

Variability, Heritability and Genetic Advance in Tomato (*Lycopersicon esculentum* Mill.) Genotypes in West Shoa, Ethiopia

¹Jiregna Tasisa, ²Derbew Belew, ²Kassahun Bantte and ²Wosene Gebreselassie

¹Mizan-Tepi University, P.O. Box 260, Mizan Teferi, Ethiopia

²Jimma University College of Agriculture and Veterinary Medicine, P.O. Box 307 Jimma, Ethiopia

Abstract: Twenty three tomato (*Lycopersicon esculentum* Mill.) genotypes were evaluated to estimate variability, heritability and genetic advance in fruit yield and yield components at Bako Agricultural Research Center (Western Ethiopia). The experiment was conducted using a randomized complete block design with three replications. Significant genotypic variability among the test genotypes was observed for all traits studied. Higher values of phenotypic coefficients of variation and genotypic coefficients of variation were observed for fruits per plant, seeds per fruit, flowers per cluster, unmarketable fruit yield per plot, fruit clusters per plant and plant height indicating the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters. Higher heritability estimates values were recorded for fruits per plant, days to maturity, nodes on the main stem, flowers per cluster, plant height, shape index, days to flowering, seeds per fruit, fruit diameter and fruit clusters per plant, indicating these traits were less influenced by environmental factors and selection for them is fairly easy. Higher values of expected genetic advance as per cent of mean was recorded for fruits per plant, seeds per fruit, flowers per cluster, plant height, fruit clusters per plant, nodes on the main stem, shape index, yield per plant and fruit diameter, indicating that selection would be more useful to improve these traits. High heritability values coupled with high genetic advance were observed in respect of seeds per fruit, fruits per plant, plant height and fruit clusters per plant, indicating selection for these traits would be most likely effective in tomato improvement.

Key words: Heritability • Genetic advance • Genotypic variation • Phenotypic variation • Tomato • Yield

INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) is one of the most important vegetables worldwide [1]. In Ethiopia, tomato is one of the most popular vegetables, produced by small farmers and commercial growers, for both local uses as well as for processing industries. It is used as fresh and processed forms in a variety of dishes. It is an important cash-generating crop for small farmers and also provides employment in production and processing industries. Considering the importance of tomato as one of the potential vegetable crops for both domestic consumption as well as export markets, it is important to increase its productivity along with desirable attributes through genetic manipulation.

The genetic improvement of any crop plant needs to have knowledge on the nature and magnitude of variability in the base population [2]. 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 [3].

Different types of tomato varieties are being cultivated in Ethiopia with varying productivity potentials. However, tomato production is confronted various constraints including diseases, insects, salinity, heat complexes, low yield and sometimes total crop failure that need systematic breeding effort. In this context, it is relevant to identify ideal plant characters or traits important to the variety development program. However, genetic information with respect to the nature and magnitude of variability for fruit yield and yield related traits are not generated on tomato germplasms maintained under Ethiopian conditions. Such information is absolutely essential to design effective breeding strategies for genetic improvement of this crop.

Hence, the study was conducted employing twenty three tomato genotypes to estimate the nature and magnitude of variability for fruit yield and related characteristics.

MATERIALS AND METHODS

Location and Season: The study was conducted from October 2007 to May 2008 under irrigation condition at Bako Agricultural Research Center (Western Ethiopia) located between 9°07'N latitude and 37°05'E longitude at an altitude of 1650 m. a. s. l [4]. The mean daily minimum and maximum temperature are 15.1°C and 30.3°C, respectively and receives an average of 1200 mm rain per year [5]. The environment is hot and humid with mean relative humidity of 60 per cent [7]. The soil type of the area belongs to the Nitosol series, which is reddish-brown in color and has a clay to sandy clay-loam texture with pH ranging from 5.3-6.0 [4].

Experimental Materials: Twenty-three tomato genotypes comprising ten determinate, five indeterminate and eight processing types including one local cultivar from Bako Agricultural Research Center, were used for the experiment. The seed material of the test genotypes were obtained from the germplasm collections maintained at Melkasa Agricultural Research Center (national tomato research coordinating center).

Experimental Design: The experiment was performed in a randomized complete block design (RCBD) with three replications and plot size of 2 x 5 m, each plot having five

rows. The net plot size was 1.8 x 3 m. Inter-row spacing of 1.0 m and intra-row spacing of 0.3 m within the block was maintained to accommodate 35 plants per gross plot. The seedlings were transplanted after six weeks of their emergence. A recommended fertilizer rate of 200 Kg/ha DAP was broadcasted at transplanting and 100 kg/ha Urea was side-dressed at early flowering stage and other management practices were performed as per as per set recommendations.

Parameter Recorded: In this study, 17 characters were studied from 15 sample plants in each net plot and the results were expressed as mean values. List of characters that were considered in this study and their descriptions are given in Table (1). All the data represent per plant observation except for marketable fruit yield and unmarketable fruit yield which were computed from the net plot observation and days to flowering and maturity were computed on the basis of harvestable rows in each net plot. Further, Total Soluble Solids (TSS) was determined following the procedures described by [7]. Aliquot of juice was extracted using a juice extractor (6001 x Model No.31JE356 x 00777) and 50 ml of the slurry was filtered using cheesecloth. The TSS was determined by refractometer 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 refractometer was standardized against distilled water (0.0 % TSS).

Table 1: Description of characters evaluated

Character	Description
Dfl = Days to 50 % flowering	The actual number of days from the transplanting to a day at which 50 per cent of flowering was attained on the harvestable rows of the each plot
Fl/C =Number of flowers/cluster	Average number of flowers on five flower clusters per plant
Fr/C =Number of fruits/cluster	Average number of fruits on five flower clusters per plant
FC/P =Number of fruit clusters/plant	Total number of fruit cluster on the plant
SD= Stem diameter (cm)	Diameter of main stem at 15 cm height from the ground level using Vernier Callipers at 50 per cent flowering.
DM =Days to maturity	The Actual number of days from transplanting to a day at which more than 50 per cent of the plant attain fruit maturity on the harvestable rows of the each plot.
PH =Plant height (cm)	The distance measured from the soil surface to the tip of the main stem at harvest
NN =Number of nodes on main stem	Number of nodes on main stem at harvest
FD =Fruit diameter (cm)	The average size measured at the widest point in the middle portion of ten mature fruits per plant expressed in cm
FL =Fruit length (cm)	The height of ten mature fruits per plant measured in cm
SI =Fruit shape index	The ratio of fruit length to fruit diameter
F/P =Number of fruits per plant	Average number of fruit on the plant
TSS =Total soluble solids	Average total soluble solids per fruit was estimated using Refractometer
S/F =Number of seed/fruits	Average number of seeds in a fruit
Marketable fruit yield (kg)	Total yield that fit for market
MFrYP =Unmarketable fruit yield/plant (kg)	Total yield that are not fit to be marketed (damaged, diseased etc.)
FYP =Average fruit yield/plant (kg)	Total fruit t yield on the plant (marketable and unmarketable)

Statistical Procedures: The data collected for each trait were subjected to analysis of variance for Randomized Complete Block Design as described in [8]. GENRES Version 7.01 Statistical Software Package [9] was employed for analysis of variance and estimation of correlation among the traits. The statistical significance was determined by using F-test. List significance difference (LSD) was used to separate the mean performance of the genotypes which were significantly different. Simple variability measures such as ranges (maximum and minimum values) and the mean along with standard error were computed for each character studied.

To estimate the extent of variability, genotypic and phenotypic coefficients of variability were estimated according to the following method suggested by [10].

$$PCV = \left(\frac{\sqrt{\sigma_p^2}}{\bar{x}} \right) \times 100$$

$$GCV = \left(\frac{\sqrt{\sigma_g^2}}{\bar{x}} \right) \times 100$$

Where,

PCV = phenotypic coefficient of variation

GCV = genotypic coefficient of variation

σ_p^2 = phenotypic variance

σ_g^2 = genotypic variance

\bar{x} = population mean

These were calculated as follows using the values from the Analysis of variance:

Environmental variance (σ_e^2) = Error mean square

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

Where,

σ_g^2 = Genotypic variance

MSg = mean square of genotypes

MSe = error mean square

r = number of replications

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

σ_e^2 = environmental variance

Broad sense heritability $h^2(b)$ of the traits was estimated according to the formula suggested by [11] 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

The genetic advance (in broad sense) expected under selection, assuming the selection intensity of five per cent, was calculated by the formula described by [10].

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

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 per cent of mean (GAM) was estimated as ratio of genetic advance to population mean in per cent

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

Where,

GAM = genetic advance as per cent of mean

GA = Genetic advance

\bar{x} = population mean

x

RESULTS

Analysis of Variance: The results on analyses of variances using RCB design revealed that the genotypes exhibited highly significant differences for all the characters studied (Table 2). This indicated the existence of sufficient genetic variability and the scope for improvement of this crop.

Estimates of Range and Mean: There were big differences observed between least and highest mean values for all characters studied (Table 3). Maximum mean value exceeded the minimum mean value by more than 50 per cent for all characters studied except for days to 50 per cent flowering (48.00 %), stem diameter (41.67 %) and days to maturity (30.42 %).

Table 2: Analyses of variances in randomized complete block design for seventeen characters in some tomato genotypes

Source of variation	df	DFI	Fl/C	Fr/C	FC/P	SD	DM	PH	NN	FD
Replication	2	7.712	0.404	0.040	10.187	0.011	5.923	35.031	0.212	0.202
Genotypes	22	39.666**	9.785**	0.649**	183.562**	0.031**	102.922**	673.106**	36.624**	1.769**
Error	44	2.059	0.236	0.156	13.717	0.005	2.049	16.851	0.880	0.112
C.V (%)		3.45	9.81	11.69	12.84	6.04	1.77	6.91	5.82	6.76
L.S.D (5%)		2.36	0.80	0.65	6.10	0.11	2.36	6.76	1.55	0.54
Source of variation	df	FL	SI	F/P	TSS	S/F	MFrYP	UFrYP	Y/P	
Replication	2	0.008	0.001	15.656	0.445	324.465	20.532	0.081	0.081	
Genotypes	22	1.04**	0.093**	672.458**	0.757**	5879.252**	50.488**	1.426**	0.236**	
Error	44	0.17	0.003	7.662	0.148	331.526	4.920	0.120	0.023	
C.V (%)		8.40	5.46	8.10	8.80	16.91	10.99	14.93	10.11	
L.S.D (5%)		0.68	0.09	4.56	0.63	29.98	3.65	0.56	0.26	

** = indicates significant differences at 1 per cent probability levels

The calculated F-value for the treatment must exceed 2.28 to be significant at 1 per cent probability level

Fl/C = Number of flowers per cluster, 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, S/F = Number of seeds per fruit, FD = Fruit diameter, FL = Fruit length, SI (ratio of FL/FD) = Fruit shape index, F/P = Number of fruits per plant, MFrYP = Marketable fruit yield per plot, TSS = Total soluble solids, DFI = Days to 50 per cent flowering, DM = Days to maturity, UFrYP = Unmarketable fruit yield per plot, Y/P = Average fruit yield per plant.

Table 3: Estimates of mean, range, phenotypic (PCV) and genotypic (GCV) coefficients of variation, phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances for different characters of tomato genotypes

Character	Range	Range of mean	Vmin (%)	Overall Mean± SE	Mean of check	PCV (%)	GCV (%)	σ^2_p	σ^2_g	σ^2_e
Dfl	33.00-51.00	33.33-49.33	48.00	41.59±1.17	37.33	9.19	8.51	14.595	12.536	2.059
Fl/C	2.91-11.08	3.28-10.62	223.78	4.96±0.40	4.98	37.28	35.97	3.419	3.183	0.236
Fr/C	2.10-4.98	2.57-4.30	67.32	3.38±0.32	3.82	16.74	11.98	0.320	0.164	0.156
FC/P	14.10-49.10	14.90-45.07	202.48	28.84±3.024	30.20	29.08	26.09	70.332	56.615	13.717
SD	0.93-1.41	0.96-1.36	41.67	1.17±0.06	1.23	10.11	8.11	0.014	0.009	0.005
DM	72.00-95.00	72.33-94.33	30.42	80.77±1.17	77.00	7.39	7.18	35.673	33.624	2.049
PH	43.00-99.30	45.20-97.47	115.64	59.44±3.35	61.10	25.82	24.88	235.603	218.752	16.851
NN	11.70-25.00	12.33-24.17	96.03	16.12±0.77	12.80	22.19	21.41	12.795	11.915	0.880
FD	3.54-6.74	3.78-6.33	67.46	4.95±0.27	4.27	16.46	15.01	0.664	0.552	0.112
FL	3.60-6.67	3.89-5.92	52.19	4.91±0.34	4.07	13.86	10.95	0.463	0.289	0.174
SI	0.67-1.36	0.73-1.30	78.08	1.003±0.05	0.95	18.11	17.27	0.033	0.030	0.003
F/P	16.00-69.20	17.13-68.77	301.46	34.19±2.26	68.77	44.29	43.54	229.261	221.599	7.662
TSS	3.00-5.30	3.33-5.00	50.15	4.37±0.31	3.40	13.56	10.31	0.351	0.203	0.148
S/F	48.00-274.20	59.47-227.20	282.04	107.65±14.87	108.00	43.38	39.95	2180.768	1849.242	331.526
MFrYP	13.05-30.90	14.20-28.75	102.46	20.17±1.81	27.90	22.23	19.32	20.109	15.189	4.920
UFrYP	0.90-3.90	1.00-3.75	275.00	2.32±0.28	2.30	32.11	28.43	0.555	0.435	0.120
Y/P	1.01-2.21	1.08-2.08	92.59	1.50±0.13	2.013	20.44	17.76	0.094	0.071	0.023

V min = Percentage of maximum mean differences from minimum mean.

Fl/C = Number of flowers per cluster, 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, S/F = Number of seeds per fruit, FD = Fruit diameter, FL = Fruit length, SI (ratio of FL/FD) = Fruit shape index, F/P = Number of fruits per plant, MFrYP = Marketable fruit yield per plot, TSS = Total soluble solids, DFI = Days to 50 per cent flowering, DM = Days to maturity, UFrYP = Unmarketable fruit yield per plot, Y/P = Average fruit yield per plant.

Higher maximum mean from minimum mean value differences was recorded for the characters such as number of fruits per plan, number of seeds per fruit, unmarketable fruit yield per plot, number of flowers per cluster, plant height, marketable fruit yield per plot, number of nodes on the main stem and average fruit yield per plant (Table 3). The maximum value of average fruit yield per plant was recorded by the

genotype Tomato 1365/13 (2.08 kg) and the minimum value was recorded by the genotype CLN2037F (1.08 kg). In general, the observation from the simple variability measures indicated the presence of wide range of variability among the genotypes for most of the characters considered in this study, which in turn indicated the existence of more scope for improvement through selection.

Estimates of Phenotypic and Genotypic Variability:

The value of genotypic variances (σ^2g) was ranged from 0.009 (stem diameter) to 1849.242 (number of seeds per fruit) and the value of phenotypic variance (σ^2p) was ranged from 0.014 (stem diameter) to 2180.768 (number of seeds per fruit) (Table 3). Relatively higher values of genotypic variances (σ^2g) and phenotypic variances (σ^2p) were observed for number of fruit clusters per plant, days to maturity, plant height, number of fruits per plant, number of seeds per fruit and marketable fruit yield per plot was observed indicating the existence of relatively higher magnitude variability among the genotypes in respect to the above characters.

The values of genotypic coefficients of variation (GCV) ranged from 7.18 per cent (days to maturity) to 43.54 per cent (number of fruits per plant) similarly, values for phenotypic coefficients of variation (PCV) ranged from 7.39 per cent (days to maturity) to 44.29 per cent (number of fruits per plant) (Table 3).

The smallest differences were observed between PCV and GCV values of characters such as days to maturity, days to 50 per cent flowering, number of fruits per plant, number of nodes on main stem, shape index, stem diameter and plant height suggesting lesser influence of environmental factors on their expression. Relatively higher differences between PCV and GCV values were recorded in respects of the characters like number of fruit per cluster, unmarketable fruit yield per plot, number of seeds per fruit, total soluble solids, number of fruit clusters per plant, marketable fruit yield per plot, fruit yield per plant, stem diameter, fruit diameter and number of flowers per cluster. The results revealed that these characters were under more influences of environmental factors than the rest of the characters studied.

For characters like number of fruits per plant, number of seeds per fruit, number of flowers per cluster, unmarketable fruit yield per plot, fruit clusters per plant and plant height, the values of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were relatively higher than the rest of the studied characters.

Estimates of Broad Sense Heritability (h^2b) and Expected Genetic Advance:

The heritability estimate was more than 50 per cent for all the characters considered in this study (Table 4). Very high values of heritability estimates were recorded for characters like number of fruits per plant (96.66 %), days to maturity (94.26 %), number of nodes on the main stem (93.12 %), number of flowers per cluster (93.10 %), plant height (92.85 %), shape index (90.91 %),

Table 4: 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
Dfl	85.89	6.76	16.25
Fl/C	93.10	3.55	71.57
Fr/C	51.25	0.60	17.66
FC/P	80.50	13.91	48.23
SD	64.29	0.16	13.68
DM	94.26	11.60	14.36
PH	92.85	29.36	49.39
NN	93.12	6.86	42.56
FD	83.13	1.40	28.18
FL	62.42	0.87	17.72
SI	90.91	0.34	33.90
F/P	96.66	30.15	88.18
TSS	57.83	0.71	16.16
S/F	84.80	81.57	75.77
Y/P	75.53	0.48	32.00

Fl/C = Number of flowers per cluster, 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, S/F = Number of seed per fruits, 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, DFl = Days to 50 per cent flowering, DM = Days to maturity, Y/P = Average fruit yield per plant

days to 50 per cent flowering (85.89 %), number of seeds per fruit (84.80 %), fruit diameter (83.13 %) and number of fruit clusters per plant (80.50 %) (Table 5) indicating the possibility of improvement through selection. The characters like number of fruit clusters per plant, plant height, number of fruits per plant and number of seed per fruits recorded very high heritability and genotypic coefficients of variation.

The expected genetic advance as per cent of mean from selecting the top 5 per cent of the genotypes ranged from 13.68 per cent for stem diameter to 88.18 per cent for number of fruits per plant (Table 4). This indicated that selecting the top 5 per cent of the base population would result an increase of 13.68 per cent for stem diameter and 88.18 per cent for number of fruits per plant over the base population mean.

Characters such as number of seeds per fruit (75.77%), number of flowers per cluster (71.57%), plant height (49.39 %), number of fruit clusters per plant (48.23%), number of nodes on the main stem (42.56%), shape index (33.9%), average fruit yield per plant (32%) and fruit diameter (28.18%) recorded relatively higher values of expected genetic advance as percent of mean next to number of fruits per plant.

High genetic advance accompanied by high heritability was observed for number of seeds per fruit ($h^2(b) = 84.8\%$ and $GA = 81.57$), number of fruits per plant ($h^2(b) = 96.66\%$ and $GA = 30.15$), plant height ($h^2(b) = 92.85\%$ and $GA = 29.36$), number of fruit clusters per plant ($h^2(b) = 80.5\%$ and $GA = 13.91$) and days to maturity ($h^2(b) = 94.26\%$ and $GA = 11.60$).

The characters like stem diameter, shape index, average fruit yield per plant, number of fruits per cluster, total soluble solids, fruit length, fruit diameter and number of flowers per cluster in spite of having relatively higher heritability estimates had recorded low to moderate genetic advance (Table 4). The result of this study indicated that selection for stem diameter, shape index, average fruit yield per plant, number of fruits per cluster, total soluble solid, fruit length, fruit diameter and number of flowers per cluster would be less effective as compared to selection for the characters that showed high heritability and high genetic advance in this crop improvement program. Characters such as number of fruit clusters per plant, plant height, number of fruits per plant and number of seed per fruits recorded very high heritability, genetic advance and genetic advance as percent of mean and genotypic coefficients of variation

DISCUSSION

Analysis of variance of genotypes exhibited highly significant differences for all the characters studied, indicating the existence of sufficient genetic variability and the scope for improvement of tomato crop. Similar findings were reported by [12, 13] who characterized different tomato varieties.

The smallest differences were observed between phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values of characters such as days to maturity, days to 50 per cent flowering, number of fruits per plant, number of nodes on main stem, shape index, stem diameter and plant height suggesting lesser influence of environmental factors on their expression. Similar results were observed for fruit shape index and days to maturity [13]. Relatively higher differences between PCV and GCV values were recorded in respects of the characters like number of fruit per cluster, unmarketable fruit yield per plot, number of seeds per fruit, total soluble solids, number of fruit clusters per plant, marketable fruit yield per plot, fruit yield per plant, stem diameter, fruit diameter and number of flowers per cluster. The results revealed that these characters were under more influences of environmental factors than the rest of the characters studied.

For characters like number of fruits per plant, number of seeds per fruit, number of flowers per cluster, unmarketable fruit yield per plot, fruit clusters per plant and plant height, the values of phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were relatively higher than the rest of the studied characters. This implied that the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters. This is in agreement with the findings of [14] for number of fruits per plant. Existence of high phenotypic variability and coefficient of genotypic variance for yield components also indicated the possibilities to improve the genotypes by selection. Intermediate PCV and GCV values were recorded for marketable fruit yield per plot, number of nodes on the main stem, average fruit yield per plant, shape index, number of fruits per cluster and fruit diameter, while they were relatively lower for days to maturity, days to 50 per cent flowering, stem diameter, total soluble solids and fruit length indicating selection for these characters is less effective as compared to the characters having higher percent of GCV and PCV values. In general, from overall result obtained, it could be concluded that the studied genotypes have sufficient genetic variability that can be utilized for further improvement of this crop through selection process.

The heritability estimate was more than 50 per cent for all the characters considered in this study. This observation is in agreement with the findings of [15] for days to flowering, [16] for plant height and fruit diameter and [17] for number of fruit per plant. According to [3], if the heritability of the character is very high e.g., 0.8 or more, selection for the character should be fairly easy. This is because there would be closer correspondence between the genotypes and phenotype due to relatively smaller contribution of environment to the phenotype. In view of this observation, selection for the above characters would be fairly effective due to smaller contribution of environment to their phenotypic expression. The characters like number of fruit clusters per plant, plant height, number of fruits per plant and number of seed per fruits recorded very high heritability and genotypic coefficients of variation. It was suggested by [12] that the magnitude of heritability is largely governed the amount of genotypic variance present in the population. Similar suggestions were forwarded [10, 18] that larger heritability and genetic progress would be obtained from larger genetic variance. This indicated that more effectiveness of selection to improve the above characters.

The expected genetic advance as per cent of mean from selecting the top 5 per cent of the genotypes indicated that selecting the top 5 per cent of the base population would result in an increase of 13.68 per cent for stem diameter and 88.18 per cent for number of fruits per plant over the base population mean. Similar result was reported [19, 17] for number of fruits per plant. This indicated that selection would be useful in improving these characters.

High genetic advance accompanied by high heritability was observed for number of seeds per fruit, number of fruits per plant, plant height, number of fruit clusters per plant and days to maturity. This result is in agreement with the findings of [14, 20-23], for number of fruits per plant, [24] for number of fruits per plant, number of seeds per fruit and plant height, [13] and [25] for number of seeds per fruit and plant height and [26] for number of fruit per plant and plant height. A suggestion by [27] stated 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 [28], 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 seeds per fruit, number of fruits per plant, plant height and number of fruit clusters per plant, would be most likely effective in tomato improvement.

The result of this study indicated that selection for stem diameter, shape index, average fruit yield per plant, number of fruits per cluster, total soluble solids, fruit length, fruit diameter and number of flowers per cluster would be less effective as compared to selection for the characters that showed high heritability and high genetic advance in this crop improvement program. Characters such as number of fruit clusters per plant, plant height, number of fruits per plant and number of seed per fruits recorded very high heritability, genetic advance and genetic advance as percent of mean and genotypic coefficients of variation. An observation made by [12] also mentioned that high heritability, genetic advance as percent of mean and genotypic coefficients of variation for number of fruits per plant. It was also found out by [29] that a genetic coefficient of variation together with a heritability estimate would seem to give the best picture of the amount of advance to be expected from selection. Therefore, this observation indicated the possibility of improving tomato crop through direct selection for the above characters.

ACKNOWLEDGEMENTS

The authors are grateful to Oromiya Rural Development and Capacity Building for sponsoring this study.

REFERENCES

1. Shankara, N., V. Joep, G. Marja, H. Martin and V. Barbara, 2005. Cultivation of tomato. Fourth completely revised edition. Agromisa Foundation and CTA, Wageningen. http://journeytoforever.org/farm_library/AD17.pdf.
2. Dudley, J.W. and R.H. Moll, 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. *Crop Science*, 9: 257-262.
3. Singh, B.D., 1993. *Plant Breeding, Principles and Methods*. Kalayani Publishers, New Delhi, pp: 103-142.
4. Tesfaye, L. and G. Diriba, 2006. Effect of stocking rate on growth of lambs grazed on dry season tropical mixed pasture in Ethiopia. *Livestock Research for Rural Development*. Volume 18, Article No. 161. <http://www.cipav.org.co/lrrd/lrrd18/11/lemm18161.htm>
5. Yohannes, G., A. Kasahun and C.J. Thwaites, 2005. Factors Influencing Survival and Growth of the Ethiopian Horro Sheep. *Ethiopian Journal of Agricultural Science*, 18(1): 41-51.
6. Kebede, M., J.P.C. Greyling and L.M.J. Schwalbach, 2007. Effect of season and supplementation on percentage live sperm and sperm abnormalities in Horro (Zebu) bulls in sub-humid environment in Ethiopia. *Tropical Animal Health and Production*, 39(2): 149-154.
7. Waskar, D.P., R.M. Kheldlar and V.K. Grande, 1999. Effect of post harvest treatment on shelf life and quality of pomegranate in evaporative cooling chamber and ambient conditions. *Journal of food sciences and technology*, 2(36): 114-117.
8. Montgomery, D.C., 2005. *Design and Analysis of Experimentals*, 6th ed. John Wiley and Sons Inc., USA., pp: 97.
9. GENRES., 1994. Version 7.01 Statistical Package for Genetical Researchers, Pascal International Software Solutions.
10. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314-318.

11. Hanson, C.H., H.F. Robinson and R.E. Comstock, 1956. Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy Journal*, 48: 268-272.
12. Pradeepkumar, T., D. Bastian, M. Joy, N.V. Radhakrishnan and K.C. Aipe, 2001. Genetic Variability in Tomato for Yield and Resistance to Bacterial Wilt. *Journal of Tropical Agriculture*, 39: 157-158.
13. Fekadu, M., H. Ravishankar and D. Lemma, 2003. Study on variability in tomato germplasm under conditions of central Ethiopia. *Vegetable Crops Research Bulletin*, 58: 41-49.
14. Sahu, G.S. and R.S. Mishra, 1995. Genetic divergence in tomato. *Journal of Agricultural Science*, 29(1): 5-8.
15. Natarajan, S., 1994. Genetics of yield and its components in tomato under moisture stress. *Madras Agricultural Journal*, 81(6): 311-312.
16. Kumari, A.N. and M. Subramanian, 1994. Genetics variability in tomato. *Madras Agricultural Journal*, 81(12): 651-653.
17. Padmini, K. and E. Vadivel, 1997. Studies on genetic variability and heritability in F2 generation of tomato (*Lycopersicon esculentum* Mill.). *South Indian Horticulture*, 45(1-2): 1-4.
18. Allard, R.W., 1999. Principles of Plant Breeding, 2nd ed. John Willey and Sons, Inc., New York, pp: 95-102, 235-236.
19. Phookan, D.B., P. Talukdar, A. Shadeque and B.K. Chakravarty, 1998. Genetic variability and heritability in tomato (*Lycopersicon esculentum* Mill.) genotypes during summer season under plastic-house condition. *Indian Journal of Agricultural Science*, 68(6): 304-306.
20. Singh, H.N., R.R. Singh and R.K. Mittal, 1974. Genotypic and phenotypic variability in tomato. *Indian Journal of Agricultural Science*, 44(12): 807-811.
21. Natarajan, S., 1991. Genetics variability and heritability in F2 generation of intervarietal crosses of tomato under moisture stress. *South Indian Horticulture*, 39(1): 27-31.
22. Sreenivasulu, B. and P.V. Rao, 1996. Variability studies in F2 generation of tomato under moisture stress. *Journal of Research APAU*, 24(3-4): 71-72.
23. Das, B., M.H. Hazarika and P.K. Das, 1998. Genetic variability and correlation in fruit characters of tomato (*Lycopersicon esculentum* Mill.). *Annals of Agricultural Research*, 19(1): 77-80.
24. Barman, D., C.K. Sharma, I.P. Singh, S. Sardana and L.C. De, 1995. Genetic variability in exotic lines of tomato (*Lycopersicon esculentum* Mill.). *International Journal of Tropical Agriculture*, 13(1-4): 265-268.
25. Ghosh, P.K., M.M. Syamal, N. Rai and A.K. Joshi, 1995. Improvement of hybrid tomato. *Advances in Plant Sciences*, 8(2): 79-83.
26. Mittal, P., S. Prakash and A.K. Singh, 1996. Variability studies in tomato (*Lycopersicon esculentum* Mill.) under sub humid conditions of Himachal Pradesh. *South Indian Horticulture*, 44(5-6): 132-134.
27. Chauhan, J.S. and M.K. Tyagi, 2002. Inheritance of Erucic Acid Content in Two Crosses of Indian Mustard (*Brassica juncea* L.). *SABRAO Journal of Breeding and Genetics*, 34(1): 19-26.
28. Rakhi, R. and L. Rajamony, 2005. Variability, heritability and genetic advances in landraces of culinary melon (*Cucumis melo* L.). *Journal of tropical agriculture*, 43(1-2): 79-82.
29. Burton, G.W., 1952. Quantitative inheritance in grasses. *Proceedings of the Sixth International Grassland Congress*, pp: 277-283.