# Genetic Analysis for Fruit Yield and its Contributing Characters in Okra (Abelmoschus esculentus L. Moench)

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## AUTHORS CONTRIBUTION

M. P. GAWAI, B. N. PATEL, D. J. PARMAR & M. M. PANDYA : Conceptualization, conducting experiment, drafting the orginal manuscript, data analysis;

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#### **ABSTRACT**

The components of gene effects for yield and its components in okra were studied using generation mean analysis from twelve generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$ ,  $B_2$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  and  $B_{2s}$ ) derived from eight different genotypes. Mean performance of  $F_1$  hybrids exceeded the value of their better parent in desired direction in the cross AOL 16-01  $\times$  AOL 18-08 for fruit weight, fruits per plant. In the cross GAO 5  $\times$  Red One Long for fruit length, fruit weight, fruits per plant, fruit yield per plant, branches per plant, plant height, internodes on main stem. In the cross AOL 19-10 × AOL 20-03 for fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, internodes on main stem, total soluble solids and in the cross Phule Prajatika  $\times$  GAO 5 for plant height, internodes on main stem, length of internode, while for days to initiation of flowering, none of the  $F_1$  *per se* performance was lower than its better parent. Mean performance of backcross progenies was not consistent in different crosses for different traits. The additive (d) gene effect found significant for all the four crosses for the traits viz., days to initiation of flowering, fruit length, fruits per plant and total soluble solid; crosses II, III and IV for the traits fruits per plant, fruit yield per plant and internode on main stem, crosses I, III, IV for traits fruit girth, crosses II and IV for the trait plant height, crosses III, IV for trait length of internode and cross I for the trait branches on main stem, cross III for trait fruit weight. Yield component traits in all crosses were governed by additive. Dominance and digenic and/or trigenic epistasis gene effects. When additive and non-additive gene effects involved, a breeding scheme efficient in exploiting both types of gene effects should be employed. Reciprocal recurrent selection could be followed which would facilitate exploitation of both gene effects. Duplicate type of gene action would be difficult for a plant breeder to get promising segregants through conventional breeding methods, so breeding procedures involving biparental mating may be used to restore transgressive segregants.

Keywords : Okra, Generation mean analysis, Gene action, Yield

CKRA, is an important annual vegetable crop raised<br>for its young, green and edible fruits without for its young, green and edible fruits without fibrous skin. In several African countries, people also consume leaves in addition to fruits. Okra is now frequently found in cafeterias, salad bars and restaurants as a fried or boiled vegetable dish. Okra stems and roots are used to purify the cane juice that is used to make gur or jaggery. Both young okra and

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133 frozen okra are in high demand right now. India is world's largest producer of okra and contributes more than 72 per cent (6 million tonnes) to the global production from an area of 0.5 million hectares. Okra with its significant share in fresh vegetable exports has immense potential for earning foreign exchange. According to FAO estimates around 75 per cent of the okra market is in India and 12 per cent is in Nigeria.

It can be cultivated both as a rainfed as well as irrigated crop. It is the most valued and popular vegetable consumed in fresh and dried forms. Over the last few years okra is gaining ground as a global crop because of the recognition of its nutritional values by the growing number of consumers. Especially after the COVID pandemic importance of healthy and balanced diet is getting ingrained in the global consumer mindset. India exports okra seeds to over 20 countries. In the recent past several research papers have been published by the Asian and African scientists working on okra genetics, breeding, genomics and agronomy. This further indicates okra's growing popularity as a global crop. Over 90 per cent of the okra seed market in India is covered by hybrid seeds. Global seed requirement of okra is expected to touch 6000 MT mark valued at \$ 300m by 2030 (GORT, 2022).

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250 million In India okra was grown in 546 thousand hectare area with production of 6700 thousand MT and 12.27 tonnes productivity. (Anonymous, 2021-22a). The important okra growing states in India are Gujarat, Maharashtra, Andhra Pradesh, Uttar Pradesh, Tamil Nadu, Karnataka, Haryana and Punjab in which it is cultivated as a kharif as well as summer season crop. The main okra growing districts in Gujarat are Surat, Tapi, Navsari, Banaskantha, Anand, Kheda, Vadodara, Dahod, Chhota Udaipur, Bharuch, Mehsana, Gandhinagar etc. In Gujarat, it was grown in 91.177 thousand hectares area and produced of 1098.021 thousand MT with 12.04 MT productivity during year 2021-22 (Anonymous, 2021-22b). This crop is highly remunerative and generates more employment opportunities in the country. Nevertheless, the amount of vegetables produced in our country falls far short of what is needed and only provides 135 g of the daily requirement for a balanced diet per person against 300g per day, as our population is increasing tremendously, there is an increasing demand for veggies. Vegetable crop demand is expected to reach 250 million tons by 2050 (Varmudy, 2001). High yielding and nutrient dense veggies must be produced immediately in our country to complete this titanic undertaking. Methods that offer information on the average effects of individual genes, interactions between alleles of the same locus and interactions

among genes of various loci were required to determine the amount of genetic influences on the expression of quantitative traits. It is preferable to effectively exploit the available genetic variability in order to improve the yield potential. The kind and extent of genetic diversity present in the population are further clarified by genetic study of quantitative traits. The estimates of gene effects in a crop improvement program directly affect the breeding method that will be used. While dominance and epistatic effects can be employed to take advantage of hybrid vigor, additive gene effects are helpful in the selection of superior genotypes.

## MATERIAL AND METHODS

Data on the crop comprising twelve generations  $(P_1, P_2, F_1, F_2, B_1, B_2, B_{11}, B_{12}, B_{21}, B_{22}, B_{1s} \text{ and } B_{2s})$  all grown in a year for each of the following four cross combinations were collected and computed in this study. Four crosses *viz.*, AOL  $16-01 \times \text{AOL}$  18-08 (cross I), GAO 5 × Red One Long (cross II), AOL 19-  $10 \times \text{AOL}$  20-03 (cross III) and Phule Prajatika  $\times$  GAO 5 (cross IV) and their parents were collected from Main Vegetable Research Station, Anand Agricultural University, Anand. These four crosses were produced at Main Vegetable Research Station, Anand Agricultural University, Anand during kharif 2020 were utilized for making further generations to obtain seeds of  $F_1$  (fresh),  $F_2$ ,  $B_1$  and  $B_2$  generations during kharif 2021. These three generations along with parents and hybrids were grown at MVRS farm, Anand Agricultural University, Anand during summer 2022 to develop the subsequent generations  $(B_{11}, B_{12}, B_{22})$  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  and  $B_{2s}$ ) and also the fresh seeds of  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$  generations. The seeds of  $P_1$ ,  $P_2$ ,  $F_2$ ,  $B_{1s}$  and  $B_{2s}$  were produced by selfing, while seeds of  $B_1$ ,  $B_2$ ,  $B_{11}$   $(B_1 \times P_1)$ ,  $B_{12}$   $(B_1 \times P_2)$ ,  $B_{21}$   $(B_2 \times P_1)$ ,  $B_{22}$  $(B_2 \times P_2)$  were produced by hand emasculation followed by pollination. The final evaluation of experimental materials was done during kharif 2022. In each replication for recording observation on eleven plant characters viz., days to initiation of flowering, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, branches per plant, plant height, internodes on main stem, length of internode and total



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soluble solids. The analysis of variance for compact family block design was performed cross-wise for all the characters as per standard procedure (Panse and sukhatme, 1969). The mean values of various generations were subjected to simple scaling test A, B, C and D (Hayman et al., 1955) to justify the adequacy of additive dominance model. In the event of significant estimates of simple scaling test and joint scaling test, i.e., inadequacy of additive dominance model, the three-parameter model (Cavalli, 1952). The joint scaling test (additive-dominance model or nonepistatic model) outlined by Cavalli (1952) was also applied to twelve generations to fit the threeparameter model (m), (d) and (h). The comparison between observed and expected generation means were made by Chi-square  $(\chi^2)$  test. When threeparameter model was inadequate as indicated by significant value, digenic interactions were estimated using six-parameter model. When the six-parameter or digenic model was inadequate  $[\chi^2_{(2)}$ -significant], a ten-parameter model was fitted which includes second order epistatic effects.

### RESULTS AND DISSCUSSION

the crosses GAO 5  $\times$  Rec<br>
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per plant crosses AOL 16-<br>
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in cross GAO 5  $\times$  Red One<br>
20-03 and Phule Prajatika<br>
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research. Considering ch The analysis of variance between generations within family revealed that all the four crosses exhibited significant differences for days to initiation of flowering, fruit length, fruit girth, fruits per plant, fruit yield per plant, plant height, length of internode and total soluble solids brix (Table 1). While, the generations differed significantly for fruit weight in the crosses GAO  $5 \times$  Red One Long, AOL 19-10  $\times$ AOL 20-03 and Phule Prajatika  $\times$  GAO 5, for branches per plant crosses AOL 16-01 × AOL 18-08 and Phule Prajatika  $\times$  GAO 5 and for internodes on main stem in cross GAO 5 × Red One Long, AOL 19-10 × AOL 20-03 and Phule Prajatika  $\times$  GAO 5. This indicates presence of sufficient variability in the material under research. Considering character-cross combinations, the significant differences were observed in 40 out of 44 cases. The data for different characters were subjected to generation mean analysis only for those crosses where significant differences were observed among the generations.

Perusal of Table 2 mean performance of  $F_1$  hybrids exceeded the value of their better parent in desired direction in the cross AOL  $16-01 \times$  AOL  $18-08$  for fruit weight. In the cross GAO  $5 \times$  Red One Long for fruit length, fruits per plant, fruit yield per plant, plant height, internodes on main stem. In the cross AOL  $19-10 \times \text{AOL}$  20-03 for fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, internodes on main stem, total soluble solids. In the cross Phule Prajatika  $\times$  GAO 5 for plant height, internodes on main stem, length of internode, while for days to initiation of flowering, none of the  $F_1$  per se performance was lower than its better parent. Mean performance of backcross progenies was not consistent in different crosses for different traits.

Days to initiation of flowering: In cross AOL 16-01  $\times$ AOL 18-08 backcross generations  $B_{12}$  and  $B_{2s}$ manifested lower mean value than both the parents revealing accumulation of desirable genes for earliness from corresponding parent, these generations could be further exploited for selection of permissible earliness.

*Fruit length:* In cross GAO  $5 \times$  Red One Long backcross generations  $B_1$  manifested higher mean value than both the parents revealing accumulation of desirable genes for big fruit length from corresponding parent, these generations could be further exploited for selection of permissible big fruit length.

*Fruit girth* : In cross AOL  $16-01 \times \text{AOL}$  18-08 backcross generations  $B_{22}$ ,  $B_{25}$  in cross GAO 5  $\times$  Red One Long backcross generations  $B_1 B_2 B_{11} B_{25}$  in cross AOL 19-10  $\times$  AOL 20-03 backcross generation B<sub>11</sub> manifested higher mean value than both the parents revealing accumulation of desirable genes for big fruit girth from corresponding parent, these generations could be further exploited for selection of permissible big fruit girth.

*Fruit weight* : In cross AOL  $16-01 \times$  AOL  $18-08$ backcross generations  $B_1$ ,  $B_2$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$ and  $B_{2s}$  in cross GAO 5  $\times$  Red One Long backcross generation  $B_{2s}$  (11.80),  $B_{21}$  (11.36) than other generation of different crosses, manifested higher



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mean value than both the parents revealing accumulation of desirable genes for more fruit weight from corresponding parent, these generations could be further exploited for selection of permissible more fruit weight. The  $B_1$  followed by  $B_2$  generation exhibited the highest fruit weight than other generations in the cross AOL  $16-01 \times$  AOL  $18-08$ indicating accumulation of genes for this trait were originated from female parent.

*Fruits per plant:* In cross GAO  $5 \times$  Red One Long backcross generations  $B_2$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  and  $B_{2s}$  in cross Phule Prajatika × GAO 5 backcross generation  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  manifested higher mean value than both the parents revealing accumulation of desirable genes for more fruits per plant from corresponding parent, these generations could be further exploited for selection of permissible more fruits per plant. Mean value of  $B_{22}$  (27.22g) showed the highest than all the other generations in the cross AOL 19-10  $\times$  AOL 20-03 for fruits per plant.

*Fruit yield per plant* : In cross AOL  $16-01 \times \text{AOL}$  18-08 backcross generations  $B_1$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{22}$ ,  $B_{1S}$  and  $B_{2S}$ in cross GAO  $5 \times$  Red One Long backcross generations  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{25}$  in cross Phule Prajatika  $\times$  GAO 5 backcross generation B<sub>1</sub>, B<sub>11</sub>, B<sub>12</sub>, B<sub>21</sub>, B<sub>22</sub>,  $B_{1s}$ , B<sub>2S</sub> manifested higher mean value than both the parents revealing accumulation of desirable genes for more fruit yield per plant from corresponding parent, these generations could be further exploited for selection of permissible more fruit yield per plant. However, the mean value of  $B_{22}$  (266.45g) backcross generation showed mean value among the other backcross generations of the cross as well as various crosses.

*Branches per plant* : In cross AOL  $16-01 \times \text{AOL}$  18-08 backcross generations  $B_{1s}$  in cross GAO 5  $\times$  Red One Long backcross generations  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$ ,  $B_{2s}$  in crosses AOL 19-10  $\times$  AOL 20-03 and Phule Prajatika × GAO 5 backcross generation  $B_{11}$ ,  $B_{12}$ manifested higher mean value than both the parents revealing accumulation of desirable genes for more branches per plant from corresponding parent, these generations could be further exploited for selection of permissible more branches per plant.

*Plant height:* In cross AOL  $16-01 \times \text{AOL}$  18-08 backcross generations  $B_2$ ,  $B_{12}$ ,  $B_{25}$  in cross GAO 5  $\times$ Red One Long backcross generation  $B_{12}$  and in cross Phule Prajatika  $\times$  GAO 5 backcross generations B<sub>12.</sub>  $B_{21}$ ,  $B_{22}$ ,  $B_{2s}$  manifested higher mean value than both the parents revealing accumulation of desirable genes for tallness from corresponding parent, these generations could be further exploited for selection of permissible tallness. Whereas, In cross AOL 16-01  $\times$  AOL 18-08 backcross generations  $B_1$  and in cross GAO 5  $\times$  Red One Long backcross generation  $B_1$ ,  $B_2$ ,  $B_{1s}$  manifested lower mean value than both the parents revealing accumulation of desirable genes for dwarfness from corresponding parent, these generations could be further exploited for selection of permissible dwarfness.

Internodes on main stem: The backcross generations  $B_2$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  and  $B_{2s}$  of the cross GAO 5  $\times$ Red One Long in cross AOL 19-10 × AOL 20-03 backcross generations  $B_{22}$ ,  $B_{1s}$  and Phule Prajatika  $\times$ GAO 5 backcross generations  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$ manifested higher mean value than both the parents revealing accumulation of desirable genes for more internodes on main stem from corresponding parent, these generations could be further exploited for selection of permissible internodes on main stem.

Length of internode: In cross AOL  $16-01 \times$  AOL  $18-$ 08 backcross generation  $B_2$  and Phule Prajatika  $\times$ GAO 5 backcross generations  $B_2, B_{2s}$  manifested higher mean value than both the parents revealing accumulation of desirable genes for length of internode from corresponding parent, these generations could be further exploited for selection of permissible length of internode.

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139 Total soluble solid: In cross AOL 16-01 × AOL 18-08 backcross generations  $B_2$ ,  $B_{11}$ ,  $B_{12}$ ,  $B_{22}$ ,  $B_{1S}$  and Phule Prajatika × GAO 5 backcross generations  $B_1 B_2$  in cross AOL 19-10  $\times$  AOL 20-03 backcross generations  $B_{11}$  and  $B_{21}$  in cross Phule Prajatika × GAO 5 backcross generations  $B_1$  and  $B_2$  manifested higher mean value than both the parents revealing accumulation of desirable genes for total soluble solid from corresponding parent, these generations could be further exploited for selection of permissible total soluble solid.

The  $F_1$  generated from the cross AOL 19-10  $\times$  AOL 20-03 manifested higher mean value than the other generations for fruit length (11.03 cm), fruit weight  $(11.01g)$  and fruit yield per plant  $(279.12 g)$ . The F<sub>1</sub> hybrid could be further tested for confirming its higher fruit yield per plant. For selection of any traits the generation which is superior to the parents can be advanced for future breeding programme. The significant estimate of scaling tests given by Hill indicated contribution of particular generation to nonallelic gene interactions contributed to higher order epistatic interactions.

The character days to initiation of flowering contribute non-allelic gene interaction exhibits by  $B_{11}$ ,  $B_{12}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in crosses AOL 16-01 × AOL 18-08 and GAO  $5 \times$  Red One Long,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{18}$  by cross AOL 19- $10 \times \text{AOL } 20-03$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{25}$  by cross Phule Prajatika × GAO 5. Whereas, character fruit length contributed for non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  in cross AOL 16-01 × AOL 18-08 and  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{25}$  for cross GAO 5  $\times$  Red One Long by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{15}$ ,  $B_{25}$  in cross AOL 19-10 × AOL 20-03, by  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{2s}$  in cross Phule Prajatika  $\times$ GAO 5.

Fruit girth: Contribution to non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{15}$ ,  $B_{25}$  in cross AOL 16-01  $\times$  AOL 18-08 by B<sub>11</sub>, B<sub>12</sub>, B<sub>21</sub>, B<sub>22</sub>,  $B_{1s}$  in cross GAO 5  $\times$  Red One Long, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross AOL 19-10 × AOL 20-03 by  $B_{22}$ ,  $B_{2s}$ in cross Phule Prajatika  $\times$  GAO 5.

Fruit weight: Contribution to non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{21}$ ,  $B_{25}$  in cross GAO 5  $\times$  Red One Long, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross AOL 19-10 × AOL 20-03, by  $B_{11}$ ,  $B_{12}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross Phule Prajatika  $\times$  GAO 5.

<sup>24</sup> Solution Sciences interactions exhibited by F<br>
<sup>24</sup> X Red One Long, by B<sub>11</sub>, B<br>
AOL 19-10 × AOL 20-03,<br>
cross Phule Prajatika × G<sub>1</sub><br>
Fruits per plant : Contril<br>
interactions exhibited by<br>
AOL 16-01×AOL 18-08, b<br>
in Fruits per plant : Contribution to non-allelic gene interactions exhibited by  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{25}$  in cross AOL 16-01×AOL 18-08, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{18}$ ,  $B_{25}$ in cross GAO 5  $\times$  Red One Long, by B<sub>11</sub>, B<sub>12</sub>, B<sub>21</sub>, B<sub>22</sub>,  $B_{1s}$ ,  $B_{2s}$  in cross AOL 19-10  $\times$  AOL 20-03, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  in cross Phule Prajatika × GAO 5.

Fruit yield per plant : Contribution to non-allelic gene interactions exhibited by  $B_{12}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross

AOL 16-01 × AOL 18-08 by  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross GAO 5 × Red One Long in cross AOL 19-10 × AOL 20-03 by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{1s}$ ,  $B_{2s}$  in Phule Prajatika  $\times$ GAO 5.

Branches per plant: Contribution to non-allelic gene interactions exhibited by  $B_{12}$ ,  $B_{22}$ ,  $B_{18}$ ,  $B_{28}$  in cross AOL  $16-01 \times \text{AOL}$  18-08, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$  in cross Phule Prajatika  $\times$  GAO 5.

Plant height: Contribution to non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{25}$  in cross AOL 16-01 × AOL 18-08, by  $B_{21}$ ,  $B_{1S}$  in cross GAO 5  $\times$  Red One Long, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$  in cross AOL 19-10 × AOL 20-03, by  $B_{11}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross Phule Prajatika  $\times$  GAO 5.

Internodes on main stem: Contribution to non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{12}$ ,  $B_{22}$ ,  $B_{15}$ ,  $B_{25}$  in cross GAO 5  $\times$  Red One Long, by B<sub>11</sub>, B<sub>12</sub>, B<sub>21</sub>, B<sub>22</sub>,  $B_{1S}$ ,  $B_{2S}$  in cross AOL 19-10 × AOL 20-03, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$  in cross Phule Prajatika × GAO 5.

Length of internode: Contribution to non-allelic gene interactions exhibited by  $B_{12}$ ,  $B_{22}$  in cross AOL 16-01  $\times$  AOL 18-08, by B<sub>11</sub>, B<sub>12</sub>, B<sub>22</sub>, B<sub>1S</sub>, B<sub>2S</sub> in cross GAO  $5 \times$  Red One Long, by  $B_{11}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1S}$  in cross AOL 19-10 × AOL 20-03, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{15}$ ,  $B_{25}$  in cross Phule Prajatika  $\times$  GAO 5.

Total soluble solids: Contribution to non-allelic gene interactions exhibited by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross AOL 16-01 × AOL 18-08, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross GAO 5  $\times$  Red One Long, by  $B_{11}$ ,  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross AOL 19-10 × AOL 20-03, by  $B_{12}$ ,  $B_{21}$ ,  $B_{22}$ ,  $B_{1s}$ ,  $B_{2s}$  in cross Phule Prajatika  $\times$ GAO 5.

Van Der Veen's tests gives idea about presence or absence of higher epistasis and further more valid conclusion can be made on the basis of  $\chi^2_{(2)}$  value at 6 degree of freedom which indicates adequacy or inadequacy of 6 parameter model and presence or absence of trigenic and higher order epistasis. The significant scaling tests of Van Der Veen and  $\chi^2_{(2)}$ together pointed out presence of trigenic or higher order epistasis in all four crosses for the characters







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\*,\*\* Significant at 5% and 1% levels respectively, C I: AOL 16-01 × AOL 18-08, C II: GAO 5 × Red One Long, C III: AOL 19-10  $\times$  AOL 20-03, C IV: Phule Prajatika  $\times$  GAO 5, D: Duplicate

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days to initiation of flowering, fruit girth, fruits per plant, total soluble solids in three crosses CII, III, IV characters fruit weight, fruit yield per plant, internodes on main stem, length of internode in crosses C I, II, IV character plant height and in cross C IV character branches per plant in all the cases Van Der Veen's tests were observed significant this indicates less influence of environment. The 3-parameter additivedominance model was found inadequate for all four crosses for the traits viz., days to initiation of flowering, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, branches on main stem, plant height, internode on main stem, length of internode and total soluble solid (brix). Surprisingly, none of the scaling tests was significant for fruits girth in the cross C IV. The 6-parameter model was also inadequate for all four crosses for all eleven characters (Table 3).

As  $\chi^2_{(2)}$  was significant so the data was subjected to 10 parameter model given by Hill for analysis of major, digenic and trigene gene effects. The additive (d) gene effect found significant for all the four crosses for the traits viz., days to initiation of flowering, fruit length, fruits per plant and total soluble solid, in crosses CII, III, IV for the traits viz., fruit weight, fruit yield per plant and internode on main stem; in crosses CI, III, IV for the trait fruit girth, in crosses CII, IV for the trait plant height, in crosses CI, IV for the trait length of internode and in cross CI for the trait branches on main stem. When the traits are controlled by such fixable type of gene effects, these could be improved through simple selection or a single seed descent method. Similar observations had earlier been reported by Srikanth et al. (2018) for fruit length, fruit weight, fruits per plant, fruit yield per plant, branches per plant, plant height and internode on main stem. Liou et al. (2002) for days to initiation of flowering, fruits per plant, fruit yield per plant and plant height. Allolli et al. (2020) for days to initiation of flowering and fruits per plant. Gediya (2020) for days to initiation of flowering, fruit yield per plant and plant height. Deshmukh et al. (2021) for fruit girth and fruits per plant. Whereas, Nichal et al. (2000) reported significant estimates of additive gene effect for days to initiation of flowering, fruit girth, fruit weight, fruit yield per plant, branches per plant and plant height. Gediya (2020) for length of internode. Deshmukh et al. (2021) for branches per plant for both additive and dominance gene effects.

In cross AOL  $16-01 \times$  AOL  $18-08$ , dominance (h), dominance  $\times$  dominance (1) and dominance  $\times$ dominance  $\times$  dominance (z) gene effect governs days to initiation of flowering, fruit length, fruit girth, plant height, total soluble solid whereas dominance (h) and  $dominance \times dominance$  (1) gene effect governs fruit yield per plant, dominance × dominance × dominance (z) gene effect governs fruit per plant. In cross GAO  $5 \times$  Red One Long dominance(h), dominance  $\times$ dominance (1) and dominance  $\times$  dominance  $\times$ dominance (z) gene effect governs days to initiation of flowering, fruit length, fruit girth, fruit weight, fruit per plant, plant height, internode on main stem, length of internode, total soluble solid, whereas dominance (h) and dominance  $\times$  dominance (l) gene effect governs fruit yield per plant. In cross AOL 19-10 × AOL 20-03 dominance (h), dominance  $\times$  dominance (1) and dominance  $\times$  dominance  $\times$  dominance (z) gene effect governs fruit per plant, internode on main stem, length of internode, total soluble solid. In cross Phule Prajatika  $\times$  GAO 5 dominance (h), dominance  $\times$ dominance (1) and dominance  $\times$  dominance  $\times$ dominance (z) gene effect governs days to initiation of flowering, fruit girth, fruit per plant, plant height, total soluble solid, dominance (h), dominance × dominance (l) gene effect governs fruit yield per plant, branches per plant, internode on main stem, dominance  $\times$  dominance (1) and dominance  $\times$ dominance  $\times$  dominance (z) gene effect governs fruit length. In a crop like okra, particularly dominance gene effects viz. (h) as well as (l) and (z) can be utilized in the form of hybrid variety.

All the three digenic interactions  $(i)$ ,  $(j)$  and  $(l)$  were significant for fruit girth and total soluble solid in cross AOL 16-01  $\times$  AOL 18-08, for days to initiation of flowering, fruit girth, fruit weight, plant height in cross GAO  $5 \times$  Red One Long, for fruit girth, fruits per plant, internode on main stem, length of internode, total soluble solid, in cross AOL 19-10 × AOL 20-03,

for days to initiation of flowering, fruit yield per plant, plant height and total soluble solid in cross Phule Prajatika  $\times$  GAO 5. All the four types of trigenic interactions  $viz.$ ,  $(w)$ ,  $(x)$ ,  $(y)$  and  $(z)$  were significant for fruit girth and total soluble solid in cross AOL 16-  $01 \times \text{AOL}$  18-08, for days to initiation of flowering, fruit yield per plant, plant height, total soluble solid in cross GAO  $5 \times$  Red One Long, for fruits per plant, fruit yield per plant, internode on main stem, length of internode, total soluble solid in cross AOL 19-10 x AOL 20-03, for days to initiation of flowering, fruit length, fruit yield per plant, total soluble solid in cross Phule Prajatika  $\times$  GAO 5. Interestingly, all digenic  $[(i), (j)$  and  $(l)]$  and trigenic  $[(w), (x), (y)$  and  $(z)]$ gene effects were significant for fruit girth and total soluble solid in cross AOL  $16-01 \times$  AOL 18-08, for days to initiation of flowering, fruit yield per plant, plant height in cross GAO  $5 \times$  Red One Long, for fruits per plant, internode on main stem, length of internode, total soluble solid, in cross AOL 19-10 × AOL 20-03, for days to initiation of flowering, fruit yield per plant and total soluble solid in cross Phule Prajatika  $\times$  GAO 5, where additive (d) and dominance (h) gene effects and/or the digenic and trigenic epistasis collectively governed the inheritance of the trait, it would be difficult to get promising segregants through conventional breeding methods. Hence, some sort of recurrent selection by ways of intermating the most desirable segregants followed by selection, diallel selective mating or the use of multiple crosses, could be effective alternative approaches for the improvement of these traits.

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18-08 for days to initiation<br>
fruit girth, fruits per plat<br>
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and total soluble solids. In<br> The  $\chi^2_{(3)}$  value at 2 degree of freedom were significant in ten parameter model in cross AOL 16-01 × AOL 18-08 for days to initiation of flowering, fruit length, fruit girth, fruits per plant, fruit yield per plant, branches per plant, plant height, length of internode and total soluble solids. In cross GAO 5 × Red One Long for days to initiation of flowering, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, plant height and total soluble solids. In cross AOL 19-10  $\times$  AOL 20-03 for fruit girth, fruit weight, fruits per plant, fruit yield per plant, plant height and total soluble solids. In cross Phule Prajatika × GAO 5

for days to initiation of flowering, fruit length, fruit girth, fruit weight, fruits per plant, fruit yield per plant, branches per plant, plant height and total soluble solids indicating presence of higher order epistasis and/or linkage. The signs of either two or all the three gene effects *viz.*, dominance (h), dominance  $\times$  dominance (1) and dominance  $\times$  dominance  $\times$  dominance (z) suggest the presence of duplicate type of epistasis. Duplicate epistasis was observed in all the crosses for all the characters may result in decreased variation in  $F_2$  and subsequent generations and consequently reduce heterosis and also might hinder the pace of crop improvement through selection alone. However, such characters including yield indicates that they might be improved through recurrent selection practiced in the progenies obtained through biparental mating system that in turn would help in exploiting the duplicate type of non-allelic interaction and allow recombination and concentration of genes resulting cumulative effects in population since this method is helpful in breaking up undesirable linkages as suggested for days to initiation of flowering, fruit length, fruit girth, fruits per plant, fruit yield per plant, branches per plant, plant height, internode on main stem and length of internode by Patel et al. (2010). Wakode et al. (2015) and Gediya (2020) reported duplicate type of epistasis for days to initiation of flowering, fruit length, fruits per plant, fruit yield per plant, branches per plant, plant height and length of internode. Akotkar et al. (2010) observed duplicate type of epistasis for days to initiation of flowering, fruit length, fruit girth, fruit weight, fruits per plant, branches per plant and plant height. Adiger et al. (2015) reported duplicate type of epistasis for days to initiation of flowering, fruit girth, fruit weight, fruits per plant, fruit yield per plant and length of internode. Balakrishnan et al. (2014) observed duplicate type of epistasis for days to initiation of flowering, fruit weight, fruits per plant, fruit yield per plant and plant height. Akhtar et al. (2010) reported duplicate type of epistasis for days to initiation of flowering, fruit length, fruits per plant, fruit yield per plant and plant height. Modha (2009) observed duplicate type of epistasis for days to initiation of flowering, fruit weight, fruit yield per plant, plant height and internode

on main stem. Deshmukh et al. (2021) also reported duplicate type of epistasis for fruit length, fruit girth and fruit weight. Overall, it could be concluded that fruit yield per plant and its component traits in all four okra crosses were governed by additive, dominance and digenic and/or trigenic epistasis gene effects. When additive and non-additive gene effects involved, a breeding scheme efficient in exploiting both types of gene effects should be employed. Reciprocal recurrent selection could be followed which would facilitate exploitation of both additive and non-additive gene effects simultaneously. Under a situation of duplicate type of gene action, it would be difficult for the plant breeders to get promising segregants through conventional breeding methods. Therefore, breeding procedures involving either multiple crosses or biparental mating may be used to restore transgressive segregants.

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