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Analysis of Generation Means for Yield and Its Components in Tomato Crosses

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ABSTRACT

Generation mean analysis was studied among hybridization of local cultivated tomato(P1) with wild type(*Lycopersicon pimpinellifolium*) (P2), the F1 plants was selfed for F2 seeds and backcrossed to get 6 tomato genotype plants P1, P2, F1, F2, BC1F1 and BC2F1 plants were planted in a randomized block design with three replications. The experiment was carried out at the Horticulture Department ,University of Mosul. The results showed that The genetic parameters was additive for number of fruits/plant vit c ,plant height ,number of seeds / fruit,and fruit weight . Whereas the dominant effect was significant for: flower number/cluster ,fruit weight(g), plant height (cm) and total yield of fruits. The values of F1, BC1F1 and BC2F1 genotypes were exceeded their parents in the characters: of yield and number of fruits per cluster , Vit C, TSS%, and were under the control of duplicate epistasis while the number of locules per fruit was governed by complementary gene interaction.

*Part of Thesis for the Second Author

INTRODUCTION

The cultivated tomato (*Lycopersicon esculentum* Mill.)is considered as one of the important vegetable crops grown throughout the world and in Iraq(Arun. and Kohli. [1]), because of its wider adaptability (Shaheen et al. [2]). high yielding potential Asati et al [3],it is used as a raw material and for processing industries(Ranganna, S. [4],. Regassa, et al[5]).

The most important traits of tomato crop are the yield and quality (Shaheen et al. [2]); they are concerned in every tomato breeding programme. Therefore the choice of parents that possess the potential to give high- yielding and good quality hybrid plants are essential (Sharma,et al. [6],. Kaushik et al., [7]). However, the character yield is a complex character , and influenced by environment,(Linda and Scott,[8]); Acquaah, G. [9]. Besides the character yield itself, the yield components or other yield contributing characters that effects yield ,Tomar, and Dixit,. [10],may be used for breeding to increase the yield, Mohanty ,[11]. The yield In tomato crop depends mainly on the number of fruit s per inflorescence and the weight of fruits ,Ramazani et al . [12] ; they are both characters are governed by many genetic factors and environmental factors ; (Sajjan et al , [13]; Singh et al., [14]; Shalaby et al, [15]). Therefore, the understanding mode of inheritance of yield and its components is important for the adequate choice of selection to develop high-yield cultivars and hybrids ,Tomar, and Dixit. [10].and Chauhan et al[16].

Analysis of generation means ,suggested by(Mather and Jinks, [17]), is a very useful method to estimate the main genetic effects for additive, dominance and their digenic interactions,(Negi et al , [18]), involved in the expression of quantitative characters , Patel , et al[19],such as yield components Mahesha et al. [20], and yield Ramzan et al.[12]. In tomato, total yield / plant depends on fruit weight, as reported by., Umesh et al., [21], and number of fruits per inflorescence ,Tasisa et al [22]; however, these characters are both determined by genetic factors and environmental factors(Sunil et al [23]). Therefore, the it is important to understanding the mode of inheritance of yield and yield components as they are important and crucial for the choice of the breeding and selection method to develop high-yield and highquality cultivars and hybrids,. Solieman et al., [24]..

The object of this experiment was to study the inheritance and performance of the early generation means of tomato genotypes and hybridsP1,P2,F1,F2,BC1 and BC2 resulted from hybridization between cultivated tomato and wild type *Lycopersicon pimpinellifolium* to improve the characters of yield and yield .



MATERIALS AND METHODS

The present experiment was conducted at the University of Mosul, College of Agriculture and Forestry, Department of Horticulture and Landscape. Tomato Local inbred lines(P1), was crossed with wild tomato. *Pimpinellifolium* (P2) to get F₁ seeds. All the F₁ seed were sown in pots, and at the time of pollination, flowers from about 10 plants were selfed to get F₂ seeds. The F₁ plant were back crossed with the parents to get BC₁ and BC₂. All the five generations genotypes namely, parent plants P₁, P₂, and F₁ hybrid plants F₂ hybrid plants, backcross (BC₁) and backcross (BC₂) of the crosses, were planted in a randomized block design (RBCD) cultivated in three replications. Therefore, the experiment was carried out in a randomized complete block design with three replications. The tomato seedlings were transplanted and cultivated at the spacing of 75 cm between rows and 60 cm between plants, and were grown in the plastic house. The data obtained for yield and biochemical traits were tested for significance by the method suggested by (Mather and Jinks [17]). The Total soluble solids (TSS) of fruits was tested using a hand refractometer calibrated in °brix values were corrected at 20°C, and the analysis of genetic parameters was carried out according to: Singh, and Chaudhary, [25].

The values of the F₁, F₂ BC₁P₁, BC₁P₂ and parents for the characters were evaluated by analysis of variance and the mean values were test. Data recorded were subjected to Analysis of Variance (ANOVA) according to the methods suggested by Al-Rawi and Khalafallah, [26].

The inheritance of quantitative characters in this experiment was calculated by generation mean analysis as follows: parents (P₁ and P₂, F₁, F₂, BC₁P₁, and BC₁P₂), using additive genes and dominance genes model parameter (Mather and Jinks [17]). The genetic effects for the genes was calculated as follows:

$$(m) = 0.5P_1 + 0.5P_2 + 4F_2 - 2BC_1P_1 - 2BC_1P_2 \quad (d) = 0.5P_1 - 0.5P_2$$

$$(a) = 6BC_1P_1 + 6BC_1P_2 - F_1 - 8F_2 - 1.5P_1 - 1.5P_2 \quad (i) = 2BC_1P_1 + 2BC_1P_2 - 4F_2$$

$$(d) = 2BC_1P_1 - P_1 - 2BC_1P_2 + P_2$$

$$(l) = P_1 + P_2 + 2F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2$$

Where (m) representing the means, and (a) additive and dominance gene effect, (d) represent additive/additive genes, and (j) additive/dominance while, (l) refers to dominance/ dominance gene effects.

Results and Discussion:

The results in table (1) shows the mean sum of squares in the analysis of variance, the results revealed a high variability among the studied genotypes. The variation due to genotypes was significant for all the characters under study both at 5 and 1 per cent probability levels (Table 1). It can be seen that there is a high variability among the studied genotypes of the parents and their segregating hybrids, this might be due to their genetic background of selected parental germplasm, and the different geographical regions from which they have been originated, (Patel, et al. [19]), Shaheen, [2]. The result of this study are in accordance with: Chauhan et al [27], Oseki et al., [28], and Chauhan et al., [16]. They also recorded highly significant difference among the tomato genotypes and resulting hybrids with respect to all the characters under studied; Kumar et al (2003).

Table.(1) Analysis of variance for yield and its components in Tomato crosses

S. No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
1-	Plant Height (cm)	142.44	13018.3**	344.75
2-	Number of branches/plant	12.46	243.6**	3.02
3-	Number of Flowers/cluster	1.38	5.28*	1.40
4-	Number seeds/ Fruit	46.48	875.17**	80.52
5-	Average Fruit Weight (g)	15.64	7336.7**	30.35

6-	Number of Fruits/ Plant	114.82	2423.8**	185.88
7-	Fruit Yield/ Plant (kg)	0.05	1.66**	0.13
8 -	TSS	0.048	3.25**	0.51
9-	(Vit C)mg/100g	36.92	37.49**	16.15
10 -	Number of Locules/ Fruit	0.05	2.56**	0.05

*Significant at 5% level of probability, ** Significant at 1% level of probability

In the character of number of flowers / inflorescence the positive significant gene effect . The analysis of generation mean for most of the characters showed the importance of both additive genes and dominant types of gene effects(Shankar et al., [29]). However, additive gene effects , was mostly positive for all of characters; Dordevic et al., [30]. The estimation of gene effect for plant characters revealed that the inheritance of the quantitative characters are more complicated inheritance, and the contribution of each gene effect are very important and become great effect . Shokat, et al[31].

From the resulted data are presented in table(2), the data shows that one or more of gene effects was significant or highly significant with positive values for the characters: number of fruits per plant., average fruit weight(gm), fruit length (cm), fruit diameter, fruit size and yield per plant (kg). Tasisa,et al. [21], Osekita,and Ademiluyi [28].

The main gene effects additive and dominance were found to be of negative significance for number of fruits / plant while among the epistatic effects, additive genes x dominant genes and components of dominance x dominance genes were positive significant and with duplicate type of epistasis was recorded in inheritance of number of fruits per plant. Solieman et al, [24], Chauhan ,et al.,[16].

Results In table(2)revealed that, The additive gene , additive and dominant gene , and dominant gene x dominant gene effect were positive significant whereas the negative significant was shown the additive x additive gene in plant height, Sharma et al[6]. The character number of fruits / plant was observed positive significant in the additive gene and dominant x dominant gene effect , while the effect of dominant gene and additive x additive gene was significant, Ahmed et al. [32]; Osekita,and Ademiluyi (2014). Plant height was showed the significant for the additive gene effect and was shown negative significant for the dominant gene effect, Tomar, and Dixit. [10] .

Table(2) Estimates of Means for six parameters model of gene effects for different characters of the tomato

Traits	m±SE	a±SE	d± SE	aa±SE	ad±SE	dd±SE
Number of fruits per plant	4.90** ± 2.48	6.509** ± 2.55	107.57 ± 10.36	104.402* ± 34.45	7.30* ± 9.29	195.85** ± 48.09
Average fruit weight (g)	0.170** ± 0.40	1.491** ± 0.36	9.46** ± 1.67	8.75** ± 2.08	2.09 ± 0.42	30.53** ± 1.88
Plant height (cm)	4.85** ± 0.22	3.83** ± 1.14	95.234 ± 9.94	93.81 ± 9.64	4.61 ± 0.33	3.25* ± 1.14
Fruit diameter (cm)	0.017** ± 0.02	0.04** ± 0.11	0.296 ± 0.25	0.25 ± 0.23	0.91** ± 0.26	147.48 ± 12.47
Fruit size	3.78** ± 0.33	4.22** ± 0.35	1.55 ± 1.65	4.54* ± 1.51	5.48** ± 1.36	-3.83 ± 2.36
Yield per plant (kg)	0.13** ± 0.13	0.257 ± 0.53	1.67 ± 1.74	1.59** ± 0.70	0.32 ± 0.25	5.75** ± 1.16

m= Mean, a= additive; aa= dominance; d= additive × additive; ad= additive × dominance; dd=dominance × dominance, SE= Standard error, D= Duplicate, C= Complimentary.

*and ** for significant and highly significant, respectively.

The results from this study revealed that, the analysis of generation means for the characters studied was shown the importance of the effect of additive genes and dominant types of gene effects, the same results obtained by : Mohanty, ([11], 30));Asati .,et al. [3], Arun., and Kohli. [1]. Shokat ,et al[34], Negi et al., [18]. However, additive gene effects, was mostly positive for all of characters studied, Singh,et al. [35]and Chauhan et al., [27]. The estimation of gene effect for plant characters indicating that the inheritance of quantitative characters become more complicated, Asati et al. [3], the contribution of gene effect become great. Sharma,et al. [6], Mohanty,. [11] Regassa, et al, [5].

The data presented in table(2) reveals that one or more of gene effects is significant and or highly significant values with positive values for the characters: number of fruits per plant, average fruit weight, fruit length, fruit diameter, fruit size and yield per plant. Concerning the average fruit weight, both main gene effects of additive and dominant gene effect was highly positive significant, Patel et al[19]., whereas among the effect of epistatic components showed that only additive \times additive effects was observed positive significant. Duplicate type epistasis was recorded for average fruit weight. Regarding fruit length the main effects of the gene was additive, and was shown to be positive significant, while in case of epistatic gene effects only the results showed that the dominant \times dominant gene effect was significant in positive direction, Solieman et al., [24]. Complimentary type epistasis was observed in inheritance of fruit length. Concerning the fruit diameter, the main effects of the additive gene was found positive significant, whereas no positive significant epistatic effects were recorded for this character and complimentary type of epistasis genes was found in inheritance of fruit diameter. Sunil ,et al. [23]. In case of fruit size, only additive effects were recorded positive significant while among epistatic effects additive \times additive effects were recorded positive significant. Regarding yield per plant, main gene effects were non- significant whereas dominance \times dominance epistatic effect were recorded positive significant for this trait among the epistatic components and duplicate type epistasis was recorded in inheritance of yield per plant. Similar results indicated that both effects of additive genes and non-additive gene effects, appeared to share and contribute to the basic genetic mechanisms which involved in the inheritance of yield and yield contributing traits of tomato Mahesha et al. [20],Asati BS, and Singh AK. . [3], Shankar,et al.(2013) Shaheen et al. [29].

Table 3:Mean and standard errors \pm for different characters of the tomato genotypes

Traits	P1	P2	F ₁	F ₂	BC ₁	BC ₂
Number of fruits per plant	56.25 \pm 3.05	308.20 \pm 6.76	231.13 \pm 7.06	175.33 \pm 7.48	104.88 \pm 4.46	202.16 \pm 7.26
Average fruit weight (g)	48.34 \pm 0.41	6.92 \pm 0.19	14.55 \pm 0.39	18.20 \pm 0.20	32.37 \pm 0.23	12.46 \pm 0.28
Fruit length (cm)	4.47 \pm 0.27	1.00 \pm 0.11	1.74 \pm 0.39	2.15 \pm 0.38	3.31 \pm 0.14	1.88 \pm 0.20
Fruit diameter (cm)	3.37 \pm 0.25	1.18 \pm 0.04	1.17 \pm 0.08	1.77 \pm 0.04	2.12 \pm 0.09	1.48 \pm 0.16
Fruit size (L \times W in cm)	15.10 \pm 2.02	1.18 \pm 0.14	2.05 \pm 0.59	3.78 \pm 0.58	7.03 \pm 0.28	2.81 \pm 0.53
Yield per plant (kg)	2.74 \pm 0.15	2.13 \pm 0.13	3.35 \pm 0.23	3.13 \pm 0.13	2.75 \pm 0.18	2.33 \pm 0.13

Table (3) Shows the means for different characters of the parents and genotypes, the values of F₂ hybrids mean values were decreased as compared to the values of F₁ means for number of fruits per plant and yield per

plant. This could be due to presence of inbreeding depression Dordevic et al[30] ., Ahmed, et al. [32]. Similarly, it was reported that inbreeding depression leads to decrease yield of tomato in F_2 generation compared to F_1 , Tomar and Dixit. [10]. These results are consistent with finding of Solieman et al (2013) Shokat. et al. [34]. On contrast, the values of F_2 means were higher than these of the values of F_1 hybrid means for the characters : average fruit weight (gm), fruit length(cm), fruit diameter(cm), and fruit size. Values for high mean of fruit weight in F_2 plant population could be due to more the number of fruits in the F_1 hybrid plants., Regassa, et al, [5]. Negi et al., [18]., Umesh .et al [21] . Generally, the results showed that the in most characters the values of the means of BC_1 plants and BC_2 plants were higher than the mean values of F_2 plants .Tasisa, et al. [22]. It is clearly shown that ,the mean values of BC_1 and BC_2 plants were less than the mean values of F_1 and F_2 values for yield per plant; it may be due to higher percentage of heterosis in F_1 Shalaby., [15] and evolution of transgressive segregates in F_2 hybrid plants., Mohanty., [11. Tomar, and Dixit., [10]. Chauhan .et al[16] .

Conclusion: The results from this experiment shows that the yield(kg) and yield components, in F_2 hybrid plant population was found to be performed better than the rest of the genotypes plants for most of the studied characters, due to transgressive segregation, and direct selection could be useful for these reproductive attributes.

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