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Genetic Variability and Association of Characters in Tomato (*Solanum lycopersicon* L.) Genotypes in Northern Ethiopia

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ABSTRACT

The aim of the study was to estimate the extent of genetic variability and association among characters. Thirty six tomato genotypes were evaluated at Humera Agricultural Research Center, Northern Ethiopia, during 2010/11 in 6×6 simple lattice design with two replications. Variance component method was used to estimate genetic variance, heritability and genetic advance. Highly significant difference ($p < 0.01$) was observed among the tested genotypes for all the characters studied. Highest phenotypic (79.13 and 74.66) and genotypic coefficient of correlation (78.47 and 73.27) were observed for number of matured fruits per plant and fruit set percentage. The highest heritability estimate was recorded for number of matured fruits per plant (98.34) and the least for number of primary branches (47.36%). Yield per hectare had highest positive and highly significant phenotypic correlation with weight of fruits per plant ($r_p = 0.89$), fruits per plant ($r_p = 0.85$) and fruit set percentage ($r_p = 0.78$). While it showed negative and highly significant phenotypic correlation with days to 50% fruiting ($r_p = -0.78$) and days to maturity ($r_p = -0.68$). The study generally, revealed the presence of adequate variability which can be exploited through direct selection or hybridization.

Key words: Genotype, phenotypic and genotypic coefficient of variation, heritability, genetic advance, correlation

INTRODUCTION

Tomato (*Solanum lycopersicon* L.) is the third most important vegetable crops in the world next to potato and sweet potato (FAO, 2005). In 2009 the world's total cultivated area under tomato was 4.98 million ha, with a production quantity of 141.14 million tons (FAOSTAT, 2011). Similarly, Ethiopia has favourable agroecology for production of the crop. In 2008, Ethiopia's total cultivated area under tomato was 5,342 ha with a production of 41,815 tons (FAOSTAT, 2011).

The national average yield of tomato is below the world average. Average yield for Ethiopia is 7.83 ton ha⁻¹ CSA (2009), which is very low, as compared to the world average yield of 28.39 ton ha⁻¹ (FAOSTAT, 2011). The major production constraints associated with yield reduction of tomato in Ethiopia are shortage of varieties and recommended package of information, unknown sources and poor quality seeds, disease and insect pests and high postharvest losses (Lemma, 2002). This shows that developing high yielding genotypes with desirable fruit characteristics should be primary task of plant breeders.

Estimating the variability present in a population is crucial for genetic improvement of a crop. Moreover, studying interrelation among characters helps in selecting important yield contributing traits.

A number of studies viz., Haydar *et al.* (2007), Hidayatullah *et al.* (2008), Mehta and Asati (2008) and Ghosh *et al.* (2010) reported a wide range of variation for yield and fruit yield related traits in tomato. However, little information is available with respect to the nature and magnitude of variability and interrelation among characters for fruit yield and yield related traits on tomato genotypes maintained under Ethiopian conditions. Thus, the present study was conducted to estimate the extent of phenotypic and genotypic variability, heritability, genetic advance expected under selection and to estimate the extent of genotypic and phenotypic correlation between pairs of characters.

MATERIALS AND METHODS

Experimental site: The experiment was conducted at Humera Agricultural Research Center experimental site, Northern Ethiopia from July 2010 to February 2011 cropping season under irrigation condition. Humera is located 960 km North of Addis Ababa, at an altitude of 604 meter a.s.l and at 14° 06' N latitudes and 38°31'E longitudes. The dominant soil type is chromic vertisol black in color characterized with very deep (>150 cm) clay textured. Agro-ecologically it is described as hot to warm semiarid plain sub agro-ecology (SA1-1). The maximum temperature varies from 42°C in April to 33°C in May while minimum temperature varies from 22.2°C in July to 17.5°C in August. Average rainfall varies from 400-650 mm per year, which last from June to September (EARO, 2002).

Experimental material: The experimental materials comprise 36 tomato genotypes introduced from Asian Vegetable Research and Development Center (AVRDC), Israel, Italy, United States of America (USA) and France (Table 1). Seedlings of each genotype were raised in nursery in August and transplanted to the main field in September.

Experimental design and management: The trial was laid out in 6×6 simple lattice design in two replications. Seedlings of each genotype were raised in a seed bed in August 2010 and transplanted to the main field in September 2010. Each genotype was planted in the main field in a plot size of 20.4 m² (4 rows, 5.1 m row length, 100 cm meter between rows and 30 cm between plants spacing). The 200 kg ha⁻¹ DAP and 100 kg ha⁻¹ Urea were applied at time of planting and two weeks after transplanting as recommended for the crop (Lemma, 2002). All agronomic practices were applied as per recommendation for the crop. The middle two rows were used for data collection leaving the two rows as borders.

Data collected: Ten plants and ten fruits were randomly sampled from the central two rows of each plot to measure growth parameters, fruit yield components and fruit characteristics data viz., Plant height (cm), primary and secondary branches, Number of flowers per plant, Average number of fruit clusters per plant, Average number of fruits per cluster, Average number of fruits per plant, Fruit set percentage (%), weight of fruit per plant (kg plant⁻¹), single fruit weight (g), fruit polar diameter (mm), equatorial diameter (mm), Fruit shape index, number of locules per fruit, Pericarp thickness (mm), Number of seeds per fruit, Total soluble solids (TSS) (°Brix). Measurements such as days to 50% flowering, days to 50% fruiting, days to maturity, number of Pickings and average total yield per hectare (ton ha⁻¹) were taken on plot basis.

Table 1: List of experimental materials

Pedigree	Year of introduction/release	Source	Growth habit	Type
CLN-2498 A	2004	AVRDC	Determinate	Fresh market
CLN-2037 E	2004	AVRDC	Indeterminate	Fresh market
CLN-2037 H	2004	AVRDC	Indeterminate	Fresh market
CLN-5915-206-D4-2-2-0	2004	AVRDC	Indeterminate	Fresh market
CLN-2037 C	2004	AVRDC	Indeterminate	Fresh market
CLN-2037 I	2004	AVRDC	Indeterminate	Fresh Market
CLN-1314 G	2004	AVRDC	Determinate	High beta carotene
CLN-2070 A	2004	AVRDC	Indeterminate	High beta carotene
CLN-2366 A	2004	AVRDC	Indeterminate	High beta carotene
CLN-2366 B	2004	AVRDC	Indeterminate	High beta carotene
CLN-2366 C	2004	AVRDC	Indeterminate	High beta carotene
CLN-2037 A	2002	AVRDC	Indeterminate	High beta carotene
CLN-1621 F	1998	AVRDC	Determinate	Cherry tomato
CLN-5915-93-D4	1998	AVRDC	Determinate	Fresh market
CLN-5915-206-D4-2-5-0	NA	AVRDC	Indeterminate	Fresh market
ARP-Tomato No.367-2	NA	AVRDC	Determinate	Fresh market
Beaf steak	NA	NA	Determinate	Fresh market
Tomato 1365/95	NA	Hazera seed company	Determinate	Fresh market
Tomato 1358/95	NA	Hazera seed company	Indeterminate	Fresh market
Supper Roma VF	NA	NA	Determinate	Processing
PT-4719 B	NA	AVRDC	Determinate	Processing
Cathrine	NA	Hazera seed company	Indeterminate	Fresh market
Melkashola	1998	Italy	Semi-determinate	Processing
Melkasalsa	1998	Italy	Determinate	Processing
Chali	2007	Italy	Determinate	Processing
Miya	2007	Italy	Semi-determinate	Fresh market
Roma VF	1992	France	Determinate	Processing
Marglobe	1994	USA	determinate	Fresh market
Eshet	2005	Italy	Determinate	Fresh market
Bishola	2005	France	Determinate	Fresh market
Metadel	2005	Guadaloupe	Semi-determinate	Fresh market
Fetan	2005	Italy	Determinate	Fresh market
H-1350	NA	NA	Determinate	Fresh market
Electra	NA	Hazera Seed Company	Indeterminate	Fresh market
Fire ball	1992	Italy	Determinate	Processing
Cochoro	2007	NA	Determinate	NA

AVRDC: Asian vegetable research and development center, NA: Information not available, USA: United States of America

Data analysis: Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2 (SAS, 2008) after testing the ANOVA assumptions. The difference between treatment means was compared using LSD at 5 and 1% probability levels. GENRES Version 7.01 (GENRES, 1994) computer software was employed for estimation of Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability in broad sense (h^2b), genetic advance as percentage of mean (GAM), genotypic and phenotypic correlation between traits.

The phenotypic and genotypic variances and coefficient of variations were estimated as per Singh and Chaudhury (1985).

Heritability in the broad sense for all the 22 quantitative characters was computed using the formula suggested by Singh and Chaudhury (1985). The genetic advance expected under selection, assuming selection intensity of the superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al.* (1955) and Allard (1960).

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

RESULTS AND DISCUSSION

Mean square values of Analysis of Variance (ANOVA) of 22 quantitative characters for the 36 tomato genotypes showed highly significant difference ($p < 0.01$) among the tested genotypes for all the characters studied (Table 2). Number of flowers per plant (1980.03**), days to maturity (1402.28**), number of seeds per fruit (1032.03**), number of matured fruits per plant (903.04**) and total fruit yield per hectare (258.55**) were some of the traits which showed highly significant variation. The significant variation among the genotypes revealed that presence of adequate variability which can be exploited through selection. This is in agreement with the findings of Mohanty (2003) who reported significant differences for all characters studied (plant height, number of branches per plant, days to first harvest, fruits per plant, average fruit weight and yield per hectare). Similarly, Pradeepkumar *et al.* (2001) and Golani *et al.* (2007) obtained highly significant difference for all characters studied among the test tomato genotypes.

Table 2: Analysis of variance for the 22 characters, using simple lattice design

Source of variation	Mean square			Efficiency relative to RCBD
	Treatments unadjusted	Treatments adjusted	Intra block error	
Degree of freedom	35	35	25	
Days to 50% flowering	79.95	74.63**	7.120	100.18
Days to 50% fruiting	702.73	647.23**	14.190	134.30
Days to maturity	1465.06	1402.28**	24.840	115.55
Plant height	961.75	823.84**	44.600	102.86
No. of primary branches	3.29	3.19**	1.080	101.80
No. of secondary branches	2.63	2.42**	0.110	80.56
No. of flowers per plant	2343.49	1980.03**	134.700	100.22
No. of fruit clusters per plant	44.30	43.59**	2.320	92.42
No. of fruits per fruit cluster	0.86	0.78**	0.083	85.57
No. of matured fruits per plant	957.71	903.04**	8.570	85.11
Fruit set percentage (%)	835.02	787.75**	14.800	100.97
Weight of fruits per plant (kg)	0.46	0.42**	0.030	85.55
Single fruit weight per plant (g)	1248.07	1112.25**	56.300	99.87
No. of pickings	2.02	1.97**	0.200	89.43
Fruit polar diameter (mm)	135.61	132.33**	5.360	101.84
Fruit equatorial diameter (mm)	89.69	86.23**	7.550	100.65
Shape index	0.14	0.14**	0.010	93.92
No. of seeds per fruit	1221.45	1032.03**	12.610	106.07
No. of locules per fruit	2.04	1.69**	0.060	88.68
Pericarp thickness (mm)	3.00	2.63**	0.250	111.00
Total soluble solids (° Brix)	0.85	0.74**	0.010	91.05
Total yield (tons ha ⁻¹)	281.38	258.55**	6.390	104.99

**Significance at 1% probability level. RCBD: Randomized complete block design

Table 3: Estimate of variability parameters for 22 characters of tomato genotypes studied

Characters	Range	Mean±SE	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	H ² (%)	GA	GAM
Days to 50% flowering	28-55	38.81±0.22	36.33	7.28	43.62	15.53	17.02	83.33	11.33	29.20
Days to 50% fruiting	31-110	75.29±0.36	339.99	22.75	362.74	24.49	25.30	93.73	36.77	48.84
Days to maturity	69-156	104.03±0.44	715.97	33.11	749.08	25.72	26.31	95.58	53.89	51.80
Plant height	59-129	91.07±0.57	456.10	49.54	505.64	23.45	24.69	90.20	41.78	45.88
No. of primary branches	1.8-9.2	6.40±0.08	1.06	1.17	2.23	16.07	23.35	47.36	1.46	22.79
No. of secondary branches	1.3-7.6	3.70±0.023	1.26	0.09	1.35	30.44	31.52	93.25	2.24	60.55
No. of flowers per plant	38-185	102.8±0.87	1102.6	1240.9	138.26	32.29	34.26	88.86	64.51	62.71
No. of fruit clusters per plant	1-22	7.80±0.112	21.07	2.15	23.22	58.87	61.80	90.75	9.01	115.53
No. of fruits per fruit cluster	0.7-4.4	1.71±0.021	0.395	0.071	0.466	36.68	39.83	84.80	1.19	69.59
No. of matured fruits per plant	4-97	27.86±0.218	475.04	8.03	483.07	78.47	79.13	98.34	44.66	160.30
Fruit set percentage (%)	3.58-80.40	27.63±0.303	409.67	425.35	15.68	73.27	74.66	96.31	40.93	148.12
Weight of fruits per plant (kg)	0.13-2.10	0.887±0.012	0.215	0.023	0.238	52.33	55.06	90.33	0.91	102.45
Single fruit weight per plant (g)	18-147	54.90±0.587	595.92	56.22	652.14	44.47	46.52	91.38	48.08	87.57
No. of pickings	2-6	4.15±0.034	0.919	0.185	1.104	23.08	25.31	83.22	1.80	43.38
Fruit polar diameter (mm)	34.0-65.3	45.61±0.180	64.90	5.82	70.72	17.66	18.44	91.77	15.90	34.86
Fruit equatorial diameter (mm)	27.5-64.4	40.77±0.196	40.10	8.15	48.25	15.55	17.06	83.10	11.90	29.20
Shape index	0.72-1.91	1.14±0.0065	0.069	0.007	0.076	22.92	24.09	90.56	0.51	44.94
No. of seeds per fruit	18-118	47.82±0.274	603.30	14.85	618.15	51.36	51.99	97.60	49.99	104.53
No. of locules per fruit	2-5	3.36±0.0175	0.990	0.056	1.047	29.69	30.52	94.62	2.00	59.49
Perricarp thickness (mm)	2.55-7.48	4.70±0.043	1.341	0.317	1.658	24.65	27.41	80.88	2.15	45.66
Total soluble solids (° Brix)	3.58-6.71	5.18±0.0093	0.420	0.013	0.433	12.52	12.71	97.07	1.32	25.41
Total yield (ton ha ⁻¹)	3.33-52.67	17.88±1.93	137.00	7.39	144.39	65.48	67.22	94.88	23.49	131.39

Mean±SE: Standard error of the mean, σ^2_g : Genotypic variance, σ^2_p : Phenotypic variance, σ^2_e : Environmental variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H²: Broad sense heritability, GA: Genetic advance and GAM: Genetic advance under selection

Efficiency of simple lattice design over randomized complete block design showed that more than half of the traits were efficient. Days to 50% fruiting (134%), days to maturity (115%) and pericarp thickness (111%) (Table 2) are among the traits which indicated high efficiency i.e., the experimental plots within replications were heterogeneous hence, making incomplete block within replication reduces the experimental error.

All the 36 genotypes studied showed wide range of variability for most of the characters studied (Table 3) indicating presence of adequate variability which can be exploited through selection. Wide range of variation was observed for days to maturity (69-156 days), number of matured fruits per plant (4-97) and total fruit yield per hectare (3.33-52.67 ton ha⁻¹). Based on mean value, the average mean value was more than twice of the minimum mean value for traits days to 50% fruiting, number of primary and secondary branches, number of flowers per plant, number of fruit clusters per plant, number of fruits per cluster, number of matured fruits per plant, fruit set percentage, weight of fruits per plant, single fruit weight, number of harvests, number of seeds per fruit and total fruit yield per hectare indicating their maximum contribution to the total variability observed among the tomato genotypes. This showed the possibility to improve the various desirable traits through direct selection as short term strategy and through hybridization as long term strategy. The wide range of variation obtained may be due divergent genotypes included in the study. In line with the present finding. Pradeepkumar *et al.* (2001) reported wide range of variation for plant height, number of fruits per plant, number of pickings single fruit weight and fruit yield per plant in tomato.

Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) Variances and Phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 3. According to Deshmukh *et al.* (2005), phenotypic and genotypic coefficient of variation values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Considering this delineation number of matured fruits per plant had the highest GCV and PCV (78.47 and 79.13) followed by fruit set percentage (73.27 and 74.66), total yield per hectare (65.48 and 67.22), number of fruit clusters per plant (58.87 and 61.80), average weight of fruits per plant (52.33 and 55.06), number of seeds per fruit (51.36 and 51.99), average single fruit weight per plant (44.47 and 46.52) and number of flowers per plant (32.29 and 34.26). Medium GCV and high PCV were observed for number of primary branches per plant (16.07 and 23.35), indicated influence of the environment in the expression of the trait. However, genotypic and phenotypic coefficients of variability were medium for fruit polar diameter (17.66 and 18.44), fruit equatorial diameter (15.55 and 17.06), days to 50 percent flowering (15.53 and 17.02) and total soluble solids (12.52 and 12.71). Phenotypic coefficient variation was generally higher than GCV values in all characters.

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

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

In this study estimate of heritability in broad sense ranged from 47.36% for number of primary branches to 98.34% for number of matured fruits per plant (Table 3). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. But, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of the environment. Considering this benchmark, heritability estimate was very high (>80%) for number of matured fruits per plant (98.34%), number of seeds per fruit (97.60%), total soluble solids (TSS) (97.07%), fruit set percentage (96.31%), days to maturity (95.58%), total fruit yield (ton ha⁻¹) (94.88%), days to 50% fruiting (93.73%), number of locules per fruit (94.62%), number of secondary branches (93.25%), plant height (90.20%) and number of flowers per plant (88.86%). It was moderate (40-80%) for number of primary branches per plant (47.36%).

Most of the characters had higher heritability estimates, indicating lesser influence of environment. The high heritability estimates obtained may be due to the divergent genotypes

included in the study. This is in harmony with the finding of Hidayatullah *et al.* (2008) who reported high heritability for plant height, number of fruits per plant, fruit weight per plant, fruit length, fruit diameter, single fruit weight, number of locules, pericarp thickness, TSS and seeds per fruit. Similarly Pradeepkumar *et al.* (2001) reported high heritability estimates for all characters studied, Mehta and Asati (2008) also found high heritability in broad sense for plant height, number of fruit clusters, weight of fruits per plant, total fruit yield per hectare, number of locules and TSS. Similarly, Golani *et al.* (2007) obtained high heritability for 10 fruits weight per plant, fruit length, number of locules per fruit and fruit yield per hectare.

Generally, genetic advance as percent of mean (GAM) at 5% selection intensity was high (>20%) for all characters studied. The highest GAM was recorded for number of matured fruits per plant (160.30%) followed by fruit set percentage (148.12%), total yield per hectare (131.39), number of fruit clusters per plant (115.53), number of seeds per fruit (104.53) and average weight of fruits per plant (102.45) showed these characters are governed by additive genes and selection will be rewarding improvement of such traits. The least GAM was recorded for number of primary branches per plant (22.79), TSS (25.41) and days to 50% flowering (29.20). This is in confirmation with the finding of Pradeepkumar *et al.* (2001) who reported high genetic advance as per cent of mean for plant height, number of fruits per plant, fruit weight, fruit yield per plant, locule number, pericarp thickness, Plant height and number of harvest. Similarly, Shashikanth *et al.* (2010) found high genetic advance as percent of mean for number of fruits per plant and fruit yield per plant. Golani *et al.* (2007) also obtained high genetic advance as percent of mean for characters average 10 fruit weight and fruit yield per hectare. In addition to the above report, Ghosh *et al.* (2010) also found high genetic advance for number of fruits per plant, fruit yield per plant and number of fruits per fruit cluster.

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

Total fruit yield per hectare showed positive and highly significant phenotypic association with average weight of fruits per plant ($r = 0.89$), number of matured fruits per plant ($r = 0.85$), fruit set percentage ($r = 0.78$), number of fruit clusters per plant ($r = 0.73$), number of pickings ($r = 0.73$) and number of fruits per fruit cluster (0.70) (Table 4). Therefore, any improvement of these characters would result in a substantial increment on fruit yield. This is in agreement with Ghosh *et al.* (2010) who reported that number of fruits per cluster, fruit clusters per plant and fruits per plant had positive and highly significant association with fruit yield. Similarly, Hidayatullah *et al.* (2008) reported positive association of fruit yield per plant with number of fruits per plant and number of pickings.

Fruit yield showed highly negative significant association with days to 50% fruiting ($r = -0.782$), days to maturity ($r = -0.68$) and days to 50% flowering ($r = -0.54$) at both phenotypic and genotypic level. This is because early genotypes gave higher fruit yield per hectare than the late genotypes in the specific environment among the specific test genotypes. There was also high flower abortion rate for the late genotypes.

Table 4: Genotypic (above diagonal) and phenotypic correlation coefficients (below diagonal) of the studied tomato genotypes

	50FL	50FR	DM	PHT	PBR	SBR	NFLO	NFCL	FRPFC	NFRPP	FSPER	WFPP	SFWt	FPD	FED	SHIN	NPICK	TSS	TYLD
50FL		0.8**	0.73**	0.29	-0.08	-0.09	-0.33	-0.68**	-0.58**	-0.61**	-0.52**	-0.55**	0.17	-0.25	-0.13	-0.11	-0.67**	-0.29	-0.58**
50FR	0.7**		0.91**	0.18	0.14	0.06	-0.28	-0.88**	-0.72**	-0.80**	-0.73**	-0.76**	0.23	-0.07	-0.12	0.02	-0.94**	-0.20	-0.81**
DM	0.69**	0.88**		0.02	0.11	0.09	-0.43**	-0.79**	-0.58**	-0.66**	-0.60**	-0.69**	0.16	-0.15	-0.15	-0.02	-0.92**	-0.15	-0.71**
PHT	0.25	0.16	0.03		0.26	-0.09	0.30	-0.20	-0.12	-0.06	-0.10	-0.01	-0.06	-0.13	0.01	-0.12	-0.01	0.17	-0.11
PBR	-0.01	0.13	0.12	0.21		0.8**	0.58**	-0.18	-0.15	-0.12	-0.31	0.003	0.33	0.41*	0.31	0.07	-0.05	-0.10	-0.09
SBR	-0.06	0.07	0.09	-0.06	0.64**		0.32	0.01	0.11	0.07	-0.07	0.03	0.42*	0.08	0.27	-0.14	-0.15	-0.02	0.04
FLO	-0.26	-0.24	-0.39*	0.30	0.46**	0.32		0.15	0.14	0.23	-0.04	0.16	-0.11	0.38*	-0.07	0.35*	0.45**	0.12	0.22
NFC	-0.58**	-0.82**	-0.73**	-0.18	-0.12	0.03	0.17		0.77**	0.78**	0.73**	0.71**	-0.17	0.01	0.18	-0.05	0.80**	0.18	0.79**
FRPC	-0.46**	-0.64**	-0.52**	-0.13	0.02	0.11	0.13	0.71**		0.81**	0.71**	0.69**	-0.15	-0.08	0.03	-0.09	0.64**	0.14	0.70**
NFRP	-0.56**	-0.77**	-0.65**	-0.05	-0.09	0.07	0.22	0.75**	0.76**		0.93**	0.81**	-0.36*	-0.21	-0.07	-0.14	0.74**	0.26	0.87**
FSP	-0.47**	-0.70**	-0.59**	-0.10	-0.25	-0.08	-0.08	0.66**	0.65**	0.92**		0.80**	-0.28	-0.25	-0.003	-0.22	0.66**	0.16	0.81**
WFP	-0.49**	-0.72**	-0.65**	0.01	-0.01	0.03	0.16	0.67**	0.65**	0.79**	0.76**		0.02	-0.02	0.35*	-0.25	0.77**	0.13	0.91**
SFWt	0.15	0.24	0.16	-0.07	0.2	0.40*	-0.09	-0.16	-0.12	-0.33	-0.26	0.03		0.14	0.76**	-0.33*	-0.22	-0.18	-0.13
FPD	-0.21	-0.07	-0.13	-0.12	0.23	0.06	0.35*	0.01	-0.09	-0.19	-0.23	-0.02	0.15		0.07	0.78**	0.19	-0.40*	-0.003
FED	-0.10	-0.1	-0.11	0.05	0.24	0.26	-0.01	0.16	-0.01	-0.07	-0.02	0.3	0.72**	0.1		-0.55**	0.21	-0.15	0.16
SHI	-0.10	0.003	-0.02	-0.14	0.004	-0.16	0.29	-0.06	-0.06	-0.13	-0.19	-0.22	-0.32	0.75**	-0.56**		0.02	-0.21	-0.10
NPIC	-0.62**	-0.83**	-0.86**	-0.04	-0.15	-0.15	0.36*	0.72**	0.55**	0.68**	0.61**	0.70**	-0.12	0.17	0.13	0.04		0.11	0.80**
TSS	-0.26	-0.19	-0.15	0.17	-0.03	-0.01	0.12	0.17	0.14	0.26	0.15	0.12	-0.18	-0.38*	-0.12	-0.21	0.1		0.21
TYL	-0.54**	-0.78**	-0.68**	-0.10	-0.07	0.05	0.21	0.74**	0.64**	0.85**	0.78**	0.89**	-0.11	0.01	0.17	-0.101	0.73**	0.19	

*And** indicate significance at 0.05 and 0.01 probability levels, respectively, 50FL: Days to 50 percent flowering, 50FR: Days to 50 percent fruiting, DM: Days to maturity, PHT: Plant height, NPBR: No. of primary branches, NSBR: No. of secondary branches, NFLO: No. of flowers per plant, NFCL: No. of fruit clusters per plant, FRPFC: No. of fruits per fruit cluster, NFRPP: No. of matured fruits per plant, FSPER: Fruit set percentage, WFPP: Average weight of fruits per plant, SFWt: Average single fruit weight per plant, FPD: Fruit polar diameter, FED: Fruit equatorial diameter, SHIN: Shape index, NPICK: No. of fruit pickings, TSS: Total soluble solids, TYLD: Total yield per hectare

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

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

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

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

Average weight of fruits per plant had positive association with fruit equatorial diameter and duration of picking. Average single fruit weight exhibited positive and significant relationship with fruit equatorial diameter and shape index. Similarly, Haydar *et al.* (2007) reported that fruit length was positively correlated with fruit diameter and single fruit weight. Total soluble solids exhibited a significant negative correlation with fruit polar diameter.

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

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