



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2020; 9(4): 314-316

Received: 25-05-2020

Accepted: 27-06-2020

Bipasha Datta

Department of Genetics and
Plant Breeding, Junagadh
Agricultural University,
Junagadh, Gujarat, India

DR Mehta

Associate Professor, Department
of Genetics and Plant Breeding,
Junagadh Agricultural
University, Junagadh, Gujarat,
India

Generation mean analysis in tomato (*Solanum lycopersicum* L.): Estimation of gene actions for fruit yield and its component traits

Bipasha Datta and DR Mehta

Abstract

Gene actions for fruit yield and its component traits of six basic generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of two crosses namely, JTL-15-02 x JT-3 and JTL-12-02 x AT-3 of tomato were estimated through generation mean analysis. The experimental material was evaluated in Compact Family Block Design with three replications at Vegetable Research Station, Junagadh Agricultural University, Junagadh. The analysis of variance revealed the significant differences between the families as well as among the generations of each family for all the characters studied. Importance of both additive as well as non-additive gene actions was realized for most of the characters in both the crosses. However, non-additive gene actions were more profound than the additive gene action for all the characters in both the crosses except for fruit length in JTL-15-02 x JT-3. Duplicate type of epistasis was observed for fruit yield and its attributing traits suggesting selection would not be effective for such traits due to its non-fixable nature in earlier generation.

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

Introduction

Tomato (*Solanum lycopersicum* L. $2n=2x=24$) is one of the most important and most popular vegetables in the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. It thrives well in temperature 10°C to 30°C (Zalom and Wilson, 1999) [8]. The mean temperature below 16°C and above 27°C is not desirable. It requires low to medium rainfall, and does well under average monthly temperature of 21°C to 23°C (Dubey, 2012) [4]. In breeding programme, fruit yield is considered as one of the essential agronomical trait and the traits like number of fruits per cluster, average fruit weight and number of fruits per plant, extensively determine the extent of fruit yield per plant and thus exploitation of such traits lead to the enhancement of fruit yield in tomato. Therefore, a better understanding of the mode of inheritance of fruit yield and its components is crucial for adequate choice of selection strategy for developing high-yielding cultivars and hybrids. Generation mean analysis (Mather and Jinks, 1982) [6] is an efficient tool to understand the nature of gene effects involved in the expression of the character. Diallel and line x tester analysis are useful for selection of parents of good combining ability but at some point it fails to detect the interaction gene effects which can be resolved by the analysis of generation means using the scaling test and different genic models. The presence or absence of epistasis detected by the analysis of generation means using the scaling test measures epistasis whether complementary (additive x additive) or duplicate (additive x dominance and dominance x dominance) at digenic level (Dutta *et al.*, 2013) [5].

Materials and methods

The experiment of six basic generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of the two crosses *viz.*, JTL-15-02 x JT-3 and JTL-12-02 x AT-3 were laid out during *Rabi*-2018-2019 at Vegetable Research Station, Junagadh Agricultural University, Junagadh in Compact Family Block Design with three replications. The observations were recorded on five randomly selected plants from P_1 , P_2 and F_1 ; 10 plants from backcrosses (B_1 and B_2) and 20 plants from F_2 generation in each cross in each replication for seven characters *viz.*, number of fruits per cluster, number of fruits per plant, average fruit weight, number of locules per fruit, fruit yield per plant, fruit length and fruit circumference. All the recommended agronomical and plant protection practices were adopted to raise healthy crops. Data were collected from all the plants of each generation of the two crosses. The gene effects were estimated for characters and crosses having significant mean sum squares.

Corresponding Author:**Bipasha Datta**

Department of Genetics and
Plant Breeding, Junagadh
Agricultural University,
Junagadh, Gujarat, India

The data was initially subjected to simple scaling tests A, B, C and D. Significant estimates of any one or more of these tests indicate the presence of digenic interactions. The results of simple scaling tests were further confirmed by joint scaling test (Cavalli, 1952) [1]. Data which were not fit under three parameter model were subjected to six-parameter model. Further, models having non-significant one or more digenic interactions namely, additive x additive (i), additive x dominance (j) and dominance x dominance (l) were required and further tested for goodness of fit by using chi square test.

Table 1: Mean performance of six generations of two crosses for seven characters in tomato

| Cross | P ₁ | P ₂ | F ₁ | F ₂ | B ₁ | B ₂ | S. E. ± | C. D. at 5% |
|------------------------------|----------------|----------------|----------------|----------------|----------------|----------------|---------|-------------|
| Number of fruits per cluster | | | | | | | | |
| JTL-15-02×JT-3 | 3.53±0.13 | 3.27±0.22 | 4.60±0.17 | 3.28±0.12 | 3.53±0.12 | 3.43±0.10 | 0.10 | 0.30 |
| JTL-12-02×AT-3 | 4.53±0.13 | 3.40±0.17 | 4.73±0.25 | 3.30±0.13 | 4.73±0.14 | 3.40±0.08 | 0.08 | 0.26 |
| Number of fruits per plant | | | | | | | | |
| JTL-15-02×JT-3 | 92.80±0.97 | 95.40±1.09 | 105.60±1.40 | 81.45±0.86 | 106.60±1.03 | 90.63±0.68 | 0.39 | 1.26 |
| JTL-12-02×AT-3 | 117.47±1.59 | 86.73±1.36 | 126.13±1.41 | 89.17±1.18 | 133.97±0.74 | 72.60±0.92 | 0.47 | 1.48 |
| Average fruit weight (g) | | | | | | | | |
| JTL-15-02×JT-3 | 58.05±0.49 | 53.22±0.65 | 63.47±0.76 | 47.62±0.62 | 50.89±0.54 | 57.52±0.36 | 0.33 | 1.05 |
| JTL-12-02×AT-3 | 49.15±0.69 | 55.08±0.70 | 59.41±0.59 | 46.49±0.56 | 45.99±0.37 | 59.13±0.49 | 0.21 | 0.67 |
| Number of locules per fruit | | | | | | | | |
| JTL-15-02×JT-3 | 3.00±0.18 | 4.00±0.20 | 2.67±0.13 | 3.20±0.09 | 3.63±0.09 | 3.33±0.11 | 0.08 | 0.24 |
| JTL-12-02×AT-3 | 3.47±0.17 | 2.60±0.13 | 3.93±0.18 | 3.32±0.12 | 4.33±0.16 | 3.47±0.18 | 0.09 | 0.29 |
| Fruit yield per plant (kg) | | | | | | | | |
| JTL-15-02×JT-3 | 5.38±0.05 | 5.11±0.07 | 6.70±0.07 | 3.88±0.07 | 5.42±0.05 | 5.21±0.02 | 0.04 | 0.08 |
| JTL-12-02×AT-3 | 5.77±0.09 | 4.78±0.08 | 7.49±0.08 | 4.14±0.03 | 6.23±0.09 | 4.29±0.07 | 0.03 | 0.06 |
| Fruit length (cm) | | | | | | | | |
| JTL-15-02×JT-3 | 4.25±0.15 | 4.01±0.11 | 4.61±0.16 | 4.02±0.08 | 4.26±0.09 | 4.05±0.11 | 0.08 | 0.26 |
| JTL-12-02×AT-3 | 5.05±0.07 | 4.34±0.09 | 4.93±0.12 | 4.52±0.06 | 4.79±0.05 | 4.40±0.05 | 0.06 | 0.20 |
| Fruit circumference (cm) | | | | | | | | |
| JTL-15-02×JT-3 | 18.17±0.30 | 14.86±0.19 | 17.50±0.27 | 15.55±0.28 | 14.65±0.20 | 14.82±0.13 | 0.19 | 0.61 |
| JTL-12-02×AT-3 | 15.23±0.25 | 16.39±0.23 | 14.63±0.23 | 13.82±0.18 | 14.34±0.21 | 14.66±0.24 | 0.10 | 0.33 |

Importance of digenic interaction effects along with additive and dominance gene effects were confirmed for fruit yield and its attributing traits in two crosses viz., JTL-15-02 x JT-3

and JTL-12-02 x AT-3 through generation mean analysis (Table 2).

Table 2: Estimates of Simple scaling test and gene effects for different characters in cross JTL-15-02 x JT-3 and JTL-12-02 x AT-3 based on best fit model

| JTL-15-02 x JT-3 | A | B | C | D | m | [d] | [h] | [i] | [j] | [l] | Epistasis |
|------------------------------|----------|----------|----------|----------|---------|---------|----------|---------|----------|----------|-----------|
| Number of fruits per cluster | -1.07** | -1.00** | -2.87** | -0.40 | 3.41** | 0.11 | -1.12* | - | - | 2.31** | D |
| Number of fruits per plant | 14.80** | -19.73** | -73.60** | -34.33** | 25.43** | -1.30 | 143.90** | 68.67** | 34.53** | -63.73** | D |
| Average fruit weight (g) | -19.73** | -1.64 | -47.71** | -13.17** | 32.37** | 2.38** | 31.46** | 23.37** | -18.44** | - | - |
| Number of locules per fruit | 1.60** | -0.06 | 0.47 | -0.57* | 2.37** | -0.50** | 3.03** | 1.13* | 1.60** | -2.73** | D |
| Fruit yield per plant (kg) | -1.24** | -1.39** | -8.35** | -2.86** | -0.48 | 0.16** | 10.07** | 5.65** | - | -2.96** | D |
| Fruit length (cm) | -0.35 | -0.53* | -1.40** | -0.26 | 4.14** | 0.15* | -0.60 | - | - | 1.06** | D |
| Fruit circumference (cm) | -6.36** | -2.73** | -5.84** | 1.62** | 19.76** | 1.65** | -14.60** | -3.25** | -3.63** | 12.34** | D |
| JTL-12-02 x AT-3 | | | | | | | | | | | |
| Number of fruits per cluster | 0.20 | -1.33** | -4.20** | -1.53** | 1.89** | 0.56** | 3.00** | 2.11** | 1.70** | - | - |
| Number of fruits per plant | 24.33** | -67.67** | -99.80** | -28.23** | 53.86** | 15.44** | 73.20** | 48.75** | 92.42** | - | - |
| Average fruit weight (g) | -16.58** | 3.77** | -37.08** | -12.14** | 27.84** | -2.96** | 43.03** | 24.27** | -20.35** | -11.47** | D |
| Number of locules per fruit | 1.27** | 0.40 | -0.67 | -1.17** | 0.65 | 0.51** | 7.40** | 2.41** | - | -4.11** | D |
| Fruit yield per plant (kg) | -0.79** | -3.70** | -8.97** | -2.24** | 0.79* | 0.49** | 6.69** | 4.48** | 2.93** | - | - |
| Fruit length (cm) | -0.41* | -0.47* | -1.17** | -0.15 | 4.69** | 0.37** | -0.75** | - | - | 0.98** | D |
| Fruit circumference (cm) | -1.17* | -1.71** | -5.62** | -1.37** | 13.00** | -0.52** | 1.62** | 2.82** | - | - | - |

Number of fruits per cluster

Parameters viz., 'm', dominance [h] and digenic [l] gene effects were significant which confirmed the adequacy of four-parameter model including 'm', [d], [h] and [l] as best fit model with duplicate epistasis for explaining the inheritance of number of fruits per cluster in JTL-15-02 x JT-3. Dominance gene effect [h] was higher than the additive gene effect [d]. The genetic model having five parameters namely, 'm', additive [d], dominance [h], digenic [i] and [j] was

adequate for studying the variations in generation means in JTL-12-02 x AT-3. Dominance gene effect [h] was higher than the additive gene effect [d] in this cross. Additive x additive [i] component was higher than additive x dominant [j] component.

Number of fruits per plant

Six-parameter model was fitted for explaining the inheritance of number of fruits per plant in JTL-15-02 x JT-3. Dominance

gene effect [h] was higher than the additive gene effect [d] in this cross. Additive x additive [i] component was higher than both the additive x dominance [j] and dominance x dominance [l] component. Genetic model including five parameters viz., 'm', additive [d], dominance [h], digenic [i] and [j] was the best fitting model to explain the trait inheritance in JTL-12-02 x AT-3. Dominance gene effect was more profound than the additive gene effect besides additive x dominance [j] component was higher than the additive x additive [i] component.

Average fruit weight (g)

Parameters namely, 'm', additive [d], dominance [h] along with digenic [i] and [j] were fitted as best fit model for studying the inheritance of this trait in JTL-15-02 x JT-3. Mean performance as well as dominance gene effect [h] was higher than the additive gene effect [d]. Additive x additive [i] component was higher than additive [d] and dominance [h] component. Six-parameter model was found adequate in JTL-12-02 x AT-3 in which dominance gene effect [h] was higher than the additive gene effect [d]. Additive x additive [i] component was higher than both the additive x dominance [j] and dominance x dominance [l] gene effect. Presence of dominance x dominance [l] interaction for fruit weight cannot be exploited through heterosis breeding due to duplicate type of epistasis (Dhaliwal *et al.* 2001)

Number of locules per fruit

The adequacy of six-parameter model with duplicate epistasis was confirmed for number of locules per fruit in JTL-15-02 x JT-3 in which dominance gene effect [h] was higher than the additive gene effect [d]. Dominance x dominance [l] gene effect was higher than both the additive x additive [i] and additive x dominance [j] component. Incorporation of two digenic gene effects [i] and [l] along with 'm', additive [d] and dominance [h] gave best fit model for number of locules per fruit in JTL-12-02 x AT-3. Dominance gene effect [h] was higher than the additive gene effect [d] as well as dominance x dominance [l] component was also higher than the additive x additive [i] component.

Fruit yield per plant (kg)

Genetic model including 'm', additive [d], dominance [h], digenic gene effects [i] and [l] with duplicate epistasis was adequate to explain the variation in generation means for this character in JTL-15-02 x JT-3 in which dominance gene effect [h] was higher than the additive gene effect [d] as well as additive x additive [i] component was also higher than dominance x dominance [l] component. Five-parameter model viz., 'm', additive [d], dominance [h] and digenic [i] and [l] was treated as best fit model in JTL-12-02 x AT-3 in which dominance gene effect [h] was higher than the additive gene effect [d] as well as additive x additive [i] component was higher than the additive x dominance [j] component. Importance of additive as well as non-additive gene effects was reported by Devi *et al.*, (2005) ^[2] for this trait.

Fruit length (cm)

Four-parameter model ('m', additive [d], dominance [h] and digenic [l]) was adequate to explain the variation in generation means for fruit length in JTL-15-02 x JT-3 and treated as best fit model with duplicate epistasis. Incorporation of two digenic parameters [j] and [l] along with duplicate epistasis i.e., five-parameter model was considered as best fit model in JTL-12-02 x AT-3. Mean performance as

well as dominance gene effect [h] was higher additive gene effect [d]. Duplicate type epistasis was confirmed from the opposite signs of [h] and [l].

Fruit Circumference (cm)

Six-parameter model with duplicate epistasis was adequate to explain the inheritance of fruit circumference in JTL-15-02 x JT-3. Dominance x dominance [l] component was also higher than both the additive x additive [i] and additive x dominance [j] component. The best fitting model for fruit circumference in JTL-12-02 x AT-3 included 'm', additive [d], dominance [h] and digenic [i]. Mean performance and dominance gene effect [h] was higher than the additive gene effect [d] in both crosses.

Positive and negative sign of dominance gene effect [h] and dominance x dominance [l] gene effect indicated enhancing and diminishing effect in expression of the characters, respectively. Positive and negative sign of additive x additive [i] gene effect indicated association and dissociation of allele in parents. Traits where both the dominance [h] and dominance x dominance [l] component were more prominent are undesirable in terms of selection as it hinders the transgressive segregation in early generations. As the contribution of dominance gene effect for its inheritance becomes greater, the inheritance of quantitative characters becomes more complex (Mohamed *et al.*, 1997) ^[7].

In above cases where additive [d] and dominance [h] gene effects and some or all the digenic epistasis collectively govern the inheritance of the trait, it would be difficult to get promising segregants through conventional breeding methods. Hence, some sort of recurrent selection by way of intermating the most desirable segregants followed by selection or diallel selective mating or the use of multiple crosses could be effective alternative approaches for the genetic improvement of these traits.

References

1. Cavalli LL. An analysis of linkage in quantitative inheritance. In: Reev, E.C.R. and Waddington, C. H. (Eds.). Quantitative Inheritance, HMSO, London. 1952, 135-144.
2. Devi ES, Singh NB, Devi AB, Singh NG, Laishram JM. Gene action for fruit yield and its components in tomato (*Lycopersicon esculentum* Mill.). Indian J Genet. 2005; 65(3):221-222.
3. Dhaliwal MS, Gupta A, Singh S, Cheema DS. Assessment of genetic potential for economically important characters in an intervarietal cross of tomato: P-4-5-2 x UC 82-B. Indian J. Genet. 2001; 61:178-179.
4. Dubey K. Climatic and temperature requirement of tomato. 2012; Available online: <http://agropedia.iitk.ac.in>
5. Dutta AK, Akhtar S, Karak C, Hazra P. Gene actions for fruit yield and quality characters of tomato through generation mean analysis. Indian J Hort. 2013; 70(2):230-237.
6. Mather K, Jinks JL. Introduction to Biometrical Genetics. Chapman and Hall Ltd., London. 1982, 19.
7. Mohamed ES, Umaharan P, Phelps RH. Genetic nature of bacterial wilt resistance in tomato (*Lycopersicon esculentum* Mill.) accession LA 1421. Euphytica. 1997; 96:323-326.
8. Zalom FG, Wilson LT. Predicting phenological events of California processing tomatoes. Acta Hort. 1999; 487:41-48.