Vegetable Science (2021) 48 (2) : 164-171

Generation mean analysis unveils genetic effects controlling major yield traits in okra [*Abelmoschus esculentus* (L.) Moench].

Vinay ND, RK Yadav*, TK Behera#, A Talukdar[1] Suma Lata and Anjan Das

Received: November 2021/ Accepted: December 2021

Abstract

The present study on generation means analysis was carried out to uncover genetics of yield traits in okra. To determine the nature and magnitude of gene action six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of cross Pusa Sawani x Pusa Bhindi- 5 was assessed. The results revealed that both additive and dominance gene effects were significant in genetic control of yield traits. However, the magnitude of dominance gene effects was significant and higher for seed germination per cent, days to first flower, node to first flower, number of fruiting nodes, plant height and fruit yield per plant. Therefore, heterosis breeding would be effective to improve these traits. Additive genetic effect was significant for days to 50 per cent flower, inter-nodal length, number of primary branches, fruit length, fruit diameter and fruit weight. Result of scaling tests confirmed the role of non-allelic interaction in genetic control of all the yield traits analysed. The opposite sign of dominance (h) and dominance x dominance interaction (l) for many yield traits suggested role of duplicate type of epistasis, while few characters exhibited complementary type of epistasis. For improving traits with higher fixable (additive and additive x additive) component of genetic variation, pedigree method of breeding would be useful. For traits showing significant values of both additive and non-additive gene effects, improvement can be done by either recurrent selection or bi-parental mating system in segregating generations followed by selection.

Key words: Generation mean, Gene action, Scaling test, Yield traits, Okra

Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] also known as lady's finger is one of the important vegetable crops of the tropical, subtropical and warmer temperate region of the world. Okra is the commercial vegetable crop of Malvaceae family, grown for its tender pods. It is rich in of protein, calcium, potassium and rich source of iodine that found only in fewer food crops which helps to control goitre (Yawalkar 1965). Okra is quite popular vegetable in Indian subcontinent due to easy cultivation, dependable yield and adaptability to varying moisture and climatic conditions (Chauhan 1972). India is the leading producer of okra in the world with cultivated area of 0.514 million hectare and total producing of 6.126 million tonnes with a productivity of 11.9 metric tonnes/ha (NHB 2018). It has immense commercial value as one of the foreign exchange earner crops and accounts for 70 per cent of the export of fresh vegetables from India (Dhankhar and Mishra 2004). Okra is a classified as an often-cross pollinated species as natural cross-pollination ranges from 4 to 19 percentage (Choudhury and Choomsai 1970), causing considerable genetic diversity. Crop improvement in okra is mostly done through breeding methods that relay on effective selection and hybridization. It has several righteous features such as, shorter life span, photo-insensitivity and adaptability to wide range of soil and climatic conditions, which help the breeders to have quick genetic analysis through crop cultivation multiple times in a year. Presence of considerable variability, ease in emasculation, very high per cent of fruit set and higher number of seeds per cross makes commercial exploitation of hybrid vigour feasible in okra. Thus, it is important to conduct genetic studies to quantify the genetic effects controlling important traits for efficient exploitation of heterosis in okra.

Okra breeding is primarily focused on improvement of yield and resistance to yellow vein mosaic virus (YVMV)

Division of Vegetable Science, ICAR-Indian Agricultural Research Institute, New Delhi-110012

[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi-110012

#Presently at ICAR-Indian Institute of Vegetable Research, Varanasi-221305, Uttar Pradesh

*Corresponding author, Email: rkyadavneh@gmail.com

and enation leaf curl virus (ELCV) diseases. Yield in okra depends on various contributing traits that are quantitatively inherited and are dependent on nature and magnitude of heritable variations. Partitioning of heritable variations into components and quantifying them will be useful to determine genetics of these quantitative traits. To enhance yield potential through efficient utilization of available genetically diverse germplasm, it is essential to understand the nature and magnitude of genetic variation present in population elucidated by genetic analysis. This helps breeders to select appropriate breeding methods to increase yield through improvement of yield contributing traits. Genetic models developed earlier for the estimation of different genetic effects are basically additive dominance models or simply additive models. Majority of the workers reported the use of line x tester analysis or diallel approach to study the genetics of growth and yield traits in okra (Arora et al. 1993). However, these methods are based on absence of epistasis. But, it is currently well-known that such inter-allelic interaction is effectively modulate quantitate trait expression (Gamil and Saheal 1986, Kearsey and Pooni 2004). Thus, epistasis should also be estimated and considered while choosing the breeding methodology in crop improvement programme. Hence in the current study, six-parameter model of generation mean analysis approach (Hayman and Mather 1955, Hayman 1958) involving scaling test (Mather 1949) as well as joint scaling tests by Cavalli (1952) was followed which is more efficient approach for estimation of all three genetic effects such as additive, non-additive and epistasis involved in control of quantitative traits (Hayman 1958, Jinks and Jones 1958).

Materials and Methods

Plant materials: A popular varieties Pusa Sawani and Pusa Bhindi-5, contrasting in multiple traits were selected. F_1 generation was developed by hand emasculation and pollination using Pusa Bhindi-5 as male and Pusa Sawani as female counterpart. F_2 populations were developed by controlled self-pollination (bagging) of the F_1 plants, in the same season back cross populations were developed by hand emasculation and pollination. F_1 plants were backcrossed with Pusa Bhindi-5 and Pusa Sawani to produce B_1 and B_2 generations respectively. The final experiment was laid out with six generations *i.e.,* P_1, P_2, F_1, F_2, B_1, and B_2 in randomized complete block design (RBD) with 3 replications. Seeds were sown in row on ridge of about 3m long and were 45 cm apart between rows. Each row consisted of 10 plants spaced at 30 cm. The numbers of plants per replication among different generations in each cross were: 50 plants for P_1, P_2 and F_1; 200 for F_2; and 50 for B1 and B2. Standard cultural practices followed on time to raise the crop (Chattopadhyay et al. 2007). Data were collected for percent seed germination, days to first flower, days to 50 percent flower, node to first flower, number of fruiting nodes, inter nodal length, plant height, fruit length, fruit diameter, fruit weight, number of fruits per plant and yield per plant from all six generations.

Statistical Analysis: Quantitative genetic analysis was done through generation mean analysis (Hayman and Mather 1955: Hayman 1958) to study the gene action of the important yield traits in okra. The means and variances of means for the three characters studied were computed for each generation as described by Panse and Sukhatme (1978). The gene effects were estimated using the scaling test (Mather 1949) and joint scaling tests (Cavalli 1952; Mather and Jinks 1982). The significance of each estimate was judged from a t-test against its standard error of estimate. The corresponding standard errors were calculated by taking the square root of the respective scaling test and tested by t-test. The calculated values of 't 'were compared with the tabular values of 't' at 5 % and 1% levels of significance, respectively. Quantitative assessment was performed using OPSTAT software of CCSHAU, Hisar.

Results and Discussion

In current study, results of scaling test viz A, B, C and D suggested the presence of appreciable amount of epistasis/non-allelic interactions in genetic control of various yield traits of okra. One or more scaling tests and chi square tests of joint scaling test was significant for all the traits under study. This proved inadequacy of additive-dominance model in explaining the genetic control of traits under study. Since three parameter model did not satisfactorily explain the gene action, six parameter model was adopted to explain epistatic interactions. Presence of epistasis in genetic control of yield and its component traits has been previously reported by Panda and Singh (2003), Akthar et al. (2010), Mistry (2013) which validated our present results. Estimates of scaling tests for yield trait of cross Pusa Sawani X Pusa Bhindi-5 are given in Table 1.

Out of four scaling tests (A, B, C and D), scale A was highly significant for number of fruiting nodes, yield per plant and number of fruits per plant and found significant for average fruit length and fruit weight. Values of scale B were highly significant for seed germination percentage, plant height, number of primary branches, fruit length, fruit weight and yield per plant while B scale was found significant for days to 50 percentage flower and inter nodal length. Scaling test C

Table 1: Scaling tests for yield traits

Traits	A	B	C	D
Germination percentage	-0.55 ± 2.87	26.67** ± 2.65	66.45** ± 9.26	-20.17 ± 4.68
Days to first Flower	-6.33* ± 1.83	0.67 ± 0.82	-0.33 ± 2.79	-2.67 ± 1.63
Days to 50 percent flowers	-3.67* ± 1.33	2.00* ± 0.82	-1.67 ± 4.9	0.12 ± 2.49
Node to first flower	-1.77* ± 0.54	3.76 ± 0.48	-1.89 ± 0.83	-1.89 ± 0.43
Number of fruiting nodes	-4.9** ± 0.61	-0.10 ± 0.778	-4.67* ± 0.93	-0.17 ± 0.52
Inter-nodal length	0.13 ± 0.57	1.94* ± 0.517	4.01** ± 0.89	-0.96* ± 0.48
Plant height	-7.73 ± 4.63	36.90** ± 6.20	25.73* ± 9.89	1.72 ± 4.80
Number of primary branches	-0.6 ± 0.49	2.00** ± 0.49	-0.73 ± 0.71	1.07* ± 0.37
Fruit length	1.10* ± 0.45	-2.42** ± 0.20	-3.62* ± 1.64	1.15 ± 0.85
Fruit diameter	4.6 ± 3.31	3.23 ± 3.31	7.66* ± 6.62	0.08 ± 0.17
Fruit weight	-1.09 ± 0.56	4.40** ± 1.03	5.15* ± 1.89	-0.92 ± 0.91
Number of fruits per plant	-6.07** ± 0.59	-0.33 ± 0.61	-4.26** ± 1.07	-1.06 ± 0.56
Yield per plant	-81.26**± 6.97	36.09** ± 7.11	39.18 ± 20.33	-42.17**±10.25

was highly significant for seed germination percentage, inter nodal length, number of fruits per plant and was found to be significant for number of fruiting nodes, plant height, fruit length, fruit diameter and fruit weight. The scale D was highly significant for yield per plant and significant for inter-nodal length and number of primary branches. Our results were consistent with the reports of Panda and Singh (2003), Akthar et al (2010), Mistry (2013), Wakode et al. (2016), Srikanth et al. (2018) and Deshmukh et al. (2021). One or more of gene effects (*m, d, h, i, j* and *l*) measured in six parameter model were either significant or highly significant with positive values for all the yield traits studied (Table 2). Mean effect of parameter (m) that affects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci were highly significant for all yield traits studied. Signs that indicates direction of values on the dominance (h) and dominance x dominance (l) gene effects specifies the type of non-allelic interaction involved in trait control. If both values are in same direction (sign) signifies complementary epistasis whereas opposite signs on value of *h* and *l* signifies duplicate epistasis.

Seed germination percentage: Significance of scale B and C suggested the contribution of all three types of non-allelic gene interaction in genetic control of seed germination percentage. Both the main gene effects additive (d) and dominance (h) were found highly significant and dominance effect (h) was much higher in magnitude. Among the non-allelic interactions additive x additive (i) and dominance x dominance (j) effects were highly significant. Higher magnitude dominance gene effect (h) and additive x additive (i) gene interaction advocated the use of recurrent selection to enhance seed germination percentage.

Days to 1st flower: Scale A was found to be significant confirming the role of all three forms of epistasis. Days

Table 2: Estimates of gene effects for various yield traits in okra [Mather and Jinks (1982) six-parameter model]

Traits	M	[*d*]	[*h*]	[*i*]	[*j*]	[*l*]	Epistasis	χ2
Seed Germination per cent	65.33** ± 2.21	10.0** ± 1.56	48.11** ± 9.46	40.33** ± 9.35	27.22 **± 3.58	-14.22 ± 11.16	Duplicate	143.46**
Days to first Flower	38.67** ± 0.67	1.33 ± 0.94	5.50** ± 3.29	5.33 ± 3.27	7.00* ± 1.94	-11* ± 4.69	Duplicate	8.98**
Days to 50% flowers	42.67** ± 1.2	0.67**± 0.67	-1.83 ± 5.01	0 .20 ± 4.99	5.67* ± 1.49	-1.67 ± 5.58	Complementary	7.01**
Node to first flower	6.422** ± 0.16	1.70** ± 0.28	-4.789** ± 0.90	-3.89** ± 0.67	5.53** ± 0.67	5.89** ± 1.39	Duplicate	97.51**
Number of fruiting nodes	11.33** ± 0.17	1.50* ± 0.40	5.27** ± 1.10	0.33** ± 1.04	4.8 ** ± 0.94	-5.33* ± 1.86	Duplicate	74.28**
Inter-nodal length	8.38** ± 0.18	-0.013 ± 0.32	4.10** ± 1.00	1.93** ± 0.96	1.82** ± 0.70	0.15 ± 1.56	Complementary	29.00**
Plant height	127.53** ± 1.93	10.53** ± 2.85	35.42** ± 10.09	-3.44 ± 9.61	44.64** ± 7.02	32.61* ± 15.10	Complementary	44.00**
Number of primary branches	4.26** ± 0.129	0.93* ± 0.273	-1.10 ± 0.79	-2.13** ± 0.75	2.6** ± 0.66	3.53* ± 1.30	Duplicate	23.92**
Fruit length	11.39** ± 0.409	-1.28** ± 0.24	-1.05 ± 1.71	-2.307 ± 1.71	-3.52** ± 0.45	0.99 ± 1.90	Duplicate	155.78**
fruit diameter	5.25** ± 0.071	-0.51* ± 0.09	2.9 ± 3.325	-0.165 ± 0.33	-1.37** ± 0.22	7.99 ± 6.63	Complementary	42.95**
Fruit weight	11.12** ± 0.403	2.35** ± 0.44	2.93 ± 1.90	1.84 ± 1.83	5.49** ± 0.991	1.47 ± 2.58	Complementary	40.36**
Number of fruits per plant	10.43** ± 0.22	1.80** ± 0.33	4.87** ± 1.16	2.13 ± 1.12	5.73** ± 0.79	-8.53** ± 1.71	Duplicate	107.90**
yield per plant	110.44** ± 4.75	41.69** ± 3.84	133.5** ± 20.82	84.35**± 20.50	117.3** ± 9.33	-129.5**± 25.49	Duplicate	186.61**

to first flower is an important indicator earliness. Among major effects, dominant gene effect (h) was found to be highly significant. For this trait, similar findings were reported by Arora et al. (2007); Singh et al. (2012) and Alolli et al. (2017). Among the non-allelic interactions, additive x dominance (j) and dominance x dominance interactions (l) were significant with later showed higher magnitude. Significant additive x dominance (j) effect was also reported by Alloli et al. (2017). Gene effect results indicated duplicate gene action in control of this trait, which was supported by earlier findings of Arora et al. (2007) and Alloli et al. (2017). Predominance of dominance gene effect (h) and dominance x dominance interactions suggests that heterosis breeding will be useful in improvement of this trait.

Days to 50% flowers: Days to 50 percentage flowers is important as it is directly measuring earliness. Early varieties are preferred as they fetch high market prices in early days of the season and these varieties fit well in multiple cropping systems. Scaling test, A and B were significant advocating the role of all the three type of non- allelic gene interaction. Hence the additive-dominance model was inadequate. Among the major genetic effects, Additive gene effect (d) was significant and positive. Among non-allelic interactions only additive x dominance (j) was found to be significant. These results support the fact that simple selection would be effective in developing early flowering types. High and significant additive dominance was previously reported by Akthar et al. (2010), Khanorkar and Kathiria (2010), Akotkar and De (2014), Wakode et al. (2015), and Deshmukh et al. (2021) in this trait control. Our results suggested role of complementary gene action in this trait.

Node to first flower: Presence of all the three types of epistasis was evident by significance of scale A. All genetic components measured were found to be significant. Among major effects magnitude of dominance effect (h) was much higher; similarly among epistatic interactions dominance x dominance (l) gene action was predominant with higher value. The type of gene action was Duplicate, similar findings were reported by Akthar et al. (2010) and Deshmukh et al. (2021). Predominance of dominant gene effect was reported previously by Wakode et al. (2016) who also reported all three significant non-allelic interactions. Dominance x dominance interaction was reported to be significant in the studies conducted by Akthar et al. (2010) and Deshmukh et al. (2021). Highly significant values of dominance genetic effect advocates use of heterosis breeding in developing varieties that bear flowers in early nodes.

Number of fruiting nodes: Scaling test results suggest the presence of epistatic interaction and inadequacy of additive-dominance model in explaining genetics of this trait. Scale A and C were significant. Number of fruiting nodes is a direct indicator of yield as it decides number of fruits per plant so, lines with higher fruiting nodes per plant is desirable. Dominance gene effect (h) was highly significant and positive with much higher magnitude the additive effect. Only dominance x dominance (l) epistatic interaction was significant among the non-allelic interaction. These results clearly suggest use of heterosis breeding to improve this trait. The type of gene action was duplicate denoted by opposite signs on the dominance (h) and dominance x dominance genetic effects.

Inter-nodal length: Scaling test B, C and D were significant which denotes presence of all three non-allelic interactions. Among major effects only additive genetic effect (d) was significant. Role of additive effect in genetic control of inter-nodal length was reported earlier by Arora et al. (2007) and Dehsmukh et al. (2021) in the inter-varietal crosses of okra. Among epistasis, additive x additive (i) and additive x dominance (j) interactions were significant, additive x additive (i) interaction was slightly higher in magnitude. Similar findings were reported by Arora et al. (2007). The type of epistasis is complementary which is in accordance with the findings of Deshmukh et al. (2021). Changes in the inter-nodal length will alter the plant architecture. Higher inter-nodal length is not always preferred since in many conditions, dwarf varieties are grown. Predominance of additive effect and additive x additive gene interaction indicates that this trait can be improved by simple selection.

Plant height: Role of epistasis was confirmed by significance of scaling test (B and C) which was supported by Lal et al. (1975) and Patel et al. (2010). Of the two major effects dominance genetic (h) effect was significant and high in magnitude than additive gene effects. Das et al. (2013) and Soher et al. (2013) also observed non-additive gene action for this trait. Similar epistatic interactions were also reported by Srikanth et al. (2018) and Arora et al. (2007). Among epistatic interactions additive x dominance (j) and dominance x dominance (l) interactions were significant. These results indicated that selection in the early segregating generation might not effective; hence, heterosis breeding or combination breeding is appropriate method. The plant height is governed by complementary epistasis as per our results. Complementary epistasis for plant height was also reported by Deshmukh et al. (2021) in all six crosses they studied. Similar findings were reported by Srikanth et al. (2018).

Number of primary branches: Scaling test B and D were significant suggesting the role of epistasis in control of this trait. Among major genetic parameters, additive genetic effect was significant and of the three epistatic interactions dominance x dominance interaction was significant. These results advocated the use of either selection or recurrent breeding method in the improvement of this trait. Significant additive gene action was reported by and Wakode et al. (2016). Significance of Additive genetic effect (d) and dominance x dominance (l) interaction was earlier reported by Patel et al. 2013 and Srikanth et al. (2018). The type of gene action is duplicate type.

Fruit length: Three scaling tests namely A, B, and C were significant indicating importance of all three non-allelic interactions in control of this trait. Among six genetic parameters, additive gene effect (d) and additive x dominance (j) interactions were predominant and were significant. The gene action involved in fruit length control was duplicate indicated by opposite signs in dominance gene effect (h) and dominance x dominance (l) interaction. Role of additive gene effect has been reported by Aher et al. (2003), Soher et al. (2013) and Wakode et al. (2016) So, simple selection or pedigree method involving hybridization and selection can be applied for the improvement if this trait. Role of duplicate epistasis for fruit length was reported by Arora et al. (2010); Akotkar and De (2014) in okra.

Fruit diameter (cm): Among major gene effects Additive gene effect (d) was found to be significant. C scale was significant suggesting presence of epistasis. Significance of C scale was reported by Arora et al. (2010). Additive x dominance (j) non allelic interaction was found to be highly significant. Absence of non-additive interaction rules out the chance of using the heterosis breeding for improving fruit diameter. Predominance of additive gene effect suggests selection or breeding methods that follow early generation selection can be employed for the improvement of this trait. Complementary of epistasis was observed in controlling Fruit diameter since both genetic parameters dominance and dominance x dominance has same sign viz negative values.

Fruit weight (g): Significance of B scaling test suggests the presence of all three types of non-allelic interactions. Of the major effects, additive gene effect (d) was significant and positive. Additive x dominant epistasis was positively significant. These results are in accordance with the report of Arora et al. 2010. Predominance of additive fraction of genetics suggests effectiveness of breeding method that relay on simple selection in improvement of this trait. The gene action controlling fruit weight was complementary. Similar gene action for fruit weight was reported by Akotkar and De (2014) and Wakode et al. (2015).

Number of fruits per plant: Scaling test, A and C were significant indicating role of epistasis in genetic control of this trait. Both additive (d) and dominant genetic effects (h) were significant. Among non-allelic interactions additive x dominance (j) and dominance x dominance interactions were significant. But predominance of dominant genetic effect and dominance x dominance interaction was more since the magnitude was high. Kulkarni et al. (1978), Kumar et al. (2005); Das et al. (2013); Seth et al. (2016) and Wakode et al. (2016) also suggested role of dominance gene effect. Srikanth et al. 2018 also reported high magnitude of dominance gene effect and dominance x dominance type of interaction in this trait. Heterosis breeding will be the most ideal methods to exploit of dominance fraction of genetic variance for increasing number of fruits per plant. The type of gene action controlling the trait was duplicate which was supported by findings of Kumar and Anandan (2006), Akthar et al. (2010), Patel et al. (2013) and Wakode et al. (2015).

Fruit yield per plant: Three (A, B and D) out of four scaling tests were found significant, which indicates the presence of all three types of non- allelic interaction in control of fruit yield per plant. All genetic parameters measured were found to be significant. Dominant effect (h) and dominant x dominant (l) gene actions were in much higher magnitude. Additive genetic effect was significant in the study of Khanorkar and Kathiria (2010) whereas evidence for dominant gene action were reported by Lal et al. (1975), Abdul et al. (2009) and Patel et al. (2010). The importance of dominant gene effect and dominance x dominance gene action was reported by Das et al. (2013) Seth et al. (2016) and Wakode et al. (2016) in the expression of fruit yield/plant. In the current study all the three types of epistatic gene interactions were significant, significance of one or more interactions were confirmed with the previous work of Lal et al. (1975), Singh and Sharma (1990) and Wakode et al. (2016). Significance of both additive and dominance effects indicates that, the trait can be improved by recurrent selection. Since the magnitude of dominance genetic effect and dominance x dominance gene actions were high, heterosis breeding will also be effective in yield improvement.

Type of gene action is one of major factors that must be measured in the analysis of quantitative genetic variation along with number of genes involved and genotype environment interaction (Sprague 1963). Generation mean analysis is the most comprehensive method for estimation of genetic effects (additive, non-additive and epistasis). Measure of gene effects and determination of gene action is instrumental in understanding the genetic architecture of crop plants to bring desirable changes through formulation of appropriate breeding strategies. From the results of our genetic analysis, it is realised that single breeding approach cannot be followed to improve all the characters under study. So, appropriate method should be followed as per the genetics of the traits. For the traits showing higher non additive effects with significant non- allelic interactions such as germination percentage, node to first flower, number of fruiting nodes and intermodal length, recurrent selection should be followed. Recurrent selection involves inter-mating among desirable segregates followed by selection and this method is proved to be effective for improving traits with non-additive gene effect and can take care of non-allelic interactions. Besides this, di-allele selective mating or multiple crosses or bi-parental mating in early segregating generations could be promising for genetic improvement of these traits. For the traits such as node to first flower, number of fruiting nodes and yield per plant we observed significant values for all three gene effects (additive, non-additive and epistasis). Hence, to improve these traits few cycles of recurrent selection followed by pedigree method will be efficient. These breeding methods are effective in creation of variability in advanced generations through mating of selected desirable plants in early segregating generations thus enhances the effectiveness of selection by maintaining considerable heterozygosity in the population.

Predominance of non–fixable (dominance and dominance × dominance) gene effects for days to first flower, node to first flower, number of fruiting nodes, plant height and number of fruits per plant, indicated that there is much scope for heterosis breeding. Whereas high magnitude and significant values of Fixable gene effects (additive effect and additive x additive interaction) for traits such as intermodal length, fruit length, fruit diameter and fruit weight suggests that simple selection methods such mass, pure line selection or hybridization and selection methods like pedigree or bulk method can be followed for genetic improvement of these traits.

In the present study, duplicate type of epistasis was found for seed germination percentage, days to first flower, node to first flower, number of fruiting nodes, number of primary branches, fruit length, number of fruits per plant and yield per plant. Prevalence of duplicate type of non-allelic interaction would hinder the pace of progress through conventional selection procedure hence, the selection intensity should be mild in the earlier and intense in the later generations and selection should be delayed for several generations (single seed descent) until a high level of gene fixation is attained. In these circumstances, recurrent selection in biparental progenies would helpful which allow recombination and concentration of genes having cumulative effects in population and helps to break undesirable linkages (Ganesh and Sakila 1999). Kulkarni et al. (1978), Panda and Singh (1998) and Tripathi (2001) have also reported role duplicate type of epistasis in okra. On the other hand, complementary type of non-allelic interaction has been observed for days to 50 percentage flowering, inter-nodal length, plant height, fruit diameter and fruit weight. Role of complementary epistasis in genetic control of various traits in okra was earlier reported by Srikanth et al. 2018 and Deshmukh et al. 2021. For the improvement of these traits heterosis breeding will be most appropriate.

Acknowledgements

The authors are highly thankful to the Director, ICAR-IARI, New Delhi for providing necessary facilities for this work. The first author also wants to extend his sincere thanks to the Head, Division of Vegetable Science, ICAR-IARI, New Delhi for giving necessary support for this work.

सारांश

भिण्डी में उपज की अनुवांशिकी ज्ञात करने के लिये पीढ़ी माध्य विश्लेषण द्वारा वर्तमान अध्ययन किया गया। जीन क्रिया कि प्रकृति और परिमाण निश्चित करने के लिये 6 पीढ़ियों (पी$_1$, पी$_2$, एफ$_1$, एफ$_2$, बीसी$_1$ व बीसी$_2$) तक पूसा सावनी x पूसा भिण्डी–5 संकरण कर मूल्यांकन किया गया। परिणाम से स्पष्ट हुआ कि योज्य एवं प्रभावी दोनों का प्रभाव उपज गुणों की अनुवांशिक नियंत्रण में पाया गया जबकि प्रभावी का प्रभाव परिमाण सार्थक रहा एवं अधिकतम बीज प्रथम पुष्पन के दिनों, प्रथम पुष्पन की गांठ, फलन गांठ की संख्या, पौध ऊँचाई व फल उपज प्रति पौध पर प्रभाव देखा गया। इसलिये इन गुणों के उन्नयन हेतु ओज प्रजनन सबसे प्रभावी होगा। योज्य अनुवांशिक प्रभाव 50 प्रतिशत पुष्पन के दिन, अंतः पार्श्व गांठ की लम्बाई, प्रथामिक शाखाओं की संख्या, फल की लम्बाई, फल व्यास तथा फल भार के लिये सार्थक पाया गया। परीक्षण परिमाण से स्पष्ट हुआ कि गैर–युग्मक पारस्परिक क्रिया सभी उपज गुणों के लिये अनुवांशिक नियंत्रण को धारित करता है। प्रभाविकता का विपरीत लक्षण (एच) तथा प्रभावी ग प्रभावी पारस्परिक क्रिया (एल) कई उपज गुणों हेतु डुप्लीकेट इपीस्टासिस के महत्व को बताता है जबकि कुछ गुणों हेतु कम्पलीमेन्टरी इपीस्टाटिसस को प्रदर्शित करता है। उच्च ताप सहन करने योग्य (योज्य व अयोज्य x अयोज्य) घटकों में उन्नयन हेतु अनुवांशिक विविधता एवं वंशावली प्रजनन विधि ज्यादा उपयोगी होगा। योज्य तथा गैर–युग्मिक जीन प्रभावों के प्रति सार्थक मूल्य प्रदर्शित करने वाले गुणों में उन्नयन या तो आवर्ती

चयन या द्विपितृ समागम पद्धति से पीढ़ियों में चयन करने से किया जा सकता है।

References

Abdul, Naveed, Asif AK, Iftikhar AK (2009) Generation means analysis of water stress tolerance in okra (*Abelmoschous esculentus* L.). Pak J Bot 41(1):195-205.

Aher RP, Mahale, VD and Aher AR (2003) Genetic studies on some quantitative characters in okra. J Maharastra Agric Uni 28(2): 151-153.

Akhtar M, Singh JN, Shahi JP and Srivastava K (2010) Generation mean analysis for yield traits in okra. Indian Journal Horticulture 67: 203-207.

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

Allolli S, Jagtap VS and Ahamed Z (2009) Generation mean analysis with respect of yield and percent incidence of fruit borer and yellow vain mosaic virus (yvmv) in okra [*Abelmoschus esculentus* (L.) Moench]. Journal of Pharmacognosy and Phytochemistry 9(1):2305-2308.

Arora D, Jindal SK and Ghai TR (2010) Generation mean analysis for earliness related traits in okra [*Abelmoschus esculentus* (L.) Moench]. Electronic Journal of Plant Breeding 1(6):1434-1442.

Arora D, Kumar Jindal S and Ghai TR (2007) Generation mean analysis for earliness related traits in okra (*Abelmoschus Esculentus* L. Moench. Journal of Genetics and Breeding 61(1):85.

Arora SK (1993) Diallel analysis for combining ability studies in okra (*Abelmoschus esculentus* L. Moench). Punjab Hort J 33: 116-22.

Cavalli LL (1952) An analysis of Linkage in quantitative inheritance. H M Stationary Office, London, pp 135-144.

Chattopadhyay A, Dutta S, Bhattacharya I, Karmakar K and Hazra P (2007) Technology for vegetable crop production. Published by AICRP-Vegetable Crops, Directorate of Research, Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal, India, pp 226.

Chauhan DVS (1972) Vegetable production in India. 3rd ed., Ram Prasad and Sons.

Choudhury B and Choomsai MLA (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.

Deshmukh KD, Khandare VS and Kharat BM (2021) Estimation of generation mean analysis and scaling test for fruit yield and its attributing traits in okra (*Abelmoschus esculentus* L. Moench). The Pharma Innovation Journal 2021 10(1): 292-295.

Dhankhar BS and Mishra JP (2004) Objectives of okra breeding. Hybrid Vegetable Development, pp 195–209.

Hayman BI (1958) The separation of epistatic from additive and dominance variation in generation means. Heredity 12:371-390.

Hayman BI and Mather K (1955) The description of genic interactions in continuous variation. Biometrics.11: 69-82.

Jinks JL and Jones RM (1958) Estimation of the components of heterosis. Genetics 43: 223-224.

Gamil KH, Saheal YA (1986) Estimation of genetic effects for agronomic traits in wheat. Wheat Inform. Service 62: 36-41

Khanorkar SM and Kathiria KB (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.

Kulkarni RS, Rao TS and Virupakshappa (1978) Epistasis should not be ignored in bhindi breeding. Curr Res UAS Bangalore 7:142-143

Kulkarni RS, Rao TS and Virupakshappa (1976) Gene action in bhindi. J Agric Res Kerala 14: 13-20.

Kumar NS and Anandan A (2006) Inheritance of fruit yield and its component characters in okra (*Abelmoschus esculentus* (L.) Moench). International Journal of Plant Sciences 12:13-15.

Lal S, Shekhar. and Shrivastava J P (1975) Genetic studies on bhindi (*Abelmoschus esculentus* (L.) Moench) gene effects and heterosis. Indian J Hort 32:175-178.

Kearsey M and Pooni HS (2004) The Genetical Analysis of Quantitative Traits (second ed.), Chapman and Hall, UK, ISBN 0-7487-4082-1.

Mather K, Jinks JL (1997) Introduction to biometrical genetics. Chapman and Hall, London, pp 237.

Mather K (1949) The Study of continuous variation. Biometrical Genetics. Methuen and Co. Ltd. London.

Mather K and Jinks JL (1982) Biometrical Genetics. III Edn, Chapman and Hall Ltd., London.

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

Panda PK and Singh KP (2003) Generation mean analysis for yield and yield traits in okra (*Abelmoschus esculentus* (L.) Moench). Vegetable Science 30(1): 25-28.

Panse VG and Sukhatme PV (1978) Statistical Methods for Agricultural Research Workers. ICAR, New Delhi.

Patel KD, Barad AV, Savaliya JJ and Butani AM (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 KD, Barad AV, Savaliya JJ and Kalaiya D (2013) Genetic architecture of fruit yield and yield attributing traits in okra. Progressive Research 8: 589-592.

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.

Singh B and Sharma AK (1990) Genetics of seed number and fruit characteristics in Okra. Haryana J Hort Sci 19(3-4): 353-357.

Singh Parjeet Aulakh, Dhall RK, Jaskanwal Singh (2012) Genetics of early and total yield in okra (*Abelmoschus esculentus* (L.) Moench). Vegetable Science 39(2):165-168.

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

Sprague GF (1963) Orientation and objectives. *In*: Statistical genetics and plant breeding. Nat Acad Sci NRC Pub.

Srikanth M, Dhankhar SK, Mamatha NC and Deswal S (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.

Wakode MM, Bhave SG, Navhale VC, Dalvi VV and Mahadik SG (2015) Genetic analysis of yield and yield contributing traits in okra (*Abelmoschus esculentus* L. Moench). Electronic Journal of Plant Breeding 6(4): 956-961.

Wakode MM, Bhave SG, Navhale VC, Dalvi VV, Devmore JP and Mahadik SG (2016) Combining ability studies in okra (*Abelmoschus esculentus* L. Moench). Electronic Journal of Plant Breeding 7(4): 1007-1013.

Yawalkar KS (1965) Vegetable Crops of India. Agri-horticulture Publishing House, Nagpur, pp 70-101.