruits per truss	4.00	0.65	0.75	0.10	20.10	21.60	7.91	87	1.54	38.54
Number of fruits per plant	11.00	66.68	66.86	0.18	74.24	74.34	3.86	100	16.80	152.72

GM = Grand mean, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 18 Estimate of variance, heritability and genetic advance for 15 fruit physical and quality characters of tomato under greenhouse conditions

Character	GM	Variance component					ECV	Heritability &genetic advance		
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV		H^2_b	EGA	GAM
Single fruit weight	68.90	685.70	696.69	10.99	38.01	38.31	4.81	98	53.52	77.67
Total fruit weight per plant	606.40	133003.00	171274.00	38271.0	60.14	68.25	32.26	78	662.04	109.18
Fruit yield per plant	52.60	1239.23	1243.87	4.65	66.93	67.05	4.10	99	71.93	136.75
Number of locules per fruit	4.00	3.09	3.09	0.00	43.97	43.97	0.00	100	3.62	90.58
Fruit length (cm)	4.65	0.48	0.50	0.02	14.90	15.20	3.04	96	1.40	30.07
Fruit diameter (cm)	5.07	1.39	1.44	0.05	23.29	23.70	4.41	97	2.39	47.13
Fruit shape index	0.95	0.03	0.03	0.00	17.78	18.99	6.64	88	0.33	34.32
Pericarp thickness	4.66	0.63	0.73	0.10	17.09	18.39	6.79	86	1.52	32.71
Fruit firmness	3.90	0.30	0.44	0.14	14.13	17.09	9.60	68	0.94	24.08
pH	4.30	0.10	0.10	0.0002	7.35	7.36	0.33	100	0.65	15.13
Total soluble solids content	4.44	1.35	1.38	0.03	26.13	26.42	3.90	98	2.36	53.24
Titrable acidity	0.32	0.01	0.01	0.0003	25.32	25.90	5.41	96	0.16	51.01
TSS/TA	14.08	7.44	7.74	0.30	19.38	19.76	3.89	96	5.51	39.14
Malic acid	0.34	0.01	0.01	0.0003	23.38	24.37	5.09	96	0.16	48.01
Fruit dry matter content	0.44	0.01	0.01	0.001	26.09	27.08	7.24	93	0.23	51.79

GM = Grand mean, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of meas.

Table 4. 19 Estimate of variance, heritability and genetic advance for 14 antioxidant characters of tomato under greenhouse conditions

Character	GM	Variance component						Heritability & genetic advance		
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV	ECV	H^2b	EGA	GAM
β-Carotene (mg/100ml)	19.89	67.37	67.62	0.25	41.27	41.34	2.51	100	16.88	84.85
Lycopene (mg/100ml)	16.22	41.83	42.01	0.18	39.87	39.96	2.62	100	13.29	81.96
Ascorbic acid (mg/100ml)	11.73	5.59	13.26	7.67	20.16	31.05	23.61	42	3.16	26.97
Gallic acid (mg/100ml)	1.58	0.01	0.01	0.001	5.04	5.42	2.00	86	0.15	9.64
Vanillic acid (mg/100ml)	0.89	0.02	0.03	0.01	14.51	18.35	11.24	63	0.21	25.62
Rosmarinicacid (mg/100ml)	0.83	0.01	0.02	0.01	12.05	17.04	12.05	50	0.15	17.55
Rutin (mg/100ml)	97.55	2131.56	2155.80	24.24	47.33	47.60	5.05	99	94.57	96.95
Quercetin(mg/100ml)	64.55	939.26	950.25	10.99	47.48	47.75	5.14	99	62.77	97.23
Catechin (mg/100ml)	105.71	1877.26	1882.27	5.01	40.99	41.04	2.12	100	89.14	84.32
Hesperetin (mg/100ml)	120.28	6065.47	6273.37	207.90	64.75	65.85	11.99	97	157.75	131.15
Kaempferol (mg/100ml)	29.76	327.52	392.49	60.81	60.81	66.57	27.08	83	34.06	114.43
Myricetin (mg/100ml)	44.02	367.02	371.05	4.03	43.52	43.76	4.56	99	39.25	89.16
Genestein (mg/100ml)	64.08	518.38	527.96	9.58	35.53	35.86	4.83	98	46.47	72.52
Antioxidant activity (IC_{50})	3.36	1.08	1.11	0.03	30.89	31.32	5.15	97	2.11	62.77

GM = Grand mean, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

4.4.5 Heritability of tomato traits studied under field conditions

Broad sense heritability estimated for all characters studied under the open field condition is presented in Table 4.20 – Table 4.22. Estimated broad sense heritability was high (> 60 %) for most of the studied traits. However, traits including stem girth, fruit set percentage, number of fruits per truss, fruit dry matter content, gallic acid, vanillic acid and rosmarinic acid recorded moderate (30-60%) heritability values. The highest broad sense heritability estimate of 100 % was recorded by flavonoid compounds, rutin, quercetin, catechin, hesperetin, Kaempferol, myricetin and genestein while the lowest value of 40 % was recorded by gallic acid.

4.4.6 Genetic gain (GAM) of tomato traits studied under field conditions

The estimated genetic gain expressed as genetic advance as percentage of mean of all tomato traits studied is presented in Table 4.20 – 4.22. Moderate (10 – 20 %) to high (> 20 %) genetic gain (GAM) was recorded by most of the tomato traits (Table 4.4 – 4.6). However, the traits percentage fruit set and pH recorded low (< 10 %) values of GAM while moderate (10 – 20 %) estimates were recorded by plant height, stem girth, chlorophyll content, number of days to 50 % flowering and gallic acid. The lowest estimated GAM was observed for percentage fruit set (9.97) and pH (5.88). Higher values were particularly observed among the quality traits compared to that of the agronomic traits. The highest estimated value of 281.59 % was recorded by Hesperetin while the lowest value of 6.03 % was recorded by fruit pH.

Table 4. 20 Estimate of variance, heritability and genetic advance for 16 vegetative and reproductive characters of tomato under field conditions

Character	GM	Variance component					Heritability & genetic advance			
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV	ECV	H_2b	EGA	GAM
Pant height (cm)	49.85	20.34	24.85	4.51	9.05	10.00	4.26	82	8.41	16.86
Stem diameter (cm)	8.35	0.47	1.14	0.67	8.24	12.81	9.80	41	0.91	10.92
Number of leaves	43.75	89.12	101.45	12.33	21.58	23.02	8.03	88	18.23	41.66
Chlorophyll content	40.03	13.78	17.66	3.88	9.27	10.50	4.92	78	6.76	16.88
Number of primary branches	4.00	0.39	0.54	0.15	15.61	18.37	9.68	72	1.09	27.33
Root length per plant	19.50	17.40	18.45	1.05	21.39	22.03	5.25	94	8.34	42.79
Number of days to 1st flowering	16.00	9.12	9.44	0.32	18.87	19.20	3.54	97	6.11	38.22
Number of days to 50 % flowering	25.00	4.95	5.53	0.58	8.90	9.40	3.05	90	4.33	17.34
Number of days to first fruit set	37.00	18.72	20.68	1.96	11.69	12.29	3.78	91	8.48	22.92
Number of days to 50 % fruit set	46.00	25.36	29.84	4.48	10.95	11.88	4.60	85	9.56	20.79
Percentage fruit set	55.39	13.79	26.48	12.69	6.71	9.29	6.43	52	5.52	9.97
Number of days to fruit maturity	66.00	28.15	29.96	1.81	8.04	8.29	2.04	94	10.59	16.05
Number of truss per plant	16.00	50.94	52.02	1.08	44.61	45.08	6.50	98	14.55	90.93
Number of flowers per truss	7.00	0.78	1.12	0.34	12.59	15.10	8.33	70	1.51	21.63
Number of fruits per truss	3.00	0.27	0.50	0.23	17.32	23.57	15.99	54	0.79	26.22
Number of fruits per plant	13.00	71.68	72.38	0.70	65.12	65.44	6.44	99	17.36	133.51

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 21 Estimate variance, heritability and genetic advance for 15 fruit physical and quality characters of tomato under field conditions

Character	GM	Variance component						Heritability & genetic advance		
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV	ECV	H^2_b	EGA	GAM
Single fruit weight	57.82	424.99	429.11	4.12	35.65	35.83	3.51	99	42.26	73.09
Total fruit weight per plant	660.70	117805.71	119198.71	1393.00	51.95	52.26	5.65	99	702.91	106.39
Fruit yield per plant	55.10	817.96	827.67	9.71	51.91	52.21	5.66	99	58.57	106.30
Number of locules per fruit	4.00	2.34	3.18	0.84	38.22	44.56	22.91	74	2.70	67.52
Fruit length (cm)	4.86	0.74	0.84	0.10	17.66	18.82	6.51	88	1.66	34.14
Fruit diameter (cm)	4.89	0.99	1.09	0.10	20.38	21.38	6.47	91	1.96	40.02
Fruit shape index	1.03	0.06	0.07	0.004	24.17	24.94	6.14	94	0.50	48.27
Pericarp thickness	4.29	0.68	1.05	0.37	19.22	23.89	14.18	65	1.37	31.87
Fruit firmness	3.18	0.15	0.24	0.09	12.31	15.51	9.43	63	0.64	20.14
pH	4.36	0.02	0.02	0.0003	2.95	2.98	0.40	98	0.26	6.03
Total soluble solids content	4.00	1.36	1.38	0.02	29.19	29.40	3.54	99	2.39	59.70
Titrable acidity	0.40	0.01	0.01	0.0004	20.21	20.82	5.00	94	0.16	40.41
TSS/TA	9.96	2.97	3.11	0.14	17.30	17.71	3.76	95	3.47	34.83
Malic acid	0.42	0.01	0.01	0.001	18.95	20.39	7.53	86	0.15	36.27
Fruit dry matter content (g)	0.36	0.003	0.005	0.002	15.21	19.64	12.42	60	0.09	24.28

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 22 Estimate of variance, heritability and genetic advance for antioxidant characters of tomato under field conditions

Character	GM	Variance component						Heritability & genetic advance		
		σ^2_G	σ^2_P	σ^2_E	GCV	PCV	ECV	H_2b	EGA	GAM
β-Carotene (mg/100 ml)	23.35	26.71	35.66	8.95	22.13	25.58	12.81	75	9.21	39.46
Lycopene (mg/100 ml)	15.41	31.24	31.79	0.55	36.27	36.59	4.82	98	11.41	74.06
Ascorbic acid (mg/100 ml)	9.41	4.75	4.96	0.21	23.16	23.67	4.87	96	4.39	46.69
Gallic acid (mg/100 ml)	1.75	0.05	0.13	0.08	13.20	20.87	16.16	40	0.30	17.19
Vanillic acid (mg/100 ml)	1.16	0.15	0.36	0.21	33.39	51.72	39.50	42	0.52	44.40
Rosmarinicacid (mg/100 ml)	1.03	0.09	0.22	0.13	29.13	45.54	35.01	41	0.40	38.38
Rutin (mg/100 ml)	83.14	6557.17	6563.52	6.35	97.40	97.44	3.03	100	166.73	200.54
Quercetin(mg/100 ml)	53.94	2910.14	2913.55	3.41	100.01	100.07	3.42	100	111.06	205.90
Catechin (mg/100 ml)	94.94	5387.53	5403.67	16.14	77.31	77.43	4.23	100	150.98	159.02
Hesperetin (mg/100 ml)	98.49	18143.76	18162.13	18.37	136.76	136.83	4.35	100	277.34	281.59
Kaempferol (mg/100 ml)	24.90	1041.21	1043.24	2.03	129.59	129.72	5.72	100	66.41	266.69
Myricetin (mg/100 ml)	34.03	1030.72	1031.98	1.26	94.34	94.40	3.30	100	66.10	194.23
Genestein (mg/100 ml)	53.55	1435.03	1437.07	2.04	70.74	70.79	2.67	100	77.98	145.62
Antioxidant activity (mg/100 ml)	4.24	6.32	6.39	0.07	59.31	59.63	6.24	99	5.15	121.50

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

4.4.7 Variance components of tomato traits estimated over combined locations

Components of variance estimated over the combined greenhouse and open field locations are presented in Tables 4.23 – 4.25. The estimated variance due to location (σ^2_L) was higher than the corresponding genotypic variance (σ^2_G) for some vegetative and reproductive traits. Such traits included plant height, stem girth, chlorophyll content, root length and number of days to first flowering. Similarly, quality traits including fruit firmness, acidity, TSS/TA, malic acid, fruit dry matter content, β-carotene, gallic acid, vanillic acid, rosmarinic acid, myricetin, genestein as well as antioxidant activity recorded higher values of variance due to location (σ^2_L) than corresponding genotypic variance (σ^2_G).

Generally, estimated values of phenotypic (σ^2_P) and interaction (σ^2_{GL}) variance were higher than the corresponding genotypic variance (σ^2_G) for most of the traits. The variances due to G x L were much larger than the environmental variance components for most of the studied characters indicating that the traits differed considerably with environment. The estimated environmental variances for stem girth, number of fruits per truss, number of locules per fruit, vanillic acid and rosmarinic acid were higher than the variance component due to G x L interaction. This indicated that those traits varied strongly with the environment as a result of unpredictable environmental factors. With the exception of characters number of days to 1st fruit set and number of flowers per truss, the ratio of the genotypic variance to genotype by location interaction variance (σ^2_G: $\sigma^2_{G\,x\,L}$) observed for almost all the studied traits were far from unity.

Among all the studied characters, high (> 20 %) estimated values of GCV and PCV were recorded by number of truss per plant, number of fruits per truss, number of fruits per plant, single fruit weight per plant, fruit weight per plant, total fruit yield per plant and number of

locules per fruit. The differences between the GCV and PCV were large for most of the studied traits indicating a significant role of the environment on the expression of those traits.

High (> 20 %) estimated GCV and PCV was recorded by number of truss per plant, number of fruits per truss, number of fruits per plant, single fruit weight per plant, fruit weight per plant, total fruit yield per plant and number of locules. The differences between the GCV and PCV were large for most of the studied traits indicating a significant role of environment on the expression of those traits.

4.4.8 Heritability of tomato traits estimated over combined locations

Heritability estimated for agronomic traits over the combined locations are presented in Tables 4.23 – 4.25. Among the vegetative and reproductive traits studied, number of leaves, number of days to first fruit set, number of days to 50 % fruit set, number of days to fruit maturity, number of truss per plant, number of flowers per truss, number of fruits per truss and number of fruits per plant recorded high (> 60 %) broad sense heritability estimates. Moderate (30 – 60 %) heritability values were observed by plant height, stem girth, number of primary branches and number of days to 1st flowering while number of days to 50 % flowering and percentage fruit set recorded low (<30 %) heritability estimates. Vanillic acid recorded the lowest heritability estimate (11 %). The highest estimated value of 96 % was recorded by number of locules per fruit.

4.4.9 Genetic gain (GAM) of tomato traits estimated over combined locations

The estimated values of genetic gain expressed as genetic advance as percentage of mean are presented in Tables 4.23 – 4.25. Number of leaves per plant, number of days to 50% fruit set, number of truss per plant, number of fruits per truss and number of fruits per plant recorded

higher values of genetic gain (> 20 %). With the exception of characters including plant height, number of primary branches per plant, number of days to 1st flowering, number of days to first fruit set, and number of flowers per truss where moderate (10 – 20 %) GAM was recorded, all other vegetative and reproductive traits had low (< 10 %) estimated values.

High (> 20 %) GAM was observed for almost all the quality traits except Pericarp thickness, fruit firmness, malic acid and fruit dry matter where low estimate of GAM was recorded. Titrable acidity and TSS/TA recorded moderate genetic gain (10 – 20 %). Among the antioxidant composition traits, very low GAM was observed for lycopene content, ascorbic acid, gallic acid, vanillic acid and rosmarinic acid contents. Non-significant estimated genetic gain values were recorded for all the other polyphenol traits.

Table 4. 23 Estimate of variance, heritability and genetic advance for 16 vegetative and reproductive characters of tomato over combined locations

Character	GM	Variance components								Heritability and genetic advance		
		σ^2_L	σ^2_G	σ^2_P	σ^2_{GL}	σ^2_E	GCV	PCV	ECV	H^2_b	EGA	GAM
Pant height (cm)	89.17	3086.69	41.03	82.55	82.03	3.06	7.18	10.19	1.96	50	9.30	10.43
Stem girth (cm)	7.91	0.37	0.20	0.35	0.16	0.40	5.65	7.46	8.00	57	0.70	8.83
Number of leaves	40.00	32.44	53.60	72.62	35.77	6.78	18.30	21.30	6.51	74	12.96	32.39
Chlorophyll content	35.57	38.44	00	12.68	24.45	2.70	-	10.01	4.62	00	00	00
Number of primary	4.00	0.00	0.20	0.36	0.27	0.11	11.18	14.90	8.29	56	0.69	17.29
Root length per plant	20.40	0.32	00	13.03	25.75	0.91	-	17.69	4.68	00	00	00
Number of days to 1st flowering	17.00	0.85	2.35	4.41	4.02	0.29	9.01	12.35	3.17	53	2.30	13.54
Number of days to 50 % flowering	23.00	10.12	1.12	4.15	5.91	0.46	4.60	8.86	2.95	27	1.13	4.92
Number of days to first fruit set	38.00	1.32	15.17	23.04	15.35	1.13	10.25	12.63	2.80	66	6.51	17.14
Number of days to 50 % fruit set	45.00	0.26	27.78	38.02	19.67	2.43	11.71	13.70	3.46	73	9.28	20.63
Percentage fruit set	56.28	00	13.02	50.11	62.96	33.69	6.41	12.58	10.31	26	3.79	6.73
Number of days to fruit maturity	66.00	00	31.46	34.61	5.93	1.06	8.50	8.91	1.56	91	11.02	16.69
Number of truss per plant	15.00	2.32	18.67	25.91	14.17	0.96	28.80	33.94	6.53	72	7.55	50.36
Number of flowers per truss	6.00	0.11	0.44	0.70	0.42	0.25	11.08	13.89	8.33	64	1.09	18.19
Number of fruits per truss	3.00	0.01	0.38	0.44	0.08	0.16	20.41	22.19	13.33	85	1.16	38.67
Number of fruits per plant	12.00	3.23	61.62	65.47	7.56	0.44	65.42	67.43	5.43	94	15.69	130.73

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 24 Estimate of variance, heritability and genetic advance for 16 fruit physical and quality characters of tomato over combined locations

Character	GM	Variance component								Heritability & genetic advance as % of mean		
		σ^2_L	σ^2_G	σ^2_P	σ^2_{GL}	σ^2_E	GCV	PCV	ECV	H^2_b (%)	EGA	GAM
Single fruit weight	63.37	56.57	456.76	507.31	98.62	7.46	33.73	35.54	4.31	90	41.78	65.92
Fruit weight per plant	633.50	92.40	104328.17	118171.67	21057.33	19889.0	50.99	54.26	22.26	88	625.19	98.69
Fruit yield per plant	53.80	00	871.66	951.32	156.98	7.05	54.88	57.33	4.94	92	58.22	108.21
No. of locules per fruit	4.00	0.02	2.65	2.75	0.06	0.44	40.70	41.48	16.58	96	3.29	82.25
Fruit length	4.76	0.01	0.39	0.51	0.22	0.06	13.04	14.95	5.15	76	1.11	23.41
Fruit diameter	4.98	0.003	0.96	1.09	0.23	0.08	19.66	20.95	5.68	88	1.89	38.00
Fruit shape index	0.99	0.002	0.03	0.04	0.02	0.004	15.97	19.34	6.39	68	0.27	27.17
Pericarp thickness	4.48	0.04	0.14	0.44	0.52	0.24	8.20	14.72	10.94	31	0.42	9.41
Fruit firmness	3.54	0.27	0.06	0.17	0.17	0.11	7.11	11.47	9.37	38	0.32	9.07
pH	4.33	00	0.16	0.32	0.33	0.02	9.09	13.13	3.27	48	0.56	12.97
Total soluble solids	4.22	0.05	0.41	0.89	0.95	0.03	15.11	22.29	4.10	46	0.89	21.10
Titrable acidity	0.36	0.003	0.001	0.004	0.005	0.0003	8.78	17.57	4.81	25	0.03	9.05
TSS/TA	12.02	8.37	1.46	3.37	3.73	0.22	10.06	15.26	3.90	43	1.64	13.67
Malic acid	0.38	0.003	0.001	0.006	0.01	0.0005	8.32	20.38	5.88	17	0.03	7.00
Fruit dry matter	0.40	0.003	0.002	0.01	0.01	0.001	11.18	18.26	7.91	38	0.06	14.10

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 25 Estimate of variance, heritability and genetic advance for antioxidant characters of tomato over combined locations

		Variance component								Heritability and genetic advance as %of mean		
Character	GM	σ^2_L	σ^2_G	σ^2_P	σ^2_{GL}	σ^2_E	GCV	PCV	ECV	H^2_b (%)	EGA	GAM
β-Carotene (mg/100 ml)	21.62	3.07	00	29.33	57.15	4.51	-	25.05	9.82	00	00	00
Lycopene (mg/100 ml)	15.19	00	2.74	19.70	33.79	0.36	11.04	29.59	4.00	14	1.27	8.49
Ascorbic acid (mg/100 ml)	10.57	2.37	00	3.26	5.21	3.93	-	17.08	18.76	00	00	00
Gallic acid (mg/100 ml)	1.66	0.01	00	0.04	0.06	0.04	-	11.79	12.05	00	00	00
Vanillic acid (mg/100 ml)	1.03	0.03	0.01	0.06	0.08	0.10	7.93	24.43	30.70	11	0.05	5.30
Rosmarinicacid (mg/100 ml)	0.93	0.02	0.01	0.04	0.04	0.07	7.60	21.05	28.45	13	0.05	5.66
Rutin (mg/100 ml)	90.34	00	00	2438.54	4872.10	14.95	-	54.66	4.28	00	00	00
Quercetin(mg/100 ml)	59.25	00	00	1099.00	2195.50	7.48	-	55.95	4.62	00	00	00
Catechin (mg/100 ml)	100.32	00	00	1986.18	3968.82	10.64	-	44.42	3.25	00	00	00
Hesperitin (mg/100 ml)	109.39	00	00	6685.07	13333.13	111.0	-	74.74	9.63	00	00	00
Kaempferol (mg/100 ml)	27.33	00	00	407.24	803.11	34.12	-	73.84	21.37	00	00	00
Myricetin (mg/100 ml)	39.03	8.50	00	414.77	828.65	2.65	-	52.18	4.17	00	00	00
Genestein (mg/100 ml)	58.82	0.06	00	553.80	1105.66	5.83	-	40.01	4.10	00	00	00
Antioxidant activity (mg/100 ml)	3.80	0.18	00	2.06	4.10	0.05	-	37.75	5.88	00	00	00

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV =Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

4.5 Character association among tomato genotypes

4.5.1 Correlation of tomato traits studied under greenhouse conditions

The Pearson's correlation coefficients among selected agronomic and fruit quality traits studied under greenhouse conditions revealed an association between trait pairs (Table 4.26). A significant and positive association was observed between number of trusses per plant (TPP) and number of primary branches per plant (NPB) (r = 0.588**). Number of fruits per plant (FPP) correlated with number of primary branches per plant (NPB) (r = 0.517*) and number of trusses per plant (TPP) (r = 0.643**). Number of fruits per plant (FPP) associated with number of primary branches per plant (NPB) (r = 0.517*) and number of trusses per plant (TPP) (r = 0.643**). Ascorbic acid content of fruit (ASC) correlated with number of primary branches per plant (NPB) (r = 0.474*), number of truss per plant (TPP) (r = 0.535**) and number of fruits per plant (FPP) (0.518*) while total fruit weight per plant (FWP) correlated with number of trusses per plant (TPP) (r = 0.559**) and number of fruits per plant (FPP) (0.687**).

Tomato fruit yield (YPP) correlated positively and significantly with number of trusses per plant (TPP) (r= 0.562**) fruit weight per plant (FWP) (r =1.00**) and number of fruits per plant (FPP) (r = 0.686**). A positive correlation was observed between each of the following trait pair: number of days to fruit maturity (DFM) and number of days to 50 % fruit set (FPFS) (r = 0.804**), fruit length (FL) and number of days to fifty percent fruit set (FPFS) (r = 0.459*) as well as titrable acidity (TA) with total soluble solids content (TSS) (0.744**). Gallic acid (GA) also showed a positive and significant association with plant height (PHT) (r = 0.457*) and number of days to fruit maturity (DFM) (0.554**).

On the other hand, a significant negative association was observed between certain trait pairs (Table 4.26). Fruit yield per plant (YPP) showed a negative significant association with

number of days to 50 % fruit set (FPFS) (r = -0.573**), number of days to fruit maturity (DFM) (-0.627**) and gallic acid content (GA) (-469**). A significant negative correlation was observed for fruit length (FL) and number of primary branches per plant (NPB) (r = -0.561**) and number of fruits per plant (FPP) (r = -0.460*), ascorbic acid content (ASC) (r = -0.557**) and quercetin content in fruit (QUE) (r = -0.447*). The association of number of fruits per plant (FPP) with number of days to 50 % flowering (FPF) (r = -0.454*), number of days to 50 % fruit set (FPFS) (r = -0.624**) and gallic acid (GA) (-460*) were found to be significantly negative.

Fruit weight per plant (FWP) correlated negatively with number of days to 50 % fruit set (FPFS) (r = -0.572**), number of days to fruit maturity (DFM) (r = -6.27**) and gallic acid content (GA) (r = -0.462*). Moreover, a negative and significant association was recorded for trait pairs including number of trusses per plant (TPP) and number of days to 50 % fruit set (FPFS) (r = -0.534**). Quercetin content in fruit (QUE) correlated negatively and significantly with fruit diameter (FD) (r = -0.481*).

4.5.2 Correlation of tomato traits studied under field conditions

The results of the correlation among selected agronomic and fruit quality traits of field-produced tomato genotypes were significant for a number of traits (Table 4.27). A significant positive association was observed between trait pairs number of trusses per plant (TPP) and number of primary branches per plant (NPB) (r = 0.605**), number of fruits per plant (FPP) and number of days to fruit maturity (DFM) (r = 0.740**). Fruit length (FL) correlated with number of days to 50 % flowering (FPF) (r = 0.630**) while fruit diameter (FD) associated with single fruit weight per plant (SFW) (r = 0.744**), titrable acidity (TA) (r = 0.744**) and total soluble solids content (TSS) (r = 0.751**). Antioxidant activity (AA) correlated with number of days to fruit maturity (DFM) (r = **0.674****)

Table 4. 26 The Pearson's correlation matrix of selected agronomic and quality traits of tomato under greenhouse conditions

Variables	PHT	NPB	FPF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE
PHT	-																		
NPB	0.185	-																	
NFF	0.116	-0.250	-																
FPFS	0.207	-0.384	0.436	-															
DFM	0.192	-0.251	0.311	**0.804****	-														
TPP	0.089	**0.588****	-0.380	**-0.534****	-0.386	-													
FPP	-0.019	**0.517***	**-0.454***	**-0.624****	**-0.607****	**0.643****	-												
FWP	0.049	0.230	-0.323	**-0.572****	**-0.627****	**0.559****	**0.687****	-											
YPP	0.050	0.231	-0.324	**-0.573****	**-0.627****	**0.562****	**0.686****	**1.000****	-										
SFW	-0.051	-0.066	0.218	0.061	0.020	-0.077	-0.360	0.309	0.308	-									
FL	-0.031	**-0.561****	0.001	**0.459***	0.307	-0.368	**-0.460***	-0.193	-0.194	0.170	-								
FD	-0.099	-0.069	-0.015	0.072	-0.023	-0.107	-0.344	0.169	0.174	**0.727****	0.426	-							
FF	0.056	-0.228	0.144	0.140	0.335	-0.064	-0.088	-0.154	-0.160	-0.011	0.229	-0.158	-						
TSS	-0.076	-0.005	-0.203	-0.015	0.225	0.101	-0.315	-0.421	-0.419	-0.134	-0.081	-0.068	-0.223	-					
TA	-0.269	-0.131	0.136	0.136	0.204	-0.149	-0.384	-0.312	-0.316	0.138	-0.063	-0.033	-0.193	**0.744****	-				
LYC	0.105	-0.022	0.301	0.182	0.418	-0.190	-0.193	-0.345	-0.344	-0.297	-0.163	-0.305	0.270	0.091	0.175	-			
ASC	0.050	**0.474***	0.141	-0.277	-0.258	**0.535****	**0.518***	0.380	0.382	-0.056	**-0.557****	-0.265	-0.163	-0.192	-0.242	-0.110	-		
GA	**0.457***	-0.211	0.394	**0.460***	**0.554****	-0.291	**-0.518***	**-0.462***	**-0.460***	-0.091	0.065	-0.224	-0.132	0.290	0.214	0.343	-0.119	-	
QUE	-0.300	0.198	-0.062	-0.332	-0.260	0.399	0.219	-0.050	-0.050	-0.200	**-0.447***	**-0.481***	0.077	0.137	0.014	-0.242	0.304	-0.209	-
AA	0.079	0.025	0.139	0.252	-0.132	-0.043	0.009	0.205	0.204	0.151	0.159	-0.005	-0.130	-0.364	-0.017	-0.172	0.184	-0.102	-0.025

** = significant at P < 0.05 (r > 0.413), ** = significant at P < 0.01 (r > 0.526), PHT = Plant height, NPB = Number of primary branches per plant, FPF = Number of days to 50 % flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, = TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.*

(r = 0.674). Number of days to fruit maturity (DFM) correlated positively and significantly with number of days to 50 % flowering (FPF) (r = 0.555**) and number of days to 50 % fruit set (FPFS) (r = 0.617**). A significantly positive association of fruit weight per plant with number of trusses per plant (TPP) (r = 0.629**) and number of fruits per plant (FPP) (r = 0.566**) was recorded.

Tomato fruit yield per plant (YPP) showed a high significant positive association with number of trusses per plant (TPP) (r = 0.628**), total fruit weight plant (FWP) (r = 1.00**) and number of fruits per plant (FPP) (r = 0.566**). The correlations between fruit firmness (FF) with number of days to 50 % flowering (FPF) (r = 0.573**) and fruit length (FL) (0.641**) were positive and significantly high. There was also significant positive association between lycopene content of fruits (LYC) and total soluble solids content of fruit (TSS) (r = 0.731**). Gallic acid content (GA) associated significantly (P < 0.5) with fruit weight per plant (FWP) (r = 0.502*) as well as yield per plant (YPP) (r=0.502*). The flavonoid compound quercetin (QUE) correlated positively and significantly with single fruit weight per plant (SFW) (r = 0.476*), total soluble solids content (TSS) (0.596**) and titrable acidity (TA) (r = 0.736**).

A significantly negative correlation was observed for some agronomic and fruit quality traits. The number of trusses per plant (TPP) showed a significant negative correlation with number of days to 50 % flowering (FPF) (r = -0.555**) and number of days to fruit maturity (DFM) (r = -0.490*). A significant negative association was observed to exist in some trait pairs including fruit weight per plant (FWP) and number of days to 50 % fruit set (FPFS)(r = -0.469*), fruit yield per plant(YPP) and number of days to 50 percent fruit set (FPFS) (r = -0.469*). Fruit length (FL) correlated with number of trusses per plant (TPP) (r = 0.495*), fruit diameter (FD) (and number of fruits per plant (FPP) (r = -0.632**), total soluble solids (TSS) and number of days to 50 % fruit set (FPFS) (r = -0.494*). Titrable acidity content of

tomato fruits (TA) correlated with number of days to 50 % fruit set (-0.669**). Quercetin content of fruit (QUE) showed a negative significant correlation with number of days to 50 percent flowering (NFPFS) (-596**).

4.5.3 Correlation among tomato traits over combined locations

The correlation among selected agronomic and fruit quality characters o f tomato determined over the combined greenhouse and open field locations are presented in Table 4.29. Positive and significant association was observed between trait pairs number of days to 50 % fruit set (NFPFS) and number of days to 1st flower observed (NFF) (r = 0.518*), number of trusses per plant (TPP) and number of primary branches per plant (NPB) (r = 0.689**), fruit length (FL) and number of days to 50 % fruit set (FPFS) (r = 0.553**), fruit diameter (FD) and single fruit weight per plant (SFW) (r = 0.826**), acidity (TA) and total soluble solids content of fruit (TSS) (r = 0.757**). Number of days to fruit maturity (DFM) correlated positively and significantly with number of days to 50 % flowering (FPF) (r = 0.514*), number of days to 50 % fruit set (FPFS)) (r = 0.791**) and lycopene content (LYC) (r = 0.702**).

Number of fruits per plant associated positively and significantly with number of primary branches per plant (NPB) (r = 0.507*), number of truss per plant (TPP) (r = 0.847**) well as ascorbic acid (ASC) (r =0.516*). There was significantly positive character association between fruit weight per plant (FWP) and number of truss per plant (TPP) (r = 0.647**) as well as number of fruits per plant (FPP) (r = 0.622**). The association of fruit yield per plant (YPP) with number of truss per plant (TPP) (r = 0.648**), fruit weight per plant (FWP) (r = 1.00**) and number of fruits per plant (FPP) (r = 0.621**) was found to be highly significant. Quercetin (QUE) showed a significantly positive correlation with titrable acidity (TA) (r = 0.536*) and ascorbic acid (ASC) (r = 0.474*).

Table 4. 27 The Pearson's correlation matrix of selected agronomic and fruit quality traits of tomato under field conditions

Variables	PHT	NPB	FPF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE
PHT	-																		
NPB	0.032	-																	
NFF	0.166	-0.425	-																
FPFS	-0.141	-0.271	0.431	-															
DFM	0.142	-0.103	**0.519***	**0.617****	-														
TPP	-0.154	**0.605****	**-0.555****	-0.382	**-0.490***	-													
FPP	-0.266	0.320	**-0.529****	-0.350	-0.334	**0.740****	-												
FWP	-0.037	0.379	-0.244	**-0.469***	-0.386	**0.629****	**0.566****	-											
YPP	-0.037	0.378	-0.244	**-0.469***	-0.386	**0.628****	**0.566****	**1.000****	-										
SFW	-0.028	0.076	0.250	-0.123	0.012	-0.226	-0.402	0.248	0.248	-									
FL	-0.090	-0.256	**0.630****	0.439	0.382	**-0.495***	-0.291	-0.152	-0.152	0.048	-								
FD	0.185	0.020	0.198	-0.102	0.081	-0.379	**-0.632****	-0.027	-0.027	**0.744****	0.097	-							
FF	0.002	0.055	**0.573****	0.106	0.284	-0.208	-0.238	0.179	0.178	0.357	**0.641***	0.423	-						
TSS	0.127	0.148	-0.286	**-0.494***	-0.227	0.043	0.209	0.039	0.039	0.245	-0.142	0.233	-0.122	-					
TA	-0.071	0.292	-0.369	**-0.669****	-0.379	0.147	0.194	0.145	0.145	0.296	-0.357	0.215	-0.108	**0.751****	-				
LYC	0.287	-0.020	-0.020	-0.086	0.050	-0.053	0.150	-0.006	-0.006	0.098	0.139	0.159	-0.009	**0.731****	0.117	-			
ASC	-0.429	-0.046	-0.046	0.207	0.345	0.030	0.406	-0.002	-0.002	-0.232	0.017	-0.360	-0.142	-0.220	-0.160	-0.151	-		
GA	-0.241	0.043	0.136	-0.010	0.049	0.015	0.135	**0.502***	**0.502***	0.329	0.008	0.031	0.212	-0.174	0.108	-0.260	0.265	-	
QUE	-0.107	0.178	-0.260	**-0.531****	-0.180	-0.008	-0.008	0.086	0.085	**0.476***	-0.293	0.299	-0.218	**0.596****	**0.736***	0.144	0.045	0.233	-
AA	0.102	-0.160	0.419	0.364	**0.674****	-0.219	-0.060	-0.255	-0.255	0.000	0.186	-0.040	0.147	-0.005	-0.395	0.408	0.201	-0.233	-0.301

** = significant at P < 0.05 (r > 0.413), ** = significant at P < 0.01 (r > 0.526), PHT = Plant height, NPB = Number of primary branches per plant, FPF = Number of days to 50 % flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, = TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.*

In addition, the antioxidant activity (AA) of tomato across the locations associated positively with number of days to 50 % fruit set (FPFS) (r = 0.505) and number of days to fruit maturity (DFM) (r = 0.555).

However, a significantly negative correlation was observed between certain traits determined over the combined locations (Table 4.28). Trait pair association was found negative and significant between number of days to 50 % flowering (FPF) and number of primary branches per plant (NPB) (r = -0.630), ascorbic acid content (ASC) and fruit length (FL) (r = -4.87). Quercetin content (QUE) associated negatively with fruit length (FL) (-0.476). Negative and significant correlation was observed for number of truss per plant (TPP) with number of days to 50 % flowering (FPF) (r = -0.673), number of days to 50 % fruit set (FPFS) (r = -0667) and number of days to fruit maturity (DFM) (r = -0.585).

Similarly, number of fruits per plant (FPP) negatively associated with number of days to 50 % flowering (FPF) (r = -0.609), number of days to 50 % fruit set (FPFS) (r = -0.580) and number of days to fruit maturity (DFM) (-0.551). Both fruit weight per plant (FWP) and fruit yield per plant (YPP) showed separate negative significant correlation with number of days to 50 % fruit set (FPFS) (r = -0.637, r = -0.636) and number of days to fruit maturity (DFM) (r = -0.576, r = -0.575). A significantly negative association was also observed for fruit length (FL) with number of primary branches per plant (NPB) (r = -0.634), number of truss per plant (TPP) (r = -0.596) and number of fruits per plant (FPP) (-0.584).

Table 4. 28 The Pearson's correlation matrix of selected agronomic and quality traits of tomato over combined greenhouse and field locations

Variables	PHT	NPB	NFF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE
PHT	-																		
NPB	0.184	-																	
NFF	0.093	**-0.630****	-																
FPFS	0.085	-0.437	**0.518***	-															
DFM	0.156	-0.284	**0.514***	**0.791****	-														
TPP	-0.109	**0.689****	**-0.673****	**-0.667****	**-0.585****	-													
FPP	-0.090	**0.507***	**-0.609****	**-0.580****	**-0.551****	**0.847****	-												
FWP	-0.004	0.326	-0.401	**-0.637****	**-0.576****	**0.647****	**0.622****	-											
YPP	-0.002	0.328	-0.400	**-0.636****	**-0.575****	**0.648****	**0.621****	**1.000****	-										
SFW	-0.066	0.041	0.205	-0.063	0.028	-0.187	**-0.453***	0.274	0.274	-									
FL	-0.064	**-0.634****	0.395	**0.553****	0.402	**-0.596****	**-0.584****	-0.286	-0.286	0.131	-								
FD	0.000	0.058	0.172	0.021	0.033	-0.249	**-0.526***	0.093	0.096	**0.826****	0.282	-							
FF	-0.226	-0.158	0.030	0.325	0.369	-0.151	-0.028	-0.250	-0.254	-0.146	0.315	-0.241	-						
TSS	0.021	0.126	-0.079	-0.191	-0.002	0.052	-0.171	-0.218	-0.218	0.080	0.068	0.149	-0.119	-					
TA	-0.087	0.092	0.065	-0.251	-0.129	-0.026	-0.124	-0.050	-0.053	0.305	-0.090	0.141	-0.126	**0.757****	-				
LYC	0.176	-0.083	0.237	0.405	**0.702****	-0.264	-0.214	-0.372	-0.373	-0.158	-0.023	-0.354	0.422	0.044	0.015	-			
ASC	-0.184	0.195	0.041	-0.252	-0.005	0.380	**0.516***	0.270	0.268	-0.145	**-0.487***	-0.404	0.154	-0.121	-0.006	0.119	-		
GA	0.202	-0.157	0.156	0.174	0.187	-0.122	0.032	0.384	0.381	0.307	0.081	-0.056	-0.028	-0.216	0.108	0.121	0.278	-	
QUE	-0.098	0.334	-0.053	-0.443	-0.204	0.296	0.140	0.124	0.122	0.359	**-0.476***	0.100	0.169	0.377	**0.536****	0.027	**0.474***	0.019	-
AA	-0.252	-0.165	0.318	**0.505***	**0.555****	-0.239	-0.255	-0.239	-0.237	0.001	0.236	0.014	0.120	-0.027	-0.190	0.370	0.145	-0.013	-0.357

** = significant at P < 0.05 (r > 0.413), ** = significant at P < 0.01 (r > 0.526), PHT = Plant height, NPB = Number of primary branches per plant, NFF = Number of days to 1st flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, = TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.*

CHAPTER FIVE

5.0 DISCUSSION

5.1 Variability in Agronomic Performance of Tomato Genotypes

5.1.1 Vegetative characteristics of tomato genotypes

Vegetative traits play significant role in the overall development of the tomato crop. In the present study, significant variation was observed among the tomato genotypes for vegetative traits in all locations as well as across locations. Plant height and root length were significantly higher under greenhouse conditions as compared with the genotypes produced under field conditions. Similar observation was made by Rajasekar *et al*. (2013) who reported 150.25 cm and 52.41 cm of plant height under greenhouse and field conditions respectively. According to this author relative humidity was higher in the greenhouse environment which consequently resulted to higher vegetative growth and improved productivity of tomato fruit yield**.**

Estimated values recorded for stem diameter, number of leaves per plant, chlorophyll content and number of primary branches per plant in this work was higher under field conditions than those of the greenhouse. Contrast to the present findings, Rajasekar *et al*. (2013) found that tomato leaves were higher in number under greenhouse conditions compared with that of the field conditions. Similarly, Atnafua and Rao (2014) recorded higher values for number of primary branches per plant under greenhouse conditions than that of the field conditions. Differences in observations made could be attributed to differences in the genotypes evaluated, surrounding environment and seasons of the study. Vicente *et al*. (2011) indicated that chlorophyll content is higher at the vegetative growth stage than at the reproductive growth stage. In this study, measurement of chlorophyll content was carried out at the reproductive growth stage of the plants and thus probably resulted to lower values recorded.

5.1.2 Reproductive and phenological characteristics of tomato genotypes

The growth and productivity of the tomato crop is significantly influenced by its reproductive or phenological characters. Understanding these economically important characters is essential in planning a crop improvement programme because genotypes with short reproductive or phenological cycle along with high fruit yield are normally selected for commercial cultivation (Singh *et al.*, 2014). The results of the present study indicated that greenhouse-produced tomato genotypes were earlier in attaining 50 % flowering as well as number of days to fruit maturity. Higher values for percentage fruit set and number of fruits per truss were also recorded under greenhouse conditions. However, the field-produced genotypes were early in attaining 1st flower opening and fruit set. Also, number of truss per plant as well as number of flowers per truss was higher under field conditions. The significance of genotype, location and Genotype x Location interaction for all the reproductive and phenological characters implied that variability existed among the genotypes evaluated in each location. According to Singh *et al.* (2014) both genotypic and environmental factors influence tomato plants to flower early or delay in flowering. Generally, the performances of the genotypes for reproductive and phenological traits were inconsistent across the experimental locations due to the interaction between genotype and the environment.

Number of days to 1st flowering varied from 15 to 20 days and 12 to 24 days after transplanting under greenhouse and field conditions respectively. The presence of variability among tomato genotypes for number of days to 1st flowering has been reported in earlier studies. Earlier report by Parvej *et al.* (2010) indicated that phenological traits such as number of days to 1st flowering, 1st fruit set and number of days to fruit maturity were earlier under greenhouse conditions as compared with results obtained under field conditions.

Amarananjundeshwara *et al.* (2008) recorded variation in number of days to 1st flowering which ranged from 25 to 30 days after transplanting.

Percentage fruit set is an important character for increasing the productivity of tomato in terms of fruit yield. It serves as a good indicator of the resistance or tolerance of a genotype to the surrounding environmental conditions particularly temperature (Singh *et al.*, 2014). According to Singh *et al.* (2014), higher percentage fruit set is required to achieve high fruit yield. High percentage fruit set was recorded under greenhouse conditions than that of the field and varied greatly among the experimental locations. Genotypes such as PLATINUM F1 (72.93 %) and NIRVANA F1 (47.76) recorded maximum and minimum values for fruit set percentage across locations. Earlier investigations reported minimum and maximum values of 50.33% to 84.09 % (Singh, 2014), 72.84 % to 86.21 % (Sharma *et al.*, 2011) and 83.1 to 93.9 % (Pandey *et al.*, 2006). Differences recorded by different authors may be due to differences in the genetic materials evaluated. Genotype PLATINUM F1, CHERRY, SUMO F1 and NKANSAH HT showed a better mean performance for this trait. They are therefore considered as superior heat resistant or tolerant genotypes.

Number of days to fruit maturity was higher under greenhouse conditions as compared with that of the field. The genotypes showed high variability for the trait in each location and across locations. Similar observations were previously reported by Nagalakshani *et al.* (2001) and Cheema *et al.* (2004). Genotypes NKANSAH HT, WOSOWOSO, COBBRA F1 and THORGAL F1 showed early fruit maturity across locations and represent good genetic materials for increasing the productivity of tomato.

Reproductive and phenological characters are influenced by both cultivar and environmental conditions. Tomato genotypes evaluated in this experiment showed variation in their reproductive development characters within and across locations as a result of genotypic differences. The results of the present study indicated that number of truss per plant and

number of flowers per truss were higher under field conditions while number of fruits per truss was higher under greenhouse conditions. A study by Parvej *et al*. (2010) revealed that reproductive development traits including number of trusses per plant, number of fruits per truss and number of flowers per truss were higher under greenhouse conditions than that of the field. Such differences may result from differences in surrounding environment as well as differential response of different genotypes to different environments. Singh *et al*. (2014) observed that higher number of flower clusters contributed to increased fruit yield in tomato and attributed this observation to inherent genetic factors. Variability in reproductive development characters has been reported in previous studies and ranged from 6.9 to 8.6 for number of truss per plant (Osekita and Ademiluyi, 2014), 2.9 to 7.8 for number of flowers per truss (Emami *et al*., 2013) and 1.72 to 5.11 for number of fruits per truss.

4.1.3 Yield and yield components characteristics of tomato genotypes

Fruit yield is an important trait in genetic improvement of tomato. It is a complex trait and thus influenced by several yield components. Considering the average performances of all genotypes under greenhouse conditions, a total of 7 genotypes (MONGALF1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, SUMO F1, and NS 504) showed superior performance for fruit yield. These genotypes are good materials for tomato production under greenhouse experimental conditions. Similarly, 7 tomato genotypes namely MONGAL F1, PLATINUM F1, NKANSAH HT, WOSOWOSO, ROMA, ROMA VF and BUFFALO exhibited better fruit yield performance among all the genotypes evaluated under open field conditions for fruit yield. The mean fruit yield of these genotypes exceeded their respective location averages. Across the two locations, four tomato genotypes showed superior performance. These genotypes were MONGAL F1, PLATINUM F1, NKANSAH HT and WOSOWOSO. They represent good materials for tomato production irrespective of differences in locations considered in this experiment. Common among most of the

genotypes with superior performance for fruit yield was high scores for one or more yield component traits including number of fruits per plant, number of trusses per plant, single fruit weight and total fruit weight per plant.

The tomato genotypes generally showed diverse yield performances which agreed with findings by other workers (Hussain *et al.*, 2001; Mansour *et al.*, 2009; Singh *et al.*, 2009). This was as a result of differences in number and type of genetic materials used, location as well as growing environment. A narrow difference in fruit yield was recorded between the genotypes produced under greenhouse and that produced under field conditions. Some genotypes including PECTOMECH, L11, NIRVANNA F1, #20880 and SHAKTIMAN performed poorly under greenhouse conditions. These genotypes showed poor adaptation to greenhouse conditions. Thus a lower average value of 52.60 t/ha under greenhouse conditions than that of the field (55.10 t/ha) was recorded. Average tomato fruit yield as reported by Atnafua (2014) was higher under polyhouse condition (80.6 t/ha) than that of the open field (57.2 t/ha). Parvej (2010) compared phenological development and productive ability of tomato and obtained high fruit yield under polyhouse condition (81 t/ha) than that of the field (57 t/ha). Also, Blay *et al.* (1999) evaluated 8 tomato genotypes under field conditions and reported low fruit yield (6 117.30 – 11 359.2 kg/ha). This was attributed to poor rainfall, high day and night temperatures in the experimental period, as well as attack by root knot nematodes. Other reports on tomato fruit yield differences among cultivars include that of Firas *et al.* (2012) who reported minimum and maximum yield of 15 907 kg/ha and 42 908 kg/ha respectively. Singh *et al.* (2014) recorded average fruit yield of tomato in a range of 135.10 – 1046.80 q/ha**.** According to this author, genotypes with medium and large numbers of fruits per plant produced more fruit yield as compared with those with large fruit sizes but smaller number of fruits per plant. This observation agrees with the present study where

genotype NKANSAH HT with medium sized fruits and higher number of fruits per plant (27, 33) produced high fruit yield per plant.

5.4 Fruit physical and quality characteristics of tomato genotypes

The quality of fruits and vegetables including tomato is determined by their chemical compositions. While inherent genetic factors play major role in determining fruit quality components, environment could alter the quantitative composition of the fruit (Mpofu *et al.*, 2006). For the fresh consumption of tomato as well as in the tomato processing industries, desirable tomato fruit physical and quality features include fruit pericarp thickness, fruit firmness, total soluble solids contents, acidity, flavour, pH, phenolic acids and flavonoid compounds (Caliman *et al.*, 2010).

Fruit firmness

Tomato fruit firmness has been reported as one of the most pertinent qualities required for processing in the canning industry. It determines fruit shelf life as well as susceptibility of tomatoes to damages associated with harvest, sorting, processing, packaging and transportability (Radzevicius *et al.*, 2013). High fruit pericarp thickness corresponds with better fruit firmness and consequently, its suitability for processing (Saimbhi *et al.*, 2001). Genotype factor is known to be the major determinant of tomato fruit firmness. In the present study, fruits obtained from greenhouse-produced genotypes were found to be relatively firmer (3.90 kg/cm^2) than fruits harvested from field-produced genotypes (3.18 kg/cm^2). Comparatively, genotypes 11 – 172, ROMA, NKANSAH HT, PECTOMECH, SUMO F1, and INLAY F1 were superior in fruit firmness in the present study.

Total soluble solids content

Between fifty and sixty-five percent (50 - 65 %) of total soluble solids content (TSS) of tomato is made up of mainly sugars (glucose and fructose) which are essential quality parameters of tomato in the processing industry. Higher amounts of TSS are correlated with

higher recovery product yield (Manashi, 2011; Emami *et al.*, 2013; Singh *et al.*, 2014). In terms of processing, a total soluble solids content range of 4 to 8 ^{0}Brix has been reported to be desirable. The present study showed a wide variability among the genotypes for TSS content and ranged from 2.26 ^{0}Brix (Roma) to 6.58 ^{0}Brix (ROMA VF) under greenhouse and 2.58 ^{0}Brix (SHAKTIMAN) to 6.98 (WOSOWOSO) under field conditions. A related range of TSS content have been reported in previous studies by Blay *et al*. (1999), Caliman *et al*. (2010), Emami *et al*. (2013) and Singh *et al*. (2014). In contrast to findings by Caliman *et al*. (2010), greenhouse-produced genotypes in this study recorded higher TSS values than the field-produced genotypes. Out of the 20 tomato genotypes evaluated, 11 genotypes under green house conditions as well as 8 genotypes under field conditions recorded TSS values in the range of 4 – 8 ^{0}Brix indicating their suitability for the processing industry.

Fruit acidity content

Acidity content of tomato fruits represents another important quality determinant trait of tomato for processing. In the processing industry, acidity reduces pH of the pulp and prevents the growth of microbes. Besides, high acidity gives better tomato flavour, improves its palatability and nutritive value of the fruit as well as reduction in processing time and temperature of the product (Manashi, 2011). Wide variations among genotypes for acidity content have been reported in tomato by previous authors (Manashi, 2011; Aoun *et al.* 2013; Singh *et al.*, 2014) and this have been mainly attributed to genetic factors. Caliman *et al* (2010) reported that tomato genotype with acidity value greater than 0.32 % is suitable for processing**.** The results of the current study revealed 10 and 11 tomato genotypes with acidity content greater than 0.30 mg/ml (0.32 %) under greenhouse and field conditions respectively. Values obtained in this study were in agreement with findings by Caliman *et al*. (2010) who recorded percentage acidity values of 0.26 – 0.37 under protected conditions and 0.28 – 0.40 under field conditions . From the results of the present work, tomato genotypes produced

under field conditions were more acidic (0.40 mg/100 ml) compared with the corresponding genotypes evaluated under greenhouse (0.32 mg/100 ml) conditions. The low acidity content under greenhouse condition could be attributed to low photosynthetic activity of the genotypes produced under greenhouse conditions as compared with that produced under field conditions (Caliman *et al.*, 2010). This is not unexpected as field-produced genotypes recorded higher mean chlorophyll content (40.30 mg/ml) than the greenhouse genotypes (31.12 mg/ml).

Fruit flavour index (TSS/TA)

Tomato fruit flavour influences consumers or processors' preference for specific tomato cultivars. It is determined by TSS/TA ratio which is also a taste determinant quality trait. Variation in tomato flavour composition among different genotypes has been attributed mainly to varietal differences and environmental factors such as plant nutrition (Caliman *et al*, 2010; Manashi, 2011; Aoun *et al* 2013). Tomato genotype with a TSS/TA value $\geq$ 10 is reported to have good flavour required for fresh fruit consumption and processing (Caliman *et al*. (2010). Among the 20 tomato genotypes evaluated, superior flavour content ($\geq$10) was recorded by almost all the tomato genotypes under greenhouse conditions except PECTOMECH (9.61). More than half of the tomato genotypes evaluated under field conditions recorded poor flavour composition of < 10 TSS/TA value. This finding suggests that better fruit flavour composition could be obtained under greenhouse environment compared with that of field conditions. The present results contradicted findings by Caliman *et al*. (2010) who recorded an average TSS/TA value of 12.07 and 16.82 for greenhouse and field conditions respectively. Differences in flavour indexes observed by different authors could be due to differences in the experimental materials used as well as the surrounding environment.

Fruit pH

Fruit pH along with TSS is desirable indexes for the assessment of related quality traits of tomato in the processing industry (Agong *et al.*, 2001). Previous study by Aoun *et al.* (2013) revealed that fruit acidity affects flavour only when pH value is lower. At pH value less than 4.1, growth of pathogens like *Bacillus coagulans* in tomato products are reduced (Majid,

2007), while values less than 4. 49 are suitable in terms of fruit sourness (Aoun *et al.*, 2013). In the processing industry, a suitable tomato genotype for processing should have pH value lower than 4.5 **(**Caliman *et al*., 2010**).** Blay *et al.* (1999) and Singh (2014) reported relatively smaller variability for pH among different genotypes. Findings from the present study showed that pH value differed among the genotypes with appreciably higher values recorded by field-produced genotypes (4.36) than those produced under greenhouse conditions (4.30). This observation was in accordance with findings by Caliman *et al.* (2010) who recorded a relatively greater pH value under field conditions (4.49) than that obtained under protected conditions (4.48). Fruit pH values obtained in this study revealed that most of the tomato genotypes recorded values that make them suitable for processing.

Carotenoids content of fruits

In the plant kingdom, beta carotene and lycopene are essential phytochemical compounds. Manashi (2011) mentioned bright colours of fruits (either yellow or red) are good quality characteristic that influence consumers' choice for tomato. Such colours are affected by the composition of β-carotene and lycopene in the fruit. Composition of carotenoids in fruits varies greatly among different genotypes as well as environments (Frusciante, 2000). Various reports have indicated the effects of light intensity and high temperature in stimulating carotenoids biosynthesis. Variation was observed among the genotypes for lycopene concentration of fruits and ranged from 7.31 mg/100 ml (ROMA VF) to 33.71 mg/100 ml (SHAKTIMAN) among the greenhouse-produced genotypes and 13.31 mg/100 ml (PECTOMECH) to 33.79 mg/100 ml (11-172) among the field-produced tomato genotypes. Generally, lycopene content under field conditions (23.35 mg/100 ml) was appreciably higher than the amount recorded by the corresponding greenhouse genotypes (19.89 mg/100 ml). A different observation was made by Caliman *et al*. (2010) who obtained higher average lycopene content under protected conditions (7.81 mg/100 ml) than field produced genotypes (7.47 mg/100 ml). Manashi *et al.* (2011) recorded a narrow difference in carotene content

when 5 tomato genotypes were evaluated under field conditions. Previous findings have also revealed an appreciable level of variation among different genotypes for lycopene content under different growing conditions. For instance, Frusciante (2000) reported lycopene content in the range for 5.5 – 7.5 mg/100 g whereas Radzevicius (2013) found 2.02 – 4.95 range of lycopene. These differences in observed values could be attributed to differences in genotypic and prevalent environmental factors such as temperature and light intensity.

Ascorbic acid content of fruit

A wide variability in ascorbic acid composition was recorded among tomato genotypes as a result of both genetic and surrounding environmental factors. Tomato genotypes that contain high ascorbic acid content are preferred for processing and determine the nutritional quality of the processed product (Singh *et al*., 2014). The results of the present study indicated that greenhouse-produced tomato genotypes are richer in ascorbic acid content than the field-produced ones. The composition of ascorbic acid was found to be variable within each location as well as across locations. Tomato varieties that contain high ascorbic acid content are suitable for consumption and thus establish the nutritional worth of the variety (Singh *et al*., 2014). Variability in ascorbic acid composition has also been recorded in previous studies by Singh *et al*. (2014) (12.6 – 15.63 mg/100 g), Sharma *et al*. (2011) (17.29 – 26.21 mg.100 g) and Vinod *et al*. (2013) (21.63 – 26.70 mg/100 g). The small fruited CHERRY variety recorded the highest ascorbic acid composition under greenhouse condition. This is in agreement with findings by Vinod *et al*. (2013) who indicated that tomato genotypes with small fruits contain high ascorbic acid content. Comparatively, the highest ascorbic acid composition across the two locations was recorded by CHERRY, NKANSAH HT, 11-172, #20880 and PLATINUM F1.

Phenolic acid compounds:

Phenolic acid compounds including gallic, vanillic and rosmarinic acids have chemo-protective or antioxidant property and thus are able to scavenge effects associated with reactive oxygen species in the human body. In this way, several human-related chronic and degenerative diseases are prevented. The composition of these compounds in the tomato fruit is not only influenced by cultivar factors but also the cultivation practice, surrounding environment, extraction procedure, temperature, processing as well as storage conditions (Supathra *et al*., 2013). For all the phenolic acid compounds, field-produced genotypes recorded maximum amount as compared with those produced under greenhouse conditions. Brezeanu *et al.* (2013) observed a significant amount of rosmarinic acid content in tomato fruits among tomato genotypes evaluated under conventional system. The results of the present study revealed five (5) tomato genotypes as comparatively better source of phenolic acid compounds. These genotypes included PLATINUM F1, 11-172, BUFFALO, SUMO F1 and SHAKTIMAN. They contain a relatively higher amounts of gallic, vanillic and rosmarinic acids composition across locations.

Flavonoid compounds

Quercetin, kaempferol and myricetin are reported to be the main flavonoid compounds present in tomato and its related products (Tokusoglu *et al*., 2003). In addition, tomato fruits also contain rutin, catechin, hesperetin and genestein as important flavonoid compounds. The concentration of these compounds in fruits varies among genotypes as a result of differences in genetic makeup and cultivation environment. In the present experiment greenhouse-produced tomato genotypes recorded high composition for all the flavonoid compounds studied. A wide variability within each location and across locations was observed among the genotypes for all the flavonoid compounds studied and this could be attributed to both genotype and environment factors. Generally, genotypes WOSOWSO, SUMO F1, NKANSAH HT, 11-172 and CHERRY displayed superior performance for all flavonoid

compounds studied across locations. Koh *et al.* (2009) recorded quercetin and Kaempferol content in commercial broccoli with a range of 0.03 to 10. 85 and 0.24 to 13.20 mg/100 g FW respectively. In this work, quercetin and kaempferol content in tomato fruits ranged from 23.71 to 126 mg/100 ml FW and 6.04 to 57 mg/100 ml respectively across locations. Differences in results could be attributed to differences in plant materials evaluated.

5.3 Antioxidant activity of tomato genotypes

Generally, the antioxidant activity of vegetables and fruits differ among different cultivars due to differences in their genotypic makeup and environmental conditions (Marsic *et al.*, 2011). The results of the present study revealed that antioxidant activity of the field-produced genotypes was higher than the same genotypes produced under greenhouse conditions. In each of the two experimental locations, variability for antioxidant activity in terms of their IC_{50} values was observed. In a related study, Ferreira *et al.* (2012) recorded the most excellent antioxidant activity in a local tomato variety whose IC_{50} value was 1.63 mg/100 ml. The results of the present work showed that the local tomato genotype WOSOWOSO proved to be the highest in antioxidant activity under field conditions as well as across locations. In a related study in organic Baby-Leaf salads, Aires *et al.* (2013) reported antioxidant activity (expressed as IC_{50}) ranged from 0.23 to 3.03 mg/ml. Generally, WOSOWOSO, BUFFALO and NS 504 recorded the lowest IC_{50} values across the two locations suggesting that their antioxidant activities were comparatively superior to the rest of the genotypes.

5.1.4 Genotype x Location interaction effects on tomato fruit yield

Though, the tomato crop is recognized to be adapted to different agro-climatic conditions and cropping systems (Sunil *et al.*, 2013**),** several studies have indicated a significant G x E interaction effects on the expression of important traits of tomato genotypes. Such interaction effects have been reported in tomato fruit yield as well as several quality characters (Kuti and Konuru, 2005; Rosello *et al.*, 2011; Cebolla-Cornejo *et al.*, 2011 and Panthee, *et al.*, 2012).

In the present study, differences in genotype, location and G x L interaction effects were significant ($P < 0.01$) for almost all the studied characters indicating the role of varietal difference, location and G x L interaction effects on the expression of individual traits. The highly significant value recorded for location suggested that the two locations were diverse. These findings are not unexpected because yield as a complex trait is influenced by a number of yield components which are quantitative in character. Such quantitative characters exhibit continuous variation in their expression and are subject to genotype-by-environment interaction effects (Causse *et al*, 2002). For instance, the genotype COBBRA F1 performed better with a total fruit yield of 88.55 t/ha relative to its overall mean performance across the two locations and also, it ranked among the top 5 genotypes with superior yield (above location mean) under greenhouse conditions. However it produced 49.78 t/ha (and ranked 15th) under the open field conditions relative to its overall mean across the locations and thus categorized outside the first 5 superior genotypes under field locations. This pattern of performance is inconsistent and a manifestation of reversibility in rank as well as differences in levels of environmental sensitivity across the two locations. This makes COBBRA F1 an unstable and environmentally sensitive for fruit yield. Apart from MONGAL F1, PLATINUM F1 and NKANSAH HT all the other genotypes evaluated exhibited irregular patterns of performance as a result of genotype-by-environment interaction effects. Similar pattern of performance was observed among the genotypes for most fruit quality traits. The present results was in conformity with earlier findings by Panthee *et al.* (2012) who reported significant effects of genotype-by-environment interaction on all studied traits except ascorbic acid content of fruits.

5.3 Genetic Variance, heritability and genetic gain of tomato characters

5.3.1 Individual location basis

Genetic variability studies in a crop are fundamental to crop improvement programmes aimed at yield and quality traits. The significant ($P < 0.01$ and $P < 0.05$) genotypic difference obtained from the results of the analysis of variance (ANOVA) and the estimate of genetic variance indicated an existence of an amount of variability in the 20 tomato genotypes evaluated. Similar findings have been reported earlier by Sharma *et al*. (2009) and Dar and Sharma (2011). Estimation of genotypic coefficient of variation (GCV) gives a true suggestion of the magnitude of genetic variation in a studied population. In the present study, moderate (10 – 20 %) to high (> 20 %) estimate of GCV and PCV for most of the agronomic traits under both greenhouse and field conditions showed appreciable amounts of phenotypic and genotypic variability. The relatively higher estimate of PCV than the corresponding GCV indicated a relative effects of environment (to some degree) on the expression of the traits. However, the narrow difference between PCV and GCV and the closeness to unity in values observed in the ratio of GCV to PCV suggest that genetic control in the expression of the traits was predominant. This suggests that simple phenotypic selection could be made among the genotypes. Also, selection could be effective for most characters at the early stage of a breeding program since response to selection is directly proportional to variability present in the experimental materials evaluated (Falconer and Mackay, 1996). Generally, the magnitude of variability observed among the genotypes for agronomic traits was higher under the greenhouse conditions than the open field conditions.

Among the quality traits studied, moderate to high estimate of PCV and GCV was observed for most traits under greenhouse and field conditions. This indicated the existence of variability in the genotypes for such traits. However, the low estimate of GCV for pH, gallic acid, rosmarinic acid and vanilic acid suggests that the expression of those traits were

influenced by environment. For crop improvement purpose, selection for such characters will need to be carried out in large replicates across multiple location and years (Hallauer, 2007). Besides, the fruit quality traits were more variable compared to the agronomic traits under both locations. The results of the present investigation were in agreement with findings by Nwosu *et al.* (2014) who recorded low difference between PCV and GCV for most of the characters studied including days to flower, days to 50 % flower, days to fruit ripening, fruit length, fruit per inflorescence, fruit diameter, fruit weight and number of days to fruit maturity. Report by Reddy *et al.* (2013) indicated an estimate of moderate to high PCV and GCV as well as smaller differences between them for most of the traits they studied. Similar findings have also been reported by other authors (Pradeepkumar *et al.*, 2001; Jiregna *et al.*, 2012; Shankar *et al.*, 2013; Shushay *et al.*, 2013)

The estimate of GCV along with heritability provides a true indication of the magnitude of heritable component of variation. Estimate of heritability enables a breeder to determine the extent to which genetic variability contributes to phenotypic variability of a trait. In the present study, broad sense heritability estimated for all traits under greenhouse and field conditions were very high with the exception of ascorbic acid and rosmarinic acid contents which recorded moderate values.

High GCV as well as high heritability are useful to breeders to make effective selection and also indicate that selection could be made on phenotypic basis. However, this does not necessarily suggest high genetic gain for a particular character unless it is associated with high genetic advance. In this study, very high heritability estimates accompanied with high genetic gain was recorded by most of the traits evaluated under each of the locations. These findings suggest that those traits could easily be passed on to the next generation. High estimate of heritability may be the result of the diverse nature of the genotypes included in the study (Shushay *et al.*, 2013). Phenotypic selection of such traits in the early generation

for further improvement could therefore be accomplished via simple selection methods like pure line, mass selection, bulk or single seed decent. High estimate of broad sense heritability (61 % to 100 %) along with high genetic advance was recorded for almost all agronomic and physicochemical traits of tomato varieties studied by Shankar *et al.* (2013). However, in the present study high heritability and moderate genetic gain was recorded for days to 50 % flowering, number of flowers per cluster and TSS. High and medium heritability estimate along with low genetic gain recorded for percentage fruit set and pH respectively under open field conditions suggested that non-additive gene action controlled their expression; hence selection cannot be achieved through simple selection methods. Instead such traits could be improved through development of hybrids or could possibly be used as transgressive segregants in heterosis breeding programme (Reddy *et al.*, 2013).

The results of the present study is in accordance with findings made by Shushay *et al.* (2013), Hadhayatullah *et al.* (2008) and Mehta and Asati (2008) who recorded very high (P > 80 %) estimates of heritability along with high genetic gain for most of the traits studied. A related study by Vinod *et al.* (2010) indicated a very high estimate of heritability for all traits with a range from 80 % to 99 %. Several related findings have been reported in tomato genetic variability and heritability studies (Kaushik *et al.*, 2011; Reddy *et al.*, 2013).

5.3.2 Combined location basis

On the basis of the combined analysis of variance, the observed variation recorded for almost all characters studied was significant ($P < 0.01$ and $P < 0.05$) among the genotypes. This observation could be attributed to environment or location or genotype-specific differences as well as G x L interaction effects. The significant ($P < 0.01$) mean squares of location and G x L interaction suggest that the locations were diverse. This resulted in differences in response of genotypes to location changes as manifested in their varied performances across different locations. The challenge then is the need to develop separate varieties tailored to each

specific location. Therefore, one of the most important rationales behind genetic variability studies is the identification of suitable environments where a trait which is intended to be improved upon is most likely to show a consistent expression. Environmental factors may influence the genotype and consequently, the expression of a trait in a cultivar evident by the magnitude of variability due to genotype-by-environment interaction (G x E).

Genotype-by-environment interaction (G x E) causes a reduction in the overall genetic gain of desired traits. This phenomenon may create difficulties in selection of desirable traits for crop improvement programmes. Knowledge about G x E interaction is therefore required in the selection of ideal location, traits and the genotype for inclusion in a breeding programme (Gruneberg *et al*, 2005). The results in the present investigation based on the combined analysis of variance indicated that the estimated variance due to location (σ^2_L) was higher than the corresponding genotypic variance (σ^2_G) for some agronomic traits including plant height, stem diameter, chlorophyll content, root length per plant and number of days to 50 % flowering confirming the significance of location effects on those traits. Among the fruit quality parameters, larger estimates of genotypic variance (σ^2_G) than variance due to location (σ^2_L) was found for most fruit physical traits including single fruit weight, fruit weight per plant, fruit yield per plant, number of locules, fruit length and diameter as well as shape index. As a result high estimate of heritability was recorded for such parameters indicating that they were predominantly affected by inherent genetic factors. It should be noted that very large variance estimates due to phenotypic, environmental and G x L as well as phenotypic coefficient of variation than the corresponding genotypic parameter were observed for almost all the fruit chemical traits. This resulted in negative GCV and heritability estimates.

Among the traits studied, the value obtained for the ratio of σ^2_G to $\sigma^2_{G \times L}$ (σ^2_G:$\sigma^2_{G \times L}$) ratio was close to unity only for number of primary branches per plant, number of days to first fruit

set, number of flowers per truss and fruit shape index. This implied that the effects of location or environment as well as G x L interaction effects accounted for variability in most of the traits. This observation gives an indication that differential response of genotypes to location difference was very possible. Highly significant genotype-by-location interaction implied that independent analysis of data for each location is required (Khan *et al.*, 2013) rather than analysis carried out on combined location basis. The present observation agrees with earlier findings by Causse *et al.* (2003) who recorded a significant G x E interaction for lycopene, TSS and TA.

Information regarding the nature of a trait, its expression as well as interaction with environment could best be understood from the estimate of broad sense heritability. The results of the present study revealed that almost all fruit quality traits recorded very low heritability estimates. This implied that most of the quality traits were environmentally sensitive and the ability to control and predict variability based on genetic information alone becomes negligible (Panthee, 2012). This also implied that selection of superior genotypes for most of the traits would not be effective at early generation. In contrast to the present findings, high heritability estimate has been reported by Premah *et al.* (2011) for TSS (77.95), ascorbic acid (74.7 %), and TA (99.94 %). Similarly, Dar and Sharma, (2011) reported high heritability estimates for lycopene (92 %) and ascorbic acid (94 %). These contrasting results could be due to differences in the experimental materials, growing conditions as well as cultural practices.

5.4 Character association of traits among tomato genotypes

In selection programs, yield, yield components and quality traits are among the most economically essential traits usually targeted by plant breeders. According to Falconer and Mackay (1996), many important characters in crops are positively or negatively correlated because they are influenced by the same gene or because they are developmentally or

structurally related. Knowledge of correlated traits is essential in determining whether or not selection for a particular trait will influence another (Girdthai *et al.*, 2012).

In the present study, number of trusses per plant, number of fruits per plant as well as total fruit weight per plant showed a significant and positive association with fruit yield irrespective of the crops growing condition considered in this experiment. This shows a consistency of correlation across the two locations. However the correlation coefficients differed due to G x L interaction effect. Indirect selection gives a correlated response in the target trait so far as the targeted trait and the secondary traits are associated (Falconer and Mackey, 1996). Those traits with significantly positive association with fruit yield could therefore be selected for maximizing fruit yield in tomato in any of the two growing conditions. This result was in agreement with findings by previous authors including Hadhayatullah *et al.* (2008), Gosh *et al.* (2010), Jiregna *et al.* (2012) and Shushay *et al.* (2013). These authors independently reported a positive and significant correlation of fruit yield with number of fruit clusters per plant and number of fruits per plant at both the genotypic and /or phenotypic levels. Singh (1993) indicated that a high fruit yield response is achieved when the secondary trait also has a high estimate of heritability as well as high correlation coefficient. The present study revealed high heritability estimates as well as high correlation coefficient for the traits associated with fruit yield.

Negative correlation of fruit yield with number of days to 50 % fruit set (under both greenhouse and open field condition) and number of days to fruit maturity (greenhouse condition only) indicated that genotypes that attain early fruit set and mature early tend to have higher fruit yield. This finding agrees with results reported by Jiregna *et al.* (2012) and Shushay *et al.* (2013).

A positive and significant correlation was observed between fruit yield and gallic acid (a phenolic and antioxidant phytochemical compound) under the field experimental location.

This indicated that indirect selection of one trait for the other could be feasible under field conditions. Moreover, the significantly positive association between most traits suggests that each of those pairs of traits is controlled by the same or similar genes or is developmentally or structurally related (Falconer and Mackay, 1996). Indirect selection of one trait for the other should then be appropriate. This is in agreement with earlier report where average fruit weight correlated positively and significantly with number of primary branches per plant at both genotypic and phenotypic levels (Vinod *et al.*, 2013), number of days to 50 % fruit set and number of days to fruit maturity (Shushay *et al.*, 2013). On the other hand, negative association observed for trait pairs point out that indirect selection for any one of those traits may possibly not be advantageous.

Antioxidant compounds considered in this discussion included lycopene, ascorbic acid, gallic acid and quercetin. Under greenhouse growing environment, ascorbic acid correlated positively and significantly with number of primary branches per plant, number of trusses per plant and number of fruits per plant suggesting that those pairs of traits are controlled by the same gene. Similar observations were made earlier by Vinod *et al.* (2013). Indirect selection for any one of those traits is therefore possible. Genotypes with superior performance for traits positively correlated with ascorbic acid could be used for further development of materials endowed with high ascorbic acid content. A negative association between ascorbic acid content and fruit length also suggests that genotypes with shorter fruit length contain higher amount of ascorbic acid content and hence could be used as indirect selection under green house conditions.

Moreover, the antioxidant compound quercetin showed a significant and positive correlation with titrable acidity and ascorbic acid. This observation indicated that indirect selection of the trait titrable acidity or ascorbic acid could contribute to enhancing quercetin content in tomato fruit over combined locations. Under the combined locations genotypes containing

high ascorbic acid content and titrable acidity content could be used to develop high quercetin content cultivars.

Quercetin showed a negative significant correlation with fruit length and fruit diameter under greenhouse conditions suggesting that indirect selection for these traits to increase gallic acid content would be less useful. Thus genotypes with reduced fruit length or reduced diameter are possibly better in terms of their gallic acid composition. Also, under field growing conditions a positive significant association of quercetin with single fruit weight per plant, total soluble solids content and titrable acidity was observed. These results revealed that the traits are under the control of the same or similar genes. Indirect selection of those traits could therefore maximize quercetin content in tomato fruits under field conditions.

However a negative and significant association of quercetin with number of days to 50 % fruit set suggests that it is undesirable to select the later trait for maximizing the amount of quercetin in the fruit. Antioxidant scavenging activity, expressed as IC_{50} (inhibition coefficient) associated positively and significantly only with number of days to 50 % fruit set implying that the two traits are being controlled by the same or similar genes or they are developmentally or structurally correlated. The lower the IC_{50} value scored for a genotype the better its antioxidant potential to deactivate the harmful effects associated with reactive oxygen species (ROS) in humans (Kipandula *et al*., 2014). This also implied that a reduction in number of days to 50 % fruit set should show a corresponding reduction in the IC_{50} value (increased antioxidant activity). Genetic and environmental variation study in bread and Durum wheat by Sukkalovic *et al.* (2013) indicated a highly significant and positive association of antioxidant capacity with total phenolic composition. The association of antioxidant activity with phenolic compound (gallic acid) studied in the present experiment was not significant.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

1. Systematic breeding programmes aimed at improving tomato fruit yield and fruit quality traits require information on the nature and magnitude of genetic variability, heritability and character association in agronomic and fruit quality traits in the crop. Results of the present study revealed an existence of useful genetic variability in the genotypes. The estimate of moderate to high GCV, high broad sense heritability as well as high genetic gain for almost all traits suggest the potential for selection and utilization of suitable genotypes based on different parameters to obtain high yield and fruit quality traits.
2. Following the present findings, promising tomato genotypes based on their fruit yield (t/ha) under greenhouse conditions were MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA, SUMO F1 and NS 504.
3. Tomato genotypes MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA, SUMO F1, ROMA VF and BUFFALO showed superior yield performance under field conditions.
4. Across the two locations, MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA and SUMO F1were superior genotypes for fruit yield. Most of the top performing genotypes for yield recorded high scores for one or more yield component traits including number of fruits per plant, trusses per plant, single fruit weight and total fruit weight per plant.
5. Highest amount of flavonoid compounds across the two locations were recorded by tomato genotypes WOSOWSO, SUMO F1, NKANSAH HT, 11-172, CHERRY and THORGAL F1.

6. The amount of phenolic acids composition was found to be highest in genotypes PLATINUM F1, BUFFALO, 11-172, SHAKTIMAN, THORGAL F1 and NIRVANA F1.
7. Genotypes produced under greenhouse conditions recorded higher amount of flavonoid composition while phenolic acids content was higher under field conditions.
8. Highest antioxidant scavenging activity among the genotypes across locations was recorded by WOSOWSO, BUFFALO and NS 504.
9. Generally, the performance of the genotypes evaluated differed across locations due to the interaction between the genotypes and environment. The expressions of most traits were influenced by genetic and environmental factors as well as their interaction.
10. Number of trusses per plant, number of fruits per plant and total fruit weight per plant showed a positive significant association with fruit yield and are potentially useful traits as indirect selection indexes for yield improvement under both greenhouse and field conditions

6.2 Recommendations

1. The results of the current study showed that tomato genotypes MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA and SUMO F1are recommended for commercial production under both greenhouse and field conditions by virtue of their superior fruit yield per plant across the two growing environments.
2. The present study was carried out under a single growing season; hence further evaluation of the genotypes could be conducted over multiple seasons or years. Evaluation of the genotypes across multiple locations and years along with appropriate stability analysis procedure will further be required to identify stable

tomato genotypes for fruit yield and other important chemical composition traits. This will also provide an in depth information regarding G x E interaction and tomato fruit yields.

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APPENDIX

Appendix 1. Means squares of PHT, SG, NL, CC, NPB, RTL, NFF, FPF and NFS measured under greenhouse conditions

		MEAN SQUARE								
Source of variation	df	PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	4.40	0.05	1.17	3.85	0.14	1.09	0.47	0.42	1.52
Genotype	19	678.90**	0.89**	270.11**	93.63**	1.74**	60.10**	11.10**	27.65**	130.00**
Residual	38	1.38	0.06	0.58	1.08	0.06	0.82	0.17	0.31	0.36
Total	59	219.60	0.32	87.40	30.98	0.61	20.25	2.91	9.12	42.45
CV (%)		11.75	7.27	27.26	18.46	24.14	21.01	11.05	13.65	16.70

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; PHT= Plant height; SG = Stem girth; NL= Number of leaves CC = Chlorophyll content; NPB = Number of primary branches per plant, RTL = Root length; NFF = Number of days to 1st flowering; FPF = Number of days to 50 % flowering and NFS = Number of days to 1st fruit set.*

Appendix 2. Mean squares of FPFS, FSP, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured under greenhouse conditions

		MEAN SQUARE								
Source of variation	df	FPFS	FSP	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	1.72	6.55	0.47	1.32	0.02	0.06	0.14	13.18	25359.00
Genotype	19	209.00**	469.18**	140.24**	45.04**	3.01**	2.04**	200.23**	2068.08**	437280.00**
Residual	78	0.49	56.07	0.33	0.88	0.18	0.10	0.18	10.99	38271.00
Total	59	67.68	187.43	45.39	15.12	1.09	0.72	64.60	673.52	166327.63
CV (%)		18.13	21.88	10.30	30.46	18.68	21.74	77.52	38.01	62.96

***Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; FPFS = Number of days to 50 % fruit set; FSP = Fruit set percentage; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of fruits per truss, NFPT = Number of fruits per truss; FPP = Number of fruits per plant; SFW =Single fruit weight and FWP = Fruit weight per plant*

Appendix 3. Means squares of YPP, LOC, PTK, FF, FL, FD, SI, FDM, and MA measured under greenhouse conditions

		MEAN SQUARE								
Source of variation	df	YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	7.66	0.00	0.11	1.03	0.04	0.03	0.00	0.00	0.00
Genotype	19	3722.33**	9.28	2.00**	1.05**	1.46**	4.23**	0.09**	0.04**	0.02**
Residual	78	4.65	0.00	0.10	0.14	0.02	0.05	0.00	0.00	0.00
Total	59	1201.97	2.99	0.71	0.46	0.49	1.39	0.03	0.01	0.01
CV (%)		66.97	48.77	17.52	15.17	15.01	23.43	18.55	26.09	23.53

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA= Malic acid content of fruit.*

Appendix 4. Mean squares of PH, TSS, TA, TSS/TA, β-CARO, LYC, ASC, GA and VA measured greenhouse conditions

		MEAN SQUARE								
Source of variation	df	pH	TSS	TA	TSS/TA	β-CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.03	0.00	0.44	0.32	0.09	8.05	0.00	0.00
Genotype	19	0.30*	4.07**	0.02**	22.63**	202.37**	125.67**	24.45**	0.02**	0.06**
Residual	78	0.00	0.03	0.00	0.30	0.25	0.18	7.67	0.001	0.01
Total	59	0.10	1.33	0.01	7.49	65.34	40.59	13.09	0.01	0.02
CV (%)		5.48	26.21	25.32	19.59	41.30	40.17	24.34	5.34	15.83

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or ripeness index; TI = Fruit taste index; β-CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit and ASC = Ascorbic acid content of fruit*

Appendix 5. Mean squares of RA, QUE, RUT, CAT, KAE, HES, MYR, GEN and AA measured under greenhouse conditions

.		Mean square								
Source of variation	df	RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.00	9.46	6.18	0.87	82.94	83.0	0.43	5.83	0.09
Genotype	19	0.04**	2828.77**	6418.92**	5636.78**	1047.25**	18404.30**	1105.10**	1564.71**	3.27**
Residual	78	0.01	10.99	24.24	5.01	64.97	207.90	4.03	9.58	0.03
Total	59	0.02	918.36	2082.93	1818.49	382.00	6063.48	358.49	510.26	1.08
CV (%)		13.71	6.87	47.42	41.01	62.79	65.12	43.60	35.64	31.03

***Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid ; MYR = Myricetin; GEN = Genestein and AA = Antioxidant activity.*

Appendix 6. Means squares of PHT, SG, NL, CC, NPB, RTL, FFF, FPF, and NFS measured under field conditions

		MEAN SQUARE								
Source of variation	df	PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	21.89	2.84	26.47	14.64	0.28	0.65	5.52	3.35	2.12
Genotype	19	65.54**	2.09**	279.69**	45.23**	1.32**	53.25**	27.68**	15.42**	58.12**
Residual	78	4.51	0.67	12.33	3.88	0.15	1.05	0.32	0.58	1.96
Total	59	24.75	1.20	98.91	17.56	0.53	17.85	9.31	5.45	20.05
CV (%)		9.40	10.00	21.61	9.70	17.76	21.60	19.83	9.15	12.25

**Significant at P < 0.01; CV = Coefficient 0f variability; PHT= Plant height; SG = Stem girth; NL= Number of leaves and RTL = Root length NFF = Number of days to 1st flowering; FPF = Number of days to 50 % flowering and NFS = Number of days to 1st fruit set.*

Appendix 7. Mean squares of FPFS, FSP, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured under field conditions

		MEAN SQUARE								
Source of variation	df	FPFS	FSP	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	2.83	15.32	0.22	1.11	0.02	0.14	0.97	0.76	2854.00
Genotype	19	80.56**	54.07**	86.26**	153.89**	2.67**	1.04**	215.73**	1279.09**	354810.14**
Residual	78	4.48	12.69	1.81	1.08	0.34	0.23	0.70	4.12	1393.00
Total	59	28.93	26.10	28.95	50.29	1.08	0.49	69.96	414.59	115255.24
CV (%)		12.21	7.66	9.14	41.89	15.85	22.20	64.08	35.60	52.05

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; FPFS = Number of days to 50 % fruit set; FSP = Fruit set percentage; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of fruits per truss, NFPT = Number of fruits per truss; FPP = Number of fruits per plant; SFW =Single fruit weight and FWP = Fruit weight per plant*

Appendix 8. Mean squares of measured traits YPP, LOC, PTK, FF, FL, FD, DI, FDM and MA measured under field conditions

		MEAN SQUARE								
Source of variation	df	YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	19.72	2.19	0.94	0.31	0.28	0.44	0.00	0.01	0.00
Genotype	19	2463.58**	7.85**	2.41**	0.55**	2.31**	3.08**	0.19**	0.01**	0.02**
Residual	78	9.71	0.84	0.37	0.09	0.10	0.10	0.00	0.00	0.00
Total	59	800.28	3.14	1.05	0.25	0.82	1.07	0.00	0.00	0.01
CV (%)		52.04	50.45	20.87	13.74	18.04	20.71	24.66	15.16	19.47

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA= Malic acid content of fruit*

Appendix 9. Mean squares of measured PH, TSS, TA, TSS/TA, B-CARO, LYC, ASC, GA and VA measured under field conditions

		MEAN SQUARE								
Source of variation	df	pH	TSS	TA	TSS/TA	β-CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.00	0.00	0.04	0.86	0.20	0.30	0.02	0.05
Genotype	19	0.05**	4.11**	0.02**	9.05**	89.09**	94.26**	14.46**	0.24**	0.66**
Residual	78	0.00	0.02	0.00	0.14	8.95	0.55	0.21	0.08	0.21
Total	119	0.02	1.34	0.01	3.01	34.49	30.72	4.80	0.13	0.35
CV (%)		2.93	29.29	19.41	17.43	23.34	36.31	23.34	16.17	40.26

**Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or ripeness index; TI = Fruit taste index; β-CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit, ASC = Ascorbic acid content of fruit, GA = Gallic acid and VA = Vanillic acid*

Appendix 10. Mean squares of RA, QUE, RUT, CAT, KAE, HES, MYR, GEN, AA measured under field conditions

		MEAN SQUARE								
Source of variation	df	RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.03	8.89	12.02	32.64	4.06	55.43	4.24	8.35	0.05
Genotype	19	0.408**	8733.82**	19677.85**	16178.73**	3125.67**	54449.66**	3093.43**	4307.14**	19.04**
Residual	78	0.13	3.41	6.35	16.14	2.03	18.37	1.26	2.04	0.07
Total	59	0.21	2815.08	6341.44	5221.60	1008.02	17548.35	997.15	1388.64	
CV (%)		35.18	100.03	97.42	77.36	129.65	136.79	94.37	70.76	59.39

***Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid ; MYR = Myricetin; GEN = Genestein and AA= Antioxidant activity*

Appendix 11. Mean squares of PHT, SG, NL, CC, NPB, RTL, NFF, FPF AND NFS measured across greenhouse and field locations

		MEAN SQUARE								
Source of variation	df	PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	16.59	1.27	8.73	7.43	0.29	1.68	4.01	2.76	3.61
Location	1	185450.69**	22.97**	2060.65**	2382.35**	0.80*	97.20**	63.08**	625.63**	126.08**
Genotype	19	495.30**	2.09**	435.70**	62.80**	2.13**	35.18**	26.43**	24.89**	138.22**
Genotype x Location	19	249.14**	0.89*	114.10**	76.06**	0.93**	78.17**	12.36**	18.18**	47.18**
Residual	78	3.06	0.40	6.78	2.70	0.11	0.91	0.29	0.46	1.13
Total	119	1679.56	0.95	109.69	44.09	0.57	19.70	6.98	12.48	31.46
CV (%)		10.21	7.46	21.48	9.23	17.64	11.90	13.11	9.02	12.79

**Significant at P < 0.05; **Significant at P < 0.01; CV = Coefficient of variability; PHT= Plant height; SG = Stem girth; NL= Number of leaves; RTL = Root length; NFF = Number of days to 1st flowering; FPF = Number of days to 50 % flowering and NFS = Number of days to 1st fruit set.*

Appendix 12: Mean squares of FPFS, FPS, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured across greenhouse and field locations

		MEAN SQUARE								
Source of variation	df	FPFS	FSP	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	4.23	14.17	0.10	2.21	0.01	0.17	0.85	10.12	6144.00
Location	1	76.80**	94.10*	5.04*	182.43**	7.86**	0.97*	217.16**	3697.22**	88605.00*
Genotype	19	228.13**	300.68**	207.64**	155.47**	4.17**	2.66**	392.84**	3043.86**	709030.00**
Genotype x Location	19	61.43**	222.57**	18.86**	43.47**	1.52**	0.41**	23.12**	303.31**	83061.00**
Residual	78	2.43	33.69	1.06	0.96	0.25	0.16	0.44	7.46	19889.00
Total	119	48.	106.66	36.90	33.96	1.14	0.61	68.54	570.55	140352.88
CV (%)		14.14	12.58	9.25	34.29	12.92	20.02	67.99	35.44	54.26

**Significant at P < 0.05; **Significant at P < 0.01; ns = Not significant at 0.05; CV = Coefficient of variability; FPFS = Number of days to 50 percent fruit set; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of flowers per truss; FPP = Number of fruits per plant; Single fruit weight and Fruit weight per plant.*

Appendix 13: Mean squares of YPP, LOC, PTK, FF, FL, FD, SI, FDM and MA measured across greenhouse and field locations.

		MEAN SQUARE								
Source of variation	df	YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	25.10	1.10	0.63	1.24	0.19	0.26	0.00	0.01	0.00
Location	1	182.18**	1.67^{ns}	3.94**	16.53**	1.36**	0.93**	0.19**	0.20**	0.19**
Genotype	19	5707.92**	16.52**	2.61**	0.99**	3.04**	6.53**	0.22**	0.02**	0.02**
Genotype x Location	19	477.98**	0.62^{ns}	1.80**	0.61**	0.73**	0.78**	0.07**	0.02**	0.02**
Residual	78	7.05	0.44	0.24	0.11	0.06	0.08	0.00	0.00	0.00
Total	119	994.24	3.06	0.91	0.49	0.66	1.23	0.05	0.01	0.01
CV (%)		57.30	48.77	14.74	11.52	14.96	20.94	19.39	15.91	16.31

***Significant at P < 0.01; ns = Not significant at P < 0.05; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA= Malic acid content of fruit.*

Appendix 14. Mean squares of PH, TSS, TA, TSS/TA, β-CARO, LYC, ASC, GA and VA measured across locations

		MEAN SQUARE								
Source of variation	df	pH	TSS	TA	TSS/TA	β-CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.02	0.00	0.26	0.23	0.03	4.85	0.01	0.03
Location	1	0.04**	5.84**	0.21**	513.72**	360.02**	3.21**	161.58**	0.80**	2.17**
Genotype	19	1.94**	5.31**	0.02**	20.20**	115.51**	118.20**	19.46**	0.14**	0.38**
Genotype x Location	19	1.01**	2.87**	0.02**	11.42**	175.95**	101.74**	19.55**	0.23**	0.34**
Residual	78	0.02	0.03	0.00	0.22	4.51	0.36	3.93	0.04	0.10
Total	119	0.05	1.37	0.01	9.52	52.52	35.38	10.23	0.07	0.20
CV (%)		4.28	22.29	16.88	15.38	20.30	27.94	17.05	9.04	15.83

**Significant at P < 0.05; **Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or flavour indicator; TI = Fruit taste index; β-CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit; ASC = Ascorbic acid content of fruit; GA= Gallic acid and VA = Vanilic acid*

Appendix 15. Mean squares of RA, RUT, CAT, KAE, HES, MYR, GEN and AA measured across greenhouse and field locations

		MEAN SQUARE								
Source of variation	df	RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.02	0.18	16.24	20.38	29.39	106.60	2.01	7.49	0.10
Location	1	0.23**	3379.34**	6231.98**	3481.66**	710.07**	14247.40**	2998.80**	3326.68**	23.09**
Genotype	19	1.28**	4968.60**	11465.53**	9898.41**	1729.73**	32743.60**	1709.91**	2549.03**	9.96**
Genotype x Location	19	0.20**	6593.99**	1463.10**	11917.09**	2443.45**	40110.40**	2488.61**	3322.81**	12.35**
Residual	78	0.07	7.48	14.95	10.64	34.12	111.00	2.65	5.83	0.05
Total	119	0.12	1879.43	4229.16	3519.72	695.13	11826	697.32	969.43	3.79
CV (%)		21.24	48.57	48.39	40.49	62.13	67.53	43.26	35.05	33.89

**Significant at P < 0.05; **Significant at P < 0.01; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid; MYR = Myricetin; GEN = Genestein and AA = Antioxidant activity*