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Generation mean analysis for processing suitable seed traits of tomato (*Solanum lycopersicum* L.)

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Abstract

Using generation mean analysis and gene actions for seed parameters of the 6 generations (P_1, P_2, F_1, F_2, B_1 and B_2) of the tomato cross IIHR 2847 X CLN3916C were estimated. The percent seed was lowest in line IIHR 2847 and highest in line CLN3916C. The hybrid IIHR 2847 X CLN3916C showed intermediate seed content. The experimental material was evaluated at the Division of Vegetable Crops, Indian Institute of Horticultural Research, Bengaluru. For characters and crosses with significant mean sum squares, gene effects were estimated. The scaling test was conducted using the standard errors, mean values and variances of several generations. The number of seeds, seed weight (g) and percent of seed content traits showed a duplicate type of epistasis, indicating that selection would not be successful for these traits because they were not fixable in earlier generations.

Keywords: Tomato, generation mean analysis, gene action, epistasis

1. Introduction

The tomato (*Solanum lycopersicum* L.; 2n=24) is the most extensively grown vegetable in the world due to its high yield potential and wider adaptability and suitability for a variety of uses in fresh as well as processed forms, such as sauce, ketchup, puree, paste and juice (Takeoka *et al.*, 2001) [12]. Therefore, in order to develop cultivars of high-quality traits for processing industries, it is essential to understand the genetics of quality characters.

Generation mean analysis (Mather and Jinks, 1982) [10] is a biometrical design that uses six generations for the assessment of genetic components of variation, *viz*. P_1, P_2, F_1, F_2, B_1 and B_2. A useful method for determining the types of gene effects involved in character expression is generation mean analysis. Although diallel analysis is commonly used to choose parents based on how ability to combine, it is unable to identify epistasis. The scaling test can be used to determine whether epistasis is present or not, which determines whether epistasis is duplicate (additive x dominance and dominance x dominance) or complementary (additive x additive). Inheritance of seed parameters is the main objective of the study.

2. Materials and Methods

Six generations of the cross IIHR 2847 X CLN3916C were tested (P1, P2, F1, F2, B1, B2) in this experiment. The genetic population contains 5 individuals of P_1, P_2, F_1 and 100 each of F_2, B_1 and B_2 of these crosses were grown in separate rows during *Rabi* 2021 at the Division of Vegetable Crops, Indian Institute of Horticultural Research, Bengaluru. The parameters were recorded on one-kilogram fruits of randomly selected plants from P_1, P_2, F_1, F_2, B_1 and B_2 generations of the cross IIHR 2847 X CLN3916C for three characters, *viz*., number of seeds, seed weight (g) and per cent of seed content. The gene effects were estimated for characters and cross having significant mean sum squares. The standard errors, variances and mean values of the diverse generations were used for the scaling test. The models proposed by Mather and Jinks (1971) [9] were used to estimate the genetic effects and variance components. Data were analyzed by Indostat Services, Hyderabad.

3. Results and Discussion

The study of the generation mean analysis was examined in the cross of IIHR 2847 x

CLN3916C for three traits, such as seed weight, number of seeds per fruit and per cent seed content. The results indicated that P_2 (CLN3916C) performed better for all the traits, followed by BC_2, F_2, F_1 and BC_1. The results showed that the number of seeds per fruit had a high mean value. The expected mean value is significant only for the number of seeds per fruit (Fig.1, 2, 3). These results were in accordance with the findings of Somraj *et al*. (2017) [11].

Generation mean analysis helps to determine the type of gene effects and interactions in the expression of the traits. The presence or absence of epistasis is distinguished by the generation means analysis using the scaling test parameters and epistasis is inferred as duplicate (additive x dominance and dominance x dominance) or complementary (additive x additive) at the digenic level (Dutta *et al*., 2013) [5].

The *per se* performance of F_1, F_2, BC_1, and BC_2 was found between the number of their respective parents means in a positive direction for the seed weight, number of seeds and percent seed content (Table 1). The highest number of seeds was observed in F_1 generation (939.2) among the hybrids; BC_2 (2.636 g) performed better for seed weight and also for seed content (0.264%). Among the six generations, parent 2 (CLN3916C) performed better for all three traits, like seed weight (3.694 g), number of seeds per fruit (1259.6) and percent seed content (0.369). This suggests positive improvements in these traits in the crosses compared to the parents. Similar results were also documented by Jasmina *et al*. (2011) [8], Dutta *et al*., (2013) [5] and Datta and Mehta (2020) [1].

The genetic model has six parameters, namely, 'm', additive [d], dominance [h], digenic [i], [j] and [l] were used for studying the variations in generation means (Table 2). In the cross, IIHR 2847 X CLN3916C dominance gene effect [h] was less than the additive gene effect [d]. Dominance x dominance [l] interaction was higher than the additive x additive [i] component and the additive x dominant [j] component. The presence of dominance x dominance [l] interaction cannot be exploited through heterosis breeding, owing to a duplicate type of epistasis (Dhaliwal *et al*. 2001) [2].

Negatively significant gene effects were observed for seed weight. The additive gene effect was higher than the dominance [h], digenic [i] and [j] gene effect. Dominance x dominance [l] interaction was higher than additive x additive [i] component and additive x dominant [j] component for seed weight. Negatively significant gene effects were observed for seed content. The additive gene effect was higher than the dominance [h], digenic [i] and [j] gene effect. Dominance x dominance [l] interaction was higher than additive x additive [i] component and additive x dominant [j] component for seed content. In this cross, the presence of duplicate epistasis was observed for all three traits studied (Table 2). Similar observations were also reported by Hayman (1958) [7] and Gabry *et al*. (2014) [6].

In the estimation of allelic interactions, seed weight and seed content exhibited implications for both additive and dominance gene effects. The number of seeds had significant dominance x dominance [l] and additive x dominance [j] gene epistasis. The duplicate type of epistasis was observed in all three traits studied, signifying that these traits cannot be exploited through heterosis breeding due to the duplicate type of epistasis. Significance of most of the scales suggested the contribution of non-allelic interaction in the genetic regulator of all three traits. In all these traits, the dominance (h) and dominance x dominance (l) effects were significant in opposite directions, suggesting a duplicate type of epistasis (Table 3). This indicated that predominantly disseminated alleles at the interacting loci will decrease the rate of advancement through selection and reduce variation in the F_2 and other succeeding generations, as recorded earlier by Dhankar *et al*. (2003) [3] and Dixit *et al*., (2006) [4].

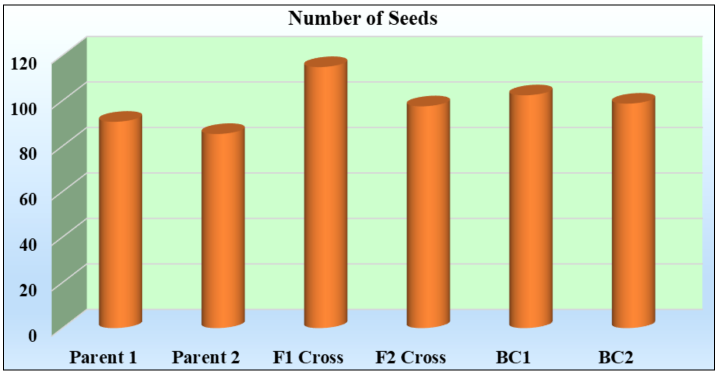

Fig 1: Graphical representation of mean performance of six generations for number of seeds in tomato

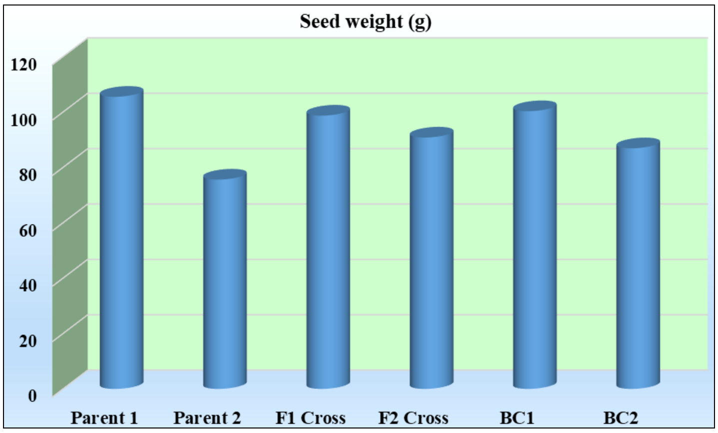

Fig 2: Graphical representation of mean performance of six generations for seed weight (g) in tomato

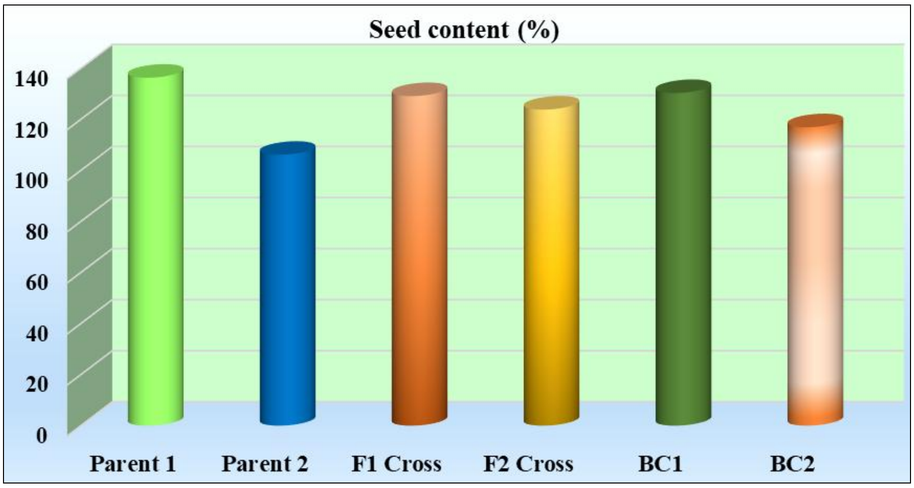

Fig 3: Graphical representation of mean performance of six generations for seed content (%) in tomato

Table 1: Generation means and ±SEm on seed parameters in 2847 X CLN3916C

Generation	Number of seeds	Seed weight (g)	Seed content (%)
P_1	486.0 ± 19.45	1.33 ± 0.06	0.13 ± 0.006
P_2	1259.6 ± 60.68	3.69 ± 0.15	0.36 ± 0.015
F_1	939.2 ± 25.19	2.23 ± 0.10	0.22 ± 0.010
F_2	843 ± 23.20	2.61 ± 0.07	0.26 ± 0.007
B_1	638.9 ± 16.55	1.98 ± 0.05	0.19 ± 0.005
B_2	838.92 ± 20.03	2.63 ± 0.06	0.26 ± 0.006

Table 2: Estimate of gene effects for seed parameters of cross 2847 X CLN3916C in tomato

Sl. No.	Character	Estimation of Genetic factors						
		[$\hat{m}$]	[$\hat{d}$]	[$\hat{h}$]	[$\hat{i}$]	[$\hat{j}$]	[$\hat{l}$]	Epistais
1	Number of seeds	1289.16**±111.06	-386.8±31.86	-1434.68±261.83	-416.36±106.39	186.78**±41.12	1084.72*±161.32	Duplicate
2	Seed weight (g)	3.72±0.34	-1.18*±0.08	-2.94*±0.79	-1.2*±0.33	0.53±0.12	1.45±0.51	Duplicate
3	Seed content (%)	0.37±0.03	-0.12*±0.01	-0.29*±0.08	-0.12*±0.03	0.05±0.01	0.15±0.05	Duplicate

Table 3: Estimate of Scaling test for seed parameters of cross 2847 X CLN3916C in tomato

Sl. No.	Character	Scaling test				Non-allelic Interaction
		A	B	C	D	
1	Number of seeds	-147.4±45.92	-520.96±76.96	-252±123.36	208.18*±53.2	Present
2	Seed weight (g)	0.4±0.16	-0.66±0.23	0.95±0.39	0.6±0.16	Present
3	Seed Content (%)	0.04±0.02	-0.07*±0.02	0.1±0.04	0.06±0.02	Present

4. Conclusion

The experiment results indicate that improving all three of the traits under investigation cannot be accomplished with a single breeding strategy. Since both additive and dominant gene effects were seen in opposite directions, the duplicate type of epistasis was observed in all three traits. This suggests that a duplicate type of epistasis prevents the exploitation of these traits through heterosis breeding.

5. Disclaimer (Artificial Intelligence)

Authors hereby declare that no generative AI technologies such as large language models (Chat GPT, COPILOT, etc) and text-to-image generators have been used during the writing or editing of manuscripts.

6. Acknowledgement

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7. Competing Interests

The authors have declared that no competing interests exist.

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