Selection for Early Flowering, Branching and Gynoecy in Cucumber (*Cucumis sativus* L.)

Ana Isabel López-Sesé and J. E. Staub
USDA-ARS Vegetable Crops Research Unit, University of Wisconsin-Madison Department of Horticulture, 1575 Linden Dr. Madison WI 53706

Introduction. The use of exotic germplasm has allowed for the incorporation of disease resistant genes (e.g., PI 198087, PI 196289, PI 220860), and opportunities to change plant architecture in cucumber (1). This has resulted in the development and release of lines with unique branching and flowering habits (2).

One of these plant types that has potential for increasing the yield of cucumber is one which is gynoecious, determinate and multiple lateral branching (3). In theory, earliness is encouraged in gynoecious flowering, and plants of shorter stature (i.e., determinate) with many lateral branches might be expected to produce a larger amount of early fruit in a reduced field space.

There are, however, problems associated with the selection of plants that possess multiple lateral branching in a determinate background (4). The problems involve the difficulty of vegetative propagation during breeding and the inability to select determinate plants in a multiple lateral branching background. This can be over come by indirect selection for DNA markers associated with target traits (5).

We have been attempting to introduce multiple lateral branching originating from exotic germplasm into commercially acceptable gynoecious lines through phenotypic selection. The research described herein provides information on the use of the multiple lateral lines H-19 (University of Arkansas) and WI 5551 (2) during backcrossing to the commercially acceptable lines G421 (released by the University of Wisconsin and North Carolina State University as Gy7) and Gy14 (released by Clemson University).

Materials and Methods. Matings were made between Gy14 and H-19 and WI 5551, and G421 and H-19 and WI 5551 to produce F_1, F_2, BC_1 and BC_2 progeny (Table 1). Plants were selected (5% selection intensity) in a field nursery at Hancock WI for gynoecy, flowering date, and lateral branch number, and were rated for relative leaf size (1 = ~ 40 cm^2 and 5 = ~ 80 cm^2).

These lines and families were evaluated in 2001 in a randomized complete block design with eight replications where rows were on 1.5 m centers and plants were planted about 10 cm apart in the row. An analysis of variance and mean separation (Least Significant Difference) was preformed ($p = 0.05$). Pearson correlations coefficients and probabilities for pair wise associations were calculated. Principal component analysis (PCA; Figure 1) was performed using number of lateral branches and sex expression (Panel A), number of lateral branches and flowering date (Panel B), number of lateral branches and leaf type (Panel C), and all trait (Panel D) data.

Results and Discussion. Mean and standard deviation (StDv) for flowering date (days to anthesis), percentage of gynoecy, number of lateral branches are given in Table 1. It is clear that progeny having either H-19 or WI 5551 have relatively more branches. However, progeny with H-19 in their pedigree tended to possess more lateral branches when compared to progeny resulting from WI 5551 matings. The mean days to flower for H-19 is significantly less than WI 5551, but H-19 produces female flowers

later than WI 5551 which has a relatively early gynoecious flowering habit.

PCA indicated that parents and progeny could be separated by their phenotypic appearance (Figure 1). For instance, three distinct groups were apparent based on differences in lateral branch number and sex expression (Panel A). Two entries (line G421 and F1 G421 x Gy14) were not associated with any group. Line H-19 differed from all other entries in number of lateral branches (relatively high) and flowering time (late) (Panel B). Likewise, many of the entries grouped into two clusters based on their lateral branch number and leaf type (Panel C). As predicted online H-19 was distinct from other entries for these traits. Other entries containing various doses of H-19 (F_2, BC_1 and BC_2) were also distant from the main groups. When all traits were considered (Panel D), two major groups could be identified, and line H-19 and BC_1 [(H-19 x 5551) x H-19] were similar. Progeny of entries F_2 (5551 x H-19), F_2 (G421 x H-19), BC_1 (H-19 x 5551) x 5551 were also distinct, but not similar to each other.

Little leaf type and flowering date (-0.06), gynoecy and lateral branch number (- 0.57), gynoecy and little leaf type (-0.35), number of lateral branches and standard leaf size (- 0.45), and little leaf size and standard leaf size (- 0.51) were negatively correlated. Normal leaf size and gynoecy (0.40) and number of lateral branches and little leaf (0.45) were positively correlated. Based on these correlations and the phenotypic similarities observed in the parents and progeny examined herein, it appears that the development of multiple branching, gynoecious, early flowering germplasm with either leaf type will be difficult. Nevertheless, the variation for the characters selected (Table 1) suggests that further selection in some families (e.g., 26, 28, 30 and 31) might result in the capture of unique individuals having potential for increasing early yield in processing cucumber while retaining acceptable fruit quality.

Literature Cited

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Figure 1. Principal component analyses of traits observed in parental and progeny (F_1, F_2, BC_1, BC_2) of cucumber.

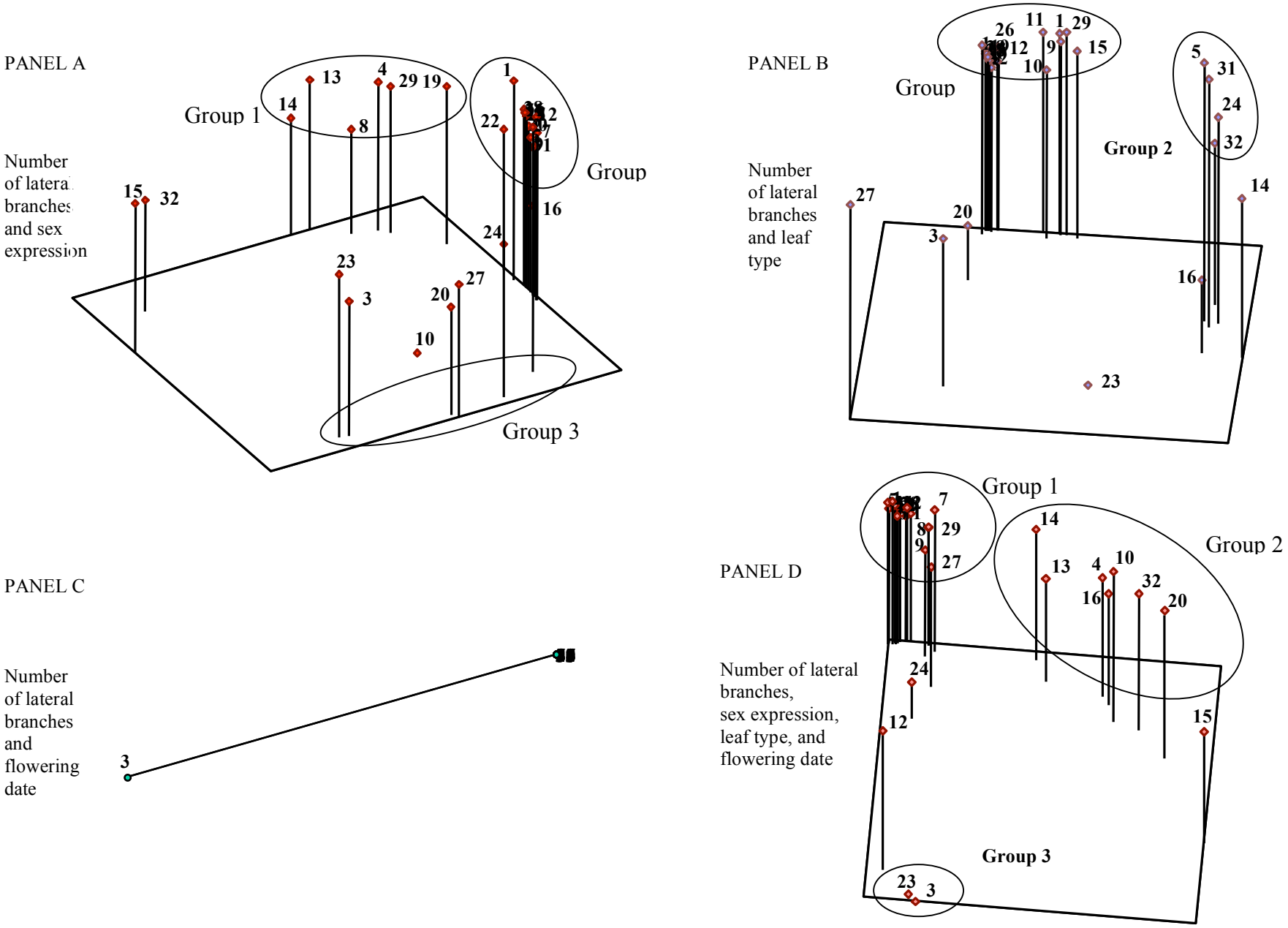

Table 1. Mean and standard deviation of traits of parental lines and progeny in cucumber.

			Flower Date[1]		Gynoecious		Lateral Branches[3]		Leaf type[4]	
Entry	Gen.	Pedigree	Mean	StDv[2]	Mean	StDv	Mean	StDv	Mean	StDv
1	P	G421	41.8	2.2	100.0	0.0	2.1	1.0	5.0	0.0
2	P	GY14	39.4	1.4	94.7	22.6	4.5	1.1	5.0	0.0
3	P	H19	39.8	6.4	0.0	0.0	11.3	2.3	1.0	0.0
4	P	5551	47.8	1.3	56.8	50.2	5.2	1.2	5.0	0.0
5	F_1	G421 x GY14	38.8	0.5	100.0	0.0	3.8	0.5	4.5	0.6
6	F_1	G421 x H19	40.8	3.0	100.0	0.0	5.1	1.3	5.0	0.0
7	F_1	G421 x 5551	42.8	2.1	88.9	33.3	4.7	1.1	5.0	0.0
8	F_1	GY14 x H19	40.1	2.7	95.0	22.1	6.2	1.6	5.0	0.0
9	F_1	5551 x GY14	41.2	2.2	96.2	19.6	5.5	1.4	4.8	0.4
10	F_1	H19 x 5551	40.4	2.7	52.5	50.6	8.1	2.2	4.9	0.3
11	F_2	(G421 x GY14)(x)	39.5	1.5	100.0	0.0	3.8	1.1	4.9	0.3
12	F_2	(G421 x H19) (x)	41.0	2.8	85.9	35.0	4.0	1.9	4.8	0.7
13	F_2	(G421 x 5551) (x)	42.5	2.9	67.3	47.1	4.5	1.5	4.8	0.4
14	F_2	(GY14 x H19) (x)	39.5	2.5	67.7	47.0	5.5	2.3	4.0	1.2
15	F_2	(5551 x GY14) (x)	43.6	2.7	21.5	41.4	6.3	1.8	4.8	0.4
16	F_2	(H19 x 5551) (x)	43.4	3.9	58.3	49.7	6.2	2.0	3.9	1.3
17	BC_1	(G421 x GY14) x G421	40.8	2.0	100.0	0.0	4.0	1.3	5.0	0.0
18	BC_1	(G421 x GY14) x GY14	40.8	2.4	98.7	11.5	3.9	1.1	5.0	0.0
19	BC_1	(G421 x H19) x G421	40.1	2.4	97.5	15.7	3.8	1.2	5.0	0.1
20	BC_1	(G421 x H19) x H19	39.8	2.6	44.3	50.0	7.7	2.8	4.0.	1.5
21	BC_1	(G421 x 5551) x G421	41.8	2.2	100.0	0.0	3.9	1.3	5.0	0.0
22	BC_1	(G421 x 5551) x H19	44.1	2.7	97.5	15.7	5.3	1.0	5.0	0.0
23	BC_1	(H19 x 5551) x 5551	39.7	2.6	0.0	0.0	8.9	3.1	3.1	1.7
24	BC_1	(H19) x 5551) x 5551	43.4	3.2	50.0	50.3	7.1	1.9	4.5	0.5
25	BC_2	[(G421 x GY14) x G421] x G421	40.8	2.0	100.0	0.0	4.0	1.0	5.0	0.0
26	BC_2	[(G421 x H19) x G421] x G421	40.3	2.0	100.0	0.0	3.8	1.1	5.0	0.2
27	BC_2	[(G421 x H19) x H19]x H19	41.0	3.8	40.0	49.3	8.6	2.4	1.4	0.5
28	BC_2	[(G421 x 5551) x G421] x G421	41.4	2.2	100.0	0.0	3.6	1.3	5.0	0.0
29	BC_2	[(G421 x 5551) x G421] x 5551	43.3	2.8	80.0	40.3	4.5	0.9	4.8	0.4
30	BC_2	[(G421 x 5551) x 5551] x G421	42.8	1.9	100.0	0.0	4.5	0.8	5.0	0.0
31	BC_2	[(G421 x 5551) x 5551] x 5551	44.5	3.0	98.6	11.9	5.6	1.4	4.5	0.5
32	BC_2	[(H19 x 5551) x 5551] x 5551	45.9	1.2	48.1	50.0	5.6	1.0	4.5.	0.6
		LSD (0.05)	1.13		13.15		0.70		0.26	