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Genetics of early and total yield in okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract An investigation was carried out during summer and rainy season of 2009 to study the gene action and inheritance pattern of early and total yield in two okra hybrids (Punjab-8 x Arya Dhanlaxhmi and Punjab-8 x Pusa Sawani) by using six generation mean analysis. F_1 means of both the crosses surpassed both of their corresponding parental means suggesting over dominance for days to first flowering, days to first fruit set and total yield per plant. Generation mean analysis of early and total yield revealed the presence of epistasis and the magnitude of dominance gene effects was more than that of additive gene effects for all the traits. The dominance (h) and dominance x dominance (l) components have opposite sign for all the traits which indicated the presence of duplicate type of epistasis. Hence this will reduce the net gain occurring from heterozygosity due to cancellation of dominance and epistasis effects. Such situation is not very conducive for exploitation in the form of F_1 hybrids. Therefore, genetic improvement of okra with respect to these characters in this material can be made through pure line breeding or inbred development.

***Key Words*:** Gene action, Heterosis, Okra, Yield

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) commonly known as lady's finger or bhindi is an important vegetable crop grown for fresh market and processing. It contains carbohydrate, proteins, minerals, iodine and vitamin C in large quantities (Adeboye and Oputa, 1996).

Expression of yield is a result of the interaction of several contributing characters; hence selection based on its components would be more effective. A number of varieties have been bred in okra in recent past but the yield plateau could not be broken to a great extent. The knowledge of genetic architecture and inheritance pattern of yield is very essential for a breeder to plan breeding programme for getting efficient results in the succeeding generations. The genetic information available so far needs further elaboration for effective implementation of breeding programme. Therefore the present investigation was undertaken to determine the inheritance pattern of days to first flowering, days to first fruit set and total yield of okra so that inference could be utilized in forming the breeding programme accordingly.

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Materials and Methods

The experimental material comprised of two F_1's of okra viz. Punjab-8 x Arya Dhanlaxhmi and Punjab-8 x Pusa Sawani. These two F_1's were sown along with their respective parents during summer, 2009. Flowers from each cross were self pollinated to produce F_2s and other back crossed with both the parents (P_c= Punjab-8, P_i= Arya Dhanlaxhmi / Pusa Sawani) in order to obtain back cross (B_c= F_1 x P_c, B_i= F_2 x P_i) seeds respectively. Moreover, the parents were again crossed to produce the seeds of F_1 hybrids because the earlier produced seeds of F_1 hybrids were utilized for production of back crosses and F_2 generations seed. The parental lines of both the crosses were selfed to produce parental seed. Seeds of all the six generations namely P_c, P_i, F_1, F_2, B_c and B_i were harvested separately. The six basic sets of generations namely P_c, P_i, F_1, F_2, B_c and B_i were sown in rainy season of the same year (2009) using randomized block design (RBD) with three replications. Both the crosses were treated as separate experiment i.e. the randomization was done within crosses between rows. The distance between row to row and plant to plant was kept at 45 x 30 cm. The crop was raised using recommended package of practices for cultivation of okra. The observations were recorded on individual plant basis for days to first flowering, days to first fruit set and total yield per plant. For each character, P_1 is higher scoring parent than P_2. So whom so ever may be higher

mean among parents (P_c, P_i) should be treated as P_1 for scaling and joint scaling test. Similarly for backcrosses (B_c, B_i), B_i and B_c generations are obtained after crossing with P_i and P_c, respectively. Scaling test of Mather (1949) and joint scaling test of Cavalli (1952) were applied to detect the non-allelic interactions and gene effects respectively. First the three-parameter model was fitted to estimate the genetic parameters. Where three-parameter model was inadequate, then adequacy of best-fit model could be tested having maximum significant genetic parameters and least non-significant chi-square value.

Results and discussion

Days to first flowering

In both the crosses *viz.* Punjab-8 x Arya Dhanlaxhmi and Punjab-8 x Pusa Sawani, the F_1 means surpass both of their corresponding parental means indicating over dominance for the character (Table 1). Some degree of inbreeding depression was also indicated by lower F_2 means than their corresponding F_1 means in both the crosses (Table 1). In cross Punjab-8 x Arya Dhanlaxhmi, B_i mean was higher than their corresponding B_c mean, as the recurrent parent involved in B_i had higher days to first flowering mean than that of the recurrent parent involved in B_c whereas in cross Punjab-8 x Pusa Sawani, B_c means was higher than their corresponding B_i mean, which indicated that mean of backcross generations were slightly deviated from expectations (Table 1).

Significant estimation of one or all A, B and C scaling test in both the crosses clearly indicated the presence of all the three type of non-allelic gene interactions *viz.* additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) for the character (Table 2). Moreover the significant value of chi-square for additive-dominance model also indicate the presence of epistasis in both the crosses (i.e. failure of additive-dominance model). After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the additive (*d*) and dominance (*h*) gene effects were significant in both the crosses. The magnitude of dominance gene effects was more than that of additive gene effects in both the crosses which confirm that dominance gene effects were found to contribute substantially in the inheritance of days to first flowering but negative sign of (*h*) in both the crosses indicates the dominance of decreaser alleles.

Among the epistatic effects, in cross Punjab-8 x Arya Dhanlaxhmi, two interaction parameters out of three interaction parameters were non-significant in the six parameter model. The non-significant interaction parameters were eliminated and the remaining four parameters were re-estimated along with testing the adequacy of the model using chi-square test. The four parameter model m, [d], [h], [l] was tested and observed that this model was best fit (Table 2). This model showed significant estimates of dominance x dominance (*l*) gene effect for the character. However, in cross Punjab-8 x Pusa Sawani, one interaction parameter was found non-significant in the six parameter model. The non-significant interaction parameter was eliminated and the remaining five parameters were re-estimated along with testing the adequacy of the model using chi-square test. The five parameter model m, [d], [h], [j], [l] was observed to be the best fit model (Table 2). This model resulted in significant estimates of additive x dominance (*j*) and dominance x dominance (*l*) gene effects. Moreover, opposite signs of dominance (*h*) and dominance x dominance (*l*) effects in both the crosses showed the presence of duplicate type of epistasis. Presence of duplicate type of epistasis is also with the agreement of Tripathi *et al.* (2002). So it can be concluded that days to first flowering is controlled by dominant effects and epistasis. Similar results were also reported by Aher *et al.* (2003).

Table 1. Generation means of days to first flowering, days to first fruit set and total yield in different crosses.

Generations	Days to first flowering		Days to first fruit set		Total yield per plant (g)	
	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani
P_c	44.0 ± 0.37	43.7 ± 0.28	45.5 ± 0.37	45.0 ± 0.17	98.9 ± 0.26	99.1 ± 0.92
P_i	45.2 ± 0.46	45.4 ± 0.46	46.7 ± 0.40	46.9 ± 0.28	79.9 ± 0.40	62.1 ± 0.80
F_1	46.0 ± 0.40	45.8 ± 0.34	47.5 ± 0.40	47.5 ± 0.21	102.6 ± 0.72	101.0 ± 0.98
F_2	44.4 ± 0.40	43.9 ± 0.40	45.9 ± 0.40	45.5 ± 0.34	88.5 ± 0.45	87.4 ± 0.92
B_c	43.7 ± 0.46	44.8 ± 0.28	45.2 ± 0.46	46.2 ± 0.46	85.7 ± 0.72	86.1 ± 0.92
B_i	43.9 ± 0.46	43.0 ± 0.34	45.4 ± 0.46	44.3 ± 0.40	74.8 ± 0.75	64.7 ± 0.86
M.P	44.6	44.55	46.1	45.95	88.65	77.5

P_c= Punjab-8, P_i= Arya Dhanlaxhmi / Pusa Sawani, F_1= P_c x P_i, B_c= F_1 x P_c, B_i= F_2 x P_i, M.P= Mid-Parent

Days to first fruit set

The F_1 means of both the crosses surpass both of their corresponding parental means indicating over dominance for the character (Table 1). The F_2 means were lower than their corresponding F_1 means in both the crosses indicating some degree of inbreeding depression. In cross Punjab-8 x Arya Dhanlaxhmi, B_i mean was higher than their corresponding B_c mean, as the recurrent parent involved in B_i had higher mean than that of the recurrent parent involved in B_c whereas in cross Punjab-8 x Pusa Sawani, B_c means was higher than their corresponding B_i mean, which indicated that means of backcross generations were slightly deviated from expectations (Table 1).

Significant estimation of one or all A, B and C scaling test in both the crosses clearly indicated the presence of epistasis (Table 2). Moreover, the significant chi-square value for additive-dominance model indicate the presence of epistasis in both the crosses and this suggested that simple additive-dominance model was inadequate to explain the total genetic variation for days to first fruit set. After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the additive (*d*) and dominance (*h*) gene effects were significant in both the crosses. The magnitude of dominance gene effects was more than that of additive effects in both the crosses which confirm that dominance gene effects were found to contribute substantially in the inheritance of days to first fruit set but negative sign of (*h*) in both the crosses indicates the dominance of decreaser alleles. Among the epistatic effects, in cross Punjab-8 x Arya Dhanlaxhmi, two interaction parameters out of three were non-significant in the six parameter model. The non-significant interaction parameters were eliminated and the remaining four parameters were re-estimated along with testing the adequacy of the model using chi-square test. The four parameter model m, [d], [h], [l] was tested and observed to be best fit model (Table 2). This model showed significant estimates of dominance x dominance (*l*) gene effect for this character.

However, in cross Punjab-8 x Pusa Sawani, one interaction parameter was found non-significant in the six parameter model. The non-significant interaction parameter was eliminated and the remaining five parameters were re-estimated along with testing the adequacy of the model using chi-square test. The five parameter model m, [d], [h], [j], [l] was considered the best fit model (Table 2). This model resulted in significant estimates of additive x dominance (*j*) and dominance x dominance (*l*) gene effects. Moreover, opposite signs of dominance (*h*) and dominance x dominance (*l*) effects in both the crosses showed the presence of duplicate type of epistasis. So it can be concluded that days to first fruit set is controlled by dominant effects and epistasis.

Table 2. Estimates of gene effects based on scaling, joint scaling tests and genetic components in the best fitting model in different crosses.

Parameter	Days to first flowering		Days to first fruit set		Total yield per plant (g)	
	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani	Punjab-8 x Arya Dhanlaxhmi	Punjab-8 x Pusa Sawani
			Scaling Test			
A	-2.7 ± 1.07*	0.1 ± 7.3	-2.7 ± 1.07*	-5.8 ± 0.88**	-17.1 ± 1.63**	-22.3 ± 2.28**
B	-3.5 ± 1.10**	-5.2 ± 0.9**	-3.4 ± 1.08**	-0.1 ± 0.96	-34.4 ± 1.71**	-28.5 ± 2.14**
C	-3.8 ± 1.90*	-5.1 ± 1.84**	-3.8 ± 1.88*	-5.0 ± 1.49**	-28.6 ± 2.38**	-7.3 ± 4.35
Joint Scaling Test						
m	44.1 ± 0.27**	43.8 ± 0.23**	45.7 ± 0.25**	45.5 ± 0.15**	87.4 ± 0.23**	74.7 ± 0.56**
[*d*]	-0.46 ± 0.27	-0.04 ± 0.23	-0.5 ± 0.25*	0.6 ± 0.16**	8.1 ± 0.23**	21.1 ± 0.55**
[*h*]	1.07 ± 0.49*	1.25 ± 0.42**	1.02 ± 0.47*	1.5 ± 0.27**	5.7 ± 0.61**	18.8 ± 1.09**
$\chi^2_{(3\ d.f.)}$	15.56**	36.98**	15.61**	50.30**	474.22**	244.21**
m	44.6 ± 0.29**	44.5 ± 0.27**	46.1 ± 0.27**	45.9 ± 0.16**	111.6 ± 2.78**	120.9 ± 4.52**
[*d*]	-0.5 ± 0.27*	-0.9 ± 0.27**	-0.5 ± 0.25*	1.0 ± 0.16**	7.2 ± 0.24**	20.6 ± 0.61**
[*h*]	-3.9 ± 1.41**	-3.9 ± 1.18**	-3.8 ± 1.37**	-3.9 ± 1.07**	-83.4 ± 7.31**	-114.1 ± 10.8**
[*i*]	-	-	-	-	-22.9 ± 2.77**	-43.4 ± 4.47**
[*j*]	-	5.3 ± 1.05**	-	-5.8 ± 1.26**	17.3 ± 2.13**	6.1 ± 2.81*
[*l*]	5.3 ± 1.42**	5.1 ± 1.18**	5.3± 1.41**	5.6± 1.07**	74.5 ± 4.79**	94.2 ± 6.68**
$\chi^2_{(d.f.)}$	$\chi^2_{(2)}$ 1.67	$\chi^2_{(1)}$ 0.0	$\chi^2_{(2)}$ 1.62	$\chi^2_{(1)}$ 0.29	-	-
Type of Epistasis	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

*,** Significant at 5% and 1% level, respectively

Total yield per plant

The F_1 means of both the crosses surpass both of their corresponding parental means indicating over dominance for the character (Table 1). Some degree of inbreeding depression was also indicated by lower F_2 means than their corresponding F_1 means in both the crosses. B_c means were higher than their corresponding B_i means in both the crosses, as the recurrent parent involved in B_c's had higher mean total yield than that of recurrent parent involved in corresponding B_i's (Table 1).

Significant estimation of scaling test A, B and C in cross Punjab-8 x Arya Dhanlaxhmi and significance of A and B scaling test in cross Punjab-8 x Pusa Sawani indicate the presence of epistasis for the character (Table 2). Moreover, the presence of epistasis and failure of additive-dominance model in both the crosses were also confirmed by the significant value of chi-square for additive-dominance model. After confirming the presence of epistasis, the search for the best fit model was done. In the best fit model of joint scaling test, the additive (*d*) and dominance (*h*) gene effects were significant in both the crosses. No doubt, the magnitude of dominance effects was higher than the additive effects in both the crosses but negative sign of (*h*) indicates the dominance of decreaser alleles. Among the epistatic effects, all the three types of gene interactions i.e. additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) were significant in both the crosses (Table 2). Thus in these crosses, the adequacy of the best fit model could not be tested for the digenic interactions. The magnitude of dominance x dominance (*l*) gene effects were higher than other two types of interactions in these crosses, which indicated that dominance x dominance (*l*) gene effects were found to contribute more than additive x additive (*i*), additive x dominance (*j*) gene effects. The negative sign of additive x additive (*i*) effects in both the crosses indicated dissociated gene pair. Moreover, opposite signs of dominance (*h*) and dominance x dominance (*l*) effects in both the crosses showed the presence of duplicate type of epistasis (Tripathi *et al*. 2002). Hence this will reduce the net gain occurring from heterozygosity due to cancellation of dominance and epistasis effects. Such situation is not very conducive for exploitation in the form of F_1 hybrids. Therefore, genetic improvement of okra with respect to early and total yield in the studied material can be made through pure line breeding or inbred development.

सारांश

वर्ष 2009 की गर्मियों और बरसात के मौसम के दौरान कुल उपज के दो ओकरा संकर (पंजाब–8 x आर्य धनलक्ष्मी और पंजाब–8 x पूसा सवानी) का उपयोग करके जीन कार्य और विश्लेषण पैटर्न का अध्ययन छह पीढ़ी तक किया गया। जल्दी पीढ़ी और कुल उपज का मतलब विश्लेषण से पता चला है कि एपिस्टासिस और प्रभुत्व जीन के प्रभाव के परिमाण भी उपस्थिति सभी लक्षण के लिए एडिटिव जीन के प्रभाव से अधिक था। प्रभुत्व (ज) और प्रभुत्व घटको (एल) के सभी लक्षण जो एपिस्टासिस की नकल प्रकार की उपस्थिति का संकेत के लिए विपरीत संकेतक है। इसलिए इस प्रभुत्व और एपिस्टासिस प्रभाव के रद्द करने के कारण हेटरोजाइगोसिटी से होने वाली शुद्ध लाभ कम हो जाएगा। इस तरह की स्थिति F1 संकर के रूम में शोषण के लिए बहुत अनुकूल नहीं है। इसलिए इस लक्षण को ध्यान में रखते हुए ओकरा की आनुवंशिक सुधार शुद्ध लाइन प्रजनन या जन्मजात विकास के माध्यम से किया जा सकता है।

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