GENETIC GAIN AND VARIABILITY IN FRUIT YIELD AND ASSOCIATED TRAITS OF TOMATO [*Lycopersicon esculuntum* (L.) Mill] VARIETIES IN ETHIOPIA

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As thesis advisors, we hereby certify that we have read and evaluated this thesis entitled "**Genetic Gain and Variability in Fruit Yield and Associated Traits of Tomato [*Lycopersicon esculuntum* (L.) Mill] Varieties in Ethiopia**" prepared under our guidance by Dagim Demelash. We recommend that it can be submitted as fulfilling the thesis requirements.

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As members of the Board Examiners of the M Sc. thesis open defense examination, we certify that we have read and evaluated the thesis prepared by: Dagim Demelash and examined the candidate. We recommend that the thesis be accepted as it fulfilling the thesis requirements for the degree of Master of Science in Horticulture.

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STATEMENT OF THE AUTHOR

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ACRONYMS AND ABBREVIATION

ANOVA	Analysis of Variance
ARARI	Amhara Regional Agricultural Research Institute
BARC	Bako Agricultural Research Center
BSM	Breeder Seed Maintenance
CSA	Central Statistical Agency
CV	Coefficient of Variation
CGIAR	Consultative Group on International Agricultural Research
CGS	Council of Graduate Studies
DMRT	Duncan's Multiple Range Test
EIAR	Ethiopian Institute of Agricultural Research
ENARS	Ethiopian National Agricultural Research System
HARC	Humera Agricultural Research Center
IARC	International Agricultural Research Centers
ICARDA	International Center for Agricultural Research in the Dry Areas
MARC	Melkassa Agricultural Research Center
MoARD	Ministry of Agriculture and Rural Development
MoSHE	Ministry of Science and Higher Educations
OARI	Oromia Agricultural Regional Institute
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
USDA-NASS	United States Department of Agriculture, National Agricultural Statistics Service

BIOGRAPHICAL SKETCH

The author, Dagim Demelash, was born on April 24, 1997, in Oromia Region. He attended elementary and preparatory schools at Ticho. After the completion of his preparatory school in 2015, he joined Gambella University and graduated with a Bachelor of Science Degree in Horticulture in June 2018. Soon after graduation, he was employed in the same university as a graduate assistant. In October 2020, he joined the School of Graduate Studies of Wolkite University to pursue his M Sc studies in Horticulture.

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DEDICATION

This thesis dedicated to my family.

TABLE OF CONTENTS

LIST OF TABLES

Tables’ **pages**

LIST OF FIGURES

LIST OF TABLES IN THE APPENDIX

ABSTRACT

Tomato is one of the most important dietary vegetable food crops in Ethiopia. It serves as a cash-generating crop to small and large scale farmers and employment for the production and processing in local industries. Notwithstanding this, information on genetic progress achieved over time from a breeding program is useful to develop effective and efficient breeding strategies for tomato improvement is very limited in Ethiopia. The objective of this study was to estimate the magnitude of genetic gain and variability of fruit yield and associated trait. In the present study, 16 (released from 1997 to 2015) tomatoes were evaluated in Sodo district using a randomized complete block design with three replications during 2021 cropping season. The analysis of variance indicated highly significant differences among the varieties for all traits except for number of primary branches per plant and number of seeds per fruit. The average annual rate of increase per year of release for the period 1997-2015 as estimated from the slope of the graph of linear regression of mean fruit yield on a year of variety release was 0.127 t ha^{-1} *with a relative genetic gain of 0.40%* yr^{-1}*. Recently released varieties demonstrate a yield improvement of 0.40 kg* ha^{-1} *(1.47%) over the oldest varieties in the last 18 years. Marketable yield, fruit diameter, fruit length, fruit width, fruit growth rate per plant and fruit yield per day showed a significant trend of increment. All other traits showed a significant decreasing trend over the year of release. High (509.61%) and low genetic advance (0.74%) was exhibited by fruit growth rate per plant and total soluble solid, respectively. Fruit yield was significantly and positively correlated with fruit diameter, fruit width, fruit length, fruit growth rate per plant, fruit yield per day and marketable yield both at the genotypic and phenotypic levels. Path coefficient analysis showed that the maximum positive direct contribution towards fruit yield was through fruit width, fruit yield per day and marketable yield. The study concluded that inconsistent yield improvement have been achieved in fruit yield through the last 18 years of tomato improvement. Therefore, further effort should be strengthened and continued to achieve more progresses in these and other relevant traits to design appropriate tomato fruit yield improvement strategy in the country.*

Keywords: Genetic variability, Correlation, Genetic progress, Tomato

1. INTRODUCTION

Tomato [*Lycopersicon esculentum (*L.*)* Mill] is a self-pollinated and diploid (2n = 24) crop with a genome size of 950MB (Hoeven *et al.,* 2002; Phillip, 2011; Caicedo *et al.,* 2013). It belongs to the family of *Solanaceae,* species of *Lycopersicon;* with 14 wild relatives (Peralta *et al.,* 2008). Globally, indeterminate and determinate tomato types are grown. Mexico and Peru are presumed to be the most probable region of domestication and center of diversity respectively (Larry *et al.,* 2007).

Globally, tomato is produced on five million hectares, more than186 million-ton ha^{-1} produced per year with China and India as the major producing countries (GTPM, 2020). In Africa, Egypt, Nigeria, Morocco and Algeria are the leading producing countries with a total production of 17.9 million tons ha^{-1} in the continent (FAOSTAT, 2019). In Ethiopia, tomato covers 6,012.28 hectare of land and 349.472 t ha^{-1} are produced per annum (CSA, 2019/20). In production and area coverage tomato ranks fourth after Red peppers, Ethiopian cabbage and Green peppers (CSA, 2019/20).

Tomato is important cash and industrial crop in many parts of the world (Ayandiji *et al*., 2011). Tomato is rich in vitamins, minerals, sugars, essential amino acids, iron, dietary fibers and phosphorus (Ayandiji *et al*., 2011). It provides nutritional value like calories, water, carbs, sugar, fiber and fat to the human diet and subsequent importance in human health (US, 2019). In addition, tomato contains higher amounts of lycopene (Arab *et al*. 2000) which is beneficial in reducing the incidence of some chronic diseases like cancer and many other cardiovascular disorders (Basu *et al.,*2007). It also provides employment opportunities in production areas and processing industries and is consumed in every household in different ways (Ambecha *et al*., 2012). Indeed, it serves both local and export markets and provides a route out of poverty for small-scale producers who live in developing countries in general and in Ethiopia in particular (Tewodros *et al*., 2013).

Ethiopia has huge potential for the production and productivity of tomatoes (Lamma, 2002). In Ethiopia, tomato is produced mainly in the northern and central rift valley areas by smallholder farmers, commercial states and private farms (Bezabih *et al*. 2014). Ethiopia has ample climatic and market opportunities for large scale and small scale production of tomatoes (Lemma, 2002). Unlike this, lack of improved varieties for a particular purpose, poor and traditional agronomic practices, and high disease (Wondirad *et al*. 2009) and weeds (Etagegnehu *et al*. 2009) are the major constraints of tomato production in Ethiopia.

The first and foremost prerequisite for crop improvement is the availability of wide genetic variability in the form of germplasm (Vavilov, 1951). The national and regional agricultural research system has been striving to improve tomato production in Ethiopia since the late 1997's, and more than twenty-five improved tomato varieties along with their management practices have been developed and released (Variety release booklet, 2018). However, as per reports of CSA (2019/2020) annual production of tomatoes is very low, but in areas where improved tomato technologies were adopted and used, yield levels of up to 56.19 ton ha^{-1} have been achieved (GTPM, 2020).

Estimation of genetic progress of the breeding program and assessment in the genetic gain of a crop is vital to understand changes produced by breeding, to assess the past efforts made in genetic yield potential and to put forward future breeding strategies (CGIAR, 2016; Wassu, 2017). Although, information on genetic progress achieved over time from a breeding program is essential to develop effective and efficient breeding strategies by assessing the efficiency of past improvement, because it suggests future selection direction to facilitate further improvement (Donmez *et al*., 2001; Abeledo *et al*., 2003). Globally genetic progress studies were conducted on different crops to determine the trends made in improving yield potential and associated changes in morphological traits concluded that genetic improvement in those crops has produced modern cultivars with improved yield potential (Muluken *et al.* 2016; Antonio *et al.* 2017; Atul *et al.* 2019; Felipe *et al.* 2020; Maria *et al.* 2020). This is also true for some crops in Ethiopia (Amsal, 1994; Yifru *et al.* 2005; Kebere *et al*. 2006; Tamene, 2008; Wondimu, 2010; Demissew, 2010; Ersullo, 2010).

Therefore, in Ethiopia, in order to enhance the production and productivity of tomatoes, there is a need to estimate genetic progress made in genetic improvement programs to design an effective and efficient breeding strategy for the future. However, information on the magnitude of genetic progress in fruit yield and yield associated traits of tomato varieties in the last breeding progress of Ethiopia is limiting. Therefore, the present study was planned to contribute efficient information on the progressive genetic gain of tomatoes in the production area of the country for sustainable uses.

The objective of the study

The general objective of the study was to determine the genetic gain of tomato varieties in fruit yield and associated traits in Ethiopia.

The specific objectives were:

- To estimate the magnitude of genetic gain of fruit yield and associated traits.
- To assess the genetic variability of yield and yield-related traits.
- To estimate the genotypic and phenotypic association among traits.

2. LITERATURE REVIEW

2.1. Origin, Domestication and Distribution of Tomato

The center of origin of tomatoes have been debated by many scientists, some are suggesting the center to be the dry coastal desert of Peru (Jenkins, 1948; Preedy *et al*. 2008), while others have suggested a dual center with one part in the coastal region between the Andes ocean and the second part from South Mexico to Guatemala (Bauchet *et al.*, 2012). The domestication is still unclear but linguistic evidence has postulated Peru and Mexico as the major regions of domestication (Peralta *et al*., 2006). Tomatoes are known to be used in cooking in Mexico by the Aztecs already 500 BC and were transferred to the rest of the world by the conquistadors after the capture of the Aztecs territory (Bergougnoux, 2014). Wild relatives of tomatoes are distributed in the Andes from Ecuador, through Peru and to Chile (Peralta *et al*., 2005).

The introduction of cultivated tomatoes into Ethiopian agriculture dates back to 1940. The Ethiopian Institute of Agricultural Research was established in 1966 in which tomato was recognized as a commodity crop (Setotaw, 2006). Since 1969 adaptation trials had been carried out but challenged by diseases (Shushay, 2013). Then the first record of commercial tomato cultivation was since 1980 with a production area of 80 ha in the upper Awash by Merti Agro-industry for both domestic and export markets (Lemma, 2002).

2.2. Morphology of Tomato

Tomato plants are vines, initially decumbent, typically growing 180 cm or more above the ground if supported, although erect bush varieties have been bred, generally 100cm tall or shorter. Indeterminate types are "tender" perennials, dying annually in temperate climates they are originally native to tropical highlands. Determinate types are annual in all climates. Tomato plants are dicots and grow as a series of branching stems, with a terminal bud at the tip that does the actual growing. When that tip eventually stops growing, whether because of pruning or flowering, lateral buds take over and grow into other, fully functional and vines (Peet, 2009).

Tomato cultivars can also be distinguished based on the indeterminate or determinate growing habit. Cultivars for processing purposes are determinate growing and plants have a compact growth habit with grouped fruits ripening at a single moment, which are suitable for a mechanical harvest. In addition, fruits for processing should have certain characteristics that are related to processing quality, such as high viscosity, dry extract, pH value and high value of total soluble acids. Indeterminate habit is typical of fresh market cultivars in a greenhouse.

Tomato possesses unique properties, as it is both an economically important crop, the first vegetable in production in the world, and a model plant species, due to its diploid, relatively compact, and recently sequenced genome and its large genetic and genomic resources (Ranjan *et al.*, 2012). Grown under optimal conditions, tomatoes have a 95 to 115-day lifecycle. The first flowers will appear and open 7 to 8 weeks after seeding and mature fruits will follow 6 to 8 weeks later. The tomato flower is normally perfect, having functional male (anthers) and female (pistil) parts. Present cultivated tomato varieties form a tight protective anther one surrounding the stigma, which greatly reduces the possibility for natural cross-fertilization. Outdoors flower movement aided by wind is sufficient to release pollen, but under greenhouse conditions, manual variation of open flowers is required to effect pollination and fruit set. Genetic and environmental modification of stigma position can affect both fruit set and degree of cross-fertilization (Maiti *et al.*, 2014).

2.3. Ecology, Adaptation and Production Practice in Ethiopia

Ethiopia is suitable for tropical and subtropical fruits and vegetables including tomato production (EIAR, 2007). According to Birhanu *et al.* (2010), this crop grows between 700 and 2000 m.a.s.l. with about 700 to over 1400 mm annual rainfall, in different areas and seasons, in different soil types, under different weather conditions. Moreover, especially in humid- and sub-humid areas of the country, tomato is cultivated mainly during the dry season using irrigation with a resultant inadequate supply of tomato (Lamma, 2002).

The climatic and soil conditions of Ethiopia allow the cultivation of a wide range of fruit and vegetable crops including tomatoes (Zeberga, 2010). It is largely grown in eastern and central parts of mid to low land areas of the country. Large-scale production of tomatoes takes place in the upper Awash valley under irrigated and rain-fed conditions whereas small-scale production for the fresh market is common practice around Koka, Ziway, Wondo-Genet, Guder, Bako and many other areas (Lemma, 2002).

In Ethiopia, tomato takes the highest share of commercial vegetables; more than 15 open-pollinated tomato varieties have been verified and are under production in Ethiopia (variety release booklet, 2018). Smallholders have grown tomatoes for a long time for their livelihood needs since the start of its commercialization. However, as observed from CSA (2019/2020) reports the average yield of tomatoes in Ethiopia is low, as compared with the world average yields. This may be related to limited genetic improvement and use of improved commercial tomato varieties and poor production management. Therefore, the crop requires further improvement to maximize productivity in the country. This can be achieved through studying the past breeding efforts under common environments to identify past breeding efforts and for effective future improvements.

2.4. Importance and Uses of Tomato

Globally, tomato is an important food and industrial crop (Ayandiji *et al*., 2011). It is a source of vitamins and pro-vitamins (vitamin C, pro-vitamin A, β carotene, folate), minerals and secondary metabolites (lycopene, Flavonoids, Phytosterols and Polyphenols) for humans (Luthria *et al.*, 2006). Intake of tomato has been related to reducing the risk of breast cancer head and neck cancers and the use of tomato as food might help reduce cardiovascular threat associated with type-2 diabetes (Friedman, 2002).

Furthermore, processed tomato such as soup, paste, concentrate, juice and ketchup contribute positively to human health by the content of the mentioned compounds in these products (Bergougnoux, 2014). It is also an important co-staple food (Ambecha *et al.,* 2012). In addition, tomato is a source of umami flavour (Fleming, 2013). It is consumed in diverse ways, raw or cooked, in many dishes, sauces and drinks. The fresh produce is sliced and used as salad. It is also cooked for making the local sauce (***Wot***) in Ethiopia. The processed products such as tomato paste, tomato juice, tomato ketchup and whole peel tomato are produced for local market and export. Such diverse uses make the tomato an important vegetable in irrigated agriculture of the country (Lemma, 2002).

2.5. Genetic Gain in Plant Breeding

Genetic gain or genetic progress is defined as the improvement in average genetic value in a population or the improvement in average phenotypic value due to selection within a population over cycles of breeding (Hazel *et al.*, 1942). Rutkoski (2019a) also described genetic gain as the expected or realized change in the average breeding value of a population over at least one cycle of selection for a particular trait or index of traits. This change is sometimes referred to as a genetic trend and can be estimated by regressing the average breeding value on year when linearity exists (Eberhart, 1964). Hill (2014) and Jessica (2019) also define genetic gain as a response to selection.

The development of methods to estimate genetic gain is of interest for breeding programs and their stakeholders, as genetic gain constitutes a highly relevant indicator of breeding program performance and a means to compare different crossing, evaluation and selection strategies, either through real experiments or simulations (Faux *et al*. 2016; Walsh *et al*. 2018; Cobb, 2019). The methods to estimate the rate of genetic gain can be separated into expected (Walsh, 2004; Falconer, 2005) and realized genetic gain (Mackay 2011; Laidig *et al*. 2014). Expected genetic gain is a prediction of the actual change in phenotype that would occur due to the genetic changes brought about by a proposed selection or a proposed breeding strategy. Expected genetic gain can be estimated using parameters obtainable from breeding experiments and given various assumptions. Realized genetic gain is the observed gain due to selection over cycles (Piepho *et al*. 2014; Rutkoski, 2019a).

Genetic gain can be achieved for virtually any trait if it is heritable. It can also be achieved for total net merit, which is a combination of multiple economically important traits. Selection for net merit is done using an economic selection index which is a linear combination of different traits of economic importance weighted optimally so that selection based on the index maximizes expected genetic gain in net merit (Hazel, 1943). Because the term genetic gain only applies to changes in population mean over cycles of selection, it makes sense to talk about genetic gain in traits that are heritable and conferred by multiple loci (Smith, 1936). This is because improving such traits can be done most effectively over multiple cycles of selection.

For a breeding program that has been in operation for several years, it is crucial to check the genetic changes that have been achieved in time through plant breeding. Genetic progress is made when the average genetic value of the offspring is higher than the average genetic value of the previous generation from which the parents were selected (Lisbeth *et al*., 2014). This is the realized genetic change, often also called genetic progress (Strandberg *et al.*, 2006). Likewise, Evans (1993) and Cox *et al*. (1988) suggested that it is quite significant to undertake genetic gain studies to find out whether the program has been successful or not and to propose new actions based on the merits and discrepancies of past results.

Understanding of changes produced by crop breeding on fruit yield and its determinants is important to evaluate the efficiency of past improvement work on the advances in genetic yield potential and to define future selection criteria to facilitate further progress (Evans, 1993). Information on genetic progress achieved over time from a breeding program is essential to develop effective and efficient breeding strategies by assessing the efficiency of past improvement works in genetic yield potential and suggesting on future selection direction to facilitate further improvement (Waddington *et al.,* 1986; Cox *et al.*, 1988; Donmez *et al.*, 2001; Abeledo *et al*., 2003). Similarly, Soares *et al.* (2005) emphasized that genetic gain studies could enhance the decision-making process regarding the preservation of varieties and implementation of vital selection methodologies of breeding programs. Hence, information on genetic progress achieved over time, be it positive or negative, is essential in any breeding program (Girum, 2019).

According to Hallauer *et al*. (2010), estimation of realized genetic gain is typically done after conducting selection experiments to compare different breeding strategies, and to a lesser extent, to assess the effectiveness of breeding programs. This may be because the adoption of varieties by growers in the targeted region has been considered to be the ultimate measure of the success of the program.

2.6. Fruit Yield Potential and Progresses through Breeding

2.6.1. Yield potential concept and measurements

According to Raggi *et al*. (2017), plant breeding has been a key science in improving crop production, with an estimated contribution to productivity increases of around 50%. Terms such as "yielding capacity" or specific "yielding ability" were quite widely used in the 1960s under an array of definitions. In considering yielding capacity, Bingham (1967) distinguished between the "potential yield" of a cultivar in farm cultivation but free from the hazards of lodging, winter killing, pests and diseases, and the "realized yield" as a result of these and other stresses. Similarly, MacKey (1979) described that the "specific yielding ability under overall optimal conditions must be complemented by protection mechanisms against outside stresses and disturbances.’’

Yield potential is a yield of a cultivar when grown in environments to which it is adapted, with nutrients and water non-limiting and with pests, diseases, weeds, lodging, and other stresses effectively controlled, whereas yield refers to the mass of product at final harvest, for which dry matter content should be specified (Evans, 1993). Yield potential is 'the yield that can be obtained with current cultivars under ideal conditions in the absence of poor weather, diseases, soil or nutritional constraints with and optimized'.

2.6.2. Genetic progress research in Ethiopia

Tomato research was started at Melkasa Agricultural Research Center in Ethiopia; currently more than 15 open-pollinated tomato varieties have been verified and are under production (Variety release booklet, 2018). Quantifying breeding achievements in yield and associated traits and understanding the crucial characteristics of the crop associated with the genetic gains achieved through breeding is an essential step for improving the current knowledge of yield-limiting factors and the design for future breeding strategies (Wassu, 2017). The main goals of of tomato breeding in Ethiopia are to maximize the productivity by increasing improved varieties high and stable yield, tolerant to both biotic and abiotic stresses that contribute to increased availability of food, improved economic and social welfare of farmers.

According to Tibebu (2011), in Ethiopia, apart from some comparative observations in variety trials by breeders and results of field demonstrations and popularization programs by different stakeholders where few varieties may be tested together under common environments, studies on the assessment of genetic progress through breeding in yield and yield related traits in important crops are very limited specially in tomato.

As presented by Wondimu (2010), grain yield has increased from 3314.8 kg ha^{-1} to 5088.6 kg ha^{-1} in the past three decades of food barley improvement program. The author also indicated that based on regression of mean grain yield versus the number of year's elapsed since 1970 and 1973, yield gain has risen at an average rate of 44.24 kg ha-1 (1.34%) and 42.96 kg ha-1 (1.19%) year^{-1}, respectively. The average annual increase in grain yield as estimated from coefficient of linear regression of variety means on year of release was 13.26 kg ha^{-1}, which represents a 1.27% relative genetic gain each year.

Similarly, Yifru *et al.* (2005) resulting in a gain of 41.44% in Tef, Tamene (2008) also reported an increment in grain yield of modern varieties as high as 907 kg ha $^{-1}$ (37%) over the older variety in Faba bean, Demissew (2010) has observed a 71.27% yield increment in soybean breeding. Similarly, Genetic gain estimates for grain yield and associated traits for the different crops in Ethiopia are often presented in various literatures (Daniel *et al*. 2011; Solomon, 2016;

Solomon *et al.,* 2018). However, there is no research have been done on genetic progress of tomato improvement in Ethiopia.

2.7. Changes in Fruit Yield Related Traits Associated with Genetic Improvement.

Identification and manipulation of traits contributing to yield are important as this increases breeding efficiency (Falconer and Mackay, 1996). Thus, giving emphasis to easily measurable characters with high heritability and having a useful relationship with yield is of paramount importance to practice indirect selection for high yield (Tibebu, 2011). To exploit the genetic potential of the crop through its improvement by pursuing an appropriate breeding strategy, researchers study the progress made by breeding in improving yield and associated agronomic and physiological traits and thereby determine the basis of yield gains of crop cultivars successively released during the past years (Yifru *et al.*, 2005). Evans (1993) also reported that it is useful to study changes produced on yield attributes with a year of cultivar release by past genetic improvements if future breeding programs aim to maximize the yield with adequate quality.

In addition to studying the genetic base and the changes in yield-related traits is valuable to recognize which of them are associated with fruit yield, to identify yield-limiting factors and specially to plan future effective approaches to increase the fruit yield genetic gains in breeding programs. Historical studies have shown that traits such as fruits per square meter, biomass and harvest index are positively associated with fruit yield progress (Shearman *et al.*, 2005).

To exploit the genetic potential of the crop through its improvement by pursuing an appropriate breeding strategy, researchers study the progress made by breeding in improving yield and associated agronomic and physiological traits and thereby determine the basis of yield gains of crop cultivars successively released during the past years (Yifru *et al.*, 2005). According to Evans (1993), it is useful to study changes produced on yield attributes with a year of cultivar release by past genetic improvements if future breeding programs aim to maximize the grain yield.

2.8. Genetic Parameters

2.8.1. Genotypic and phenotypic variability

Variability describes the potential for variation and the occurrence of differences among individuals due to differences in their genetic composition or environment in which they are raised (Allard, 1960). Phenotypic variability is the observable variation present in a character in a population; it includes both genotypic and environmental variation and, as a result, its magnitude differs under different environmental conditions. Genotypic variability, on the other hand, is the component of variation, which is due to the genotypic differences among individuals within a population and it is the main concern of plant breeders (Singh, 2005).

According to Govindaraj *et al.* (2015), the presence of genetic variability in crops is essential for its further improvement by providing options for the breeders to develop new varieties and hybrids. This can be achieved through phenotypic and molecular characterization of plant genetic resources (PGR). Likewise, Allard (1964) reported that; 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. In initiating a breeding program 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.

Genetic variability is the formation of individuals differing in genotypes, or the presence of genotypic different individuals, in contrast to environmentally induced differences which, as a rule, cause only temporary, non-heritable changes of the phenotype (Rieger *et al.,* 1968). Genetic variability in a population is important for biodiversity (Sousa, 2011). Genetic variability is of immense importance to the breeders because it can be transmitted to the progeny and the proper management of this diversity can produce a permanent gain in the performance of the plant because identification of superior genotype by selection is dependent on the existence of reliable genetic variability (Welsh, 1981). Therefore, the existence of genotypic variability is a key component of breeding programs for broadening the gene pool of crops (Ahmad *et al.,* 2011).

2.8.2. Heritability

Heritability is often used by plant breeders and geneticists as a measure of the precision of a trial or a series of trials. It is often used by plant breeders to quantify the precision of single field trials or series of field trials. It is defined as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects, also known as heritability in the narrow sense (Holland, 2003). The success of any crop improvement program is not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Sumathi *et al.* 2005; Najeeb *et al.* 2009; Wang *et al.*, 2011).

In any crop-improvement programme the success of selection as a breeding method is determined by the magnitude of genetic variability for yield and yield components (Dudley, 1969). The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. In genetic studies, characters with high genotypic coefficient of variation indicate the potential for an effective selection (Sadiq *et al.*, 1986). Determining the components of variability in yield and its components enable us to know the extent of environmental influence on yield, taking into consideration of the fact that yield and its component are quantitative characters that are affected by the environment (Ahmed *et al.*, 2006). Heritability provides an idea of the extent of genetic control for expression of a particular character and the reliability of phenotype in predicting its breeding value and the extent of which a particular genetic character can be transmitted to the successive generations (Mangi *et al.*, 2010). High heritability indicates less environmental influence in the observed variation (Songsri *et al.*, 2008).

Heritability assumes that individuals more closely related are more likely to resemble one another than distant ones (Falconer *et al.*, 1996). Estimate of heritability assists breeders to allocate the resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources. It may be estimated as broad-sense or narrow-sense, on a single plant, individual plot, or mean of entry (Nyquist *et al.*, 1991). Studies by Mahesh *et al*. (2006); Ahmed *et al*. (2006); Asati *et al*. (2008); Ara *et al*. (2009) and Reddy *et al*. (2013) indicates that; high heritability along with high estimates of genetic gain was observed for number of fruits per cluster, number of seeds per fruit, average fruit weight, fruit yield per plant and fruit yield per hectare in tomato.

2.8.3. Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. It also indicates the presence of additive genes in the trait and further suggests reliable crop improvement through a selection of such traits. The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer *et al.*, 1996). Traits with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Najeeb *et al.,* 2009) because genetic advance shows the degree of the gain obtained in a character under particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection.

Heritability estimates help to predict the possible progress that can be attained by making the selection process effective. Moreover, genetic advance estimates give a clear picture of segregating generations to make selection effective. Several studies have been conducted on the genetic advances of tomatoes (Singh, 2005; Hayder *et al.* 2006; Hidayatullah *et al.* 2008; Haq *et al.* 2008; Kahrizi *et al.* 2010; Gulnaz *et al.* 2011; Arshad *et al.* 2011; Koundinya, 2014).

2.9. Trait Associations

2.9.1. Correlation analysis

Correlation is the association between two variables and measures the strength and/or direction (i.e., positive or negative) of the relationship (Miller *et al.,* 1958). Correlation measures the degree of association, genetic or non-genetic, between two or more traits. If a genetic association exists, selection for one trait will cause changes in other traits (Hallauer *et al.*, 1988). Chen *et al.* (2002) suggested that the choice of the coefficient type depends on several factors, including the scale measurement, assumptions about the bivariate distribution, and whether population parameters are estimated. According to Monica *et al*. (2019), correlation analysis is a statistical method used to evaluate the strength of the relationship between two quantitative variables. Correlation analyses help to determine 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 traits and yield as well as among the trait themselves.

Research conducted on tomatoes by Ara *et al*. (2009) and Khapte *et al*. (2014) indicates that the correlation analysis results of the yield per plant were positively and significantly correlated with number of primary branches, percent fruit set, number of flower trusses per plant, fruit length, pericarp thickness.

2.9.2. Path coefficient analysis

Path coefficient indicates the direct effect of a variable assumed to be a cause on another variable assumed to be an effect. Path coefficients are standardized because they are estimated from correlations (Dewey *et al.,* 1959). Therefore, partitioning the observed correlation coefficients into components of direct and indirect influences provide perceptions in the characterizations of more complex traits, like yield (Baloch *et al.,*1994). Path coefficient analysis provides precise information on the direct and indirect effects to perceive the most influencing characters to be utilized as selection criteria in tomato breeding programs.

Path analysis was used in numerous researches to determine the effects of important yield components (Naazar *et al*., 2003). In tomato, earlier studies made by Bodende (2002), Hayder *et al.* (2007) and Khapte *et al*. (2014) indicates that there were positives and negative significant effects among tomato traits.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted during January 2021 under irrigation condition at Sodo district, Gurage Zone. The district is located 103 Km away from Addis Ababa, in south-west direction. Located at 8°20’46.58” N latitude and 38°34’33.83’’ E longitude and the altitude is between 1800 and 2900 m.a.s.l and the annual rainfall is less than 1500 mm. Average temperature ranges between 10 and 27.5°C. The soil type of the site is vertisols (Sodo woreda Farming and Natural Resources Development, 2011). According to Sodo woreda farming and natural resources development (2011), teff, wheat, pepper, tomato and onion are the main crops produced in the districts.

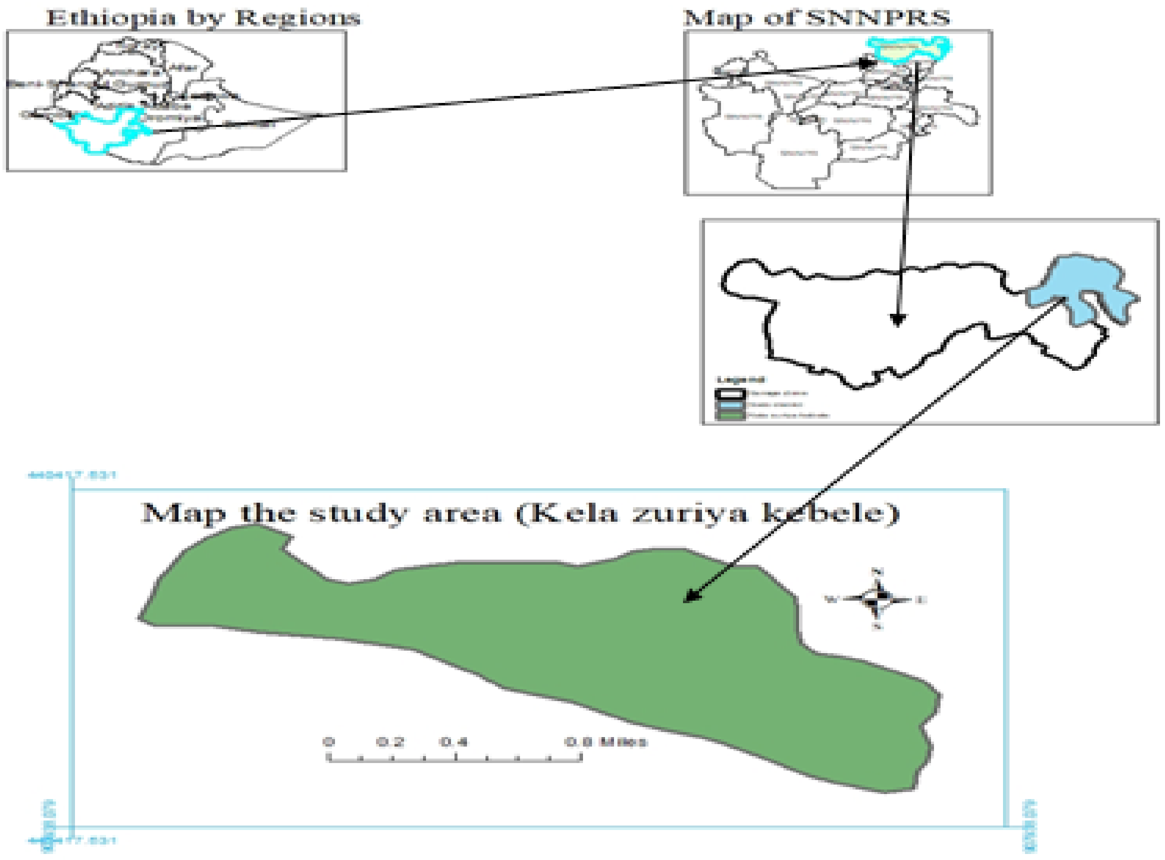


Figure 1 Geographical location of the study area

3.2. Experimental Materials

Sixteen open-pollinated tomato varieties released over 18 years (since 1997-2015) were used in this study. These released varieties were obtained from federal and regional agricultural research centers of Ethiopia (Table 1).

Table 1List of tomato varieties.

SN	Variety/name	Year of released	Altitude (m)	Days to maturity	Average yield (t ha^{-1})	BSM	Remarks
1	Melka Salsa (Serio).	1997	700-2000	100-110	45.0	MARC/EIAR	OPV
2	Melka Shola (Red Pear)	1997	>>	100-120	43.0	MARC/ EIAR	OPV
3	Eshet (Calypso)	2005	>>	75-80	39.7	MARC/ EIAR	OPV
4	Metadel (Caraibo)	2005	>>	75-90	34.5	MARC/ EIAR	OPV
5	Fetan (Picador)	2005	>>	75-80	45.4	MARC/ EIAR	OPV
6	Bishola(Floradado)	2005	>>	85-90	34.0	MARC/ EIAR	OPV
7	Woyno (Fireball)	2006	>>	85	24.9	SRARC/ARARI	OPV
8	Mersa (Carman)	2006	>>	100-120	27.6	SRARC/ARARI	OPV
9	Sirinka-1 (Cardinal).	2006	>>	95-100	38.2	SRARC/ARARI	OPV
10	Tekeze-I	2006	>>	90	25.2	HARC/TARI	OPV
11	Miya (Floralou)	2007	>>	90-100	47.1	BARC/OARI	OPV
12	Cochoro (pace setter)	2007	>>	85-90	45.0	MARC/ EIAR	OPV
13	Chali (Riogrande)	2007	>>	85-100	46.2	MARC/ EIAR	OPV
14	Marglobe	2007	>>			MARC/ EIAR	OPV
15	ARP tomato d2	2012	>>	100-120	37.2	MARC/ EIAR	OPV
16	Gelilema(Oval red)	2015	>>	100-110	42.0	MARC/ EIAR	OPV

EIAR= Ethiopian Institute of Agricultural Research, MARC= Melkasa Agricultural Research Center, SRARC= Sirinka Regional Agricultural Research Center, ARARI= Amhara Regional Agricultural Research Institute, OARI = Oromia Agricultural Regional Institute, BSM = Breeder Seed Maintenance, OPV= Open Pollinated Varieties, BARC= Bako Agricultural Research Center, HARC = Humera Agricultural Research Center, TARI =Tigray Agricultural Research Institute.

3.3. Experimental Design and Procedures

The experiment was carried out using a randomized complete block design (RCBD) with three replications. Seedlings of each variety were raised on seedbeds with the size of 3mx10m. Uniform and vigorous seedlings of each variety were selected and transplanted to a well-prepared field. Each experimental plot has four rows, each 4 m long, 2.1 m width and 8.4 m^2 plot areas. A total of 7 and 28 plants per row and plot were planted respectively. The spacing between rows and plants 1 m and 0.3 m were used respectively. The central two rows (4.2 m^2) were used for data collection.

Tomato seeds for each variety were raised on January 2, 2021 near the experimental field separately and transplanted on February 5, 2021. All agronomic practices (fertilizer application, disease management, and irrigation, cultivation, weeding and stacking) were applied uniformly as per recommendation for all plots.

3.4. Data Collection

As per descriptors of tomato (IPGRI, 1996), the following parameters were collected on plot and plant basis from two middle rows.

Phonological traits

1. **Days to 50% flowering (DF):** The number of days was counted from planting to the date on which 50% of plants on the two middle rows produce at least their first flower.
2. **Days to 90% physiological maturity (DM):** The number of days was counted from planting to the stage when 90% of the plants in a plot have reached physiological maturity.
3. **Fruit filling period (FFP):** The number of days between days to flowering and days to physiological maturity.

   Fruit filling period (FFP) = Days to 90% physiological maturity - Days to 50% flowering

Yield and yield related traits:

1. **Total fruit yield:** It was obtained by adding marketable and unmarketable fruit yields and expressed as t ha^{-1}.
2. **Fruit growth rate per plant:** Computed by dividing the total fruit yield to days to fruit filling period and expressed as kg ha^{-1} day^{-1}.
3. **Fruit yield per day:** Calculated as the ratio of gain yield to days to physiological maturity and expressed as kg ha^{-1}day^{-1}.
4. **Plant height (**cm**):** The height of five randomly taken plants from each of the two middle rows were measured from the ground level to the tip of the plant at maturity and expressed in centimeters and the mean was computed.
5. **Number of primary branches per plant:** The number of primary branches of five randomly taken plants from each of the two middle rows excluding the main stem was counted at maturity and the average was taken per plant.
6. **Number of secondary branches per plant:** The average number of secondary branches formed on the primary branches per plant was counted at harvesting on individual plant basis.
7. **Number of fruits per clusters:** Number of fruits per clusters were counted from five randomly taken plants from the middle two rows and expressed as an average for each plant.
8. **Number of seeds per fruit:** The number of seeds were counted from five random fruits from each of five randomly taken plants per plot and expressed as an average of five plants per plot of two middle rows.
9. **Fruit diameter** (cm)**:** Average diameter of five fruits from each sampled plant was measured using Venire caliper at the highest bulged portion of the fruit in centimeters.
10. **Fruit width** (cm)**:** The width of five randomly selected fruits at each harvest was measured using a caliper and the mean values were taken for analysis.
11. **Fruit length** (cm): Average fruit length of five fruits from five plants was measured using a Vernier caliper from the tip to the base of the fruit and expressed in centimeters.

12. **Number of fruits per plant**: The total number of fruits harvested from the five plants was counted and the average number of fruits per plant was calculated.
13. **Total soluble solids content of fruit (%Brix):** Brix percentage was measured by Portable Refractometer at room temperature. Single fruit was blended, and juice was collected to measure Brix.
14. **Marketable and unmarketable yield (t/ha):** Diseased, insect pests, physiologically, and mechanically damaged fruits were considered as unmarketable (Lemma, 2000), while fruits free from any visible damages were considered as marketable. Both marketable and unmarketable fruits obtained from each plot area were weighed in kg and converted into a hectare basis.

3.5. Data Analysis

3.5.1. Analysis of variance

All collected data were subjected to analysis of variance (ANOVA) to check the presence of variation among the varieties for tested traits using statistical analysis software, version 9.3 (SAS, 2008). analysis of variance was computed using the following mathematical model:

$$Y_{ij}= \mu +rj+gi+ \varepsilon ij$$

Where: Y_{ij} =the observed value of the trait Y for the i^{th} genotype in j^{th} replication

μ= the general mean of trait Y

rj = the effect of j^{th} replication

gi= the effect of i^{th} genotypes and

εij= the experimental error associated with the trait y for the i^{th} genotype in j^{th} replication.

Duncan's Multiple Range Test (DMRT) at 5% probability level was used for mean separation and coefficient of percent variation (CV %) for all characters was computed (Gomez and Gomez, 1984).

3.5.2. Estimation of genetic gain

Linear regression analysis was used to calculate the genetic gain for yield and other yield-related traits (Moyer *et al*., 2004). The breeding effect was estimated as a genetic gain for fruit yield and associated traits in tomato improvement by regressing the mean of each character for each variety against the year of release of that variety (Singh and Chaudhary, 2007). The year of release of variety was determined as the number of years since 1997-2015.

The regression equation was $Y = a + bx$

Where Y- Mean value of dependent variables

x- Mean value of an independent variable

a- The constant value of dependent variable and

b- The regression coefficient or the changes in y per unit change in x.

The relative annual gain achieved over the last 18 (1997-2015) years for tomatoes was determined as a ratio of genetic gain to the corresponding mean value of the oldest variety and expressed as a percentage (Singh and Chaudhary, 1996).

Relative annual rate of gain $=\frac{\text{COV XY}}{\text{Var X}}$

Where: Cov= covariance

Var= variance

X= the year of variety release

Y= the mean value of each trait for each variety

3.5.3. Estimation of genetic parameters

3.5.3.1. Estimation of variance components

The genotypic and phenotypic variance components and their coefficient of variability were estimated based on the method suggested by Burton *et al.* (1953) as follows:

- Genotypic variance (σ^2g) = $\frac{MS_g - MS_e}{r}$

  Where: MS_g = mean square due to genotypes,

  MS_e = error mean square

  r = the number of replications

- Environmental variance (σ^2e) = error mean square = MSe
- Phenotypic variance (σ^2p) = $\sigma^2{}_g + \sigma^2{}_e$
- Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$
- Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma^2 g}}{\bar{x}}$ x100

  Where: $\bar{x}$ = grand mean of traits

3.5.3.2. Estimation of heritability in a broad sense

Heritability (H^2) in a broad sense for all traits was computed using the formula given by Falconer (1996). Broad sense heritability (H^2) is expressed as a percentage of the ratio of the genotypic variance **(**σ^2g**)** to the phenotypic variance **(**σ^2p) and estimated on genotype mean base as described by Allard (1960) as:

Heritability (H^2) = $\frac{\sigma_g{}^2}{\sigma_p{}^2}$ x100

Where: H^2 = Heritability in a broad sense

$\sigma^2{}_p$ = Phenotypic variance

$\sigma^2{}_g$ = Genotypic variance

3.5.3.3. Estimation of genetic advance

Genetic advance in the absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated by the methods illustrated by Johnson *et al.* (1955), as:

$GA = K\sigma_P H^2$

Where, K=the standardized selection differential at 5% selection intensity (k=2.063)

σ_p =phenotypic standard deviation on a mean basis

H^2=heritability in a broad sense

Genetic advance as percent of mean was calculated to compare the extent of the predicted advance of different traits under selection, using the following formula.

$$GAM = \frac{GA}{\overline{X}} X100$$

Where: GAM= genetic advance as percent mean

GA=genetic advance under selection

$\overline{X}$ = Mean of the population in which selection employed

3.5.4. Association of traits

3.5.4.1. Genotypic and phenotypic correlations

Phenotypic and genotypic correlations between yield and yield-related traits were estimated using the method described by Miller *et al*. (1958) as follows:

Phenotypic correlation coefficient (rp_{xy}) between trait x and y

$$rp_{xy} = \frac{Covp_{xy}}{\sqrt{Vp_x Vp_y}}$$

Where, Cov_{pxy} = Phenotypic covariance between trait x and y

Vp_x = Phenotypic variance for trait x

Vp_y = Phenotypic variance for trait y

Genotypic correlation coefficient (rg_{xy}) between trait x and y

$$rg_{xy} = \frac{Covg_{xy}}{\sqrt{Vg_x Vg_y}}$$

Where, Cov_{gxy} = Genotypic covariance between trait x and y

Vg_x = Genotypic variance for trait x

Vg_y = Genotypic variance for trait y

The coefficients of correlations at a phenotypic and genotypic level were tested for their significance by comparing the value of the correlation coefficient with tabulated t-value at g-2 degree of freedom. However, the coefficients of correlations at a genotypic level were tested for their significance using the formula described by Robertson (1959) as follows:

$$t = \frac{(rg_{xy})}{SEg_{xy}}$$

The calculated t-value was compared with the t-tabulated value at g-2 degree of freedom at 5% level of significance.

$$SEg_{xy} = \sqrt{\frac{(1 - r^2 g_{xy})}{2h_x . h_y}}$$

Where SEg_{xy} standard error of genotypic correlation coefficient between trait x and y

h_x = Heritability value of trait x

h_y = Heritability value of trait y

g = number of varieties

3.5.4.2. Path coefficient analysis

Path coefficient analysis was conducted as worked out by Dewey *et al.* (1959) using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effect of yield components on fruit yield based on the following relationship.

$$r_{ij}= p_{ij} +\sum r_{ik}p_{kj}$$

Where, r_{ij} = Mutual association between the independent trait (i) and dependent trait, fruit yield (j) measured by the correlation coefficients.

P_{ij} = Component of direct effects of the independent trait (i) as measured by the path coefficients and

$\sum r_{ik}p_{kj}$ = Summation of components of the indirect effect of a given independent trait (i) on a given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated as $P_R= (1- \sum r_{ij}p_{ij})$ ½, the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor. That is if PR value is small (for instance, nearly zero), the dependent trait considered (fruit yield) is fully explained by the variability in the independent trait, whereas a higher P_R value indicates that some other factors which were not considered, need to be included in the analysis to account fully the variation in the dependent trait (fruit yield).

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

Mean squares for all the traits were highly significant ($P \leq 0.01$) except for number of primary branches per plant and number of seed per fruit (Table 2), indicating the presence of sufficient genetic variability in the studied varieties for fruit yield and yield related traits. This result is in agreement with the findings of Aysh *et al*. (2012) and Meitei *et al.* (2014).

4.2. Simple Measure of Variability

The means mean squares and their coefficient of variation of the studied traits are presented in Table 2. A wide range of variability was recorded for days to 50% flowering, days to 90% maturity, plant height, number of secondary branches per plant, number of fruits per cluster, fruit width, fruit diameter, fruit length, and number of fruits per plant, fruit growth rate per plant, fruit yield per day, total soluble solid, marketable yield, unmarketable yield and total fruit yield. This significant variation in studied tomato varieties showed the presence of high variability which can exploited through selection (Hidayatullah *et al*., 2008). Previous works in tomato by Aysh *et al.* (2012) and Meena *et al*. (2015) had also observed similar progress.

Days to 50% flowering is one of the crucial parameters of tomato observed to determine the earliness of variety. The mean values of days to 50% flowering varied from 53 (Fetan) to 69 (Bishola) days with an overall mean of 57.00 days. Similarly, Masho *et al.* (2015) observed wide variation for days to 50% flowering in tomato varieties. The longer fruit filling period (50.17 days) was observed in Melkashola variety. However, the short fruit filling period value was recorded in Bishola (25.8 days) variety. Earliness is the utmost desirable parameter, as the early crop produce can obtain a higher price in the market due to its high demand and less produce at that time. Extended days to 90 % maturity was observed by variety Melkashola (109 days), whereas variety Fetan required lower number of days (84.3 days) to 90% maturity. Overall mean values was 97.00 days. Considerable variation for days to 90% of maturity were also reported by Moraru *et al.* (2004) and Fayaz *et al*. (2007) in tomato.

The mean values for plant height varied from 68 (Metadel) to 108.3 cm (Sirinka-I) with an overall mean of 85.5 cm. This result are in agreement with the findings of Hussain *et al.* (2001) and Dufera (2013), who observed a wide range for plant height in different tomato varieties. The maximum number of secondary branches per plant was recorded by variety Miya followed by Melkashola and Sirinka-1 varieties, while the smallest number of secondary branches per plant was scored by variety Mersa and Marglobe (Table 3). The number of secondary branches per plant was recorded in the range of 11-14.3. Significant variation in number of secondary branch has also been recorded in the findings of Shushay *et al.* (2013) and Masho *et al.* (2015) in tomato.

It is evident from Table 3 that significant differences were recorded in number of fruits per cluster by tomato varieties. The highest number of fruits per cluster was recorded from variety Melkasalsa, and the lowest number of fruits per cluster was recorded from variety Cochoro. The observation showed that the mean values for this trait was ranged 3.1- 5.9 with an overall means of 4.13 (Table 2). In general, the higher the number of fruits per cluster, the more fruit yield is expected, although fruit size also determines the yield estimation (Pandey, 2007), which is in line with these results.

Fruit shape and size are important not only for the consumer but also for the market. Fruit diameter is a very important parameter in tomato fruit, as fruit diameter is desirable for preference and appearance of tomato. The variety Gelilema gave the highest mean value of fruit diameter (7.13 cm), while the lowest fruit diameter (3.53 cm) was observed in Tekeze-I variety with an overall mean of 5.18 cm. The variety Marglobe had the highest (7.2 cm) fruit width which was significantly superior to all other varieties; on the other hand, variety Sirinka-1 had the lowest (3.83 cm) fruit width. The highest fruit length was scored by variety Marglobe followed by Eshet and Melkasalsa varieties (Table 3). The lowest fruit length was recorded by

Sirinka-1 variety with overall ranges from 4.1 – 7.6 cm. The ranges reported for fruit width was in line with the ranges (3.2-10.6 cm) reported by Kaushik *et al.* (2011) and Rashidi *et al.* (2011) in tomato.

The highest fruit growth rate per plant (1306 Kg ha^{-1} day^{-1}) was observed in Bishola and the lowest fruit growth rate per plant (454 Kg ha^{-1} day^{-1}) was observed in the Woyno variety. Fruit yield per day was high (154.67 Kg ha^{-1} day $^{-1}$) for the variety Chali. The variety Melkashola had the lowest fruit yield per day (218 Kg ha^{-1} day^{-1}). Total soluble solids are a desirable quality attribute for tomato in processing as well as for fresh consumption. Variety Mersa had the highest (5.0%) total soluble solid value which was significantly different from others, whereas the lowest total soluble solid value was recorded by variety Chali (3.3 %). These results conform to the findings Caliman *et al*. (2010), who reported that the total soluble solid of cultivated tomato comprised 3-7.5 % total soluble solid of its fresh weight.

Variation was observed among the varieties for number of fruits per cluster. Mersa variety had the highest (5.9) number of fruits per cluster and the lowest (3.16) number of fruits per cluster was observed for the Cochoro variety. Melkasalsa, Miya and Melkashola varieties gave the highest number of fruits per plant 36.8, 30.1 and 28.2, respectively. While the smallest number of fruits per plant were recorded by variety ARP d2 and Cochoro (Table 3). This result was in accordance with the findings of Eshteshabul *et al.* (2010), Falak *et al.* (2011) and Tadele (2016). The result of these findings showed an increasing tendency in the number of secondary branches per plant with an increase in the fruit number. These results are also in close conformity with the findings of Rastogi (1993) who reported significant variations among cultivars of tomato for the number of branches and fruits per plant.

Variety Melkasalsa (33.9 t ha^{-1}) recorded maximum marketable fruit yield, while the lowest was recorded by Tekeze-1 (19.1 t ha^{-1}). This result was in agreement with the work of Shushay *et al.* (2014), who reported that marketable tomato yield ranges from 17-56 tha^{-1}. According to Lemma (2002), sun burnt, small-sized, cracked disease and insect pest damaged fruits are considered as unmarketable. Accordingly, the highest unmarketable fruit yield was recorded in variety Fetan

(5.05 tha^{-1}) and Sirinka-1 (4.57 tha^{-1}), while the least was recorded in Gelilema (1.1 t ha^{-1}) and Metadel (1.7 tha^{-1}) varieties.

Fruit yield is one of the major goals of tomato breeding. The total fruit yield is the yield gain from any commodity both marketable and unmarketable yields. The mean average total fruit yield of all varieties was 30.3 t ha^{-1} ranged from 22.8 to 36.1 t ha^{-1} (Table 3). The highest total fruit yield (36.1 t ha^{-1}) was obtained from Melkasalsa and the lowest yielding (22.8 t ha^{-1}) variety was Tekeze-I (Table 3). The range obtained in this result was in agreement with Lemma (2002), Znidarcic *et al.* (2003) and Ketema *et al.* (2015) in tomato.

Table 2 Mean squares, CV and R^2 from analysis of variance for fruit yield and related traits in tomato varieties evaluated in 2021.

Traits	Source variation				
	Variety (15)	Error (30)	Mean	CV (%)	R^2
PH	560.77**	46.52	85.50	7.99	0.79
NPBPP	0.63^{ns}	0.53	5.09	14.42	0.38
NSBPP	2.15**	0.43	12.61	5.05	0.73
DT 50% F	54.55**	6.40	57.00	4.41	0.81
DT 90 % M	144.12**	6.61	97.00	2.71	0.91
FFP	206**	15.24	40.04	9.74	0.87
NSPF	991.69^{ns}	3539.40	123.90	47.90	0.12
NFPC	1.36**	0.31	4.13	13.16	0.68
FD	3.84**	0.43	5.18	12.64	0.81
FW	2.92**	0.15	5.20	7.67	0.90
FL	3.14**	0.04	5.53	4.02	0.97
SGR	204641.08**	5735.61	806.10	9.39	0.93
FYPD	9927.08**	91.89	314.50	3.05	0.96
TSS	0.71**	0.11	3.93	8.16	0.77
NFPP	77.80**	12.04	23.70	14.40	0.77
UMY	3.94**	0.69	3.07	26.42	0.76
MY	83.10**	0.98	27.18	3.64	0.97
TY	67.33**	0.75	30.30	2.80	0.97

**, ^{ns} = *highly significant at $P \leq 0.01$ and non-significant ($P < 0.05$) respectively.*

PH=Plant height, NPBPP= Number of primary branches per plant, NSBPP= Number of secondary branches per plant, DTM= Days to 90% maturity, DTF= Days to 50% flowering, FFP= Fruit filling period, NSPF= Number of seeds per fruit, NFPC= Number of fruits per cluster, FD=Fruit diameter, FW=Fruit Width, FL= Fruit length, SGR= Seed growth rate per plant, FYPD= Fruit yield per day, TSS= Total soluble solid, NFPP= Number of fruits per plant, UMY= Unmarketable yield, MY=Marketable yield, TY= Total yield, CV= Coefficient of variation,R^2=Coefficientofdetermination.

Table 3 Mean of yield and yield related traits of 16 tomato varieties.

	Mean of traits															
Varieties	PH	NSBPP	DTF	DTM	FFP	NFPC	NFPP	FD	FW	FL	SGR	FYD	TSS	UMY	MY	TY
Melkasalsa	74.0^{f}	13.0^{bdc}	59.1^{cbd}	102.0^{cbd}	42.6^{bdc}	3.7^{ced}	36.8^{a}	5.8^{bc}	5.7^{cb}	6.2^{c}	851.0^{dce}	354.0^{bc}	3.67^{edf}	3.5^{bdc}	32.58^{a}	36.1^{a}
Melkashola	83.3^{fdec}	13.8^{a}	59.1^{cebd}	109.0^{a}	50.1^{a}	4.1^{cebd}	28.2^{cb}	4.1^{fe}	4.1^{e}	4.1^{h}	474.1^{i}	218.4^{g}	4.1^{bdc}	3.1^{dec}	20.7^{ed}	23.8^{i}
Eshete	97.0^{bac}	12.7^{bdc}	60.0^{bc}	88.67^{ihj}	28.6^{e}	4.5^{cbd}	21^{fed}	7.0^{a}	6.4^{b}	7.2^{b}	1158.3^{b}	371.4^{ba}	3.4^{ef}	3.5^{bdac}	29.4^{bc}	32.9^{edc}
Metadel	68.0^{f}	12.0^{dec}	54.7^{efd}	94.3^{feg}	39.7^{dc}	3.6_{ced}	25.9^{cbd}	5.2^{dce}	5.5^{e}	5.5_{e}	796.3^{dfe}	330.3^{d}	3.6^{edf}	1.7^{ef}	29.4^{bc}	31.2^{ef}
Fetane	78.3^{fe}	12.2^{dec}	53.0^{f}	84.3^{j}	31.1^{e}	4.5^{cb}	24.0^{cbd}	5.1^{dce}	5.8^{cb}	5.8^{de}	928.7^{dc}	342.8^{cd}	3.7^{edf}	5.1^{a}	23.8^{d}	28.8^{g}
Bishola	89.3^{bac}	12.3^{bdc}	69.3^{a}	95^{feg}	25.8^{e}	4.1^{cebd}	22.1^{cfed}	5.5^{dc}	5.5^{cd}	5.8^{de}	1306.3^{a}	352.6^{bcd}	4.4^{bac}	1.8^{fe}	31.6^{ba}	33.5^{bdc}
Woyno	95.3^{bac}	12.9^{bdc}	54.0^{f}	93^{fhg}	39.3^{d}	4.9^{b}	20.5^{fed}	4.0^{fe}	3.8^{e}	4.4^{hg}	657^{gf}	276.6^{f}	3.8^{edf}	4.3^{ba}	21.4^{ed}	25.8^{h}
Mersa	107.3^{a}	11.0^{e}	55.0^{efd}	97.7^{fed}	42.8^{bdac}	5.9^{a}	23.0^{ced}	5.1^{dce}	5.5^{cd}	6.1^{dc}	621^{gh}	267.3^{f}	5.0^{a}	2.5^{fdec}	23.5^{d}	26.1^{h}
Sirinka-I	108.3^{a}	13.3^{bac}	55.3^{cefd}	103.7^{cb}	48.4^{ba}	4.5^{cb}	20.1^{fed}	4.0^{fe}	3.8^{e}	4.5^{g}	489.0^{ih}	226.7^{g}	3.6^{edf}	4.5^{ba}	19.0^{e}	23.5^{i}
Tekeze-I	100.0^{ab}	13.2^{bac}	54.0^{f}	104.3^{b}	50.0^{ba}	4.4^{cbd}	23.8^{cbd}	3.53^{f}	4.2^{hg}	4.2^{hg}	457.1^{i}	219.9^{g}	3.5^{edf}	3.8^{bac}	19.0^{e}	22.8^{i}
Miya	72.7^{f}	14.3^{a}	54.3^{ef}	101.3^{cbd}	47.1^{bac}	4.3^{cebd}	30.1^{b}	4.17^{fe}	4.1^{e}	4.5^{hg}	763.2^{gfe}	354.3^{bc}	4.6^{ba}	4.3^{ba}	31.5^{ba}	35.8^{ba}
Cochoro	71.7^{f}	12.1^{dec}	53.7^{f}	99.9^{ced}	45.5^{bdac}	3.2^{e}	17.2^{fe}	5.53^{dc}	5.4^{cd}	5.8^{de}	758.5^{gfe}	346.4^{cd}	4.5^{bdc}	2.1^{fde}	32.2^{a}	34.3^{bac}
Chali	80.7^{fde}	12.2^{dec}	62.0^{b}	99.9^{ihg}	29.3^{e}	3.4^{ced}	245.2^{cbd}	5.8^{bc}	5.9^{cb}	6.1^{dc}	1210.0^{ba}	389.4^{a}	3.3^{f}	3.4^{bdec}	32.1^{a}	35.5^{ba}
Marglobe	91.3^{bdec}	11.9^{de}	56.0^{cefd}	102.0^{cbd}	46.0^{bdac}	3.9^{cebd}	24.2^{cbd}	6.8^{ba}	7.2^{a}	7.6^{a}	684.0^{gf}	308.5^{e}	4.0^{edc}	2.5^{fdec}	28.9^{c}	31.4^{edf}
ARP d2	72.0^{f}	12.6^{bdc}	57^{cefd}	87.6^{ij}	30.5^{e}	3.4^{ed}	16.6^{f}	4.37^{dfe}	4.8^{d}	5.1^{f}	982.0^{c}	338.4^{cd}	3.6^{edf}	1.8^{fe}	28.2^{c}	30.6^{gf}
Gelilema	78.6^{fe}	12.2^{dec}	54.33^{ef}	98.0^{ed}	43.6^{bdac}	3.8^{ced}	21.1^{fed}	7.13^{a}	5.2^{cd}	5.5^{e}	761.9^{gfe}	342.8^{cd}	3.7^{edf}	1.1^{f}	31.6^{ba}	32.8^{edc}

Means followed by the same letter within a column are not significantly different from each other at $P \leq 0.05$ according to Duncan’s Multiple Range Test. For table foot note refer Table 3

4.1. Estimation of Genetic Gain

4.1.1. Genetic gain in fruit yield

Improvement of fruit yield is the major priority for tomato breeding in Ethiopia. Means of total fruit yield (t ha^{-1}), genetic progress in total fruit yield, average increments over the averages of older varieties, mean regression of varieties and annual relative genetic gains were presented in tables 4 to 8.

As presented in table 4, the estimated average annual rate of increase in total fruit yield potential of recently released variety Gelilema was 2900 kg ha^{-1} (9.7%) increments over the average total fruit yield of the oldest varieties (Table 4). Miya was the superior variety had yield increments of 5900 kg ha^{-1} (19.73%) over the average of the two oldest varieties followed by Chali (5600 kg ha^{-1} or 18.7%) and Cochoro (4400 kg ha^{-1} or 14.7%) varieties. These yield increments in 18 years occurred due to increase both in fruit diameter and fruit length of recently released varieties (Table 8). In different crops similar increment of varieties over oldest varieties were reported by Shearman *et al*. (2005), Yifru *et al.* (2005), Kebere *et al*. (2006), Tamene, (2008) and Demissew (2010) on wheat, tef, haricot bean, faba bean and soyabean varieties, respectively.

In contrary, the means total fruit yield of Woyno, Mersa, Sirinka-I and Tekeze-1 varieties were -4100 kg ha^{-1}, -3800 kg ha^{-1}, -6400 kg ha^{-1} and -7100 kg ha^{-1} respectively reduction over means of the oldest varieties. This showed that these varieties were lower than the mean total fruit yield of the first two released varieties (Table 4). In general, the released varieties had yield advantage over the first released one by 440 kg ha^{-1} or 1.47% (Table 6). Similarly, Yifru *et al.* (2005) in tef, Tamene (2008) in faba bean, Hailu *et al.* (2009) and Demissew (2010) in soya bean reported 71.27%, 41.44%, 37% and 67.8% grain yield increment, respectively.

Table 4 Mean fruit yield (kg ha^{-1}) and trends in genetic progress in total fruit yield released from 1997 to 2015of tomato varieties

Varieties	Year	Mean (kg ha^{-1})	Yield increment over older varieties	
			kg ha^{-1}	%
Melkashola Melkasalsa	1997	29950	—	—
Eshete	2005	32900	300	10.03
Metadel	2005	31000	1100	3.67
Fetane	2005	28800	-1100	-3.67
Bishola	2005	33500	3600	12.04
Woyno	2006	25800	-4100	-13.71
Mersa	2006	26100	-3800	-12.70
Sirinka-I	2006	23500	-6400	-21.40
Tekeze-I	2006	22800	-7100	-23.74
Miya	2007	35800	5900	19.73
Cochoro	2007	34300	4400	14.71
Chali	2007	35500	5600	18.72
Marglobe	2007	31400	1500	5.01
ARP d2	2012	30600	700	2.34
Gelilema	2015	32800	2900	9.69
Mean		30311		
CV		2.80		
R^2		0.97		

Trends in genetic progress in fruit yield of tomato varieties released during 2005, 2007, 2012 and 2015 exceed the average of the first two oldest varieties released in 1997 by 1650 (5.51%), 700 (2.34%), 4350 (14.60%) and 2900 (9.70%) kg ha^{-1}, respectively. Whereas varieties released in 2006 indicated yield reduction by -5350 (-17.90). This result showed inconsistency in fruit yield increment among varieties with respect to their year of release; this inconsistency could be due to some of the varieties released in 2006 had low yield performance than the oldest varieties and due to the variety Melkasalsa performed well in fruit yield. Similar finding was recorded by Wassu (2017) and some recently released varieties showed lower yield performance than the oldest variety of potato in Eastern Ethiopia. Tessema *et al.* (2020) also reported some recently released varieties with lower yield performance than the oldest variety in faba bean.

The average annual rate of increase per year of release for the period 1997-2015 as estimated from the slope of the graph of linear regression of mean total fruit yield on a year of variety release was 0.127 t ha^{-1} yr^{-1} (Figure 1c). It is positive and significantly different from zero. These indicated that genetic change was an important source to increase total fruit yield, and this gives an insight into possible future opportunities to exploit the genetic potential of the tomato for enhancing total fruit yield increment for sustainable future tomato production. Similarly, Tibebu *et al.* (2011) reported similar result for the chickpea genotypes with an 18.42 kg ha^{-1} yr^{-1} average rate of increase in grain yield per year of release. Hailu *et al.* (2010) also indicated a 23.61 kg ha^{-1} yr^{-1} annual rate of gain for medium maturing genotypes of soyabean.

The average relative annual gain in fruit yield of tomato varieties since 1997 was 0.40% yr^{-1} (Table 8). This implies that tomato improvement had significant efforts over the last 18 years to improve the fruit yields of tomatoes in the country. This result also revealed that genetic improvement for fruit yield has important enhancement and the best level of tomato breeder’s efforts made for past 18 years breeding progress. The result is in agreement with the findings of Grandilo *et al.* (2004), who reported an average genetic gain for yield with 1.54%/yr for California and of 0.4%/yr for Israel tomato. On the other hand, the average annual increment of this study is greater than progress made in tef and faba bean varieties in Ethiopia as reported by Yifru *et al.* (2005) and Tamene (2008), respectively.

The present investigation indicated that the last 18 (1997-2015) years tomato improvement program showed inconsistent increment in fruit yield in Ethiopia through different breeding strategies. Therefore, it is more likely that the productivity of fruit yield in the future can be increased by developing varieties using similar and other modern approaches, since the objective of tomato breeding is to increase fruit yield (Sanchez *et al*., 2019). However, there was no indication of a yield potential plateau in tomato improvement over the period studied indicating that the opportunity for breeders to further improve tomato fruit yield. In agreement with the findings of these results, Wondimu (2010) in food barley, Wassu (2017) and Tesama *et al.* (2020) in potato; reported that no evidence of a yield plateau was found, and the genetic improvement has not reached this stage.

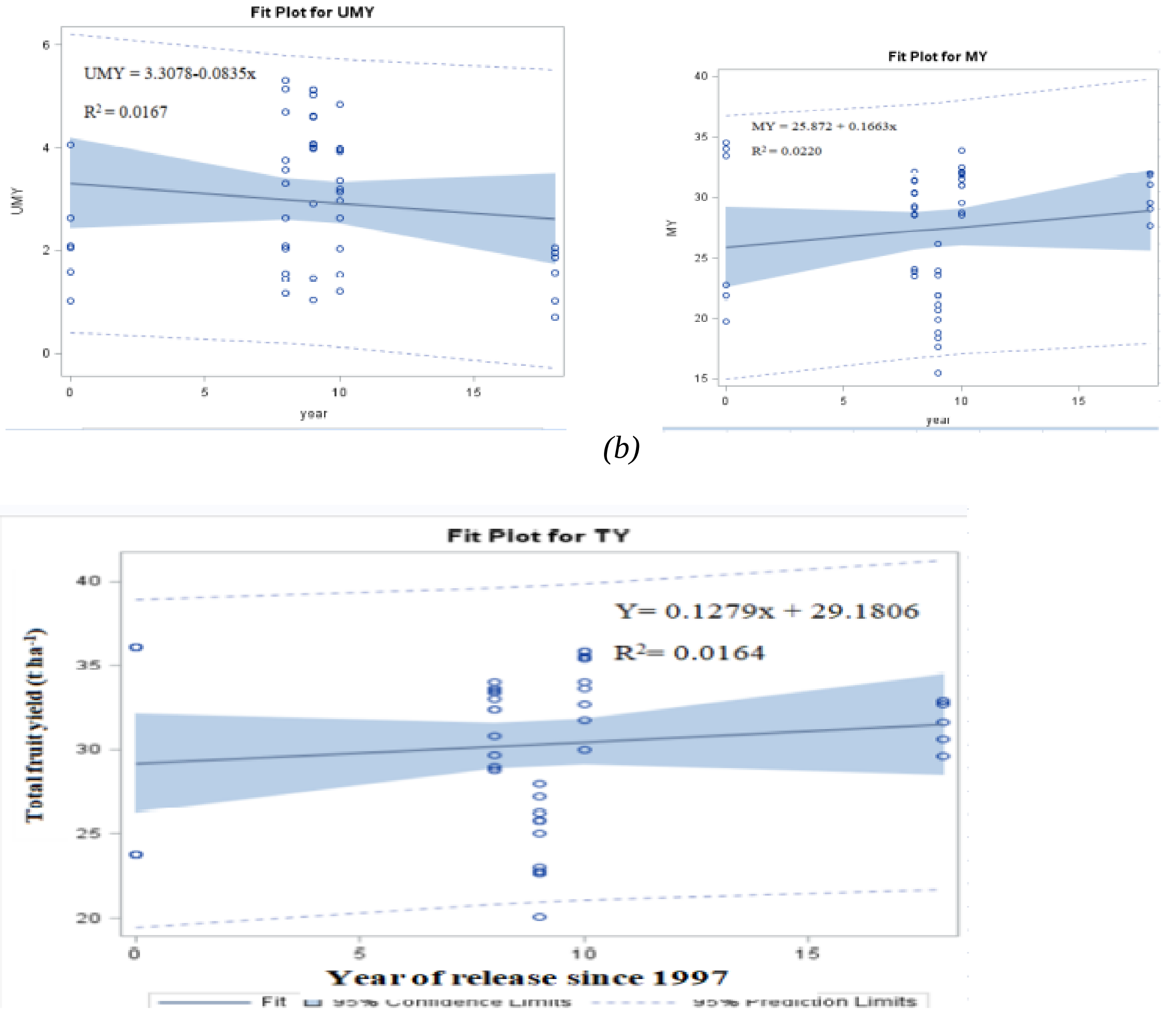
Similar genetic gain progress in crop improvement has been reported by Shukula *et al.* (2005) in Amaranths, Dilip *et al.* (2011) in fresh market tomatoes, Thirupathi *et al.* (2012) in Okra; Muluken *et al.* (2016) and Maria *et al.* (2020) in sweet potato, Antonio *et al.* (2017) in Valenciana onion, Atul *et al.* (2019) in vegetable Chenopodium and Felipe *et al.* (2020) in cherry tomatoes.

Table 5 Trends in genetic progress in fruit yield of tomato varieties released in 2005s, 2006s, 2007s, 2012 and 2015 over the average of the first two older varieties (Melkasalsa and Melkashola) released in 1997s.

Varieties	Year of release	Mean fruit yield (kg ha^{-1})	Increment over an average of the first two older varieties (1997s)	
			Kg ha^{-1}	%
Melkashola	1997	29950		-
Melkasalsa	1997			
Eshet	2005	31550	1650	5.50
Metadel	2005			
Fetan	2005			
Bishola	2005			
Woyno	2006	24550	-5350	-17.90
Mersa	2006			
Sirinka-1	2006			
Tekeze-I	2006			
Miya	2007	34250	4350	14.60
Cochoro	2007			
Chali	2007			
Marglobe	2007			
ARP d2	2012	30600	700	2.34
Gelilema	2015	32800	2900	9.71

Table 6 Average increments in fruit yield over the averages of older varieties (Melkashola and Melkasalsa).

Varieties	Average fruit yield (kg ha^{-1})	Average fruit yield increment over an older variety	
		Kg ha^{-1}	%
Older varieties	29950	-	-
New varieties	30340	440	1.47



(a) (b)

(c)

Figure 2 A fit plots of unmarketable yield (a), marketable yield (b) and total fruit yield (t ha^{-1}) (c) against the year of varieties released since 1997.

4.1.2. Genetic gain in fruit yield-related traits and total soluble solid

As it was estimated from regression of variety means against the year of release, the tested varieties correspondingly with the year of variety release over the past 18 (1997-2015) years exhibited significant amount of annual and average relative genetic gain in fruit yield-related traits and TSS value (Table 7 and 8). As it was estimated from regression of variety means against the year of release, there was -0.23 cm plant^{-1} year^{-1} (Figure 2a) and 0.27% year^{-1} annual rate of gain and relative annual genetic gain in plant height, respectively. In line with this result, Wondimu (2010) found a significant ($P < 0.05$) negative reduction trend on the year of release for plant height with an average annual genetic gain of -0.39 cm plant^{-1} (-0.33%) year^{-1} in barley. Likewise, significant reduction in plant height in linseed and wheat has been reported by Donmez *et al*. (2001) and Ersullo (2010), respectively.

In addition, the regression analysis indicated a significant and negative regression coefficient and relative genetic gain in days to flowering with -0.223 days year^{-1} and -0.38 % year^{-1} (Figure 2c), respectively. This significant reduction in days to flowering was recorded due to the early flowering traits of some recently released varieties like Chali and Bishola as compared to the average of the oldest varieties (Table 3). This result indicated that the genetic change had a vitally important source to reduce days to flowering in the past 18 years. Tessema *et al.* (2020) also reported negative genetic gain for days to flowering in potatoes. As evident from regression of variety means against the year of release, a significant negative annual genetic gain and annual relative change of fruit filling period were -0.839 days year^{-1} and -0.78% year^{-1}, respectively (Table 8).

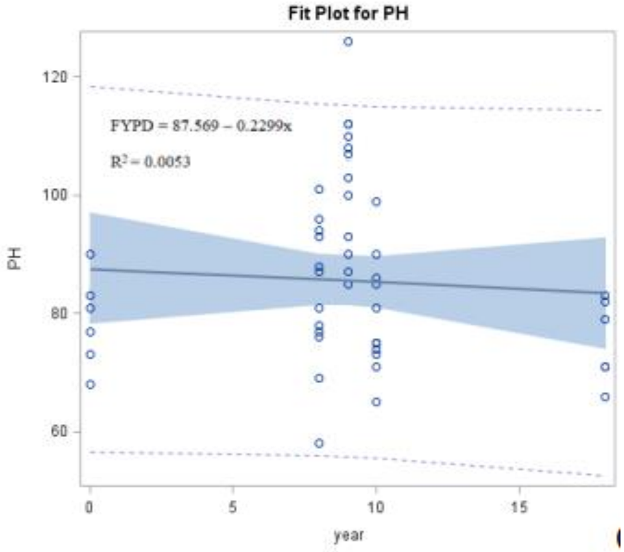
The relative annual genetic gain since 1997 was found significantly negative with -0.56 days year^{-1} (Table 8) for days to 90% physiological maturity. Days to 90% maturity are important phonological parameters showed an annual reduction of -0.58 % day's year^{-1} over the past 18 years (Figure 2c). The estimated annual rate of change was in the same direction as that of days to flowering; however, it was significant reduced, as it was observed for days to flowering (Table 8). This indicates that there was no continuous improvement in 18 years of tomato breeding for reduction of the number of days to 90% maturity. Genetic gain in a short fruit filling period may have an advantage over the longer fruit filling period of old varieties to withstand unexpected stress in a growth period and early matured varieties are important for early marketing in the season which mostly earns a good price. Likewise, a significant reduction in days to maturity was reported in desi type chickpea by Tibebu (2011).

The average relative genetic gain of fruit diameter over the last 18 years was 1.21% year^{-1}. This gain was highly significantly ($p \leq 0.01$) and different from zero and showed that fruit diameter was increased parallel with the release of new varieties with an annual increase of 0.064 cm fruit^{-1} year^{-1}. Like fruit diameter, the regression analysis indicated a positive regression coefficient in fruit width with 0.01% year^{-1}. This value was significantly different from zero (Table 7). The average relative genetic gain of fruit width was found to be 0.19% year^{-1}. Linear regression coefficient indicated that fruit length for the period studied was significantly different from zero (Table 7).

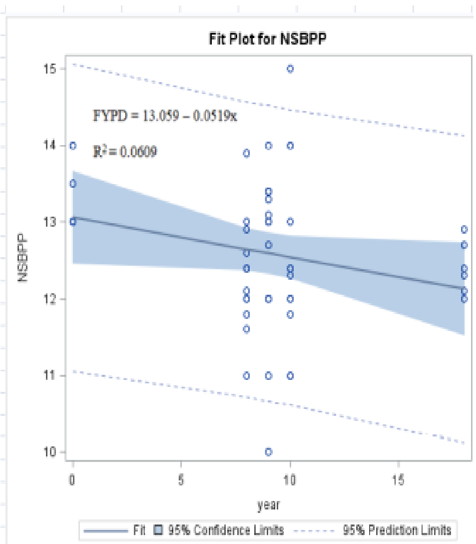
As evident from regression of variety means against the year of release, the annual rate of gain for fruit length was 0.008 cm fruit^{-1} year^{-1} with the average relative genetic gain of 0.19% year^{-1}. This result implies that the tomato improvement program has made substantial progress in improving these traits in 18 years of breeding progress in parallel to fruit yield. Likewise, a positive significant annual genetic improvement trend was made over tomato varieties for these traits (Table 8) reveals that, efforts of the breeder to satisfy customers' needs in preference and appearance in 18 years breeding cycles, since these traits are an important parameter for variety selection and customer preference (Meneberu *et al*., 2011). Similarly, Finzi *et al*. (2020) reported 5.50 to 9.41% average relative genetic gain for fruit diameter in tomato. However, in opposition to these results, Enrique *et al*. (2018) reported fruit length and fruit diameter had negative values of gains in his work of stability and breeding potential of tomato hybrids.

The regression of the mean fruit growth rate per plant of studied varieties on the year of release showed that there was 9.82 kg ha^{-1} year^{-1} average annual rate of increase over the past 18 years improvement (Table 7). This highly significant and different from zero value indicates the positive progress from the old to the recently released varieties in fruit growth rate per plant. The relative annual fruitd growth rate per plant increase in tomato varieties was estimated to be a

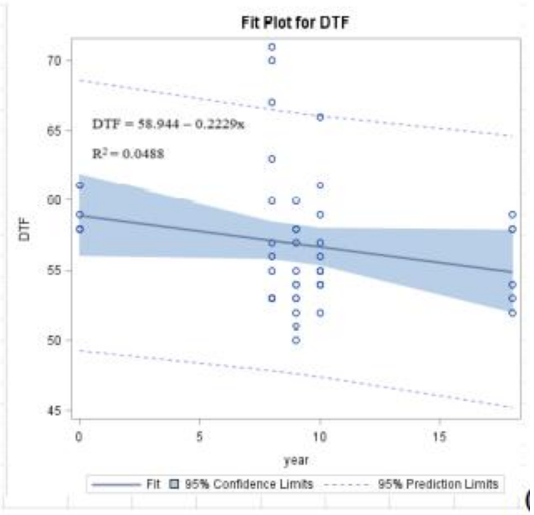
1.48% year^{-1} for the last 18 years (Table 7). Similarly, result of linear regression analysis showed that fruit yield per day in recently released varieties increased significantly (Table 7) with the average annual rate of 3.05 kg ha^{-1} day^{-1}. The relative genetic gains of fruit yield per day were 1.06% year^{-1}, indicating that these traits were effectively and significantly improved for the last 18 years of the tomato improvement program. From the result of linear regression of these findings, fruit growth rate per plant and fruit yield day^{-1} against the years of release scored the maximum relative genetic gain (Table 8), these reflecting that better genetic improvement was obtained from breeding for these traits than it was from breeding for fruit yield and other traits. A significant increase in fruit growth rate per plant and fruit yield per day was also reported by Tibebu (2011) in chickpea. This was also in agreement with the investigation of Yifru *et al* (2005) on tef and Kebere *et al*. (2006) on haricot bean.



(a)



(b)


Fit Plot for DTF
DTF = 58.944 – 0.2229x
R² = 0.0488
DTF
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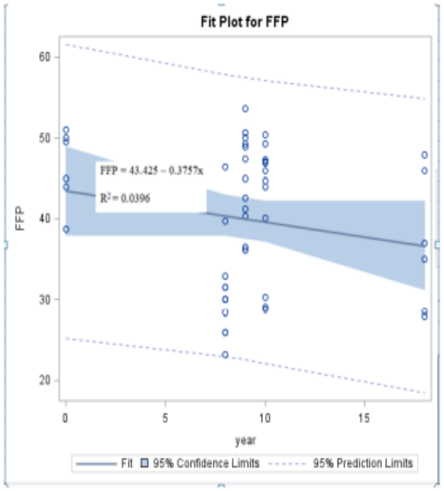
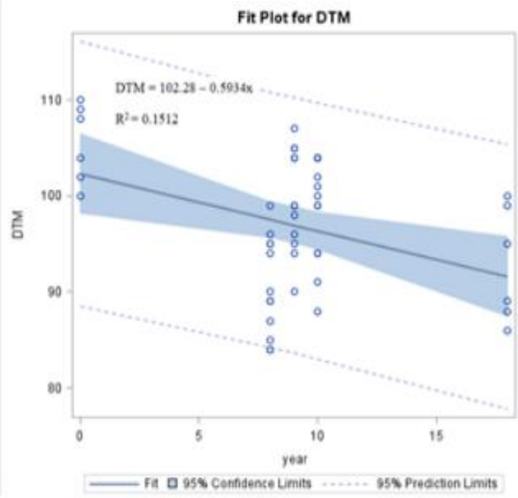
65
60
55
50
45
0
5
10
15
year
Fit
95% Confidence Limits
95% Prediction Limits

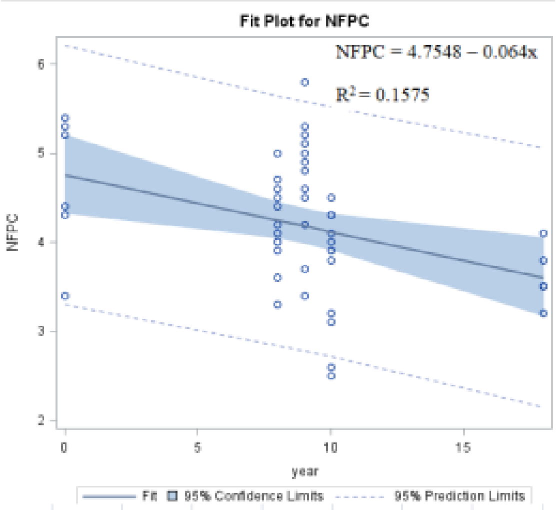
(c)

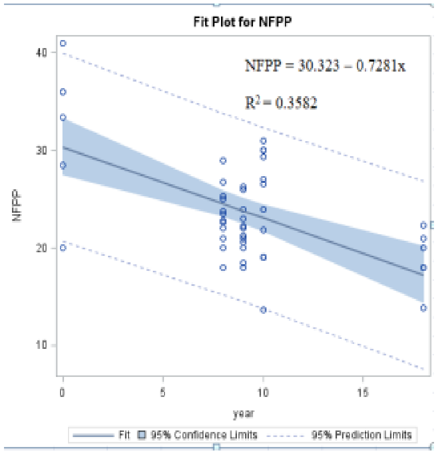

Fit Plot for FFP
FFP = 43.425 – 0.3757x
R² = 0.0396
FFP
60
50
40
30
20
0
5
10
15
year
Fit
95% Confidence Limits
95% Prediction Limits

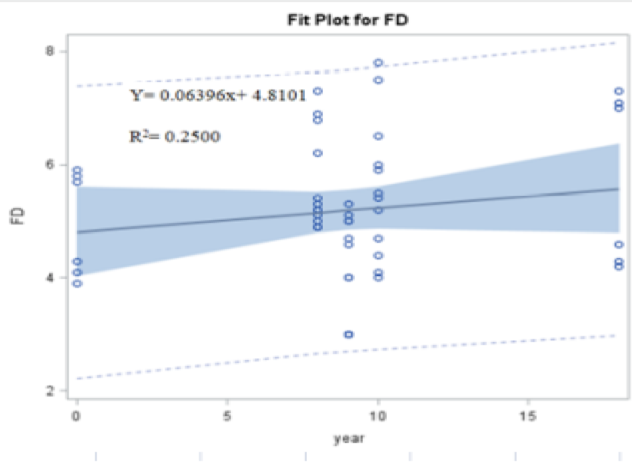
(d)


Fit Plot for DTM
DTM = 102.28 – 0.5934x
R² = 0.1512
DTM
110
100
90
80
0
5
10
15
year
Fit
95% Confidence Limits
95% Prediction Limits

(e)


Fit Plot for NFPC
NFPC = 4.7548 – 0.064x
R² = 0.1575
NFPC
6
5
4
3
2
0
5
10
15
year
Fit
95% Confidence Limits
95% Prediction Limits

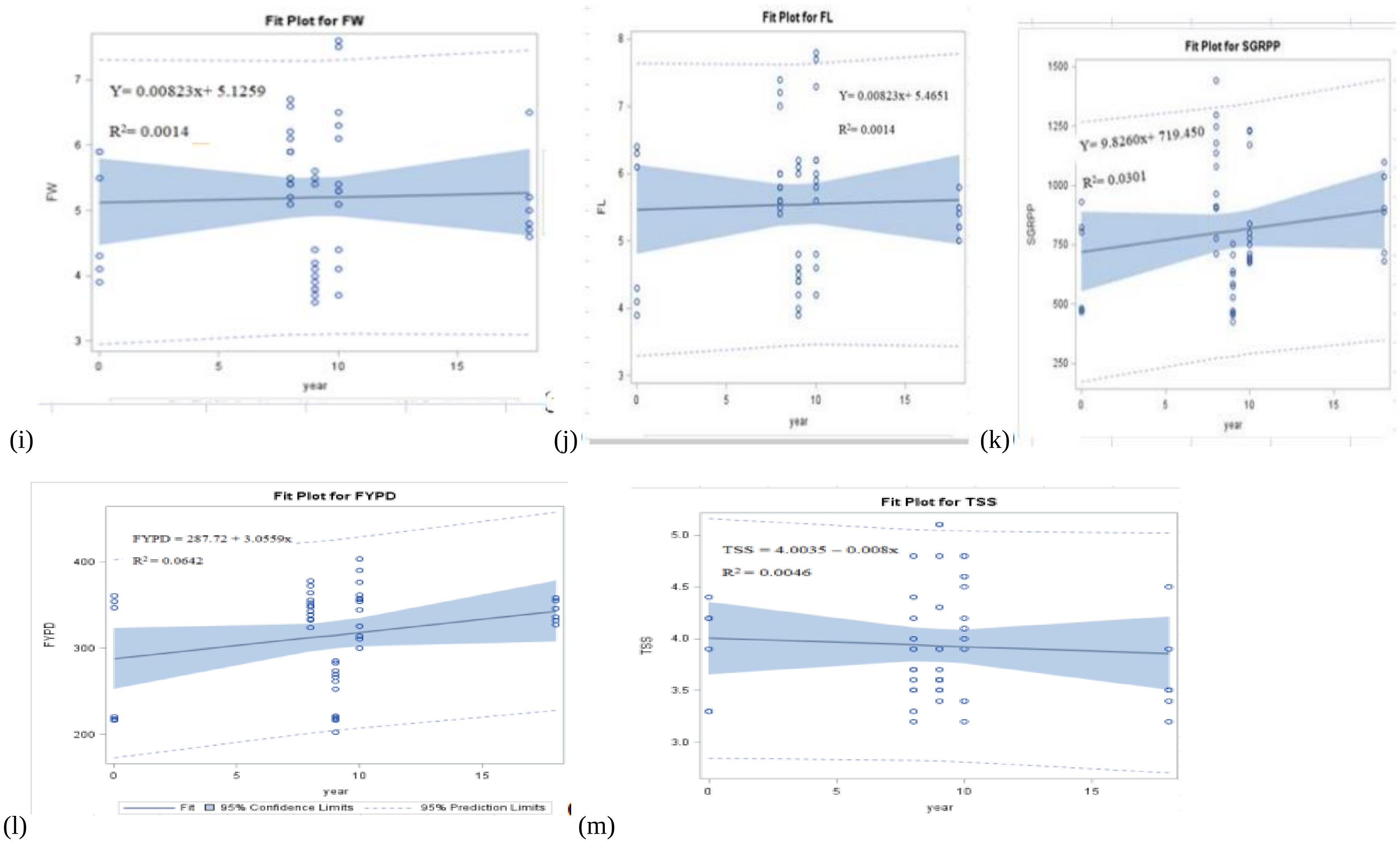

Fit Plot for NFPP
NFPP = 30.323 – 0.7281x
R² = 0.3582
NFPP
40
30
20
10
0
5
10
15
year
Fit
95% Confidence Limits
95% Prediction Limits


Fit Plot for FD
Y= 0.06396x+ 4.8101
R²= 0.2500
FD
8
6
4
2
0
5
10
15
year

(f)

(g)

(h)



(i) (j) (k)

(l) (m)

Figure 3 A fit plot of plant height (a), number of secondary branches per plant (b), days to 50% flowering (c), fruit filling period (d), days to 90 % maturity (e), number of fruits per cluster (f), number of fruits per plant (g), fruit diameter (h), fruit width (i), fruit length (j), fruit growth rate per plant(k), fruit yield per day (l) and total soluble solid(m).

Table 7 Mean regression of varieties (2005-2015), gain in percentage and regression coefficient (b) in 18 years compared to an average of oldest varieties (Melkasalsa and Melkashola).

Traits	Regression means (1997-2015)	Intercept	Regression coefficient (b)
Plant height	87.57	85.57	-0.22^{**}
Number of secondary branches per plant	12.59	13.06	-0.05^{**}
Days to 50% flowering	56.93	58.94	-0.22^{**}
Days to 90% maturity	96.93	102.27	-0.59^{**}
Fruit filling period	40.05	43.43	-0.36^{**}
Number of fruits per cluster	4.18	4.75	-0.06^{**}
Number of fruits per plant	23.77	30.32	-0.72^{**}
Fruit diameter	5.19	4.81	0.06^{**}
Fruit width	5.20	5.12	0.01^{**}
Fruit length	5.54	5.46	0.01^{**}
Fruit growth rate per plant (kg ha^{-1} day^{-1})	807.88	719.45	9.82^{**}
Fruit yield per day (kg $ha^{-1}day^{-1}$)	315.23	287.72	3.05^{**}
TSS (%)	3.93	4.01	-0.01^{**}
Unmarketable yield (t ha^{-1})	3.067	3.39	-0.08^{**}
Marketable yield (t ha^{-1})	27.24	25.26	0.16^{**}
Total yield (t ha^{-1})	30.30	29.18	0.12^{**}

*** = Significant ($P \leq 0.01$) at distribution of t Probability*

Table 8 Mean of regression, coefficient of determination (R^2) and average relative genetic gain (% $year^{-1}$) of the studied varieties since 1997-2015.

Traits	Average means of oldest varieties (1997s)	Coefficient of determination (R^2)	ARGG (% $year^{-1}$)
Plant height	78.66	0.01	-0.27
Number of secondary branches per plant	59.16	0.61	-0.08
Days to 50% flowering	56.93	0.05	-0.38
Days to 90% maturity	105.50	0.59	-0.56
Fruit filling period	46.38	0.01	-0.78
Number of fruits per cluster	4.66	0.03	-1.28
Number of fruits per plant	32.48	0. 35	-2.21
Fruit diameter	4.95	0.25	1.21
Fruit width	4.93	0.01	0.20
Fruit length	5.18	0.01	0.19
Fruit growth rate per plant (kg ha^{-1} day^{-1})	662.76	0.03	1.48
Fruit yield per day (kg $ha^{-1}day^{-1}$)	286.18	0.06	1.06
Total soluble solid (%)	3.88	0.01	-0.25
Unmarketable yield (t ha^{-1})	2.24	0.09	-3.57
Marketable yield (t ha^{-1})	27.71	0.03	0.58
Total yield (t ha^{-1})	29.95	0.02	0.40

ARGG= Average relative genetic gain

Number of secondary branches showed significant and negative genetic reduction against years of variety released (Table 7). This proves the challenges to increase these traits over the last 18 years of tomato breeding progress. This could be due to the oldest varieties having greater number of secondary branches per plant than recently released varieties. Results of the linear regression showed that, the significant reduction progress in relative and annual genetic improvement in the number of secondary branches per plant with -0.08% year^{-1} and -0.051 year^{-1}, respectively (Table 8 and Figure 2b). It is true that as the number of secondary branches increased fruit yield also increased. This is contrary to the regression analysis result of these findings, i.e. this is due to mean regression of older varieties that had more secondary branches and fruit number with low fruit yield than average of recently released varieties. This is in agreement with the findings of Masho *et al.* (2015), who reported varieties with the highest number of secondary branches recorded gave low yield.

The regression mean value of number of fruits per cluster and number of fruits per plant of tomato varieties on the year of release was -0.05191 and -0.72814 year^{-1} of average annual rate of reduction, respectively (Figure 2f and g). The regression mean of these traits also implies that there was a significant and negative relative and annual reduction of -1.24% and -2.41 year^{-1}, respectively for the past 18 years. This indicated that the breeding progress on tomatoes has failed to bring substantial progress on these traits. Hence this is due to the average of older varieties being greater than the average of recently released varieties in these traits. Similarly, Finzi *et al.* (2020) reported reduction trends in the number of fruits per plant in their studies of genetic gain in advanced tomato lines. Significant reduction progress in the number of secondary branches per plant, number of fruit per clusters and number of fruit per plant may be considered as the result of a positive need response to the increment in fruit size through the period of variety development. However, for the selection of superior varieties all traits must make simultaneously.

From results of linear regression, total soluble solid value for studied tomato varieties on a year of variety release indicated significant trends of reduction throughout study (Table 7). Total soluble solid scored a relative gain of -0.25 % year^{-1} and an annual gain of -0.008 year^{-1}, these results confirming that improvements on fruit quality (TSS) traits through breeding for the last 18 years breeding progress was relatively moderate as compared to fruit yield and fruit yield-related traits.

Generally, from the present findings the newly released varieties were the most important sources of genetic material contributing to the genetic improvement of fruit yield in 18 years of breeding progress. These imply that concerns of the breeder to increase in fruit yield of tomato varieties in the last 18 years of breeding progress. However, the significant and strong relationship between fruit yield and fruit size (fruit diameter and fruit length) and non-significant relationship of number of secondary branches per plant, number of fruits per cluster and number of fruits per plant with total fruit yield showed the compensatory relationship between the two traits. Therefore, selection of superior tomato varieties should be made considering several traits simultaneously, in order to maximize genetic gains for the greatest number of traits possible (Vasconcelos *et al*., 2010; Rezende *et al*., 2014).

4.2. Estimation of Genetic Parameters

4.2.1. Estimations of variance components

The results of genotypic variance (σ^2g), phenotypic variance (σ^2p) and the genotypic coefficient of variations (GCV) and phenotypic coefficient of variations (PCV) are presented in table 9. As per Deshmukh *et al. (*1986), phenotypic and genotypic variance and their coefficient can be categorized as low (<10%), moderate (10-20%) and high (>20%).

Accordingly, higher genotypic variances (σ^2_g) was observed for days to 90 % maturity (45.89%), fruit filling period (63.58%), fruit growth rate per plant (66301.00%), fruit yield per day (3278.39%), number of fruits per plant (21.92%), marketable yield (27.37%), total fruit yield (22.19%) and plant height (171.41%). High genotypic variance indicates more contribution of genetic component for the total variation of the varieties. These traits are a key component of breeding programs for broadening the gene pool of tomato (Ahmad *et al.*, 2011). Therefore, these traits considered to be the most important in formulating an efficient breeding program since they have high nature and extent of genetic variability (Pradipta *et al*., 2014). These results are in accordance with the results obtained by Hermanpreet *et al.* (2018).

Moderate genotypic (σ^2g) variance was observed for days to 50% flowering (16.05%), whereas low genotypic variance was observed by total soluble solid (0.22%), number of secondary branches per plant (0.57%), number of fruits per clusters (0.35%), fruit diameter (1.13%), fruit length (1.03%), fruit width (0.92%) and unmarketable yield (1.08%). Low genotypic variance revealed the genotypic component of variation had a low contributor to total variation. This result agrees with the findings of Dasta *et al.* (2020) reported that low genotypic variance for fruit diameter, fruit length, total soluble solid, number of branches per plant and number of fruits per cluster in tomato varieties.

Higher phenotypic variances ($\sigma^2{}_p$) were recorded for days to 90% maturity (52.44%), fruit filling period (78.82%), fruit growth rate per plant (72037.80%), fruit yield per day (3370.28%), marketable yield (28.55%), and number of fruits per plant (33.96%), total fruit yield (22.94%) and plant height (217.93%). High phenotypic variance implies the strong influence of environmental factors during the growth period of the varieties for their expression. These results are in accordance of Desta *et al*. (2021). Low phenotypic variance was observed by total soluble solid (0.31%), number of secondary branches per plant (1.01%), number of fruits per cluster (0.66%), fruit diameter (1.56%), fruit length (1.08%), fruit width (1.07%) and unmarketable yield (1.77%), indicates a low influence of environmental factors on these traits during the growth period. These results are in accordance of Kashif *et al.* (2013) for total soluble solid and Mehedi *et al.* (2016) for fruit diameter in their findings of genetic variability of tomato.

4.2.2. Estimates of genotypic and phenotypic coefficient of variation

The estimates of genotypic coefficient of variation (GCV) were highest for fruit growth rate per plant (31.94%), fruit diameter (20.58%) and unmarketable yield (33.91%). High genotypic coefficient of variation showed the presence of exploitable genetic variability among the studied varieties. This result agrees with the findings of Anjum *et al.* (2009) and Prema *et al*. (2011a).

Moderate genotypic coefficients of variations (GCV) were observed for plant height (15.31%), number of fruits per cluster (14.32%), fruit width (18.47%), fruit yield per day (18.21%), total soluble solid (11.37%), marketable yield (19.24%) and total fruit yield (15.54%). These revealed the presence of moderate generic variability with these traits. This result is in agreement with the findings of Ara *et al.* (2009) for the number of fruits per cluster and plant height in tomato.

Higher phenotypic coefficients of variations (PCV) were recorded for fruit growth rate per plant (33.29%), fruit diameter (24.67%), number of fruits per plant (24.58%), fruit filling period (22.17 %) and unmarketable yield (43.37%), indicated the higher magnitude of variability and huge potential for improvement of these traits through direct selection to enhance the potentiality of fruit yield and related traits. Similar highest PCV values for these traits were reported by Hermanpreet *et al.* (2018), Sharma *et al.* (2019) and Sunanda *et al.* (2019) in their genetic variability findings in tomato. A moderate amount of PCV was recorded for plant height (17.26%), number of fruits per cluster (19.67%), fruit width (19.92%), fruit yield per day (18.45%), total soluble solid (14.16%), marketable yield (19.59%) and total fruit yield (15.54%). These revealed the presence of moderate environmental influence on these traits and a favorable situation for selection (Sharma *et al.*, 2009). Dasta *et al.* (2020) also observed high phenotypic variations for the number of fruits per clusters and plant height; Kumar (2010) for plant height and total fruit yield and Rakesh *et al.* (2017) for the number of fruit per cluster in tomato.

Among studied traits, the lowest GCV were observed for number of secondary branches per plant (6.04%), days to 50 % flowering (7.02%) and days to 90% maturity (6.97%%). Moderate rate of GCV is an indication of the existence of variability in the varieties to a certain extent for these traits and low genetic contribution of these traits. It is in harmony with the report of Dasta *et al.* (2020) for the number of secondary branches per plant. The lowest PCV value was observed for number of secondary branches per plant (7.94%), days to 50 % flowering (8.31%) and days to 90% maturity (7.46%). Similarly, Suma (2014) reported low PCV for days to flowering (5.16%) in tomato.

In general, the phenotypic coefficient of variances was slightly greater than genotypic coefficient of variances for all studied traits, which implies that all these traits are less influenced by environmental variations. However, the genotypic coefficient of variation had the same progress as the phenotypic coefficient of variation and there was a close correspondence between GCV and PCV values, except for plant height, fruit filling period, fruit diameter, fruit length, TSS and number of fruits per plant (Table 9). The close correspondence of GCV and PCV values for these traits are indication of the major variation observed is genetic and these traits less influenced by an environmental factor. This also suggested that selection for such traits effective based on phenotypic performance (Khanom *et al*., 2008).

Thereby, narrow differences between GCV and PCV also confirmed the small effect of the environment. The highest estimate of PCV than the corresponding GCV indicated the relative effects of the environment (to some degree) on the expression of the traits. In general, existence of phenotypic and genotypic coefficient of variations suggested that there are good opportunities for the scope of tomato improvement through selection. It is in agreement with the report of Renuka *et al.* (2017) in his findings of genetic variability studies in cherry tomato. The result was also in line with the findings of Islam *et al.* (2010) and Patil *et al.* (2013). .

Table 9 Estimates of genotypic and phenotypic variance components, coefficient of variances, broad-sense heritability and genetic advance for 16 quantitative traits in tomato

Traits	Mean	σ^2_e	σ^2_g	σ^2_P	GCV %)	PCV (%)	H^2 (%)	GA at 5%	GAM (%)
Plant height (cm)	85.50	46.52	171.41	217.93	15.31	17.26	78.65	23.95	28.01
Number secondary branches per plant	12.61	0.43	0.57	1.01	6.04	7.94	57.14	1.18	9.36
Days to 50% flowering	57.01	6.4	16.05	22.45	7.02	8.31	71.49	6.98	12.26
Days to 90 % maturity	97.00	6.61	45.83	52.44	6.97	7.46	87.39	13.05	13.46
Fruit filling period	40.04	15.24	63.58	78.82	19.91	22.17	80.66	14.77	36.91
Number of fruits per cluster	4.13	0.31	0.35	0.66	14.32	19.67	53.03	0.89	21.52
Fruit diameter (cm)	5.18	0.43	1.13	1.56	20.58	24.67	72.55	1.87	36.16
Fruit width (cm)	5.2	0.15	0.92	1.07	18.47	19.92	86.02	1.83	35.35
Fruit length (cm)	5.53	0.04	1.03	1.08	18.38	18.73	96.27	2.05	37.02
Fruit growth rate per plant (kg ha^{-1} day^{-1})	806.1	5735.61	6630.00	72037.33	31.94	33.29	92.03	509.61	63.22
Fruit yield per day (kg ha^{-1} day^{-1})	314.5	91.89	3278.39	3370.28	18.21	18.45	97.27	116.51	37.04
Total soluble solids (%)	3.93	0.11	0.22	0.31	11.37	14.16	64.51	0.74	18.85
Number of fruits per plant	23.70	12.04	21.92	33.96	19.75	24.58	64.54	7.75	32.74
Unmarketable yield (t ha^{-1})	3.07	0.69	1.08	1.77	33.91	43.37	61.09	1.67	54.66
Marketable yield (t ha^{-1})	27.18	0.98	27.37	28.55	19.24	19.59	96.54	10.61	39.01
Total yield (t ha^{-1})	30.30	0.75	22.19	22.94	15.54	15.81	96.73	9.55	31.54

σ^2e= environmental variability or mean square of error, σ^2g= Genotypic variability, σ^2p= Phenotypic variability, PCV=Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation, H^2= Heritability in broad sense, GA= Genetic Advance at 5%, GAM= Genetic Advance as percentage of Mean

4.2.3. Estimate of broad-sense heritability

The results of the broad sense heritability for 16 traits of tomato varieties are presented in table 9. Heritability estimates for the studied traits varied from 53.03% for number of fruits per cluster to 97.27% for fruit yield per day. According to Dabholkar (1992) heritability is generally classified as low (<10%), moderate (10-30%) and high (>30%). In this study, high broad-sense heritability was observed in all traits (Table 9), indicating the variation observed was mainly under genetic control and traits were least influenced by the environmental factors (Songsri *et al.*, 2008). Although, high heritability for these traits showed that direct selection based on these traits is efficient because this parameter corresponds to the proportion of total variability that is genetic (Falconer and Mackay, 1996). High heritability estimates worked out in the present investigation align with reports by Jiregna *et al.* (2011) and Renuka (2017) in tomato.

Besides these, selection for improvement on such traits may be useful always, because of broad-sense heritability is based on total genetic materials which include both fixable (additive and additive x additive components) and non-fixable (dominance and epistatic minus additive x additive, and environmental fractions) variances components. Shushay *et al.* (2014) stated that the genetic constitution in the expression of these traits and indicated the relatively by small contribution of the environmental factors for these traits. High heritability value for these traits helps to make a selection of superior varieties based on phenotypic performances (Hayder *et al.*, 2007) and to estimate the information which helps the breeders for selecting the varieties for further use (Neeraj *et al.*, 2015).

4.2.4. Estimates of genetic advance

According to Johnson *et al.* (1955) genetic advances classified as low (<10%), moderate (10-20%) and high (>20%). Accordingly, high genetic advance was observed for plant height (23.95%), fruit growth rate per plant (509.61%) and fruit yield per day (116.51%). Such high values of genetic advance indicating that the expressions of those traits are majorly governed by additive gene action and the possibility of genetic improvement of those traits through direct selection could be effective. High estimates of genetic advances for these traits are in agreement with the results reported by Anjum *et al*. (2009) and Prema *et al*. (2011a) in tomato.

Estimates of genetic advance as percent of mean (GAM) at 5% selection intensity varied from 9.36 to 63.22% for the number of secondary branches per plant and fruit growth rate per plant, respectively. Genetic advance in percent of mean was high for all studied traits except for number of secondary branches per plant (9.36%), days to 50% flowering (12.36%) and days to 90% maturity (13.46%). High genetic advance as percentage of mean showed that selection for such traits could be effective for tomato improvements as they governed by additive genes and are less influenced by environmental factors. There is an influence of fixable additive gene effects for the inheritance of these traits; therefore, selection for these traits may lead to fast genetic improvement. Sunanda *et al*. (2019) also reported high GAM for plant height, number of fruits per plant and number of fruits per cluster in tomato. Whereas number of secondary branches per plant had low GAM, indicating that these traits are mainly under the control of non-additive gene action.

High heritability and genetic advance as percent of mean attributable to highly additive gene effects for plant height, fruit filling period, number of fruits per cluster, fruit diameter, fruit width, and fruit length, fruit growth rate per plant, fruit yield per day, number of fruits per plant, unmarketable yield, marketable yield, and total fruit yield (Table 9). High heritability and high genetic advance for these traits indicates that it is governed by additive gene action and, therefore, it provides the most effective condition for selection (Nwosu *et al*., 2014). This result is in agreement with the findings of Bharti *et al.* (2002), Singh *et al.* (2002) and Khanom *et al.* (2008) in their genetic variability studies of tomato. On the other hand, high heritability with low advance as percent of mean for number of secondary branches per plant indicated these traits which are mainly governed by nonadditive gene action, improving them through simple or the selection upon this trait might not be promising. Similar results were reported by Pradipta *et al.* (2014) and Meena *et al.* (2015) in tomato.

4.3. Association of Traits

4.3.1. Correlation of analysis

4.3.1.1. Phenotypic and genotypic correlation of fruit yield with yield related traits and total soluble solid

Estimates of genotypic and phenotypic correlations coefficient between fruit yield and fruit yield related traits are presented in table 10 and 11. Fruit yield had positive significant association ($p \leq 0.01$) at genotypic level with fruit growth rate per plant (0.724), fruit yield per day (0.935) and marketable yield (0.984). These indicated the progressive improvement in these traits were successful in developing varieties and selection of these traits might have good impact on fruit yield. These also indicates that varieties with high fruit growth rate, fruit yield per day and marketable yield producing high fruit yield. Total fruit yield also showed a significant positive correlation ($p \leq 0.05$) with fruit width (0.558) and fruit length (0.558) at genotypic level (Table 10). These traits offered much scope for selection towards yield improvement and could be given due importance for further breeding programs (Adnan *et al.,* 2017). Mehedi *et al.* (2016) also reported that significant and positive association between traits suggested additive genetic model thereby less affected by the environmental fluctuation. Similarly, significant positive associations of fruit yield with fruit diameter and fruit length were also reported by Islam *et al*. (2010) and Harmanpreet *et al.* (2018).

Total fruit yield exhibited significant positive ($p \leq 0.01$) correlation at phenotypic level with fruit growth rate per plant (0.700), fruit yield per day (0.930) and marketable yield (0.979). Total fruit yield also showed a significant and positive ($p \leq 0.05$) correlation with fruit width (0.508), fruit length (0.520) and fruit diameter (0.592) at phenotypic level indicating that how these traits are important yield components and critical determinants of fruit yield in tomato (Table 11). This result is similar to the findings of Ullah *et al.* (2015) for fruit diameter and fruit width of tomato.

In general, the correlation coefficient analysis revealed that, in many cases, the values of genotypic correlations were found to be slightly higher than phenotypic correlation values, revealing the presence of inherent association among traits and the presence of inherent genetic relationships among various traits and the phenotypic expression of these traits were less influenced by the environment (Islam *et al.,* 2010). In support to this, Kotal *et al*. (2010), Dabi *et al*. (2016), Ambresh *et al.* (2017) and Ashebr *et al*. (2020) were found a higher magnitude of genotypic correlations as compared to phenotypic correlation coefficients in their findings of genetic variability in tomato.

Table 10 Genotypic correlation coefficient for the 16 studied traits.

Traits	PH	NSB	DTF	DTM	FFP	NFPC	FD	FW	FL	SGR	FYPD	NFPP	TSS	UMY	MY
NSB	0.007														
DTF	0.012	-0.076													
DTM	0.208	0.493	-0.067												
FFP	0.164	0.449	-0.557*	0.867**											
NFPC	0.653**	0.293	-0.070	0.173	0.177										
FD	-0.208	-0.580*	0.254	-0.237	-0.328	-0.229									
FW	-0.165	-0.728**	0.326	-0.379	-0.480	-0.230	0.944**								
FL	-0.040	-0.701**	0.270	-0.346	-0.424	-0.099	0.928**	0.999**							
SGR	-0.359	-0.359	0.685**	-0.701**	-0.926**	-0.325	0.513*	0.566*	0.521*						
FYPD	-0.649**	-0.330	0.356	-0.626**	-0.700*	-0.429	0.642**	0.603*	0.583*	0.867**					
NFPP	-0.251	0.474	0.154	0.509*	0.339	0.500*	-0.096	0.008	-0.038	-0.140	-0.004				
TSS	0.056	-0.201	-0.057	0.329	0.308	0.024	-0.095	-0.080	-0.054	0.196	-0.098	0.026			
UMY	0.459	0.690**	-0.282	-0.046	0.099	0.757*	-0.504*	-0.401	-0.341	-0.260	-0.335	0.283	-0.250		
MY	-0.708**	-0.320	0.387	-0.270	-0.420	-0.528*	0.701**	0.583*	0.569*	0.703**	0.906**	0.143	0.102	-0.594*	
TY	-0.690**	-0.202	0.369	-0.313	-0.445	-0.423	0.671**	0.560*	0.558*	0.724**	0.935**	0.222	0.055	-0.43	0.984**

For Abbreviation refer table 2

Table 11 Phenotypic correlation coefficient for the 16 studied traits.

Traits	PH	NSB	DTF	DTM	FFP	NFPC	FD	FW	FL	SGRPP	FYPD	NFPP	TSS	UMY	MY
NSB	-0.019														
DTF	-0.003	0.024													
DTM	0.2187	0.445	-0.106												
FFP	0.177	0.369	-0.588*	0.866**											
NFPC	0.556*	0.212	-0.038	0.220	0.191										
FD	-0.146	-0.500*	0.221	-0.290	-0.340	-0.15									
FW	-0.10	-0.660**	0.242	-0.440	-0.480	-0.08	0.858**								
FL	-0.005	-0.625**	0.217	-0.400	-0.430	0.142	0.845**	0.971**							
SGR	-0.341	-0.290	0.672**	-0.730**	-0.93**	-0.28	0.470	0.524*	0.497*						
FYPD	-0.620*	-0.280	0.318	-0.65**	-0.69**	-0.36	0.583*	0.573*	0.563*	0.854**					
NFPP	-0.22	0.383	0.127	0.424	0.278	0.483	-0.087	-0.040	-0.070	-0.140	-0.01				
TSS	0.001	-0.140	0.008	0.284	0.232	0.039	-0.130	-0.100	-0.040	-0.140	-0.07	0.011			
UMY	0.357	0.504*	-0.230	0.014	0.125	0.527*	-0.430	-0.270	-0.250	-0.220	-0.27	0.291	-0.200		
MY	-0.670**	-0.260	0.340	-0.310	-0.410	-0.41	0.629**	0.519*	0.525*	0.682**	0.900**	0.094	0.104	-0.530*	
TY	-0.661**	-0.160	0.321	-0.330	-0.430	-0.330	0.592*	0.508*	0.520*	0.700**	0.930**	0.174	0.067	-0.350	0.979**

For Abbreviation refer to table 2

4.3.1.2. Correlation among yield-related traits and TSS

Plant height showed a significant positive ($p \leq 0.01$) correlation with number of fruits per cluster (0.653) at genotypic level. But, plant height had significant ($p \leq 0.05$) and negatively correlated with fruit yield per day (-0.649) and marketable yield (-0.708) at genotypic level. Plant height had also highly significant and negative correlation with fruit yield per day (-0.624) and marketable yield (-0.671) at phenotypic level, which indicated that as the plant height increases, the number of fruit per clusters increase and leads to decrease in fruit yield per day and marketable yield.

Number of secondary branches per plant also exhibited significant and positive correlation with unmarketable yield (0.504), significant and negative correlation with fruit diameter (-0.501), fruit width (-0.660) and fruit length (-0.625) at phenotypic level. This implies that increase in number of secondary branches per plant leads to decrease in fruit diameter, fruit length and fruit width. Days to flowering showed a positive significant ($p \leq 0.01$) association with fruit growth rate per plant (0.685), but significant negative ($p \leq 0.05$) association with fruit filling period (-0.588) at genotypic level, which revealed that as days to flowering increase days to fruit filling and fruit growth rate per plant leads to decrease and increase, respectively. Days to flowering also showed a positive significant ($p \leq 0.01$) association with fruit growth rate per plant (0.672) at phenotypic levels, but significant and negative correlation with fruit filling period (-0.588). Similar results were also reported by Shushay *et al.* (2014) in his findings of evaluation of tomato varieties for fruit yield and yield components.

The correlation analysis showed that fruit diameter had exhibited positive significant ($P \leq 0.01$) correlation with fruit width (0.944), fruit length (0.928), fruit yield per day (0.642) and marketable yield (0.671) at genotypic level. Fruit diameter had positive significant ($P \leq 0.01$) correlation with fruit width (0.858), fruit length (0.875) and marketable yield (0.629) at phenotypic level. However, fruit diameter had a negative and significant correlation with unmarketable yield (-0.504) at the genotypic level. This result implies that an increase in fruit diameter leads to an increase in fruit width, fruit length, fruit yield per day and marketable yield. But, fruit diameter had s significant negative association with the unmarketable yield at both genotypic and phenotypic levels. Similarly, Islam *et al.* (2010) found a significant and positive correlation of fruit diameter with fruit length both at the genotypic and phenotypic levels in tomato.

Fruit width had a highly positive and significant correlation with fruit length (0.999) and positive and significant ($p \leq 0.05$) with fruit growth rate (0.566), fruit yield per day (0.603) and marketable yield (0.560) at genotypic level. Fruit length shows a positive and significant association with fruit growth rate per plant (0.524), fruit yield per day (0.573) and marketable yield (0.508) at phenotypic level, which implies an increase in fruit length, will lead to increase in these traits. The fruit growth rate had highly significantly and positively correlated with fruit yield per day (0.867, 0.854) and marketable yield (0.703, 0.682) and fruit yield per day was correlated strong significant and positive with marketable yield (0.906, 0.930) both at genotypic and phenotypic levels, respectively implies that these traits could be improved simultaneously. The unmarketable yield was negatively and significantly correlated with marketable (-0.594, -0.530) yield at both phenotypic and genotypic levels, which implies an increase in marketable yield leads to a decrease in unmarketable yield. These also suggested that the larger the marketable yield, the lower the unmarketable yield.

4.3.2. Path coefficient analysis

4.3.2.1. Phenotypic path coefficient analysis of fruit yield with other traits

According to Reed *et al.* (2001), the characterization of genetic diversity of varieties can be achieved with phenotypic traits. Phenotypic traits have the advantage that they may be directly related to the fitness of the populations and usefulness for plant breeding (Berecha, 2015). This author also stated that analyses of phenotypic diversity as well as attempts at predicting the breeding value for different phenotypic traits depending on the genotype of the parents. Accordingly, results of these findings for path coefficient were done using phenotypic correlation, this is also due to phenotypic observations based on adequately large sample sizes and the physical traits measured show significant differences among populations, they can provide a reasonable representation of overall genetic performance (Velasco *et al*., 2007).

Phenotypic direct and indirect effects of traits on total fruit yield are presented in table 12. The path coefficient analysis at the phenotypic level based on total fruit as dependent variable showed that the independent variables were plant height, fruit diameter, fruit width, fruit length, seed growth rate per plant, fruit yield per day and marketable yield. Accordingly, marketable yield revealed the highest positive phenotypic direct effect (0.78) followed by fruit yield per day (0.48,), plant height (0.07) and fruit width (0.04). These traits are the main contributors to fruit yield. This also suggested that direct selection based on these traits will be rewarding for crop yield improvement (Sushma *et al.,* 2020). Phenotypic positive correlation of these traits except plant height with total fruit yield was the cumulative contribution of these direct and indirect effects. Islam *et al.* (2010) also observed that plant height exhibited positive direct effect on yield of tomato. The positive direct effect of marketable fruit yield with yield is similar to Monamodi *et al*. (2013). Similarly, Reddy *et al.* (2013) reported that the height of the plant and width of the fruit had high direct positive effects on fruit yield.

Table 12 Phenotypic direct effect path (bold face) and indirect effect (off diagonal) of various traits on total fruit.

Traits	PH	FD	FW	FL	SGRPP	FYPD	MY	rp
PH	**0.07**	0.01	0.00	0.00	0.03	-0.21	-0.45	-0.66*
FD	-0.01	**-0.12**	0.03	-0.01	-0.10	0.34	0.58	0.52*
FW	0.00	-0.12	**0.04**	-0.01	-0.10	0.33	0.50	0.50*
FL	0.01	-0.12	0.04	**-0.01**	-0.10	0.32	0.50	0.52*
FGRPP	-0.01	-0.07	0.02	0.00	**-0.16**	0.42	0.58	0.70**
FYPD	-0.03	-0.09	0.02	0.00	-0.14	**0.48**	0.72	0.93**
MY	-0.04	-0.09	0.02	0.00	-0.12	0.44	**0.78**	0.97**

Residual= 0.032.

PH= plant height, FD= Fruit diameter, FW= Fruit width, FL= Fruit length, FGRPP= Fruit growth rate per plant, FYPD= Fruit yield per day and MY= Marketable yield

The path coefficient analysis also revealed that fruit growth rate per plant (-0.16), fruit diameter (-0.12) and fruit length (-0.01) had negative direct effect on total fruit yield. But all these traits have strong positive association with total fruit yield. Similarly, Islam *et al.* (2010) observed negative direct effect of fruit length and fruit diameter on total fruit yield.

According to Mehedi *et al.* (2016), the residual effect determines how best the causal factors account for the variability of the dependent factor, the total fruit yield in this case. Accordingly, the result of the present study revealed that the residual effect was 96.8%. The high residual effect showed that the studied traits explained high variability towards total yield. Similar results were also obtained by Kumar *et al*. (2008).

5. SUMMARY, CONCLUSIONS AND RECOMENDATIONS

Tomato is one of the most economically important and widely consumed vegetable crops grown around the world. In Ethiopia, tomato produced under wide spectrum of altitude in humid and sub-humid areas of the country, mainly during the dry season using irrigation with a resultant inadequate supply of tomato. The national and regional agricultural research system has been striving to improve tomato production in Ethiopia since the late 1997's. Estimation of genetic progress of a breeding program through genetic gain of a crop is vital to understand changes produced by breeding, to assess the past efforts made in genetic yield potential and to put forward future breeding strategies. Regardless of considerable effort and devotion of resources, the magnitude of genetic progress from tomato improvement made since its early inception and the associated traits of genetic improvement achieved so far from the same efforts from different years in a common environment are virtually absent in Ethiopia.

Thus, this research was conducted based on the following specific objectives: (1) to estimate the magnitude of genetic gain of fruit yield and associated traits, (2) to assess the genetic variability of yield and yield-related traits and (3) to estimate the genotypic and phenotypic association among traits. As per the specific objectives; field and laboratory experiments were conducted, and data collection were made during 2021 cropping season. The field experiment was conducted at Sodo district, Guraghe zone. The field study was made on 16 open-pollinated tomato varieties using randomized complete block design with three replications and 18 traits data were collected for genetic gain, genetic variability, and trait association studies during the 2021 cropping season.

As per result of analysis of variance, mean squares for all the traits were highly significant ($P \leq 0.01$) except for number of primary branches per plant and number of seeds per fruit. The mean average total fruit yield of all varieties was 30.3 t ha^{-1} ranged from 22.8 to 36.1 t ha^{-1}. Miya was the superior variety in total fruit yield showed an increment of 5900 kg ha^{-1} or 19.732% over the average of the two older varieties followed by Chali, Cochoro and Bishola 5600 kg ha^{-1} (18.7%), 4400 kg ha^{-1} (14.7%), 3600 kg ha^{-1} (12.04%), respectively. The average rate of increase in total fruit yield of tomato varieties per year of release was 0.12 t ha^{-1} (0.40%) year^{-1}.

For the past 18 years tomato improvement fruit diameter, fruit width, fruit length, fruit growth rate per plant, fruit yield per day and marketable yield increased significantly. Unlikely, linear regression analysis revealed that there was significant reduction progress across the year of release for plant height, days to 50% flowering, fruit filling period, days to 90% maturity, secondary branches per plant, number of fruit per cluster, number of fruit per plant and TSS.

Extensive range of genotypic and phenotypic variability values were observed by plant height, days to flowering, days to maturity, fruit filling period, fruit growth rate per plant, fruit yield per day, number of fruits per plant and marketable yield showed the presence offering greater scope for selecting desirable varieties. Low genotypic variance for number of secondary branches per plant, number of fruits per cluster, fruit width, fruit length and TSS deals that the major part of the total variation was not heritable.

The magnitude of phenotypic coefficients of variation (PCV) was higher than the corresponding genotypic coefficients of variation (GCV) for all traits under study. The high differences between the estimates of GCV and PCV for number of fruits per cluster, fruit diameter, number of fruits per plant and unmarketable yield were observed. All traits exhibited high heritability. High heritability with high genetic advance were observed for plant height, fruit filling period, number of fruits per cluster, fruit diameter, fruit width, fruit length, fruit growth rate per plant, fruit yield per day, number of fruits per plant, unmarketable yield, marketable yield, and total fruit yield.

From the correlation study, total fruit yield was significantly and positively correlated with fruit diameter, fruit width, fruit length, fruit growth rate per plant, fruit yield per day and marketable yield both at the genotypic and phenotypic levels. These traits had probably contributed to the changes in fruit yield during the past 18 years of tomato breeding in Ethiopia. However, total fruit yield correlated significantly and negatively with plant height at both genotypic and phenotypic levels.

Generally, research efforts made for the last 18 years brought considerable improvement in genetic potential of tomato varieties. However, to increase production and fulfill market demands, it’s recommended to disseminate seeds of improved varieties and associated technology packages to the farmers in major tomato producing areas of the country. This study found that among studied varieties, Miya, Melkasalsa, Gelilema, Mersa and Marglobe varieties were higher yield. So, recommended to use them as major sources of crossing material for future tomato breeding program. Genetic yield potential improvement of open-pollinated tomato varieties over the last 18 years have been significant increase, but not consistent. Therefore, it is suggested that the tomato breeding program should revise its breeding methodology and plan a new strategy.

Finally, great emphasis should be given on varieties of high yield potential. It’s also recommended that during varietal development combined selection of varieties for multi traits that contributing for yield, and yield potential and using modern science and technology is mandatory in breeding program.

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7. APPENDICES

Appendix Table 1 Mean of yield and yield related traits of 16 tomato varieties.

Varieties	Mean of traits														
	PH	NSBPP	DTF	DTM	FFP	NFPC	NFPP	FD	FW	FL	SGR	FYD	TSS	UMY	MY	TY
Melkasalsa	74^{f}	13^{bdc}	59^{cbd}	102^{cbd}	42.6^{bdc}	3.7^{ced}	36.8^{a}	5.8^{bc}	5.7^{cb}	6.2^{c}	851^{dce}	354^{bc}	3.67^{edf}	3.52^{bdc}	32.58^{a}	36.1^{a}
Melkashola	83.33^{fdec}	13.83^{a}	59^{cebd}	109^{a}	50.17^{a}	4.03^{cebd}	28.2^{cb}	4.1^{fe}	4.13^{e}	4.1^{h}	474.1^{i}	218.4^{g}	4.1^{bdc}	3.1^{dec}	20.7^{ed}	23.8^{i}
Eshete	97^{bac}	12.77^{bdc}	60^{bc}	88.67^{ihj}	28.67^{e}	4.5^{cbd}	21^{fed}	7.0^{a}	6.47^{b}	7.2^{b}	1158.3^{b}	371.4^{ba}	3.4^{ef}	3.5^{bdac}	29.4^{bc}	32.9^{edc}
Metadel	68^{f}	12^{dec}	54.67^{efd}	94.3^{feg}	39.7^{dc}	3.63_{ced}	25.9^{cbd}	5.17^{dce}	5.5^{e}	5.5_{e}	796.3^{dfe}	330.3^{d}	3.66^{edf}	1.7^{ef}	29.4^{bc}	31^{ef}
Fetane	78.3^{fe}	12.2^{dec}	53^{f}	84.3^{j}	31.1^{e}	4.5^{cb}	24^{cbd}	5.1^{dce}	5.83^{cb}	5.8^{de}	928.7^{dc}	342.8^{cd}	3.73^{edf}	5.05^{a}	23.8^{d}	28.8^{g}
Bishola	89.3^{bac}	12.3^{bdc}	69.3^{a}	95^{feg}	25.8^{e}	4.1^{cebd}	22.1^{cfed}	5.5^{dc}	5.53^{cd}	5.8^{de}	1306.3^{a}	352.6^{bcd}	4.47^{bac}	1.85^{fe}	31.6^{ba}	33.5^{bdc}
Woyno	95.33^{bac}	12.9^{bdc}	54^{f}	93^{fhg}	39.3d	4.9^{b}	20.5^{fed}	4^{fe}	3.87^{e}	4.4^{hg}	657^{gf}	276.6^{f}	3.87^{edf}	4.39^{ba}	21.4^{ed}	25.8^{h}
Mersa	107.3^{a}	11^{e}	55^{efd}	97.7^{fed}	42.8^{bdac}	5.9^{a}	23^{ced}	5.03^{dce}	5.5^{cd}	6.1^{dc}	621^{gh}	267.3^{f}	5^{a}	2.53^{fdec}	23.5^{d}	26.1^{h}
Sirinka-I	108.33^{a}	13.23^{bac}	55.3^{cefd}	103.7^{cb}	48.4^{ba}	4.53^{cb}	20.1^{fed}	4^{fe}	3.83^{e}	4.5^{g}	489^{ih}	226.7^{g}	3.67^{edf}	4.57^{ba}	19^{e}	23.5^{i}
Tekeze-I	100^{ab}	13.17^{bac}	5478.3^{f}	104.3^{b}	50^{ba}	4.4^{cbd}	23.8^{cbd}	3.53^{f}	4.23^{hg}	4.23^{hg}	457^{i}	219.9^{g}	3.5^{edf}	3.83^{bac}	19^{e}	22.8^{i}
Miya	72.67^{f}	14.33a	54.33^{ef}	101.3^{cbd}	47.03^{bac}	4.3^{cebd}	30.1^{b}	4.17^{fe}	4.07^{e}	4.53^{hg}	763.2^{gfe}	354.3^{bc}	4.6^{ba}	4.25^{ba}	31.5^{ba}	35.8^{ba}
Cochoro	71.67^{f}	12.07^{dec}	53.7^{f}	99.9^{ced}	45.57^{bdac}	3.16^{e}	17.2^{fe}	5.53^{dc}	5.47^{cd}	5.8^{de}	758.5^{gfe}	346.4^{cd}	4.5^{bdc}	2.1^{fde}	32.2^{a}	34.3^{bac}
Chali	80.67^{fde}	12^{dec}	62^{b}	99.91^{ihg}	29.37^{e}	3.43^{ced}	24.52^{cbd}	5.8^{bc}	5.93^{cb}	6.1^{dc}	1210^{ba}	389.4^{a}	3.3^{f}	3.4^{bdec}	32.1^{a}	35.5^{ba}
Marglobe	91.33^{bdec}	11.9^{de}	56^{cefd}	102^{cbd}	46^{bdac}	3.9^{cebd}	24.2^{cbd}	6.8^{ba}	7.2^{a}	7.6^{a}	684^{gf}	308.5^{e}	4^{edc}	2.5^{fdec}	28.9^{c}	31.4^{edf}
ARP d2	72^{f}	12.63^{bdc}	57^{cefd}	87.67^{ij}	30.5^{e}	3.4^{ed}	16.6^{f}	4.37^{dfe}	4.83^{d}	5.13^{f}	982^{c}	338.4^{cd}	3.63^{edf}	1.86^{fe}	27.7^{c}	29.6^{gf}
Gelilema	78.66^{fe}	12.17^{dec}	54.33^{ef}	98^{ed}	43.67^{bdac}	$3.8c^{ed}$	21.1^{fed}	7.13^{a}	5.23^{cd}	5.57^{e}	761.9^{gfe}	342.8^{cd}	3.7^{edf}	1.1^{f}	31.6^{ba}	32.8^{edc}

Means followed by the same letter with in a column are not significantly different from each other at $P \leq 0.05$ according to Duncan’s Multiple Range Test
For Abbreviation refer Table 2.