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**Research Article**

# Genetic analysis of yield and yield contributing traits in okra (*Abelmoschus esculentus* L. Moench)

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## Abstract

The generation mean analysis involving six generations ($P_1$, $P_2$, $F_1$, $F_2$, $B_1$ and $B_2$) was carried out to study the nature and magnitude of gene effects for eleven characters in okra. The study was conducted at Departmental Farm of Department of Agricultural Botany, College of Agriculture, Dr. B.S.K.K.V., Dapoli during *Kharif*-12 season. The Mather's individual scaling tests and Cavalli's joint scaling tests were used to detect the presence or absence of the epistatic interactions. The results obtained showed the importance of additive, dominant and all three types of epistatic interactions for most of the crosses and characters viz., nodal position for first flowering, days to first flowering, days to first picking, plant height, number of branches per plant fruit length, fruit weight, number of fruiting nodes per plant, number of fruits per plant, internodal length and yield per plant. For majority of crosses duplicate epistasis was observed while for fruit weight complementary epistasis was observed.

**Key words**

Gene action, Generation Mean, Okra, epistasis

## Introduction

Okra (*Abelmoschus esculentus* L. Moench) is considered as one of the most popular vegetable crop grown in the tropical, subtropical, low altitude region of Asia, Africa, America and warmer region of tropical Mediterranean basin. It is grown commercially in most of the states of India as *Kharif* as well as summer season crop with area 532.66 thousand hectare production 6346 thousand metric tonnes and productivity 12 tonnes/ha (Anonymous 2014 ) .

In this crop all the traits of economical importance are qualitatively inherited and are dependent on nature and magnitude of heritable variations. Yield ultimately is the final product is the result of complex of several yield attributing traits and being govern by polygenes are highly influence by environmental fluctuations. Therefore, a breeder should have information on the mode of inheritance and genetic architecture of yield and it's attributing traits. Information of gene actions thus enables the breeder to decide the suitable breeding method and selection strategy form crop improvement programme. Partitioning the heritable variations in to components is useful to provide information on inheritance of these quantitative traits. Most widely used approach for understanding the nature of gene action is growing the different generations to carry out the generation mean analysis. Although, it is widely used in several crops, very little information on these aspects is available in the literature on okra crop. The present study was undertaken to study nature and magnitude of gene action for yield and its components traits in okra.

## Materials and Methods

Six basic sets of generations viz., P1, P2, F1, F2, B1 and B2 were derived from three crosses involving five genotypes of okra. These six generations of three crosses viz., AKO-101-5-2 x Tarjani, AKO 101-5-2 x Evergreen and Parbhani Kranti x Shegaon local were produced and grown in RBD with three replications during Kharif season of 2012 at Botany farm, College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Maharashtra. The parental genotypes and $F_1$s were grown in two rows, the $F_2$s were grown in five rows and each backcross in three rows each of net 10 plants. The data was recorded on five plants for parents and $F_1$s, twenty plants for backcrosses and fourty plants for $F_2$s in each replication. The observations were recorded on nodal position for first flowering, days to first flowering, days to first picking, plant height, number of branches per plant, fruit length, fruit weight, number of fruits per plant, number of fruiting node per plant, internode length and yield per plant.

Individual scaling tests (A,B,C and D) and their variances were computed for each trait and cross for testing their deviations of segregation from the additive-dominance model of gene effects according to Mather and Jinks (1982). The joint scaling test was also implemented for confirmation of adequacy of additive-dominance model as provided by Cavelli (1952). The cases where the model was adequate i.e. no epistasis was present, three parameter model of Jinks and Jones (1958) was used for estimation of genetic components. When the scaling tests were significant i.e. inter allelic interactions were present six parameter model suggested by Hayman (1958), Jinks and Jones (1958) was used for estimation of genetic components of variation.

**Results and discussion**

The individual scaling tests for most of the characters and crosses were significant except for number of branches per plant. For nodal position for first flowering, plant height and fruit length, A or B scaling test were non significant, while C and D were highly significant for all the traits except cross 2 of nodal position for first flowering, cross three of fruit weight and all the crosses for number of branches per plant. For the joint scaling tests, ‘m’, ‘d’ and ‘h’ for all the crosses and traits were significant with some exceptions. While, $\chi^2$ tests were significant for all the characters and crosses except cross 2 for nodal position for first flowering and all the crosses for number of branches per plant. The individual scaling test and joint scaling test behaves in accordance with each other and confirm the presence of inter allelic gene interaction. The accordance of individual and joint scaling tests was earlier reported by Khanorkar and Kathiria (2010).

For three parameter model, additive gene effects (*d*) were significant for all crosses for nodal position for first flowering and number of branches per plant (except cross 2) while dominant gene effects (*h*) were non significant in these crosses for these two traits. The adequacy of additive dominance model for these traits are in conformity with the results obtained by Lal *et al.* (1975), Randhawa (1989), Aher *et al.* (2003) and Khanorkar and Kathiria (2010) for number of branches per plant. Under six parameter model, additive gene effects (*d*) was significant for seven cases such as, nodal position for first flowering , days to first flowering, days to first picking, plant height , number of fruits per plant and number of fruiting nodes per plant.

The additive and dominance gene effects were found significant for nodal position for first flowering (C1 and C3), days to first flowering (C2 and C3), days to first picking (C3), plant height (C1 and C3), fruit length, fruit weight (C2 and C3), number of fruits per plant, number of fruiting nodes per plant (C1 and C2), internode length and yield per plant all three crosses. The significant positive dominant effect is suppose to enhance the expression of the traits like fruit length, fruit weight and yield per plant (C3), while negative but in desirable directions, dominant gene action were also found significant for nodal position for first flowering (C1 and C3), days to first flowering (C2 and C3), days to first picking and internode length (C3).

Additive gene effects was reported significant for days to first flowering Lal et al. (1975), Poshiya and Shukla (1986), Ahlavat (2004), Ahmed et al. (2004), for days to first flowering and days to first picking by Khanorkar and Kathiria (2010), for node number for first flowering by Panda and Singh (2003), for plant height by Randhawa (1989) and Pawar el al. (1999). Additive gene effects for number of branches per plant were earlier depicted by Randhawa (1989), Patel et al. (1990) and Khanorkar and Kathiria (2010). For fruit length and fruit weight, significance of both additive and dominant gene effects were quoted by Aher et al. (2003), Chandra Deo et al. (2004), Arora et al. (2010), Khanorkar and Kathiria (2010) and Patel et al (2010).

The estimates of significant gene action either additive, dominance or both these gene actions are in complete agreement with the findings of Kulkarni et al. (1978), Kumar et al (2005), Arora et al. (2010) and Aulakh and Dhall (2012) for number of fruits per plant, Patel et al (2010) for internode length and Elongovan et al (1981), Singh and Singh (1984), Tripathi et al. (2002), Khanorkar and Kathiria (2010), Panda and Singh (2003) and Soher and Al-Aziz (2013) for yield per plant.

The epistatic gene effects i.e. additive x additive (*i*), additive x dominant (*j*) and dominant x dominant (*l*) were estimated significant at least for one case in cross 3 for nodal position for first flowering days to first flowering, days to first picking, cross 1 for plant height, number of fruits per plant and number of fruiting nodes per plant, cross 2 and 3 for fruit length and cross 1 and 2 for internode length. Additive x additive and dominant x dominant epistasis were significant for nodal position for first flowering and fruit length (C1), plant height (C3), fruit weight and number of fruits per plant (C2), number of fruiting nodes per plant (C2 and C3) and yield per plant (C1 and C2).

Additive x dominant and dominant x dominant gene effects were present for days to first flowering (C1), days to first picking (C1) and fruit weight (C3), while one case of significant ‘*i*' (cross 3 for number of fruits per plant) and two cases of significant *‘l’* (cross 2, plant height and cross 3, yield per plant). Significance of one or more types of the epistatic interaction for the characters under study were earlier quoted by Lal et al. (1975), Kulkarni et al. (1978), Pullaih *et al* (1996), Panda and Singh (2003), Khanorkar and Kathiria (2010) ad Akhtar et al (2010).

Regarding the type of epistasis, the complementary type of epistasis was detected for trait fruit weight in cross 3, while majority of cases duplicate epistasis was detected for nodal position for first flowering and plant height (C1 and C3), days to first flowering and days to first picking (C3), fruit weight (C2), number of fruits per plant and internode length (C1 and C2), while all the three crosses for fruit length, number of fruiting nodes per plant and yield per plant. The evidence of complementary epistasis for fruit weight was provided by earlier findings of Arora et al. (2010), while evidence of duplicate epistasis for one or more the traits studied was provide by the experiments of Kulkarni et al (1978), Panda and Singh (2003), Arora et al (2010), Khanorkar and Kathiria (2010), Patel et al (2010) and Soher and El-Aziz (2013).

The estimates of different types of gene effect provided the test for gene action and useful in analyzing genetic architecture of crop for future improvement for desirable characters. The estimates obtained from each cross may be unique in varying degrees and may not be applicable to the parental population (Sprague, 1966). Dominant followed by additive variance was major part of genetic variances for the yield and its component character. Also complexities in expression of epistatic variances would not give the desired improvement for yield and yield related characters. Therefore, use of bi-parental mating in early segregating generations, recurrent selection is suggested. The intermating would allow the undesirable linkages to break and establish the useful and unique recombinants. The selection should be delayed in late segregating generations so that considerable homozygosity is reached.

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Table 1: Scaling and joint scaling test for yield and yield contributing traits in okra.

| Traits | Cross | A | B | C | D | m | d | h | $x^2$ |
|---|---|---|---|---|---|---|---|---|---|
| Nodal position for first flowering | $C_1$ | -0.33 | -0.3 | 2.60** | 1.62** | 3.10** | 0.97** | 1.12** | 37.32** |
| | $C_2$ | -0.03 | 0.13 | 1 | 0.45 | 4.28** | -0.26** | 1.22** | 3.9 |
| | $C_3$ | -2.23** | -4.80** | -3.97** | 1.53** | 5.91** | -2.72** | -0.27 | 141.81** |
| Days to first flowering | $C_1$ | 1.40* | 8.07** | 10.47** | 0.5 | 42.5** | 4.88** | 4.11** | 173.58** |
| | $C_2$ | 1.87** | 1.07 | 4.2** | 0.63 | 49.71** | -2** | -1.41** | 14.14** |
| | $C_3$ | 3.80** | -0.47 | 17.53** | 7.1** | 51.16** | -6.03** | 3.58** | 197.28** |
| Days to first picking | $C_1$ | 2.13** | 8** | 13.2** | 1.53 | 50.84** | 4.58** | 4.6** | 145.06** |
| | $C_2$ | 2.80** | 1.53* | 4.8** | 0.23 | 58.56** | -2.99** | 0.08 | 19.95** |
| | $C_3$ | 2.93** | -2.33* | 15.6** | 7.5** | 60.46** | -7.13** | 4.3** | 128.37** |
| Plant height (cm) | $C_1$ | -6.30 | -22.97** | 120.37** | 74.82** | 124.63** | 18.21** | 44.61** | 415.42** |
| | $C_2$ | -12.80** | -15.13** | -14.57* | 6.68 | 142.5** | -6.38** | 19.86** | 29.66** |
| | $C_3$ | -19.73** | -16.1** | 104.1** | 69.97** | 151.35** | -31.54** | 53.17** | 165.38** |
| No. of branches per plant | $C_1$ | | | 0.267 | 0.133 | 2.17** | 1.51** | 1.05** | 0.267 |
| | $C_2$ | -0.33 | 0.07 | 0.83 | 0.55 | 3.72** | -0.1 | 0.17 | 6.82 |
| | $C_3$ | 0.07 | -0.43 | 0.57 | 0.47 | 3.38** | -1.42** | 2.22** | 3.42 |
| Fruit length (cm) | $C_1$ | -0.66** | -0.26 | 0.63** | 0.77** | 7.7** | 0.11** | 1.03** | 31.74** |
| | $C_2$ | -0.71** | -0.18 | 1.17** | 1.03** | 8.46** | -0.63** | 1.13** | 50.46** |
| | $C_3$ | 1.00** | -0.21 | -0.76** | -0.77** | 8.87** | -0.22** | 0.81** | 51.06** |
| Fruit weight (g) | $C_1$ | -0.27 | 2.15** | 3.48** | 0.8 | 7.84** | 1.2** | 2.63** | 244.81** |
| | $C_2$ | -0.31 | -0.34 | 2.94** | 1.79** | 9.58** | -0.51** | 1.32** | 79.99** |
| | $C_3$ | 0.49** | -1.19** | -0.28 | 0.21 | 10.26** | -0.46** | 1.19** | 51.23** |
| No. of fruits per plant | $C_1$ | 2.63** | -0.43 | 14.77** | 6.28** | 13.41** | 2.09** | 4.49** | 194.64** |
| | $C_2$ | -2.17** | -1.57** | 4.57** | 4.15** | 15.73** | -0.93** | 3.12** | 58.32** |
| | $C_3$ | 0.77 | 0.20 | 4.53** | 1.78** | 11.64** | 1.72** | 3** | 28.51** |
| No. of fruiting node per plant | $C_1$ | 3.87** | -1.73** | 18.17** | 8.02** | 19.1** | -2.26** | 4.51** | 177.80** |
| | $C_2$ | -2.67** | -1.43 | 7** | 5.55** | 20.96** | 1.1** | 4.27** | 52.19** |
| | $C_3$ | -0.13 | 0.43 | 4.97** | 2.33** | 16.49** | -2.62** | 3.09** | 23.31** |
| Inter-node length (cm) | $C_1$ | -0.02 | 1.40** | -1.66** | -1.52** | 9.28** | -0.35** | 0.3* | 52.47** |
| | $C_2$ | 1.26** | -0.03 | -1.18** | -1.2** | 9.41** | -0.26** | 0.08 | 65.24** |
| | $C_3$ | 0.96** | 2.72** | 9.21** | 2.76** | 11.10** | -1.43** | 1.66** | 239.81** |
| Days to last picking | $C_1$ | -6.60** | 1.33 | -10.13** | -2.43 | 102.79** | 10.26** | 9.43** | 15.07** |
| | $C_2$ | 0.47 | -0.73 | 3.6 | 1.93 | 113.11** | 1.79** | 0.77 | 2.97 |
| | $C_3$ | 0.87 | 17.80** | 26.73** | 4.03 | 122.55** | -7.8** | -2.33** | 107.87** |
| Yield per plant (g) | $C_1$ | 15.22** | 15.77** | 181.26** | 75.14** | 106.59** | 31.44** | 74.42** | 221.22** |
| | $C_2$ | -29.58** | -24.45** | 93.36** | 73.69** | 150.58** | -16.6** | 52.67** | 111.87** |
| | $C_3$ | 34.25** | 18.54** | 53.50** | 0.36 | 126.78** | 17.02** | 49.04** | 46.22** |

C1 = AKO-101-5-2 x Tarjani, , C2= AKO-101-5-2 x Evergreen and C3= Parbhani Kranti x Shegaon Local

* and ** indicate significance at $P<0.05$ and $P<0.01$ respectively.

Table 2: Estimates of gene effects for yield and yield contributing traits in okra using six parameter model

| Traits | Cross | m | d | h | i | j | l | Type of epistasis |
|---|---|---|---|---|---|---|---|---|
| Nodal position for first flowering | $C_1$ | 4.17** | 0.95** | -2.27** | -3.23** | -0.02 | 3.87** | Duplicate |
| | $C_2$ | 5.13** | -0.23* | -0.53 | | | | |
| | $C_3$ | 5.69** | -1.55** | -2.03* | -3.07** | 1.28** | 10.1** | Duplicate |
| Days to first flowering | $C_1$ | 45.93** | 1.97** | 1.57 | -1 | -3.33** | -8.47** | |
| | $C_2$ | 49.57** | -1.7** | -3.1* | -1.27 | 0.4 | -1.67 | |
| | $C_3$ | 56.17** | -4.17** | -11.77** | -14.20** | 2.13** | 10.87** | Duplicate |
| Days to first picking | $C_1$ | 55.05** | 2.03** | 0.1 | -3.07 | -2.93** | -7.07** | |
| | $C_2$ | 59.22** | -2.4** | -0.77 | -0.47 | 0.63 | -3.87 | |
| | $C_3$ | 65.68** | -4.73** | -11.63** | -15** | 2.63** | 14.4** | Duplicate |
| Plant height (cm) | $C_1$ | 173.28** | 25.58** | -106.62** | -149.63** | 8.33** | 178.9** | Duplicate |
| | $C_2$ | 152.39** | -4.83** | 8.83 | -13.37 | 1.17 | 41.3** | - |
| | $C_3$ | 203.8** | -32.77** | -86.75** | -139.93** | -1.82 | 175.77** | Duplicate |
| No. of branches per plant | $C_1$ | 2.43** | 1.5** | 0.5 | | | | |
| | $C_2$ | 4.8** | -0.03 | -2.3 | | | | |
| | $C_3$ | 4.33** | -1.47** | -0.03 | | | | |
| Fruit length (cm) | $C_1$ | 8.4** | -0.06 | -0.48 | -1.55** | -0.2 | 2.47** | Duplicate |
| | $C_2$ | 9.29** | -0.86** | -0.93** | -2.05** | -0.27* | 2.94** | Duplicate |
| | $C_3$ | 9.1** | 0.29** | 2.39** | 1.55** | 0.61** | -2.33** | Duplicate |
| Fruit weight (g) | $C_1$ | 9.69** | 0.1 | 0.59 | -1.6** | -1.21** | -0.28 | |
| | $C_2$ | 10.91** | -0.5** | -2.32** | -3.58** | 0.02 | 4.23** | Duplicate |
| | $C_3$ | 10.87** | 0.24* | 0.8* | -0.43 | 0.84* | 1.13* | Complementary |
| No. of fruits per plant | $C_1$ | 18.81** | 3.37** | -8.53** | -12.57** | 1.53** | 10.37** | Duplicate |
| | $C_2$ | 18.54** | -1.17** | -5.1** | -8.3** | -0.3 | 12.03** | Duplicate |
| | $C_3$ | 13.92** | 1.92** | -0.87 | -3.57** | 0.28 | 2.6 | |
| No. of fruiting node per plant | $C_1$ | 25.23** | 4.35** | -11.68** | -16.03** | 5.6** | 13.9** | Duplicate |
| | $C_2$ | 24.91** | -1.53** | -6.75** | -11.1** | -1.23 | 15.2** | Duplicate |
| | $C_3$ | 18.95** | 2.4** | -1.95 | -4.67** | -0.57 | 4.37** | Duplicate |
| Inter-node length (cm) | $C_1$ | 9.02** | -0.98** | 3.38** | 3.03** | -0.71** | -4.41** | Duplicate |
| | $C_2$ | 9.11** | 0.23* | 2.38** | 2.41** | 0.65** | -3.64** | Duplicate |
| | $C_3$ | 13.57** | -2.22** | -4.62** | -5.52** | -0.88** | 1.84 | |
| Yield per plant (g) | $C_1$ | 182.21** | 30.58** | -84.41** | -150.2** | -0.28 | 119.28** | Duplicate |
| | $C_2$ | 201.74** | -19.25** | -93.59** | -147.4** | -2.57 | 201.41** | Duplicate |
| | $C_3$ | 157.49** | 25.61** | 37.58** | -0.71 | 7.86 | -52.08** | Duplicate |

C1 = AKO-101-5-2 x Tarjani, , C2= AKO-101-5-2 x Evergreen and C3= Parbhani Kranti x Shegaon Local, m=mean, d=additive effect, h= dominance effect, i= additive x additive type gene interaction, j= additive x dominance type gene interaction and l= dominance x dominance type gene interaction.
* and ** indicate significance at $P<0.05$ and $P<0.01$ respectively.