

Genetic Variability Study in Some Quantitative Traits of Tomato (*Solanum Lycopersicum* L.)

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ABSTRACT

Genetic variability study was conducted in some quantitative traits of tomato. The cultivars were evaluated under greenhouse and field conditions at the University of Ghana Forest and Horticultural Crops Research Center (FOHCREC) in Ghana. The experimental layout in each location was Randomized Complete Block Design (RCBD) with three (3) replications. The individual analysis of variance performed for the data gathered revealed a significant ($P<0.01$) variability among the cultivars for most of the traits. Variance components estimated on individual location basis indicated a moderate to high genotypic coefficient of variability (GCV), high broad sense heritability as well as high genetic gain for most of the traits. The present study provides significant information for selecting desirable cross combinations for conventional breeding targeting yield improvement of tomato in Ghana.

Keywords: Coefficient of variability; Greenhouse; Heritability; Genetic gain; Tomato; Variance components

INTRODUCTION

Tomato (*Solanum lycopersicum* L., $2n=24$) is one of the most widely produced, consumed and processed vegetable crops [1-5] largely due to the many important nutritional and health promoting elements present in the fruits [5,6]. The suitability of the crop for production in different cropping systems, seasons and both close and open environments has contributed to its popularity across the globe [7]. In Ghana, tomato is extensively cultivated throughout the year for the fresh consumption of the fruits. Tomato fruits are the commonest solanaceous vegetable in almost all markets across the country. Over the years, open field tomato production systems have been the main system of production practiced in the country. Nonetheless, open environment-derived tomato fruits alone are not able to meet consumer demands for fresh fruits, especially during lean seasons. To ensure year-round tomato production and thus satisfy

the rising consumer and processors' demand for quality tomato fruits, greenhouse production systems have been recommended and currently in use. Tomato production is a major source of income generation to many farmers in the country. Therefore, there is increasing need to develop improved cultivars adapted for production in the local environment. Meanwhile, the success of conventional plant breeding relies very much on knowledge about the extent of genetic variability present in quantitative traits of cultivated genetic resources and the ability to select cultivars more appropriate for better a cross combination required for achieving a desirable genetic gain [8-10]. During genetic variability analysis, genetic component of variance, genetic coefficient of variability (GCV), heritability and genetic gain are estimated and serve as reference and indicators for planning breeding strategies [11-14].

Agronomic traits evaluation is an essential technique frequently used for genetic variability analysis in conventional crop breeding

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programmes. Though the method is simple, fast and cost effective, as quantitative traits, their expressions are associated with the masking effects of several interrelated environmental factors [15,16]. Consequently, a cultivar is likely to perform differently across diverse environments irrespective of the inherent genetic potential. It is therefore highly significant that genetic assessment of a crop is carried out over different locations to facilitate breeding of crops for specific environmental conditions [4,17]. This study was therefore carried out with the intent to evaluate tomato cultivars for genetic variability in some quantitative traits under greenhouse and field conditions. Results of the study provide useful information for selection of desirable cultivars and cross combinations in genetic improvement programmes aimed at optimizing tomato fruit yield.

MATERIALS AND METHODS

A total of 20 tomato cultivars were evaluated for their genetic variability in agronomic traits [17]. The experimental procedure used in this study to raise tomato seedlings to the stage of harvest has been previously reported [17]. In brief, the experiments were arranged in a Randomized Complete Block Design (RCBD) with three replications. The climatic conditions including mean monthly temperature, relative humidity, and rainfall (for field ex-

periment only) prevalent in the two experimental sites were recorded. A composite soil sample taken from 15 locations in the field at 0-20 cm depth was analyzed for physical and chemical properties using standard laboratory procedure. Important agronomic practices including daily watering, fertilizer application, plant protection, weed control, pruning and plant support were followed to raise the crop. Fruits were harvested by hand picking when they had reached their physiological maturity (fully ripe) stage.

Statistical analysis of data

Data collected under the two growing conditions (Tables 1 and 2) were used for individual analysis of variance [17]. GENSTAT statistical software (12th edition) was used for the data analysis. The variance component format was employed in the computation of variances, coefficient of variability, heritability and genetic advance.

Estimation of variance components: The variance component of each trait was estimated separately for the field and greenhouse data gathered as per the methods suggested by [18] (Tables 3 and 4).

Estimation of coefficient of variability: Estimates of coefficient

Table 1. Analysis of variances of 24 quantitative characters

Greenhouse experimental location												
Source	PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS	FPFS	FSP	DFM
R	4.4	0.05	1.17	3.85	0.14	1.09	0.47	0.42	1.52	1.72	6.55	0.47
G	678.90**	0.89**	270.11**	93.63**	1.74**	60.10**	11.10**	27.65**	130.00**	209.0**	469.18**	140.24**
ERR	1.38	0.06	0.58	1.08	0.06	0.82	0.17	0.31	0.36	0.49	56.07	0.33
CV (%)	11.75	7.27	27.26	18.46	24.14	21.01	11.05	13.65	16.7	18.13	21.88	10.3
Field experimental location												
Source	PHT	SG	NL	CC	NPB	RTL	NFF	FPF	NFS	FPFS	FSP	DFM
R	21.89	2.84	26.47	14.64	0.28	0.65	5.52	3.35	2.12	2.83	15.32	0.22
G	65.54**	2.09**	279.69**	45.23**	1.32**	53.25**	27.68**	15.42**	58.12**	80.56**	54.07**	86.26**
ERR	4.51	0.67	12.33	3.88	0.15	1.05	0.32	0.58	1.96	4.48	12.69	1.81
CV (%)	9.4	10	21.61	9.7	17.76	21.6	19.83	9.15	12.25	12.21	7.66	9.14

*Significant P<0.01; CV=Coefficient of variability; 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, FPFS=Number of days to 50 % fruit set; FSP=Fruit set percentage; DFM=Number of days to fruit maturity.

Table 2. Analysis of variance of 24 quantitative characters

Greenhouse experimental location												
Source	TPP	FPT	NEFT	FPP	SFW	FWP	YPP	LOC	PTK	FL	FD	SI
R	1.32	0.02	0.06	0.14	13.18	25359.00	7.66	0.00	0.11	0.04	0.03	0.00
G	45.04**	3.01**	2.04**	200.23**	2068.08**	437280.0**	3722.33**	9.28	2.00**	1.46**	4.23**	0.09**
ERR	0.88	0.18	0.10	0.18	10.99	38271.00	4.65	0.00	0.10	0.02	0.05	0.00
CV (%)	30.46	18.68	21.74	77.52	38.01	62.96	66.97	48.77	17.52	15.01	23.43	18.55
Field experimental location												
Source	TPP	FPT	NEFT	FPP	SFW	FWP	YPP	LOC	PTK	FL	FD	SI
R	1.11	0.02	0.14	0.97	0.76	2854.00	19.72	2.19	0.94	0.28	0.44	0.00

G	153.89**	2.67**	1.04**	215.73**	1279.09**	354810.14**	2463.58**	7.85**	2.41**	2.31**	3.08**	0.19**
ERR	1.08	0.34	0.23	0.70	4.12	1393.00	9.71	0.84	0.37	0.10	0.10	0.00
CV (%)	41.89	15.85	22.20	64.08	35.60	52.05	52.04	50.45	20.87	18.04	20.71	24.66

Table 3. Format for individual analysis of variance

Source of variation	df	MS	EMS	F-test
Replication	r-1	MS _R	$\sigma^2E + g\sigma^2R$	MS _G /MS _E
Genotype	g-1	MS _G	$\sigma^2E + r\sigma^2G$	
Error	(r-1)(g-1)	MS _E	σ^2E	
Total	gr-1			

MS_R=mean square due to replication; MS_G=mean square due to genotypes; MS_E=mean square of error; σ^2G , σ^2R and σ^2E are variances due to genotype, replication and Error variance respectively; r=Number of replications; g=number of genotypes

Table 4. Estimation of variances on individual location basis

Genotypic parameter	Symbol	Determination method
Environmental variance	σ^2E	MS _E
Genotypic variance	σ^2G	(MS _G - MS _E)/r
Phenotypic variance	σ^2P	$\sigma^2p = \sigma^2G + \sigma^2E$

MS_G=mean square due to genotypes; MS_E=mean square of error; σ^2p , σ^2G , and σ^2E are variances due to phenotype, genotype, and Error variance respectively; r=Number of replications; g=number of genotypes.

of variation (PCV) were performed according to the formulae adopted by [11,18] and categorized as high (>20%), moderate (10%–20%) and low (<10%) following the procedure adopted by Reddy et al. [6]. $PCV\% = (\sqrt{\sigma^2p}/GM) \times 100$; $GCV\% = (\sqrt{\sigma^2G}/GM) \times 100$; $ECV\% = (\sqrt{\sigma^2E}/GM) \times 100$, Where GM=grand mean value.

Estimation of heritability and genetic gain (GAM): For heritability in broad sense (h_{2b}), the method adopted from [19] Allard (1960) was used for the computation of all the key traits using the following procedure, Heritability (h_{2b}%)=(σ^2G/σ^2P) × 100.

The expected genetic advance (EGA) for selection intensity (k) at 5% (2.06) and the genetic advance as percentage of mean (GAM) were estimated according to the procedure of [11] adopted from [20]. The expected genetic advance (EGA) for selection intensity (k) at 5% (2.06) and the genetic advance as percentage of mean were estimated according to the procedure adopted by [20] where $EGA = k \times \sigma^2p \times h_{2b}$; Genetic advance as percentage of mean (GAM)=(EGA/GM) × 100, where GM=grand mean.

RESULTS

Analysis of variance and components of variance

The analysis of variance (ANOVA) revealed a significant (P<0.01) difference among the genotypes evaluated (Tables 1 and 2). Components of variance estimated for all the quantitative traits under greenhouse and field conditions are presented in (Tables 5-8). Generally, the estimated phenotypic variance (σ^2P) was significantly higher than the corresponding genotypic variance (σ^2G) for all the characters studied in each of the two conditions. Similarly, the estimated phenotypic coefficient of variation (PCV) was greater than the corresponding genotypic coefficient of variation (GCV) for all the characters. Besides, the ratio of the GCV to PCV was either unity or near unity for almost all the characters.

Estimate of heritability and genetic gain

The estimates of broad sense heritability for six (6) quantitative traits (Table 9) of genotype cultivated under greenhouse and field experimental conditions were high (>60%) except stem diameter

Table 5. Estimate of variance components of six (6) quantitative traits of genotypes evaluated in each of the growth conditions

Character	Greenhouse experimental location							
	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Pant height (cm)	128.24	225.81	227.19	1.38	11.72	11.75	0.92	1
Stem diameter (cm)	7.48	0.28	0.34	0.06	7.03	7.76	3.27	0.91
Number of leaves	35	89.84	90.42	0.58	27.08	27.17	2.18	1
Chlorophyll content (nm)	31.12	30.63	32.37	1.74	17.79	18.28	4.24	0.97

NO. primary branches	3	0.56	0.62	0.06	24.94	26.25	8.16	0.95
Root length per plant (cm)	21.31	19.76	20.58	0.82	20.86	21.29	4.25	0.98
Field experimental location								
Character	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Pant height (cm)	49.85	20.34	24.85	4.51	9.05	10	4.26	0.91
Stem diameter (cm)	8.35	0.47	1.14	0.67	8.24	12.81	9.8	0.64
Number of leaves	43.75	89.12	101.45	12.33	21.58	23.02	8.03	0.94
Chlorophyll content (nm)	40.03	13.78	17.66	3.88	9.27	10.5	4.92	0.88
NO. of primary branches	4	0.39	0.54	0.15	15.61	18.37	9.68	0.85
Root length per plant (cm)	19.5	17.4	18.45	1.05	21.39	22.03	5.25	0.97
MS _G =mean square due to genotypes; MS _E =mean square of error; σ^2P , σ^2G , and σ^2E are variances due to phenotype, genotype, and Error variance respectively; r=Number of replications; g=number of genotypes.								

Table 6. Estimate of variance components of ten (10) quantitative traits of genotypes evaluated under greenhouse growth conditions

Character	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Days to 1st flowering	17	3.64	3.81	0.17	11.23	11.49	2.43	0.98
Days to 50 % flowering	21	9.11	9.42	0.31	14.38	14.62	2.65	0.98
Days to first fruit set	38	43.21	43.57	0.36	17.37	17.37	1.58	1
Days to 50 % fruit set	46	69.5	69.99	0.49	18.12	18.19	1.52	1
Fruit set percentage (%)	57.16	137.7	193.77	56.07	20.53	24.35	13.1	0.84
Days to fruit maturity	65	46.64	46.97	0.33	10.51	10.54	0.88	1
No. of truss per plant	13	14.72	15.6	0.88	29.51	30.38	7.22	0.97
No. of flowers per truss	6	0.94	1.12	0.18	16.19	17.66	7.07	0.92
No. of fruits per truss	4	0.65	0.75	0.1	20.1	21.6	7.91	0.93
No. of fruits per plant	11	66.68	66.86	0.18	74.24	74.34	3.86	1

Table 7. Estimate of variance components of ten (10) quantitative traits of genotypes evaluated under field growth conditions

Character	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Days to 1st flowering	16	9.12	9.44	0.32	18.87	19.2	3.54	0.98
Days to 50 % flowering	25	4.95	5.53	0.58	8.9	9.4	3.05	0.95
Days to first fruit set	37	18.72	20.68	1.96	11.69	12.29	3.78	0.95
Days to 50 % fruit set	46	25.36	29.84	4.48	10.95	11.88	4.6	0.92
Fruit set percentage (%)	55.39	13.79	26.48	12.69	6.71	9.29	6.43	0.72
Days to fruit maturity	66	28.15	29.96	1.81	8.04	8.29	2.04	0.97
No. of truss per plant	16	50.94	52.02	1.08	44.61	45.08	6.5	0.99
No. of flowers per truss	7	0.78	1.12	0.34	12.59	15.1	8.33	0.83

No. of fruits per truss	3	0.27	0.5	0.23	17.32	23.57	15.99	0.73
No. of fruits per plant	13	71.68	72.38	0.7	65.12	65.44	6.44	1

GM=Grand mean, σ^2G =Genotypic variance, σ^2P =phenotypic variance, σ^2E =Environmental variance, GCV=Genotypic coefficient of variability, PCV=Phenotypic coefficient of variability, ECV=Environmental coefficient of variability.

Table 8. Estimate of variance components for tomato fruit traits

Greenhouse experimental location								
Character	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Single fruit weight (g)	68.9	685.7	696.69	10.99	38.01	38.31	4.81	0.99
Total fruit weight per plant (g)	606.4	133003	171274	38271	60.14	68.25	32.26	0.88
Fruit yield per plant (t/ha)	52.6	1239.23	1243.87	4.65	66.93	67.05	4.1	1
No. of locules per fruit	4	3.09	3.09	0	43.97	43.97	0	1.00
Fruit length (cm)	4.65	0.48	0.5	0.02	14.9	15.2	3.04	0.98
Fruit diameter (cm)	5.07	1.39	1.44	0.05	23.29	23.7	4.41	0.98
Fruit shape index	0.95	0.03	0.03	0	17.78	18.99	6.64	0.94
Pericarp thickness (mm)	4.66	0.63	0.73	0.1	17.09	18.39	6.79	0.93
Root length per plant (cm)	21.31	19.76	20.58	0.82	20.86	21.29	4.25	0.98
Root length per plant (cm)	21.31	19.76	20.58	0.82	20.86	21.29	4.25	0.98
Field experimental location								
Character	GM	σ^2G	σ^2P	σ^2E	GCV	PCV	ECV	GCV/PCV
Single fruit weight (g)	57.82	424.99	429.11	4.12	35.65	35.83	3.51	0.99
Total fruit weight per plant (g)	660.7	117805.71	119198.71	1393	51.95	52.26	5.65	0.99
Fruit yield per plant (t/ha)	55.1	817.96	827.67	9.71	51.91	52.21	5.66	0.99
No. of locules per fruit	4	2.34	3.18	0.84	38.22	44.56	22.91	0.86
Fruit length (cm)	4.86	0.74	0.84	0.1	17.66	18.82	6.51	0.94
Fruit diameter (cm)	4.89	0.99	1.09	0.1	20.38	21.38	6.47	0.95
Fruit shape index	1.03	0.06	0.07	0.004	24.17	24.94	6.14	0.97
Pericarp thickness (mm)	4.29	0.68	1.05	0.37	19.22	23.89	14.18	0.8
Root length per plant (cm)	19.5	17.4	18.45	1.05	21.39	22.03	5.25	0.97
Root length per plant (cm)	19.5	17.4	18.45	1.05	21.39	22.03	5.25	0.97

GM=Grand mean, σ^2G =Genotypic variance, σ^2P =phenotypic variance, σ^2E =Environmental variance, GCV=Genotypic coefficient of variability, PCV=Phenotypic coefficient of variability, ECV=Environmental coefficient of variability.

which recorded moderate (30-60%) value under field conditions. Generally, broad sense heritability estimates for six (6) of the vegetative traits were comparatively higher under greenhouse conditions than estimates recorded under field condition. The estimates of heritability of ten (10) additional traits most of which

were reproductive related, and yield traits (Table 10) revealed a higher percentage (>60%) for the genotypes cultivated in both field and greenhouse environments. However, fruit set percentage and number of fruits per truss under field conditions were moderate (30-60%).

Table 9. Estimate of heritability and genetic gain six quantitative traits of tomato evaluated in each growth

Greenhouse experimental location			
Character	H ² b (%)	EGA	GAM
Pant height (cm)	99	30.86	24.07
Stem diameter (cm)	82	0.98	13.13
Number of leaves	99	19.46	55.61
Chlorophyll content (nm)	95	11.25	35.64
Number of primary branches	90	1.47	48.84
Root length per plant (cm)	96	8.97	42.11
Field experimental location			
Character	H ² b (%)	EGA	GAM
Pant height (cm)	82	8.41	16.86
Stem diameter (cm)	41	0.91	10.92
Number of leaves	88	18.23	41.66
Chlorophyll content (nm)	78	6.76	16.88
Number of primary branches	72	1.09	27.33
Root length per plant(cm)	94	8.34	42.79

H²b=Broad sense heritability, EGA=Expected genetic advance and GAM=Genetic advance as percentage of mean.

Table 10. Estimate of heritability and genetic gain six quantitative traits of tomato evaluated in each growth condition

Greenhouse experimental location			
Character	H ² b (%)	EGA	GAM
No. of days to 1st flowering	96	3.84	22.61
No. of days to 50 % flowering	97	6.12	29.12
No. of days to first fruit set	99	13.49	35.49
No. of days to 50 % fruit set	99	17.11	37.2
Fruit set percentage	71	20.38	35.65
No. of days to fruit maturity	99	14.02	21.57
No. of truss per plant	94	7.68	59.06
No. of flowers per truss	84	1.83	30.56
No. of fruits per truss	87	1.54	38.54
No. of fruits per plant	100	16.8	152.72
Single fruit weight (g)	98	53.52	77.67
Total fruit weight per plant (g)	78	662.04	109.18
Fruit yield per plant (t/ha)	99	71.93	136.75
Field experimental location			
Character	H ² b (%)	EGA	GAM
No. of days to 1st flowering	97	6.11	38.22

No. of days to 50 % flowering	90	4.33	17.34
No. of days to first fruit set	91	8.48	22.92
No. of days to 50 % fruit set	85	9.56	20.79
Fruit set percentage	52	5.52	9.97
No. of days to fruit maturity	94	10.59	16.05
No. of truss per plant	98	14.55	90.93
No. of flowers per truss	70	1.51	21.63
No. of fruits per truss	54	0.79	26.22
No. of fruits per plant	99	17.36	133.51
Single fruit weight (g)	99	42.26	73.09
Total fruit weight per plant (g)	99	702.91	106.39
Fruit yield per plant (t/ha)	99	58.57	106.3

H²b=Broad sense heritability, EGA=Expected genetic advance and GAM=Genetic advance as percentage of mean.

DISCUSSION

Genetic Variance, heritability and genetic gain

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 a substantial amount of variability in the 20 tomato genotypes. Similar findings have been reported earlier [21,22]. Estimate of genotypic coefficient of variation (GCV) gives a true suggestion of the magnitude of genetic variation in a study population. In this study, moderate (10%–20%) to high (>20%) estimate of GCV and PCV for most of the traits under both greenhouse and field conditions indicated the presence of appreciable amount of genotypic and phenotypic variability in the studied genetic materials. The higher estimate of PCV than the corresponding GCV indicated a relative effect of environment on the expression of the traits. However, the narrow difference between PCV and GCV and the closeness to unity in values observed in GCV to PCV ratio suggested that genetic control of the expression of the traits was predominant. This result implies that simple phenotypic selection could be made among the genotypes. Also, selection could be effective for most traits at the early stage of a breeding program since response to selection is directly proportional to variability present in the experimental materials [23].

Generally, the magnitude of variability observed among the genotypes for most traits was higher under greenhouse conditions than the corresponding genotypes evaluated open field. Our results in the present study were in agreement with findings by Nwosu [24] who recorded a narrow difference between PCV and GCV for most of the traits that were studied. A related finding reported by Reddy et al. [6] revealed an estimate of moderate to high PCV and GCV as well as smaller differences between PCV and GCV for most of the traits studied. Similar results have also been reported in other previous studies [25-28].

The estimate of GCV along with heritability provides a true indication of the magnitude of heritable component of variation [11,12]. Estimate of heritability enables a breeder to determine the extent to which genetic variability contributes to phenotypic variability of a trait [11,12]. In the present study, broad sense heritability estimated for all traits in each experimental condition were very high with the exception of stem diameter, fruit

set percentage and number of fruits per truss which recorded moderate values. High GCV as well as high heritability estimates 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 observed for most of the traits evaluated in each of the two locations. These findings suggest that those traits could easily be passed on to the next generation [11,12,28]. High estimate of heritability may be the result of the diverse nature of the genotypes included in the study [28]. 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%–100%) along with high genetic advance was recorded for most of traits of tomato varieties studied by Shankar et al. [27]. In the present study, high heritability and moderate genetic gain was recorded for stem diameter (greenhouse conditions) as well as number of leaves, chlorophyll content and number of days to 50% flowering under field conditions. High and moderate heritability estimate along with low genetic gain recorded for fruit set percentage under 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 [6]. Results of the present study is in accordance with previous findings [28-30] where very high ($P > 80\%$) estimates of heritability along with high genetic gain for most of the related traits studied was observed. A study by Vinod et al. [31] revealed a very high estimate of heritability for all traits ranging from 80%–99%. Several of such findings have been reported in tomato genetic variability and heritability studies [6,32]. Results of the present study revealed the existence of useful genetic variability among the genotypes.

CONCLUSION

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.

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CONFLICT OF INTEREST

There is no conflict of interest.

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