Preliminary Study on Heritability, Genetic Advances and Correlation of Tomato (*Solanum lycopersicum* L.) Germplasms Traits in Bench Maji, Southwest Ethiopia

Tewoderos Legesse and Jiregna Tasisa

Mizan-Tepi University, College of Agriculture and Natural Resources,
Department of Horticulture, P.O. Box: 260, Mizan Teferi, Ethiopia

Abstract: Twenty one tomato (*Lycoperscion esculentum* Mill.) genotypes were evaluated during 2011/2012 to estimate the magnitude of heritability, genetic advances and to obtain information on association of different characters with fruit yield and among themselves. The experiment was conducted at Mizan-Tepi University trial field using Randomized Complete Block Design (RCBD) with three replications. High genetic advance accompanied by high heritability was observed for plant height, number of fruit clusters per plant and fruits per plant, suggesting that selection for number of fruits per plant, plant height and number of fruit clusters per plant would be most likely effective in tomato improvement. Number of fruits per plant showed positive and significant correlation with number fruits per cluster ($r_g = 0.680**$, $r_p = 0.601**$) and shape index ($r_g = 0.595**$, $r_p = 0.544*$) at both genotypic and phenotypic levels, indicating the above characters play important role in yield improvement and that they are more useful in selection process.

Key words: Tomato · Yield · Phenotypic variance · Genotypic variance · Lycopene · Genotypic correlation

INTRODUCTION

Tomato (*Lycoperscion esculentum* Mill) is one of the most important edible and nutritious vegetable crops in the world. it belongs to the Solanaceae family. It ranks next to potato and sweet potato with respect to world vegetable production. it is widely cultivated in tropical, sub tropical and temperate climates and thus ranks third in terms of world vegetable production [1]. The leading tomato producing countries are china, the United State of America, India, Egypt, Turkey, Iran, Mexico, brazil and Indonesia [2]. It is one of the most economically important vegetable crops and it is widely cultivated in the world with the total area and production of 5, 227, 883 Ha and 129, 649, 883 tons in 2008 [2]. It is the most frequently consumed vegetable in many countries, becoming the main supplier of several plant nutrients and providing an important nutritional value to the human diet [3]. The crop generally requires warm weather and abundant sunshine for best growth and development. vegetative and reproductive growth at lower temperature are very limited

and an extended period of plant growth at 12°C or less can result in chilling injury. Moreover, the plant grows best when provided with uniform moisture and well-drained soils [4]. The climatic soil conditions of Ethiopia allow cultivation of a wide range of fruit and vegetable crops including tomato, which is largely grown in the eastern and central parts of the mid to low land areas of the country. Large scale production of tomato takes place in the upper awash valley, under irrigated and rain fed conditions whereas small scale production for fresh market is a common practice around koka, Ziway, Wondo-Genet, Guder, Bako and many other areas [5] in 2016, tomato p roduction in Ethiopia reached about 41, 815 tons from a total harvested area of 3542 ha. The shortage of varieties and recommended information packages, poor quality seeds, poor irrigation systems, lack of information on soil fertility, disease and insect pests, high post harvest loss, lack of awareness of existing improved varieties and poor marketing system are the major constraints in Ethiopian tomato production [6].

Corresponding Author: Tewoderos Legesse, Mizan-Tepi University, College of Agriculture and Natural Resources, Department of Horticulture, P.O. Box: 260, Mizan Teferi, Ethiopia.

Therefore, it is important to increase its productivity along with desirable attributes through genetic manipulation. Hence, generating information about the extents of heritablities of the characters and association between the yield and related traits is important task in genetic improvement of any crop. Information about the relative contribution of the various component traits to yield aid the isolation of superior yielding genotypes from genetically variable populations by providing information on indirect selection for yield (Singh, 2015). But information in respects of the relationship between yield and yield components is rare for the tomato germplams grown in Ethiopian condition. Hence this study is started to estimate the extent of heritablities of different characters and to generate the information on association among yield and related traits.

MATERIALS AND METHODS

Study Location and Season: The study has been conducted under irrigation condition during main production season from September 2011/2012 to May 2012/2013 under Mizan agro-ecology at trial field (farm field) of Mizan-Tepi University, which is located between 6°09'N latitude and 35°E longitude at an altitude of 1400m above sea level, in sub humid tropic Southwest part of Ethiopia. The area receives annual rain fall of 2000mm and average mean annual minimum and maximum temperature are 20°C and 28°C respectively.

Experimental Materials: The study was conducted using 21 tomato genotypes (Table 3) of different origin. The seeds of the germplasms were obtained from Melkasa agricultural Research Center where they were collected from different part of the world and maintained.

Experimental Design and Trial Management: The experiment was conducted using Randomized Complete Block Design (RCBD) with three replications and with plot size of 2.10 m x 5.0 m each having five rows. Inter-row spacing of 1m and intera-row spacing of 0.3m was maintained during the layout. Fertilizer 200 Kg/ha DAP was (is used to be) broadcasted at transplant & 100 Kg/ha urea was side dressed at early flowering stage. All agronomic requirements were performed as per recommendation [7].

Data Collection: In this study, 15 parameters were evaluated on sample plants in each plot and the results were expressed as mean values. List of characters considered in this study and their descriptions are given in Table 4. All the data were represent per plant observation except for marketable fruit yield and unmarketable fruit yield which were computed from the plot observation.

Total Soluble Contents Assessment: Total Soluble Solids (TSS) was determined following the procedures described by [8]. Aliquot of juice was extracted using a juice extractor (6001× Model No.31JE356× 00777) and 50 ml of the slurry was filtered using cheesecloth. The TSS was determined by refractometer (Model Misco®) with a range of 0.0 to 32.0 °Brix and a resolution of 0.2 °Brix by placing 1 to 2 drops of clear juice on the prism. Between samples the prism of refractometer was washed with distilled water and dried before use. The referactometer was standardized against distilled water (0.0 % TSS).

Lycopene Contents Assessment: The lycopene content of the fruits was measured following the procedures described by Ranganna, (2016). Three to four tomato fruits (sample) were taken and pulped using blender. Five milligram of the pulp was taken and extracted repeatedly using pestle and mortar. The acetone extracts was pooled and transferred to separating funnel containing 20 ml petroleum ether and mixed gently. About 20 ml of 5% sodium sulphate solution was added to the separating funnel and shaken gently. The two phases was separated and the lower aqueous phase was re-extracted using additional 20 ml petroleum ether. The petroleum extract was pooled and washed with distilled water and poured into brown bottle containing 10mg anhydrous sodium sulphate and kept for 30 min. And the petroleum extract was decanted in to a 100 ml volumetric flask through a funnel containing cotton wool and sodium sulphate slurry was washed with petroleum ether and transferred to volumetric flask. The volume was made up and the absorbance was measured in spectrophotometer at 503 nm using petroleum ether as blank

Statistical Procedures
Analysis of Variance: The data collected for each trait was subjected to analysis of variance for Randomized Complete Block Design as per Montgomery[9]. SAS statistical software package[10] was employed for analysis of variance and estimation of correlation among the traits.

Table 3: Name/identity, pedigree name and source/origin of the test genotypes

S.N.	Name/Identity	Pedigree name	Origin/Source/Collection region
1	BL1198=NCEBR-1	N/A	North Carolina State University, USA
2	Metadal(Caraibo)	N/A	MARC/EIAR
3	Melkasalsa	N/A	MARC/EIAR
4	Beefsteak	N/A	MARC/EIAR
5	CLN2037F	CLN657BC1F2-285-0-21-0 x (Moneymaker x (Moneymaker x L3708))	The World Vegetable Center-AVRDC
6	CLN-2037H	CLN657BC1F2-285-0-21-0 x (Moneymaker x (Moneymaker x L3708))	The World Vegetable Center-AVRDC
7	Cochoro(Pace setter)	N/A	MARC/EIAR
8	Tomato 1365/95	N/A	Israel
9	CHali(Rio Grande)	N/A	MARC/EIAR
10	Unknown 13	N/A	MARC/EIAR
11	Bishola(Floradado)	N/A	MARC/EIAR
12	Eshete (Calypso)	N/A	MARC/EIAR
13	Melkashola (Red pear)	N/A	MARC/EIAR
14	Fetene (Picador)	N/A	MARC/EIAR
15	H-1350	N/A	MARC/EIAR
16	CLN-2037E	CLN657BC1F2-285-0-21-0 x (Moneymaker x (Moneymaker x L3708))	The World Vegetable Center-AVRDC
17	CL-5915 D4-2-2-0	N/A	The World Vegetable Center-AVRDC
18	Pirson	N/A	France
19	CLN-2037 I	CLN657BC1F2-285-0-21-0 x (Moneymaker x (Moneymaker x L3708))	The World Vegetable Center-AVRDC
20	Roma VF	N/A	MARC/EIAR
21	Marglobe	N/A	MARC/EIAR

N/A = Information not available.

Table 4: Description of characters evaluated

S.N	Character	Unit	Code	Description
1	Number of fruit clusters per plant	Number	FC/P	Total number of fruit cluster on the plant
2	Number of fruits per cluster	Number	Fr/C	Average number of fruits on five flower clusters per plant
3	Stem diameter	Centemeter	SD	Diameter of main stem at 15 cm height from the ground level at 50 per cent flowering.
4	Days to maturity	Days	DM	The Actual number of days from transplanting to a day at which more than 50 per cent of the plant will attain fruit maturity on the harvestable rows of the each plot.
5	Plant height	Centimeter	PH	The distance measured from the soil surface to the tip of the main stem at harvest
6	Number of nodes on main stem	Number	NN	Number of nodes on main stem at harvest
7	Fruit diameter	Centimeter	FD	The average size measured at the widest point in the middle portion of ten mature fruits per plant expressed in cm)
8	Fruit length	Centimeter	FL	The height of ten mature fruits per plant measured in cm
9	Fruit shape index	-	SI	The ratio of fruit length to fruit diameter
10	Number of fruits per plant	Number	F/P	Average number of fruit on the plant
11	Total soluble solids	°Brix	TSS	Average total soluble solids per fruit will be estimated using Refractometer
12	Lycopne content	mg/100g	Ly Co	Average lycopene content of the genotypes estimated in milligram per 100gram extracted sample
14	Marketable fruit yield	Kilogram	MFrYP	Total yield that fit for market
15	Unmarketable fruit yield per plant	Kilogram	UFrYP	Total yield that are not fit to be marketed (damaged, diseased etc.)
16	Average fruit yield per plant	Kilogram	FY/P	Total fruit yield on the plant (marketable and unmarketable)

Heritability in the Broad Sense: Broad sense heritability $h^2(b)$ of the traits was estimated according to the formula suggested by Hanson *et al.* (2016) as follows:

$$h^2(b) = \left(\frac{\sigma_g^2}{\sigma_p^2}\right) \times 100$$

where,
$h^2(b)$ = heritability in broad sense
σ_g^2 = genotypic variance and
σ_p^2 = phenotypic variance

Genetic Advance (Genetic Advance as per Cent of Mean): The genetic advance (in broad sense) expected under selection, assuming the selection intensity of five per cent, were calculated by the formula described by[11].

$$GA = K\sigma_p\left(h^2(b)\right)$$

where,
GA = Genetic advance
σ_p = the phenotypic standard deviation of the character,

$h^2(b)$ = heritability estimate in broad sense and
K = the selection differential (K = 2.06 at 5 % selection intensity).

Genetic advance as percent of mean (GAM) will be estimated as ratio of genetic advance to population mean in percent.

$$GAM = \left(\frac{GA}{\bar{x}} \right) \times 100$$

where,
GAM = genetic advance as percent of mean
GA = Genetic advance
$\bar{x}$ = population mean

Correlations Analysis: Phenotypic correlation, genotypic correlation and environmental correlation, were estimated using the formula given by [12] as follows:

$$r_p = \frac{P\cos XY}{\sqrt{\sigma^2 pX \sigma^2 pY}}$$

$$r_g = \frac{G\cos XY}{\sqrt{\sigma^2 gX \sigma^2 gY}}$$

where,

Pcov XY = Phenotypic covariance of character X and character Y
rp = phenotypic correlation
σ_p^2 X = phenotypic variance for character X,
σ_p^2 Y = phenotypic variance for character Y,
G cov XY = genotypic covariance of character X and character Y
rg = genotypic correlation
σ_g^2 X = genotypic variance for character X and
σ_g^2 Y = genotypic variance for character Y

The significances of phenotypic and genotypic correlation coefficients were tested by referring the standard table [13] at n-2 degree of freedom. Where, n is number of genotypes.

RESULTS AND DISCUSSION

Estimates of Broad Heritability ($h^2(b)$) and Expected Genetic Advances: The expected genetic advance as per cent of mean from selecting the top 5 per cent of the genotypes ranged from 16.51 per cent for days to maturity to 136.45 per cent for number of fruit cluster per plant (Table 1). This indicated that selecting the top 5 per cent of the base population would result an increase of 16.51 per cent for days to maturity and136.45 per cent for number of fruit cluster per plant over the base population mean.

High genetic advance accompanied by high heritability was observed for plant height ($h^2(b)$ = 97.35 % and GA = 49.65), number of fruit clusters per plant ($h^2(b)$ = 95.90 % and GA = 22.14) and fruits per plant ($h^2(b)$ = 90.08 % and GA = 28.64) (Table 1). This result is in agreement with the findings of [14])], Natarajan [15], [16], [17], [18] and for number of fruits per plant, [19] for number of fruits per plant and plant height, [20] for plant height and for number of fruit per plant and plant height. [21] suggested that heritability estimates with genetic advance enable breeders to predict the real genetic gain under selection so that they can anticipate improvements from different types and intensities of selection. According to [22], if a character exhibited high heritability with genetic advance variation for this is due to highly additive gene effect and consequently the scope for improving the trait through selection is more. In general, this observation suggested that selection for number of fruits per plant, plant height and number of fruit clusters per plant would be most likely effective in tomato improvement.

Analyses of Correlations at Genotypic (r_g) and Phenotypic (r_p) Levels: N umber of fruit clusters per plant showed positive and highly significant association with number of node on the main branch (r_g = 0.894**, r_p = 0.865**) and total soluble solids (r_g = 0.629**, r_p = 0.572**) at both phenotypic and genotypic level, which revealed strong relationship between the characters. Number of fruits per cluster showed positive highly significant correlation with number of fruits per plant (r_g = 0.450*, r_p = 0.680**) at both phenotypic and genotypic level, indicating their strong relationship. Similarly days to maturity and plant showed positive and highly significant with each other at genotypic and phenotypic levels (r_g = 0.685**, r_p = 0.655**) (Table 2).

The character number of fruits per plant showed positive and significant correlation with number fruits per cluster (r_g = 0.680**, r_p = 0.601**) and shape index (r_g = 0.595**, r_p = 0.544*) at both genotypic and phenotypic levels (Table 2). This indicated that the above characters play important role in yield improvement and that they are more useful in selection process.

Table 1: Heritability in broad sense ($h^2(b)$), genetic advance (GA) and genetic advance as per cent of mean (GAM) for different characters of tomato genotypes

Character	h^2 (b) (%)	GA	GAM
FC/P	95.90	22.14	136.45
Fr/C	80.25	1.37	44.53
SD	75.85	0.25	22.04
DM	94.31	13.27	16.51
PH	97.35	49.65	65.06
NN	98.01	11.44	118.39
FD	87.18	1.51	34.16
FL	83.42	1.48	33.71
SI	93.98	0.59	56.77
F/P	90.08	28.64	106.21
TSS	85.26	1.61	43.15
LyCo	87.45	1.42	83.26
Y/P	74.98	0.62	78.38

Fr/C = Number of fruits per cluster, FC/P = Number of fruit clusters per plant, SD = Stem diameter, PH = Plant height, NN = Number of nodes on main stem, FD= Fruit diameter, FL= Fruit length, SI (ratio of FL/FD) = Fruit shape index, F/P = Number of fruits per plant, TSS = Total soluble solids, DM = Days to maturity, LyCo= Lycopene content, Y/P = Average fruit yield per plant

Table 2: Correlation coefficients at genotypic (above diagonal) and phenotypic (below diagonal) level of various characters in some tomato genotypes

Chanter	FC/P	Fr/C	SD	DM	PH	NN	FD	FL	SI	F/P	TSS	LyCo	Y/P
FC/P	1	0.463*	-0.030	-0.452*	-0.393	0.894**	0.138	0.387	0.109	0.488*	0.629**	-0.436*	-0.241
Fr/C	0.417	1	0.010	-0.421	-0.249	0.511*	-0.145	0.471*	0.421	0.680**	0.358	-0.013	0.099
SD	-0.032	0.044	1	0.261	0.382	0.005	0.392	0.083	-0.161	0.114	-0.061	0.197	0.383
DM	-0.425	-0.357	0.223	1	0.685**	-0.358	0.034	-0.522*	-0.316	-0.330	-0.387	0.139	-0.214
PH	-0.373	-0.224	0.318	0.655**	1	-0.306	0.013	-0.420	-0.215	-0.182	-0.425	0.281	-0.155
NN	0.865**	0.453*	0.001	-0.338	-0.302	1	0.223	0.261	-0.009	0.413	0.737**	-0.308	-0.236
FD	0.128	-0.091	0.317	0.021	0.014	0.201	1	-0.129	-0.704**	-0.437*	0.047	0.175	-0.020
FL	0.354	0.353	0.002	-0.464*	-0.366	0.240	-0.117	1	0.772**	0.417	0.432	-0.430	0.139
SI	0.105	0.364	-0.136	-0.292	-0.219	-0.003	-0.687**	0.708**	1	0.595**	0.188	-0.310	0.209
F/P	0.450*	0.601**	0.113	-0.313	-0.176	0.386	-0.391	0.369	0.544*	1	0.389	-0.068	0.236
TSS	0.572**	0.319	-0.012	-0.327	-0.386	0.671**	0.024	0.369	0.172	0.327	1	-0.260	-0.062
LyCo	-0.404	-0.019	0.148	0.132	0.252	-0.272	0.143	-0.386	-0.281	-0.043	-0.247	1	0.067
Y/P	-0.196	0.080	0.209	-0.195	-0.125	-0.200	-0.016	0.147	0.192	0.201	-0.064	0.060	1

*, ** = Indicate significant at 5 per cent and 1 per cent probability levels respectively.

The correlation coefficient must exceed 0.433 and 0.549 to be significant at 5 per cent and 1 per cent probability levels, respectively.

Fr/C = Number of fruits per cluster, FC/P = Number of fruit clusters per plant, SD = Stem diameter, PH = Plant height, NN = Number of nodes on main stem, FD= Fruit diameter, FL= Fruit length, SI (ratio of FL/FD) = Fruit shape index, F/P = Number of fruits per plant, TSS = Total soluble solids, DM = Days to maturity, LyCo= Lycopene content, Y/P = Average fruit yield per plant

Negative and highly significant association was observed between the character fruit diameter and shape index (r_g = 0.680**, r_p = 0.601**) and both genotypic and phenotypic levels, indicating their negative relationship (Table 2).

CONCLUSION

High genetic advance accompanied by high heritability was observed for plant height, number of fruit clusters per plant and fruits per plant, suggesting that selection for number of fruits per plant, plant height and number of fruit clusters per plant would be most likely effective in tomato improvement.

The character number of fruits per plant showed positive significant correlation with number fruits per cluster and shape index at both genotypic and phenotypic levels. This indicated that the above characters play important role in yield improvement and that they are more useful in selection process.

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