Study Of Heritability And Genetic Variability Among Different Plant And Fruit Characters Of Tomato (Solanum Lycopersicum L.)

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Abstract: Heritability, genetic advance, genetic advanced as percentage over mean and genetic variability among different plant and fruit characters of thirty tomato genotypes were studied at Hudeiba Research Station (ARC) during the winter of 2007- 08. Analysis of variance showed significant variation among the genotypes for all tested characters. Fruit weight showed the highest genotypic and phenotypic variance (1642.9 and 1779.1) whereas fruit yield per plant showed the lowest ones (0.17 and 0.39). High genotypic variance was observed for most of the characters indicating more contribution of genetic component for the total variation. Genotypic coefficients of variations (GCV) and phenotypic coefficient of variation (PCV) were highest for fruit weight (0.4885 and 0.4905) whereas the lowest ones were for days to 50% flowering (0.0552 and 0.0665). Higher GCV and PVC were recorded for most of the characters indicating higher magnitude of variability for these characters. The highest heritability was recorded on plant height (97%), while the lowest was for fruit yield per plant (43%). High heritability (broad senses) estimates were observed for all the tested characters indicating that these characters are controlled by additive genes action which is very useful in selection.

Key words: Tomato, genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance

1 INTRODUCTION

The tomato (Solanum lycopersicum L.) is one of the most popular and widely consumed vegetable crops throughout the world, both for the fresh fruit market and the processed food industry. Its adaptation to fit many diverse uses and environments is a reflection of the great wealth of genetic variability existent in the genus Solanum, which can be exploited in applied breeding programs [1]. Systematic study and evaluation of tomato germplasm is of great importance for current and future agronomic and genetic improvement of the crop. Furthermore, if an improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and the breeding value of the available germplasm [2]. The genetic variance of any quantitative trait is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction). Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. So Proper evaluation of genetic resources is essential to understand and estimate the genetic variability and heritability. Studies on genetic parameters and character associations provide information about the expected response of various characters to selection and it will help in developing optimum breeding procedure. Hence the present study was conducted to study heritability and the genetic variability among different tomato genotypes.

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2 MATERIALS AND METHODS

The experiment was conducted in the Hudeiba Research Station, Agricultural Research Corporation (ARC), Sudan. Thirty tomato genotypes were evaluated for different plant and fruit characters during winters of 2007 -08. The genotypes were grown in a randomized complete block design (RCB) with three replications. Plot size was 8 meters x 1.8 meters with spacing of 0.5 meter between plants. All the technical packages recommended by ARC for tomato cultivation were followed. Ten plants were tagged for recording both quantitative and qualitative characters, which included plant height (cm), number of primary branches per plant, days to 50% flowering, number of flowers per inflorescence, number of fruits per cluster, fruit yield per plant (kg) and fruit weight (g). Analysis of variance, genotypic variance (σ^2g), phenotypic variances (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability in broad sense (h^2 bs), genetic advance (GA) and genetic advance as percentage over mean were analyzed following the formula illustrated by Singh and Chaudhary [3].

3 RESULTS AND DISCUSSION

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied (table 1). Estimates of different genetic variability parameters are presented in table 2. Results showed that the highest genotypic variance was for fruit weight (1642.97), followed by plant height (1383.71), days to 50% flowering (9.097), number of branches per plant (4.32), number of fruits per cluster (0.74), number of flowers per inflorescence (0.65) and the lowest genotypic variance was that of fruit yield per plant (0.17). Phenotypic variance was also the highest for fruit weight (1779.11), followed by plant height (1421.92), days to 50% flowering (13.183), number of branches per plant (6.12), number of fruits per cluster (1.08), number of flowers per inflorescence (1.03), whereas the lowest phenotypic variance was for fruit yield per plant (0.39). Genotypic coefficient of variation (GCV) was the highest for fruit weight (0.4885) followed by plant height (0.3436), fruit yield per plant (0.2591), number of branches per plant (0.2039), number of fruits per cluster (0.1829), number of flowers per inflorescence (0.1337), whereas the lowest GCV was found for days to 50% flowering (0.0552). The highest phenotypic coefficient of variation (PCV) was for fruit weight (0.4905) followed by fruit yield per plant (0.3924), plant height (0.3483), number of branches per plant (0.2433), number of fruits per cluster (0.221), number of flowers per inflorescence (0.1728), whereas the lowest PCV was for days to 50% flowering (0.0665). Similarly, the highest GCV and PCV values were reported for fruit weight by [4] and [5]. Genotypic coefficient of variation, which is the true indicator of the extent of genetic variability in a population, was high for all the characters, except days to 50% flowering. Similar results were obtained by [6]. Generally, higher PCV values than GCV were obtained for all tested traits. The highest heritability was recorded on plant height (97%) with an expected genetic advance over percentage of mean of 69.6%, followed by fruit weight (92%) with an expected genetic advance over percentage of mean of 92.9%, number of branches per plant (70%) with an expected genetic advance over percentage of mean of 35.07%, days to 50% flowering (69%) with an expected genetic advance over percentage of mean of 9.4%, number of fruits per cluster (68%) with an expected genetic advance over percentage of mean of 30.8% and number of flowers per inflorescence (63%) with an expected genetic advance over percentage of mean of 22.3%, while the lowest heritability was that of fruit yield per plant (43%) with an expected genetic advance over percentage of mean of 33.9%. These results agreed with those of [6]. All the tested characters have high heritability estimates illustrated that they will be affected by environmental condition. High genotypic variance was observed for most of the characters indicating more contribution of genetic component for the total variation. Therefore, these characters (table 2) could be considered and exploited for selection purpose. Whereas, the characters like fruit weight, plant height, days to 50% flowering and number of branches in the main stem showed high phenotypic variance indicating the strong influence of environmental factors for their expression. These results are in accordance of the results obtained by [7], [8], [5] and [9]. Higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PVC) were recorded for characters like fruit yield per plant, fruit weight, number of branches per plant, and plant height indicating higher magnitude of variability for these characters. The results are in conformity with the findings of [10],[4] and [9]. Heritability (bs) was observed for the characters like plant height, average fruit weight, number of branches per plant, and days to 50% flowering indicating that these traits are controlled by additive gene action which is very useful in selection. Similar results were noticed by [11], [12], [13] and Singh [8] and [9]. The estimates of heritability alone fail to indicate the response to selection [9]. Therefore, heritability estimates appear to be more meaningful when accompanied by estimates of genetic advance and genetic advance as percentage over mean.

TABLE 1: *Analysis of variance for different characters in tomato genotypes*

Character	Genotypes Mean	S.E (±)	F-value
Plant height (cm)	108.22	3.56	109.64**
No. of branches per plant	10.15	0.77	8.17**
Days to 50% flowering	54.57	1.16	7.68 **
No. of flowers per inflorescence	5.87	0.35	6.06 **
No. of fruits per cluster	4.70	0.33	7.57 **
Fruit yield per plant (kg)	1.59	0.27	3.27 **
Fruit weight (g)	85.96	6.70	37.2 **

*** - Significant at 1%probability level*

TABLE 2: *Estimates of genetic parameters for seven traits of tomato germplasm used in this study*

Character	Variance		GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GA Over mean (%)
	σ^2g	σ^2p					
Plant height (cm)	1383.71	1421.92	34.36	34.83	97	75.33	69.6
Number of branches per plant	4.32	6.12	20.39	24.33	70	3.56	35.07
Days to 50% flowering	9.097	13.183	5.52	6.65	69	5.15	9.4
Number of flowers per inflorescence	0.65	1.03	13.37	17.28	63	1.31	22.3
Number of fruits per cluster	0.74	1.08	18.29	22.10	68	1.45	30.8
Fruit yield per plant (kg)	0.17	0.39	25.91	39.24	43	0.54	33.9
Fruit weight (g)	1642.97	1779.11	48.85	49.05	92	79.92	92.9

GA=Genetic advanced

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