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

Parjeet Singh Aulakh, RK Dhall and Jaskanwal Singh

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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. 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.

The experimental material comprised of two F_1's of okra viz. Punjab-8 x Arya Dhanlaxhmi, Punjab-8 x Pusa were sown along with their respective parents during summer 2009. Some flowers from each cross was self pollinated to produce F_2's and other back crossed with both the parents (P_c, P_i) in order to obtain back cross (B_c, B_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 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 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 teasts. 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 has fitted to estimate the genetic parameters. Where three-parameter model was inadequate, than adequacy of best-fit model could be tested having maximum significant genetic parameters and least non-significant chi-square value.

In both the crosses *viz.* Punjab-8 x Arya Dhanlaxhmi and Punjab-8 x Pusa Sawani, the F_1 means surpasses both of their corresponding parental means indicating over dominance for days to first flowering and days to first fruit set (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 and days to first fruit set 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 days to first flowering and presence of epistasis for days to first fruit set (Table 2). Moreover the significant value of chi-square for additive-dominance model also indicating the presence of epistasis in both the crosses (i.e. failure of additive-

Parjeet Singh Aulakh, RK Dhall and Jaskanwal Singh
Department of Vegetable crops, Punjab Agricultural University, Ludhiana 141 004, India

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

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 and 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 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 both 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

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

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).

The F_1 means of both the crosses surpasses both of their corresponding parental means indicating over dominance for total yield per plant (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 indicating 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). Thus it can be concluded that total yield per plant is mainly governed by dominant gene effects (Singh *et al*. 2002; Kumar *et al*. 2005).

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