

The evaluation of genetic inheritance, heritability and correlations coefficient of mutant tomato

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Abstract: The present study was evaluated genetic inheritance, heritability and correlation coefficient for some quantitative traits of tomato by using six generations (P_1 , P_2 , F_1 , F_2 , BC_1P_1 and BC_1P_2) from a cross between X604-1(P_1) with indeterminate growth habit and the immature fruit have green shoulder with tomato TTD302A (P_2) determinate growth habit without green shoulder. The results indicated that the analysis of mean values of plant characters in six population were found tomato X604-1 (P_1) could be a good parental species, the development of yield were high. The study of heterosis were found highly significant related to plant height number of branches per plant and significant negative heterosis for days to 50% flowering, number of flower per cluster, number of fruit per cluster and average fruit weight. The correlation coefficient of variability was found positive significant in all of characters. Generation mean analysis were shown the influence of additive and dominant types of gene effect. However, both of gene effects were found mostly significant in all of plant characters, heritability in broad sense was observed high for all of the plant characters.

Keywords: tomato, mutation, phenotype, inheritance

INTRODUCTION

Tomatoes are the top economic crops in the worldwide. Knowledge about the inheritance of traits were used as a tool for generally improves breeding efficiency. Investigation of inheritance of some characterization and agronomic traits in tomato is very important for the selection of plant breeding in the future [1, 13]. It has been a superior model for studying and applied plant research. This has been due to many purposes including short life cycle, photoperiod insensitivity, high self-fertility, homozygosis and simple of controlled pollination and hybridization, diploid species with a rather small genome (950 Mb) [6]. Tomatoes are efficiency and adapted of plant material to study of inheritance. The cross-breeding of the different varieties is comparatively and readily propagated in a vegetative way. The tomato contains many heritable units; the inheritance of characters may be studied. They can grow without difficulty and mature normal fruit readily under greenhouse conditions.

Many of the agronomic traits of tomato are quantitative traits therefore careful attention is paid to the question of their variability and inheritance, mostly for the preparation of selection and genetic programs and successful conduction of the selection process. The inheritance studies in tomato are the basic foundation to

derive such information which can be used as guidelines in breeding.

MATERIAL AND METHOD

Plant materials

Tomato mutant line X604-1 (P_1) has in indeterminate growth habit and the immature fruit have green shoulder. It was crossed with TTD302A (P_2), determinate growth habit without green shoulder in immature fruit color to obtain F_1 , the F_1 was self-pollinated to obtain F_2 . The F_1 was crossed with P_1 and P_2 to obtain BC_1P_1 and BC_1P_2 respectively. Seeds of P_1 , P_2 , F_1 , F_2 , BC_1P_1 and BC_1P_2 were sown in plug trays. Individual seedling in each population was transplanted to the greenhouse and observed separately for all characters. All populations were arranged in completely randomized design. P_1 and P_2 had 25 and 27 plants per plot, F_1 had 34 plants and F_2 had 252 plants, while the BC_1P_1 and BC_1P_2 had 70 and 72 plant per plot, respectively.

Data to be collected

Six of quantitative traits were measured in the greenhouse. The data collection and recording for traits were carried out as follow plant height, number of branches per plant, days to 50% flowering, number of flower per cluster, number of fruit per cluster and average fruit weight.

Statistical analysis of variance (ANOVA)

The values of the F₁, F₂ BC₁P₁, BC₁P₂ and parental lines for all traits were evaluated by ANOVA and the mean values compared by Duncan's test. Also, the traits among the segregating generations (F₂ and backcross generations).

Estimation of Generation means analysis

The inheritance of quantitative traits in tomato was estimated by generation mean analysis (P₁, P₂, F₁, F₂, BC₁P₁, and BC₁P₂), using additive/dominance model parameter [7]. The effects of genes were calculated as:

$$\begin{aligned} (m) &= 0.5P_1 + 0.5P_2 + 4F_2 - 2BC_1P_1 - 2BC_1P_2 \\ (d) &= 0.5P_1 - 0.5P_2 \\ (h) &= 6BC_1P_1 + 6BC_1P_2 - F_1 - 8F_2 - 1.5P_1 - 1.5P_2 \\ (i) &= 2BC_1P_1 + 2BC_1P_2 - 4F_2 \\ (j) &= 2BC_1P_1 - P_1 - 2BC_1P_2 + P_2 \\ (l) &= P_1 + P_2 + 2F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2 \end{aligned}$$

Where (m) representing means, (d) additive and (h) dominance effect, (i) represent additive/additive, (j) additive/dominance and (l) dominance/ dominance effects.

Estimation of heterosis

Heterosis in F₁ hybrid was calculated as the difference and expressed as increase or decrease over mid parent value [3].

$$\text{Heterosis (\%)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Where $\overline{F_1}$ = Mean performance of F₁
 \overline{MP} = Mean performance of parent lines

Estimation of Heritability (H²_b)

Broad sense heritability (H²_b) was expressed as the percentage of the ratio of the genotypic variance mean basis as described by [12].

$$H^2_b = \frac{VF_2 - (VP_1 + VP_2 + VF_1) / 3}{VF_2}$$

Where; H²_b = heritability in broad sense, V representing variances.

Estimation of Correlation Coefficient

Phenotypic correlation is the relationship between two variables, which includes both genotypic and environmental effects and genotypic correlation the inherit association between two variables, phenotypic and genotypic by [2].

$$\text{Phenotypic correlation} = r_p(xy) = \frac{\text{COV}_p(xy)}{\sqrt{V_p(x)} \times \sqrt{V_p(y)}}$$

$$\text{Genotypic correlation} = r_g(xy) = \frac{\text{GOV}_g(xy)}{\sqrt{V_g(x)} \times \sqrt{V_g(y)}}$$

Where; COV_p(xy) and GOV_g(xy) are phenotypic and genotypic covariance between x and y characters, V_p(x) and V_g(x) represent variances of x character and V_p(y) and V_g(y) denote variance of Y character at phenotypic and genotypic level, respectively.

RESULTS AND DISCUSSION

The analysis of mean and standard error (±SE) of P₁, P₂, F₁, F₂ BC₁P₁ and BC₁P₂ for different agronomic traits in tomato a cross of X604-1 × TTD302A

The mean values of plant height in F₂ population (126.62 cm.) were similar to the P₁ values (127.35 cm.) because tomato X604-1 (P₁), there were observed growth habit to be indeterminate type whereas the mean values of plant height in P₂ and BC₁P₂ also were observed 54.20 cm. and 53.79 cm. that refer to P₂ and BC₁P₂ had plant height values in the same direction and plant growth habit were determinate type. For the number of branches per plant, the P₂ mean were lower than among six populations. However, the mean of F₁, F₂, BC₁P₁ and BC₁P₂ were intermediate between the two parents (6.45, 6.08, 6.44, 5.02 and 6.45 respectively). The mean of days to 50% flowering in P₂ and BC₁P₂ populations were earlier (46.85 and 42.45 days) than other population. In addition, the mean value for number of flowers per cluster (7.55), the number of fruits per cluster (5.35) and average fruit weight (43.53) were observed highest in P₁ population. On the contrary, the F₁ mean values were lowest in the number of fruit per cluster. The results were shown in table 1. In the present study, the mean values of F₁ hybrid in plant height, number of branches per plant, number of flower per cluster, number of fruit per cluster and average fruit weight were not exceeding over the better parent values. These might infer to the role of incomplete dominant effect or possibly epistatic gene action, this results were observed similar to previous study [10].

Table 1: Mean and standard error (\pm SE) of quantitative traits in parents and their generation of tomato a cross of X604-1 \times TTD302A

Population	Plant height (cm)	No. of branches/plant	Days to 50% flowering (day)	Number of flowers/cluster	Number of fruits/cluster	Average fruit weight (kg)
P ₁	127.35 \pm 0.63	6.45 \pm 0.19	52.35 \pm 0.53	7.55 \pm 0.18	5.35 \pm 0.18	0.43 \pm 0.90
P ₂	54.20 \pm 0.81	4.60 \pm 0.18	46.85 \pm 0.75	3.70 \pm 0.16	3.05 \pm 0.18	0.30 \pm 1.68
F ₁	108.45 \pm 0.87	6.45 \pm 0.19	53.75 \pm 1.09	4.55 \pm 0.13	2.95 \pm 0.15	0.29 \pm 0.96
F ₂	126.62 \pm 1.00	6.08 \pm 0.05	52.35 \pm 0.15	4.65 \pm 0.03	4.17 \pm 0.03	0.37 \pm 0.48
BC ₁ P ₁	115.92 \pm 0.61	6.44 \pm 0.08	51.31 \pm 0.77	5.74 \pm 0.07	4.70 \pm 0.05	0.30 \pm 0.64
BC ₁ P ₂	53.79 \pm 0.33	5.02 \pm 0.08	42.45 \pm 0.42	4.65 \pm 0.03	4.13 \pm 0.1	0.31 \pm 0.62
%CV	12.18	3.69	0.80	0.65	0.66	6.80

Heterosis and mean performance of F₁ hybrid with mid-parents (MP) and better-parent (BP).

In the present study, F₁ hybrid giving the mean values of plant height, number of branches per plant, number of flowers per cluster, numbers of fruit per cluster and average fruit weight (108.5, 5.3, 4.6, 3 and 29.3 respectively). The mean value of these characters were not exceeding over that of the better parent values whereas except of day to first flowering, the mean value showed 53.8 in F₁ that took longest time (53.8 days) than parent. The heterosis of F₁ hybrid (table 2) were found highly significant from parents for plant height was 17.6%, number of branches per plant was 8.4% and

significant negative heterosis for days to 50% flowering was -4.5%, number of flowers per cluster, number of fruits per cluster and average fruit weight were -18.6, -36.8 and -21.1%, respectively at significant level 0.05 and 0.01. Heterosis is demonstrated of greater vigour of F₁ hybrid over their parents. The heterosis study were suggested that an increase or decrease vigours of F₁ hybrids over mid parent or better parent values for plant breeding, superiority of F₁ over mid parent is of little value it does not offer any advantage [11]. Heterosis provides the opportunity for improvement productivity and development of crop breeding.

Table 2: Mean performance of F₁, mid-parents (MP), better-parent (BP) and heterosis of six characters in tomato from a cross between X604-1 and TTD302A

Character	F ₁	M	BP	Heterosis (%)
Plant height	108.5	92.3	127.4	17.6**
Number of branches/ plant	5.3	5.5	6.5	8.4*
Days to 50% flowering	53.8	49.6	52.4	-4.5*
Number of flowers/cluster	4.6	5.7	7.6	-18.6**
Number of fruits/cluster	3	4.8	5.4	-36.8**
Average fruit weight	29.3	37.2	43.5	-21.1**

*, ** Significant at P < 0.05 and P < 0.01, respectively

Estimation of Correlation coefficient of quantitative trait in tomato

Correlation coefficient analysis measures the extent of closeness of the component traits. The data are presented in table 3. Plant height recorded positive and highly significant correlation with number of branches per plant (r=0.600) and followed by the day to 50% flowering (r=0.465) were observed at 0.01 level. Number of branches per plant showed significant positive with the day to flowering (r=0.303) at 0.05. For days to 50% flowering were observed significant correlation at 0.01 level with number of flower per cluster (r=0.260) and number of fruit per cluster (r=0.125) and at 0.05 level with average fruit number (r=0.121). In addition, numbers of flowers per cluster were showed significant correlated with number of fruits per cluster and average fruit weight. And number

of fruits per cluster exhibited significant correlation with average fruit weight at 0.05 level. The correlation coefficient of variability was found significant in the component traits, its referred to the important of characters for example; plant height, number of branches per plant, the days to flowering and number of flower per cluster. This observation indicated that selection for the traits will be effective good indexes for improvement of breeding programme [9]. Correlation studies provide detail of the nature and extent of association between characters. It could be due to genetic controlling in one character by selection of the other of character. The positive significant correlation occurs might be due to coupling phase of linkage of gene controlling in different traits. Number of flower per cluster had positive significant correlation with number of fruit per cluster [5].

Table 3: Correlation coefficient for among six quantitative traits in tomato

Character	Plant height	No. of branches/plant	Days to 50% flowering	Number of flowers/cluster	Number of fruits/cluster	Average fruit weight
Plant height	-	0.600**	0.465**	0.203**	0.185**	0.329
No. of branches/ plant		-	0.303*	0.056	0.072	0.225
Days to 50% flowering			-	0.260**	0.125**	0.121*
No. of flowers/cluster				-	0.445**	0.096*
No. of fruits/cluster					-	0.120*
Average fruit weight						-

*, ** Correlation is significant at the 0.05 and 0.01 level, respectively

Estimation of heritability

The analysis of heritability which derived from the variance of each population was observed high for all of the plan characters. For plant height was highly heritability of 0.8 which approaches 1 and the other of plant characters had ranged from 0.5-0.8, the results as showed in table 4. Estimation of broad sense heritability was high for all studied characters. High heritability indicates that the proportion of the variability of plant characters are transmitted to progeny, a large portion is caused by genetic variation [4].

The generations mean analysis

The generation mean analysis is effective method of genetic analysis for quantitative traits that provide the relative effect in gene level. The additive gene [d], additive dominant gene [j] and dominant x dominant gene [l] effect were observed positive significant whereas the negative significant were showed the dominant gene [h] and additive x additive gene [i] in plant height. In number of branches per plant were

observed positive significant in the additive gene [d] and dominant x dominant gene [l] while the dominant gene [h] and additive x additive gene [i] were negative significant. Days to 50% flowering were showed the significant positive for the additive gene [d] effect and were showed negative significant for the dominant gene [h] and additive x additive gene [i]. In parameter of number of flowers per cluster the positive significant gene effect were showed the additive gene [d], dominant gene [h] additive x additive gene [i] and the additive gene [d] and only dominant x dominant gene [l] were observed negative significant. The generation mean analysis for most of the characters were showed the importance of both additive and dominant types of gene effects. However, additive gene effects [d] were mostly positive for all of characters. The estimation of gene effect of d, h, i, j and l for plant characters indicating that the inheritance of quantitative characters become more complex, the contribution of gene effect become greater [8].

Table 4 Generation mean analysis and heritability of plant characters in six population (P₁, P₂, F₁, F₂, BC₁P₁ and BC₁P₂) of tomato

Generation mean	Plant Characters					
	Plant height	No. of branches/plant	Days to 50% flowering	No. of flowers/cluster	No. of fruits/cluster	Average fruit weight
[m]	322.7**	75.3**	7.2**	3.9*	3.5*	63.9**
[d]	35.1**	2.8**	1.9*	1.9	1.2	6.4
[h]	-380**	-70.4	-2.4**	2.7**	3.5**	-70.4**
[i]	-167**	-25.6**	-1.6*	1.8*	0.8*	-26.8**
[j]	54**	8.1	0.9	-0.1	-1.1	13.5
[l]	229.2**	48.9**	0.5*	-1.9*	-3.9**	35.7**
H _b ²	0.8	0.6	0.5	0.6	0.7	0.6

*, ** Significant at 0.05 and 0.01, respectively

CONCLUSION

The evaluation of genetic inheritance, heritability, heterosis, correlation and the interaction of gene effects of quantitative traits in six populations P₁, P₂, F₁, F₂, BC₁P₁ and BC₁P₂ of tomato a cross between X604-1xTTD302A were concluded as follows:

Generation mean analysis was shown the influence of additive and dominant types of gene effect. However, both of gene effects were found mostly

significant in all of plant characters. Heritability were observed high for all of the plant characters. The study on heterosis were found highly significant related to plant height number of branches per plant and significant negative heterosis for days to 50% flowering, number of flower per cluster, number of fruit per cluster and average fruit weight. The correlation coefficient of variability was found positive significant in all of characters.

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parents of F1, F2, BC1 and BC2 progeny. *Acta Physiologiae Plantarum*. 2000 Sep 1; 22(3):261-5.

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