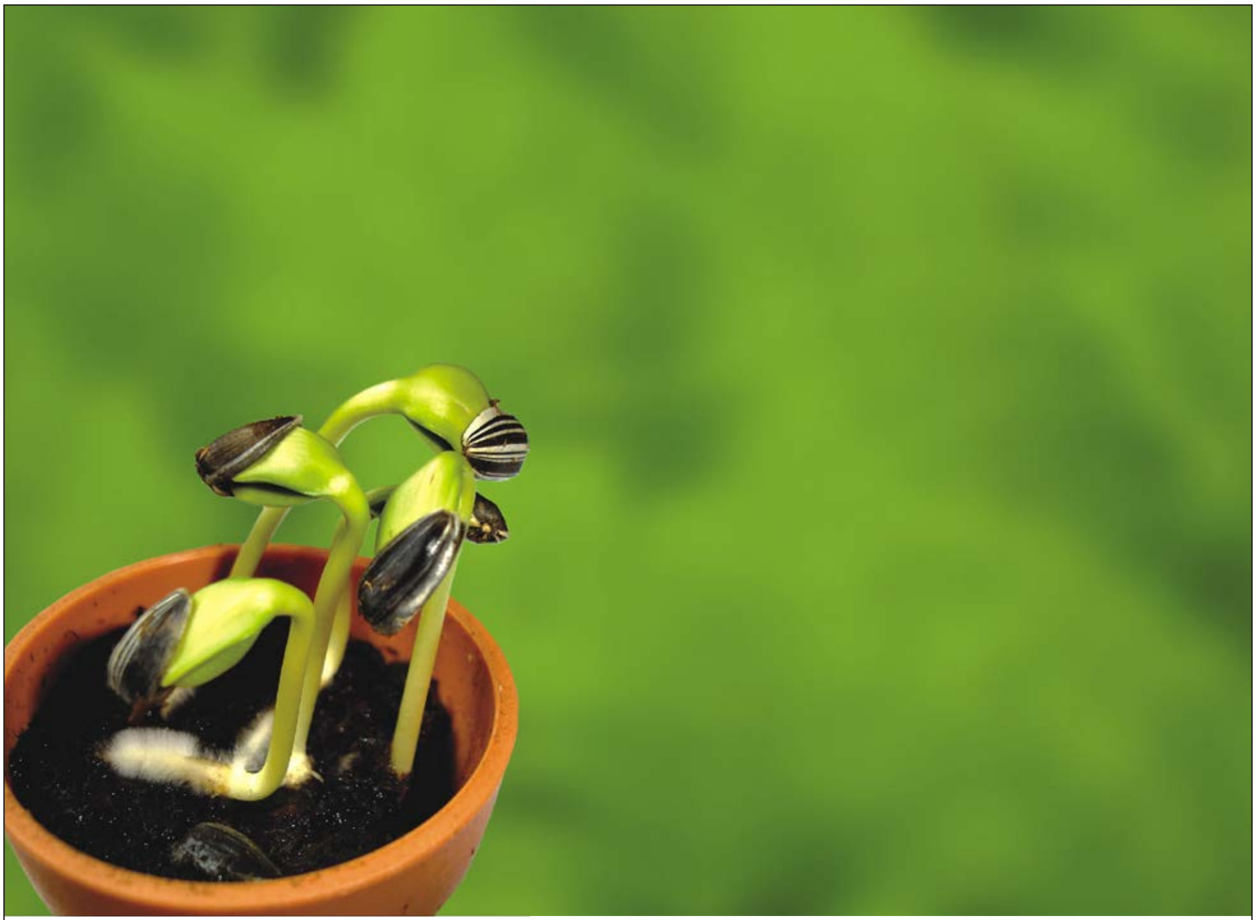

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Genetic Associations Analysis among Some Traits of Tomato (*Lycopersicon esculentum* Mill.) Genotypes in West Showa, Ethiopia

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ABSTRACT

The study was initiated to generate genetic information on characters associations for tomato genotypes maintained under Ethiopian conditions. Twenty three tomato (*Lycopersicon esculentum* Mill.) genotypes were evaluated to estimate the nature and magnitude of associations of different characters with fruit yield and among themselves at Bako Agricultural Research Center (Western Ethiopia) during October 2007 to May 2008. The experiment was conducted using a Randomized Complete Block Design with three replications. Yield per plant showed positive and significant genotypic and phenotypic correlation with fruit clusters per plant ($r_g = 0.448^*$, $r_p = 0.442^*$) and fruits per plant ($r_g = 0.505^*$, $r_p = 0.461^*$) which indicated that these traits play important role in yield improvement. Fruit clusters per plant showed positive and significant genotypic and phenotypic correlation with yield per plant by having positive direct effect at both levels, indicating the true relationship between them and the feasibility to exploit the potentiality of this trait for effective direct selection to improve yield per plant. Genotypic and phenotypic path coefficient analysis revealed that positive direct effects were exerted by days to flowering, fruit clusters per plant and plant height on yield per plant, suggesting their importance in yield improvement and that these traits would be considered in selection program.

Key words: Fruit cluster, genotypic correlation, path coefficient analysis, phenotypic correlation, traits

INTRODUCTION

Tomato (*Lycopersicon esculentum* Mill.) is native of West Coast of South America (Mexico and Peru) and was cultivated by Indians about 500 B.C. long before arrival of Spaniards (Rehman *et al.*, 2000). It is a widely disseminated vegetable crop all over the world (Adebooye *et al.*, 2006) and is among the world's major traded vegetable crops (Dar and Sharma, 2011).

Tomato is consumed as a fresh or processed product in different part of the world (Adebooye *et al.*, 2006). The fresh fruits of tomato possess several nutritive value traits including antioxidant compounds which are being use in formulation of several commercial therapeuticals (Dar and Sharma, 2011). Consuming vegetables rich in lycopene, such as tomatoes or tomato-based products, may reduce the risk of getting breast, cervical, gastrointestinal, colorectal, lung and prostate cancer (Mahajan *et al.*, 2009).

In Ethiopia, tomato is produced in the state and private horticultural enterprises, commercial farms and small farmers scattered in different parts of Ethiopia. It is produced mainly as a source of food and income both under rain fed as well as irrigated conditions. Tomato is among the most important vegetable crops in Ethiopia.

Lemma and Geleti (2006) indicated that the total production of tomato in the country has shown a marked increase since it became the most profitable crop providing a higher income to small scale farmers compared to other vegetable crops. However, the average national yield (7 t ha^{-1}) still remains very low (CSA, 2009) as compared to the world average yield of 28.39 t ha^{-1} (FAOSTAT, 2011). This indicates that there is a need to increase the productivity of this crop. In this context, developing superior yielding varieties through appropriate breeding work is mandatory to satisfy ever increasing demand of domestic and export markets for this crop. As indicated by Ashrafuzzaman *et al.* (2010), conventional breeding techniques is appropriate to improve the yield and quality of this crop.

Generating information about the relationships between yield and other economic attributes is the key task in genetic improvement of any crop plant. Exploiting genetically desirable traits is important in order to achieve the rapid genetic improvement of a crop (Denton and Nwangburuka, 2011). According to Singh (1993), understanding the relative contribution of the various component traits to yield could play significant role in identifying high yielding genotypes from genetically variable populations by providing information on indirect selection for yield. Information on genetic associations among traits and variability is important for plant breeding program and it guides the plant breeders to use appropriate breeding techniques (Ekvised *et al.*, 2006; Khan *et al.*, 2001; Bashir *et al.*, 2001).

Lemma (2002) stated that various factors contribute to low yield of tomato in Ethiopia including shortage of improved varieties. The best alternative to overcome such problem is developing improved varieties through genetic manipulation of this crop. In order to achieve this goal, it is important to identify ideal plant traits relevant to variety development program. However, there is limited genetic information with respect to relationships between fruit yield and yield related traits on tomato genotypes under production in Ethiopian. This study was therefore conducted to estimate the nature and magnitude of relationship and to obtain information on the associations among fruit yield and related characteristics in some tomato genotypes.

MATERIALS AND METHODS

Testing location and season: The study was conducted under irrigation condition from October 2007 to May 2008 at Bako Agricultural Research Center which is located between 9°07'N latitude and 37°05'E longitude at an altitude of 1650 m above sea level. The mean daily minimum and maximum temperature are 15.1 and 30.3°C, respectively and receives an average of 1200 mm rain per year (Kebede *et al.*, 2007). The soil type of the area belongs to the Nitosol series which is reddish-brown in color and has clay to sandy clay-loam texture with pH ranging from 5.3-6.0 (Lemma and Geleti, 2006).

Experimental materials and design: Twenty three tomato genotypes, 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). The experiment was laid out in a Randomized

Complete Block Design with three replications and each plot having five rows. Inter-row spacing of 1.0 m and inter-row spacing of 0.3 m within the block was maintained to accommodate 35 plants per gross plot.

Data collection: In this study, 17 characters were studied from 15 sample plants in each net plot and the results were expressed as mean values. 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 Waskar *et al.* (1999) using handheld refractometer with a range of resolution 0.0 to 32.0°Brix to 0.2°Brix by standardizing against distilled water (0.0% TSS). One to two drops of extracted juice was placed on the prism of refractometer and to avoid error data collection, the prism of refractometer was properly washed with distilled water and dried between using each samples.

Statistical procedures: The data collected for each trait were subjected to analysis of variance for Randomized Complete Block Design as per Montgomery (2005). GENRES Statistical Software Package (GENRES, 1994) 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.

Phenotypic correlation, genotypic correlation and environmental correlation, were estimated using the formula given by Miller *et al.* (1958) as follows:

$$r_p = \frac{P\mathrm{cov}XY}{\sqrt{\sigma^2 pX.\sigma^2 pY}}$$

$$r_g = \frac{G\mathrm{cov}XY}{\sqrt{\sigma^2 gX.\sigma^2 gY}}$$

where, PcovXY = Phenotypic covariance of character x and character y, r_p = phenotypic correlation, σ^2_pX = phenotypic variance for character x, σ^2_pY = phenotypic variance for character y, GcovXY = Genotypic Covariance of character x and character y, r_g = genotypic correlation, σ^2_gX = genotypic variance for character x and σ^2_gY = genotypic variance for character y.

The significance of phenotypic and genotypic correlation coefficients was tested by referring the standard table (Snedecor and Cochran, 1967) at n-2 degree of freedom. Where, n is number of genotypes.

In path coefficient analysis, fruit yield per plant was considered as resultant (dependent) variable and the rest of the characters considered as causal (independent) variables. The direct and indirect effects of independent characters on fruit yield per plant were estimated by using the following formula as applied by Dewey and Lu (1959):

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

where, r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficients. P_{ij} = direct effects of the independent character (i) on the dependent variable (j) as measured by the genotypic path coefficients and $\sum r_{ik}p_{kj}$ = Summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

The residual effects were estimated using the formula: $\sqrt{1-R^2}$, where, $R^2 = \sum P_{ij}r_{ij}$.

RESULTS AND DISCUSSION

Analyses of correlations at genotypic (r_g) and phenotypic (r_p) levels: For most of the characters studied, phenotypic correlation coefficients were lower in magnitude than that of corresponding genotypic correlation coefficients (Table 1). This clearly indicated inherent association among various characters independent of environmental factors influence.

Positive and significant genotypic and phenotypic correlation of average fruit yield per plant with fruit clusters per plant (r_g = 0.448*, r_p = 0.442*) and fruits per plant (r_g = 0.505*, r_p = 0.461*) was recorded (Table 1). Nair and Thamburaj (1995), Moya *et al.* (1996), Singh *et al.* (1997), Verma *et al.* (1997), Das *et al.* (1998), Prasad *et al.* (1998), Wang *et al.* (1998) and Yadav and Singh (1998) also observed that positive and significant phenotypic and genotypic correlation of average fruit yield per plant with fruits per plant. According to Singh (1993), greater yield response is obtained when the character for which indirect selection is practiced has a high heritability and a high correlation with yield. The practical utility of selecting for a given character as a means of improving another depends on the extent to which improvement in the major character is facilitated by selection for the indicators (Johnson *et al.*, 1955). Such improvement depends on genotypic and phenotypic correlations of the characters. This implied that any increase in either of the above characters would result in significant increase in average fruit yield per plant. Similarly, characters such as total soluble solids, seeds per fruit, shape index, fruit length and fruits per cluster showed positive and low genotypic and phenotypic association with average fruit yield per plant (Table 1). This result is in agreement with findings of Cuartero and Cubero (1982) for fruits per cluster. This pointed that keeping other components constant; any increase in either of above characters would lead to increase in average fruit yield per plant.

Negative and low genotypic and phenotypic correlation of average fruit yield per plant with plant height, nodes on main stem, flowers per cluster, days to maturity and days to 50% flowering was recorded (Table 1). This implied that keeping other components constant any decrease in the above factors would lead to increase in average fruit yield per plant. Average fruit yield per plant showed negative and low association at genotypic level and positive and low association at phenotypic level (which is nearer to null at both levels) with stem diameter (r_g = -0.054, r_p = 0.056) and fruit diameter (r_g = -0.073, r_p = 0.039) (Table 1). This indicated that the weaker relationship between these characters and average fruit yield per plant.

Fruits per cluster showed positive and significant association with fruits per plant at genotypic (r_g = 0.465*) level and positive non significant association at phenotypic (r_p = 0.317) level. And the characters like fruit clusters per plant (r_g = 0.506*, r_p = 0.459*) and shape index (r_g = 0.446*, r_p = 0.428*) showed positive and significant correlation with fruits per plant at both genotypic and phenotypic levels (Table 1). This indicated that the above characters play important role in yield improvement and that they are more useful in selection process. Fruit diameter (r_g = -0.667**, r_p = -0.743**) showed negative and highly significant genotypic and phenotypic correlation with fruits per plant, while days to 50% flowering, fruit length,

Table 1: Correlation coefficients at genotypic (above diagonal) and phenotypic (below diagonal) level of various characters in some tomato genotypes

Chanter	DFl	Fl/C	Fr/C	FC/P	SD	DM	PH	NN	FD	FL	SI	F/P	TSS	S/F	Y/P
DFl	1	0.065	-0.407	0.023	0.441*	0.771**	0.229	0.165	0.280	-0.342	-0.413	-0.371	0.101	0.195	-0.279
Fl/C	0.065	1	0.576**	0.066	-0.122	0.432*	0.745**	0.708**	-0.268	-0.636**	-0.207	0.232	0.079	0.283	-0.189
Fr/C	-0.227	0.443*	1	-0.084	-0.188	-0.122	0.335	0.266	-0.555**	-0.336	0.234	0.465*	0.149	-0.052	-0.117
FC/P	0.043	0.063	0.008	1	0.188	0.284	0.363	0.307	-0.271	-0.334	0.013	0.506*	0.332	-0.013	0.448*
SD	0.377	-0.072	-0.023	0.151	1	0.495*	0.231	0.151	0.371	-0.377	-0.548**	-0.081	-0.308	0.361	-0.054
DM	0.738**	0.409	-0.046	0.252	0.407	1	0.754**	0.623**	0.051	-0.645*	-0.452*	-0.074	0.086	0.250	-0.189
PH	0.187	0.703**	0.339	0.310	0.189	0.703**	1	0.897**	-0.132	-0.743**	-0.375	0.289	0.023	0.244	-0.056
NN	0.133	0.641**	0.183	0.306	0.123	0.562**	0.850**	1	-0.165	-0.511*	-0.217	0.246	0.019	0.034	-0.183
FD	0.265	-0.206	-0.255	-0.158	0.329	0.042	-0.089	-0.123	1	-0.023	-0.767**	-0.743**	-0.285	0.653**	-0.073
FL	-0.224	-0.467*	-0.059	-0.144	-0.191	-0.466*	-0.537**	-0.376	0.134	1	0.660**	-0.185	0.181	-0.548**	0.050
SI	-0.366	-0.207	0.131	0.029	-0.419*	-0.404	-0.351	-0.186	-0.702**	0.547**	1	0.446*	0.392	-0.853**	0.080
F/P	-0.354	0.218	0.317	0.459*	-0.064	-0.075	0.278	0.236	-0.667**	-0.126	0.428*	1	0.165	-0.389	0.505*
TSS	0.029	0.042	-0.112	0.088	-0.176	0.029	0.023	0.002	-0.293	0.003	0.264	0.118	1	-0.119	0.259
S/F	0.146	0.258	-0.019	0.004	0.214	0.204	0.225	0.032	0.517*	-0.467*	-0.760**	-0.352	-0.090	1	0.109
Y/P	-0.167	-0.153	0.054	0.442*	0.056	-0.143	-0.007	-0.154	0.039	0.178	0.074	0.461*	0.056	0.072	1

*, **: Indicate significant at 5 and 1% probability levels respectively. The correlation coefficient must exceed 0.413 and 0.526 to be significant at 5% and 1% probability levels, respectively. Fl/C: Flowers per cluster, Fr/C: Fruits per cluster, FC/P: Fruit clusters per plant, SD: Stem diameter, PH: Plant height, NN: Nodes on main stem, S/F: Seeds per fruit, FD: Fruit diameter, FL: Fruit length, SI (ratio of FL/FD: Fruit shape index, F/P: Fruits per plant, TSS: Total soluble solids, DFl: Days to 50% flowering, DM: Days to maturity, Y/P: Average fruit yield per plant

stem diameter and days to maturity recorded negative but lower association with fruits per plant at both level (Table 1). Raijadhav *et al.* (1996) found similar result for days to 50% flowering. Genotypic correlation coefficients provide a measure of genetic association between traits and thus help identify the more important as well as the lesser important traits to be considered in breeding program (Pandey and Gritton, 1975). This indicated that these characters play important role in this crop's improvement program. And this pointed that the need of focus in selecting genotypes with smaller fruit diameter and length, lesser days to 50% flowering and days to maturity for average fruit yield improvement.

Positive and significant genotypic and phenotypic association of flowers per cluster with fruits per cluster, plant height and nodes on the main stem and seeds per fruit with fruit diameter, shape index with fruit length, days to maturity with plant height, nodes on the main stem and days to 50% flowering indicating the strong positive relationship between the characters (Table 1).

Negative and significant genotypic and phenotypic correlation flowers per cluster with fruit length, stem diameter with shape index, plant height with fruit length, seeds per fruit with fruit length and shape index, fruit diameter with shape index and fruit length with days to maturity, was recorded. And negative and significant genotypic and non significant phenotypic association of fruits per cluster with fruit diameter, nodes on the main stem with fruit length and shape index with days to maturity was observed (Table 1). This indicated the existence of strong negative relationship between these each pair traits.

Path coefficient analysis: In order to measure the relative magnitude of each causal factors contributing to correlations and determine the specific effects acting to produce the correlations, the observed correlations were further partitioned into their direct and indirect components by path coefficient analysis. Path coefficient analysis is useful in partitioning the correlation coefficients into direct and indirect effects to measure the relative importance of causal factors and permits critical determination of the specific forces acting to produce a given correlation (Bhatt, 1973; Khan and Qureshi, 2001). As yield is influenced by many components or contributing traits both in positive and negative directions, it was considered as resultant (dependent) variable and the rest of the characters considered as causal (independent) variables.

At phenotypic level characters like plant height, days to 50% flowering, fruits per plant (0.021), shape index (0.015) and fruit clusters per plant (0.008) exerted relatively higher magnitude positive direct effect on yield per plant (Table 2). This observation is in agreement with the findings of Mohanty (2003) and Mariame *et al.* (2004) for fruits per plant. But it is contrasting with results reported by Rani *et al.* (2008) for plant height. This is probably due to the influences of environmental factors on inherent association of the characters. According to Dewey and Lu (1959), if environmental variances and covariance of the two characters is reduced to zero, the phenotypic and genotypic correlation coefficients will of necessity be identical. This clearly indicated that inherent association between these characters is more influenced by environmental factors. Among the above characters, only fruits per plant (r_p = 0.461*), fruit clusters per plant (r_p = 0.442*) and shape index (r_p = 0.074), showed positive phenotypic correlation with average fruit yield per plant, while the rest rerecorded negative phenotypic association with average fruit yield per plant. This revealed the existence of true relationship between fruit yield per plant and fruits per plant, fruit cluster per plant and shape index, indicating selection for such characters would be most likely effective for yield improvement.

Even though the characters like days to maturity (-0.045), fruit length (-0.024), fruits per cluster (-0.016), flowers per cluster (-0.014) exerted relatively stronger negative direct effects on yield per plant, only days to maturity and flowers per cluster showed negative phenotypic correlation with yield per plant. This indicated that the characters such as days to maturity and flowers per cluster could have inverse relationship with yield per plant.

The phenotypic positive indirect effects of fruits per cluster, stem diameter, fruit length and total soluble solids were counteracted by their own respective phenotypic negative direct effects leading to positive phenotypic correlation with yield per plant. This indicated that the roles of positive indirect effects of these characters should be given appropriate focus in selection for higher yield per plant.

Genotypic path coefficient analysis indicated that positive direct effects were exerted by fruits per cluster, days to 50% flowering, nodes on the main stem, fruit clusters per plant, stem diameter and plant height on average fruit yield per plant (Table 3). Haydar *et al.* (2007) also observed similar results for days to 50% flowering and plant height and Mariame *et al.* (2004) for fruits per plant and nodes on the main stem. This suggested that the above characters play important role in improvement of average fruit yield per plant. However, fruits per cluster, stem diameter, plant height, nodes on the main stem and days to 50% flowering had positive genotypic direct effects on average fruit yield per plant, they exhibited negative genotypic correlation with average fruit yield per plant. And only fruit clusters per plant showed positive and significant genotypic correlation (r_g = 0.448*) with average fruit yield per plant by having positive genotypic direct effect (Table 3). If the correlation between yield and a character is due to direct effects of the character, it reflects a true relationship between them and selection can be practiced for such a character in order to improve yield (Singh, 1993). This observation revealed that the existence of true relationship between fruit clusters per plant and average fruit yield per plant which suggested that direct selection for such character to improve average fruit yield per plant would be effective.

Table 2: Phenotypic direct effect (underlined and bold face) and indirect effects of various characters on fruit yield per plant of tomato genotypes studied under Bako, Southwestern Ethiopia condition

Chanter	DFl	Fl/C	Fr/C	FC/P	SD	DM	PH	NN	FD	FL	SI	F/P	TSS	S/F	r_p
DFl	0.035	-0.001	0.004	0.001	-0.003	-0.033	0.009	-0.001	0.002	0.005	-0.006	-0.007	-0.001	0.001	-0.167
Fl/C	0.002	-0.014	-0.007	0.001	0.001	-0.018	0.034	-0.001	-0.002	0.011	-0.003	0.005	-0.001	0.002	-0.153
Fr/C	-0.008	-0.006	-0.016	0.001	0.001	0.002	0.016	-0.001	-0.002	0.001	0.002	0.007	0.001	-0.001	0.054
FC/P	0.002	-0.001	-0.001	0.008	-0.001	-0.011	0.015	-0.001	-0.001	0.003	0.001	0.020	-0.001	0.001	0.442*
SD	0.013	0.001	0.001	0.001	-0.008	-0.018	0.009	-0.001	0.002	0.005	-0.006	-0.001	0.001	0.002	0.056
DM	0.026	-0.006	0.001	0.002	-0.003	-0.045	0.034	-0.002	0.001	0.011	-0.006	-0.002	-0.001	0.002	-0.143
PH	0.007	-0.010	-0.005	0.003	-0.002	-0.031	0.048	-0.003	-0.001	0.013	-0.005	0.006	0.001	0.002	-0.007
NN	0.005	-0.009	-0.003	0.003	-0.010	-0.025	0.041	-0.003	-0.001	0.010	-0.003	0.005	-0.001	0.001	-0.154
FD	0.0092	0.003	0.0040	-0.001	-0.003	-0.002	-0.004	0.001	0.006	-0.003	-0.011	-0.014	0.001	0.004	0.039
FL	-0.008	0.007	0.001	-0.001	0.002	0.021	-0.026	0.001	0.001	-0.024	0.008	-0.003	-0.001	-0.003	0.178
SI	-0.013	0.003	-0.002	0.001	0.003	0.018	-0.017	0.001	-0.004	-0.013	0.015	0.009	-0.001	-0.006	0.074
F/P	-0.012	-0.003	-0.005	0.004	0.001	0.003	0.013	-0.001	-0.004	0.003	0.007	0.021	-0.001	-0.003	0.461*
TSS	0.001	-0.001	0.002	0.001	0.001	-0.001	-0.002	-0.001	-0.002	-0.001	0.004	0.003	-0.002	-0.001	0.056
S/F	0.005	-0.004	0.001	0.001	-0.002	-0.009	0.011	-0.001	0.003	0.011	-0.012	-0.007	0.001	0.007	0.072

*: Indicate significant at 5% probability levels. The phenotypic correlation must exceed 0.413 to be significant at 5% probability level. Residual effect = 0.0737, r_p: Phenotypic correlation, Fl/C: Flowers per cluster, Fr/C: Fruits per cluster, FC/P: Fruit clusters per plant, SD: Stem diameter, PH: Plant height, NN: Nodes on main stem, S/F: Seeds per fruit, FD: Fruit diameter, FL: Fruit length, SI (ratio of FL/FD): Fruit shape index, F/P: Fruits per plant, TSS: Total soluble solids, DFl: Days to 50% flowering, DM: Days to maturity

Table 3: Genotypic direct effect (underlined and bold face) and indirect effects of various characters on fruit yield per plant of tomato genotypes studied under Bako, Southwestern Ethiopia condition

Chanter	DFl	Fl/C	Fr/C	FC/P	SD	DM	PH	NN	FD	FL	SI	F/P	TSS	S/F	r_g
DFl	0.074	-0.003	-0.031	0.001	0.014	-0.115	0.004	0.012	-0.049	0.003	0.064	0.099	-0.003	-0.027	-0.279
Fl/C	0.005	-0.048	0.044	0.004	-0.004	-0.064	0.014	0.05	0.047	0.005	0.032	-0.062	-0.002	-0.039	-0.189
Fr/C	-0.030	-0.027	0.076	-0.004	-0.006	0.018	0.006	0.020	0.097	0.003	-0.036	-0.124	-0.005	0.007	-0.117
FC/P	0.002	-0.003	-0.006	0.045	0.006	-0.042	0.007	0.02	0.047	0.003	-0.002	-0.135	-0.010	0.002	0.448*
SD	0.03	0.006	-0.014	0.009	0.031	-0.074	0.004	0.011	-0.065	0.003	0.0846	0.022	0.009	-0.050	-0.054
DM	0.057	-0.021	-0.009	0.013	0.016	-0.149	0.014	0.046	-0.008	0.005	0.0698	0.020	-0.003	-0.035	-0.189
PH	0.017	-0.035	0.025	0.016	0.007	-0.113	0.018	0.066	0.023	0.006	0.0579	-0.077	-0.001	-0.034	-0.056
NN	0.012	-0.034	0.020	0.014	0.005	-0.093	0.016	0.073	0.029	0.004	0.0335	-0.066	-0.001	-0.005	-0.183
FD	0.021	0.013	-0.042	-0.012	0.012	-0.008	-0.002	-0.012	-0.174	0.001	0.1185	0.198	0.009	-0.091	-0.073
FL	-0.025	0.030	-0.025	-0.015	-0.012	0.096	-0.014	-0.038	0.004	-0.008	-0.102	0.049	-0.006	0.076	0.050
SI	-0.0316	0.010	0.018	0.001	-0.017	0.067	-0.007	-0.016	0.134	-0.005	-0.154	-0.119	-0.012	0.119	0.080
F/P	-0.028	-0.011	0.035	0.023	-0.003	0.011	0.005	0.018	0.129	0.002	-0.069	-0.267	-0.005	0.054	0.505*
TSS	0.008	-0.004	0.011	0.015	-0.010	-0.013	0.001	0.001	0.050	-0.003	-0.061	-0.044	-0.031	0.017	0.259
S/F	0.014	-0.013	-0.004	-0.001	0.011	-0.037	0.005	0.003	-0.114	0.005	0.132	0.104	0.004	-0.139	0.109

*: Indicate significant at 5% probability level. The genotypic correlation must exceed 0.413 to be significant at 5% probability levels, Residual effect = 0.0662, r_g: Genotypic correlation, Fl/C: Flowers per cluster, Fr/C: Fruits per cluster, FC/P: Fruit clusters per plant, SD: Stem diameter, PH: Plant height, NN: Nodes on main stem, S/F: Seeds per fruit, FD: Fruit diameter, FL: Fruit length, SI (ratio of FL/FD): Fruit shape index, F/P: Fruits per plant, TSS: Total soluble solids, DFl: Days to 50% flowering, DM = Days to maturity

Negative genotypic direct effects were exerted on average fruit yield per plant by fruit diameter (-0.174) and flowers per cluster (-0.047), having negative genotypic correlation coefficient of r_g = -0.073, r_g = -0.189, respectively, with average fruit yield per plant (Table 3). Mariame *et al.* (2004) observed similar results for days to maturity, seeds per fruit, flowers per cluster and shape index. This indicated that the negative association of these characters with average fruit yield per plant which implied that any decrease in magnitude of either flower per cluster or fruit diameter would result in increase in average fruit yield per plant.

The positive genotypic indirect effects by seeds per fruit through days to 50% flowering, fruits per plant, shape index and stem diameter, could have counteracted with its own negative genotypic direct effect (-0.139) giving the over all correlation with average fruit yield per plant positive (r_g = 0.109). In spite of having negative genotypic direct effect (-0.008) on average fruit yield per plant, fruit length had positive genotypic indirect effects through days to maturity, fruits per plant, seeds per fruit and flowers per cluster which contributed to positive genotypic correlation (r_g= 0.050) with average fruit yield per plant. In addition, the possibilities that positive genotypic indirect effects by shape index through days to maturity, fruit diameter, seeds per fruit and fruits per cluster could have counteracted with its own negative genotypic direct effect (-0.154) leading to positive genotypic correlation (r_g = 0.080) with average fruit yield per plant. Similarly, the positive genotypic indirect effects of fruits per plant through days to maturity, fruit diameter, seeds per fruit, nodes on the main stem, fruit clusters per plant and fruits per cluster counteracted with its own negative direct effect (-0.267) leading to positive genotypic correlation (r_g = 0.505*) with average fruit yield per plant (Table 2).

In view of results of the present observation, indirect causal factors of seeds per fruit, fruit length, shape index, fruits per plant and total soluble solids need to be considered simultaneously for selection. Singh and Chaudhary (1977) also stated that the causal factors of indirect effects could be the cause of correlation, when the correlation coefficient is positive but the direct effect is negative or negligible.

CONCLUSION

Fruit clusters per plant showed positive and significant genotypic and phenotypic correlation with average fruit yield per plant by having positive direct effect on average fruit yield per plant at both levels. This indicated the true relationship between fruit clusters per plant and average fruit yield per plant. In turn this indicates the feasibility to exploit the potentiality of fruit clusters per plant for effective direct selection to improve average yield per plant. Fruits per plant showed negative and significant association with fruit diameter and negative and low association with days to 50% flowering, fruit length, stem diameter and days to maturity at both genotypic and phenotypic levels. This indicated that the importance of these characters in tomato improvement program through selection.

The genotypic and phenotypic positive indirect effects of fruit length and total soluble solids were counteracted by their own respective genotypic and phenotypic negative direct effects leading to positive genotypic and phenotypic correlation with average fruit yield per plant. The genotypic positive indirect effects of seeds per fruit, shape index, fruits per plant were counteracted by their own respective genotypic negative direct effects leading to positive genotypic correlation with average fruit yield per plant. In light of this observation, the indirect causal factors of the above characters need to be considered simultaneously for selection. Hence, it may also be possible to consider the indirect positive effects fruits per plant, total soluble solids, seeds per fruit, shape index and fruit length in overall selection process. In addition, the undesirable indirect negative effects fruits per cluster, days to flowering, nodes on main stem, stem diameter and plant height need to be nullified through imposing appropriate selection model in order to make use of their positive direct effects for yield improvement. In view of the above, it would be advisable to continue this study across locations and seasons with additional genotypes.

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