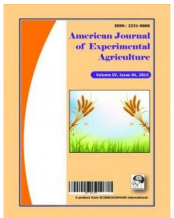

*American Journal of Experimental Agriculture*
*13(6): 1-8, 2016, Article no.AJEA.28424*
*ISSN: 2231-0606*

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# Genetic Studies of Agronomic and Physiological Traits in Tomato (*Lycopersicon lycopersicum* Mill.) Under Heat Stress Conditions

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***Authors' contributions***

*This work was carried out in collaboration between all authors. Author HSH designed the study, wrote the protocol and wrote the first draft of the manuscript. Authors SGA, MYY, ISU and SOA reviewed the experimental design and all drafts of the manuscript. Authors HSH and AU managed the analyses of the study. Author BAI identified the plants. Author HSH performed the statistical analysis. All authors read and approved the final manuscript.*

***Article Information***

DOI: 10.9734/AJEA/2016/28424
*Editor(s):*
(1) Dalong Guo, College of Forestry, Henan University of Science and Technology, Luoyang, 471003, Henan, People's Republic of China.
*Reviewers:*
(1) Funda Eryilmaz Acikgoz, Namik Kemal University, Turkey.
(2) Kojo Ahiakpa, College of Agriculture and Sustainable Development, Cuttington University, Liberia.
(3) Sahib Gul Afridi, Abdul Wali Khan University, Mardan, Pakistan.
Complete Peer review History: http://www.sciencedomain.org/review-history/16121

***Original Research Article***

***Received 19th July 2016***
***Accepted 24th August 2016***
***Published 9th September 2016***

## ABSTRACT

Field experiments were conducted at National Horticultural Research Institute, Bagauda (11°33´N; 8°23´E) in the Sudan Savannah and Institute for Agricultural Research, Samaru (11°11´N; 07°38'E) in the Northern Guinea Savanna ecological zones of Nigeria between July-October, 2014 rainy season to estimate Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, Genetic Advance (GA) and Genetic Advance as percent of Mean (GAM) for agronomic and physiological traits of tomato under heat stress conditions. The study comprised 15 hybrids, their parental lines along with four checks were laid out in partially balanced lattice design with three replications. Analysis of variance revealed significant variation among the genotypes for

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all traits except fruit diameter, indicating sufficient variability existed among the genotypes. The estimates of PCV were higher than GCV. High GCV and PCV values were recorded for number of clusters per plant, and number of fruits per plant suggesting high genetic variability for these traits. Broad-sense heritability varied from 5.20% to 98.92%, while the estimates of GA showed a wide range from 0.09 to 161.13. High estimates of Broad-sense heritability coupled with high GAM were observed for the number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit shape index and yield per plant indicating additive gene effects for the hereditary pattern of roles. Based on the results of the study, simple selection based on phenotypic performance of these traits would provide better response and also considered for higher fruit yield under heat stress conditions.

*Keywords: Tomato; variability; heritability; genetic advance; heat stress.*

## 1. INTRODUCTION

Tomato (*Lycopersicon lycopersicum* Mill.) belongs to the family Solanaceae, genus Lycopersicon, subfamily Solanoideae and tribe Solaneae where pepper, potato, tobacco and eggplant belong [1]. Tomato is very rich in vitamins, minerals (iron and phosphorus), essential amino acids, sugars and dietary fibers. It contains a high level of lycopene, an antioxidant that reduces the risks related to several cancers and neurodegenerative diseases [2]. The optimal temperatures required for tomato cultivation are between 25-30℃ during photoperiod and 20℃ during the dark period [3], and an increase of 2-4℃ over optimal temperature adversely affects gamete development and inhibits the ability of pollinated flowers to develop into fruits and thus reduced fruit yield [4-6]. Heat stress becomes a major limiting factor for field production of tomatoes [7]. High temperature during the growing season is detrimental to growth and reproductive development which reduces fruit size, yield and fruit quality [8-11]. In Nigeria, the major growing area of tomato lies between latitudes 7.5° 11´ and 13.0° N and within a temperature range of 22-30℃. Tomato is usually grown during the rainy season in Nigeria and high temperature during the rainy season, causing a significant reduction in fruit size, increment in flower abortion, decrease in fruit set which reduced fruit yield and shortage of supply which results in high cost. Thus, there is need to develop high yielding variety with acceptable fruit setting ability under high temperature through proper breeding program to fulfill the demand of tomato production during rainy season. It is vital to have knowledge of the nature and magnitude of genetic variability created through hybridization for various traits under heat stress conditions, since the nature and magnitude of variability are pre-requisite for any crop improvement which would assist breeders in planning a successful breeding program. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful for finding the amount of variability present among the genotypes. Heritability is the proportion of genetic variance to the total variance which help in determining the influence of location in the expression of the trait and the extent to which improvement is feasible after selection [12]. However, heritability alone is not adequate to make an efficient selection in segregating generation. Therefore, high heritability accompanied by Genetic Advance (GA) is appropriate factor for selection of a trait and serves as an indication of additive gene action for such trait. [13] recorded higher PCV values than GCV for all traits under rainy season. High PCV and GCV were observed for number of fruits per plant, number of flowers per plant, average fruit weight, number of clusters per plant and fruit yield per plant, while high broad-sense heritability and genetic advance as percent over mean were recorded for number of fruit per plant, number of flowers per plant, average fruit weight and fruit set percentage [14]. [15,16] reported higher PCV values than GCV for days to 50% flowering, plant height, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit weight, fruit length, fruit diameter, fruit yield per plant and high heritability was also recorded for the traits. The present investigation was conducted to study nature and magnitude of variability, heritability and genetic advance of agronomic and physiological traits under heat stress conditions.

## 2. MATERIALS AND METHODS

The experiment consists of two heat tolerant (Icrixina and Rio Grande) and four heat susceptible tomato (Tima, Tropimech, Petomech and Roma Savana) genotypes which were crossed using half diallel mating design in the screen house. The 15 hybrids, 6 parents and 4 checks (Roma VF, UC82 B, Thorgal $F_1$ and Jaguar $F_1$) were evaluated at National Horticultural Research Institute, Bagauda Research Farm (11°33´N; 8°23´E) in the Sudan Savannah and Institute for Agricultural Research Farm, Samaru (11°11´N; 07°38'E) in the Northern Guinea Savanna ecological zones of Nigeria in a 5X5 partially balanced lattice design with three replications; between July to October, 2014 rainy season to synchronize flowering stage with heat period (September and October) as shown in Table 1. The plot size was 2X2 m and 1 m alleys. Seedlings were raised in nursery17$^{th}$ July, 2014 and transplanted to the field about 30 days after sowing on three rows at inter-row spacing of 60cm and intra-row spacing of 50 cm on 17$^{th}$ August, 2014. Fertilizer (N.P.K 15:15:15) was split applied at the rate of 45kgN, 45 kg $P_2O_5$ and 45 kg$K_2O$/ha and Urea (46%) at the rate of 64.4 kgN/ha at two and five weeks after transplanting, respectively. All agronomic practices were kept uniform in all plots. Data were randomly taken on five centered plants for observations and measurements leaving the plants on either end of the plot to avoid the border effect. Data were recorded for agronomic traits (plant height, days to 50% flowering, number of branches per plant, number of clusters per plant, number of flowers per cluster, number of flowers per plant, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length, fruit diameter, fruit shape index, fruit yield per plant and percentage fruit set) and physiological traits (leaf chlorophyll content and canopy temperature depression). The leaf chlorophyll content and canopy temperature depression were measured using SPAD chlorophyll meter (SPAD 502plus. Konica Minolta, Tokyo, Japan) and handheld infrared Thermometer (Spectrum Technologies, Inc. U.S.A), respectively. Canopy temperature depression was calculated using equation 1. Analysis of variance was computed using Statistical Analysis System [17]. Genotypic variance, genotypeXlocation variance, phenotypic variance and environmental variance were estimated from Table 2 using equation 2, 3, 4 and 5, respectively. The estimates of the Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV) and classified according to [18] as: low = 0-10%, moderate = 10-20% and high = 20% and above. Heritability were calculated according to [19] and categorized according to [12] as follows: low = 0-30%, moderate = 30-60% and high = 60% and above, while Genetic Advance (GA) and Genetic Advance as percent of Mean (GAM) were computed according to formula of [20].

$$\text{Canopy temperature depression} = T_a - T_c \quad (1)$$

Where:

$T_a$ = Air temperature
$T_c$ = canopy temperature

$$\sigma_g^2 = \frac{M_g - M_{gl}}{rl} \quad (2)$$

$$\sigma_{gl}^2 = \frac{(M_{gl} - M_e)/r}{l} \quad (3)$$

$$\sigma_{ph}^2 = \sigma_g^2 + \sigma_{gl}^2 + \sigma_e^2 \quad (4)$$

$$\sigma_e^2 = \frac{M_e}{rl} \quad (5)$$

Where: $\sigma_g^2$ = Genotypic variance, $\sigma_{ph}^2$ = Phenotypic variance, $\sigma_{gl}^2$ = Genotype × location variance, $\sigma_e^2$ = environmental variance, $r$ = Replications, $l$ = Locations, $M_g$ = Genotype mean square, $M_{gl}$ = Genotype × location mean square and $M_e$ = Error mean square.

**Table 1. Average temperature and rainfall for the experimental sites**

| Month | Bagauda | | | Samaru | | |
|---|---|---|---|---|---|---|
| | Maximum temperature (℃) | Minimum temperature (℃) | Rainfall (mm) | Maximum temperature (℃) | Minimum temperature (℃) | Rainfall (mm) |
| July | 32.2 | 22.6 | 24.06 | 30.9 | 22.38 | 11.71 |
| August | 31 | 24.13 | 30.86 | 29.83 | 22.43 | 26.74 |
| September | 32.67 | 27.11 | 14.07 | 31.17 | 21.72 | 11.04 |
| October | 32.92 | 24 | 45.2 | 33.73 | 21.23 | 2.33 |

*Source: National Horticultural Research Institute, Bagauda and Institute for Agricultural Research, Samaru, meteorological data units*

## 3. RESULT AND DISCUSSION

### 3.1 Variability

Analysis of variance revealed highly significant ($P$ = .01) differences for all traits except fruit diameter and significant ($P$ =.05) for canopy temperature depression (Table 2), indicating presence of sufficient and significant variability existing among genotypes selected for the study which can be exploited through selection. Similar results were reported by [14,21]. [15] also observed highly significant variation for plant height, fruits per cluster, fruit length, fruit diameter, number of fruits per plant and fruit yield per plant. The genotype × location mean squares were highly significant ($P$ = .01) for number of branches per plant, number of flowers per plant, percentage fruit set and leaf chlorophyll content and significant ($P$ = .05) for plant height and number of clusters per plant; while days to 50% flowering, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length, fruit diameter, fruit shape index, fruit yield per plant and canopy temperature depression recorded non-significant difference among genotypes. The significant genotype × location suggested that the locational conditions have influence on the performance of the genotypes regards to the traits, hence there is need to test the genotypes over different locations across years to identify their suitability for utilization as suitable germplasm for tomato improvement under heat stress.

Genotypic variance was higher than the environmental variance for all traits (Table 3) except fruit diameter, leaf chlorophyll content and canopy temperature depression, indicating more contribution of genetic variance to the total variation and therefore the characters could be considered and exploited for selection in earlier generations. GCV and PCV are important in studying of the nature and magnitude of variability of different traits, because it measures the range of variability which is prerequisite for any crop improvement. The PCV values were higher than the GCV, thereby suggesting the strong influence of the environmental factors on the expression of the characters (Table 3). The results confirmed the findings of [14,15,22,13, 16]. The difference between GCV and PCV values were minimum for the number of flowers per cluster, number of fruits per cluster and fruit diameter, indicating there is least effect of environment on the expression of the traits, hence selection could be applied to improve these traits in an early segregating population. Similar results were also reported by [23] for number of flowers per cluster and number of fruits per cluster and [14] for fruit diameter. The results (Table 3) showed that GCV value was high for number of fruits per plant (27.46) and number of clusters per plant (20.22) indicating that genetic variance contributing more to total variation, hence selection could be carried out in earlier generations. Moderate GCV values were observed for number of branches per plant (10.94), number of flowers per cluster (12.05), number of fruits per cluster (11.73), average fruit weight (19.44), fruit length (12.44), fruit shape index (13.15), fruit yield per plant (19.32) and percentage fruit set (16.85); Whereas, lowest GCV values were recorded for plant height (5.51), days to 50% flowering (2.35), fruit diameter (3.13), leaf chlorophyll content (4.92) and canopy temperature depression (2.18). The results correspond to findings [24,15,16]. The highest PCV values were observed for number of fruits per plant (30.31) followed by average fruit weight (25.52), number of flowers per plant (24.46), number of clusters per plant (22.96), fruit yield per plant (22.40), percentage fruit set (22.52) and number of branches per plant (21.25). High PCV values were recorded for these traits shows that the traits are under influence of environmental effects than of genetic effects. Number of flowers per cluster (12.32), number of fruits per cluster (11.88), fruit length (13.34) and fruit shape index (14.26) also exhibited Moderate PCV values, while the lowest PCV values were recorded for plant height (8.51), days to 50% flowering (3.07), fruit diameter (3.83), leaf chlorophyll content (6.76) and canopy temperature depression (9.55). The moderate GCV and PCV values observed for the traits indicated the presence of moderate variability among the genotypes for these traits suggesting improvement of base population through intercrossing in $F_2$ followed by recurrent selection. GCV and PCV values were higher for the number of clusters per plant and number of fruits per plant, suggesting the presence of high genetic variability of the traits. The results were in accordance with findings of [25,13].

### 3.2 Heritability and Genetic Advance

Highest estimates of broad sense heritability (Table 3) was noticed for days to 50% flowering (68.00), number of clusters per plant (77.51), number of flowers per cluster (95.68), number of fruits per cluster (98.92), number of fruit per plant (82.02), fruit length (86.86),

**Table 2. Mean squares for sixteen agronomic and Physiological characters combined across locations**

| Source of variation | df | PHT | DFPFL | NBPP | NCPP | NFLPC | NFLPP | NFRPC | NFRPP |
|---|---|---|---|---|---|---|---|---|---|
| Location | 1 | 6084.75 | 74.91 | 7408.92 | 1912.66 | 0.52 | 182490.07 | 0.02 | 8198.32 |
| Block(replication × location) | 24 | 73.19 | 12.56 | 49.26 | 14.56 | 0.53 | 232.19 | 0.73 | 52.44 |
| Replication(location) | 4 | 128.97 | 10.17 | 39.59 | 14.23 | 0.78 | 796.08 | 0.28 | 91.45 |
| Genotype | 24 | 138.51** | 27.53** | 74.18** | 57.40** | 3.01** | 1535.64** | 1.86** | 200.66** |
| Genotype × location | 24 | 80.47* | 8.81 | 54.51** | 12.91* | 0.13 | 639.14** | 0.02 | 36.01 |
| Error | 72 | 42.13 | 5.53 | 11.65 | 6.85 | 1.09 | 205.10 | 0.31 | 33.15 |

*df: Degree of freedom, PHT: Plant height, DFPFL: Days to 50% flowering, NBPP: Number of branches per plant, NCPP: Number of clusters per plant, NFLPC: Number of flowers per cluster, NFLPP: Number of flowers per plant, NFRPC: Number of fruits per cluster and NFRPP: Number of fruits per plant. ** and * are significantly different at 1% and 5% levels of probability, respectively.*

**Table 2 continued**

| Source of variation | df | AFW | FRL | FRD | FRSI | FRYPP | PFRS | LCC | CTD |
|---|---|---|---|---|---|---|---|---|---|
| Location | 1 | 29.06 | 0.57 | 0.69 | 0.01 | 6507841.92 | 1082.13 | 3080.85 | 338.19 |
| Block(replication × location) | 24 | 198.45 | 0.30 | 0.13 | 0.04 | 23057.13 | 38.21 | 70.80 | 2.59 |
| Replication(location) | 4 | 255.96 | 0.40 | 1.23 | 0.16 | 1921.78 | 56.10 | 151.88 | 10.65 |
| Genotype | 24 | 325.04** | 2.36** | 0.12 | 0.20** | 66310.62** | 491.53** | 71.41** | 4.23* |
| Genotype × location | 24 | 136.43 | 0.31 | 0.04 | 0.03 | 16974.22 | 213.03** | 109.22** | 4.01 |
| Error | 72 | 99.24 | 0.25 | 0.12 | 0.03 | 14090.34 | 69.53 | 42.67 | 2.47 |

*df: Degree of freedom, AFW: Average fruit weight, FRL: Fruit length, FRD: Fruit Diameter, FRSI: Fruit shape index, FRYPP: Fruit yield per plant, PFRS: Percentage fruit set, LCC: Leaf chlorophyll content and CTD: Canopy temperature depression. ** and * are significantly different at 1% and 5% levels of probability, respectively.*

**Table 3. Genetic parameters for sixteen agronomic and Physiological characters combined across locations**

| Parameter | PHT (cm) | DFPFL | NBPP | NCPP | NFLPC | NFLPP | NFRPC | NFRPP |
|---|---|---|---|---|---|---|---|---|
| Mean | 56.44 | 69.76 | 16.55 | 13.47 | 5.75 | 65.41 | 4.72 | 19.08 |
| $\sigma_e^2$ | 7.02 | 0.92 | 1.94 | 1.14 | 0.18 | 34.18 | 0.05 | 5.53 |
| $\sigma_g^2$ | 9.67 | 3.12 | 3.28 | 7.42 | 0.48 | 149.42 | 0.31 | 27.44 |
| $\sigma_{gl}^2$ | 6.39 | 0.55 | 7.14 | 1.01 | -0.16 | 72.34 | -0.05 | 0.48 |
| $\sigma_{ph}^2$ | 23.09 | 4.59 | 12.36 | 9.57 | 0.50 | 255.94 | 0.31 | 33.44 |
| GCV (%) | 5.51 | 2.53 | 10.94 | 20.22 | 12.05 | 18.69 | 11.73 | 27.46 |
| PCV (%) | 8.51 | 3.07 | 21.25 | 22.96 | 12.32 | 24.46 | 11.80 | 30.31 |
| $h_b^2$ (%) | 41.90 | 68.00 | 26.52 | 77.51 | 95.68 | 58.38 | 98.92 | 82.05 |
| GA | 4.15 | 3.00 | 1.92 | 4.94 | 1.40 | 19.24 | 1.13 | 9.78 |
| GAM (%) | 7.35 | 4.30 | 11.61 | 36.66 | 24.28 | 29.41 | 24.04 | 51.23 |

*PHT: Plant height, DFPFL: Days to 50% flowering, NBPP: Number of branches per plant, NCPP: Number of clusters per plant, NFLPC: Number of flowers per cluster, NFLPP: Number of flowers per plant, NFRPC: Number of fruits per cluster and NFRPP: Number of fruits per plant*

**Table 3 continued**

| Parameter | AFW (g) | FRL (cm) | FRD (cm) | FRSI | FRYPP (g) | PFRS (%) | LCC | CTD (℃) |
|---|---|---|---|---|---|---|---|---|
| Mean | 28.84 | 4.70 | 3.69 | 1.28 | 469.29 | 40.43 | 51.02 | 8.79 |
| $\sigma_e^2$ | 16.54 | 0.04 | 0.02 | 0.01 | 2348.39 | 11.59 | 7.11 | 0.41 |
| $\sigma_g^2$ | 31.44 | 0.34 | 0.01 | 0.03 | 8222.73 | 46.42 | -6.30 | 0.04 |
| $\sigma_{gl}^2$ | 6.20 | 0.01 | -0.01 | 0.00 | 480.65 | 23.92 | 11.09 | 0.26 |
| $\sigma_{ph}^2$ | 54.17 | 0.39 | 0.02 | 0.03 | 11051.77 | 81.92 | 11.90 | 0.71 |
| GCV (%) | 19.44 | 12.44 | 3.13 | 13.15 | 19.32 | 16.85 | 4.92 | 2.18 |
| PCV (%) | 25.52 | 13.34 | 3.83 | 14.26 | 22.40 | 22.39 | 6.76 | 9.55 |
| $h_b^2$ (%) | 58.03 | 86.86 | 66.67 | 85.00 | 74.40 | 56.66 | 52.95 | 5.20 |
| GA | 8.80 | 1.12 | 0.19 | 0.32 | 161.13 | 10.56 | 3.76 | 0.09 |
| GAM (%) | 30.51 | 23.88 | 5.26 | 24.98 | 34.33 | 26.13 | 7.38 | 1.02 |

*AFW: Average fruit weight, FRL: Fruit length, FRD: Fruit Diameter, FRSI: Fruit shape index, FRYPP: Fruit yield per plant, PFRS: Percentage fruit set, LCC: Leaf chlorophyll content and CTD: Canopy temperature depression.*

fruit diameter (66.67), fruit shape index (85.00), fruit yield per plant (74.40) and moderate for plant height (41.09), number of branches per plant (26.52), number of flowers per plant (58.38), percentage fruit set (56.66) and leaf chlorophyll content (52.95). Whereas, the lowest broad-sense heritability was recorded by canopy temperature depression (5.20). The high broad sense heritability values indicated that the location has less influence on the expression of the traits, hence the traits were heritable, which can be transferred to the progeny and improved by simple selection under heat stress conditions. Moderate heritability values show both additive and non-additive gene actions are important in influencing the expression of these traits under high temperature across locations. Low broad-sense heritability might be due to confounded effects of other stresses such as drought and mineral imbalance; therefore selection should be delayed to later segregating generations. [16] reported high broad sense heritability for days to 50% flowering, flowers per cluster, fruits per cluster, number of fruits per plant, fruit length, fruit diameter, fruit yield and [26] for number of fruits per plant. Nevertheless, high heritability alone is not enough to demonstrate the response to selection. Hence, high heritability coupled with high genetic advance as percent of mean are important parameters in response to selection of a trait. Estimates of genetic advance showed a wide range from 0.09 for canopy temperature depression to 161.13 in fruit yield per plant. High broad-sense heritability and genetic advance as percent of mean were recorded for number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit shape index and fruit yield per plant indicating additive gene effects for the inheritance of the traits. The traits can be considered and selected for further improvement through simple breeding methods like pure line, single seed descent and mass selection for higher fruit yield under high temperature conditions. [23] observed high heritability and GAM for number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit yield per plant and [15] for fruit diameter. High estimates of heritability with low GAM observed for days to 50% flowering and fruit diameter attributed to non-additive gene effects in controlling their inheritance.

## 4. CONCLUSION

The results show that there is adequate and significant variability existing among the genotypes which could be harnessed through selection to improve traits under heat stress. High heritability and genetic advance as percent of mean were observed for most of the traits indicating existence of additive gene effects in the expression of the traits. Therefore, pure line, single seed decent and mass selection could be exploited to improve the traits under heat stress conditions.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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*Peer-review history:*
*The peer review history for this paper can be accessed here:*
*http://sciencedomain.org/review-history/16121*