

Short communication

Genetics of fruit size in chilli

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Chilli (*Capsicum annum* L.) is an important spice or condiment as well as vegetable crop of India and is mostly grown in the tropical and sub-tropical regions. Fruit length and breadth are important traits influencing chilli yield. A number of varieties/hybrids have been bred in chilli in the recent past, but the yield and quality plateau could not be broken simultaneously. This is because of poor understanding of the nature of gene action for various yield attributes. Therefore, the present investigation was taken up with the objective of studying the gene action for fruit length and breadth so that inference drawn from the study could be utilized in formulating breeding strategies.

The experimental material comprised of seven genotypes namely PBC 830, Punjab Lal, S-2530, Ludhiana Local Selection (LLS), Anaheim Thick Green (ATG), Ooty Round and Pepsi-7. PBC 830 was used as female parent (P_c) while rest of six was used as male parents (P_i). The hybridization programme consisting of above material was started in end June, 1999 at Department of Vegetable Crops, Punjab Agricultural University, Ludhiana, in order to produce six F_1 hybrids namely PBC 830 × S-2530, PBC 830 × Punjab Lal, PBC 830 × LLS, PBC 830 × Ooty Round, PBC 830 × ATG and PBC 830 × Pepsi-7. The F_1 seeds from the above crosses were sown on November 8, in first year under the same conditions. Some flowers from each cross were self-pollinated and other back crossed with both the parents (P_c , P_i) in order to obtain F_2 and back cross (B_c , B_i) seeds, respectively. Six generations, viz., P_c , P_i , F_1 , F_2 , B_c and B_i developed from above crosses were sown on 10th November in second year. The seedlings were than transplanted in the experimental field on 7th March of the third year on following year using single plant randomization for each cross keeping 10 plants of parents (P_c , P_i) and F_1 (each); 20 plants of B_c and B_i (each) and 40 plants of F_2 . The distance between row to row and plant to plant was kept at 100 m × 30 cm. The generation means were worked out by taking the average over all the plants used for each generation. To test the adequacy of additive-dominance model, scaling test of Mather (6) was applied. The generation means were analyzed following weighed least square method (Mather and Jinks, 7). 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 case of fruit length, the F_1 mean of the cross PBC 830 × S-2530, PBC 830 × LLS and PBC 830 × Pepsi-7 surpasses both of their corresponding parental means indicating over dominance for the character (Table 1). In crosses PBC 830 × Pb Lal and PBC 830 × Ooty Round, the F_1 means were intermediate between their respective parental means but higher than the corresponding mid parental means, suggesting partial dominance towards the higher parent (P_c). Though mean fruit length of F_1 of PBC 830 × ATG lied in between its parental means, it skewed too much towards the better parental (P_c) mean and was almost equal to it, indicating complete dominance. The F_2 means were lower than their corresponding F_1 means in all the crosses indicating some degree of inbreeding depression. Mean of segregating generations (F_2 s) were as per expectations in all the crosses except PBC 830 × Pepsi-7, in which transgressive segregants were noticed in F_2 as indicated by its F_2 mean surpassing both of its parental means. B_c means were higher than their corresponding B_i means in all the crosses except PBC 830 × Pepsi-7, as the recurrent parent involved in B_c s had higher mean fruit length than that of recurrent parent involved in corresponding B_i s. The significance of one or all of the A, B and C scaling tests (Table 2) in all the crosses clearly indicated the presence of non-allelic gene interactions, which was further confirmed by the significant chi-square value of simple additive-dominance model. In best fit model of joint scaling test, the additive (d) and dominance (h) gene effects were significant in all the crosses except PBC 830 × S-2530 in which only dominance (h) component was significant. Moreover the magnitude of dominance gene effects was more than that of additive gene effects in all the crosses which confirms that dominance gene effects were found to contribute substantially in the inheritance of fruit length. Similar results were also reported by Muthukrishnan *et al.* (8), and Lohithaswa *et al.* (5). Among the epistatic effects, all the three types of gene interactions were significant in crosses PBC 830 with S-2530, Ooty Round and ATG. Thus in these crosses, the adequacy of the best fit model could not be tested

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Table 1. Generation means \pm SE of fruit length (cm) and fruit breadth (cm) in six generations of six different crosses.

Generation	PBC 830 x S-2530	PBC 830 x Pb. Lal	PBC 830 x LLS	PBC 830 x Ooty Round	PBC 830 x ATG	PBC 830 x Pepsi-7
Fruit length						
P _c	7.59 \pm 0.15	7.55 \pm 0.16	8.02 \pm 0.13	7.79 \pm 0.19	7.73 \pm 0.12	7.80 \pm 0.18
P _i	7.27 \pm 0.12	3.74 \pm 0.05	6.65 \pm 0.12	1.82 \pm 0.04	6.11 \pm 0.13	8.93 \pm 0.17
F ₁	8.73 \pm 0.17	6.92 \pm 0.13	8.45 \pm 0.17	5.47 \pm 0.08	7.71 \pm 0.16	9.60 \pm 0.19
F ₂	7.54 \pm 0.12	6.76 \pm 0.09	7.89 \pm 0.11	4.58 \pm 0.07	6.75 \pm 0.07	8.99 \pm 0.08
B _c	8.79 \pm 0.08	8.00 \pm 0.09	8.23 \pm 0.12	6.94 \pm 0.11	8.19 \pm 0.10	9.10 \pm 0.11
B _i	7.70 \pm 0.09	5.46 \pm 0.09	7.55 \pm 0.09	3.32 \pm 0.13	6.46 \pm 0.11	9.40 \pm 0.09
MP	7.43	5.65	7.34	4.81	6.92	8.37
Fruit breadth						
P _c	1.485 \pm 0.015	1.510 \pm 0.019	1.499 \pm 0.016	1.504 \pm 0.015	1.514 \pm 0.012	1.501 \pm 0.017
P _i	1.269 \pm 0.009	0.762 \pm 0.004	1.346 \pm 0.017	1.901 \pm 0.035	1.896 \pm 0.029	1.248 \pm 0.020
F ₁	1.384 \pm 0.022	1.162 \pm 0.016	1.370 \pm 0.014	1.573 \pm 0.016	1.637 \pm 0.015	1.368 \pm 0.012
F ₂	1.280 \pm 0.014	1.195 \pm 0.017	1.322 \pm 0.009	1.424 \pm 0.016	1.628 \pm 0.012	1.292 \pm 0.014
B _c	1.321 \pm 0.022	1.272 \pm 0.016	1.361 \pm 0.016	1.487 \pm 0.020	1.607 \pm 0.012	1.315 \pm 0.013
B _i	1.296 \pm 0.018	0.921 \pm 0.008	1.336 \pm 0.012	1.746 \pm 0.018	1.749 \pm 0.012	1.256 \pm 0.012
MP	1.377	1.136	1.423	1.703	1.705	1.375

P_c = PBC830, P_i = S-2530 / Pb Lal / LLS / Ooty Round / ATG / Pepsi-7, F₁ = P_c x P_i, B_c = F₁ x P_c, B_i = F₁ x P_i, MP = Mid-parent

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

Estimate	PBC830 x S-2530		PBC830 x Pb Lal		PBC830 x LLS		PBC830 x Ooty Round		PBC830 x ATG		PBC830 x Pepsi-7	
	FL	FB	FL	FB	FL	FB	FL	FB	FL	FB	FL	FB
Scaling test												
A	1.26 ± 0.28**	-0.226 ± 0.051**	1.54 ± 0.28**	-0.128 ± 0.040**	1.10 ± 0.33**	-0.148 ± 0.038**	0.62 ± 0.31*	-0.103 ± 0.046*	0.94 ± 0.28**	0.063 ± 0.031*	0.81 ± 0.34*	-0.239 ± 0.033**
B	-0.60 ± 0.29*	-0.061 ± 0.043	0.26 ± 0.23	-0.083 ± 0.023**	0.01 ± 0.28	-0.044 ± 0.032	-0.65 ± 0.27*	0.019 ± 0.053	-0.91 ± 0.30**	-0.035 ± 0.041	0.26 ± 0.31	-0.104 ± 0.033**
C	-2.18 ± 0.65**	-0.403 ± 0.073**	1.92 ± 0.49**	0.183 ± 0.079*	0.81 ± 0.60	-0.297 ± 0.050**	-2.25 ± 0.38**	-0.855 ± 0.080**	-2.27 ± 0.46**	-0.172 ± 0.065**	0.04 ± 0.56	-0.317 ± 0.068**
Joint scaling test												
<i>m</i>	7.50 ± 0.09**	1.359 ± 0.009**	5.93 ± 0.07**	1.130 ± 0.008**	7.34 ± 0.08**	1.390 ± 0.010**	4.73 ± 0.07**	1.649 ± 0.015**	6.80 ± 0.08**	1.689 ± 0.012**	8.44 ± 0.11**	1.322 ± 0.011**
(<i>d</i>)	0.53 ± 0.08**	0.095 ± 0.009**	2.19 ± 0.07**	0.370 ± 0.008**	0.68 ± 0.08**	0.065 ± 0.010**	2.95 ± 0.07**	0.184 ± 0.015**	1.07 ± 0.07**	0.168 ± 0.011**	0.46 ± 0.09**	0.109 ± 0.011**
(<i>h</i>)	1.27 ± 0.18**	-0.057 ± 0.019**	1.36 ± 0.14**	-0.007 ± 0.015	1.11 ± 0.17**	-0.068 ± 0.018**	0.54 ± 0.12**	-0.135 ± 0.024**	0.60 ± 0.16**	-0.053 ± 0.020**	1.33 ± 0.21**	0.004 ± 0.017
$\chi^2_{(3 d.f.)}$	61.98**	39.32**	33.72**	35.33**	12.77**	40.62**	64.91**	141.48**	71.29**	15.44**	8.58*	64.33**
<i>m</i>	4.59 ± 0.58**	1.170 ± 0.035**	5.64 ± 0.09**	1.505 ± 0.075**	7.27 ± 0.09**	1.272 ± 0.022**	2.58 ± 0.45**	0.937 ± 0.085**	4.61 ± 0.41**	1.505 ± 0.062**	7.39 ± 0.45**	1.375 ± 0.013**
(<i>d</i>)	0.16 ± 0.10	0.107 ± 0.009**	1.90 ± 0.09**	0.369 ± 0.008**	0.55 ± 0.09**	0.077 ± 0.012**	2.99 ± 0.10**	0.219 ± 0.016**	0.81 ± 0.09**	0.191 ± 0.016**	0.45 ± 0.09**	0.126 ± 0.013**
(<i>h</i>)	7.63 ± 1.32**	0.205 ± 0.051**	3.12 ± 0.36**	-0.898 ± 0.163**	1.96 ± 0.41**	0.094 ± 0.033**	5.08 ± 1.19**	1.311 ± 0.214**	5.44 ± 1.08**	0.360 ± 0.152*	4.21 ± 1.15**	-0.343 ± 0.051**
(<i>l</i>)	2.84 ± 0.57**	0.206 ± 0.036**	—	-0.374 ± 0.075**	—	0.148 ± 0.025**	2.22 ± 0.44**	0.779 ± 0.083**	2.31 ± 0.40**	0.200 ± 0.060**	0.99 ± 0.43*	—
(<i>l</i>)	1.86 ± 0.32**	-0.152 ± 0.058**	1.28 ± 0.31**	—	0.35**	-0.096 ± 0.045	1.27 ± 0.39**	—	1.85 ± 0.34**	-0.098 ± 0.047*	—	-0.135 ± 0.044**
(<i>l</i>)	-3.49 ± 0.82**	—	-1.84 ± 0.38**	0.555 ± 0.095**	-1.02 ± 0.47*	—	-2.20 ± 0.77**	-0.676 ± 0.135**	-2.34 ± 0.74**	-0.228 ± 0.096*	-1.99 ± 0.80**	0.336 ± 0.046**
$\chi^2_{(d.f.)}$	—	$\chi^2_{(1)} = 1.62$	$\chi^2_{(1)} = 0.07$	$\chi^2_{(1)} = 1.28$	$\chi^2_{(1)} = 0.31$	$\chi^2_{(1)} = 0.87$	—	$\chi^2_{(1)} = 3.34$	—	—	$\chi^2_{(1)} = 2.06$	$\chi^2_{(1)} = 0.15$
Type of epistasis	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

*, ** Significant at 5 and 1%, respectively. FL = Fruit length, FB = Fruit breadth

for the digenic interactions. The magnitude of dominance \times dominance (l) gene effects were higher than other two type of interactions in these three crosses, which indicated that dominance \times dominance (l) gene effects were more important followed by additive \times additive (i) and additive \times dominance (j) gene effects. In all the crosses except PBC 830 \times Pb Lal and PBC 830 \times LLS, additive \times additive effects were significant and positive, which indicates the presence of associated gene pairs. Significant and higher magnitude of dominance \times dominance (l) interactions among the other epistatic interactions in all the crosses except PBC 830 \times LLS indicated the importance of dominance \times dominance (l) gene interaction but the negative sign of (l) indicated higher frequencies of decreaser alleles. Moreover, the opposite signs of dominance (h) and dominance \times dominance (l) effects in all the crosses indicated the presence of duplicate type of epistasis. Therefore, it can be concluded that fruit length is controlled by additive effects along with partial dominance and epistasis. In the presence of sufficient magnitude of additive variance, selection can be used for improving fruit length. However, in view of partial dominance and epistasis, selection for the improvement of fruit length should be more effective in the later generations. Similar results were also reported by Krishnamurthy and Deshpande (4), Sarma and Talukdar (9), and Bal and Singh (1).

In case of Fruit Breadth, the F_1 means were intermediate between their respective parental means in crosses PBC 830 \times LLS, PBC 830 \times Ooty Round, PBC 830 \times ATG and PBC 830 \times Pepsi-7, but lower than their corresponding mid-parental means, suggesting partial dominance of the smaller sized fruits over the larger sized fruits whereas F_1 means of the crosses PBC 830 \times S-2530 and PBC 830 \times Pb Lal suggested partial dominance towards the higher parent (P_2) (Table 1). The F_2 means were lower than their corresponding F_1 means in all the crosses (except PBC 830 \times Pb Lal), suggesting some degree of inbreeding depression. The F_2 mean of crosses PBC 830 \times LLS and PBC 830 \times Ooty Round were lower than both of their respective parental means, which might be due to negative heterosis for the character. Mean of the backcross generations were on expected lines. In all the crosses, the significance of one or all of the A, B and C scaling tests (Table 2) indicated the presence of epistasis. Moreover the presence of epistasis and failure of additive-dominance model in all the crosses were also confirmed by the significant value of chi-square for additive dominance model. Both the additive (d) and dominance (h) gene effects were significant in best fit model of all the crosses. No doubt, the magnitude of dominance (h) effects were higher than the additive (d) effects in all the crosses but positive

sign of (h) in crosses PBC 830 \times S-2530, PBC 830 \times LLS, PBC 830 \times Ooty Round and PBC 830 \times ATG indicates the dominance of increaser alleles, whereas negative sign of (h) in crosses PBC 830 \times Pb Lal and PBC 830 \times Pepsi-7 indicates the dominance of decreaser alleles. Similar results of dominance gene effects were reported for fruit breadth in chilli (Singh, 10; Krishnamurthy and Deshpande, 4; Devi and Arumugam, 3; Ben-chain and Paran, 2). Among the epistatic effects, all the three interaction parameters were significant in the cross PBC 830 \times ATG. So the adequacy of best fit model could not be tested for this cross. The magnitude of dominance \times dominance (l) effects was higher, indicating their importance among the other interactions for the character but the negative sign of (l) indicates higher frequencies of decreaser alleles. In the remaining five crosses, only two interaction parameters were significant in the six-parameter model. The negative sign of additive \times additive (i) effects indicated dissociated gene pairs in cross PBC 830 \times Pb Lal while positive sign of (i) in PBC 830 \times Ooty Round indicated association of favourable alleles. In the crosses PBC 830 \times S-2530 and PBC 830 \times LLS, additive \times additive (i) and additive \times dominance (j) effects were present but the magnitude of (i) component was more than (j) component. Moreover the positive sign of (i) component indicated the presence of associated gene pairs. The additive \times dominance and dominance \times dominance effects were present in the remaining cross PBC 830 \times Pepsi-7 but the magnitude of dominance \times dominance interaction was higher as compared to additive \times dominance effects. It is observed that magnitude and signs of all the three interaction parameters varied from cross to cross showing lot of variability for the character. In four crosses of PBC 830 with Pb Lal, Ooty Round, ATG and Pepsi-7, highly significant values of (h) and (l) components with opposite sign indicated duplicate type of epistasis for this character.

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