

Table 4. 24 Estimate of variance, heritability and genetic advance for 16 fruit physical and quality characters of tomato over combined locations

Character	GM	Variance component							Heritability & genetic advance as % of mean			
		σ^2_L	σ^2_G	σ^2_P	σ^2_{GL}	σ^2_E	GCV	PCV	ECV	H^2_b (%)	EGA	GAM
Single fruit weight	63.37	56.57	456.76	507.31	98.62	7.46	33.73	35.54	4.31	90	41.78	65.92
Fruit weight per plant	633.50	92.40	104328.17	118171.67	21057.33	19889.0	50.99	54.26	22.26	88	625.19	98.69
Fruit yield per plant	53.80	00	871.66	951.32	156.98	7.05	54.88	57.33	4.94	92	58.22	108.21
No. of locules per fruit	4.00	0.02	2.65	2.75	0.06	0.44	40.70	41.48	16.58	96	3.29	82.25
Fruit length	4.76	0.01	0.39	0.51	0.22	0.06	13.04	14.95	5.15	76	1.11	23.41
Fruit diameter	4.98	0.003	0.96	1.09	0.23	0.08	19.66	20.95	5.68	88	1.89	38.00
Fruit shape index	0.99	0.002	0.03	0.04	0.02	0.004	15.97	19.34	6.39	68	0.27	27.17
Pericarp thickness	4.48	0.04	0.14	0.44	0.52	0.24	8.20	14.72	10.94	31	0.42	9.41
Fruit firmness	3.54	0.27	0.06	0.17	0.17	0.11	7.11	11.47	9.37	38	0.32	9.07
pH	4.33	00	0.16	0.32	0.33	0.02	9.09	13.13	3.27	48	0.56	12.97
Total soluble solids	4.22	0.05	0.41	0.89	0.95	0.03	15.11	22.29	4.10	46	0.89	21.10
Titration acidity	0.36	0.003	0.001	0.004	0.005	0.0003	8.78	17.57	4.81	25	0.03	9.05
TSS/TA	12.02	8.37	1.46	3.37	3.73	0.22	10.06	15.26	3.90	43	1.64	13.67
Malic acid	0.38	0.003	0.001	0.006	0.01	0.0005	8.32	20.38	5.88	17	0.03	7.00
Fruit dry matter	0.40	0.003	0.002	0.01	0.01	0.001	11.18	18.26	7.91	38	0.06	14.10

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV = Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

Table 4. 25 Estimate of variance, heritability and genetic advance for antioxidant characters of tomato over combined locations

Character	GM	Variance component							Heritability and genetic advance as % of mean			
		σ^2_L	σ^2_G	σ^2_P	σ^2_{GL}	σ^2_E	GCV	PCV	ECV	H^2_b (%)	EGA	GAM
β -Carotene (mg/100 ml)	21.62	3.07	00	29.33	57.15	4.51	-	25.05	9.82	00	00	00
Lycopene (mg/100 ml)	15.19	00	2.74	19.70	33.79	0.36	11.04	29.59	4.00	14	1.27	8.49
Ascorbic acid (mg/100 ml)	10.57	2.37	00	3.26	5.21	3.93	-	17.08	18.76	00	00	00
Gallic acid (mg/100 ml)	1.66	0.01	00	0.04	0.06	0.04	-	11.79	12.05	00	00	00
Vanillic acid (mg/100 ml)	1.03	0.03	0.01	0.06	0.08	0.10	7.93	24.43	30.70	11	0.05	5.30
Rosmarinic acid (mg/100 ml)	0.93	0.02	0.01	0.04	0.04	0.07	7.60	21.05	28.45	13	0.05	5.66
Rutin (mg/100 ml)	90.34	00	00	2438.54	4872.10	14.95	-	54.66	4.28	00	00	00
Quercetin (mg/100 ml)	59.25	00	00	1099.00	2195.50	7.48	-	55.95	4.62	00	00	00
Catechin (mg/100 ml)	100.32	00	00	1986.18	3968.82	10.64	-	44.42	3.25	00	00	00
Hesperitin (mg/100 ml)	109.39	00	00	6685.07	13333.13	111.0	-	74.74	9.63	00	00	00
Kaempferol (mg/100 ml)	27.33	00	00	407.24	803.11	34.12	-	73.84	21.37	00	00	00
Myricetin (mg/100 ml)	39.03	8.50	00	414.77	828.65	2.65	-	52.18	4.17	00	00	00
Genestein (mg/100 ml)	58.82	0.06	00	553.80	1105.66	5.83	-	40.01	4.10	00	00	00
Antioxidant activity (mg/100 ml)	3.80	0.18	00	2.06	4.10	0.05	-	37.75	5.88	00	00	00

GM = Grand mean, σ^2_L = Variance due to location, σ^2_G = Genotypic variance, σ^2_P = Phenotypic variance, σ^2_{GL} = Genotype x location variance, σ^2_E = Environmental variance, GCV = Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, ECV = Environmental coefficient of variability, h^2_b = Broad sense heritability, EGA = Expected genetic advance and GAM = Genetic advance as percentage of mean.

4.5 Character association among tomato genotypes

4.5.1 Correlation of tomato traits studied under greenhouse conditions

The Pearson's correlation coefficients among selected agronomic and fruit quality traits studied under greenhouse conditions revealed an association between trait pairs (Table 4.26). A significant and positive association was observed between number of trusses per plant (TPP) and number of primary branches per plant (NPB) ($r = 0.588^{**}$). Number of fruits per plant (FPP) correlated with number of primary branches per plant (NPB) ($r = 0.517^*$) and number of trusses per plant (TPP) ($r = 0.643^{**}$). Number of fruits per plant (FPP) associated with number of primary branches per plant (NPB) ($r = 0.517^*$) and number of trusses per plant (TPP) ($r = 0.643^{**}$). Ascorbic acid content of fruit (ASC) correlated with number of primary branches per plant (NPB) ($r = 0.474^*$), number of truss per plant (TPP) ($r = 0.535^{**}$) and number of fruits per plant (FPP) (0.518^*) while total fruit weight per plant (FWP) correlated with number of trusses per plant (TPP) ($r = 0.559^{**}$) and number of fruits per plant (FPP) (0.687^{**}).

Tomato fruit yield (YPP) correlated positively and significantly with number of trusses per plant (TPP) ($r = 0.562^{**}$) fruit weight per plant (FWP) ($r = 1.00^{**}$) and number of fruits per plant (FPP) ($r = 0.686^{**}$). A positive correlation was observed between each of the following trait pair: number of days to fruit maturity (DFM) and number of days to 50 % fruit set (FPFS) ($r = 0.804^{**}$), fruit length (FL) and number of days to fifty percent fruit set (FPFS) ($r = 0.459^*$) as well as titrable acidity (TA) with total soluble solids content (TSS) (0.744^{**}). Gallic acid (GA) also showed a positive and significant association with plant height (PHT) ($r = 0.457^*$) and number of days to fruit maturity (DFM) (0.554^{**}).

On the other hand, a significant negative association was observed between certain trait pairs (Table 4.26). Fruit yield per plant (YPP) showed a negative significant association with

number of days to 50 % fruit set (FPFS) ($r = -0.573^{**}$), number of days to fruit maturity (DFM) (-0.627^{**}) and gallic acid content (GA) (-469^{**}). A significant negative correlation was observed for fruit length (FL) and number of primary branches per plant (NPB) ($r = -0.561^{**}$) and number of fruits per plant (FPP) ($r = -0.460^*$), ascorbic acid content (ASC) ($r = -0.557^{**}$) and quercetin content in fruit (QUE) ($r = -0.447^*$). The association of number of fruits per plant (FPP) with number of days to 50 % flowering (FPF) ($r = -0.454^*$), number of days to 50 % fruit set (FPFS) ($r = -0.624^{**}$) and gallic acid (GA) (-460^*) were found to be significantly negative.

Fruit weight per plant (FWP) correlated negatively with number of days to 50 % fruit set (FPFS) ($r = -0.572^{**}$), number of days to fruit maturity (DFM) ($r = -0.627^{**}$) and gallic acid content (GA) ($r = -0.462^*$). Moreover, a negative and significant association was recorded for trait pairs including number of trusses per plant (TPP) and number of days to 50 % fruit set (FPFS) ($r = -0.534^{**}$). Quercetin content in fruit (QUE) correlated negatively and significantly with fruit diameter (FD) ($r = -0.481^*$).

4.5.2 Correlation of tomato traits studied under field conditions

The results of the correlation among selected agronomic and fruit quality traits of field-produced tomato genotypes were significant for a number of traits (Table 4.27). A significant positive association was observed between trait pairs number of trusses per plant (TPP) and number of primary branches per plant (NPB) ($r = 0.605^{**}$), number of fruits per plant (FPP) and number of days to fruit maturity (DFM) ($r = 0.740^{**}$). Fruit length (FL) correlated with number of days to 50 % flowering (FPF) ($r = 0.630^{**}$) while fruit diameter (FD) associated with single fruit weight per plant (SFW) ($r = 0.744^{**}$), titrable acidity (TA) ($r = 0.744^{**}$) and total soluble solids content (TSS) ($r = 0.751^{**}$). Antioxidant activity (AA) correlated with number of days to fruit maturity (DFM) ($r = 0.674^{**}$).

Table 4. 26 The Pearson’s correlation matrix of selected agronomic and quality traits of tomato under greenhouse conditions

Variables	PHT	NPB	FPF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE
PHT	-																		
NPB	0.185	-																	
NFF	0.116	-0.250	-																
FPFS	0.207	-0.384	0.436	-															
DFM	0.192	-0.251	0.311	0.804**	-														
TPP	0.089	0.588**	-0.380	-0.534**	-0.386	-													
FPP	-0.019	0.517*	-0.454*	-0.624**	-0.607**	0.643**	-												
FWP	0.049	0.230	-0.323	-0.572**	-0.627**	0.559**	0.687**	-											
YPP	0.050	0.231	-0.324	-0.573**	-0.627**	0.562**	0.686**	1.000**	-										
SFW	-0.051	-0.066	0.218	0.061	0.020	-0.077	-0.360	0.309	0.308	-									
FL	-0.031	-0.561**	0.001	0.459*	0.307	-0.368	-0.460*	-0.193	-0.194	0.170	-								
FD	-0.099	-0.069	-0.015	0.072	-0.023	-0.107	-0.344	0.169	0.174	0.727**	0.426	-							
FF	0.056	-0.228	0.144	0.140	0.335	-0.064	-0.088	-0.154	-0.160	-0.011	0.229	-0.158	-						
TSS	-0.076	-0.005	-0.203	-0.015	0.225	0.101	-0.315	-0.421	-0.419	-0.134	-0.081	-0.068	-0.223	-					
TA	-0.269	-0.131	0.136	0.136	0.204	-0.149	-0.384	-0.312	-0.316	0.138	-0.063	-0.033	-0.193	0.744**	-				
LYC	0.105	-0.022	0.301	0.182	0.418	-0.190	-0.193	-0.345	-0.344	-0.297	-0.163	-0.305	0.270	0.091	0.175	-			
ASC	0.050	0.474*	0.141	-0.277	-0.258	0.535**	0.518*	0.380	0.382	-0.056	-0.557**	-0.265	-0.163	-0.192	-0.242	-0.110	-		
GA	0.457*	-0.211	0.394	0.460*	0.554**	-0.291	-0.518*	-0.462*	-0.460*	-0.091	0.065	-0.224	-0.132	0.290	0.214	0.343	-0.119	-	
QUE	-0.300	0.198	-0.062	-0.332	-0.260	0.399	0.219	-0.050	-0.050	-0.200	-0.447*	-0.481*	0.077	0.137	0.014	-0.242	0.304	-0.209	-
AA	0.079	0.025	0.139	0.252	-0.132	-0.043	0.009	0.205	0.204	0.151	0.159	-0.005	-0.130	-0.364	-0.017	-0.172	0.184	-0.102	-0.025

* = significant at $P < 0.05$ ($r > 0.413$), ** = significant at $P < 0.01$ ($r > 0.526$), PHT = Plant height, NPB = Number of primary branches per plant, FPF = Number of days to 50 % flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, = TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.

($r = 0.674$). Number of days to fruit maturity (DFM) correlated positively and significantly with number of days to 50 % flowering (FPF) ($r = 0.555^{**}$) and number of days to 50 % fruit set (FPFS) ($r = 0.617^{**}$). A significantly positive association of fruit weight per plant with number of trusses per plant (TPP) ($r = 0.629^{**}$) and number of fruits per plant (FPP) ($r = 0.566^{**}$) was recorded.

Tomato fruit yield per plant (YPP) showed a high significant positive association with number of trusses per plant (TPP) ($r = 0.628^{**}$), total fruit weight plant (FWP) ($r = 1.00^{**}$) and number of fruits per plant (FPP) ($r = 0.566^{**}$). The correlations between fruit firmness (FF) with number of days to 50 % flowering (FPF) ($r = 0.573^{**}$) and fruit length (FL) (0.641^{**}) were positive and significantly high. There was also significant positive association between lycopene content of fruits (LYC) and total soluble solids content of fruit (TSS) ($r = 0.731^{**}$). Gallic acid content (GA) associated significantly ($P < 0.5$) with fruit weight per plant (FWP) ($r = 0.502^*$) as well as yield per plant (YPP) ($r=0.502^*$). The flavonoid compound quercetin (QUE) correlated positively and significantly with single fruit weight per plant (SFW) ($r = 0.476^*$), total soluble solids content (TSS) (0.596^{**}) and titrable acidity (TA) ($r = 0.736^{**}$).

A significantly negative correlation was observed for some agronomic and fruit quality traits. The number of trusses per plant (TPP) showed a significant negative correlation with number of days to 50 % flowering (FPF) ($r = -0.555^{**}$) and number of days to fruit maturity (DFM) ($r = -0.490^*$). A significant negative association was observed to exist in some trait pairs including fruit weight per plant (FWP) and number of days to 50 % fruit set (FPFS) ($r = -0.469^*$), fruit yield per plant (YPP) and number of days to 50 percent fruit set (FPFS) ($r = -0.469^*$). Fruit length (FL) correlated with number of trusses per plant (TPP) ($r = 0.495^*$), fruit diameter (FD) (and number of fruits per plant (FPP) ($r = -0.632^{**}$), total soluble solids (TSS) and number of days to 50 % fruit set (FPFS) ($r = -0.494^*$). Titrable acidity content of

tomato fruits (TA) correlated with number of days to 50 % fruit set (-0.669**). Quercetin content of fruit (QUE) showed a negative significant correlation with number of days to 50 percent flowering (NFPFS) (-596**).

4.5.3 Correlation among tomato traits over combined locations

The correlation among selected agronomic and fruit quality characters of tomato determined over the combined greenhouse and open field locations are presented in Table 4.29. Positive and significant association was observed between trait pairs number of days to 50 % fruit set (NFPFS) and number of days to 1st flower observed (NFF) ($r = 0.518^*$), number of trusses per plant (TPP) and number of primary branches per plant (NPB) ($r = 0.689^{**}$), fruit length (FL) and number of days to 50 % fruit set (FPFS) ($r = 0.553^{**}$), fruit diameter (FD) and single fruit weight per plant (SFW) ($r = 0.826^{**}$), acidity (TA) and total soluble solids content of fruit (TSS) ($r = 0.757^{**}$). Number of days to fruit maturity (DFM) correlated positively and significantly with number of days to 50 % flowering (FPF) ($r = 0.514^*$), number of days to 50 % fruit set (FPFS) ($r = 0.791^{**}$) and lycopene content (LYC) ($r = 0.702^{**}$).

Number of fruits per plant associated positively and significantly with number of primary branches per plant (NPB) ($r = 0.507^*$), number of truss per plant (TPP) ($r = 0.847^{**}$) well as ascorbic acid (ASC) ($r = 0.516^*$). There was significantly positive character association between fruit weight per plant (FWP) and number of truss per plant (TPP) ($r = 0.647^{**}$) as well as number of fruits per plant (FPP) ($r = 0.622^{**}$). The association of fruit yield per plant (YPP) with number of truss per plant (TPP) ($r = 0.648^{**}$), fruit weight per plant (FWP) ($r = 1.00^{**}$) and number of fruits per plant (FPP) ($r = 0.621^{**}$) was found to be highly significant. Quercetin (QUE) showed a significantly positive correlation with titrable acidity (TA) ($r = 0.536^*$) and ascorbic acid (ASC) ($r = 0.474^*$).

Table 4. 27 The Pearson’s correlation matrix of selected agronomic and fruit quality traits of tomato under field conditions

Variables	PHT	NPB	FPF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE	
PHT	-																			
NPB	0.032	-																		
NFF	0.166	-0.425	-																	
FPFS	-0.141	-0.271	0.431	-																
DFM	0.142	-0.103	0.519*	0.617**	-															
TPP	-0.154	0.605**	-0.555**	-0.382	-0.490*	-														
FPP	-0.266	0.320	-0.529**	-0.350	-0.334	0.740**	-													
FWP	-0.037	0.379	-0.244	-0.469*	-0.386	0.629**	0.566**	-												
YPP	-0.037	0.378	-0.244	-0.469*	-0.386	0.628**	0.566**	1.000**	-											
SFW	-0.028	0.076	0.250	-0.123	0.012	-0.226	-0.402	0.248	0.248	-										
FL	-0.090	-0.256	0.630**	0.439	0.382	-0.495*	-0.291	-0.152	-0.152	0.048	-									
FD	0.185	0.020	0.198	-0.102	0.081	-0.379	-0.632**	-0.027	-0.027	0.744**	0.097	-								
FF	0.002	0.055	0.573**	0.106	0.284	-0.208	-0.238	0.179	0.178	0.357	0.641*	0.423	-							
TSS	0.127	0.148	-0.286	-0.494*	-0.227	0.043	0.209	0.039	0.039	0.245	-0.142	0.233	-0.122	-						
TA	-0.071	0.292	-0.369	-0.669**	-0.379	0.147	0.194	0.145	0.145	0.296	-0.357	0.215	-0.108	0.751**	-					
LYC	0.287	-0.020	-0.020	-0.086	0.050	-0.053	0.150	-0.006	-0.006	0.098	0.139	0.159	-0.009	0.731**	0.117	-				
ASC	-0.429	-0.046	-0.046	0.207	0.345	0.030	0.406	-0.002	-0.002	-0.232	0.017	-0.360	-0.142	-0.220	-0.160	-0.151	-			
GA	-0.241	0.043	0.136	-0.010	0.049	0.015	0.135	0.502*	0.502*	0.329	0.008	0.031	0.212	-0.174	0.108	-0.260	0.265	-		
QUE	-0.107	0.178	-0.260	-0.531**	-0.180	-0.008	-0.008	0.086	0.085	0.476*	-0.293	0.299	-0.218	0.596**	0.736*	0.144	0.045	0.233	-	
AA	0.102	-0.160	0.419	0.364	0.674**	-0.219	-0.060	-0.255	-0.255	0.000	0.186	-0.040	0.147	-0.005	-0.395	0.408	0.201	-0.233	-0.301	

* = significant at $P < 0.05$ ($r > 0.413$), ** = significant at $P < 0.01$ ($r > 0.526$), PHT = Plant height, NPB = Number of primary branches per plant, FPF = Number of days to 50 % flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.

In addition, the antioxidant activity (AA) of tomato across the locations associated positively with number of days to 50 % fruit set (FPFS) ($r = 0.505$) and number of days to fruit maturity (DFM) ($r = 0.555$).

However, a significantly negative correlation was observed between certain traits determined over the combined locations (Table 4.28). Trait pair association was found negative and significant between number of days to 50 % flowering (FPF) and number of primary branches per plant (NPB) ($r = -0.630$), ascorbic acid content (ASC) and fruit length (FL) ($r = -4.87$). Quercetin content (QUE) associated negatively with fruit length (FL) (-0.476). Negative and significant correlation was observed for number of truss per plant (TPP) with number of days to 50 % flowering (FPF) ($r = -0.673$), number of days to 50 % fruit set (FPFS) ($r = -0.667$) and number of days to fruit maturity (DFM) ($r = -0.585$).

Similarly, number of fruits per plant (FPP) negatively associated with number of days to 50 % flowering (FPF) ($r = -0.609$), number of days to 50 % fruit set (FPFS) ($r = -0.580$) and number of days to fruit maturity (DFM) (-0.551). Both fruit weight per plant (FWP) and fruit yield per plant (YPP) showed separate negative significant correlation with number of days to 50 % fruit set (FPFS) ($r = -0.637$, $r = -0.636$) and number of days to fruit maturity (DFM) ($r = -0.576$, $r = -0.575$). A significantly negative association was also observed for fruit length (FL) with number of primary branches per plant (NPB) ($r = -0.634$), number of truss per plant (TPP) ($r = -0.596$) and number of fruits per plant (FPP) (-0.584).

Table 4. 28 The Pearson's correlation matrix of selected agronomic and quality traits of tomato over combined greenhouse and field locations

Variables	PHT	NPB	NFF	FPFS	DFM	TPP	FPP	FWP	YPP	SFW	FL	FD	FF	TSS	TA	LYC	ASC	GA	QUE
PHT	-																		
NPB	0.184	-																	
NFF	0.093	-0.630**	-																
FPFS	0.085	-0.437	0.518*	-															
DFM	0.156	-0.284	0.514*	0.791**	-														
TPP	-0.109	0.689**	-0.673**	-0.667**	-0.585**	-													
FPP	-0.090	0.507*	-0.609**	-0.580**	-0.551**	0.847**	-												
FWP	-0.004	0.326	-0.401	-0.637**	-0.576**	0.647**	0.622**	-											
YPP	-0.002	0.328	-0.400	-0.636**	-0.575**	0.648**	0.621**	1.000**	-										
SFW	-0.066	0.041	0.205	-0.063	0.028	-0.187	-0.453*	0.274	0.274	-									
FL	-0.064	-0.634**	0.395	0.553**	0.402	-0.596**	-0.584**	-0.286	-0.286	0.131	-								
FD	0.000	0.058	0.172	0.021	0.033	-0.249	-0.526*	0.093	0.096	0.826**	0.282	-							
FF	-0.226	-0.158	0.030	0.325	0.369	-0.151	-0.028	-0.250	-0.254	-0.146	0.315	-0.241	-						
TSS	0.021	0.126	-0.079	-0.191	-0.002	0.052	-0.171	-0.218	-0.218	0.080	0.068	0.149	-0.119	-					
TA	-0.087	0.092	0.065	-0.251	-0.129	-0.026	-0.124	-0.050	-0.053	0.305	-0.090	0.141	-0.126	0.757**	-				
LYC	0.176	-0.083	0.237	0.405	0.702**	-0.264	-0.214	-0.372	-0.373	-0.158	-0.023	-0.354	0.422	0.044	0.015	-			
ASC	-0.184	0.195	0.041	-0.252	-0.005	0.380	0.516*	0.270	0.268	-0.145	-0.487*	-0.404	0.154	-0.121	-0.006	0.119	-		
GA	0.202	-0.157	0.156	0.174	0.187	-0.122	0.032	0.384	0.381	0.307	0.081	-0.056	-0.028	-0.216	0.108	0.121	0.278	-	
QUE	-0.098	0.334	-0.053	-0.443	-0.204	0.296	0.140	0.124	0.122	0.359	-0.476*	0.100	0.169	0.377	0.536**	0.027	0.474*	0.019	-
AA	-0.252	-0.165	0.318	0.505*	0.555**	-0.239	-0.255	-0.239	-0.237	0.001	0.236	0.014	0.120	-0.027	-0.190	0.370	0.145	-0.013	-0.357

* = significant at $P < 0.05$ ($r > 0.413$), ** = significant at $P < 0.01$ ($r > 0.526$), PHT = Plant height, NPB = Number of primary branches per plant, NFF = Number of days to 1st flowering, FPFS = Number of days to 1st fruit set, DFM = Number of days to fruit maturity, TPP = Number of truss per plant, FPP = Number of fruits per plant, FWP = Fruit weight per plant, YPP = Yield per plant, FL = Fruit length, FD = Fruit diameter, FF = Fruit firmness, TSS = Total soluble solids content, TA = Titrable acidity content, LYC = Lycopene content, ACS = Ascorbic acid content, GA = Gallic acid content, QUE = Quercetin content, AA = Antioxidant activity.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Variability in Agronomic Performance of Tomato Genotypes

5.1.1 Vegetative characteristics of tomato genotypes

Vegetative traits play significant role in the overall development of the tomato crop. In the present study, significant variation was observed among the tomato genotypes for vegetative traits in all locations as well as across locations. Plant height and root length were significantly higher under greenhouse conditions as compared with the genotypes produced under field conditions. Similar observation was made by Rajasekar *et al.* (2013) who reported 150.25 cm and 52.41 cm of plant height under greenhouse and field conditions respectively. According to this author relative humidity was higher in the greenhouse environment which consequently resulted to higher vegetative growth and improved productivity of tomato fruit yield.

Estimated values recorded for stem diameter, number of leaves per plant, chlorophyll content and number of primary branches per plant in this work was higher under field conditions than those of the greenhouse. Contrast to the present findings, Rajasekar *et al.* (2013) found that tomato leaves were higher in number under greenhouse conditions compared with that of the field conditions. Similarly, Atnafua and Rao (2014) recorded higher values for number of primary branches per plant under greenhouse conditions than that of the field conditions. Differences in observations made could be attributed to differences in the genotypes evaluated, surrounding environment and seasons of the study. Vicente *et al.* (2011) indicated that chlorophyll content is higher at the vegetative growth stage than at the reproductive growth stage. In this study, measurement of chlorophyll content was carried out at the reproductive growth stage of the plants and thus probably resulted to lower values recorded.

5.1.2 Reproductive and phenological characteristics of tomato genotypes

The growth and productivity of the tomato crop is significantly influenced by its reproductive or phenological characters. Understanding these economically important characters is essential in planning a crop improvement programme because genotypes with short reproductive or phenological cycle along with high fruit yield are normally selected for commercial cultivation (Singh *et al.*, 2014). The results of the present study indicated that greenhouse-produced tomato genotypes were earlier in attaining 50 % flowering as well as number of days to fruit maturity. Higher values for percentage fruit set and number of fruits per truss were also recorded under greenhouse conditions. However, the field-produced genotypes were early in attaining 1st flower opening and fruit set. Also, number of truss per plant as well as number of flowers per truss was higher under field conditions. The significance of genotype, location and Genotype x Location interaction for all the reproductive and phenological characters implied that variability existed among the genotypes evaluated in each location. According to Singh *et al.* (2014) both genotypic and environmental factors influence tomato plants to flower early or delay in flowering. Generally, the performances of the genotypes for reproductive and phenological traits were inconsistent across the experimental locations due to the interaction between genotype and the environment.

Number of days to 1st flowering varied from 15 to 20 days and 12 to 24 days after transplanting under greenhouse and field conditions respectively. The presence of variability among tomato genotypes for number of days to 1st flowering has been reported in earlier studies. Earlier report by Parvej *et al.* (2010) indicated that phenological traits such as number of days to 1st flowering, 1st fruit set and number of days to fruit maturity were earlier under greenhouse conditions as compared with results obtained under field conditions.

Amarananjundeshwara *et al.* (2008) recorded variation in number of days to 1st flowering which ranged from 25 to 30 days after transplanting.

Percentage fruit set is an important character for increasing the productivity of tomato in terms of fruit yield. It serves as a good indicator of the resistance or tolerance of a genotype to the surrounding environmental conditions particularly temperature (Singh *et al.*, 2014). According to Singh *et al.* (2014), higher percentage fruit set is required to achieve high fruit yield. High percentage fruit set was recorded under greenhouse conditions than that of the field and varied greatly among the experimental locations. Genotypes such as PLATINUM F1 (72.93 %) and NIRVANA F1 (47.76) recorded maximum and minimum values for fruit set percentage across locations. Earlier investigations reported minimum and maximum values of 50.33% to 84.09 % (Singh, 2014), 72.84 % to 86.21 % (Sharma *et al.*, 2011) and 83.1 to 93.9 % (Pandey *et al.*, 2006). Differences recorded by different authors may be due to differences in the genetic materials evaluated. Genotype PLATINUM F1, CHERRY, SUMO F1 and NKANSAH HT showed a better mean performance for this trait. They are therefore considered as superior heat resistant or tolerant genotypes.

Number of days to fruit maturity was higher under greenhouse conditions as compared with that of the field. The genotypes showed high variability for the trait in each location and across locations. Similar observations were previously reported by Nagalakshani *et al.* (2001) and Cheema *et al.* (2004). Genotypes NKANSAH HT, WOSOWOSO, COBBRA F1 and THORGAL F1 showed early fruit maturity across locations and represent good genetic materials for increasing the productivity of tomato.

Reproductive and phenological characters are influenced by both cultivar and environmental conditions. Tomato genotypes evaluated in this experiment showed variation in their reproductive development characters within and across locations as a result of genotypic differences. The results of the present study indicated that number of truss per plant and

number of flowers per truss were higher under field conditions while number of fruits per truss was higher under greenhouse conditions. A study by Parvej *et al.* (2010) revealed that reproductive development traits including number of trusses per plant, number of fruits per truss and number of flowers per truss were higher under greenhouse conditions than that of the field. Such differences may result from differences in surrounding environment as well as differential response of different genotypes to different environments. Singh *et al.* (2014) observed that higher number of flower clusters contributed to increased fruit yield in tomato and attributed this observation to inherent genetic factors. Variability in reproductive development characters has been reported in previous studies and ranged from 6.9 to 8.6 for number of truss per plant (Osekita and Ademiluyi, 2014), 2.9 to 7.8 for number of flowers per truss (Emami *et al.*, 2013) and 1.72 to 5.11 for number of fruits per truss.

4.1.3 Yield and yield components characteristics of tomato genotypes

Fruit yield is an important trait in genetic improvement of tomato. It is a complex trait and thus influenced by several yield components. Considering the average performances of all genotypes under greenhouse conditions, a total of 7 genotypes (MONGALF1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, SUMO F1, and NS 504) showed superior performance for fruit yield. These genotypes are good materials for tomato production under greenhouse experimental conditions. Similarly, 7 tomato genotypes namely MONGAL F1, PLATINUM F1, NKANSAH HT, WOSOWOSO, ROMA, ROMA VF and BUFFALO exhibited better fruit yield performance among all the genotypes evaluated under open field conditions for fruit yield. The mean fruit yield of these genotypes exceeded their respective location averages. Across the two locations, four tomato genotypes showed superior performance. These genotypes were MONGAL F1, PLATINUM F1, NKANSAH HT and WOSOWOSO. They represent good materials for tomato production irrespective of differences in locations considered in this experiment. Common among most of the

genotypes with superior performance for fruit yield was high scores for one or more yield component traits including number of fruits per plant, number of trusses per plant, single fruit weight and total fruit weight per plant.

The tomato genotypes generally showed diverse yield performances which agreed with findings by other workers (Hussain *et al.*, 2001; Mansour *et al.*, 2009; Singh *et al.*, 2009). This was as a result of differences in number and type of genetic materials used, location as well as growing environment. A narrow difference in fruit yield was recorded between the genotypes produced under greenhouse and that produced under field conditions. Some genotypes including PECTOMECH, L11, NIRVANNA F1, #20880 and SHAKTIMAN performed poorly under greenhouse conditions. These genotypes showed poor adaptation to greenhouse conditions. Thus a lower average value of 52.60 t/ha under greenhouse conditions than that of the field (55.10 t/ha) was recorded. Average tomato fruit yield as reported by Atnafua (2014) was higher under polyhouse condition (80.6 t/ha) than that of the open field (57.2 t/ha). Parvej (2010) compared phenological development and productive ability of tomato and obtained high fruit yield under polyhouse condition (81 t/ha) than that of the field (57 t/ha). Also, Blay *et al.* (1999) evaluated 8 tomato genotypes under field conditions and reported low fruit yield (6 117.30 – 11 359.2 kg/ha). This was attributed to poor rainfall, high day and night temperatures in the experimental period, as well as attack by root knot nematodes. Other reports on tomato fruit yield differences among cultivars include that of Firas *et al.* (2012) who reported minimum and maximum yield of 15 907 kg/ha and 42 908 kg/ha respectively. Singh *et al.* (2014) recorded average fruit yield of tomato in a range of 135.10 – 1046.80 q/ha. According to this author, genotypes with medium and large numbers of fruits per plant produced more fruit yield as compared with those with large fruit sizes but smaller number of fruits per plant. This observation agrees with the present study where

genotype NKANSAH HT with medium sized fruits and higher number of fruits per plant (27, 33) produced high fruit yield per plant.

5.4 Fruit physical and quality characteristics of tomato genotypes

The quality of fruits and vegetables including tomato is determined by their chemical compositions. While inherent genetic factors play major role in determining fruit quality components, environment could alter the quantitative composition of the fruit (Mpofu *et al.*, 2006). For the fresh consumption of tomato as well as in the tomato processing industries, desirable tomato fruit physical and quality features include fruit pericarp thickness, fruit firmness, total soluble solids contents, acidity, flavour, pH, phenolic acids and flavonoid compounds (Caliman *et al.*, 2010).

Fruit firmness

Tomato fruit firmness has been reported as one of the most pertinent qualities required for processing in the canning industry. It determines fruit shelf life as well as susceptibility of tomatoes to damages associated with harvest, sorting, processing, packaging and transportability (Radzevicius *et al.*, 2013). High fruit pericarp thickness corresponds with better fruit firmness and consequently, its suitability for processing (Saimbhi *et al.*, 2001). Genotype factor is known to be the major determinant of tomato fruit firmness. In the present study, fruits obtained from greenhouse-produced genotypes were found to be relatively firmer (3.90 kg/cm^2) than fruits harvested from field-produced genotypes (3.18 kg/cm^2). Comparatively, genotypes 11 – 172, ROMA, NKANSAH HT, PECTOMECH, SUMO F1, and INLAY F1 were superior in fruit firmness in the present study.

Total soluble solids content

Between fifty and sixty-five percent (50 - 65 %) of total soluble solids content (TSS) of tomato is made up of mainly sugars (glucose and fructose) which are essential quality parameters of tomato in the processing industry. Higher amounts of TSS are correlated with

higher recovery product yield (Manashi, 2011; Emami *et al.*, 2013; Singh *et al.*, 2014). In terms of processing, a total soluble solids content range of 4 to 8 °Brix has been reported to be desirable. The present study showed a wide variability among the genotypes for TSS content and ranged from 2.26 °Brix (Roma) to 6.58 °Brix (ROMA VF) under greenhouse and 2.58 °Brix (SHAKTIMAN) to 6.98 (WOSOWOSO) under field conditions. A related range of TSS content have been reported in previous studies by Blay *et al.* (1999), Caliman *et al.* (2010), Emami *et al.* (2013) and Singh *et al.* (2014). In contrast to findings by Caliman *et al.* (2010), greenhouse-produced genotypes in this study recorded higher TSS values than the field-produced genotypes. Out of the 20 tomato genotypes evaluated, 11 genotypes under green house conditions as well as 8 genotypes under field conditions recorded TSS values in the range of 4 – 8 °Brix indicating their suitability for the processing industry.

Fruit acidity content

Acidity content of tomato fruits represents another important quality determinant trait of tomato for processing. In the processing industry, acidity reduces pH of the pulp and prevents the growth of microbes. Besides, high acidity gives better tomato flavour, improves its palatability and nutritive value of the fruit as well as reduction in processing time and temperature of the product (Manashi, 2011). Wide variations among genotypes for acidity content have been reported in tomato by previous authors (Manashi, 2011; Aoun *et al.* 2013; Singh *et al.*, 2014) and this have been mainly attributed to genetic factors. Caliman *et al.* (2010) reported that tomato genotype with acidity value greater than 0.32 % is suitable for processing. The results of the current study revealed 10 and 11 tomato genotypes with acidity content greater than 0.30 mg/ml (0.32 %) under greenhouse and field conditions respectively. Values obtained in this study were in agreement with findings by Caliman *et al.* (2010) who recorded percentage acidity values of 0.26 – 0.37 under protected conditions and 0.28 – 0.40 under field conditions . From the results of the present work, tomato genotypes produced

under field conditions were more acidic (0.40 mg/100 ml) compared with the corresponding genotypes evaluated under greenhouse (0.32 mg/100 ml) conditions. The low acidity content under greenhouse condition could be attributed to low photosynthetic activity of the genotypes produced under greenhouse conditions as compared with that produced under field conditions (Caliman *et al.*, 2010). This is not unexpected as field-produced genotypes recorded higher mean chlorophyll content (40.30 mg/ml) than the greenhouse genotypes (31.12 mg/ml).

Fruit flavour index (TSS/TA)

Tomato fruit flavour influences consumers or processors' preference for specific tomato cultivars. It is determined by TSS/TA ratio which is also a taste determinant quality trait. Variation in tomato flavour composition among different genotypes has been attributed mainly to varietal differences and environmental factors such as plant nutrition (Caliman *et al.*, 2010; Manashi, 2011; Aoun *et al.* 2013). Tomato genotype with a TSS/TA value ≥ 10 is reported to have good flavour required for fresh fruit consumption and processing (Caliman *et al.* (2010). Among the 20 tomato genotypes evaluated, superior flavour content (≥ 10) was recorded by almost all the tomato genotypes under greenhouse conditions except PECTOMECH (9.61). More than half of the tomato genotypes evaluated under field conditions recorded poor flavour composition of < 10 TSS/TA value. This finding suggests that better fruit flavour composition could be obtained under greenhouse environment compared with that of field conditions. The present results contradicted findings by Caliman *et al.* (2010) who recorded an average TSS/TA value of 12.07 and 16.82 for greenhouse and field conditions respectively. Differences in flavour indexes observed by different authors could be due to differences in the experimental materials used as well as the surrounding environment.

Fruit pH

Fruit pH along with TSS is desirable indexes for the assessment of related quality traits of tomato in the processing industry (Agong *et al.*, 2001). Previous study by Aoun *et al.* (2013) revealed that fruit acidity affects flavour only when pH value is lower. At pH value less than 4.1, growth of pathogens like *Bacillus coagulans* in tomato products are reduced (Majid,

2007), while values less than 4.49 are suitable in terms of fruit sourness (Aoun *et al.*, 2013). In the processing industry, a suitable tomato genotype for processing should have pH value lower than 4.5 (Caliman *et al.*, 2010). Blay *et al.* (1999) and Singh (2014) reported relatively smaller variability for pH among different genotypes. Findings from the present study showed that pH value differed among the genotypes with appreciably higher values recorded by field-produced genotypes (4.36) than those produced under greenhouse conditions (4.30). This observation was in accordance with findings by Caliman *et al.* (2010) who recorded a relatively greater pH value under field conditions (4.49) than that obtained under protected conditions (4.48). Fruit pH values obtained in this study revealed that most of the tomato genotypes recorded values that make them suitable for processing.

Carotenoids content of fruits

In the plant kingdom, beta carotene and lycopene are essential phytochemical compounds. Manashi (2011) mentioned bright colours of fruits (either yellow or red) are good quality characteristic that influence consumers' choice for tomato. Such colours are affected by the composition of β -carotene and lycopene in the fruit. Composition of carotenoids in fruits varies greatly among different genotypes as well as environments (Frusciante, 2000). Various reports have indicated the effects of light intensity and high temperature in stimulating carotenoids biosynthesis. Variation was observed among the genotypes for lycopene concentration of fruits and ranged from 7.31 mg/100 ml (ROMA VF) to 33.71 mg/100 ml (SHAKTIMAN) among the greenhouse-produced genotypes and 13.31 mg/100 ml (PECTOMECH) to 33.79 mg/100 ml (11-172) among the field-produced tomato genotypes. Generally, lycopene content under field conditions (23.35 mg/100 ml) was appreciably higher than the amount recorded by the corresponding greenhouse genotypes (19.89 mg/100 ml). A different observation was made by Caliman *et al.* (2010) who obtained higher average lycopene content under protected conditions (7.81 mg/100 ml) than field produced genotypes (7.47 mg/100 ml). Manashi *et al.* (2011) recorded a narrow difference in carotene content

when 5 tomato genotypes were evaluated under field conditions. Previous findings have also revealed an appreciable level of variation among different genotypes for lycopene content under different growing conditions. For instance, Frusciante (2000) reported lycopene content in the range for 5.5 – 7.5 mg/100 g whereas Radzevicius (2013) found 2.02 – 4.95 range of lycopene. These differences in observed values could be attributed to differences in genotypic and prevalent environmental factors such as temperature and light intensity.

Ascorbic acid content of fruit

A wide variability in ascorbic acid composition was recorded among tomato genotypes as a result of both genetic and surrounding environmental factors. Tomato genotypes that contain high ascorbic acid content are preferred for processing and determine the nutritional quality of the processed product (Singh *et al.*, 2014). The results of the present study indicated that greenhouse-produced tomato genotypes are richer in ascorbic acid content than the field-produced ones. The composition of ascorbic acid was found to be variable within each location as well as across locations. Tomato varieties that contain high ascorbic acid content are suitable for consumption and thus establish the nutritional worth of the variety (Singh *et al.*, 2014). Variability in ascorbic acid composition has also been recorded in previous studies by Singh *et al.* (2014) (12.6 – 15.63 mg/100 g), Sharma *et al.* (2011) (17.29 – 26.21 mg/100 g) and Vinod *et al.* (2013) (21.63 – 26.70 mg/100 g). The small fruited CHERRY variety recorded the highest ascorbic acid composition under greenhouse condition. This is in agreement with findings by Vinod *et al.* (2013) who indicated that tomato genotypes with small fruits contain high ascorbic acid content. Comparatively, the highest ascorbic acid composition across the two locations was recorded by CHERRY, NKANSAH HT, 11-172, #20880 and PLATINUM F1.

Phenolic acid compounds:

Phenolic acid compounds including gallic, vanillic and rosmarinic acids have chemoprotective or antioxidant property and thus are able to scavenge effects associated with reactive oxygen species in the human body. In this way, several human-related chronic and degenerative diseases are prevented. The composition of these compounds in the tomato fruit is not only influenced by cultivar factors but also the cultivation practice, surrounding environment, extraction procedure, temperature, processing as well as storage conditions (Supathra *et al.*, 2013). For all the phenolic acid compounds, field-produced genotypes recorded maximum amount as compared with those produced under greenhouse conditions. Brezeanu *et al.* (2013) observed a significant amount of rosmarinic acid content in tomato fruits among tomato genotypes evaluated under conventional system. The results of the present study revealed five (5) tomato genotypes as comparatively better source of phenolic acid compounds. These genotypes included PLATINUM F1, 11-172, BUFFALO, SUMO F1 and SHAKTIMAN. They contain a relatively higher amounts of gallic, vanillic and rosmarinic acids composition across locations.

Flavonoid compounds

Quercetin, kaempferol and myricetin are reported to be the main flavonoid compounds present in tomato and its related products (Tokusoglu *et al.*, 2003). In addition, tomato fruits also contain rutin, catechin, hesperetin and genestein as important flavonoid compounds. The concentration of these compounds in fruits varies among genotypes as a result of differences in genetic makeup and cultivation environment. In the present experiment greenhouse-produced tomato genotypes recorded high composition for all the flavonoid compounds studied. A wide variability within each location and across locations was observed among the genotypes for all the flavonoid compounds studied and this could be attributed to both genotype and environment factors. Generally, genotypes WOSOWSO, SUMO F1, NKANSAH HT, 11-172 and CHERRY displayed superior performance for all flavonoid

compounds studied across locations. Koh *et al.* (2009) recorded quercetin and Kaempferol content in commercial broccoli with a range of 0.03 to 10.85 and 0.24 to 13.20 mg/100 g FW respectively. In this work, quercetin and kaempferol content in tomato fruits ranged from 23.71 to 126 mg/100 ml FW and 6.04 to 57 mg/100 ml respectively across locations. Differences in results could be attributed to differences in plant materials evaluated.

5.3 Antioxidant activity of tomato genotypes

Generally, the antioxidant activity of vegetables and fruits differ among different cultivars due to differences in their genotypic makeup and environmental conditions (Marsic *et al.*, 2011). The results of the present study revealed that antioxidant activity of the field-produced genotypes was higher than the same genotypes produced under greenhouse conditions. In each of the two experimental locations, variability for antioxidant activity in terms of their IC_{50} values was observed. In a related study, Ferreira *et al.* (2012) recorded the most excellent antioxidant activity in a local tomato variety whose IC_{50} value was 1.63 mg/100 ml. The results of the present work showed that the local tomato genotype WOSOWOSO proved to be the highest in antioxidant activity under field conditions as well as across locations. In a related study in organic Baby-Leaf salads, Aires *et al.* (2013) reported antioxidant activity (expressed as IC_{50}) ranged from 0.23 to 3.03 mg/ml. Generally, WOSOWOSO, BUFFALO and NS 504 recorded the lowest IC_{50} values across the two locations suggesting that their antioxidant activities were comparatively superior to the rest of the genotypes.

5.1.4 Genotype x Location interaction effects on tomato fruit yield

Though, the tomato crop is recognized to be adapted to different agro-climatic conditions and cropping systems (Sunil *et al.*, 2013), several studies have indicated a significant G x E interaction effects on the expression of important traits of tomato genotypes. Such interaction effects have been reported in tomato fruit yield as well as several quality characters (Kuti and Konuru, 2005; Rosello *et al.*, 2011; Cebolla-Cornejo *et al.*, 2011 and Panthee, *et al.*, 2012).

In the present study, differences in genotype, location and G x L interaction effects were significant ($P < 0.01$) for almost all the studied characters indicating the role of varietal difference, location and G x L interaction effects on the expression of individual traits. The highly significant value recorded for location suggested that the two locations were diverse. These findings are not unexpected because yield as a complex trait is influenced by a number of yield components which are quantitative in character. Such quantitative characters exhibit continuous variation in their expression and are subject to genotype-by-environment interaction effects (Causse *et al*, 2002). For instance, the genotype COBBRA F1 performed better with a total fruit yield of 88.55 t/ha relative to its overall mean performance across the two locations and also, it ranked among the top 5 genotypes with superior yield (above location mean) under greenhouse conditions. However it produced 49.78 t/ha (and ranked 15th) under the open field conditions relative to its overall mean across the locations and thus categorized outside the first 5 superior genotypes under field locations. This pattern of performance is inconsistent and a manifestation of reversibility in rank as well as differences in levels of environmental sensitivity across the two locations. This makes COBBRA F1 an unstable and environmentally sensitive for fruit yield. Apart from MONGAL F1, PLATINUM F1 and NKANSAH HT all the other genotypes evaluated exhibited irregular patterns of performance as a result of genotype-by-environment interaction effects. Similar pattern of performance was observed among the genotypes for most fruit quality traits. The present results was in conformity with earlier findings by Panthee *et al.* (2012) who reported significant effects of genotype-by-environment interaction on all studied traits except ascorbic acid content of fruits.

5.3 Genetic Variance, heritability and genetic gain of tomato characters

5.3.1 Individual location basis

Genetic variability studies in a crop are fundamental to crop improvement programmes aimed at yield and quality traits. The significant ($P < 0.01$ and $P < 0.05$) genotypic difference obtained from the results of the analysis of variance (ANOVA) and the estimate of genetic variance indicated an existence of an amount of variability in the 20 tomato genotypes evaluated. Similar findings have been reported earlier by Sharma *et al.* (2009) and Dar and Sharma (2011). Estimation of genotypic coefficient of variation (GCV) gives a true suggestion of the magnitude of genetic variation in a studied population. In the present study, moderate (10 – 20 %) to high (> 20 %) estimate of GCV and PCV for most of the agronomic traits under both greenhouse and field conditions showed appreciable amounts of phenotypic and genotypic variability. The relatively higher estimate of PCV than the corresponding GCV indicated a relative effects of environment (to some degree) on the expression of the traits. However, the narrow difference between PCV and GCV and the closeness to unity in values observed in the ratio of GCV to PCV suggest that genetic control in the expression of the traits was predominant. This suggests that simple phenotypic selection could be made among the genotypes. Also, selection could be effective for most characters at the early stage of a breeding program since response to selection is directly proportional to variability present in the experimental materials evaluated (Falconer and Mackay, 1996). Generally, the magnitude of variability observed among the genotypes for agronomic traits was higher under the greenhouse conditions than the open field conditions.

Among the quality traits studied, moderate to high estimate of PCV and GCV was observed for most traits under greenhouse and field conditions. This indicated the existence of variability in the genotypes for such traits. However, the low estimate of GCV for pH, gallic acid, rosmarinic acid and vanilic acid suggests that the expression of those traits were

influenced by environment. For crop improvement purpose, selection for such characters will need to be carried out in large replicates across multiple location and years (Hallauer, 2007). Besides, the fruit quality traits were more variable compared to the agronomic traits under both locations. The results of the present investigation were in agreement with findings by Nwosu *et al.* (2014) who recorded low difference between PCV and GCV for most of the characters studied including days to flower, days to 50 % flower, days to fruit ripening, fruit length, fruit per inflorescence, fruit diameter, fruit weight and number of days to fruit maturity. Report by Reddy *et al.* (2013) indicated an estimate of moderate to high PCV and GCV as well as smaller differences between them for most of the traits they studied. Similar findings have also been reported by other authors (Pradeepkumar *et al.*, 2001; Jiregna *et al.*, 2012; Shankar *et al.*, 2013; Shushay *et al.*, 2013)

The estimate of GCV along with heritability provides a true indication of the magnitude of heritable component of variation. Estimate of heritability enables a breeder to determine the extent to which genetic variability contributes to phenotypic variability of a trait. In the present study, broad sense heritability estimated for all traits under greenhouse and field conditions were very high with the exception of ascorbic acid and rosmarinic acid contents which recorded moderate values.

High GCV as well as high heritability are useful to breeders to make effective selection and also indicate that selection could be made on phenotypic basis. However, this does not necessarily suggest high genetic gain for a particular character unless it is associated with high genetic advance. In this study, very high heritability estimates accompanied with high genetic gain was recorded by most of the traits evaluated under each of the locations. These findings suggest that those traits could easily be passed on to the next generation. High estimate of heritability may be the result of the diverse nature of the genotypes included in the study (Shushay *et al.*, 2013). Phenotypic selection of such traits in the early generation

for further improvement could therefore be accomplished via simple selection methods like pure line, mass selection, bulk or single seed decent. High estimate of broad sense heritability (61 % to 100 %) along with high genetic advance was recorded for almost all agronomic and physicochemical traits of tomato varieties studied by Shankar *et al.* (2013). However, in the present study high heritability and moderate genetic gain was recorded for days to 50 % flowering, number of flowers per cluster and TSS. High and medium heritability estimate along with low genetic gain recorded for percentage fruit set and pH respectively under open field conditions suggested that non-additive gene action controlled their expression; hence selection cannot be achieved through simple selection methods. Instead such traits could be improved through development of hybrids or could possibly be used as transgressive segregants in heterosis breeding programme (Reddy *et al.*, 2013).

The results of the present study is in accordance with findings made by Shushay *et al.* (2013), Hadhayatullah *et al.* (2008) and Mehta and Asati (2008) who recorded very high ($P > 80\%$) estimates of heritability along with high genetic gain for most of the traits studied. A related study by Vinod *et al.* (2010) indicated a very high estimate of heritability for all traits with a range from 80 % to 99 %. Several related findings have been reported in tomato genetic variability and heritability studies (Kaushik *et al.*, 2011; Reddy *et al.*, 2013).

5.3.2 Combined location basis

On the basis of the combined analysis of variance, the observed variation recorded for almost all characters studied was significant ($P < 0.01$ and $P < 0.05$) among the genotypes. This observation could be attributed to environment or location or genotype-specific differences as well as G x L interaction effects. The significant ($P < 0.01$) mean squares of location and G x L interaction suggest that the locations were diverse. This resulted in differences in response of genotypes to location changes as manifested in their varied performances across different locations. The challenge then is the need to develop separate varieties tailored to each

specific location. Therefore, one of the most important rationales behind genetic variability studies is the identification of suitable environments where a trait which is intended to be improved upon is most likely to show a consistent expression. Environmental factors may influence the genotype and consequently, the expression of a trait in a cultivar evident by the magnitude of variability due to genotype-by-environment interaction (G x E).

Genotype-by-environment interaction (G x E) causes a reduction in the overall genetic gain of desired traits. This phenomenon may create difficulties in selection of desirable traits for crop improvement programmes. Knowledge about G x E interaction is therefore required in the selection of ideal location, traits and the genotype for inclusion in a breeding programme (Gruneberg *et al*, 2005). The results in the present investigation based on the combined analysis of variance indicated that the estimated variance due to location (σ^2_L) was higher than the corresponding genotypic variance (σ^2_G) for some agronomic traits including plant height, stem diameter, chlorophyll content, root length per plant and number of days to 50 % flowering confirming the significance of location effects on those traits. Among the fruit quality parameters, larger estimates of genotypic variance (σ^2_G) than variance due to location (σ^2_L) was found for most fruit physical traits including single fruit weight, fruit weight per plant, fruit yield per plant, number of locules, fruit length and diameter as well as shape index. As a result high estimate of heritability was recorded for such parameters indicating that they were predominantly affected by inherent genetic factors. It should be noted that very large variance estimates due to phenotypic, environmental and G x L as well as phenotypic coefficient of variation than the corresponding genotypic parameter were observed for almost all the fruit chemical traits. This resulted in negative GCV and heritability estimates.

Among the traits studied, the value obtained for the ratio of σ^2_G to $\sigma^2_{G \times L}$ ($\sigma^2_G:\sigma^2_{G \times L}$) ratio was close to unity only for number of primary branches per plant, number of days to first fruit

set, number of flowers per truss and fruit shape index. This implied that the effects of location or environment as well as G x L interaction effects accounted for variability in most of the traits. This observation gives an indication that differential response of genotypes to location difference was very possible. Highly significant genotype-by-location interaction implied that independent analysis of data for each location is required (Khan *et al.*, 2013) rather than analysis carried out on combined location basis. The present observation agrees with earlier findings by Causse *et al.* (2003) who recorded a significant G x E interaction for lycopene, TSS and TA.

Information regarding the nature of a trait, its expression as well as interaction with environment could best be understood from the estimate of broad sense heritability. The results of the present study revealed that almost all fruit quality traits recorded very low heritability estimates. This implied that most of the quality traits were environmentally sensitive and the ability to control and predict variability based on genetic information alone becomes negligible (Panthee, 2012). This also implied that selection of superior genotypes for most of the traits would not be effective at early generation. In contrast to the present findings, high heritability estimate has been reported by Premah *et al.* (2011) for TSS (77.95), ascorbic acid (74.7 %), and TA (99.94 %). Similarly, Dar and Sharma, (2011) reported high heritability estimates for lycopene (92 %) and ascorbic acid (94 %). These contrasting results could be due to differences in the experimental materials, growing conditions as well as cultural practices.

5.4 Character association of traits among tomato genotypes

In selection programs, yield, yield components and quality traits are among the most economically essential traits usually targeted by plant breeders. According to Falconer and Mackay (1996), many important characters in crops are positively or negatively correlated because they are influenced by the same gene or because they are developmentally or

structurally related. Knowledge of correlated traits is essential in determining whether or not selection for a particular trait will influence another (Girdthai *et al.*, 2012).

In the present study, number of trusses per plant, number of fruits per plant as well as total fruit weight per plant showed a significant and positive association with fruit yield irrespective of the crops growing condition considered in this experiment. This shows a consistency of correlation across the two locations. However the correlation coefficients differed due to G x L interaction effect. Indirect selection gives a correlated response in the target trait so far as the targeted trait and the secondary traits are associated (Falconer and Mackey, 1996). Those traits with significantly positive association with fruit yield could therefore be selected for maximizing fruit yield in tomato in any of the two growing conditions. This result was in agreement with findings by previous authors including Hadhayatullah *et al.* (2008), Gosh *et al.* (2010), Jiregna *et al.* (2012) and Shushay *et al.* (2013). These authors independently reported a positive and significant correlation of fruit yield with number of fruit clusters per plant and number of fruits per plant at both the genotypic and /or phenotypic levels. Singh (1993) indicated that a high fruit yield response is achieved when the secondary trait also has a high estimate of heritability as well as high correlation coefficient. The present study revealed high heritability estimates as well as high correlation coefficient for the traits associated with fruit yield.

Negative correlation of fruit yield with number of days to 50 % fruit set (under both greenhouse and open field condition) and number of days to fruit maturity (greenhouse condition only) indicated that genotypes that attain early fruit set and mature early tend to have higher fruit yield. This finding agrees with results reported by Jiregna *et al.* (2012) and Shushay *et al.* (2013).

A positive and significant correlation was observed between fruit yield and gallic acid (a phenolic and antioxidant phytochemical compound) under the field experimental location.

This indicated that indirect selection of one trait for the other could be feasible under field conditions. Moreover, the significantly positive association between most traits suggests that each of those pairs of traits is controlled by the same or similar genes or is developmentally or structurally related (Falconer and Mackay, 1996). Indirect selection of one trait for the other should then be appropriate. This is in agreement with earlier report where average fruit weight correlated positively and significantly with number of primary branches per plant at both genotypic and phenotypic levels (Vinod *et al.*, 2013), number of days to 50 % fruit set and number of days to fruit maturity (Shushay *et al.*, 2013). On the other hand, negative association observed for trait pairs point out that indirect selection for any one of those traits may possibly not be advantageous.

Antioxidant compounds considered in this discussion included lycopene, ascorbic acid, gallic acid and quercetin. Under greenhouse growing environment, ascorbic acid correlated positively and significantly with number of primary branches per plant, number of trusses per plant and number of fruits per plant suggesting that those pairs of traits are controlled by the same gene. Similar observations were made earlier by Vinod *et al.* (2013). Indirect selection for any one of those traits is therefore possible. Genotypes with superior performance for traits positively correlated with ascorbic acid could be used for further development of materials endowed with high ascorbic acid content. A negative association between ascorbic acid content and fruit length also suggests that genotypes with shorter fruit length contain higher amount of ascorbic acid content and hence could be used as indirect selection under green house conditions.

Moreover, the antioxidant compound quercetin showed a significant and positive correlation with titrable acidity and ascorbic acid. This observation indicated that indirect selection of the trait titrable acidity or ascorbic acid could contribute to enhancing quercetin content in tomato fruit over combined locations. Under the combined locations genotypes containing

high ascorbic acid content and titrable acidity content could be used to develop high quercetin content cultivars.

Quercetin showed a negative significant correlation with fruit length and fruit diameter under greenhouse conditions suggesting that indirect selection for these traits to increase gallic acid content would be less useful. Thus genotypes with reduced fruit length or reduced diameter are possibly better in terms of their gallic acid composition. Also, under field growing conditions a positive significant association of quercetin with single fruit weight per plant, total soluble solids content and titrable acidity was observed. These results revealed that the traits are under the control of the same or similar genes. Indirect selection of those traits could therefore maximize quercetin content in tomato fruits under field conditions.

However a negative and significant association of quercetin with number of days to 50 % fruit set suggests that it is undesirable to select the later trait for maximizing the amount of quercetin in the fruit. Antioxidant scavenging activity, expressed as IC_{50} (inhibition coefficient) associated positively and significantly only with number of days to 50 % fruit set implying that the two traits are being controlled by the same or similar genes or they are developmentally or structurally correlated. The lower the IC_{50} value scored for a genotype the better its antioxidant potential to deactivate the harmful effects associated with reactive oxygen species (ROS) in humans (Kipandula *et al.*, 2014). This also implied that a reduction in number of days to 50 % fruit set should show a corresponding reduction in the IC_{50} value (increased antioxidant activity). Genetic and environmental variation study in bread and Durum wheat by Sukkalovic *et al.* (2013) indicated a highly significant and positive association of antioxidant capacity with total phenolic composition. The association of antioxidant activity with phenolic compound (gallic acid) studied in the present experiment was not significant.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

1. Systematic breeding programmes aimed at improving tomato fruit yield and fruit quality traits require information on the nature and magnitude of genetic variability, heritability and character association in agronomic and fruit quality traits in the crop. Results of the present study revealed an existence of useful genetic variability in the genotypes. The estimate of moderate to high GCV, high broad sense heritability as well as high genetic gain for almost all traits suggest the potential for selection and utilization of suitable genotypes based on different parameters to obtain high yield and fruit quality traits.
2. Following the present findings, promising tomato genotypes based on their fruit yield (t/ha) under greenhouse conditions were MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA, SUMO F1 and NS 504.
3. Tomato genotypes MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA, SUMO F1, ROMA VF and BUFFALO showed superior yield performance under field conditions.
4. Across the two locations, MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA and SUMO F1 were superior genotypes for fruit yield. Most of the top performing genotypes for yield recorded high scores for one or more yield component traits including number of fruits per plant, trusses per plant, single fruit weight and total fruit weight per plant.
5. Highest amount of flavonoid compounds across the two locations were recorded by tomato genotypes WOSOWOSO, SUMO F1, NKANSAH HT, 11-172, CHERRY and THORGAL F1.

6. The amount of phenolic acids composition was found to be highest in genotypes PLATINUM F1, BUFFALO, 11-172, SHAKTIMAN, THORGAL F1 and NIRVANA F1.
7. Genotypes produced under greenhouse conditions recorded higher amount of flavonoid composition while phenolic acids content was higher under field conditions.
8. Highest antioxidant scavenging activity among the genotypes across locations was recorded by WOSOWSO, BUFFALO and NS 504.
9. Generally, the performance of the genotypes evaluated differed across locations due to the interaction between the genotypes and environment. The expressions of most traits were influenced by genetic and environmental factors as well as their interaction.
10. Number of trusses per plant, number of fruits per plant and total fruit weight per plant showed a positive significant association with fruit yield and are potentially useful traits as indirect selection indexes for yield improvement under both greenhouse and field conditions

6.2 Recommendations

1. The results of the current study showed that tomato genotypes MONGAL F1, PLATINUM F1, NKANSAH HT, COBBRA F1, WOSOWOSO, ROMA and SUMO F1 are recommended for commercial production under both greenhouse and field conditions by virtue of their superior fruit yield per plant across the two growing environments.
2. The present study was carried out under a single growing season; hence further evaluation of the genotypes could be conducted over multiple seasons or years. Evaluation of the genotypes across multiple locations and years along with appropriate stability analysis procedure will further be required to identify stable

tomato genotypes for fruit yield and other important chemical composition traits. This will also provide an in depth information regarding G x E interaction and tomato fruit yields.



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APPENDIX

Appendix 1. Means squares of PHT, SG, NL, CC, NPB, RTL, NFF, FPF and NFS measured under greenhouse conditions

Source of variation	df	MEAN SQUARE								
		PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	4.40	0.05	1.17	3.85	0.14	1.09	0.47	0.42	1.52
Genotype	19	678.90**	0.89**	270.11**	93.63**	1.74**	60.10**	11.10**	27.65**	130.00**
Residual	38	1.38	0.06	0.58	1.08	0.06	0.82	0.17	0.31	0.36
Total	59	219.60	0.32	87.40	30.98	0.61	20.25	2.91	9.12	42.45
CV (%)		11.75	7.27	27.26	18.46	24.14	21.01	11.05	13.65	16.70

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; PHT= Plant height; SG = Stem girth; NL= Number of leaves CC = Chlorophyll content; NPB = Number of primary branches per plant, RTL = Root length; NFF = Number of days to 1st flowering; FPF = Number of days to 50 %flowering and NFS = Number of days to 1st fruit set.

Appendix 2. Mean squares of FPFS, FSP, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured under greenhouse conditions

		MEAN SQUARE								
Source of variation	df	FPFS	FSP	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	1.72	6.55	0.47	1.32	0.02	0.06	0.14	13.18	25359.00
Genotype	19	209.00**	469.18**	140.24**	45.04**	3.01**	2.04**	200.23**	2068.08**	437280.00**
Residual	78	0.49	56.07	0.33	0.88	0.18	0.10	0.18	10.99	38271.00
Total	59	67.68	187.43	45.39	15.12	1.09	0.72	64.60	673.52	166327.63
CV (%)		18.13	21.88	10.30	30.46	18.68	21.74	77.52	38.01	62.96

***Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; FPFS = Number of days to 50 % fruit set; FSP = Fruit set percentage; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of fruits per truss, NFPT = Number of fruits per truss; FPP = Number of fruits per plant; SFW = Single fruit weight and FWP = Fruit weight per plant*

Appendix 3. Means squares of YPP, LOC, PTK, FF, FL, FD, SI, FDM, and MA measured under greenhouse conditions

Source of variation	df	MEAN SQUARE								
		YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	7.66	0.00	0.11	1.03	0.04	0.03	0.00	0.00	0.00
Genotype	19	3722.33**	9.28	2.00**	1.05**	1.46**	4.23**	0.09**	0.04**	0.02**
Residual	78	4.65	0.00	0.10	0.14	0.02	0.05	0.00	0.00	0.00
Total	59	1201.97	2.99	0.71	0.46	0.49	1.39	0.03	0.01	0.01
CV (%)		66.97	48.77	17.52	15.17	15.01	23.43	18.55	26.09	23.53

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA = Malic acid content of fruit.

Appendix 4. Mean squares of PH, TSS, TA, TSS/TA, β -CARO, LYC, ASC, GA and VA measured greenhouse conditions

MEAN SQUARE										
Source of variation	df	pH	TSS	TA	TSS/TA	β -CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.03	0.00	0.44	0.32	0.09	8.05	0.00	0.00
Genotype	19	0.30*	4.07**	0.02**	22.63**	202.37**	125.67**	24.45**	0.02**	0.06**
Residual	78	0.00	0.03	0.00	0.30	0.25	0.18	7.67	0.001	0.01
Total	59	0.10	1.33	0.01	7.49	65.34	40.59	13.09	0.01	0.02
CV (%)		5.48	26.21	25.32	19.59	41.30	40.17	24.34	5.34	15.83

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or ripeness index; TI = Fruit taste index; β -CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit and ASC = Ascorbic acid content of fruit

Appendix 5. Mean squares of RA, QUE, RUT, CAT, KAE, HES, MYR, GEN and AA measured under greenhouse conditions

Source of variation	df	Mean square								
		RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.00	9.46	6.18	0.87	82.94	83.0	0.43	5.83	0.09
Genotype	19	0.04**	2828.77**	6418.92**	5636.78**	1047.25**	18404.30**	1105.10**	1564.71**	3.27**
Residual	78	0.01	10.99	24.24	5.01	64.97	207.90	4.03	9.58	0.03
Total	59	0.02	918.36	2082.93	1818.49	382.00	6063.48	358.49	510.26	1.08
CV (%)		13.71	6.87	47.42	41.01	62.79	65.12	43.60	35.64	31.03

**Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid ; MYR = Myricetin; GEN = Genestein and AA = Antioxidant activity.

Appendix 6. Means squares of PHT, SG, NL, CC, NPB, RTL, FFF, FPF, and NFS measured under field conditions

Source of variation	df	MEAN SQUARE								
		PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	21.89	2.84	26.47	14.64	0.28	0.65	5.52	3.35	2.12
Genotype	19	65.54**	2.09**	279.69**	45.23**	1.32**	53.25**	27.68**	15.42**	58.12**
Residual	78	4.51	0.67	12.33	3.88	0.15	1.05	0.32	0.58	1.96
Total	59	24.75	1.20	98.91	17.56	0.53	17.85	9.31	5.45	20.05
CV (%)		9.40	10.00	21.61	9.70	17.76	21.60	19.83	9.15	12.25

*Significant at $P < 0.01$; CV = Coefficient of variability; PHT= Plant height; SG = Stem girth; NL= Number of leaves and RTL = Root length
 NFF = Number of days to 1st flowering; FPF = Number of days to 50 % flowering and NFS = Number of days to 1st fruit set.

Appendix 7. Mean squares of FPFS, FSP, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured under field conditions

Source of variation	df	MEAN SQUARE								
		FPFS	FSP	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	2.83	15.32	0.22	1.11	0.02	0.14	0.97	0.76	2854.00
Genotype	19	80.56**	54.07**	86.26**	153.89**	2.67**	1.04**	215.73**	1279.09**	354810.14**
Residual	78	4.48	12.69	1.81	1.08	0.34	0.23	0.70	4.12	1393.00
Total	59	28.93	26.10	28.95	50.29	1.08	0.49	69.96	414.59	115255.24
CV (%)		12.21	7.66	9.14	41.89	15.85	22.20	64.08	35.60	52.05

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; FPFS = Number of days to 50 % fruit set; FSP = Fruit set percentage; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of fruits per truss, NFPT = Number of fruits per truss; FPP = Number of fruits per plant; SFW = Single fruit weight and FWP = Fruit weight per plant

Appendix 8. Mean squares of measured traits YPP, LOC, PTK, FF, FL, FD, DI, FDM and MA measured under field conditions

Source of variation	df	MEAN SQUARE								
		YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	19.72	2.19	0.94	0.31	0.28	0.44	0.00	0.01	0.00
Genotype	19	2463.58**	7.85**	2.41**	0.55**	2.31**	3.08**	0.19**	0.01**	0.02**
Residual	78	9.71	0.84	0.37	0.09	0.10	0.10	0.00	0.00	0.00
Total	59	800.28	3.14	1.05	0.25	0.82	1.07	0.00	0.00	0.01
CV (%)		52.04	50.45	20.87	13.74	18.04	20.71	24.66	15.16	19.47

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA = Malic acid content of fruit

Appendix 9. Mean squares of measured PH, TSS, TA, TSS/TA, B-CARO, LYC, ASC, GA and VA measured under field conditions

		MEAN SQUARE								
Source of variation	df	pH	TSS	TA	TSS/TA	β -CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.00	0.00	0.04	0.86	0.20	0.30	0.02	0.05
Genotype	19	0.05**	4.11**	0.02**	9.05**	89.09**	94.26**	14.46**	0.24**	0.66**
Residual	78	0.00	0.02	0.00	0.14	8.95	0.55	0.21	0.08	0.21
Total	119	0.02	1.34	0.01	3.01	34.49	30.72	4.80	0.13	0.35
CV (%)		2.93	29.29	19.41	17.43	23.34	36.31	23.34	16.17	40.26

*Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or ripeness index; TI = Fruit taste index; β -CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit, ASC = Ascorbic acid content of fruit, GA = Gallic acid and VA = Vanillic acid

Appendix 10. Mean squares of RA, QUE, RUT, CAT, KAE, HES, MYR, GEN, AA measured under field conditions

		MEAN SQUARE								
Source of variation	df	RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.03	8.89	12.02	32.64	4.06	55.43	4.24	8.35	0.05
Genotype	19	0.408**	8733.82**	19677.85**	16178.73**	3125.67**	54449.66**	3093.43**	4307.14**	19.04**
Residual	78	0.13	3.41	6.35	16.14	2.03	18.37	1.26	2.04	0.07
Total	59	0.21	2815.08	6341.44	5221.60	1008.02	17548.35	997.15	1388.64	
CV (%)		35.18	100.03	97.42	77.36	129.65	136.79	94.37	70.76	59.39

**Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid ; MYR = Myricetin; GEN = Genestein and AA= Antioxidant activity

Appendix 11. Mean squares of PHT, SG, NL, CC, NPB, RTL, NFF, FPF AND NFS measured across greenhouse and field locations

Source of variation	df	MEAN SQUARE								
		PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS
Replication	2	16.59	1.27	8.73	7.43	0.29	1.68	4.01	2.76	3.61
Location	1	185450.69**	22.97**	2060.65**	2382.35**	0.80*	97.20**	63.08**	625.63**	126.08**
Genotype	19	495.30**	2.09**	435.70**	62.80**	2.13**	35.18**	26.43**	24.89**	138.22**
Genotype x Location	19	249.14**	0.89*	114.10**	76.06**	0.93**	78.17**	12.36**	18.18**	47.18**
Residual	78	3.06	0.40	6.78	2.70	0.11	0.91	0.29	0.46	1.13
Total	119	1679.56	0.95	109.69	44.09	0.57	19.70	6.98	12.48	31.46
CV (%)		10.21	7.46	21.48	9.23	17.64	11.90	13.11	9.02	12.79

**Significant at $P < 0.05$; **Significant at $P < 0.01$; CV = Coefficient of variability; PHT= Plant height; SG = Stem girth; NL= Number of leaves; RTL = Root length; NFF = Number of days to 1st flowering; FPF = Number of days to 50 % flowering and NFS = Number of days to 1st fruit set.*

Appendix 12: Mean squares of FPFS, FPS, DFM, TPP, FPT, NFPT, FPP, SFW and FWP measured across greenhouse and field locations

		MEAN SQUARE								
Source of variation	df	FPFS	FPS	DFM	TPP	FPT	NFPT	FPP	SFW	FWP
Replication	2	4.23	14.17	0.10	2.21	0.01	0.17	0.85	10.12	6144.00
Location	1	76.80**	94.10*	5.04*	182.43**	7.86**	0.97*	217.16**	3697.22**	88605.00*
Genotype	19	228.13**	300.68**	207.64**	155.47**	4.17**	2.66**	392.84**	3043.86**	709030.00**
Genotype x Location	19	61.43**	222.57**	18.86**	43.47**	1.52**	0.41**	23.12**	303.31**	83061.00**
Residual	78	2.43	33.69	1.06	0.96	0.25	0.16	0.44	7.46	19889.00
Total	119	48.	106.66	36.90	33.96	1.14	0.61	68.54	570.55	140352.88
CV (%)		14.14	12.58	9.25	34.29	12.92	20.02	67.99	35.44	54.26

*Significant at $P < 0.05$; **Significant at $P < 0.01$; ns = Not significant at 0.05; CV = Coefficient of variability; FPFS = Number of days to 50 percent fruit set; DFM = Number of days to fruit maturity; TPP = Number of truss per plant; FPT = Number of flowers per truss; FPP = Number of fruits per plant; Single fruit weight and Fruit weight per plant.

Appendix 13: Mean squares of YPP, LOC, PTK, FF, FL, FD, SI, FDM and MA measured across greenhouse and field locations.

MEAN SQUARE										
Source of variation	df	YPP	LOC	PTK	FF	FL	FD	SI	FDM	MA
Replication	2	25.10	1.10	0.63	1.24	0.19	0.26	0.00	0.01	0.00
Location	1	182.18**	1.67 ^{ns}	3.94**	16.53**	1.36**	0.93**	0.19**	0.20**	0.19**
Genotype	19	5707.92**	16.52**	2.61**	0.99**	3.04**	6.53**	0.22**	0.02**	0.02**
Genotype x Location	19	477.98**	0.62 ^{ns}	1.80**	0.61**	0.73**	0.78**	0.07**	0.02**	0.02**
Residual	78	7.05	0.44	0.24	0.11	0.06	0.08	0.00	0.00	0.00
Total	119	994.24	3.06	0.91	0.49	0.66	1.23	0.05	0.01	0.01
CV (%)		57.30	48.77	14.74	11.52	14.96	20.94	19.39	15.91	16.31

***Significant at $P < 0.01$; ns = Not significant at $P < 0.05$; CV = Coefficient of variability; df = degree of freedom; YPP = Yield per plant; LOC = Number of locules per fruit; PTK = Pericarp thickness; FF = Fruit firmness; FL = Fruit length; FD = Fruit diameter; SI = Fruit shape index; FDM = Fruit dry matter content and MA = Malic acid content of fruit.*

Appendix 14. Mean squares of PH, TSS, TA, TSS/TA, β -CARO, LYC, ASC, GA and VA measured across locations

Source of variation	df	MEAN SQUARE								
		pH	TSS	TA	TSS/TA	β -CARO	LYC	ASC	GA	VA
Replication	2	0.00	0.02	0.00	0.26	0.23	0.03	4.85	0.01	0.03
Location	1	0.04**	5.84**	0.21**	513.72**	360.02**	3.21**	161.58**	0.80**	2.17**
Genotype	19	1.94**	5.31**	0.02**	20.20**	115.51**	118.20**	19.46**	0.14**	0.38**
Genotype x Location	19	1.01**	2.87**	0.02**	11.42**	175.95**	101.74**	19.55**	0.23**	0.34**
Residual	78	0.02	0.03	0.00	0.22	4.51	0.36	3.93	0.04	0.10
Total	119	0.05	1.37	0.01	9.52	52.52	35.38	10.23	0.07	0.20
CV (%)		4.28	22.29	16.88	15.38	20.30	27.94	17.05	9.04	15.83

*Significant at $P < 0.05$; **Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; pH = fruit pH; TSS = Total soluble solid content; TA = Titrable acidity content of fruit; TSS/TA = TSS: TA ratio or flavour indicator; TI = Fruit taste index; β -CARO = Beta carotene content of fruit; LYC = Lycopene content of fruit; ASC = Ascorbic acid content of fruit; GA = Gallic acid and VA = Vanilic acid

Appendix 15. Mean squares of RA, RUT, CAT, KAE, HES, MYR, GEN and AA measured across greenhouse and field locations

Source of variation	df	MEAN SQUARE								
		RA	QUE	RUT	CAT	KAE	HES	MYR	GEN	AA
Replication	2	0.02	0.18	16.24	20.38	29.39	106.60	2.01	7.49	0.10
Location	1	0.23**	3379.34**	6231.98**	3481.66**	710.07**	14247.40**	2998.80**	3326.68**	23.09**
Genotype	19	1.28**	4968.60**	11465.53**	9898.41**	1729.73**	32743.60**	1709.91**	2549.03**	9.96**
Genotype x Location	19	0.20**	6593.99**	1463.10**	11917.09**	2443.45**	40110.40**	2488.61**	3322.81**	12.35**
Residual	78	0.07	7.48	14.95	10.64	34.12	111.00	2.65	5.83	0.05
Total	119	0.12	1879.43	4229.16	3519.72	695.13	11826	697.32	969.43	3.79
CV (%)		21.24	48.57	48.39	40.49	62.13	67.53	43.26	35.05	33.89

*Significant at $P < 0.05$; **Significant at $P < 0.01$; CV = Coefficient of variability; df = degree of freedom; RA = Rosmarinic acid; QUE = Quercetin; RUT = Rutin; CAT= Catechin; KAE = Kaempferol; HES = Hesperetin acid; MYR = Myricetin; GEN = Genestein and AA = Antioxidant activity



