GENETIC VARIABILITY AND ASSOCIATION OF CHARACTERS IN TOMATO (*Lycopersicon esculentum* Mill.) GENOTYPES AT HUMERA, NORTHERN ETHIOPIA

M.Sc. Thesis

BY

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October, 2011

Jimma University

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As thesis research advisors we hereby certify that we have read and evaluated the thesis prepared under our direction by **Shushay Chernet**, entitled "**Genetic Variability and Association of Characters in Tomato (*Lycopersicon esculentum* Mill.) Genotypes at Humera, Northern Ethiopia**" We recommend that it be accepted as fulfilling the thesis requirements.

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DEDICATION

I dedicate this thesis manuscript to my family

STATEMENT OF THE AUTHOR

I declare that this thesis is my original work and that all sources of materials used for writing it have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for M.Sc. degree at Jimma University, College of Agriculture and Veterinary Medicine and put at the University Library to be made available to borrowers under the rules of the library. I declare that this thesis is not submitted by any other institution anywhere for the award of academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

The author was born on June 6, 1983 in Axum, Tigray region. He attended primary, junior and secondary school education at Axum Elementary School, Abreha -Weatsbha Elementary and Junior School and Axum Comprehensive Secondary High School, respectively. After the completion of his high school education, he joined Haramaya University in 2003 and graduated with B.Sc. Degree in Plant Sciences in 2006. After graduation, he was employed by Bureau of Agriculture and Rural Development of Tigray Regional State at Wukro- Kilte awla'elo wereda as crop protection expert. After three months of work he left the office and was employed by Tigray Agricultural Research Institute (TARI), Humera Agricultural Research Center (HuARC) as junior researcher in crop improvement case team and served from February 2007 until he joined the School of Graduate Studies at Jimma University in September 2009 to pursue a study leading to the Degree of Master of science in Horticulture.

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LIST OF ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of variance
AVRDC	Asian Vegetable Research and Development Center
CA	Cluster Analysis
CSA	Central Statistics Agency
DAP	Diammonium phosphate
EARO	Ethiopian Agricultural Research Organization
EIAR	Ethiopian Institute of Agricultural Research
EU	European Union
FAOSTAT	Food and Agriculture Organization Statistics
GA	Genetic advance
GAM	Genetic advance as percent of mean
GCV	Genotypic Coefficient of Variation
GLM	General linear model
h^2	Heritability in broad sense
IPGRI	International Plant Genetic Resources Institute
LSD	Least significant differnce
MARC	Melkasa Agricultural Research Center
MoARD	Ministry of Agriculture and Rural Development
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
SAS	Statistical Analysis System
TSS	Total Soluble Solids

GENETIC VARIABILITY AND ASSOCIATION OF CHARACTERS IN TOMATO (*Lycopersicon esculentum* Mill.) GENOTYPES AT HUMERA, NORTHERN ETHIOPIA

ABSTRACT

Thirty six tomato genotypes obtained from Melkassa Agricultural Research Center were tested at Humera, Northern Ethiopia, in 2010/11. A 6 x6 simple lattice design was used to estimate the extent of genetic variability, association among characters and genetic divergence among the genotypes thereby clustering them into divergent groups. Data on 24 quantitative traits were recorded and subjected to analysis. Analysis of variance for 24 quantitative traits revealed that there was highly significant difference (P<0.01) among the thirty six genotypes for all the characters studied. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)(> 20 %) were recorded for number of matured fruits per plant, fruit set percentage, total fruit yield per hectare, number of fruit clusters, weight of fruits per plant, number of seeds per fruit, average single fruit weight, number of fruits per fruit cluster, number of flowers per plant, number of secondary branches per plant, locule number, pericarp thickness, days to maturity, days to 50 percent fruiting and shape index. All the traits except number of primary branches per plant (47.36%) had very high heritability (> 80 %) indicating these traits were less influenced by environmental factors and selection for them is fairly easy. High GCV along with high heritability and genetic advance was obtained for number of matured fruits per plant, fruit set percentage, total yield per hectare, number of seeds per fruit, number of fruit clusters per plant, average weight of fruits per plant and average single fruit weight per plant indicating that the characters can be improved through selection. Fruit yield per hectare had positive and highly significant phenotypic and genotypic correlation with average weight of fruits per plant, number of matured fruits per plant, fruit set percentage, number of fruit clusters per plant, number of pickings and number of fruits per fruit cluster while it showed negative and highly significant genotypic and phenotypic correlation with days to 50% fruiting, days to maturity and days to 50% flowering. Estimates of genotypic direct and indirect effects of various characters on fruit yield (tonnes/ha) showed that number of matured fruits per plant and average weight of fruits per plant had the highest positive direct contribution to fruit yield indicating that selection based on these characters will improve fruit yield. However, fruit set percentage, fruit polar diameter, days to 50 % fruiting and number of fruits per cluster exerted negative direct effect on fruit yield per hectare. Cluster analysis revealed that the 36 genotypes were grouped in to 6 distinct clusters. Distance between clusters showed very highly significant difference for all traits considered. The maximum and minimum distances were recorded between clusters IV and V (1805.00) and cluster II and III (81.94). This indicated the existence of a possibility to improve genotypes through hybridization from any pair of clusters and subsequent selection can be made from the segregant generations. Principal component analysis showed that the first six principal components explained about 83.03% of the total variation. It can be suggested that more number of genotypes in multiple location and season may be tested with due attention given to fruit yield, disease and pest resistant, fruit size and shelf life characteristics.

1. INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) is one of the most important vegetables worldwide (Naika *et al*., 2005). It belongs to the genus *Lycopersicon*, family *Solanaceae* (also known as the nightshade family), subfamily *Solanoidae* and tribe *Solaneae* (Taylor, 1986). All related wild species of tomato are native to the Andean region that includes parts of Chile, Ecuador, Bolivia and Peru (Sims, 1980). The most likely ancestor is the wild *L. esculentum* var. *cerasiforme* (cherry tomato), which is indigenous throughout the tropical America. Tomatoes were domesticated in America; however, the original site of domestication and the early events of domestication are largely obscure (Peralta and Spooner, 2007). Although definite proof for the time and place of domestication is lacking, Mexico is presumed to be the most probable region of domestication, with Peru as the centre of diversity for wild relatives (Larry and Joanne, 2007). Tomato is a diploid species with 2n = 2x = 24 chromosomes.

Tomato requires warm and dry climate (MoARD, 2009). However, it is adapted to a wide range of climatic conditions from temperate to hot and humid tropics. The plants can survive a range of temperatures, grow best under temperatures of 20–27°C, but the plant tissues are damaged below 10 °C and above 38 °C (Naika *et al*., 2005). Under the low and high temperature conditions it end up with poor fruit setting. Tomatoes prefer a well-drained soil because they are sensitive to water-logging. Optimum soil pH is 6.0-7.0 (Hanson *et al*., 2001). Tomato should be cultivated below 2000 m.a.s.l (MoARD, 2009).

Tomato is the third most important vegetable crops in the world next to potato and sweet potato (FAO, 2005). In 2009 the world's total cultivated area under tomato was 4.98 million ha, with a production quantity of 141.14 million tons (FAOSTAT, 2011). China is the world's leading tomato producer with a production of 34.12 million tons followed by the United States and Turkey (FAOSTAT, 2011). China is not only the world's largest fresh tomato producer, but also the world's largest tomato paste producer, followed by the EU and the United States. In 2008, the export quantity reached 818,512 tonnes, a sharp increase from 106,667 tons in the previous year (Zhang *et al*., 2010).

Tomato is the most widely grown vegetable in the world being recognized as a reach source of vitamins and minerals. Tomatoes are extremely beneficial to human health for they are rich in minerals, vitamins, essential amino acids, sugars and dietary fibers. Tomato fruits are consumed fresh in salads or cooked in sauces, soup and meat or fish dishes. They can be processed into purées, juices and ketchup (Naika *et al*., 2005). It is also among the most important vegetable crops in Ethiopia. The total production of this crop in the country has shown a marked increase (Lemma *et al*., 1992) since it became the most profitable crop providing a higher income to small scale farmers compared to other vegetable crops. In 2008, Ethiopia s' total cultivated area under tomato was 5,342 ha with a production of 41,815 tonnes (FAOSTAT, 2011). In Tigray, for 2008/09 cropping season tomato production was 34,607 quintals, produced from 433.52 hectares of land (CSA, 2009). The national average yield of tomato is below the world average. Average yield for Ethiopia is 7.83 tonnes/ha (CSA, 2009) which is very low, as compared to the world average yield of 28.39 tonnes/ha (FAOSTAT, 2011).

According to Lemma (2002), the major production constraints of tomato production in Ethiopia are shortage of varieties and recommended package of information, unknown sources and poor quality seeds, poor irrigation system, lack of information on soil fertility, disease and insect pests, high post harvest loses, lack of awareness of existing improved technologies and poor marketing system.

So far a number of research activities have been conducted by different research institutions and researchers in Ethiopia. Since 1969, about 300 tomato lines/cultivars of both short and tall set open-pollinated genotypes and hybrids have been introduced by Melkassa Agricultural Research Centre (MARC) from international seed companies, and from Asian Vegetable Research and Development Center (AVRDC). The lines have been tested at different research centers to identify lines having high fruit yield and good quality, resistance/ tolerance to diseases as well as insect pests (Lemma, 2002). Similarly from 1990 to 1992, 90 fresh and processing tomato genotypes were tested at Melkassa and superior genotypes were identified. It was because of these efforts that many varieties have been released. Similarly, Jiregna

(2008) studied genetic variability of tomato genotypes for fruit yield and yield related traits at Bako condition.

The western zone of Tigray (Humera) is one of the potential areas for tomato production. The crop is produced by 655 small holder farmers in the zone (CSA, 2009); however, no any varietal evaluation trials have been conducted so far under Humera condition. Hence, evaluation of different genotypes or varieties of tomato is crucial for effective selection. Effectiveness of selection depends on the amount of variability present in the genetic material for yield and yield related characters. Hence, the estimation of variability is of prime importance. The majority of traits including most of those important to crop productivity are controlled by the combined effects of a number of genes that influence the trait, each of which has a similar small influence (Pike, 1986).

Knowledge on the extent and pattern of genetic variability present in a population is essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection. Besides, knowledge of the naturally occurring diversity in a population helps identify diverse groups of genotypes that can be useful for the breeding program. To have this type of knowledge, research on diversity is crucial. Therefore, this study was carried out with the following objectives:

1. To estimate the extent of phenotypic and genotypic variability, heritability and the genetic advance expected under selection of tomato genotypes.
2. To estimate the extent of genotypic and phenotypic association between pairs of characters in the crop and compare the direct and indirect effects of the characters on fruit yield
3. To cluster the test tomato genotypes into different homogenous groups and estimate the genetic distance between the clusters

2. LITERATURE REVIEW

2.1. Botany, Origin and Ecological Adaptation of Tomato

Tomatoes belong to the genus *Lycopersicon* and family Solanaceae. The genus consists of 14 closely related species or subspecies including the domesticated tomato (Peralta *et al*., 2005; Spooner *et al*., 2005). The genus *Lycopersicon* includes a relatively small collection of species: the cultivated tomato *L. esculentum* Mill. and several closely related wild species, namely, *L. esculentum* var. *ceraciforme*, *L. pimpinellifolium* (Jusl.), *L. cheesmanni*, *L. Parviflorum*, *L. chmielewski*, *L. hirustum* Humb., *L. chilense* Dun. and *L. peruvianum* (L.) Mill. (Taylor, 1986).

All members of the genus are closely related diploids (2n =24) (Moyle, 2008) and have perfect flowers (hermaphroditic). Cultivated tomato is self fertile, whereas all other members of the genus are self-incompatible (Simpson, 1986), with the exception of *L. pimpinellifolium*, which undergoes various degrees of self-fertilization. The major feature of domestication, aside from increased fruit size, is the gradual shortening of the flower style length from being very long that predisposes the crop to out crossing, to very short that inhibits out crossing (Cox, 2000).

Tomato originated from the Andean region now encompassed by part of Chile, Boliva, Ecuador, Colombia and Peru (Yulling and Limdhout, 2007). Tomatoes were domesticated in America; however, the original site of domestication and the early events of domestication are largely obscure (Peralta and Spooner, 2007). Two hypotheses have been advanced for the original place of tomato domestication, one Peruvian and the other Mexican. Although definite proof for the time and place of domestication is lacking, Mexico is presumed to be the most probable region of domestication, with Peru as the centre of diversity for wild relatives (Larry and Joanne, 2007). *Lycopersicum esculentum* var *cerasiforme* is thought to be the ancestor of cultivated tomato, based on its wide presence in Central America and the presence of a shorten style length in the flower (Cox, 2000). However, recent genetic investigations have shown that the plants known as ‘cerasiforme’ are a mixture of wild and cultivated

tomatoes rather than being 'ancestral' to the cultivated tomatoes (Nesbitt and Tanksley, 2002).

The cultivated tomato was brought to Europe by the Spanish conquistadors in the sixteenth century and later introduced from Europe to southern and eastern Asia, Africa and the Middle East (Naika *et al*., 2005).There is no definite time recorded regarding the introduction of cultivated tomato to Ethiopia. However, cherry type has been growing for long around big cities and in small gardens (Lemma, 2002).

Tomato is adapted to a wide range of climatic conditions from temperate to hot and humid tropical. The optimum temperature for most varieties lies between 21 and 24 °C (Naika *et al*., 2005). Studies in different research centers/ testing sites in Ethiopia such as Debre Zeit, Werer, Jimma, Alemaya, Awasa, Gambella, Zway, Bako and the Rift Valley region located in various agro ecological zones as well as research document on horticultural genetic resource in the country indicated that tomato is grown in limited land but widely distributed in all regions of the country (Lemma, 2002).

2.2. Genotypic and Phenotypic Variations

The selection of plants from a population is almost always based on their appearance, i.e., phenotypic. Phenotype variation has both heritable and non-heritable components. The value of progeny obtained from a selected plant, therefore, would largely depend upon the relative contributions by the heritable and non-heritable components to its phenotype (Singh, 1983).

Variation is the occurrence of differences among individuals due to the differences in their genetic composition and/ or the environment in which they are growing (Allard, 1960). Progress in plant breeding depends on variability because superior genotypes obviously cannot be selected from homogenous populations, but homogeneity is desirable in the final product. Success in improving adaptation requires that the population under selection be genetically variable (Allard and Hansche, 1964). In initiating a breeding programme with any crop, information on the nature and magnitude of genetic variation within the species for traits

of agronomic importance greatly helps in formulating a sound crop breeding program and in efforts to breed better varieties (Dudley and Moll, 1969).

Phenotypic variability is the observable variation present in a character in a population; it includes both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions. Genotypic variation, on the other hand is the component of variation, which is due to genotypic differences among individuals within a population, and is the main concern of plant breeding (Singh, 2001).

The amount of variation present in any population is measured and expressed in terms of variance (Falconer and Mackay, 1996). Estimates of genotypic and phenotypic coefficients of variations are used to study the variability that exists in a given population (Kalloo, 1988). According to Deshmukh *et al.* (1986) PCV and GCV values > 20% regarded as high, PCV and GCV values between 10 and 20% medium, PCV and GCV values < 10% low.

So far a number of studies have been made on genetic variability of tomato. Mohanty (2003) reported high PCV and GCV for average fruit weight, number of branches and number of fruits per plant. Golani *et al.* (2007) also reported high PCV and GCV for number of locules per fruit, ten fruit weight, fruit yield and plant height while the same was medium for number of branches per plant, fruit length and fruit diameter and it was low for total soluble solids (TSS). Similarly, Pradeepkumar *et al*. (2001) obtained high GCV and PCV for plant height, number of fruits per plant, pericarp thickness, locule number, total soluble solids (TSS), single fruit weight, yield per plant and number of harvest. Moreover, Shashikanth *et al*. (2010) reported high GCV and PCV for number of fruits per plant, average fruit weight per plant and fruit yield per plot while low GCV and PCV for days to first and 50 % flowering and days to first fruit set.

2.3. Heritability

The proportion of total variation caused by genotype is called heritability. Theoretically heritability can range from one where all variation is due to genetic, to zero where all the

variation results from the environment. Actual heritability value will fall somewhere between these two extreme values. It is very difficult to determine the presence, amount or types of genetic variability if phenotypic expressions are strongly influenced by the environment (Welsh, 1990). If heritability is high it means that the genotype play more important role than the environment in determining the phenotype. Normally heritability values for quantitative characters are low due to their sensitivity to environment but also with the nature of the test population (Briggs and Knowels, 1987).

It is obvious that difference due to environment may tend to obscure genotypic variations. The greater the proportion of the total variability that is due to the environment the more difficult it will be to select for inherited differences. On the other hand, if environmental variability is small in relation to heritable differences, selection will be efficient because the characters to be selected will be transmitted to its progeny (Briggs and Knowles, 1987). If genetic variation in a progeny is large in relation to the environmental variation the heritability will be high or if genetic variation is small in relation to the environmental variation, then heritability will be low (Mittal and Sethi, 2004).

Heritability percentage estimate from total genetic variance without taking into a consideration the components of genetic variance is referred to as heritability in broad sense, because it estimates heritability on the basis of all genetic effects. Heritability expressed as percentage of additive component of variance is referred as narrow sense heritability (Mittal and Sethi, 2004). Heritability indicates the effectiveness with which selection of phenotypes can be based on phenotypic performance. If heritability were 100% then phenotypic performance would be perfect indication of genotypic value (Johnson *et al.*, 1955). Heritability enables the plant breeder to recognize the genetic difference among strains and variance indicates the potential for the improvement of a population (Mittal and Sethi, 2004).

Ghosh *et al*. (2010), reported high heritability(> 60 %) in tomato genotypes for days to first flowering, plant height, number of branches per plant, flowers per plant, fruits per cluster, fruit clusters per plant, fruits per plant, fruit length, fruit diameter, individual fruit weight and fruit yield per plant. While it was medium for number of flowers per cluster (47.83%).

Similarly, Hidayatullah *et al.* (2008) obtained high heritability for days to first harvest, number of fruits per plant, single fruit weight and number of locules indicated less influence of environments within specific year that could be exploited through simple selection from this material to improve yield. Pradeepkumar *et al.* (2001) also reported higher heritability (>80%) for plant height, days to maturity, number of fruits per plant, pericarp thickness, locule number, total soluble solids (TSS), average fruit weight and fruit yield per plant.

2.4. Genetic Advance

Genetic advance measures the expected genetic progress that would result from selecting the best performing genotypes for a character being evaluated. Genetic advance under selection indicates measure of the difference between the mean genotypic values of the selected population over the mean genotypic value of the original population for a given character (Allard, 1960). Genetic advance is the improvement over the base population that can potentially be made from selection for a given character. It is a function of the heritability of the trait, the amount of phenotypic variation and the selection differential that the breeder uses. The selection differential is defined as "the average phenotypic value of the selected individuals, expressed as a deviation from the population mean" (Kalloo, 1988). Heritability value in itself provides no indication of the amount of genetic progress that would result from selecting the best individuals. High heritability value could be obtained with genotypes having small or large genetic variance but genetic progress would be larger with larger genotypic variance (Johnson *et al*., 1955; Allard, 1960).

Recently, Shashikanth *et al.* (2010) reported high heritability in broad sense and genetic advance as percent of mean in tomato genotypes. The characters which had high genetic advance as percent of mean were plant height (28.45), number of branches per plant (39.62), number of fruits per plant (62.68), average fruit weight per plant (40.21), number of flowers per cluster (52.48), number of clusters per plant (24.96), fruit shape index (34.74), pericarp thickness (26.19) and TSS (28.89). Mehta and Asanti (2008) obtained very high value of heritability along with high magnitude of genetic advance as percent of mean for characters like fruit yield per hectare, plant height, number of clusters per plant and TSS. Similarly,

characters like number of locules per fruit, number of branches per plant, weight of fruits per plant exhibited high estimate of heritability and high genetic advance as percent of mean. According to Haydar *et al. (*2007), genetic advance as percentage of mean was maximum for fruit weight followed by number of flowers in three cluster/plant and number of fruits in three cluster/plant indicating the presence of additive gene effects.

2.5. Inter-relationship between Characters

2.5.1. Correlation coefficients

The degree of a linear association between two characters is measured by the correlation coefficient. Correlation, therefore, is helpful in determining the component characters of a complex trait, like yield. Such studies are useful in disclosing the magnitude and direction of these relationships between the different characters and yield as well as among the characters themselves (Falconer and Mackay, 1996).

Characters of crop plants are generally correlated. There are three types of correlations; phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlation. The phenotypic correlation measures the extent to which the two observed characters are linearly related. Genetic correlation is the association of breeding values (additive genetic variance) of the two characters. The genetic causes of correlation are mainly pleiotropic effects of genes affecting different characters. Pleiotropy is the property of a gene whereby it affects two or more characters, so that if the gene is segregating it causes simultaneous variation in the two characters it affects (Falconer and Mackay, 1996). In early segregating generations, genetic correlation determines the degree of association between characters and how they may enhance selection. Depending on the sign, genetic correlations between two characters can either facilitate or impede selection progress. High values of genetic correlations may indicate considerable genetic association between the characters tested.

Ghosh *et al.* (2010) reported significant positive genetic and phenotypic correlation in tomato for number of fruits per plant and fruit yield per plant, fruit length and individual fruit weight, fruit diameter and individual fruit weight, number of flowers per plant and number of fruits per plant, flowers per plant and fruit yield per plant. On the contrary he obtained significant negative correlation for number of flowers per cluster and fruit diameter, flowers per cluster and individual fruit weight and flowers per plant with individual fruit weight. Agong (2001) obtained negative genotypic and phenotypic association for fresh fruit weight and total soluble solids, single fruit weight and number of fruits per plant and number of fruits per plant and fruit width. He also reported positive association of fresh fruit weight with fruit width, fresh fruit weight and equatorial length.

According to Haydar *et al*. (2007) fruit weight per plant had significant correlation with number of flowers in three cluster/plant and number of fruits in three clusters/ plant in tomato. Similarly, Hidayatullah *et al*. (2008) indicated number of pickings had positive correlation with fruit weight per plant and 1000 seed weight and number of fruits per plant had positive association with fruit weight per plant and seeds per fruit at both genotypic and phenotypic level in tomato.

2.5.2. Path coefficient

Correlation between yield and its components simply measures mutual relationships without presumption of causation (Puri *et al.,* 1982) but the result of path coefficient analysis for fruit yield and yield components can describe genotypic correlations to direct and indirect effects. Path coefficient analysis is a very important statistical tool that indicates which variables (causes) exert influence on other variables (effects), while recognizing the impacts of multicolinearity (Akanda and Mundt, 1996). Path coefficient analysis specifies the cause and measures the relative importance of the characters, while correlation measures only mutual association without considering causation (Dewey and Lu, 1959).

In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959; Samonte *et al*.,

1998). In any breeding program of complex characters such as yield for which direct selection is not effective, it becomes essential to measure the contribution of each of the component variables to the observed correlation and to partition the correlation into components of direct and indirect effect (Giriraji and Vijayakumar, 1974).

Tiwari and Upadhyay (2011) obtained positive direct effect of characters like number of locules per fruit (0.846), fruit weight (0.546) and days from fruit setting to green mature stage (0.264) on fruit yield per plant in tomato genotypes. Fruit width (-0.874) and plant height (-0.706) showed negative direct effect on fruit yield per plant. However, fruit width exhibited positive indirect effect on fruit yield via number of locules (0.329), days to 50% flowering (0.318), fruit weight (0.157), days from fruit setting to mature green stage (0.136), days to first flowering (0.041) and number of calyx per fruit (0.041) and results in a positive coorelation.

Ghosh *et al.* (2010) reported that the number of fruit per plant exhibited highest positive direct effect on fruit yield per plant followed by number of flowers per plant while the characters which had highest negative direct effect on fruit yield per plant were number of flowers per cluster, fruit clusters per plant and fruit diameter. Days to first flowering, plant height, number of branches per plant and fruit length also showed negative direct effect on fruit yield per plant. He also reported highest indirect effect of fruit clusters on fruit yield per plant via number of fruits per plant.

According to Mehta and Asati (2008) plant height, weight of fruits per plant, days to first fruiting and days to 50% fruiting had the highest positive direct effect on fruit yield whereas number of branches per plant, TSS and days to 50 % flowering had the highest direct negative effect. Similarly Hidayatullah *et al.* (2008) found that days to first harvest, number of pickings, fruits per plant, fruit diameter, pericarp thickness and number of locules had positive direct effect on fruit weight per plant while plant height, fruit length, TSS and number of seeds per fruit showed negative direct effect on fruit weight.

2.6. Genetic Divergence and Cluster Analysis

Genetic divergence is the statistical distance between the genotypes. The use of D^2 statistic (Mahalanobis, 1936) is one of the most important biometrical techniques for estimating genetic divergences present in a population. It is determined by using cluster analysis, which assigns genotypes into different groups (Singh and Chaudhary, 1999). Cluster analysis is a process of identification and categorization of subsets of objects that are more often than not, continuously distributed or it refers to "a group of multivariate techniques whose primary purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptions are mathematically gathered into the same cluster". The resulting clusters of individuals should then exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. Thus, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart (Hair *et al.*, 1995).

Crossing of genotypes belonging to the same cluster would not be expected to yield desirable recombinants. Consequently, a crossing programme might be formulated in such a way that parents belong to different clusters. Information on the extent of genetic diversity amongst breeding materials is very important in the crosses between groups with maximum genetic divergence so that they would be more responsive for improvement since they are likely to produce desirable recombination and segregation in their progenies after hybridization (Norden, 1980; Reddy, 1988). The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining higher among of heterotic expression of F_1's and broad spectrum of variability in segregating populations (Norden, 1980; Rao *et al.*, 1981).

Another important aspect in cluster analysis is determining the optimal number of clusters or number of acceptable clusters. In essence, this involves deciding where to "cut" a dendrogram to find the true or natural groups. An "acceptable cluster" is defined as "a group of two or more genotypes with and within-cluster genetic distance less than the overall mean genetic distance and between cluster distances greater than their within cluster distance of the two clusters involved" (Mohammadi *et al.*, 2003).

Yashavantakumar *et al.* (2009) clustered 70 tomato genotypes in to 7 clusters based on D^2 distance. Similarly, Shashikanth *et al*. (2010) clustered 30 tomato genotypes in to 10 clusters using Mahlanobis D^2 distance. Moreover, Sekhar *et al.* (2008) grouped ten hybrids of tomato in to three clusters using Mahlanobis D^2 statistics.

2.7. Principal Component Analysis

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). PCA can be used to drive a two dimensional scatter plot of individuals, such that the geometrical distance among individuals in the plot reflect the genetic distances among them with minimal distortion. Aggregates of individuals in such a plot will reveal sets of genetically similar individuals (Warburton and Crossa, 2000).

PCA will allow visualization of the differences among the individuals and identify possible groups. The reduction is achieved by linear transformation of the original variables into a new set of uncorrelated variables known as principal components (PCs). The first step in PCA is to calculate eigenvalues, which define the amount of total variation that is displayed on the PC axes. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on (Jollife, 1986).

Agong *et al.* (2000) reported genetic variability of Kenyan tomato germplasm based on the first three principal components sufficiently explained more than 70 % of the phenotypic variation in the germplasm.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted at Humera Agricultural Research Center experimental site during 2010/11 cropping season under irrigation condition. Humera is located 600 km west of Mekelle and 960 km north of Addis Ababa, at an altitude of 604 metres a.s.l and at 14^{o} 06' N latitudes and 38^{o} 31' E longitudes. The dominant soil type is chromic vertisol black in color characterized with very deep (>150 cm) clay texture. Agro-ecologically the Western lowland of Tigray (Humera) is described as hot to warm semiarid plain sub agro-ecology (SA1-1). The maximum temperature varies from 42 ^{o}C in April to 33 ^{o}C in May while minimum temperature varies from 22.2 ^{o}C in July to 17.5 ^{o}C in August. Average rainfall varies from 400-650mm per year, which lasts from June to September (EARO, 2002).

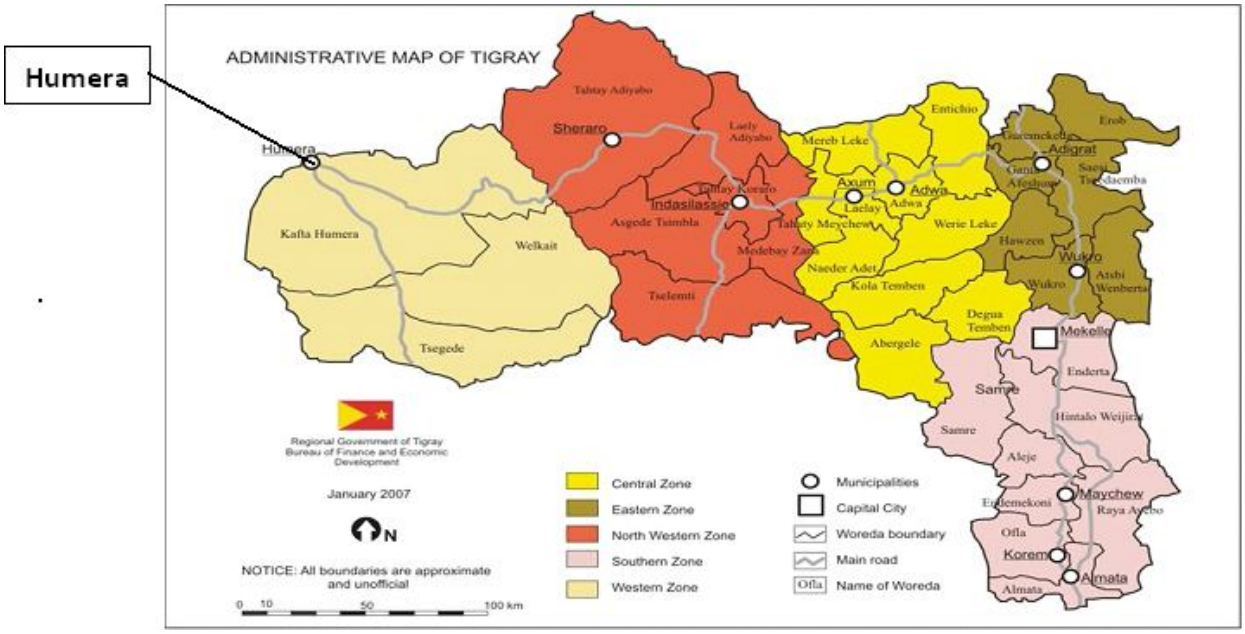

Figure 1. Map of Tigray Regional State showing experimental location

Source: Livingstone *et al.*, 2006

3.2. Experimental Materials

A total of 36 tomato genotypes obtained from Melkassa Agricultural Research Center (MARC) were tested for their genetic variability. Of the 36 testing materials 13 were released varieties. Detail information of the genotypes is presented in Table 1.

Table 1. List of tomato genotypes obtained from MARC

No.	Pedigree	Year of introduction/release	Source	Growth habit	Type	Remark
1	CLN-2498 A	2004	AVRDC	Determinate	Fresh Market	
2	CLN-2037 E	2004	AVRDC	Indeterminate	Fresh Market	
3	CLN-2037 H	2004	AVRDC	Indeterminate	Fresh Market	
4	CLN-5915-206-D4-2-2-0	2004	AVRDC	Indeterminate	Fresh Market	
5	CLN-2037 C	2004	AVRDC	Indeterminate	Fresh Market	
6	CLN-2037 I	2004	AVRDC	Indeterminate	Fresh Market	
7	CLN-1314 G	2004	AVRDC	Determinate	High beta carotene	
8	CLN-2070 A	2004	AVRDC	Indeterminate	High beta carotene	
9	CLN-2366 A	2004	AVRDC	Indeterminate	High beta carotene	
10	CLN-2366 B	2004	AVRDC	Indeterminate	High beta carotene	
11	CLN-2366 C	2004	AVRDC	Indeterminate	High beta carotene	
12	CLN-2037 A	2002	AVRDC	Indeterminate	High beta carotene	
13	CLN-1621 F	1998	AVRDC	Determinate	Cherry Tomato	
14	CLN-5915-93-D4	1998	AVRDC	Determinate	Fresh Market	
15	CLN-5915-206-D4-2-5-0	NA	AVRDC	Indeterminate	Fresh Market	
16	ARP-Tomato No.367-2	NA	AVRDC	Determinate	Fresh Market	
17	Beaf steak	NA	NA	Determinate	Fresh Market	
18	Tomato1365/95	NA	Hazera Seed Company	Determinate	Fresh Market	
19	Tomato1358/95	NA	Hazera Seed Company	Indeterminate	Fresh Market	
20	Supper Roma VF	NA	NA	Determinate	Processing	
21	PT-4719 B	NA	AVRDC	Determinate	Processing	
22	Cathrine	NA	Hazera Seed Company	Indeterminate	Fresh Market	
23	Melkashola	1998	Italy	Semi-determinate	Processing	Released
24	Melkasalsa	1998	Italy	Determinate	Processing	Released
25	Chali	2007	Italy	Determinate	Processing	Released
26	Miya	2007	Italy	Semi-determinate	Fresh Market	Released
27	Roma VF	1992	France	Determinate	Processing	Released
28	Marglobe	1994	USA	determinate	Fresh Market	Released
29	Eshet	2005	Italy	Determinate	Fresh Market	Released
30	Bishola	2005	France	Determinate	Fresh Market	Released
31	Metadel	2005	Guadaloupe	Semi-determinate	Fresh Market	Released
32	Fetan	2005	Italy	Determinate	Fresh Market	Released
33	H-1350	NA	NA	Determinate	Fresh Market	Released
34	Electra	NA	Hazera Seed Company	Indeterminate	Fresh Market	
35	Fire ball	1992	Italy	Determinate	Processing	Released
36	Cochoro	2007	NA	Determinate	NA	Released

NA= information not available

3.3. Experimental Design and Procedures

The trial was laid out in 6x6 simple lattice design with two replications at Humera Agricultural Research Center main research site during 2010/11 cropping season under irrigation condition. Seeds of each tomato genotypes were sown in seed bed of 1.05 m^2 (7 rows, 0.15 m spacing between rows, 1 meter row length) on August 4/2010 to raise seedlings. Land preparation of main field was done after seed sowing. Seedlings were transplanted to main field 27 days after seed sowing i.e. when the seedlings attained 15 cm height. Each genotype was planted in the main field in a plot size of 20.4 m^2 (4 rows, 5.1m row length and the spacing between and within plants was 100 x 30 cm). The middle two rows were used for data collection leaving the two rows as borders. 200 kg/ha DAP and 100 kg/ha Urea were applied at time of sowing and two weeks after transplanting as of recommended for the crop (Lemma, 2002). Irrigation was applied in furrows. The field was irrigated at the interval of four days until start of fruiting while it was applied in three days interval after fruit set started.

3.4. Data Collected

The following data were collected from the central two rows both per plot and plant basis, leaving the two rows as borders. The data's were collected according to the procedures given by IPGRI descriptors list for tomato,

3.4.1. Data collected per plot basis

1. **Days to 50% flowering**: number of days from transplanting to the day on which 50 percent of plants start flowering within a plot.
2. **Days to 50% fruiting**: number of days from transplanting to the day on which 50 percent of plants start fruit setting within the plot.
3. **Days to maturity**: numbers of days from transplanting to the day on which 50 % of plants have at least one fruit ripened within plots.
4. **Number of Pickings**: number of pickings from initial to the final picking.

5. **Marketable and unmarketable fruit yield per hectare (tonnes):** fruits with cracks, damaged by insect, disease, birds, small size fruits and sun burn are considered as unmarketable (l-Lemma, 2002). Those which are free from visible symptoms are considered as marketable.
6. **Total fruit yield per hectare (tonnes)**: This was obtained by summation of marketable and unmarketable fruit yield.

3.4.2. Data collected per plant basis

1. **Plant height (cm)**: measured from ground level to the main apex of the stem from ten plants at maturity.
2. **Number of primary and secondary branches per plant**: numbers of branches were counted from ten plants at maturity.
3. **Number of flowers per plant**: Numbers of flowers were counted at initial fruit setting from ten plants.
4. **Average number of fruit clusters per plant**: number of fruit clusters per plant was counted from pre- tagged ten plants at maturity.
5. **Average number of fruits per cluster**: counted as average number of fruits from five randomly taken fruit clusters in a plant at maturity.
6. **Average number of fruits per plant**: counted as the sum total number of fruits picked per plant in successive harvest from ten plants.
7. **Fruit set percentage (%)**: Calculated as the number of matured fruits per plant divided by number of flowers per plant.
8. **Average weight of fruit per plant (kg)**: measured by taking the mean weight of fruits in successive harvest from the sampled ten plants.
9. **Average single fruit weight (g)**: measured by taking the mean weight of single fruits from ten matured fruits.
10. **Average fruit polar diameter (mm):** measured the diameter of the fruit from steam to blossom end (polar) using vernier caliper from ten matured fruits.
11. **Average equatorial diameter (mm):** measured the diameter of the fruit in the transverse section (equatorial) using vernier caliper from ten matured fruits.

12. **Fruit shape index:** calculated as fruit polar diameter divided by fruit equatorial diameter.
13. **Average number of locules per fruit**: locules were counted after dissecting the fruit into equal halves through the equatorial portion from the sampled ten fruits.
14. **Pericarp thickness (mm):** measured from an equatorial of the fruit using vernier caliper from the sampled ten fruits.
15. **Number of seeds per fruit:** determined by counting the total number of seeds per fruit from the sampled ten fruits.
16. **Total soluble solids (TSS) (^{0}Brix):** measured from two composite raw juice samples of five fruits per juice using hand refractometere.

3.5. Statistical Analysis

3.5.1. Analysis of variance (ANOVA)

Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2, (SAS Institute, 2008) after testing the ANOVA assumptions. The difference between treatment means was compared using LSD at 1% probability level.

The model used for simple lattice design is given as:

$$y_{ijk} = \mu + \tau_i + \rho_j + \beta_{jk} + e_{ijk}$$

Where,

y_{ijk} =denotes the value of the observed trait for i^{th} treatment received in the k^{th} block within j^{th} replicate

μ = over all mean

τ_i = fixed effect of the i^{th} treatment (i = 1,2,…,t)

ρ_j =effect of the jth replicate (j = 1,2,…,r);

β_{jk}= effect of the k^{th} incomplete block within the j^{th} replicate (k = 1,2,…s)

e_{ijk}= an experimental error associated with the observation of the i th treatment in the kth incomplete block within the jth complete replicate.

Table 2. ANOVA Table for simple lattice

Source of variation	Df
Treatment (Unadj.)	K^2-1
Treatment (adj.)	K^2-1
Block (Adj.)	r(K-1)
Intra block error	(K-1) (rk-K-1)
RCBD error	K^2-1
Total	rt-1

Where,

r = number of replication,

t = treatment number and

k = the block size.

3.5.2. Estimation of genetic parameters

GENRES Version 7.01 (Pascal Institute, 1994) computer software was employed for estimation of phenotypic and genotypic variances and coefficient of variability, heritability in the broad sense, genetic advance as percent of mean, genotypic and phenotypic correlation between traits and path coefficient analysis.

3.5.2.1. Estimation of variance components

The phenotypic and genotypic variances and coefficients of variation were estimated according to the method suggested by Singh and Chaudhary (1985) as follows:

Environmental variance (σ^2e)

$$\sigma^2 e = MSe$$

Genotypic variance (σ^2 g)

$$\sigma^2 g = \frac{MSg - MSe}{r}$$

Phenotypic variance (σ^2 p)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

r = number replication,

MSg = mean square due to genotypes and

MSe = mean square of error (Environmental variance).

Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma 2\ p}}{\bar{X}} * 100$$

Where, σ^2 p = phenotypic variance and

$\bar{X}$= mean of the character being evaluated.

Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma 2\ g}}{\bar{X}} * 100$$

Where, σ^2 g = genotypic variance and

$\bar{X}$= grand mean of the character studied.

3.5.2.2. Estimation of heritability in broad sense (h^2)

Heritability (h^2) in broad sense was computed using the formula adopted by Allard (1960) as:

$$h^2 = \frac{\sigma 2g}{\sigma 2p} * 100$$

Where, h^2= heritability in the broad sense,

σ^2g = genotypic variance and

σ^2p = phenotypic variance.

3.5.2.3. Estimation of genetic advance

The genetic advance expected under selection assuming selection intensity of the superior 5% of the plants was estimated in accordance with the methods illustrated by Allard (1999):

$$GA=K*\sigma_p*h^2$$

Where, GA = expected genetic advance,

h^2 = heritability in the broad sense,

K = the standardized selection differential at 5% selection intensity (K = 2.063) and

$\sigma p=$ is phenotypic standard deviation on mean basis.

Genetic advance as % of mean (GAM) was computed as:

$$GAM=\frac{GA}{\bar{X}}*100$$

Where, GAM = genetic advance as percent of mean,

GA = genetic advance under selection and

$\bar{X}$= mean of the population in which selection was employed.

3.5.3. Estimation of correlation coefficients

Phenotypic correlation (the observed correlation between two variables, which includes both genotypic and environmental components between two variables) and genotypic correlation was computed following the method described by Singh and Chaundhary (1985):

$$r_p=\frac{P\operatorname{cov}x.y}{\sqrt{\sigma^2{}_p x.\sigma^2{}_p y}}$$

$$r_g=\frac{g\operatorname{cov}x.y}{\sqrt{\sigma^2{}_g x.\sigma^2{}_g y}}$$

Where,

r_p and r_g are phenotypic and genotypic correlation coefficients, respectively;

p covx.y and g covx.y are phenotypic and genotypic, covariance between variables x and y;
σ^2px and σ^2gx are phenotypic and genotypic, variances for variable x; and
σ^2py and σ^2gy are phenotypic and genotypic variances for the variable y, respectively.

The significance or non significance of the coefficients of correlations were tested using 'r' tabulated value at n-2 degrees of freedom at 5% and 1% probability level, where n is the number of treatments (genotypes).

3.5.4. Path coefficient analysis

Path coefficient analysis was conducted as suggested by Wright (1921) and worked out according to Dewey and Lu (1959) using the genotypic correlation coefficients to determine the direct and indirect effects of yield components on fruit yield based on the following relationship.

$$rij = Pij + \sum rik\ Pkj$$

where,
rij = mutual association between the independent character (i) and dependent character, fruit yield (j) as measured by the correlation coefficients,
Pij = components of direct effects of the independent character (i) as measured by the path coefficients and
$\sum rik\ pkj$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The contribution of the remaining unknown factor was measured as the residual factor (PR), which is calculated as

$$PR = \sqrt{\left(1 - \sum rij\ pij\right)}$$

3.5.5. Cluster analysis (CA)

Clustering of genotypes into different groups was carried out by average linkage method and the appropriate numbers of clusters were determined from the values of Pseudo F and Pseudo t^2 statistics, i.e., local peaks of the cubic clustering criterion (CCC) and pseudo F statistic combined with a small value of the pseudo t^2 statistics and a larger pseudo t^2 for the next cluster, using the procedures of SAS computer software version 9.2 facilities so as to group sets of genotypes into homogeneous clusters (SAS Institute, 2008).

3.5.6. Genetic divergence analysis

A measure of a group distance based on multiple characters was given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for 24 quantitative characters and was analyzed using the procedure Proc discrim of SAS version 9.2 facilities (SAS Institute, 2008).

Squared distance (D^2) for each pair of genotype combinations was computed using the following formula:

$$D^2ij = (X_i\text{-}X_j)S^{-1}(X_i\text{-}X_j)$$

Where, D^2ij = the square distance between any two genotypes i and j;

Xi and Xj = the vectors for the values for genotype ith and jth genotypes; and

S^{-1} = the inverse of pooled variance covariance matrix within groups.

Testing the significance of the squared distance values obtained for a pair of clusters was taken as the calculated value of χ^2 (chi-square) and tested against the tabulated χ^2 values at p-1 degree of freedom at 1% and 5% probability level, where p = number of characters used for clustering the genotypes.

3.5.7. Principal component analysis (PCA)

Principal components analysis was performed using correlation matrix by employing Pastogram software of version 2.02 (Hammer *et al.*, 2001) in order to evaluate the relationships among characters that are correlated among each other by converting into uncorrelated characters called principal components. The contribution of each character in PCA is determined by eigenvector that is greater than half divided by the square root of the standard deviation of the eigenvalue of the respective PCA as suggested by Johnson and Wichern (1988). Principal components (PCs) with eigenvalue > 1.0 were used as criteria to determine the number of PCs (Kaiser, 1960).

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance (ANOVA)

Results of analysis of variance (ANOVA) of 24 quantitative characters for the 36 tomato genotypes are presented in Appendix Table 1. There was highly significant difference ($P< 0.01$) among the tested genotypes for all the characters studied indicating presence of adequate variability which can be exploited through selection.

Efficiency of simple lattice design over RCB design showed that more than half of the traits were efficient. Days to 50 % fruiting (134 %), days to maturity (115 %) and pericarp thickness (111 %) are among the traits which indicated high efficiency over RCB design i.e., the experimental plots within replications were heterogeneous hence, making incomplete block within replication reduces the experimental error. The coefficient of determination (R^2) used to measure the proportion of variability in a data set that is accounted for by the statistical model. All the traits scored more than 90 % estimate of R^2 except number of primary branches per plant (80.82 %), showed that the adequacy of the model in explaining the variation.

Mean square values of all attributes showed highly significant differences ($P < 0.01$) in all the traits which is in agreement with the finding of Jiregna (2008) who reported highly significant different for 17 characters studied in tomato genotypes under Bako condition. Mohanty (2003) also reported significant differences for all characters studied (plant height, number of branches per plant, days to first harvest, fruits per plant, average fruit weight and yield per hectare). Similarly, Pradeepkumar *et al*. (2001) and Golani *et al*. (2007) obtained highly significant difference for all characters studied among the test tomato genotypes.

4.2. Mean, Range and Estimates of Genetic Parameters

4.2.1. Mean and range

The mean performance of the 36 genotypes for 24 traits is presented in Appendix Table 2. All the 36 genotypes studied showed wide range of variability for most of the characters studied (Table 3). Days to 50% flowering ranged from 28 to 55 with a mean of 39 days. Days to 50% fruiting varied from 31 to110 days with a mean of 75days. Similarly Ghosh *et al*., 2010 reported a wide range of variation for days to initial flowering in tomato. Days to maturity ranged from 69 to 156 with a mean of 104 days. CLN 5915-93-D4 genotype, the second high yielder genotype, was the earliest to mature (69 days) whereas Cathrine was the late matured (156 days).

A wide range of variation was observed for plant height (59 - 129cm) with a mean of 91.07 cm. Number of flowers (38-185) with a mean of 103 flowers per plant. Total number of matured fruits per plant ranged from 4 to 96 with an average of 28 fruits per plant and there was a wide range of variation for fruit set percentage ranged from 3.58 to 80.40 percent with a mean value of 27.6 percent. This is in agreement with the finding of Pradeepkumar *et al.* (2001) who reported a wide range of variation for plant height, number of fruits per plant and number of pickings. CLN 5915-93-D4 genotype had the highest number of fruits (97) while tomato 1358 genotype had the least number of matured fruits per plant (4).

Average weight of fruits per plant ranged from 0.13 to 2.10 kg/plant with an average weight of 0.887 kg/plant. The highest yield per plant were recorded by CLN 5915-93-D4 genotype (2.102 kg) and CLN-2037-A (1.716 kg). Average single fruit weight per plant varied from 18 to 147 gram with a mean of 54.9 gram. Similarly, Pradeepkumar *et al*. (2001), reported wide range of variability for single fruit weight and fruit yield per plant. Number of pickings ranged from 2 to 6 with an average of 4 times picking. Total fruit yield per hectare ranged from 3.33 to 52.67 tonnes/ha which showed wide variation with a mean value of 17.88 tonnes/ha. The maximum yield was obtained from CLN-2037-A (52.67 tonnes/ha) followed by CLN 5915-93-D4 (44.73 tonnes/ha) and Miya (39.06 tonnes/ha) (Appendix Table 2).

Fruit polar and equatorial diameter ranged from 34.0 to 65.3 mm and 27.5 to 64.4 mm with a mean of 45.6 and 40.8 mm. Fruit shape index varied from 0.72 to 1.91 with a mean of 1.14. Number of locules per fruit ranged from 2 to 5 with a mean of 3.4. Pericarp thickness varied from 2.55 to 7.48 mm with a mean of 4.7 mm. Number of seeds per fruit ranged from 18 to 118 with an average of 48 and total soluble solids (TSS) varied from 3.33 to 6.71 ^{0}Brix with a mean of 5.18 ^{0} Brix. Similar results on pericarp thickness, TSS, fruit shape index and number of locules were also reported by Shashikanth *et al*. (2010).

4.2.2. Estimates of genetic parameters

4.2.2.1. Estimates of variance components

Generally characters or agronomic traits are highly influenced by the environment. In this study, characters were reacting in different way i.e. the magnitude of response was quite different that was measured by the phenotypic coefficient of variation. According to Deshmukh *et al*. (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium.

Estimates of phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 3. In general, most of the characters had high genotypic and phenotypic coefficients of variability. Number of matured fruits per plant had the highest GCV and PCV (78.47 and 79.13) followed by fruit set percentage (73.27 and 74.66), total yield per hectare (65.48 and 67.22), number of fruit clusters per plant (58.87 and 61.80), average weight of fruits per plant (52.33 and 55.00), number of seeds per fruit (51.36 and 51.99), average single fruit weight per plant (44.47 and 46.52) and number of flowers per plant (32.29 and 34.26). Medium GCV and high PCV were observed for number of primary branches per plant (16.07 and 23.35), indicated influence of the environment in the expression of the trait. However, genotypic and phenotypic coefficients of variability were medium for fruit polar diameter (17.44 and 18.66), fruit

equatorial diameter (17.06 and 17.55), days to 50 percent flowering (15.55 and 17.02) and total soluble solids (12.52 and 12.71). Phenotypic coefficient variation was generally higher than GCV values in all characters in this study (Table 3).

A similar result was reported by Pradeepkumar *et al*. (2001) for most of the characters i.e. number of fruits per plant, fruit weight, yield per plant, locule number, pericarp thickness, Plant height and number of harvest showed high PCV and GCV values. Mohanty (2003) also found high GCV and PCV for number of fruits per plant and average weight of fruits per plant. High GCV value of characters suggest that the possibility of improving these trait through selection. Similarly high GCV and PCV were also reported by Golani *et al.* (2007) for 10 fruits weight and fruit yield per hectare. Moreover, Mehta and Asati (2008) obtained high GCV and PCV for weight of fruits per plant, single fruit weight per plant and number of clusters per plant.

The difference between PCV and GCV values was high for number of primary branches, number of fruits per fruit cluster, average weight of fruits per plant, duration of picking and average single fruit weight per plant indicating influence of the environment in the expression of the traits. However, this difference was low for total soluble solids, number of matured fruits per plant, fruit set percentage, number of seeds per fruit and fruit equatorial diameter suggesting minimal influence of environment on the expression of the characters so that it is easy to improve these characters/traits.

4.2.2.2. Estimation of broad-sense heritability and genetic advance

In this study estimate of heritability in broad sense ranged from 47.36 % for number of primary branches to 98.34 % for number of matured fruits per plant (Table 3). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly feasible. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 40% or less,

selection may be considerably difficult or virtually impractical due to the masking effect of the environment.

Considering this benchmark, heritability estimate was very high (>80%) for number of matured fruits per plant (98.34 %), number of seeds per fruit (97.60%), total soluble solids (TSS) (97.07%), fruit set percentage (96.31%), days to maturity (95.58 %), total fruit yield (tonnes/ha) (94.88%), days to 50 % fruiting (93.73%),number of locules per fruit (94.62%), number of secondary branches (93.25%), plant height (90.20%) and number of flowers per plant (88.86%). It was moderate (40-80%) for number of primary branches per plant (47.36%).

Most of the characters had higher heritability estimates, indicating lesser influence of environment on them. The high heritability estimates obtained may be due to the divergent genotypes included in the study. This is in harmony with the finding of Hidayatullah *et al.* (2008) who reported high heritability for plant height, number of fruits per plant, fruit weight per plant, fruit length, fruit diameter, single fruit weight, number of locules, pericarp thickness, TSS, and seeds per fruit. Similarly, Pradeepkumar *et al*. (2001) reported high heritability estimates for all characters studied, Mehta and Asati, 2008 also found high heritability in broad sense for plant height, number of fruit clusters, weight of fruits per plant, total fruit yield per hectare, number of locules and TSS. Golani *et al*. (2007) also obtained high heritability for fruits weight per plant, fruit length, number of locules per fruit, and fruit yield per hectare.

Genetic advance under selection (GA) refers to improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001).

Generally, genetic advance as percent of mean (GAM) at 5% selection intensity was high (> 20%) for all characters studied. The highest GAM was recorded for number of matured fruits per plant (160.30%) followed by fruit set percentage (148.12%), total yield per hectare (131.39), number of fruit clusters per plant (115.53), number of seeds per fruit (104.53) and

average weight of fruits per plant (102.45) showed these characters are governed by additive genes and selection will be rewarding improvement of such traits and the least GAM was recorded for number of primary branches per plant (22.79), TSS (25.41) and days to 50% flowering (29.20). This is in consistent with the finding of Pradeepkumar *et al.* (2001) who reported high genetic advance as per cent of mean for plant height, number of fruits per plant, fruit weight, fruit yield per plant, locule number, pericarp thickness, plant height and number of harvest. Similarly Shashikanth *et al.* (2010) found high genetic advance as percent of mean for number of fruits per plant and fruit yield per plant. Golani *et al.* (2007) also obtained high genetic advance as percent of mean for average 10 fruit weight and fruit yield per hectare. In addition to the above report Ghosh *et al.* (2010) also found high genetic advance for number of fruits per plant, fruit yield per plant and number of fruits per fruit cluster.

Generally, characters such as number of fruits per plant, total fruit yield per hectare, number of fruit clusters per plant, fruit set percentage, average weight of fruits per plant, number of seeds per fruit, single fruit weight, number of fruits per cluster, number of flowers, number of secondary branches, locule number per fruit, days to maturity, pericarp thickness, number of pickings and plant height with very high heritability, high genetic advance as per cent of mean and high GCV indicate a possibility of improving these characters through direct selection.

Table 3. Estimates of range, mean, variance components, broad sense heritability and genetic advance of the studied tomato genotypes

Characters	Range	Mean ± S.E Mean	σ^2g	σ^2e	σ^2p	GCV (%)	PCV (%)	h^2 (%)	GA	GAM
Days to 50 % flowering	28-55	38.81±0.22	36.33	7.28	43.62	15.53	17.02	83.33	11.33	29.20
Days to 50 % fruiting	31-110	75.29±0.36	339.99	22.75	362.74	24.49	25.30	93.73	36.77	48.84
Days to maturity	69-156	104.03±0.44	715.97	33.11	749.08	25.72	26.31	95.58	53.89	51.80
Plant height	59-129	91.07±0.57	456.10	49.54	505.64	23.45	24.69	90.20	41.78	45.88
Number of primary branches	1.8-9.2	6.40±0.08	1.06	1.17	2.23	16.07	23.35	47.36	1.46	22.79
Number of secondary branches	1.3-7.6	3.70±0.023	1.26	0.09	1.35	30.44	31.52	93.25	2.24	60.55
Number of flowers per plant	38- 185	102.8±0.87	1102.6	1240.9	138.26	32.29	34.26	88.86	64.51	62.71
Number of fruit clusters per plant	1-22	7.80±0.112	21.07	2.15	23.22	58.87	61.80	90.75	9.01	115.53
Number of fruits per fruit cluster	0.7-4.4	1.71±0.021	0.395	0.071	0.466	36.68	39.83	84.80	1.19	69.59
Number of matured fruits per plant	4-97	27.86±0.218	475.04	8.03	483.07	78.47	79.13	98.34	44.66	160.30
Fruit set percentage (%)	3.58-80.40	27.63±0.303	409.67	425.35	15.68	73.27	74.66	96.31	40.93	148.12
Weight of fruits per plant (Kg)	0.13-2.10	0.887±0.012	0.215	0.023	0.238	52.33	55.06	90.33	0.91	102.45
Single fruit weight per plant (g)	18-147	54.90±0.587	595.92	56.22	652.14	44.47	46.52	91.38	48.08	87.57
Number of pickings	2-6	4.15±0.034	0.919	0.185	1.104	23.08	25.31	83.22	1.80	43.38
Fruit polar diameter (mm)	34.0-65.3	45.61±0.180	64.90	5.82	70.72	17.66	18.44	91.77	15.90	34.86
Fruit equatorial diameter (mm)	27.5-64.4	40.77±0.196	40.10	8.15	48.25	15.55	17.06	83.10	11.90	29.20
Shape index	0.72-1.91	1.14±0.0065	0.069	0.007	0.076	22.92	24.09	90.56	0.51	44.94
Number of seeds per fruit	18-118	47.82±0.274	603.30	14.85	618.15	51.36	51.99	97.60	49.99	104.53
Number of locules per fruit	2-5	3.36±0.0175	0.990	0.056	1.047	29.69	30.52	94.62	2.00	59.49
Perricarp thickness (mm)	2.55-7.48	4.70±0.043	1.341	0.317	1.658	24.65	27.41	80.88	2.15	45.66
Total soluble solids (^{0} Brix)	3.58-6.71	5.18±0.0093	0.420	0.013	0.433	12.52	12.71	97.07	1.32	25.41
Total yield (tons/ha)	3.33-52.67	17.88±1.93	137.00	7.39	144.39	65.48	67.22	94.88	23.49	131.39

S.E Mean= Standard error of the mean, σ^2g= Genotypic variance, σ^2e = Environmental variance, σ^2p= Phenotypic variance, h^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, GA= Genetic advance and GAM= Genetic advance as percent of mean

4.3. Association among Characters

4.3.1. Estimates of correlation coefficients at phenotypic and genotypic levels

Yield is the result of many characters which are interdependent. Breeders always look for genetic variation among traits to select desirable types. Some of these characters are highly associated among themselves and with fruit yield. The analysis of the relationship among these characters and their association with fruit yield is essential to establish selection criteria (Singh *et al*., 1990). Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 4 and 5. The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the presence of inherent or genetic association among various characters.

4.3.2. Correlation of fruit yield with other characters

Total fruit yield per hectare showed positive and highly significant phenotypic association with average weight of fruits per plant (r=0.887), number of matured fruits per plant (r=0.849), fruit set percentage (r=0.783), number of fruit clusters per plant (r=0.735), number of pickings (r=0.729) and number of fruits per fruit cluster (r=0.636) (Table 5). Therefore, any improvement of these characters may result in a substantial increment on fruit yield. This is in agreement with the suggestion of Ghosh *et al.* (2010) who reported that the number of fruits per cluster, fruit clusters per plant and fruits per plant had positive and highly significant association with fruit yield. Similarly Hidayatullah *et al.* (2008) reported positive association of fruit yield per plant with number of fruits per plant and number of pickings.

Fruit yield showed highly negative significant association with days to 50% fruiting (r=-0.782), days to maturity (r=-0.682) and days to 50% flowering (r=-0.537) at both phenotypic and genotypic level. This is because early genotypes gave higher fruit yield per hectare than the late genotypes in the specific environment among the specific test genotypes. In line with

this Jiregna (2008) reported negative and low genotypic and phenotypic association of fruit yield per plot with days to maturity, days to flowering, plant height and number of flowers per cluster.

From the correlation analysis, it can be concluded that average weight of fruits per plant, number of matured fruits per plant, fruit set percentage, number of fruit clusters per plant, number of pickings and number of fruits per fruit cluster were found to be important yield components in the studied tomato genotypes.

4.3.3. Correlations among other characters

Days to 50% flowering showed positive and significant genotypic and phenotypic correlation with days to 50% fruiting and days to maturity. It showed negative and significant genotypic and phenotypic correlation with number of fruits per fruit cluster, number of matured fruits per plant, average weight of fruits per plant and number of pickings. Days to 50% fruiting exhibited positive and significant genotypic and phenotypic correlation with days to maturity and negative and significant genotypic and phenotypic correlation with number of fruits per fruit cluster, number of matured fruits per plant, average weight of fruits per plant and number of pickings. Days to maturity showed negative and significant genotypic and phenotypic correlation with number of flowers per plant, number of fruits per fruit cluster, number of matured fruits per plant, average weight of fruits per plant and number of pickings. Similarly, Mehta and Asati (2008) reported that days to 50% flowering had positive association with days to 50% fruiting and negative correlation with number of fruits per cluster and number of fruits per plant.

Plant height had a significant negative association with pericarp thickness. Number of primary branches per plant exhibited a significant positive association with number of secondary branches and number of flowers per plant. In line with this Ghosh *et al*. 2010 reported that number of branches per plant had positive correlation with number of flowers per plant.

Number of flowers had significant positive correlation with number of pickings. Number of fruit clusters per plant had a significant positive correlation with number of matured fruits per plant, number of fruits per fruit cluster, fruit set percentage, average weight of fruits per plant and number of pickings. Number of matured fruits per plant showed positive and significant positive correlation with fruit set percentage, average weight of fruits per plant and number of pickings. This result is in agreement with the finding of Haydar *et al*., 2007 who reported that number of fruits per plant was positively correlated with fruit weight per plant. Similarly the result of Ghosh *et al*., 2010 demonstrated positive association of number of fruits per cluster with number of fruit clusters per plant, number of fruits per plant and fruit yield per plant and number of fruit clusters per plant with number of fruits per plant.

Average weight of fruits per plant had positive association with fruit equatorial diameter and duration of picking. Average single fruit weight exhibited positive and significant relationship with fruit equatorial diameter and shape index. Fruit polar had significant positive correlation with pericarp thickness. Fruit equatorial diameter showed significant positive correlation with number of locules and pericarp thickness. Similarly, Haydar *et al.* (2007) reported that fruit length was positively correlated with fruit diameter, single fruit weight and pericarp thickness. Shape index exhibited significant negativ correlation with number of locules. Similar results were also reported by Ghosh *et al*., 2010. Total soluble solids exhibited a significant negative correlation with pericarp thickness and fruit polar diameter while it showed positive association with number of seeds per fruit.

Generally, positive and significant association of pairs of characters at phenotypic and genotypic level justified the possibility of correlated response to selection. The negative correlations may prohibit the simultaneous improvement of those traits.

Table 4. Genotypic coefficient of correlation for 22 quantitative traits of the studied tomato genotypes

	50FL	50FR	DM	PHT	PBR	SBR	NFLO	NFCL	FRPFC	NFRPP	FSPER	WFPP	SFWPP	FPD	FED	SHIN	NPICK	NSEE	NLOC	PETI	TSS	TYLD
50FL	1.0	0.8**	0.73**	0.29	-0.08	-0.09	-0.326	-0.682**	-0.58**	-0.614**	-0.521**	-0.551**	0.171	-0.251	-0.129	-0.112	-0.670**	-0.230	0.031	-0.40*	-0.285	-0.581**
50FR		1.000	0.91**	0.18	0.138	0.057	-0.267	-0.875**	-0.72**	-0.795**	-0.725**	-0.762**	0.230	-0.066	-0.120	0.024	-0.935**	-0.241	-0.076	-0.208	-0.199	-0.807**
DM			1.00	0.02	0.111	0.085	-0.43**	-0.786**	-0.58**	-0.662**	-0.600**	-0.686**	0.164	-0.147	-0.152	-0.018	-0.919**	-0.155	-0.060	-0.293	-0.154	-0.710**
PHT				1.00	0.263	-0.09	0.298	-0.199	-0.118	-0.056	-0.095	-0.005	-0.064	-0.127	0.008	-0.121	-0.011	0.228	0.280	-0.40*	0.173	-0.110
PBR					1.000	0.8**	0.58**	-0.180	-0.147	-0.118	-0.307	0.003	0.326	0.41*	0.314	0.069	-0.053	0.37*	0.118	0.315	-0.101	-0.093
SBR						1.000	0.320	0.004	0.105	0.066	-0.074	0.026	0.42*	0.076	0.267	-0.144	-0.145	0.143	0.015	0.339*	-0.021	0.044
FLO							1.000	0.152	0.139	0.225	-0.035	0.163	-0.112	0.38*	-0.065	0.354*	0.454**	0.140	-0.159	0.295	0.117	0.218
NFCL								1.000	0.77**	0.778**	0.728**	0.705**	-0.172	0.012	0.184	-0.053	0.796**	0.284	0.158	0.205	0.175	0.785**
FRPFC									1.000	0.812**	0.711**	0.687**	-0.148	-0.084	0.028	-0.088	0.641**	0.250	0.047	0.123	0.136	0.703**
NFRPP										1.000	0.933**	0.809**	-0.36*	-0.205	-0.074	-0.142	0.739**	0.168	0.109	0.034	0.261	0.870**
FSPER											1.000	0.796**	-0.281	-0.249	-0.003	-0.224	0.664**	0.091	0.163	-0.001	0.160	0.814**
WFPP												1.000	0.016	-0.021	0.351*	-0.252	0.766**	0.239	0.323	0.223	0.132	0.910**
SFWPP													1.000	0.143	0.76**	-0.33*	-0.224	0.097	0.317	0.374*	-0.182	-0.127
FPD														1.000	0.069	0.78**	0.187	-0.056	-0.183	0.76**	-0.40*	-0.003
FED															1.000	-0.55**	0.208	0.227	0.631**	0.417*	-0.153	0.163
SHIN																1.000	0.023	-0.158	-0.538**	0.336*	-0.205	-0.103
NPICK																	1.000	0.062	0.108	0.368*	0.114	0.803**
NSEE																		1.000	0.359**	-0.091	0.361*	0.114
NLOC																			1.000	-0.099	0.245	0.216
PETI																				1.000	-0.46**	0.206
TSS																					1.000	0.211
TYLD																						1.000

* and ** indicate significance at 0.05 and 0.01 probability levels, respectively. 50FL=days to 50 percent flowering, 50FR= days to 50 percent fruiting, DM= days to maturity, PHT= plant height, NPBR= number of primary branches, NSBR= number of secondary branches, NFLO= number of flowers per plant, NFCL= number of fruit clusters per plant, FRPFC= number of fruits per fruit cluster, NFRPP= number of matured fruits per plant, FSPER= fruit set percentage, WFPP= average weight of fruits per plant, SFWPP= average single fruit weight per plant, FPD= fruit polar diameter, FED= fruit equatorial diameter, SHIN= shape index, NPICK= number of fruit pickings, NSEE= number of seeds per fruit, NLOC= number of locules per fruit, PETI= pericarp thickness, TSS= total soluble solids, TYLD= total yield per hectare

Table 5. Phenotypic coefficient of correlation for 22 quantitative traits of the studied tomato genotypes

	50FL	50FR	DM	PHT	PBR	SBR	NFLO	NFCL	FRPFC	NFRPP	FSPER	WFPP	SFWPP	FPD	FED	SHIN	NPICK	NSEE	NLOC	PETI	TSS	TYLD
50FL	1.0	0.7**	0.686**	0.252	-0.01	-0.059	-0.263	-0.575**	-0.463**	-0.555**	-0.471**	-0.493**	0.148	-0.209	-0.098	-0.094	-0.617**	-0.193	0.017	-0.34*	-0.262	-0.537**
50FR		1.000	0.883**	0.158	0.129	0.069	-0.237	-0.815**	-0.640**	-0.769**	-0.701**	-0.720**	0.242	-0.065	-0.082	0.003	-0.831**	-0.221	-0.055	-0.195	-0.189	-0.782**
DM			1.000	0.028	0.119	0.087	-0.39*	-0.727**	-0.520**	-0.645**	-0.586**	-0.647**	0.158	-0.125	-0.111	-0.023	-0.858**	-0.146	-0.042	-0.252	-0.153	-0.682**
PHT				1.000	0.207	-0.056	0.299	-0.175	-0.125	-0.054	-0.101	0.011	-0.068	-0.120	0.045	-0.139	-0.037	0.200	0.270	-0.284	0.171	-0.095
PBR					1.000	0.64**	0.46**	-0.116	0.022	-0.087	-0.254	-0.006	0.196	0.233	0.239	0.004	-0.152	0.240	0.130	0.234	-0.026	-0.070
SBR						1.000	0.320	0.026	0.114	0.067	-0.080	0.034	0.402*	0.057	0.264	-0.163	-0.147	0.143	0.029	0.313	-0.014	0.054
FLO							1.000	0.172	0.131	0.220	-0.077	0.162	-0.085	0.352*	-0.007	0.291	0.357*	0.135	-0.122	0.256	0.116	0.214
NFCL								1.000	0.714**	0.751**	0.664**	0.669**	-0.159	0.012	0.163	-0.059	0.719**	0.276	0.126	0.200	0.174	0.735**
FRPFC									1.000	0.759**	0.646**	0.652**	-0.124	-0.087	-0.012	-0.061	0.548**	0.219	0.013	0.079	0.136	0.636**
NFRPP										1.000	0.917**	0.786**	-0.327	-0.185	-0.067	-0.126	0.676**	0.163	0.098	0.023	0.255	0.849**
FSPER											1.000	0.757**	-0.261	-0.226	-0.019	-0.190	0.610**	0.082	0.142	-0.014	0.152	0.783**
WFPP												1.000	0.025	-0.017	0.295	-0.222	0.698**	0.210	0.285	0.198	0.118	0.887**
SFWPP													1.000	0.153	0.72**	-0.319	-0.184	0.092	0.299	0.266	-0.175	-0.112
FPD														1.000	0.098	0.75**	0.168	-0.046	-0.161	0.66**	-0.38*	0.011
FED															1.000	-0.56**	0.129	0.218	0.595**	0.357*	-0.120	0.168
SHIN																1.000	0.044	-0.155	-0.513**	0.281	-0.205	-0.101
NPICK																	1.000	0.057	0.087	0.283	0.098	0.729**
NSEE																		1.000	0.351**	-0.077	0.351*	0.111
NLOC																			1.000	-0.089	0.237	0.212
PETI																				1.000	-0.40*	0.192
TSS																					1.000	0.194
TYLD																						1.000

* and ** indicate significance at 0.05 and 0.01 probability levels, respectively. 50FL=days to 50 percent flowering, 50FR= days to 50 percent fruiting, DM= days to maturity, PHT= plant height, NPBR= number of primary branches, NSBR= number of secondary branches, NFLO= number of flowers per plant, NFCL= number of fruit clusters per plant, FRPFC= number of fruits per fruit cluster, NFRPP= number of matured fruits per plant, FSPER= fruit set percentage, WFPP= average weight of fruits per plant, SFWPP= average single fruit weight per plant, FPD= fruit polar diameter, FED= fruit equatorial diameter, SHIN= shape index, NPICK= number of fruit pickings, NSEE= number of seeds per fruit, NLOC= number of locules per fruit, PETI= pericarp thickness, TSS= total soluble solids, TYLD= total yield per hectare

4.4. Path Coefficient Analysis

Path coefficient analysis involves partitioning of the correlation coefficients into direct and indirect effects via alternative characters. Fruit yield is the final products of various characters and here it was considered to be the resultant variable while the rest of the variables were casual variables.

Each character influence fruit yield by its direct and indirect contributions with other characters to fruit yield. An aggregate residual factor that includes all other factors affecting fruit yield and not yet accounted for was treated as independent of the rest of factors considered. The residual factor 0.235 (Table 6) implied that characters included in the path analysis explained 76.5 % of the total variation in fruit yield per hectare while the remaining 23.5 % was contributed by other factors not included in the path analysis. The direct and indirect effects of twenty one traits on total fruit yield per hectare are presented in Table 6.

Estimates of direct and indirect effects of various characters on fruit yield (tonnes/ha) are indicated in Table 6. Number of matured fruits per plant had the highest direct positive contribution to fruit yield (tonnes /ha) (0.798) followed by average weight of fruits per plant (0.644) and shape index (0.549) indicating that selection based on these characters will improve the total fruit yield at this particular location for the particular crop.

Characters that had negative direct effects for total fruit yield/ha (Table 6) were fruit set percentage (-0.447), fruit polar diameter (-0.392), days to 50 % fruiting (-0.220) and number of fruits per cluster (-0.208). However, the negative direct effect of fruit set percentage (-0.447) was compensated by its indirect positive effect via number of matured fruits per plant (0.744), weight of fruits per plant (0.512) and days to 50% fruiting (0.160) and resulted in positive effect (0.814). Similarly the negative direct effect of number of fruits per cluster (-0.208) was compensated by its indirect positive effect via number of matured fruits per plant (0.647), weight of fruits per plant (0.442), days to 50% fruiting (0.159) and number of fruit clusters per plant (0.102), which resulted in positive effect (0.218).

The positive direct effect of days to maturity on total fruit yield per hectare (0.030) was nullified by its indirect negative effects on number of matured fruits per plant (-0.528), weight of fruits per plant (-0.441), days to 50% fruiting (-0.201) and number of fruit clusters per plant (-0.103) and resulted in negative effect (-0.710). Similarly the positive direct effect of average single fruit weight per plant (0.112) was nullified by its indirect negative effects via on number of matured fruits per plant (-0.284) and resulted in negative effect (-0.127).In line with this, Ghosh *et al*. (2010) reported that number of fruits per plant showed highest positive direct effect on fruit yield per plant and number of flowers per cluster showed negative direct effect on fruit yield per plant. Similarly Hidayatullah *et al*., 2008; Mehta and Asati, 2008; Tiwari and Upadhyay, 2011 reported that weight of fruits per plant had the highest positive direct effect on fruit yield per plot in tomato. Jiregna (2008) also reported that days to 50% fruiting had direct negative effect on fruit yield.

Generally, the path analysis revealed that highest positive direct effect of number of fruits per plant and weight of fruits per plant on total fruit yield per hectare in conjunction with the highest positive indirect effect of number of fruits per plant and weight of fruits per plant on total fruit yield per hectare indicating these two traits could be considered simultaneously as selection criterion for improving total fruit yield per hectare of tomato.

Table 6. Path coefficients of direct (main diagonal) and indirect effects of the characters studied

	50FL	50FR	DM	PHT	PBR	SBR	NFLO	NFCL	FRPFC	NFRPP	FSPER	WFPP	SFWPP	FPD	FED	SHIN	NPICK	NSEE	NLOC	PETI	TSS	r_g
50FL	**0.066**	-0.176	0.022	0.009	0.001	-0.003	0.046	-0.089	0.120	-0.477	0.227	-0.348	0.019	0.098	-0.016	-0.064	0.003	0.037	0.004	-0.039	-0.019	-0.581**
50FR	0.053	**-0.220**	0.027	0.005	-0.001	0.003	0.038	-0.115	0.150	-0.634	0.324	-0.490	0.026	0.026	-0.015	0.013	0.004	0.040	-0.007	-0.021	-0.013	-0.807**
DM	0.049	-0.201	**0.030**	0.001	-0.001	0.003	0.061	-0.103	0.120	-0.528	0.268	-0.441	0.018	0.058	-0.020	-0.010	0.004	0.026	-0.005	-0.030	-0.010	-0.710**
PHT	0.019	-0.040	0.001	**0.030**	-0.002	-0.004	-0.042	-0.026	0.024	-0.045	0.042	-0.002	-0.007	0.050	0.000	-0.066	0.000	-0.038	0.025	-0.041	0.012	-0.110
PBR	-0.005	-0.030	0.003	0.008	**-0.008**	0.033	-0.082	-0.024	0.031	-0.094	0.137	0.001	0.037	-0.160	0.046	0.039	0.000	-0.061	0.010	0.032	-0.007	-0.093
SBR	-0.005	-0.014	0.003	-0.003	-0.007	**0.041**	-0.048	0.002	-0.024	0.052	0.035	0.019	0.046	-0.039	0.038	-0.060	0.001	-0.023	-0.001	0.034	-0.001	0.044
FLO	-0.021	0.059	-0.013	0.009	-0.005	0.014	**-0.142**	0.020	-0.029	0.182	0.015	0.104	-0.013	-0.147	-0.008	0.195	-0.002	-0.023	-0.014	0.030	0.008	0.218
NFCL	-0.045	0.193	-0.024	-0.006	0.001	0.001	-0.022	**0.131**	-0.160	0.621	-0.325	0.453	-0.019	-0.005	0.024	-0.029	-0.004	-0.047	0.014	0.021	0.012	0.785**
FRPFC	-0.038	0.159	-0.017	-0.004	0.001	0.005	-0.020	0.102	**-0.208**	0.647	-0.318	0.442	-0.017	0.033	0.003	-0.048	-0.003	-0.041	0.004	0.012	0.009	0.703**
NFRPP	-0.040	0.175	-0.020	-0.002	0.001	0.003	-0.032	0.102	-0.169	**0.798**	-0.416	0.521	-0.040	0.078	-0.010	-0.076	-0.003	-0.028	0.010	0.004	0.017	0.870**
FSPER	-0.034	0.160	-0.018	-0.003	0.002	-0.003	0.005	0.096	-0.148	0.744	**-0.447**	0.512	-0.032	0.097	-0.001	-0.123	-0.003	-0.015	0.015	0.000	0.011	0.814**
WFPP	-0.036	0.168	-0.021	0.000	0.000	0.001	-0.023	0.093	-0.143	0.646	-0.355	**0.644**	0.002	0.008	0.047	-0.138	-0.004	-0.039	0.029	0.022	0.009	0.910**
SFWP	0.011	-0.051	0.005	-0.002	-0.003	0.017	0.016	-0.023	0.031	-0.284	0.126	0.011	**0.112**	-0.056	0.104	-0.180	0.001	-0.016	0.028	0.038	-0.012	-0.127
FPD	-0.017	0.015	-0.004	-0.004	0.003	0.004	-0.053	0.002	0.017	-0.160	0.111	-0.013	0.016	**-0.392**	0.010	0.428	-0.001	0.009	-0.017	0.076	-0.027	-0.003
FED	-0.008	0.024	-0.004	0.000	-0.003	0.011	0.008	0.023	-0.004	-0.061	0.004	0.219	0.085	-0.029	**0.137**	-0.300	-0.001	-0.036	0.056	0.043	-0.010	0.163
SHIN	-0.008	-0.005	-0.001	-0.004	-0.001	-0.004	-0.050	-0.007	0.018	-0.110	0.100	-0.162	-0.037	-0.305	-0.075	**0.549**	0.000	0.026	-0.048	0.034	-0.014	-0.103
NPICK	-0.044	0.206	-0.027	0.000	0.000	-0.005	-0.064	0.105	-0.133	0.590	-0.297	0.493	-0.025	-0.074	0.027	0.013	**-0.005**	-0.010	0.010	0.037	0.008	0.803**
NSEE	-0.015	0.053	-0.005	0.007	-0.003	0.006	-0.020	0.037	-0.052	0.134	-0.041	0.153	0.011	0.022	0.030	-0.087	0.000	**-0.165**	0.032	-0.009	0.024	0.114
NLOC	0.003	0.017	-0.002	0.008	-0.001	0.000	0.023	0.021	-0.010	0.087	-0.073	0.209	0.035	0.072	0.086	-0.296	-0.001	-0.059	**0.089**	-0.010	0.017	0.216
PETI	-0.025	0.046	-0.009	-0.012	-0.003	0.014	-0.042	0.027	-0.025	0.029	0.001	0.142	0.042	-0.297	0.058	0.185	-0.002	0.015	-0.009	**0.101**	-0.031	0.206
TSS	-0.019	0.044	-0.005	0.005	0.001	-0.001	-0.017	0.023	-0.028	0.207	-0.072	0.085	-0.020	0.157	-0.020	-0.113	-0.001	-0.060	0.022	-0.046	**0.067**	0.211

Residual effect= 0.235

* and ** indicate significance at 0.05 and 0.01 probability levels, respectively. 50FL=days to 50 percent flowering, 50FR= days to 50 percent fruiting, DM= days to maturity, PHT= plant height, NPBR=number of primary branches, NSBR= number of secondary branches, NFLO= number of flowers per plant, NFCL= number of fruit clusters per plant, FRPFC= number of fruits per fruit cluster, NFRPP= number of matured fruits per plant, FSPER= fruit set percentage, WFPP= average weight of fruits per plant, SFWPP= average single fruit weight per plant, FPD= fruit polar diameter, FED= fruit equatorial diameter, SHIN= shape index, NPICK= number of fruit pickings, NSEE= number of seeds per fruit, NLOC= number of locules per fruit, PETI= pericarp thickness, TSS= total soluble solids, TYLD= total yield per hectare and r_g= genotypic coefficient of correlation

4.5. Cluster Analysis

The dendrogram obtained from the cluster analysis grouped the 36 tomato genotypes into six clusters (Appendix Figure 1) based on the value of Pseudo F and Pseudo t-square results obtained from SAS. Clusters II was the largest cluster (55.56%) containing 20 genotypes together followed by cluster I (19.44 %) containing 7 genotypes, cluster III (11.11%) comprises 4 genotypes, clusters IV and V (5.56 %) each containing 2 genotypes and cluster VI (2.78) containing one genotype (Table 7). Genotypes in cluster III had the highest fruit yield per hectare than any other clusters. Most of the released varieties were grouped in cluster II except Metadel and Bishola which were grouped in cluster I and VI respectively, Miya, which was grouped in cluster II, showed moderate performance for total fruit yield per hectare next to the genotypes in cluster III (CLN-2037-Aand CLN 5915-93-D4. In line with this, Yashavantakumar *et al*., 2009 grouped 70 tomato genotypes in to 7 clusters. Similarly, Shashikanth *et al*. (2010) clustered 30 tomato genotypes in to 10 clusters using Mahlanobis D^2 distance.

Table 7. Distribution of 36 tomato genotypes in to different cluster groups

Cluster	**No. of Genotypes**	**Name of genotypes**
Cluster I	7	Tomato 1358/95, Metadel, H-1350, ARP Tomato No 367-2, CLN-13114-G, Cathrine and Beaf steak
Cluster II	20	Melka salsa, CLN-2366-B, Melka Shola, Chali, Cochora, 5915-206-d4-2-2-0, CLN-2037-E, CLN-2366-A, CLN-2366-C, CLN-2037-I, Fire ball, Marglobe, Roma-VF, Supper Roma-VF, CLN-2037-H, Eshet, Miya, 5915-206-d4-2-5-0, Fetan and CLN-1621-F
Cluster III	4	PT-4719B, CLN-2070-A, CLN-2037-A and CLN 5915-93-D4
Cluster IV	2	CLN-2498 and CLN-2037-C
Cluster V	2	Tomato 1365/95 and Electra
Cluster VI	1	Bishola

4.5.1. Cluster mean analysis

The mean value of the quantitative characters in each cluster is presented in Table 8. Cluster I consisted of 7 genotypes having the characteristic of late flowering (46 days), fruiting (101 days) and maturity (151 days) than remaining clusters. The genotypes had relatively moderate height (90.94 cm), number of primary and secondary branches per plant (6.3 and 3.4) and average single fruit weight (57.05 g). On the contrary cluster I had the least number of flowers per plant (61 flowers), number of fruit clusters per plant (2.4), number of matured fruits per plant (6.1), number of pickings (2.6) and average weight of fruits per plant (0.390 kg) as compared to the rest of clusters . As a result of less score from the yield contributing characters it had less total fruit yield per hectare (4.38 tonnes/ha). Fruit characteristics data of cluster I showed moderate fruit length and width (40.8 and 38.9 mm) with shape index of (1.07) implies almost round shape. It had also thinner pericarp thickness (3.73 mm) than other clusters.

Cluster II consisted of majority of the test genotypes (55.65 %) having the characteristic of moderate maturity period (94 days) as compared to cluster I and IV. Majority of the genotypes in this cluster showed moderate performance in most of the fruit yield and yield related traits as compared to clusters I, IV and VI i.e. moderate number of flowers per plant (108) with relatively moderate number of matured fruits per plant (28.1). It had relatively medium single fruit weight (50.58 g), moderate fruit weight per plant (0.920 kg), relatively many times of pickings (4.50) next to cluster III, moderate total fruit yield per hectare (19.51 tonnes/ha) as compared to clusters I, IV and VI. It also showed relatively highest value of shape index (1.22) next to cluster IV (1.27) implied the fruit was cylinder or pear shaped. It also had relatively thick pericarp thickness (5.05 mm) next to cluster V (5.45) and less TSS content (5.05 ^{o}Brix) next to cluster VI (4.93^{o}Brix). This cluster consists of the third high yielding genotype, Miya.

Cluster III, which comprised the highest yield bearing genotypes, contained four genotypes characterized by the earliest genotypes in days to 50% flowering, 50% fruiting and maturity (31, 46 and 76 days respectively). Moreover, they had the highest number of fruit clusters per

plant (14.3), number of fruits per fruit cluster (2.8), number of matured fruits per plant (76), fruit set percentage (65.66 %), average weight of fruits per plant (1.520 kg), number of pickings (5.3), total fruit yield per hectare (36.36 tonnes/ha) and TSS(5.83 ^{0}Brix). On the contrary it had the least average single fruit weight per plant (33.41 g), fruit length and width (37.3 and 37.8 mm) with shape index of (0.99), plant height (87.96 cm). It had also high number of primary and secondary branches (6.5 and 4.2) next to cluster IV (8.0 and 4.2) and number of flowers per plant (116) next to cluster IV (185).

Cluster IV comprised two genotypes having characteristics of moderate maturity period (106 days) as compared to cluster I (151 days). The genotypes in this cluster had the highest number of flowers per plant (185), longest plant height (120.5 cm), relatively few matured fruits per plant (19) as compared to cluster III (76), least fruit set percentage (10.12 %) next to cluster (VI), low fruit yield per hectare (12.14 tons per hectare) next to cluster IV and I, relatively long fruit length and moderate width (49.7 and 40.4 mm) with the highest fruit shape index (1.27) indicated the fruit had cylinder or pear shape. It also had least number of locules (2.90) among other clusters.

Cluster V contained two genotypes having a property of early flowering, fruiting and maturity period (38, 64 and 87 days) next to cluster III. It showed high fruit yield per plant (1.26 kg) next to cluster III, high average single fruit weight (90.98 g) next to cluster VI, relatively moderate fruit yield per hectare (23.32 tons per hectare) as compared to cluster II, IV,VI and I. Similarly it had the longest fruit length and width (51.1 and 53.2 mm) with shape index of (1.02) i.e. almost round shape, highest seed per fruit (102) and relatively high TSS (5.55^{o}Brix) as compared to cluster III (5.83 ^{o}Brix).

Cluster VI which contained single genotypes had a characteristic of relatively late matured (112 days) as compared to clusters II, III, IV and V. This genotype also had the highest single fruit weight (146.5 g), least number of harvesting (3 times) next to cluster I, less total yield per hectare (6.19 tons per hectare) next to cluster I, moderate fruit length and larger fruit width (41.1 and 50.6mm) with the least fruit shape index (0.81) implied the fruit had flattened shape. It also had the least TSS content (4.93 ^{o}Brix) as compared to the rest of clusters.

Table 8. Cluster-wise mean values of characters in the studied tomato genotypes

Character	Cluster					
	I	II	III	IV	V	VI
Days to 50 % flowering	46**	38	31*	38	36	42
Days to 50 % fruiting	101**	71	46*	84	65	93
Days to maturity	151**	94	76*	106	87	112
Plant height (cm)	90.94	87.66*	91.71	120.50**	89.44	101.82
Number of primary branches	6.33	6.21*	6.53	8.03**	6.42	6.70
Number of secondary branches	3.37*	3.53	4.22	4.23	3.47	6.30**
Number of flowers per plant	61*	108	116	185**	83	119
Number of fruit clusters per plant	2.44*	8.25	14.31**	3.72	13.92	4.86
Number of fruits per fruit cluster	1.34	1.62	2.80**	1.07*	1.26	1.89
Number of matured fruits per plant	6*	28	76**	19	20	10
Fruit set percentage (%)	11.33	28.33	65.66**	10.12	24.73	8.54*
Weight of fruits per plant (Kg)	0.39*	0.92	1.52**	0.68	1.36	0.59
Single fruit weight per plant (g)	57.05	50.58	33.41*	51.65	90.98	146.5**
No of pickings	2.64*	4.50	5.25**	4.25	4.25	3.00
Fruit polar diameter (mm)	40.8	48.2	37.3*	49.7	51.1**	41.1
Fruit equatorial diameter (mm)	38.9	40.4	37.8*	40.4	53.2**	50.7
Shape index	1.07	1.22	0.99	1.27**	1.02	0.81*
Number of seeds per fruit	44.1	38.5*	74.5	48.6	102.0**	44.0
Number of locules per fruit	3.31	3.17	3.60	2.80*	5.65**	2.90
Perricarp thickness (mm)	3.73**	5.05	4.10	4.99	5.45**	4.81
Total soluble solids (^{0} Brix)	5.10	5.06	5.83**	5.08	5.55	4.93*
Marketable fruit yield (tonnes/ ha)	3.89*	17.64	34.35**	10.93	20.25	5.58
Un-marketable fruit yield (tonnes/ha)	0.50*	1.86	2.01	1.22	3.07**	0.60
Total fruit yield (tonnes/ha)	4.38*	19.51	36.36**	12.14	23.32	6.19

* and ** indicate the smallest and highest mean value of the character

4.5.2. Estimation of inter cluster square distances (D^2)

The distance between clusters were assessed by the so called Mahalanobis distance such that the values calculated between pairs of clusters (Table 9) were considered as Chi-square values and tested for significance using P-1 degrees of freedom, where 'P' is the number of characters used in the study (Singh and Chaudhary, 1985).

The χ^2- test for the six clusters indicated that there was a very highly significant difference among the clusters. The highest inter-cluster distance was exhibited by cluster IV and V (D^2 =

1805.00), followed by cluster I and V (D^2 = 1102), cluster III and V (D^2 =808.72) and cluster I and IV (D^2 =806.10) which implied these clusters were genetically more divergent from each other than any other pairs of cluster. Cluster II and III showed the least inter cluster distance (81.94) compared to other pair of clusters.

Increasing parental distance implies a great number of contrasting alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors (Ghaderi *et al.,* 1984). Generally, divergence analysis showed presence of high genetic divergence among the tested tomato genotypes evaluated at Humera. Hence, hybridization of these genetically divergent parents could lead to the development of desirable recombinants and transgresive segregants, that in turn, may lead to the development of better performing varieties. Therefore, maximum recombination and segregation of the progenies is expected from crosses involving parents selected from cluster IV, I or III with parents selected from genotypes in cluster V as compared to others, however the breeder must specify his objectives in order to make best use of the characters where the characters are divergent.

Table 9. Mahalanobis distance between groups of tomato genotypes

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I	___	132.44***	269.91***	480.45***	1102.00***	806.10***
II		___	81.94***	323.76***	756.56***	505.87***
III			___	403.10***	808.72***	525.17***
IV				___	1805.00***	787.94***
V					___	684.56***
VI						___

χ^2=48.27 at 0.1% probability level. ***, indicate very highly significant at 0.1% probability level

4.6. Principal Component Analysis

The principal component analysis (Table 10) revealed that six principal components PC1, PC2, PC3, PC4, PC5 and PC6 with eigenvalues 8.915, 3.309, 3.104, 2.012, 1.430 and 1.330 respectively, have accounted for 83.03% of the total variation. The first two principal components PC1 and PC2 with a proportion of 37.14 % and 13.79 %, respectively, contributed more to the total variation. According to Chahal and Gosal (2002), characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the contribution of specific few characters.

Characters having relatively higher value in the first principal component (PC1) were total fruit yield per hectare, marketable yield per hectare, days to 50 % fruiting, average weight of fruit per plant, number of matured fruits per plant, number of picking, days to maturity, number of fruit clusters per plant and fruit set percentage had more contribution to the total diversity and they were responsible for the differentiation of the six clusters. The second principal component, which accounted for 13.79 % of the total variation contributed to pericarp thickness, fruit polar diameter, number of primary branches per plant, number of secondary branches per plant, fruit equatorial diameter and single fruit weight per plant. Characters like fruit shape index, number of locules per fruit, fruit equatorial diameter and average single fruit weight per plant were the characters which contributed to the third principal component (PC 3). Similarly number of seeds per fruit, number of flowers per plant, plant height, TSS and number of primary branches were the characters contributed to the fourth cluster (PC4). Fifth Principal component (PC5) contributed to characters such as number of seeds per fruit, number of flowers per plant and number of matured fruits per plant. The sixth principal component (PC6) contributed from plant height, number of secondary branches, number of fruits per fruit cluster, number of locules per fruit and un marketable yield per hectare.

In line with the present finding, Agong *et al.* (2000) employed PCA for detecting variation in 35 tomato germplasm in which the first three PCs were adequate in determining more than 70 % of total variation.

Table 10. Eigenvectors and eigenvalues of the first six principal components (PCs) of the studied tomato genotypes

	Eigenvectors					
Characters	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Days to 50 % flowering	-0.244	-0.084	0.123	-0.118	0.191	0.219
Days to 50 % fruiting	-0.310	0.021	0.080	-0.046	0.134	0.052
Days to maturity	-0.285	-0.037	0.092	-0.074	0.129	-0.107
Plant height (cm)	-0.035	-0.049	0.166	0.385	0.093	0.507
Number of primary branches	-0.028	0.358	0.107	0.354	0.196	-0.128
Number of secondary branches	0.003	0.316	0.135	0.146	0.353	-0.422
Number of flowers per plant	0.090	0.249	-0.150	0.401	0.270	0.176
Number of fruit clusters per plant	0.281	0.008	0.003	0.005	-0.172	-0.104
Number of fruits per fruit cluster	0.219	-0.106	-0.030	0.016	0.065	-0.319
Number of matured fruits per plant	0.298	-0.128	-0.020	0.044	0.215	-0.105
Fruit set percentage (%)	0.277	-0.181	0.021	-0.112	0.124	-0.064
Weight of fruits per plant (Kg)	0.299	0.022	0.120	-0.062	0.057	0.083
Single fruit weight per plant (g)	-0.053	0.315	0.322	-0.191	-0.083	-0.090
Number of pickings	0.294	0.038	-0.097	0.009	-0.057	0.175
Fruit polar diameter (mm)	0.011	0.405	-0.284	-0.011	-0.177	0.196
Fruit equatorial diameter (mm)	0.063	0.295	0.398	-0.159	-0.168	0.029
Shape index	-0.034	0.141	-0.485	0.095	-0.056	0.142
Number of seeds per fruit	0.071	0.058	0.219	0.403	-0.277	-0.129
Number of locules per fruit	0.065	0.006	0.437	0.004	-0.113	0.284
Perricarp thickness (mm)	0.083	0.436	-0.134	-0.192	-0.069	-0.067
Total soluble solids (^{0} Brix)	0.074	-0.216	0.139	0.373	0.001	-0.053
Marketable fruit yield (tonnes/ ha)	0.314	-0.019	0.021	-0.069	0.159	0.051
Un-marketable fruit yield (tonnes/ha)	0.241	0.138	0.088	-0.166	-0.049	0.281
Total fruit yield (tonnes/ha)	0.314	-0.005	0.028	-0.079	0.143	0.073
Eigenvalue	**8.915**	**3.309**	**3.104**	**2.012**	**1.430**	**1.133**
Proportion	**37.143**	**13.786**	**12.932**	**8.385**	**5.959**	**4.721**
Cumulative	**37.143**	**50.929**	**63.961**	**72.346**	**78.305**	**83.026**

5. SUMMARY AND CONCLUSION

Information on the extent and pattern of genetic variability in a population, interrelationship among different characters and knowledge of the naturally occurring diversity are essential to design breeding strategies in crop improvement. To generate such information 36 tomato genotypes obtained from Melkassa Agricultural Research Center, including 13 released varieties were evaluated using 6 X 6 simple lattice design at Humera Agricultural Research Center experimental site during 2010/11 cropping season under irrigation condition. The data generated from the experiment were subjected to analysis of variance, computation of genotypic and phenotypic coefficients of variations, estimations of heritability in broad sense and expected genetic advance, phenotypic and genotypic correlations, path analysis, genetic divergence analysis and principal component analysis. Results of analysis of variance showed highly significant difference among the tested genotypes for all the characters considered.

Phenotypic coefficient of variation (PCV) values ranged from 12.71 for total soluble solids to 79.13 for number of matured fruits per plant, while the genotypic coefficient of variability (GCV) ranged from 12.52 for total soluble solids to 78.47 for number of matured fruits per plant. GCV and PCV were medium for days to 50 percent flowering, fruit polar diameter, fruit equatorial diameter and TSS. GCV and PCV was high for number of matured fruits per plant, fruit set percentage, total fruit yield per hectare, number of fruit clusters, weight of fruits per plant, number of seeds per fruit, average single fruit weight, number of fruits per fruit cluster, number of flowers per plant, number of secondary branches per plant, locule number, pericarp thickness, days to maturity, days to 50 % fruiting, shape index and number of primary branches per plant.

The difference between PCV and GCV values was high for number of primary branches, number of fruit per fruit cluster, average weight of fruits per plant, duration of picking and average single fruit weight per plant. This indicates that there is high influence of the environment on these characters. However, this difference was low for total soluble solids, number of matured fruits per plant, fruit set percentage, number of seeds per fruit and fruit equatorial diameter suggesting minimal influence of environment on the expression of the

characters so that it is easy to improve these characters/traits which indicated their repeatability.

High GCV coupled with very high heritability and high genetic advance as percent of mean was observed for number of fruits per plant, total fruit yield per hectare, number of fruit clusters, average weight of fruits per plant, number of seeds per fruit, single fruit weight, number of fruits per cluster, number of flowers, number of secondary branches, locule number per fruit, days to maturity, pericarp thickness, number of pickings and plant height showed these characters are governed by additive genes and selection will be rewarding improvement of such traits.

Correlation analysis showed that fruit yield per hectare had positive and highly significant association with average weight of fruits per plant, number of matured fruits per plant, fruit set percentage, number of fruit clusters per plant, number of pickings and number of fruits per fruit cluster at both genotypic and phenotypic level while it showed highly negative significant association with days to 50% fruiting, days to maturity and days to 50% flowering. Therefore, average weight of fruits per plant, number of matured fruits per plant, fruit set percentage, number of fruit clusters per plant, number of pickings and number of fruits per fruit cluster were the important yield components in the studied tomato genotypes and these characters can be used for yield improvement in tomato breeding program.

Genotypic correlation coefficients of various characters with fruit yield per hectare were partitioned in to direct and indirect effects, genotypic path coefficient analysis revealed that the highest positive direct effect on fruit yield per hectare was exerted by number of matured fruits per plant followed by average weight of fruits per plant, shape index, fruit equatorial diameter and number of clusters per plant. However, fruit set percentage, fruit polar diameter, days to 50 % fruiting and number of fruits per cluster exerted negative direct effect on fruit yield per hectare. Generally, number of matured fruits per plant and average weight of fruits per plant, which had highest positive direct effect on fruit yield and fruit set percentage and number of fruits per cluster which had the highest indirect effect via number of matured fruits

per plant and weight of fruits per plant on total fruit yield per hectare should be considered as selection criterion in the tomato improvement program.

Genetic distance is very important for hybridization program to get better yield and best recombinant parents. Generally the genetic distance (Mahlanobis D^2 statistics) showed very highly significant difference for all pairs of clusters and the highest inter-cluster distance were exhibited between cluster IV and V (D^2 = 1805.00), cluster I and IV (D^2 = 1102.00) and cluster III and V (D^2=808.72) indicating wider genetic divergence while cluster II and III showed the least distance (D^2=81.94) indicating relatively less genetically divergent.

The principal component analysis revealed that six principal components (PC1, PC2, PC3, PC4, PC5 and PC6) with eigenvalues of 8.92, 3.31, 3.10, 2.01, 1.43 and 1.33 respectively, have accounted for 83.03% of the total variation existed among the genotypes with regard to the characters studied.

This study generally indicated that there was significance genetic variability or diversity among the test genotypes. Thus, there is enormous opportunity in the improvement program of tomato through direct selection or hybridization involving crossing of the genotypes from different clusters would produce viable and potential segregant populations. Finally, the results and conclusions made on the genetic diversity of tomato genotypes are based on data obtained from one year at a single location. Therefore, more number of genotypes needs to be studied with different characters at different locations. In such an effort due attention should be given to fruit yield, disease and pest reaction, fruit size and post harvest characteristics to exploit genetic potential of the crop.

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7. APPENDICES

Appendix Table 1. Analysis of variance for the 24 characters of tomato genotypes, using simple lattice design

Source of variation	Mean square						R^2(%)	Efficiency relative to RCBD (%)
	Replication	Treatments		Block with in reps (adj)	Error			
		Un-adj	Adj		Intra block	RCBD		
Degree of freedom	1	35		10	25			
Days to 50 % flowering	0.056	79.95	74.63**	7.71	7.12	7.28	92.19	100.18
Days to 50 % fruiting	7.347	702.73	647.23**	44.15	14.19	22.75	97.42	134.30
Days to maturity	20.06	1465.06	1402.28**	53.81	24.84	33.11	98.10	115.55
Plant height	26.25	961.75	823.84**	61.89	44.60	49.54	95.27	102.86
Number of primary branches	4.972	3.29	3.19**	1.40	1.08	1.17	80.82	101.80
Number of secondary branches	0.306	2.63	2.42**	0.04	0.11	0.09	97.04	80.56
Number of flowers per plant	147.17	2343.49	1980.03**	147.17	134.70	138.26	95.59	100.22
Number of fruit clusters per plant	0.087	44.30	43.59**	1.71	2.32	2.15	96.07	92.42
Number of fruits per fruit cluster	0.281	0.86	0.78**	0.04	0.083	0.07	92.75	85.57
Number of matured fruits per plant	27.257	957.71	903.04**	4.10	8.57	7.29	99.28	85.11
Fruit set percentage	0.009	835.02	787.75**	17.87	14.80	15.68	98.41	100.97
Weight of fruits per plant	0.074	0.46	0.42**	0.01	0.03	0.02	95.71	85.55
Single fruit weight per plant	48.741	1248.07	1112.25**	56.04	56.30	56.22	96.14	99.87
Number of pickings	0.014	2.02	1.97**	0.13	0.20	0.19	92.37	89.43
Fruit polar diameter	14.815	135.61	132.33**	6.96	5.36	5.82	96.65	101.84
Fruit equatorial diameter	10.573	89.69	86.23**	8.80	7.55	7.90	94.29	100.65
Shape index	0.002	0.14	0.14**	0.01	0.01	0.01	95.86	93.92
Number of seeds per fruit	0.011	1221.45	1032.03**	20.41	12.61	14.85	99.12	106.07
Number of locules per fruit	0.00001	2.04	1.69**	0.04	0.06	0.05	97.87	88.68
Perricarp thickness	0.046	3.00	2.63**	0.48	0.25	0.32	91.70	111.00
Total soluble solids	0.083	0.85	0.74**	0.01	0.01	0.01	98.56	91.05
Marketable yield	2.921	243.17	223.08**	9.08	5.94	6.84	97.97	104.78
Un-marketable yield	1.010	2.35	2.215**	0.0216	0.02	0.02	99.43	103.14
Total yield	2.60	281.38	258.55**	9.866	6.39	7.38	98.23	104.99

**, indicate significance at 1% probability level. Un-adj= unadjusted treatment mean square, adj= adjusted treatment mean square, RCBD= randomized complete block design error and R^2= coefficient of determination

Appendix Table 2. Mean values of the studied 36 tomato genotypes

No	Name of genotype	50FL	50FR	DM	PHT (cm)	NPBR	NSBR	NFLO	NFCL	FRPFC	NFRPP	FSPER (%)	WFPP (kg)
1	Fetan	40.0^{hefdjgi}	98.5^{bc}	131.5^{dc}	68.9^{jlk}	9.2 ^{a}	7.6 ^{a}	123.3^{cfde}	3.87^{kjm}	1.14^{kjli}	15.28^{lk}	12.38^{khjlim}	0.504^{kljm}
2	5915-206-d4-2-2-0	51.5^{ba}	75.5^{ehfg}	103.0^{fih}	102.8^{fdc}	5.8^{edhgcf}	2.5^{nomp}	126.9^{cde}	7.50^{hegdfi}	1.60^{gkejfidh}	30.35^{egdf}	23.90^{egf}	1.400^{cbd}
3	Beaf steak	54.5 ^{a}	106.0^{ba}	152.5^{ba}	71.8^{jlik}	6.2^{edhgcf}	3.95^{hdgfe}	49.3^{mn}	3.45^{lkm}	1.2800^{kjlih}	6.35^{lm}	12.95^{khjli}	0.392^{lonm}
4	CLN-2037-H	45.5^{bdce}	75.5^{ehfg}	104.5^{fgh}	120.1^{bc}	6.4^{ebdhgcf}	4.5^{dc}	91.1^{kji}	10.20 ^{d}	1.82^{gcefidh}	41.50^{c}	45.55^{c}	1.020^{fgeh}
5	CLN-2366-C	40.0^{hefdjgi}	75.5^{ehfg}	92.5^{igh}	88.2^{fhig}	1.8^{i}	1.3^{q}	90.5^{kji}	9.35^{edf}	1.40^{gkjlih}	30.59^{egdf}	33.82 ^{d}	0.409^{klonm}
6	Chali	36.5^{hlmkjgi}	68.0^{ijhlgk}	98.5^{figh}	62.3^{lk}	7.3^{ebdagcf}	4.0^{hdgfe}	116.5^{gcfdih}	7.59^{hegdf}	1.65^{gkejfidh}	31.82^{ed}	27.8^{edf}	0.660^{ikljm}
7	CLN-2498	41.0^{hefdgi}	95.0 ^{c}	107.0^{fg}	120.2^{bc}	7.7^{ebdacf}	3.5^{hjglki}	185.8 ^{a}	1.72 ^{lm}	1.00^{kl}	6.65^{m}	3.58 ^{m}	0.125^{o}
8	CLN-2037-C	35.0^{hlmnkji}	72.5^{ihfg}	105.5^{fh}	120.8^{ba}	8.4^{bac}	5.0^{c}	183.9 ^{a}	4.50^{lkji}	1.20^{kjlih}	30.82^{edf}	16.79^{hjgi}	1.219^{fed}
9	Miya	29.5^{no}	60.0^{onlmk}	79.0^{kjl}	67.1^{jlk}	6.8^{ebdhagcf}	4.3^{dce}	91.1^{kji}	10.75^{d}	2.15^{cefd}	41.78^{c}	46.02 ^{c}	1.633^{cb}
10	Roma-VF	37.5^{hfkjgi}	73.5^{iehg}	120.0^{de}	73.1^{jlik}	6.9^{ebdhagcf}	3.9^{hdgfei}	129.8^{cd}	7.26^{hegdjfi}	1.56^{gkjfih}	24.45^{ijghf}	18.91^{hgf}	0.665^{iklhm}
11	CLN-2037-A	30.0^{mno}	48.5^{p}	78.5^{kl}	106.1^{bdec}	6.4^{ebdhgcf}	4.3^{dfe}	116.^{gcfdieh}	15.25^{bc}	2.36^{cb}	94.09^{a}	80.47^{a}	1.717 ^{b}
12	PT-4719B	36.0^{hlmnkjgi}	50.0^{po}	79.5^{kjl}	92.5^{fheg}	5.8^{edhgf}	4.5^{dc}	99.8^{gkfjieh}	13.88^{c}	2.25^{cebd}	58.68^{b}	59.32 ^{b}	1.168^{fed}
13	Fire ball	34.5^{lmnkjoi}	80.5^{ef}	100^{figh}	60.5^{lk}	5.0 ^{hg}	2.8^{nomlk}	90.8^{kji}	8.59^{egdf}	1.38^{gkjlih}	28.37^{ieghf}	31.46^{ed}	1.119^{fged}
14	Supper Roma-VF	36.5^{hlmkjg}i	81.5^{ef}	104.5^{fgh}	72.1^{jlik}	7.1^{ebdagcf}	4.4^{dce}	157.9^{b}	10.25^{d}	1.86^{gcefdh}	28.82^{eghf}	18.29^{hgi}	0.933^{ifgeh}
15	CLN-2037-E	41.5^{hefdg}	73.5^{iehfg}	89.5^{kij}	117.8^{bdac}	8.7^{ba}	4.1^{dgfe}	135.4^{cb}	5.09^{hlkji}	1.41^{gkjlih}	24.45^{ijghf}	18.12^{hgi}	1.198^{fed}
16	Bishola	42.0^{efdg}	93.0^{dc}	112.0^{fe}	101.8^{fdeg}	6.6^{ebdhgcf}	6.3^{b}	119.1^{gcfdeh}	5.02^{hlkji}	1.88^{gcefdh}	10.17^{lm}	8.54^{kjlm}	0.591^{ikljnm}
17	CLN-2037-I	38.0^{hefkjgi}	70.5^{ijhfgk}	96.0^{igh}	102.5^{fdec}	4.4^{h}	1.3^{qp}	85.7^{kjl}	5.50^{hgkji}	1.72^{gcejfidh}	28.07^{ieghf}	33.07^{ed}	1.024^{fgeh}
18	Tomato 1358/95	44.5^{edc}	93.0 ^{dc}	153.5^{ab}	61.5	5.5^{ehgf}	3.2^{jmlki}	38.0^{m}	1.0^{m}	0.75^{l}	3.45^{m}	9.21^{kjlim}	0.249^{on}
19	CLN-1621-F	37.5^{hfkjgi}	64.0^{ijlmk}	82.5^{kj}	91.2^{fheg}	5.3^{hgf}	2.3^{op}	63.5^{mln}	7.58^{hegdfi}	1.63^{gkejfidh}	50.67^{b}	82.86^{a}	1.616^{cb}
20	Eshet	42.0^{efdg}	84.0^{ed}	99.0^{figh}	129.0 ^{a}	6.5^{ebdhgcf}	3.2^{jmlki}	117.6^{gcfdieh}	8.29^{hegdf}	1.59^{gkejfidh}	23.88^{ijgh}	20.30^{hgf}	0.720^{ikljh}
21	Marglobe	42.5^{efdg}	75.5^{ehfg}	92.5^{igh}	67.1^{jlk}	5.7^{edhgf}	3.7^{hjgfei}	92.7^{gkjih}	6.40^{hegkjfi}	1.86^{gcefdh}	21.90^{ij}	24.28^{egf}	0.565^{ikljnm}
22	CL 5915-93-D4	28.0^{o}	31.0^{q}	68.5^{l}	59.5^{l}	6.1^{edhgcf}	4.3^{dce}	126.4^{cde}	18.08^{ba}	4.55^{a}	97.00^{a}	77.04^{a}	2.10 ^{a}
23	5915-206-d4-2-5-0	37.0^{hlkjgi}	63.5^{ijlmk}	81.5^{kjl}	112.9^{bdac}	6.1^{edhgcf}	3.4^{hjglki}	92.0^{kjih}	9.82^{ed}	2.34^{cb}	31.40^{ed}	34.15^{d}	1.447^{cbd}
24	Metadel	36.0^{hlmnkjgi}	96.0^{bc}	148.5^{ba}	59.0 ^{l}	6.2^{edhgcf}	3.4^{hjglki}	39.5^{mn}	1.65 ^{lm}	1.35^{gkjlih}	5.85^{m}	14.78^{khjgi}	0.380^{lonm}
25	ARP Tomato No 367-2	41.0^{hefdgi}	102.0^{bac}	153.0^{ba}	108.5^{bdec}	6.2^{ebdhgcf}	3.3^{hjlki}	64.0^{ml}	3.50^{lkm}	1.60^{gkejfidh}	8.10^{m}	12.73^{khjlim}	0.465^{klonm}
26	Cathrine	50.0^{bac}	109.5^{a}	156.0^{a}	116.5^{bdac}	8.1^{bdac}	4.4^{dce}	98.5^{gkfjih}	1.75^{lm}	1.05^{kjl}	5.05^{m}	5.13^{lm}	0.325^{onm}
27	Tomato 1365/95	34.0^{lmnkjo}	52.0^{pon}	78.0^{kl}	72.3^{jlik}	6.4^{ebdhgcf}	3.4^{hjglki}	80.4^{kl}	19.40 ^{a}	1.78^{gcefidh}	22.28^{igh}	28.15^{edf}	1.426^{cbd}
28	Electra	38.0^{hefkjgi}	77.5^{efg}	96.5^{igh}	106.6^{bdec}	6.4^{ebdhgcf}	3.5^{hjgfki}	86.4^{kjl}	5.02^{hlkji}	1.47^{gkjfih}	18.40^{jk}	21.31^{hgf}	1.292^{ced}
29	CLN-13114-G	44.0^{efdc}	100.5^{bac}	140.5^{bc}	126.4^{a}	6.9^{ebdhagcf}	2.4^{nop}	92.4^{kjih}	1.74^{lm}	1.55^{gkjfih}	6.60^{m}	7.15^{klm}	0.539^{kljnm}
30	H-1350	51.0^{ab}	101.5^{bac}	155.0^{a}	93.0^{fheg}	5.4^{ehgf}	3.1^{njmlk}	43.5^{mn}	3.95^{lkjm}	1.30^{kjlih}	7.55^{m}	17.38^{hjgi}	0.374^{lonm}
31	Cochora	34.0^{lmnkjo}	65.0^{ighlmk}	81.0^{kjl}	73.7^{jlik}	6.0^{edhgcf}	3.4^{hjglki}	108.6^{gcfjdieh}	14.17 ^{c}	2.27^{cbd}	35.55^{d}	33.00^{ed}	0.870^{ifgjh}
32	CLN-2366-A	37.5^{hfkjgi}	71.0^{ijhfg}	82.0^{kjl}	84.5^{jhig}	6.3^{ebdhgcf}	2.8^{noml}	111.2^{gcfjdieh}	6.05^{hgkjfi}	1.60^{gkejfidh}	14.42^{lk}	12.27^{khjli}	0.605^{ikljnm}
33	Melka salsa	35.0^{hlmnkji}	59.0^{ponlm}	89.5^{kij}	87.3^{fhig}	7.0^{ebdagcf}	4.5^{dc}	105.5^{gkfjdieh}	9.49^{edf}	2.01^{gcefd}	18.95^{jk}	18.03^{hjgi}	0.783^{ikgjh}
34	CLN-2366-B	32.0^{lmnko}	61.5^{jnlmk}	79.5^{kjl}	77.8^{jhik}	6.1^{edhgcf}	3.4^{hjglki}	115.8^{gcfdieh}	7.33^{hegdjfi}	0.98^{kl}	18.33^{jk}	15.79^{khjgi}	0.645^{ikljm}
35	CLN-2070-A	30.5^{lmno}	56.0^{ponm}	76.5^{kl}	108.8^{bdec}	7.8^{ebdac}	3.8^{hdgfei}	119.9^{gcfde}	15.42^{bc}	2.84^{b}	55.05^{b}	47.53^{c}	1.090^{fged}
36	Melka Shola	33.0^{lmnko}	52.0^{po}	77.5^{kl}	94.4^{fheg}	6.2^{edhgcf}	2.9^{nomlk}	112.3^{gcfjdieh}	10.33^{d}	1.59^{gkejfih}	24.33^{ijghf}	21.78^{hgf}	0.650^{ikljm}
	Mean	**38.81**	**75.29**	**104.03**	**91.07**	**6.40**	**3.70**	**102.82**	**7.80**	**1.71**	**27.86**	**27.63**	**0.887**
	CV (%)	**7.27**	**6.21**	**5.53**	**8.21**	**15.87**	**8.30**	**10.99**	**18.73**	**16.45**	**10.22**	**14.36**	**17.50**
	LSD at 1%	**7.27**	**11.48**	**14.92**	**18.19**	**2.83**	**0.89**	**31.61**	**4.15**	**0.78**	**7.97**	**10.48**	**0.443**

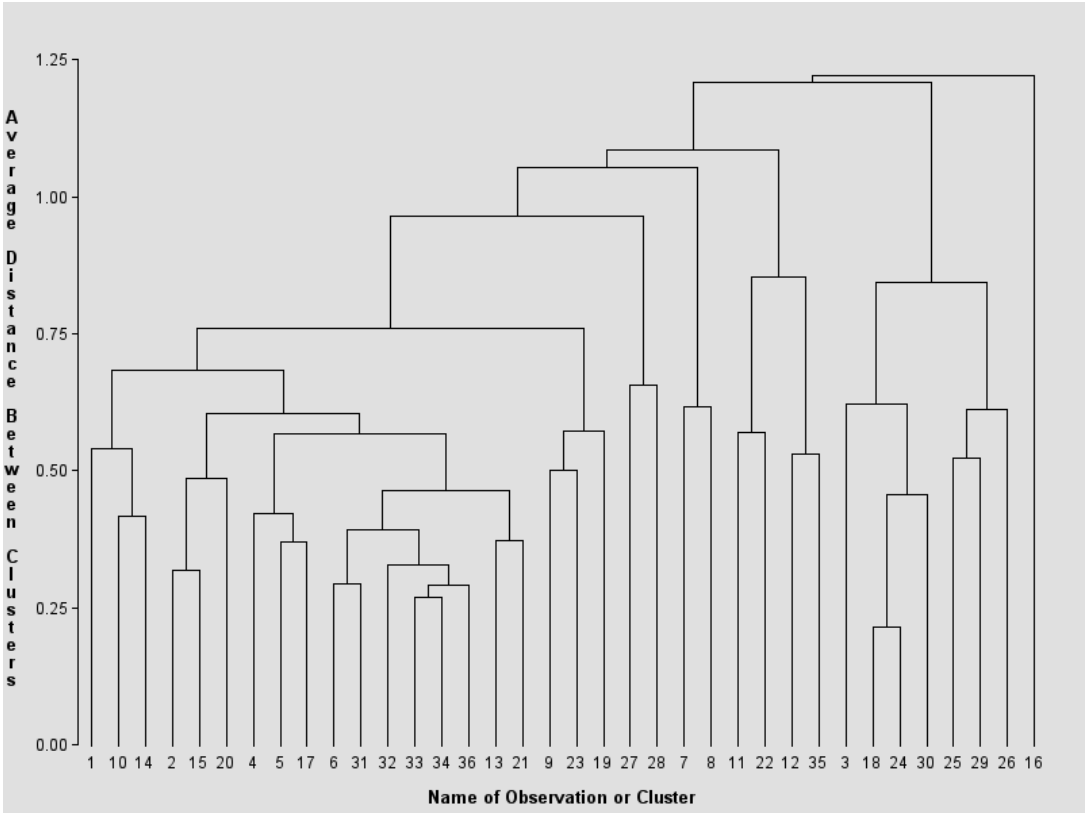
Appendix Table 2. Mean values (Continued)

No	Name of genotype	SFWPP (g)	NPICK	FPD (mm)	FED (mm)	SHIN	NSEE	NLOC	PETI (mm)	TSS (^{O}Brix)	MYLD (tons/ha)	UMYLD (tons/ha)	TYLD (tons/ha)
1	FETAN	73.40^{dfce}	3.0^{egf}	49.20^{efg}	47.60^{cbd}	1.030^{fghi}	37.5^{mlkjn}	3.95^{egf}	6.65^{bac}	5.420^{gfh}	8.49^{qopn}	0.82^{kml}	9.31^{knml}
2	5915-206-D4-2-2-0	59.53^{gdfjcieh}	5.0^{bac}	42.9^{hijk}	45.79^{cefd}	0.940^{jghi}	39.5^{lkji}	4.50^{cd}	4.33^{fhjlkig}	4.825^{jmlk}	25.67^{edf}	2.36^{d}	28.02^{ed}
3	Beaf steak	95.4 0^{b}	3.0^{egf}	41.50^{hijkm}	40.2^{ghlfjki}	1.03^{fghi}	15.0^{q}	3.00^{kji}	5.03^{fhdeg}	4.500^{o}	5.35^{qop}	0.71^{mnl}	6.05^{nml}
4	CLN-2037-H	29.60^{opn}	4.5^{bdc}	36.3^{nm}	39.00^{ghlmnjki}	0.930^{jhi}	16.5^{q}	4.45^{ed}	3.37^{mnlk}	4.975^{jlk}	18.94^{hgji}	1.72^{fi}	20.66^{gfh}
5	CLN-2366-C	17.98^{p}	4.0^{edc}	36.07 ^{nm}	27.45^{p}	1.315^{cd}	32.3^{mlon}	2.47^{kl}	3.17^{mnl}	6.115^{b}	13.18^{kmjln}	1.26^{hgi}	14.44^{kijh}
6	Chali	49.49^{mljkih}	4.0^{edc}	54.29^{ecd}	44.79^{gcefd}	1.210^{fde}	36.5^{mlkjn}	3.65^{hg}	5.93^{bdec}	3.775 ^{p}	12.76^{kmln}	17.50^{fe}	14.52^{kijh}
7	CLN-2498	43.25^{mlojkn}	4.0^{edc}	57.94^{bc}	35.8^{olmnjki}	1.615^{b}	27.8^{po}	2.55^{k}	5.15^{fhdeg}	4.520^{no}	5.89^{qop}	0.47^{on}	6.36^{nml}
8	CLN-2037-C	60.05^{gdfjcieh}	4.5^{bdc}	41.49^{lhijkm}	44.96^{gcefd}	0.920^{jhi}	67.5^{e}	3.25^{hji}	4.83^{fhjeig}	5.635^{gdfce}	15.96^{khjli}	1.96^{fe}	17.92^{gih}
9	Miya	66.98^{gdfceh}	5.0^{bac}	52.03^{ed}	46.96^{cebd}	1.110^{fghe}	29.5^{pon}	2.50^{kl}	7.48^{a}	4.825^{jmlk}	35.28 ^{c}	3.78^{b}	39.05^{c}
10	Roma-VF	57.00^{glfjkieh}	4.0^{edc}	60.63^{a}	34.19^{olmn}	1.915^{a}	60.0^{fe}	2.60^{k}	5.70^{fbdec}	5.260^{ih}	20.74^{hgf}	1.81^{fe}	22.501^{gfe}
11	CLN-2037-A	25.65^{op}	5.0^{bac}	34.16^{n}	36.66^{olmnjki}	0.930^{jhi}	44.5^{hji}	5.00^{bc}	3.03^{mnl}	6.705^{a}	49.20 ^{a}	3.47^{c}	52.67 ^{a}
12	PT-4719B	42.40^{mlojkn}	5.0^{bac}	37.09^{lnm}	38.98^{ghlmnjki}	0.950^{jghi}	77.5 ^{d}	2.75^{kj}	4.75^{fhjeig}	5.390	28.65 ^{d}	2.02^{e}	30.67 ^{d}
13	Fire ball	54.49^{gljkih}	4.5^{bdc}	50.13^{ef}	43.56^{ghefd}	1.150^{fgde}	22.5^{pq}	3.00^{kji}	6.35^{bdac}	3.795 ^{p}	19.06^{hgi}	2.32^{d}	21.38^{gf}
14	Supper Roma-VF	46.21^{mljkin}	4.5^{bdc}	60.6^{ba}	33.1^{on}	1.830^{a}	37.5^{mlkjn}	2.00^{ml}	5.38^{fhdecg}	5.38^{gh}	17.47^{khjgi}	1.85^{fe}	19.32^{gifh}
15	CLN-2037-E	62.38^{gdfcieh}	4.5^{bdc}	46.15^{hifg}	42.1^{ghefdi}	1.110^{fghe}	50.8^{hg}	3.25^{hji}	5.10^{fhdeg}	4.785^{nmlk}	20.13^{hgi}	1.91^{fe}	22.04^{gfe}
16	Bishola	146.50 ^{a}	3.0^{egf}	41.12^{lhijkm}	50.65^{cb}	0.810^{jk}	42.5^{hkji}	2.95^{kj}	4.81^{fhjeig}	4.925^{jmlk}	5.58^{qop}	0.60^{omn}	6.19^{nml}
17	CLN-2037-I	46.39^{mljkin}	5.0^{bac}	42.04^{lhijk}	41.21^{ghefjki}	1.020^{fghi}	44.0^{hkji}	3.50^{hgi}	4.05^{mhjlki}	5.810^{c}	19.00^{hgi}	1.36^{hg}	20.36^{gfh}
18	Tomato 1358/95	40.00^{mlokn}	2.5^{gf}	34.00 ^{n}	33.75^{omn}	1.01^{jfghi}	30.5^{mpon}	2.75^{kj}	2.55 ^{n}	5.625^{gdfce}	3.02^{q}	0.31^{p}	3.33^{n}
19	CLN-1621-F	69.00^{gdfce}	5.0^{bac}	46.53^{hfg}	44.5^{gefd}	1.045^{fghi}	35.0^{imlkon}	3.75^{hgf}	4.65^{fhjekig}	4.700^{nmlo}	22.81^{egf}	1.88^{fe}	24.68^{ef}
20	Eshet	28.89^{opn}	4.0^{edc}	40.94^{lhijkm}	1.08^{fgh}	1.080^{fgh}	39.8^{lkji}	2.75^{kj}	4.08^{mhjlki}	5.37^{gh}	9.77^{mopn}	0.85^{kmjl}	10.62^{kml}
21	Marglobe	57.66^{gdlfjkie}	4.5^{bdc}	37.22^{lnkm}	40.0^{ghlfjkl}	0.955^{jghi}	50.8^{hg}	4.25^{edf}	4.28^{hjlkig}	5.275^{ih}	15.78^{khjli}	1.26^{hgi}	17.04^{gijh}
22	CLN 5915-93-D4	31.29^{mopn}	6.0 ^{a}	39.33^{lnjkm}	36.34^{olmnjki}	1.080^{fgh}	64.0^{e}	2.50^{kl}	4.95^{fheig}	5.45^{gfeh}	43.27 ^{b}	1.45^{g}	44.73^{b}
23	5915-206-d4-2-5-0	74.81^{dce}	5.0^{bac}	49.60^{efg}	46.58^{cebd}	1.070^{fgh}	33.0^{mlon}	3.90^{gf}	4.06^{mhjlki}	4.875^{jmlk}	26.78^{ed}	4.86 ^{a}	31.64^{d}
24	Metadel	57.50^{gdlfjkiel}	2.5^{gf}	38.00^{lkm}	36.8^{olmnjki}	1.030^{fghi}	29.5^{pon}	2.85^{kj}	3.15^{mnl}	5.46^{gdfeh}	3.01 ^{q}	o.35 ^{op}	3.35^{n}
25	ARP Tomato No 367-2	77.00^{c}	3.0^{egf}	44.10^{hijg}	52.25^{b}	0.845^{jki}	53.0^{fg}	5.00^{bc}	5.65^{fbdecg}	5.050^{jik}	4.84^{qp}	0.73^{mnl}	5.56^{nm}
26	Cathrine	58.45^{gdfjkieh}	2.0 ^{g}	41.40^{lhijkm}	39.60^{ghlmjki}	1.045^{fghi}	101.5^{b}	2.95^{kj}	2.75^{mn}	5.68^{dfce}	3.14 ^{q}	0.37 ^{op}	3.51^{n}
27	Tomato 1365/95	106.26^{b}	5.0^{bac}	46.61^{hfg}	64.44^{a}	0.725^{k}	93.5^{c}	6.05 ^{a}	5.15^{fhdeg}	5.56^{gdfce}	25.82^{edf}	3.86^{b}	29.63^{ed}
28	Electra	75.70 ^{dc}	3.5^{edf}	55.55^{bcd}	41.8^{ghefjdi}	1.325^{cd}	103.0^{b}	5.250^{b}	5.75^{bdec}	5.53^{gdfceh}	14.67^{kmjli}	2.33^{d}	17.01^{gijh}
29	CLN-13114-G	45.00^{mljkin}	3.5^{edf}	46.16^{hifg}	38.3^{hlmnjki}	1.205^{fde}	38.8^{mlkji}	4.55^{cd}	3.49^{mnjlk}	5.750 ^{dc}	4.85^{qp}	0.68^{mnl}	5.54^{ml}
30	H-1350	26.00^{op}	2.0^{g}	40.50^{lijkm}	31.0^{op}	1.305^{cde}	44.0^{hji}	2.00^{ml}	3.47^{mnjlk}	3.575 ^{p}	3.00^{q}	0.35^{op}	3.35 ^{m}
31	Cochora	35.97^{mopn}	5.0^{bac}	54.09^{ecd}	37.13^{olmnjki}	1.480^{cb}	31.5^{mlonj}	1.95^{m}	6.85^{ba}	5.100	18.00^{khjgi}	1.93^{fe}	19.94^{gifh}
32	CLN-2366-A	40.56^{mlokn}	3.5^{edf}	38.83^{lnjkm}	35.2^{olmnk}	1.100^{fgh}	35.0^{mlkon}	2.60^{k}	3.15^{mnl}	5.810^{c}	8.45^{qopn}	1.03^{kji}	9.48^{kml}
33	Melka salsa	56.28^{glfjkih}	4.5^{bdc}	59.02^{bc}	38.29^{hlmnjki}	1.540^{b}	46.3^{hgi}	2.60^{k}	5.65^{fbdecg}	4.68^{nmo}	16.90^{khji}	2.59 ^{dc}	19.48^{gifh}
34	CLN-2366-B	45.36^{mljkin}	5.0^{bac}	44.29^{hijg}	41.6^{ghefIki}	1.065^{fghi}	50.3^{hg}	2.75^{kj}	5.05^{fhdeg}	5.72^{dce}	13.02^{kmln}	1.11^{hji}	14.12^{kij}
35	CLN-2070-A	34.33^{mopn}	5.0^{bac}	38.78^{lnjkm}	39.12^{ghlmnjki}	0.990^{jghi}	123.8^{a}	4.25^{edf}	3.65^{mnjlki}	5.750 ^{dc}	16.25^{khjli}	1.10^{hji}	17.36^{gih}
36	Melka Shola	39.56^{mlon}	5.5^{ba}	58.59^{bc}	39.9^{ghlmjki}	1.470^{cb}	37.3^{mlkjn}	2.75^{kj}	5.73^{bdec}	4.70^{nmlo}	10.67^{moln}	0.91^{kjl}	11.58^{kji}
	Mean	**54.90**	**4.15**	**45.61**	**40.77**	**1.144**	**47.82**	**3.36**	**4.70**	**5.18**	**16.26**	**1.61**	**17.89**
	CV (%)	**13.96**	**10.68**	**5.16**	**6.27**	**7.49**	**7.47**	**6.80**	**12.06**	**2.34**	**14.98**	**7.77**	**14.13**

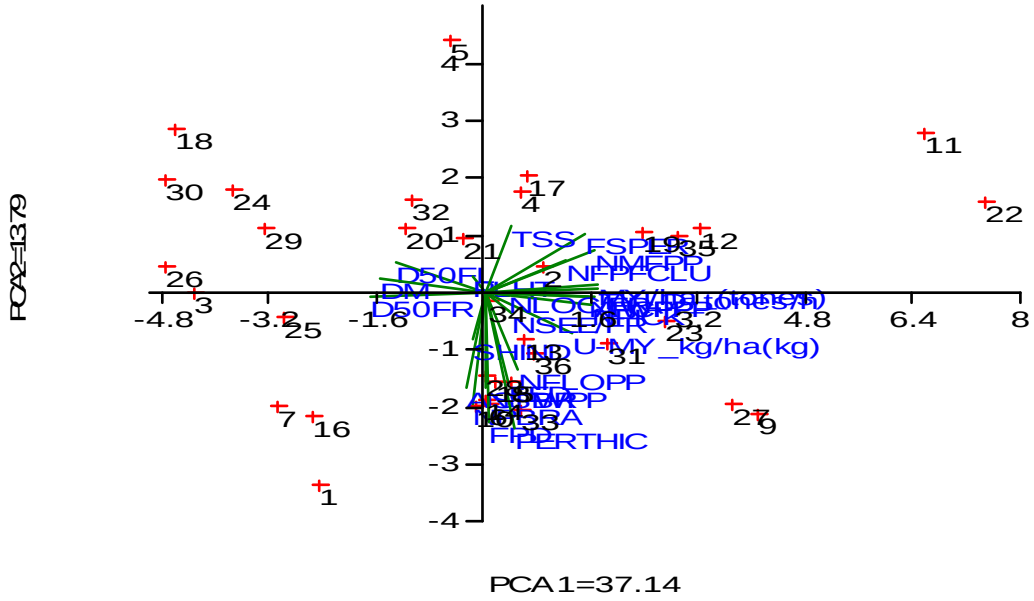
Appendix Table 2. Mean values (Continued)

	SFWPP (g)	NPICK	FPD (mm)	FED (mm)	SHIN	NSEE	NLOC	PETI (mm)	TSS (^{0}Brix)	MYLD (tons/ha)	UMYLD (tons/ha)	TYLD (tons/ha)
LSD at 1%	**20.437**	**1.24**	**6.31**	**7.48**	**0.246**	**10.43**	**0.66**	**1.49**	**0.32**	**6.64**	**0.34**	**6.39**

50FL=days to 50 percent flowering, 50FR= days to 50 percent fruiting, DM= days to maturity, PHT= plant height, NPBR= number of primary branches, NSBR= number of secondary branches, NFLO= number of flowers per plant, NFCL= number of fruit clusters per plant, FRPFC= number of fruits per fruit cluster, NFRPP= number of matured fruits per plant, FSPER= fruit set percentage, WFPP= average weight of fruits per plant, SFWPP= average single fruit weight per plant, FPD= fruit polar diameter, FED= fruit equatorial diameter, SHIN= shape index, NPICK= number of fruit pickings, NSEE= number of seeds per fruit, NLOC= number of locules per fruit, PETI= pericarp thickness, TSS= total soluble solids, MYLD=marketable yield per hectare, UMYLD= un marketable yield per hectare ,TYLD= total yield per hectare, CV= coefficient of variation and LSD= least significant difference

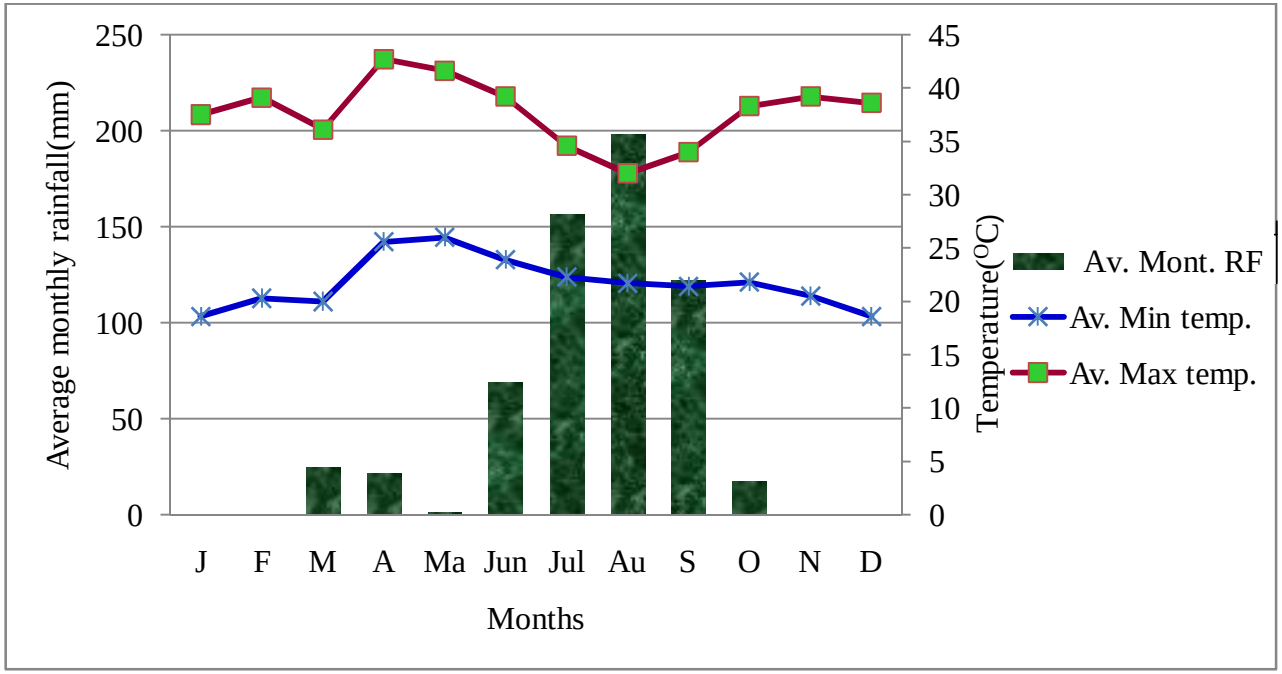


Appendix Figure 1. Dendrogram of 36 genotypes of tomato based on evaluation for 24quantitative traits



50FL=days to 50 percent flowering, 50FR= days to 50 percent fruiting, DM= days to maturity, PHT= plant height, NPBR= number of primary branches, NSBR= number of secondary branches, NFLO= number of flowers per plant, NFCL= number of fruit clusters per plant, FRPFC= number of fruits per fruit cluster, NFRPP= number of matured fruits per plant, FSPER= fruit set percentage, WFPP= average weight of fruits per plant, SFWPP= average single fruit weight per plant, FPD= fruit polar diameter, FED= fruit equatorial diameter, SHIN= shape index, NPICK= number of fruit pickings, NSEE= number of seeds per fruit, NLOC= number of locules per fruit, PETI= pericarp thickness, TSS= total soluble solids, MYLD=marketable yield per hecare, UMYLD= un marketable yield per hectare and TYLD= total yield per hectare

Appendix Figure 2. PCA scatter diagram for 24 quantitative traits of tomato genotype



Appendix Figure 3. Mean monthly rainfall (mm) for the year 2007 – 2010 and average monthly maximum and minimum temperature (^{O}C) for the year 2008 – 2010 at Humera

Source: National Meteorology Agency, 2010