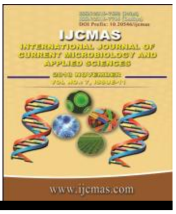
Int.J.Curr.Microbiol.App.Sci (2018) *7*(11): 2369-2379

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 7 Number 11 (2018)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2018.711.268

Assessment of Genetic Architecture of Some Economic Traits in Okra (*Abelmoschus esculentus* (L.) Moench) through Generation Mean Analysis

Mekala Srikanth*, S.K. Dhankhar, N.C. Mamatha and Sumit Deswal

Department of Vegetable Science, CCS Haryana Agricultural University, Hisar, Haryana – 125004, India

**Corresponding author*

ABSTRACT

The nature and magnitude of gene action was analysed using six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 for yield and yield contributing characters in four inter varietal crosses of okra. The scaling and joint scaling tests indicated the presence of epistatic gene effect for all the characters in four crosses. Duplicate epistasis was predominant in most of the yield and yield attributing characters in all the four crosses except number of fruits per plant, which showed complimentary epistasis. Study of gene action revealed that both additive and non-additive components of genetic variations were found important for the inheritance of fruit yield and its attributes. However, fixable components of genetic variation *i.e.*, Additive gene effects with additive x additive interactions for yield contributing traits *i.e.* fruit length and number of fruits per plant in all crosses except HB-25-2 x HB-32, for fruit diameter in all crosses except HB-40 x HB-27 and for fruit weight in crosses Hisar Naveen x Varsha Uphar and HB-25-2 x HB-32 were found significant. These traits in these crosses can be improved through pedigree method. The rest of the characters in respective cross combinations showed additive and non-additive type of gene effects. These traits would be possible to improve by either recurrent selection or bi-parental mating system in segregating generations followed by selection. Further, all the three types of gene actions *viz.*, additive (d), dominance (h) and epistatic gene effects [additive x additive (i), additive x dominance (j) and dominance x dominance (l)] were involved in the inheritance of number of fruits per plant in the crosses HB-25-2 x HB-32 and HB-1157 x Pusa Sawani.

Keywords

Scaling, Joint scaling, Additive, Dominance, Epistasis, Okra

Article Info

Accepted:
18 October 2018
Available Online:
10 November 2018

Introduction

Okra, [*Abelmoschus esculentus* (L.) Moench] also known as lady's finger is one of the important fruit vegetable crop mainly grown for its tender green fruits. It is the preferred fruit vegetable crop grown extensively in the tropical, subtropical and warmer parts of the temperate zones of the world. Basically, okra is a self-pollinated crop but natural cross-pollination occurs up to an extent of 4-19% (Choudhury and Choomsai, 1970), thus it is classified as an often cross-pollinated crop, which renders considerable genetic diversity. It has several virtuous features, which help the breeders and geneticists to have quick genetic results. Among these features *i.e.* short life span, adaptability to wide range of soil and climatic conditions, ease in emasculation, very high per cent of fruit set and large number of seeds per fruit makes commercial exploitation of hybrid vigour easy. Thus, it is one of the best-suited crops for genetic studies.

Number of workers either using line x tester analysis or diallel approach has reported predominant role of either additive or non-additive gene actions in the inheritance of growth and fruit yield parameters in okra. However, these procedures are based on absence of epistasis, which is also important genetic component should also be estimated for better breeding strategies. Among several genetic models, the six-parameter model of generation mean analysis approach of Hayman (1958) involving the joint scaling test of Cavalli (1952) for estimation of additive, non-additive and epistasis is simple and an efficient approach. According to this model, six components *viz.*, population mean (m), additive effect (d), dominance effect (h) and additive × additive (i), additive × dominance (j) and dominance × dominance (l) type of epistatic effects, could be estimated (Hayman, 1958; Jinks and Jones, 1958), which would certainly provide a sound basis for formulating the suitable breeding strategy. Generation mean analysis, even though an efficient tool to understand the nature of gene action and is employed in different crops, limited information on inheritance and gene action of morphological traits, fruit yield component traits is available in okra (Patel *et al.*, 2010).

Materials and Methods

Six basic sets of generations namely P_1, P_2, F_1, F_2, BC_1 and BC_2 were derived from four inter varietal crosses (Hisar Naveen x Varsha Uphar, HB 25-2 x HB-32, HB-40 x HB-27, HB-1157 x Pusa Sawani) involving eight contrasting genotypes of okra. The experimental materials comprised of six generations for each of the four crosses were sown during rainy season 2016 in Compact Family Block Design at spacing of 60 x 30 cm replicated thrice. Each replication consisted two rows for each of non-segregating generations (P_1, P_2 and F_1), ten rows for each of BC_1 and BC_2 generations and twenty-five rows of each F_2 generation. Each row was three meters long accommodating ten plants thereby maintaining 20 plants of each non-segregating generations (P_1, P_2& F_1), 100 plants of each back cross (BC_1 & BC_2) and 250 plants of each F_2 in every replication. The recommended package of practices of CCS Haryana Agricultural University, Hisar followed to raise the crop. Observations for yield and its traits was recorded on randomly selected five competitive plants from each non-segregating generations and 50 plants in each back cross generations and 150 plants per replication of each F_2 generation were recorded.

Statistical and genetic analysis

Using OPSTAT developed by statistic department CCS HAU, analyses of variances were done for six populations (The two parents, F_1, F_2, BC_1 and BC_2) within each cross with respect to all the studied traits. The type of interactions in crosses was sorted out with the help of scaling test (Mather, 1949) as well as joint scaling tests by Cavalli (1952) and the gene effects were estimated using the model as suggested by Hayman (1958) and Jinks and Jones (1958).

Results and Discussion

In this study, yield and yield attributing traits were investigated. Therefore, analyses of variances were made in order to test the significance of differences among crosses as well as populations within crosses. Analysis of variance for generation means comprising six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of four crosses were computed for yield and its traits of each cross and mean sum of squares for treatments with their degrees of freedom are presented in Table 1. Perusal of the data revealed that mean sum of squares for treatments was highly significant for all the characters in all the four crosses studied except for fruit length in cross HB-1157 x Pusa Sawani.

The generation means of six population was further carried out to determine scaling test to detect the presence or absence of epistasis and the estimation of the genetic components for growth, yield and its traits in okra. This indicates the presence of an appreciable amount of variability in the base material as well as in the generated materials. The results are in harmony with the findings of Abdelmageed *et al.,* (2012), Mistry (2013) and Soher *et al.,* (2013).

Gene action

Days to fifty per cent flowering

The additive-dominance model was inadequate in all four crosses for days to fifty per cent flowering (Table 2). The results obtained from six-parameter model revealed that earliness is a highly desirable attribute in okra as the market prices are invariably high in the season. The days to fifty per cent flowering are one particular indicator for earliness. Fitting of six-parameter model revealed that additive [d] gene effects were positive and significant in the crosses Hisar Naveen x Varsha Uphar and HB-40 x HB-27. However, the crosses HB-25-2 x HB-32 and HB-1157 x Pusa Sawani exhibited significant negative additive [d] gene effects. Significant negative dominance [h] gene effects, and non-allelic gene interactions were observed in the cross HB-1157 x Pusa Sawani, however dominance [h] gene effects and additive x additive gene interaction were found negative and significant in HB-40 x HB-27, so pedigree method should be followed for effective selection of segregants. Positive significant non-allelic gene interaction additive × dominance [j] and dominance × dominance [l] were observed in HB-40 x HB-27. The cross HB-25-2 x HB-32 exhibited significant negative dominance [h] gene effects and significant negative additive x additive gene interaction. Additive x dominance [j] gene interaction were positively significant in the cross Hisar Naveen x Varsha Uphar, while dominance x dominance [l] gene interaction were negatively significant in the same cross. Opposite signs for dominance [h] and dominance × dominance [l] interactions were observed in the crosses HB-40 x HB-27 and HB-1157 x Pusa Sawani, which implied the presence of duplicate type of gene action suggesting the selection intensity should be mild in the earlier and intense in the later generations because it marks the progress through selection. In another two crosses, simple selection procedure might followed for selection of early segregants. Additive, dominance, and duplicate type of epistasis was depicted by Akthar *et al.,* (2010), Khanorkar and Kathiria (2010), Akotkar and De (2014) and Wakode *et al.,* (2015) whereas, non-additive type of effects were reported by Das *et al.,* (2013).

Branches per plant

Additive [d] and dominance [h] gene effects were positive and significant in Hisar Naveen x Varsha Uphar and HB-1157 x Pusa Sawani crosses. However, the magnitude of dominance gene effects was higher than additive gene effects, which suggested greater role of dominance in the expression of this trait and dominant tend to increase the branches per plant. Additive x additive [i] and additive x dominance [j] interactions were observed positively significant in Hisar Naveen x Varsha Uphar, while additive x additive [i] and additive x dominance [j] epistasis were observed significant and negative in the crosses HB-25-2 x HB-32 and HB-40 x HB-27, respectively while both the crosses exhibited dominance x dominance [l] interaction in a positive significant manner. All three type of epistasis additive x additive [i], additive x dominance [j] and dominance x dominance [l] were found positively significant which specifies the presence of complementary type of epistasis in the cross HB-1157 x Pusa Sawani. Okra being often cross-pollinated, progeny selection might be adopted for the improvement of this trait. In rest of the crosses HB-25-2 x HB-32 and HB-40 x HB-27, only epistasis interactions were noted significant which showed that inheritance is complex in nature. Involvement of additive gene effect in the expression of this trait has been reported by Patel *et al.*, (2013) and Wakode *et al.*, (2015). Whereas, Kumar and Anandan (2006) and Mistry (2013) portrayed the presence of additive x additive (i) and dominance x dominance (l) epistatic gene effects for branches per plant.

Plant height

Additive [d] gene effects were found positive and significant in HB-25-2 x HB-32 and negatively significant in HB-40 x HB-27. Significant and negative dominance [h] gene effects were observed in the cross HB-40 x HB-27 while, cross HB-1157 x Pusa Sawani exhibited positive significant with relatively higher magnitude of gene effects than additive [d].

Additive × additive [i] gene interaction were found significant and negative in HB-25-2 x HB-32 and HB-40 x HB-27, while HB-1157 x Pusa Sawani exhibited positive and significant Additive × additive [i] gene interaction. Additive x dominance [j] gene interaction were found significant in HB-25-2 x HB-32 and HB-1157 x Pusa Sawani, while dominance x dominance [l] gene interaction in all the four crosses found positive and significant. The opposite signs of [h] and [l] in HB-40 x HB-27 suggested duplicate type of gene action whereas, same signs of [h] and [l] in the HB-1157 x Pusa Sawani advocated the presence of complementary type of gene action indicated that simple selection may be followed for improvement of okra. Das *et al.*, (2013) and Soher *et al.*, (2013) observed non-additive gene action for this trait while Kumar and Anandan (2006), Akthar *et al.*, (2010), Mistry (2013), Akotkar and De (2014) and Wakode *et al.*, (2015) reported duplicate type of epistasis for plant height.

Nodes per plant

Additive [d] gene effects were found positive and significant in all the crosses except in HB-40 x HB-27 found negative and significant. Positive and significant dominance [h] gene effects were observed in Hisar Naveen x Varsha Uphar, HB-40 x HB-27 and HB-1157 x Pusa Sawani. Additive x additive [i] gene interaction were found positive and significant in all the crosses this indicated that this trait can be improved through progeny selection in these crosses, Additive × dominance [j] gene interaction were recorded as negative and significant in the cross HB-40 x HB-27 whereas, dominance x dominance [l] gene interaction were recorded negatively significant in Hisar Naveen x Varsha Uphar opposite signs of [h] and [l] in this cross suggested duplicate type of gene interaction which suggested greater role of dominance in the expression of this trait so, selection in the later generations will be effective. Involvement of additive gene effect in the expression of this trait has been reported by Patel *et al.*, (2013) and Wakode *et al.*, (2015). Whereas, Kumar and Anandan (2006) and Mistry (2013) portrayed the presence of additive x additive (i) and dominance x dominance (l) epistatic gene effects for nodes per plant.

Table.1 Analysis of variance of six-generations means in four different crosses for growth, yield and its attributing traits in okra

Crosses	Sources of variation	d.f	DTF	BR	PH	NPP	FL	FW	No. F/P	YLD/P
Hisar Naveen x Varsha Uphar	Replications	2	2.642	0.135	7.047	0.418	0.045	0.050	3.872	585.410
	Treatments	5	3.608*	0.700**	141.897**	1.275*	0.381**	1.436**	24.872**	4791.637**
	Error	10	1.031	0.102	14.621	0.326	0.035	0.151	2.218	406.284
HB-25-2 x HB-32	Replications	2	1.034	0.300	19.961	0.205	0.036	0.121	0.277	30.630
	Treatments	5	4.107*	0.346*	442.321**	3.639*	0.774**	1.297**	28.655**	3528.664**
	Error	10	1.201	0.073	14.392	0.840	0.119	0.084	2.399	103.372
HB-40 x HB-27	Replications	2	0.393	0.150	74.330	0.619	0.019	0.049	1.457	174.791
	Treatments	5	5.518*	0.811**	117.725**	1.324*	0.852**	1.061**	8.421**	1609.903**
	Error	10	1.023	0.130	19.557	0.246	0.077	0.144	0.910	140.918
HB-1157 x Pusa Sawani	Replications	2	2.695	0.201	26.666	0.553	0.036	0.064	13.148	1372.889
	Treatments	5	5.039*	1.576**	539.418**	2.134*	0.102	0.381**	13.522**	2054.104**
	Error	10	0.557	0.040	47.947	0.463	0.067	0.102	1.644	259.867

*, ** Significant at 5 and 1% respectively

DTF-Days to fifty per cent flowering, BR- Branches per plant, PH-Plant height (cm), NPP- Nodes per plant, FL-Fruit length (cm), FW- Fruit weight (cm), No. F/P-Number of fruits per plant, YLD/P –Fruit yield per plant

Table.2 Estimates of gene effects (±SE of mean) for various yield traits in four crosses using Mather and Jinks (1982) six-parameter model

Characters Gene effects								
	m ± SE	**[d] ± SE**	**[h] ± SE**	**[i] ± SE**	**[j] ± SE**	**[l] ± SE**	**χ2**	**Epistasis**
Days to 50 % flowering								
C-1	44.66 ± 0.09**	1.56 ± 0.20**	-0.06 ± 0.71	-0.12 ± 0.56	5.93 ± 0.78**	-2.81 ± 1.26*	71.58**	--
C-II	45.31 ± 0.10**	-0.87 ± 0.24**	-3.95 ± 0.98**	-4.35 ± 0.65**	1.18 ± 0.85	2.39 ± 1.81	54.55**	--
C-III	45.48 ± 0.14**	0.46 ± 0.27	-9.90 ± 0.97**	-8.10 ± 0.80**	2.52 ± 0.87**	15.18 ± 1.65**	116.26**	**Duplicate**
C-IV	46.36 ± 0.06**	-1.01 ± 0.16**	-12.25 ±0.67**	-10.85 ± 0.41**	-2.82 ± 0.68**	9.73 ± 1.26**	747.47**	**Duplicate**
Branches per plant								
C-1	3.08 ± 0.05**	0.77 ± 0.12**	2.18 ± 0.41**	1.31 ± 0.32**	1.01 ± 0.42*	0.09 ± 0.75	41.65**	**--**
C-II	3.03 ± 0.03**	-0.02 ± 0.08	-0.29 ± 0.35	-0.72 ± 0.21**	-1.04 ± 0.35**	2.29 ± 0.67**	25.21**	--
C-III	3.69 ± 0.04**	-0.06 ± 0.10	-0.64 ± 0.41	-1.77 ± 0.28**	-0.66 ± 0.34*	4.65 ± 0.75**	53.57**	--
C-IV	3.01 ± 0.03**	0.82 ± 0.10**	2.72 ± 0.42**	1.62 ± 0.25**	1.17 ± 0.45**	2.24 ± 0.80**	99.11**	**Complimentary**
Plant height								
C-1	89.63 ± 0.94**	2.40 ± 2.19	4.56 ± 6.67	5.79 ± 5.78	-0.26 ± 5.64	39.77 ± 11.66**	47.49**	--
C-II	92.04 ± 0.65**	3.82 ± 1.23**	-3.18 ± 4.81	-20.75 ± 3.59**	-11.61 ± 5.34*	97.91 ± 8.50**	162.30**	--
C-III	113.53 ± 0.81**	-3.50 ± 1.67*	-56.5 ± 6.12**	-62.13 ± 4.68**	-3.08 ± 4.17	84.73 ± 10.84**	177.67**	**Duplicate**
C-IV	80.23 ± 0.77**	-0.9 ± 1.64	30.95 ± 6.37**	19.85 ± 4.51**	-21.86± 4.94**	60.89 ± 11.57**	139.39**	**Complimentary**
Nodes per plant								
C-1	14.38 ± 0.08**	0.78 ± 0.16**	3.27 ± 0.72**	3.67 ± 0.47**	0.36 ± 0.78	-3.02 ± 1.32*	68.37**	**Duplicate**
C-II	14.29 ± 0.07**	0.78 ± 0.17**	-0.24 ± 0.73	2.04 ± 0.47**	-0.82 ± 0.70	2.23 ± 1.35	21.05**	--
C-III	13.6 ± 0.07**	-0.74 ± 0.18**	2.58 ± 0.63 **	1.01 ± 0.47*	-2.09 ± 0.59**	-1.16 ± 1.15	17.12**	--
C-IV	12.94 ± 0.09**	0.78 ± 0.21**	5.78 ± 0.80**	4.62 ± 0.55**	0.84 ± 0.77	-1.83 ± 1.48-	91.03**	--

Note- C-I- Hisar Naveen x Varsha Uphar, C-II- HB-25-2 X HB-32, C-III- HB-40 X HB-27, C-IV-HB-1157 X Pusa Sawani.

Conti…

Characters Gene effects								
	m ± SE	**[d] ± SE**	**[h] ± SE**	**[i] ± SE**	**[j] ± SE**	**[l] ± SE**	**χ2**	**Epistasis**
Fruit length								
C-1	8.21 ± 0.03**	0.14 ± 0.05**	-0.32 ± 0.24	-0.94 ± 0.16**	-0.17 ± 0.20	3.21 ± 0.44**	57.97**	--
C-II	8.62 ± 0.02**	0.96 ± 0.07**	0.63 ± 0.25**	-0.16 ± 0.18	1.07 ± 0.22**	-0.08 ± 0.46	24.27**	--
C-III	7.49 ± 0.01**	0.13 ± 0.05*	1.96 ± 0.20**	0.60 ± 0.13**	-0.37 ± 0.24	0.07 ± 0.39	33.53**	--
C-IV	7.72 ± 0.01**	0.19 ± 0.05**	0.73 ± 0.16**	0.57 ± 0.12**	-0.04 ± 0.18	-0.16 ± 0.30	38.58**	--
Fruit weight								
C-1	8.09 ± 0.03**	0.38 ± 0.09**	2.51 ± 0.30**	1.98 ± 0.23**	0.33 ± 0.30	2.17 ± 0.57**	255.15**	**Complementary**
C-II	8.69 ± 0.03**	0.38 ± 0.03**	-1.77 ± 0.36**	-3.15 ± 0.22**	-0.07 ± 0.29	5.87 ± 0.68**	204.00**	**Duplicate**
C-III	7.27 ± 0.03**	-0.02 ± 0.10	1.26 ± 0.35**	0.70 ± 0.25**	0.16 ± 0.34	3.45 ± 0.65**	99.00**	**Complementary**
C-IV	8.95 ± 0.03**	-0.02 ± 0.09	0.47 ± 0.33	-0.02 ± 0.24	-0.02 ± 0.34	2.60 ± 0.60**	33.41**	--
Number of fruits per plant								
C-1	18.50 ± 0.21**	1.91 ± 0.52**	5.99 ± 1.64**	5.06 ± 1.35**	-0.30 ± 1.72	11.59 ± 2.94**	115.01**	**Complementary**
C-II	18.97 ± 0.15**	-4.82 ± 0.45**	5.71 ± 1.49**	2.88 ± 1.09**	-12.24 ± 1.73**	15.06 ± 2.80**	174.86**	**Complementary**
C-III	16.55 ± 0.24**	-0.84 ± 0.50	12.08 ± 1.65**	8.94 ± 1.39**	-2.76 ± 1.24*	-3.97 ± 2.86	73.62**	--
C-IV	18.9 ± 0.22**	3.62 ± 0.48**	4.62 ± 1.79**	2.69 ± 1.31*	6.18 ± 1.44**	9.28 ± 3.24**	51.88**	**Complementary**
Fruit yield per plant								
C-1	152.00 ± 2.25**	25.54 ± 6.02**	103.10 ± 19.29**	83.34 ± 15.05**	2.44 ± 21.32	153.48 ± 35.27**	163.51**	**Complementary**
C-II	165.33 ± 1.60**	-30.17 ± 4.26**	17.26 ± 15.87	-38.23 ± 10.66**	-99.59 ± 17.41**	252.91 ± 29.73**	117.68**	--
C-III	121.99 ± 2.09**	-8.06 ± 4.76	115.15 ± 16.56**	77.544 ± 12.70**	-21.06 ± 13.96	42.40 ± 29.76	93.60**	--
C-IV	171.14 ± 2.55**	32.49 ± 5.07**	48.90 ± 21.00*	17.70 ± 14.40	55.09 ± 16.12**	149.87 ± 38.09**	46.51**	**Complementary**

Note- C-I- Hisar Naveen x Varsha Uphar, C-II- HB-25-2 X HB-32, C-III- HB-40 X HB-27, C-IV-HB-1157 X Pusa Sawani

Fruit length

Positive and significant additive [d] gene effects were observed in all the four cross combinations whereas, dominance [h] gene effects were positive and significant in three crosses *viz.*, HB-25-2 x HB-32, HB-40 x HB-27 and HB-1157 x Pusa Sawaniindicating its major role in inheritance of this trait. Additive × additive [i] gene interactions were recorded as negatively significant in Hisar Naveen x Varsha Uphar, while it was positively significant in the crosses HB-40 x HB-27 and HB-1157 x Pusa Sawani. Additive x dominance [j] were found significant in HB-25-2 x HB-32 whereas, dominance × dominance [l] gene interactions found significant in Hisar Naveen x Varsha Uphar. Okra is often-cross pollinated crop and majority of varieties developed in pedigree selection. Therefore, progeny selection can be followed for improvement of this trait. Soher *et al.*, (2013) reported additive type of reactions for the trait. On the other hand, the importance of non-additive gene actions in the expression of fruit length were reported by Das *et al.*, (2013) and Seth *et al.*, (2016) Akthar *et al.*, (2010). Duplicate and complimentary gene actions for fruit length reported by Akotkar and De (2014) in okra.

Fruit weight

Fitting of six- parameter model revealed that additive [d] gene effects were observed as positive and significant in Hisar Naveen x Varsha Uphar and HB-25-2 x HB-32 crosses. Dominance [h] gene effects were positive and significant in Hisar Naveen x Varsha Uphar and HB-40 x HB-27 whereas, it was negative and significant in the cross HB-25-2 x HB-32indicating that the dominant gene effect is prominent in these two crosses. Additive × additive [i] gene interactions were significant and positive in the crosses Hisar Naveen x Varsha Uphar and HB-40 x HB-27 while, it was negatively significant in the cross HB-25-2 x HB-32. Positive and significant dominance × dominance [l] gene interactions were observed in all the crosses along with complimentary type of epistasis in the crosses Hisar Naveen x Varsha Uphar and HB-40 x HB-27indicated that simple selection may be followed. The values of [h] and [l] were of the opposite sign, which indicated the presence of duplicate type (gene effect) of epistasis in HB-25-2 x HB-32indicating that selection in later generation adopted. Both additive and non-additive gene action for fruit weight depicted by Seth *et al.*, (2016). Das *et al.*, (2013) observed preponderance of dominance effects. Complementary type of epistasis for fruit weight reported by Akotkar and De (2014) and Wakode *et al.*, (2015).

Number of fruits per plant

Six-parameter model indicated positive and significant additive [d] gene effects in Hisar Naveen x Varsha Uphar and HB-1157 x Pusa Sawani crosses. Whereas, it displayed significant and negative in HB-25-2 x HB-32 cross. Dominance [h] gene effects were positively significant in all the crosses with relatively higher magnitude than additive [d]. The magnitude of dominance type of gene effects were higher for all the crosses indicating that the dominance type of gene action contributed maximum for inheritance of this trait. Additive x additive epistasis was also found positively significant in all the crosses. Additive × dominant [j] gene interactions were observed significant and negative in HB-25-2 x HB-32 while, positive significance in HB-1157 x Pusa Sawani. Dominance × dominance [l] gene interactions revealed positively significant with complementary type of epistasis in the crosses Hisar Naveen x Varsha Uphar, HB-25-2 x HB-32 and HB-1157 x Pusa Sawani. This indicated that adoption of simple selection procedure would be more effective for improvement of this trait. Das *et al.,* (2013) and Seth *et al.,* (2016) reported importance of dominance effect in the inheritance of this trait, while Pullaiah *et al.,* (1996) reported the additive type of gene action. Duplicate type of gene action was portrayed by the works of Kumar and Anandan (2006), Akthar *et al.,* (2010), Patel *et al.,* (2013) and Wakode *et al.,* (2015), whereas Akotkar and De (2014) recorded the complementary epistasis for this character in okra.

Fruit yield per plant

Six-parameter model estimates indicated the presence of positive and significant additive [d] gene effects in the crosses Hisar Naveen x Varsha Uphar and HB-1157 x Pusa Sawani while, negative in HB-25-2 x HB-32. Dominance [h] gene effects were positively significant and higher in magnitudes than additive [d] gene effect in Hisar Naveen x Varsha Uphar, HB-40 x HB-27 and HB-1157 x Pusa Sawani crosses. Whereas, Additive × additive [i] genic interactions was recorded positively significant in Hisar Naveen x Varsha Uphar and HB-40 x HB-27 crosses while, it exhibited negatively significant effects for HB-25-2 x HB-32. Additive × dominance [j] gene interactions was significant and negative in HB-25-2 x HB-32 whereas, it displayed positive significance in HB-1157 x Pusa Sawani. Dominance × dominance [l] type of interactions were positive and significant in the crosses *viz*., Hisar Naveen x Varsha Uphar, HB-25-2 x HB-32 and HB-1157 x Pusa Sawani. Complimentary type of epistasis was evident in Hisar Naveen x Varsha Uphar and HB-1157 x Pusa Sawani. Therefore, for improvement of this trait, population improvement approaches would be beneficial and selection may be followed in later segregating generations with dilution of dominance. Among digenic epistasis, additive x additive and dominance x dominance interactions were observed significant for majority of crosses. However, dominance x dominance gene effects had significant highest positive effect in all the crosses except HB-40 x HB-27. Among three types of epistasis, sign attached to dominance x dominance effects is more important since the negative effects of dominance x dominance was undesirable (Gamble, 1962). This causes the reduction of the effect of dominant gene and decreasing phenotypic expression of the trait. Complementary type of epistasis played significant role in the inheritance of fruit yield per plant in Hisar Naveen x Varsha Uphar and HB-1157 × Pusa Sawani. Hence, fruit yield can be improved by simple selection procedure in theses crosses. Several workers like Kumar and Anandan (2006), Akthar *et al.,* (2010), Khanorkar and Kathiria (2010), Mistry (2013), Patel *et al.,* (2013), Akotkar and De (2014) and Wakode *et al.,* (2015) reported that both additive and non-additive gene action were important in the inheritance of fruit yield in okra. The importance of dominance and dominance x dominance gene action reported by Das *et al.,* (2013) and Seth *et al.,* (2016) in the expression of fruit yield/plant.

The results showed that as a consequence of higher magnitude of interactions, the non-fixable gene effects were higher than the fixable. Further, duplicate type of epistasis was also found in majority of traits in one or the other cross combinations. In such crosses, the selection intensity should be mild in the earlier and intense in the later generations because it marks the progress through selection. Therefore, methods which exploit non-additive gene effect and take care of non-allelic interactions such as restricted recurrent selection by the way of intermating among desirable segregates, followed by selection or diallel selective mating or multiple crosses or biparental mating in early segregating generations could be promising for genetic improvement of fruit yield traits. In addition, few cycles of recurrent selection, followed by pedigree method may also be useful for the effective utilization of all three types of gene effects simultaneously. It will lead toward an increased variability in later generations for effective selection by maintaining considerable heterozygosity through mating of selected plants in early segregating generations.

Acknowledgement

Authors take this opportunity to express their gratitude to the CCS Haryana Agricultural University for providing all necessary facilities for smooth conduct of research.

References

Abdelmageed, A. H. A., Faridah, Z. Q. and El Hassan, G. M. (2012). Inheritance studies of some pod traits in okra [*Abelmoschus esculentus* (L.) Moench]. *Journal of Medicinal Plant Research*, 49 (6): 5905-5911.

Akhtar, M., Singh, J. N., Shahi, J. P. and Srivastava, K. (2010). Generation mean analysis for yield traits in okra. *Indian Journal Horticulture*, 67(Special Issue): 203-207.

Akotkar, P.K. and De, D.K. (2014). Genetic analysis for fruit yield and yield attributes in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*, 5 (4): 735-742.

Cavalli, I. L. (1952). An analysis of linkage in quantitative inheritance. In: Quantitative Inheritance (Ed. E.C.R. Reeve and C. H. Waddington) HMSO, London. pp. 135-144.

Choudhury, B. and Choomsai, M.L.A. (1970). Natural cross-pollination in some vegetable crops. *Indian Journal of Agricultural Sciences*, 40 (9): 805-812.

Das, S., Arup, C., Subrata, D., Sankhendu, B. and Pranab, H. (2013). Breeding okra for higher productivity and yellow vein mosaic tolerance. *International Journal of Vegetable Science*, 19: 58-77.

Gamble, E. E. (1962). Gene effects in corn (*Zea mays* L.) I. separation and relative importance of gene effects for yield. *Canadian Journal of Plant Science*, 42: 339-48.

Hayman, B. I. (1958). The theory and analysis of diallel crosses. *Genetics*, 43: 63-85.

Jinks, J. H. and Jones, R. M. (1958). Estimation of components of heterosis. *Genetics*, 43: 223-234.

Khanorkar, S. M. and Kathiria, K. B. (2010). Genetic architecture of fruit yield and its contributing quantitative traits in *Abelmoschus esculentus* (L.) Moench. *Electronic Journal of Plant Breeding*, 1(4): 716-730.

Kumar, N. S. and Anandan. A. (2006). Inheritance of fruit yield and its component characters in okra (*Abelmoschos esculentus* (L.) Monech). *International Journal of Plant Sciences*, 1 (1): 27-28.

Mather, K. (1949). Biometrical Genetics. *1st edition*, Methuen, London.

Mistry, P. M. (2013). Generation mean analysis in okra [*Abelmoschus esculentus* (L.) Moench]. *Agriculture Science Digest*, 33(1): 21-26.

Patel, K. D., Barad, A. V., Savaliya, J. J. and Butani, A. M. (2010). Generation mean analysis for fruit yield and its attributing traits in okra [*Abelmoschus esculentus* (L.) Moench]. *The Asian Journal of Horticulture*, 5 (2): 256-259.

Patel, K. D., Barad, A.V., Savaliya, J. J. and Kalaiya, D. S. (2013). Genetic architecture of fruit yield and yield attributing traits in okra. *Progressive Research*, 8: 589-592.

Pullaiah, N., Reddy, T. B., Resdisekhar, M. and Reddy, M. (1996). Inheritance of yield components in okra (*Abelmoschus esculentus* (L). Moench). *Vegetable Science*, 23 (1): 52-56.

Seth, T., Chattopadhyay, A., Dutta, S., Hazra, P. and Singh, B. (2016). Evidence of economic heterosis and genetic control of fruit yield and yellow vein mosaic virus disease severity traits of okra. *Vegetos*, 29 (3): 46-53.

Soher, E. A., El-Gendy and El-Aziz, M. H. A. (2013). Generation mean analysis of some economic traits in okra. *Journal of Applied Sciences*, 13 (6): 810-818.

Wakode, M. M., Bhave, S. G., Navhale, V. C., Dalvi, V. V. and Mahadik, S. G. (2015). Genetic analysis of yield and yield contributing traits in okra (*Abelmoschus esculentus* L. Moench). *Electronic Journal of Plant Breeding*, 6(4): 956-961

How to cite this article:

Mekala Srikanth, S.K. Dhankhar, N.C. Mamatha and Sumit Deswal. 2018. Assessment of Genetic Architecture of Some Economic Traits in Okra (*Abelmoschus esculentus* (L.) Moench) through Generation Mean Analysis. *Int.J.Curr.Microbiol.App.Sci.* 7(11): 2369-2379.
doi: https://doi.org/10.20546/ijcmas.2018.711.268