F_2 segregation pattern for fruit shape and pedicel character in tomato

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ABSTRACT

The present investigation was designed to study the segregation pattern of fruit shape and pedicel character in tomato. Semi dominance and gene interactions were operative for the control of fruit shape. Segregation analysis in the F_2 population indicated the involvement of two genes controlling fruit shape. It could be determined that 'jointed pedicel' character controlled by the single gene 'JJ' was completely dominant over 'jointless pedicel' character controlled by 'jj'.

Different characters of tomato have been exploited extensively through breeding. Objectives of tomato breeding initially aimed at yield, plant growth habits, shelf life and processing qualities. Later, resistance breeding became the prime objective. Breeding for improvement of fruit quality came into existence somewhat later. Breeding strategy for development of improved variety with resistance properties, good fruit size and other characters require understanding of the nature and relative magnitude of gene action governing the important quantitative characters as well as the segregation pattern of both the quantitative and quantitative characters. The present investigation was, therefore, designed to study the segregation pattern of fruit shape and pedicel character in different cross combinations involving some promising genotypes of tomato with a view to elucidate the genetic architecture for fruit shape and pedicel character.

MATERIALS AND METHODS

Five genotypes of tomato, divergent for different qualitative and quantitative characters viz., Bilahi (BCT 53), CLN 200 IA (BCT 82), T 4099 dg og (BCT 115), T 4065 hp $\underline{og}^c$ (BCT 119) , HBP-2 (BCT 132) collected from Jorhat, Assam, AVRDC, Taiwan and USDA, USA have been utilized in the present study. The five parental genotypes BCT-53, BCT-82, BCT-115, BCT-119 and BCT-132 and the six F_1 hybrids BCT-82 x BCT-53, BCT-53 x BCT-82, BCT-119 x BCT-115, BCT-115 x BCT-119, BCT-132 x BCT-119 and BCT-119 x BCT-132 were grown during the autumn-winter season (2007-08). The parental genotypes were selectively (on the basis of the concerned character) crossed to develop the reciprocal crosses. The F_1 hybrids were selfed to develop the F_2 segregants. The six F_1 hybrids, their respective six F_2 segregants were grown along with their parental lines during autumn winter season in lines with 75 cm x 75 cm spacing Recommended cultural practices have been followed. In this investigation 20 plants were allotted to each parent and F_1 while 70 plants to each F_2 population. Observations on the different qualitative and quantitative characters were recorded from all the plants of the parental, F_1 and F_2 populations. The segregation pattern of the qualitative characters was analyzed by the chi-square test.

RESULTS AND DISCUSSION

Segregation Pattern of fruit shape

Segregation pattern of fruit shape was determined through the nature of expression of the respective character in the parental, F_1 and F_2 populations. The expression of these characters has been presented.

First cross : BCT 82 x BCT 53

P_1 (Heart shape)　　　x　　　P_2 (Round)

BBRR　　　↓　　　B′B′ RŔ (It is the gene symbol we proposed for round fruit shape)

F_1

BB′RR′ (Roundish-heart to heart shape)

BB′RR′　　x　　BB′RR′

F_2 :

Gametes →↓	BR	BR'	B'R	B'R'
BR	BBRR	BBRR′	BB′RR	BB′RR′
BR′	BBR′R	BBR′R′	BB′R′R	BB′R′R′
B'R	BB′RR	B′BRR′	B′B′RR	B′B′RR′
B′R′	B'BR'R	B′BRR′	B′B′R′R	B′B′R′R′

9 Roundish-heart : 5 Round : 2 Flatty-round

Genotype	Frequency
BBRR	1
BBRR′	2
BBR′R′	1
BB′RR	2
BB′RR′	4
BB′R′R′	2
B′B′RR	1
B′B′RR′	2
B′B′R′R′	1

Observed frequency: 40 Roundish-heart : 24 round : 6 Flatty-round

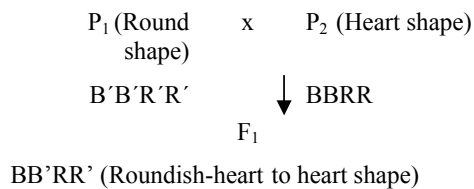Expected frequency: 39 Roundish-heart : 22 Round : 9 Flatty round to heart

Chi-square analysis

Expected Ratio	Observed (o)	Expected (e)
9/16	40	39
5/16	24	22
2/16	6	9

$\chi^2 = 1.20$, p = 0.56 at d. f. = 2

'p' value of 0.05 or greater (0.05 to 1.0) indicate that the observed deviation will be obtained by chance alone for 5 percent or more times. In this case 'p' value indicated that if the same experiment is repeated many times, 56% of the trials would be expected to exhibit chance deviation as great as or greater than that is seen in the initial trial.

Reciprocal cross :   BCT 53 x BCT 82

P_1 (Round shape)   x P_2 (Heart shape)

B′B′R′R′   ↓   BBRR

F_1

BB'RR' (Roundish-heart to heart shape)

F_2 segregation: 39 Roundish-heart : 26 Round : 5 Flatty round

Chi-square analysis

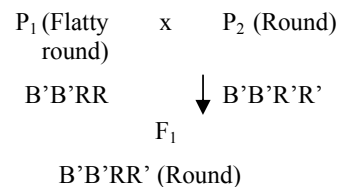| Expected Ratio	Observed (o)	Expected (e)
9/16	39	39
5/16	26	22
2/16	5	9

$\chi^2 = 2.49$, p = 0.32 at d.f. = 2

In this case also the 'p' value is greater than 0.05. Hence, the null hypothesis is accepted.

The hypothesis for the genetic control of fruit shape

Semi dominance and gene interactions were operative for the control of fruit shape which corroborated to the findings of Zdravkovic *et al.* (2003). Gene interaction produces novel or new phenotype in the F_2 segregation, effecting a modified dihybrid cross in addition. Segregation analysis in the F_2 population as recorded by Aggour (1999) indicated the involvement of two genes controlling fruit shape. In the present investigation, heart shaped fruits are controlled by two pairs of genes in homozygous condition (BBRR). Similarly, plants with round fruits have also homozygous gene arrangements (B'B'R'R'). A cross between BBRR X B'B'R'R' produced plants with somewhat intermediate fruit shape roundish-heart shape to heart shape fruits. It might be the case of semi dominant alleles. Semi dominant alleles may produce the same genetic product but in unequal quantity. In heterozygous condition the total product is the sum of two separate quantities of the two alleles. The heterozygous BB'RR' produced heart to roundish-heart shaped fruits. The gene combination of B_R_ produced heart to roundish-heart shaped fruits. B'B'R'R or B'BR'R or B'B'R'R' gene combination always produced round fruits. Interaction of either BBR'R' or B'B'RR in homozygous condition produced the new fruit shape: flatty-round which was quite different than the parental fruit shapes.

Second cross : BCT 119 x BCT 115

P_1 (Flatty round)   x P_2 (Round)

B'B'RR   ↓   B'B'R'R'

F_1

B'B'RR' (Round)

F_2 segregation :

B′B′R′R′	1	Round
B′B′R′R	2	Round
B′B′RR	1	Flatty round

Expected frequency: 3 Round : 1 Flatty round

Observed frequency: 41 Round : 19 Flatty round

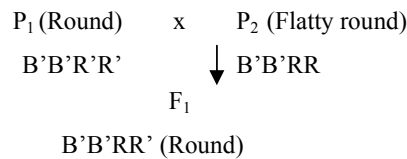**Chi-square analysis**

Expected Ratio	Observed (o)	Expected (e)
3/4	41	45
1/4	19	15

$\chi^2 = 1.41$, p = 0.25 at d.f. = 1

The null hypothesis is accepted that fruit shape is controlled by two genes. B'B'R'R' or B'B'R'R or B'BR'R' combination produced round fruits and B'B'RR produced the flatty-round fruits which were also recorded from studying the previous cross.

Reciprocal cross :   BCT 115 x BCT 119

P$_1$ (Round)   x   P$_2$ (Flatty round)

B'B'R'R'   ↓   B'B'RR

F$_1$

B'B'RR' (Round)

F$_2$ segregation : 42 Round : 20 Flatty round

Chi-square analysis

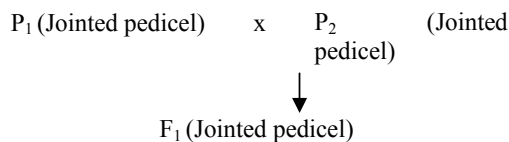| Expected Ratio	Observed (o)	Expected (e)
3/4	42	46
1/4	20	16

$\chi^2 = 1.35$, p = 0.27 at d.f. = 1

In reciprocal cross also, the null hypothesis is accepted because the p value is greater than 0.05. So, digenic inheritance of fruit shape is demonstrated. All the three fruit shapes may breed true provided the genetic control is as follows.

Genotype	Phenotype
BBRR	Heart shaped fruit
B'B'R'R	Round shaped fruit
B'B'RR/BBR'R'	Flatty-round fruit

Segregation Pattern of pedicel character (jointed/jointless)
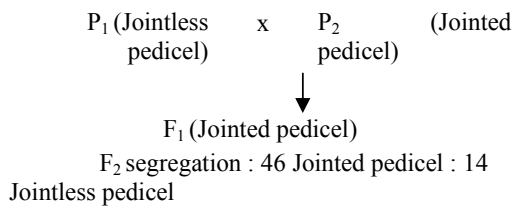
Cross 1 : BCT-82 x BCT-53

P$_1$ (Jointed pedicel)   x   P$_2$ (Jointed pedicel)

↓

F$_1$ (Jointed pedicel)

F$_2$: All plants with the fruits having jointed pedicel

Reciprocal Cross : BCT 53 x BCT 82
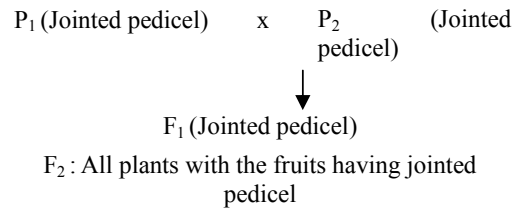
P$_1$ (Jointed pedicel)   x   P$_2$ (Jointed pedicel)

↓

F$_1$ (Jointed pedicel)

F$_2$: All plants with the fruits having jointed pedicel

Cross 2 : BCT 119 x BCT 115

P$_1$ (Jointless pedicel)   x   P$_2$ (Jointed pedicel)

↓

F$_1$ (Jointed pedicel)

F$_2$ segregation : 46 Jointed pedicel : 14 Jointless pedicel

Chi square analysis

Expected Ratio	Observed (o)	Expected (e)
3/4 Jointed pedicel	46	45
1/4 Jointless pedicel	14	15

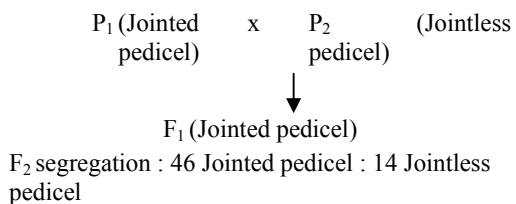$\chi^2 = 0.08$, p = 0.85 at d.f.=1

Reciprocal Cross : BCT 115 x BCT 82

P$_1$ (Jointed pedicel)   x   P$_2$ (Jointless pedicel)

↓

F$_1$ (Jointed pedicel)

F$_2$ segregation : 47 Jointed pedicel : 15 Jointless pedicel
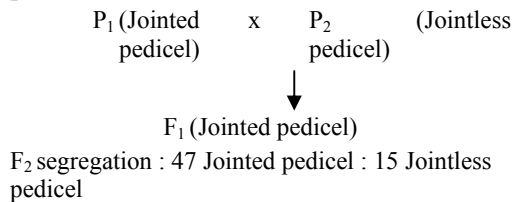
Chi square analysis

Expected Ratio	Observed (o)	Expected (e)
3/4 Jointed pedicel	47	46
1/4 Jointless pedicel	15	16

$\chi^2 = 0.08$, p = 0.85 at d.f.=1

Cross 3 : BCT 132 x BCT 119

P$_1$ (Jointed pedicel)   x   P$_2$ (Jointless pedicel)

↓

F$_1$ (Jointed pedicel)

F$_2$ segregation : 46 Jointed pedicel : 14 Jointless pedicel

Chi square analysis

Expected Ratio	Observed (o)	Expected (e)
3/4 Jointed pedicel	46	45
1/4 Jointless pedicel	14	15

χ^2= 0.08, p = 0.85 at d.f.=1

Reciprocal Cross : BCT-119 x BCT-132

P_1 (Jointless pedicel)   x P_2 (Jointed pedicel)

$\downarrow$

F_1 (Jointed pedicel)

F_2 segregation : 46 Jointed pedicel : 14 Jointless pedicel

Chi square analysis

Expected Ratio	Observed (o)	Expected (e)
3/4 Jointed pedicel	46	45
1/4 Jointless pedicel	14	15

χ^2= 0.08, p = 0.85 at d.f.=1

Hypothesis for the genetic control of pedicel character

From all the six crosses including reciprocals, the null hypothesis was highly accepted because 'p' values were much higher than 0.05. It could be proved that 'jointed pedicel' character controlled by the single gene 'JJ' was completely dominant over 'jointless pedicel' character controlled by 'jj'. The non-allelic mutations jointless and jointless-2 have been discovered as recessive mutations that completely suppress the formation of pedicel abscission zones. Based on high resolution genetic and physical mapping, it was concluded that the jointless-2 gene is located within or near the chromosome 12 (Budiman *et al.*, 2004). Previously, Rick and Butler (1956), Kravchenko (1980) and Rick and Butler (1956) opined that the locus of jointless (j) gene regulating the jointless pedicel character has locus at 11-28.

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