Theor. Appl. Genet. 58, 253-256 (1980)

The Effect of Distance Between Parents on the Yield of Sweet Pepper × Hot Pepper Hybrids, *Capsicum annuum* L. in a Single Harvest*

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Summary. Crosses between a cytoplasmic male-sterile sweet pepper and 14 hot pepper lines were often heterotic for the traits yield/plant and red yield/plant. All the F_1 crosses were fertile and hot. All other F_1 traits were intermediate to the parents' values. Phenotypic diversity among parents is not related to heterotic yield performance. Superior crosses must be found by trial and error.

Key words: *Capsicum* – Cytoplasmic male sterility – Heterosis

Introduction

Heterosis for yield in pepper, *Capsicum annuum* L. has been documented in both hot and sweet cultivars (Deshpande 1933, Gill et al. 1973. Lippert 1975, Martin 1949, Rocchetta et al. 1976, Pochard 1966, Shifriss and Rylski 1973). However, commercial exploitation on a large scale is limited (Breuils and Pochard 1975) due to the inefficient systems of male sterility-male fertility restoration (Daskalof 1976, Peterson 1958, Shifriss and Guri 1979).

In the present research, an attempt is made to predict heterotic hybrids by studying yield performance of F_1's in relation to the phenotypic distance among their parental inbreds. Furthermore, it was hypothesized that crosses among sweet and unrelated hot cultivars have new potential for heterotic hot hybrids. The feasibility of using sweet-fruited, cytoplasmic male-sterile lines which yield fertile F_1 hybrids is an integral part of the study.

Materials and Methods

Female Parent

A cytoplasmic male sterile line (S), msms, was originated from seven backcross generations of (S)-type lines to the sweet-fruited (N) msms inbred 7771 (Fig. 1). This male sterile line served as the female parent in crosses with 14 hot inbreds. Horticultural data on performance of the male sterile parent line were taken from the recurrent fertile inbred 7771.

Male Parents

Fourteen hot inbreds (Fig. 1) were isolated following selfing and progeny testing of lines collected in Mexico during 1976. The original open-pollinated lines represent large intercultivar variation typical of Mexico.

Technical Procedures

Crosses were made in the greenhouse among the male sterile line and the 14 hot inbreds. Parental and F_1 seeds were started in the greenhouse and transplanted to the field on May 17, 1979. A completely randomized design was used with two replications and eight plants per plot in a uniform field with drip irrigation, with spacing of 0.3 m and 1.0 m within and between rows, respectively, and standard cultivation techniques. All fruits were harvested when the first red fruits started to dehydrate. The following 15 traits were recorded from seven randomly selected plants per line: number of fruits, total yield, red yield, fruit weight, number of seeds per fruit, stem length, number of leaves to bifurcation, node

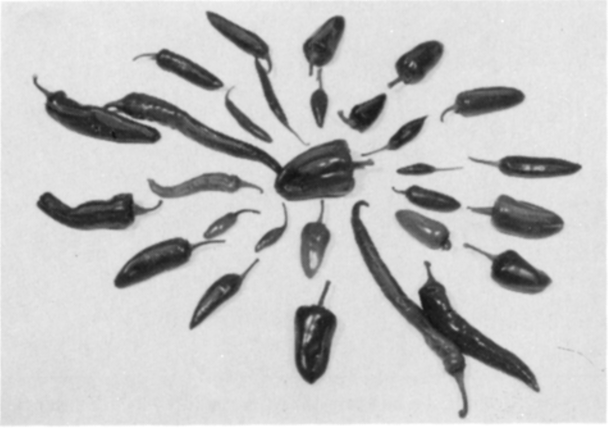

Fig. 1. Female parent (inbred 7771) in the center is surrounded by 14 male parents (inner circle) and their respective F_1's (external circle)

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* Contribution No. 128-E, 1980 Series

length, number of auxiliary shoots, pedicle length, fruit length and width, days to flowering, days to harvest, and pungency. A spectrophotometric quantitative method, Palacio (1977), was used to measure Capsaicin, the chemical responsible for pungency. The spectrophotometric readings were transformed to a log scale in the analysis.

Results

The average values of the 15 traits measured in the parents and the F_1 crosses are shown in Tables 1a-1c. Trait means for the 14 hot lines and their 14 F_1's appear at the bottom of each column along with the mean midparent value. Mean midparent is calculated as $\frac{1}{2}$ (Mean hot line + sweet line). For total yield, the mean midparent = $\frac{1}{2}$ (994 + 926) = 960 g. In Tables 1a-1c, F_1 values are indicated by an (a) or (b) if they exceed their midparent average or the larger parent respectively. The level of dominance is judged as dominant (D) or recessive (R) if a trait deviates by more than 10% from its mean midparent value. Deviations of less than 10% are classified as an essentially additive system (A).

An Euclidean measure of distance (Dis) between each hot parent and the common sweet parent is shown in Table 1a. This value has been calculated by the formula:

$$\mathrm{Dis} = \sum_{i=1}^{15} [(H_i - S_i)/S_i]^2$$

where: H_i is the mean of trait i in the hot line

S_i is the mean of trait i in the sweet line

s_i is the standard deviation of trait i.

The distance between the two parents has been calculated using standardized variables to remove the arbitrary weighting that scale effects could introduce. By standardizing the traits, the magnitude of Dis is invariant with respect to choice of scale.

Table 2 presents the correlations between the distance Dis and the corresponding F_1 trait averages.

Discussion

The yield performance of the crosses is very promising. The mean of the crosses exceeds the mean of the hot lines by some 30% and the best crosses are as good as the best parent in total yield/plant and substantially superior in red yield/plant. The crosses have fewer and larger fruits than their hot parents.

Heterosis in total yield/plant does not reflect any heterosis in either of these two yield components. In fact, these two components are recessive.

Table 1a. Yield components, number of seeds/fruit, and pungency of parents and the F_1 crosses

Line	Distance between parents	Total yield/Plant		Red yield/Plant		No. of fruits		Fruit weight		No. of seeds/fruit		Pungency	
		P	F_1	P	F_1	P	F_1	P	F_1	P	F_1	P	F_1
Sweet	0	926	–	844	–	14	–	64	–	247	–	0	–
Hot 1	85	1604	1455^a	1067	1040^a	189	61	8	24	83	167	0.3	1.1^b
2	100	617	1012^b	265	647^b	195	94	3	11	65	106	0.6	1.3^b
3	53	964	1337^b	371	926^b	63	33	15	40	78	171	1.4	1.1^a
4	39	1100	1514^b	367	1218^b	50	53	22	30	112	122	0.6	0.7^b
5	105	1110	1128^a	400	742^a	206	60	5	19	83	141	1.0	1.3^b
6	85	612	1535^b	207	1048^b	99	76	6	21	125	102	0.3	0.8^b
7	101	1234	1104	797	884^b	200	49	6	22	81	165	1.3	1.1^a
8	36	1037	1594^b	564	1265^a	28	49	39	33	152	83	0.5	1.1^b
9	36	1021	1328^b	1017	908	31	35	33	38	163	73	0.8	0.3^b
10	90	831	1118^b	221	567^a	166	62	5	34	97	158	1.4	1.1^a
11	68	660	1138^b	452	795^a	95	46	7	25	182	184	1.4	1.1^a
12	40	1214	1057	958	838	70	44	17	25	144	117	0.9	1.1^b
13	35	991	1115^b	734	825^a	55	57	18	20	145	52	1.0	1.2^b
14	79	925	1671^b	590	748^a	131	60	7	28	116	170	1.2	0.8^a
Mean of males and F_1's	68	994	1293	572	831	113	56	13.6	26.4	116	130	0.9	0.1
Mean midparent traits			960		707		64		39		181		0.45
Classification of traits			OD		D		R		R		R		OD

OD = Over dominance, majority of crosses exceeded larger parent; D = Mean F_1 exceeds mean midparent by 10% or more; R = Mean midparent exceeds mean F_1 by 10% or more; A = Mean F_1 is within 10% of mean midparent

[a] F_1 exceeds midparent

[b] F_1 exceeds larger parent

Table 1b. Plant size parameters of parents and F_1 crosses

Line	Stem length (cm)		No. of leaves to bifurcation		Node length (mm)		No. of side branches/plant	
	P	F_1	P	F_1	P	F_1	P	F_1
Sweet	12	–	7	–	16		0.1	–
Hot 1	35	18	21	9	17	20^{b}	7.3	3.6
2	35	22	15	11	23	20	5.3	3.8^{a}
3	15	14^{a}	10	7	16	19^{b}	3.1	2.4^{a}
4	18	15	8	8	22	18	3.7	2.4^{a}
5	40	15	18	8	22	18	4.7	2.9^{a}
6	24	16	17	10	13	17^{b}	6.4	4.1^{a}
7	24	17	9	7	26	23^{a}	5.4	3.4^{a}
8	15	13	8	7	19	19^{a}	2.0	1.0
9	13	12	7	7	18	18^{a}	2.0	0.9
10	26	17	15	10	17	17^{a}	4.7	2.7^{a}
11	22	15	11	8	20	20^{a}	3.2	2.1^{a}
12	17	13	8	8	22	17	3.1	1.2
13	15	12	7	7	20	17	1.6	0.9
14	32	16	21	10	15	17	6.1	3.4^{b}
Mean of male parents and F_1's	23.6	15.4	12.5	8.3	19.4	18.7	4.2	2.5
Mean midparents	17.7			10.0		17.7		2.2
Classification of traits^{c}	A			A		A		A

^{a} F_1 exceeds midparent average, ^{b} F_1 exceeds larger parent, ^{c} See Table 1a for explanation

Table 1c. Fruit size parameters, days to flowering and days to harvest of parents and F_1 crosses

Line	Pedicle length (mm)		Fruit length (mm)		Fruit width (mm)		Days to			
							Flowering		Harvest	
	P	F_1	P	F_1	P	F_1	P	F_1	P	F_1
Sweet	26	–	100	–	52	–	58	–	75	–
Hot 1	29	27	52	81^{a}	15	29	73	59	101	81
2	32	39^{b}	42	82^{a}	10	20	79	63	103	92^{a}
3	21	24^{a}	54	84^{a}	23	38	77	61	96	81
4	21	26^{a}	52	84^{a}	31	41	66	58	92	83
5	32	29	46	81^{a}	11	27	80	58	96	81
6	27	26	66	98^{a}	11	26	70	55	103	81
7	52	41^{a}	83	118^{b}	10	26	68	59	96	96^{a}
8	44	40^{a}	199	173^{a}	24	31	57	66^{a}	80	92^{b}
9	43	34	196	167^{a}	24	29	57	65^{b}	80	81^{b}
10	32	29	34	76^{a}	11	25	86	67	101	87^{a}
11	41	31	51	99^{a}	15	29	69	61	96	83
12	38	26	59	94^{a}	30	41	58	60^{b}	81	80^{a}
13	20	26	61	73	28	29	55	74^{a}	83	87^{b}
14	28	33^{b}	94	119^{b}	20	36	78	70^{a}	101	87
Mean of male parents and – F_1's	32.8	30.8	77.8	102.0	18.8	30.6	69.5	62.6	93.5	85.1
Mean midparents		29.4		88.9		35.4		63.7		84.2
Classification of traits^{c}		A		D		R		A		A

^{a} F_1 exceeds midparent, ^{b} F_1 exceeds larger parent, ^{c} See Table 1a for explanation

Table 2. Correlation between distance (Dis) and F_1 values

Trait	Correlation with F_1 values
Total yield/plant g.	– 0.23
Red yield/plant g.	– 0.49
No. of fruits/plant	0.0[a]
Weight/fruit g.	– 0.68
No. of seeds/fruit	0.51
Pungency	0.26
Stem length	0.78[a]
No. of leaves to bifurcation	– 0.60[a]
Node length	0.37
No. of side branches	0.84[a]
Pedicle length	0.29
Fruit length	– 0.32
Fruit width	– 0.65[a]
Days to flowering	– 0.31
Days to harvest	0.28

[a] Statistically significant ($p < 0.05$)

The distance between parents is not a useful predictor of promising crosses. The correlations between distance and total yield/plant or red yield/plant are small, negative and statistically non-significant. Gill et al (1973) performed a half diallel among six lines of sweet peppers. He also obtained an average F_1 superiority in total yield over the parent lines. Out of 15 F_1 crosses, nine were heterotic and six exceeded the best parent line. The number of fruits/plant and fruit weight were both higher on the average in the F_1 and several crosses were heterotic. Using the traits days to flowering, number of fruits/plant, fruit size and fruit weight, we calculated a distance measure, and the correlation between this distance and total yield was –0.22. These results are in close agreement with our findings: that distance between parents is of no predictive value for the heterotic trait total yield/plant in peppers.

Pollen Fertility Restoration

Pollen fertility restoration is a prerequisite for exploiting cytoplasmic male sterility in producing hybrid pepper cultivars. The 14 hot cultivars were, as expected (Peterson 1958), homozygotic MsMs for pollen restoration. The fertility restoration can be judged by the F_1 seed number.

Acknowledgement

We are grateful to Mr. Y. Hakim and Dr. J. Kanner for their help. This research was supported by a grant from the United States-Israel Binational Science Foundation (BSF), Jerusalem, Israel.

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Received May 8, 1980
Communicated by A. Gustafsson

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