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Estimates of Heritabilities and Genetic Variances of Three Yield and Five Quality Traits in Three Fresh-market Cucumber Populations

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Abstract. Variance components for 3 fruit yield and 5 fruit quality traits in 3 cucumber (*Cucumis sativus* L.) populations were estimated using a North Carolina Design I analysis. Three populations were studied (elite, medium base, and wide base), having been formed by intercrossing lines to produce 3 levels of genetic diversity. Families were evaluated in 1.5 × 1.5 m plots using once-over harvest at the stage of 15% oversized fruits. Heritabilities based on full-sib family selection for fruit yield ranged from 0.03 to 0.25, and for the fruit quality traits 0.00 to 0.30. The wide base population would be best for long-term selection for the traits studied, because it had the highest predicted means for all traits except percentage of culls, fruit shape, and overall performance after 15 cycles of full-sib family selection.

Since the introduction of North Carolina Designs I, II, and III by Comstock and Robinson (1, 2) in 1948, these designs

have been used by many plant breeders for estimating genetic variance components in plant populations. The N.C. Design I has been used successfully in obtaining estimates of genetic variance components for pickling cucumber populations. McCreight et al. (5) used a N.C. Design I to estimate the half-sib heritability of reducing sugars in cucumber. Expected gains per cycle of selection, based on half-sib progeny testing and half-sib testing, were 0.42 and 0.21 mg reducing sugar per g of fruit tissue, respectively. Smith et al. (8) estimated the variance components for 3 fruit yield and 5 fruit quality traits, and number of days to harvest in a monoecious pickling cucumber

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population using a N.C. Design I and found that most of the genetic variance was additive for all traits except fruit color. Heritabilities based on full-sib family selection for fruit value and fruit number were 0.19 and 0.17, respectively. Wehner (10) used a N.C. Design I to estimate the genetic variance and heritability of low-temperature germination ability in the cucumber. Dominance variance was greater than additive variance for percentage of germination and days to 50% germination, but additive variance accounted for all of the genetic variance for actual days to germination.

This study was undertaken because no estimates of genetic variance components were available for fresh-market cucumbers or for cucumber populations differing in genetic diversity. The objectives of this study were to obtain estimates of the genetic variance components for 3 fruit yield and 5 fruit quality traits in 3 fresh-market cucumber populations, to predict gain from selection for each population based on the above estimates using a N.C. Design I, and to determine the best population to use for improvement of fresh-market cucumbers for fruit yield and quality.

Materials and Methods

Populations tested. Three North Carolina fresh-market (slicer) cucumber populations were used for this experiment: NC Elite Slicer 1 (NCES1), NC Medium Base Slicer (NCMBS), and NC Wide Base Slicer (NCWBS).

The NCES1 population was developed by intercrossing the following cultivars or lines in 1981: WI 1321 and WI 1394

(C.E. Peterson, USDA-Wisconsin), Exp 7 and Exp 22 (T. Sakata & Co., Japan), Sprint 440 (Asgrow Seed), Tablegreen 72F and Poinsett 76 (H.M. Munger, Cornell Univ.), and Dasher (PetoSeed). The F_1 progenies of paired crosses were intercrossed in all possible combinations in the greenhouse in Spring 1982, and the F_2 plants were intercrossed in the field in Summer 1982.

The NCMBS population was developed by intercrossing 152 lines (96 cultivars from the United States, 31 cultivars from the Netherlands, 18 breeding lines from the United States and the Netherlands, and 7 plant introduction lines from the People's Republic of China) in the field in 1981. The fruit were harvested and seeds from each planted in 1982 for intercrossing half-sib families as described for the NCWBS population below.

The NCWBS population was developed by intercrossing 1063 lines (including 720 plant introduction lines from the USDA Regional Plant Introduction Station, Ames, Iowa, and 343 cultivars and breeding lines from seed companies and breeding programs around the world) in the field in 1981. Seeds from the long fruits (>150 mm in length) were then planted as half-sib families in 1982, with family rows alternating with rows of composite pollinator (seed of all families mixed together), for a 2nd intercross. Pollen rows were sprayed with silver nitrate and family rows were sprayed with (2-chloroethyl) phosphonic acid (ethrel) as suggested by Wehner and Jenkins (11) to maximize intercrossing and minimize self- and sib-pollination.

A N.C. Design I (1, 2) mating design was used to estimate the variance components in the reference populations. In this study, 72 S_0 plants were chosen at random from each population and designated as males. Each male was mated with 3 S_0 plants chosen at random and designated as females. Pollinations were made in the field and in the greenhouse, with one cross between each pair of plants to produce about 100 seeds per full-sib family. In order to estimate genotype \times environment interaction, 2 environments were used in the experiment in 1984—the spring and summer planting seasons.

Field evaluation. Seeds of the families produced by the mating design were planted at the Horticultural Crops Research Station near Clinton, N.C. using a nested design with full-sib families (females) nested in the half-sib families (males). The experiment was planted on 11 May 1984 for the spring season and 7 Aug. 1984 for the summer season, with 2 replications in each.

Plots were thinned to 15 plants and maintained with standard cultural practices. The soil had been treated the previous October with the nematicide (\pm)-2-(2,4-dichlorophenoxy)propanoic acid (dichloropropene) at a rate of 93.1 liters a.i./ha⁻¹. Prior to bed formation in the spring, fertilizer (90N-

Table 1. Rating scale and descriptions for evaluation of 4 fresh-market cucumber fruit quality traits of families developed from 3 populations using a North Carolina Design I analysis.

Score	Trait			
	Shape	Color	Seedcell size	Overall performance
1	Pointed, crooked	White	Extra-large	Poor
2		Yellow-white	Very large	Fair
3		Yellow-green	Large	Average
4		Light green	Medium-large	Good-
5	Tapered, curved	Med.-light green	Medium	Good
6		Medium green	Medium-small	Good+
7		Med.-dark green	Small	Excellent-
8	Blocky, straight	Dark green	Very small	Excellent
9		Very dark green	Extra-small	Excellent+

Table 2. Analysis of variance and expected mean squares for full-sib families nested in half-sib families in a North Carolina Design I analysis.

Source of variation	Degrees of freedom	Expected mean squares
Season (S)	1	---
Set (St)	1	---
Rep/St	2	---
S \times Rep/St	3	---
Male/St (M/St)	70	$\sigma^2 + 2\sigma^2_{S \times F/M/St} + 4\sigma^2_{F/M/St} + 6\sigma^2_{S \times M/St} + 12\sigma^2_{M/St}$
S \times M/St	70	$\sigma^2 + 2\sigma^2_{S \times F/M/St} + 6\sigma^2_{S \times M/St}$
Female/M/St	144	$\sigma^2 + 2\sigma^2_{S \times F/M/St} + 4\sigma^2_{F/M/St}$
S \times Female/M/St	144	$\sigma^2 + 2\sigma^2_{S \times F/M/St}$
Error	428	σ^2

Table 3. Means, estimates of design components, genetic variances, and heritabilities for 3 yield and 5 quality traits studied in the elite slicer cucumber population.

Statistic and heritability estimate ^a	Fruit yield (no./plot)			Culls (%)	Fruit quality score ^a			Overall performance
	Total	Marketable	Early ^b		Shape	Color	Seed-cell size	
\bar{x}_O	23.8	19.4	2.8	22.8	6.2	7.7	5.7	6.1
σ^2_M	5.06	3.17	0.40	0.00	0.07	-0.04	0.07	0.07
	$\pm 3.46^w$	± 2.67	± 0.36	± 0.00	± 0.07	± 0.05	± 0.08	± 0.12
$\sigma^2_{F/M}$	11.28	7.17	0.40	0.00	0.05	0.11	0.14	-0.03
	± 2.58	± 1.96	± 0.33	± 0.00	± 0.05	± 0.04	± 0.06	± 0.09
σ^2_A	20.22	12.68	0.34	0.00	0.27	-0.16	0.27	0.30
	± 6.95	± 5.34	± 0.71	± 0.00	± 0.14	± 0.09	± 0.16	± 0.24
σ^2_D	24.91	15.99	1.26	0.00	-0.09	0.61	0.29	-0.42
	± 8.66	± 6.63	± 0.97	± 0.00	± 0.18	± 0.12	± 0.20	± 0.29
$\sigma^2_{E \times M}$	2.94	3.63	1.00	0.00	0.15	0.14	0.13	0.29
	± 1.64	± 1.57	± 0.39	± 0.00	± 0.06	± 0.04	± 0.06	± 0.11
$\sigma^2_{E \times F/M}$	1.25	0.88	0.15	0.00	0.03	-0.09	-0.07	0.00
	± 2.38	± 2.06	± 0.49	± 0.00	± 0.08	± 0.05	± 0.08	± 0.15
$\sigma^2_{E \times A}$	11.77	14.54	4.00	0.01	0.59	0.55	0.53	1.14
	± 4.91	± 4.76	± 1.17	± 0.00	± 0.18	± 0.13	± 0.18	± 0.34
$\sigma^2_{E \times D}$	-6.79	-11.01	-3.40	0.00	-0.46	-0.92	-0.82	-1.14
	± 5.79	± 5.22	± 1.23	± 0.00	± 0.20	± 0.13	± 0.20	± 0.36
σ^2_e	33.21	29.22	6.82	0.02	1.08	0.83	1.32	2.13
$\sigma^2_{P(FS)}$	57.81	42.17	4.92	0.02	0.95	0.48	1.09	1.34
$\sigma^2_{P(HS)}$	73.06	57.84	8.51	0.02	1.28	1.11	1.38	1.83
$h^2_{N(FS)}$	0.18	0.15	0.03	0.13	0.14	0.00	0.12	0.10
$h^2_{N(HS)}$	0.07	0.06	0.01	0.05	0.05	0.00	0.05	0.04

^a $h^2_{N(FS)}$ and $h^2_{N(HS)}$ are the heritabilities based on full-sib and half-sib family selection, respectively.

^bEarly yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.

^aScored 1 to 9 (1 = poor, 5 = good, 9 = excellent); except for color, which was scored 1 = white, 5 = med.-light green, 9 = very dark green).

^wSE.

20P-74K, kg·ha⁻¹) was broadcast. After bed formation and seeding, ethylfluralin was applied to the soil surface at a rate of 1 kg a.i.·ha⁻¹. Post-planting fertilization consisted of a sidedress application of 34 kg·ha⁻¹ N just before the vines began spreading between rows. Irrigation was applied as needed to supplement natural rainfall and to provide about 25 to 35 mm of water to the field each week.

Fruit yield and quality traits were measured using once-over harvest of small plots. This method was more efficient in evaluating families for yield than single-plant or multiple harvest systems (12). Rows were 1.5 m apart center-to-center and plots were 1.5 m long, the optimum plot size for measurement of yield of fresh-market cucumbers in a once-over harvest system (14). Plots were separated at each end by alleys 1.5 m wide. Plot end borders were not used, since previous trials showed no genotype × end border interaction (9).

Plots were evaluated 62 and 66 days after planting in the spring, and 56 and 71 days after planting in the summer for sets 1 and 2, respectively. Fruit were harvested at the green stage when about 15% of the fruits were >60 mm in diameter. The stage at which 9% to 20% of the fruit are oversized was recommended by Miller and Hughes (6) for optimum yield in pickling cucumbers harvested once-over, so we used a similar standard for the fresh-market cucumbers.

Plots were defoliated using paraquat as recommended by Wehner et al. (13) to ease data collection at harvest. Occasional spotting of fruits by paraquat was taken into consideration when scoring fruit for color and fruit quality. Total fruit number and marketable fruit number (total fruit number - number of culls) per plot were used rather than fruit value or weight. Use of fruit

number was recommended by Ells and McSay (3) for reliable yield measurement in a once-over harvest system. Early yield was calculated by counting the number of oversized fruits per plot. Fruit shape, seedcell size, and overall performance (a rating for the plot's overall performance in both yield and quality) were rated on a scale of 1 to 9 (Table 1).

Data analysis. An analysis of variance (ANOVA) was conducted for each population. Variance components were obtained using the Varcomp procedure of the Statistical Analysis System. Components were obtained using expected mean squares from the ANOVA (Table 2). For each of the 3 populations, 14 variables were calculated as described by Hallauer and Miranda (4). These were as follows:

\bar{x}_O	=	initial mean
σ^2_M	=	variance of the males
$\sigma^2_{F/M}$	=	variance of females in males
σ^2_A	=	additive variance
σ^2_D	=	dominance variance
$\sigma^2_{E \times M}$	=	environment by male interaction variance
$\sigma^2_{E \times F/M}$	=	environment by female in male interaction variance
$\sigma^2_{E \times A}$	=	environment by additive variance
$\sigma^2_{E \times D}$	=	environment by dominance variance
σ^2_e	=	error variance
$\sigma^2_{P(FS)}$	=	phenotypic variance of full-sib families
$\sigma^2_{P(HS)}$	=	phenotypic variance of half-sib families
$h^2_{N(FS)}$	=	narrow-sense heritability based on full-sib family selection
$h^2_{N(HS)}$	=	narrow-sense heritability based on half-sib family selection

Table 4. Means, estimates of design components, genetic variances, and heritabilities for 3 yield and 5 quality traits studied in the medium base slicer cucumber population.

Statistic and heritability estimate ^z	Fruit yield (no./plot)				Fruit quality score ^x			
	Total	Market-able	Early ^y	Culls (%)	Shape	Color	Seed-cell size	Overall performance
\bar{x}_0	21.9	17.4	2.52	24.5	5.9	7.2	5.8	5.6
σ^2_M	5.80	2.26	0.12	-0.01	0.17	0.06	0.01	0.20
	$\pm 3.52^w$	± 2.26	± 0.42	± 0.00	± 0.07	± 0.07	± 0.10	± 0.46
$\sigma^2_{F/M}$	8.79	5.21	0.37	0.02	0.06	0.06	0.10	0.20
	± 2.33	± 1.67	± 0.29	± 0.00	± 0.05	± 0.06	± 0.08	± 0.38
σ^2_A	23.20	9.04	0.50	-0.02	0.66	0.23	0.06	0.81
	± 7.03	± 4.52	± 0.85	± 0.00	± 0.15	± 0.14	± 0.19	± 0.91
σ^2_D	11.96	11.78	0.98	0.10	0.41	0.19	0.68	-1.18
	± 8.44	± 5.62	± 1.03	± 1.01	± 0.18	± 0.19	± 0.66	± 1.19
$\sigma^2_{E \times M}$	6.49	6.02	1.37	0.00	0.02	0.06	0.19	0.43
	± 2.19	± 1.84	± 0.41	± 0.00	± 0.04	± 0.05	± 0.08	± 0.37
$\sigma^2_{E \times F/M}$	-1.37	-3.06	-0.08	-0.00	0.04	0.18	-0.15	-0.35
	± 2.19	± 2.10	± 0.43	± 0.00	± 0.08	± 0.08	± 0.10	± 0.66
$\sigma^2_{E \times A}$	25.95	24.10	5.46	0.02	0.08	0.24	0.77	1.70
	± 6.49	± 5.53	± 1.23	± 0.01	± 0.13	± 0.15	± 0.23	± 1.12
$\sigma^2_{E \times D}$	-31.43	-36.34	-5.78	-0.02	0.08	0.46	-1.37	-3.10
	± 6.16	± 5.59	± 1.19	± 0.01	± 0.18	± 0.18	± 0.26	± 1.51
σ^2_c	38.71	34.48	6.34	0.04	1.06	0.83	1.70	9.95
$\sigma^2_{P(FS)}$	62.52	38.07	5.50	0.04	1.12	0.88	1.13	3.73
$\sigma^2_{P(HS)}$	80.37	55.97	10.17	0.10	0.71	1.25	1.74	2.51
$h^2_{N(FS)}$	0.19	0.12	0.05	0.00	0.30	0.13	0.03	0.11
$h^2_{N(HS)}$	0.07	0.04	0.01	0.00	0.23	0.05	0.01	0.08

^z $h^2_{N(FS)}$ and $h^2_{N(HS)}$ are the heritabilities based on full-sib and half-sib family selection, respectively.

^yEarly yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.

^xScored 1 to 9 (1 = poor, 5 = good, 9 = excellent*); except for color, which was scored 1 = white, 5 = med.-light green, 9 = very dark green).

^wSE.

Cross products were computed for all pairs of traits using analogous procedures for variance components as described by Mode and Robinson (7). Covariance components were handled in a manner similar to the way variance components were handled by Mode and Robinson (7). The genetic correlation, r_{Gij} , for a pair of traits i and j was estimated as $r_{Gij} = \sigma_{Gij} / (\sigma^2_{Gi} \times \sigma^2_{Gj})^{1/2}$, where σ_{Gij} was the estimated genetic covariance component, and σ^2_{Gi} and σ^2_{Gj} were the estimated genetic variance components for characters i and j , respectively. The phenotypic correlation (r_{Pij}) for means of unrelated full-sib families grown in 2 replications and 2 environments was estimated as $r_{Pij} = \sigma_{P(FS)ij} / (\sigma^2_{P(FS)i} \times \sigma^2_{P(FS)j})^{1/2}$, where $\sigma_{P(FS)ij}$ was the phenotypic estimate of covariance, and $\sigma^2_{P(FS)i}$ and $\sigma^2_{P(FS)j}$ were the estimated phenotypic variance components for traits i and j , respectively.

Narrow-sense heritability (h^2_N) for use in selecting among half-sib and full-sib families tested in 2 replications and 2 environments was calculated as follows:

$$h^2_{N(HS)} = (1/4) \sigma^2_A / \sigma^2_{P(HS)}, \text{ and}$$

$$h^2_{N(FS)} = (1/2) \sigma^2_A / \sigma^2_{P(FS)}$$

The term σ^2_A was estimated as $4\sigma^2_M$. The term σ^2_M , the variance among males that estimates the covariance among half-sib families, is $(1/4)\sigma^2_A$, given the above assumptions.

Gain per cycle of selection (G) was calculated as follows:

$$G = k (1/2) \sigma^2_A / \sigma_{P(FS)},$$

where k was the selection intensity in units of standard deviation

(= 1.775). Gain from selection was calculated for all traits and reported as means after n cycles of selection as follows:

$$\bar{x}_n = nG + \bar{x}_0,$$

where \bar{x}_n is the mean after n cycles of selection, G is the gain per cycle of selection, and \bar{x}_0 is the initial mean.

Genetic expectations for the variance components were derived using the following assumptions for the populations studied: a) random mating, b) regular diploid behavior, c) no maternal effects, d) no epistasis, and e) linkage equilibrium or no linkage. All but 2 of the assumptions appear to be reasonable, except that epistasis and linkage could have affected the traits studied.

Results and Discussion

As expected, means for the 3 fruit yield traits (total, marketable, and early fruit number per plot) and 5 fruit quality traits (scores for percentage of culls, fruit shape, color, seedcell size, and overall performance) differed among populations. In general, the elite population had the highest means for the 8 traits measured, and the wide base population had the lowest means. The only exception was the mean for early yield, which was highest in the wide base population.

Genetic variances. As expected, additive variances for the 3 fruit yield traits and 5 fruit quality traits differed among populations. The wide base population had the largest variances for all traits except fruit shape, which was largest in the medium base population (Tables 3-5).

For the 3 yield traits, the elite population had the largest dominance variance and the wide base population the smallest

Table 5. Means, estimates of design components, genetic variances, and heritabilities for 3 yield and 5 quality traits studied in the wide base slicer cucumber population.

Statistic and heritability estimate ^z	Fruit yield (no./plot)				Fruit quality score ^a			
	Total	Market-able	Early ^y	Culls (%)	Shape	Color	Seed-cell size	Overall performance
\bar{x}_O	20.5	14.1	4.5	36.9	4.9	3.5	4.4	4.2
σ^2_M	8.41	5.21	1.87	0.01	0.16	0.13	0.15	0.09
	3.30 ^w	±2.37	±1.02	±0.00	±0.09	±0.08	±0.11	±0.11
$\sigma^2_{F/M}$	8.30	5.31	1.48	0.01	0.24	0.21	0.12	0.15
	±1.83	±1.29	±0.57	±0.00	±0.06	±0.06	±0.07	±0.08
σ^2_A	33.63	20.84	7.48	0.03	0.62	0.54	0.60	0.34
	±6.59	±4.74	±2.05	±0.01	±0.17	±0.16	±0.22	±0.23
σ^2_D	-0.42	0.39	-1.54	-0.09	0.34	0.30	-0.12	0.26
	±7.54	±5.39	±2.34	±0.01	±0.21	±0.20	±0.25	±0.28
$\sigma^2_{E \times M}$	5.50	5.23	2.78	0.00	0.03	0.08	0.23	0.25
	±1.62	±1.45	±0.78	±0.00	±0.04	±0.04	±0.08	±0.09
$\sigma^2_{E \times F/M}$	0.46	-1.21	0.40	0.00	0.06	-0.05	-0.12	-0.02
	±1.71	±1.31	±0.69	±0.00	±0.06	±0.07	±0.10	±0.11
$\sigma^2_{E \times A}$	20.21	21.30	11.11	0.05	0.10	0.31	0.92	1.00
	±4.86	±4.34	±2.33	±0.01	±0.11	±0.13	±0.25	±0.28
$\sigma^2_{E \times D}$	-18.39	-26.13	-9.50	-0.00	0.12	-0.51	-1.38	-1.08
	±4.71	±3.91	±4.32	±0.01	±0.15	±0.16	±0.26	±0.29
σ^2_e	24.49	21.11	9.60	0.04	0.87	1.04	1.64	1.70
$\sigma^2_{P(FS)}$	66.76	46.57	18.67	0.05	1.41	1.33	1.63	1.55
$\sigma^2_{P(HS)}$	74.88	57.73	26.07	0.04	1.45	1.42	1.91	2.29
$h^2_{N(FS)}$	0.25	0.22	0.20	0.25	0.22	0.20	0.19	0.11
$h^2_{N(HS)}$	0.11	0.09	0.07	0.19	0.11	0.10	0.08	0.04

^z $h^2_{N(FS)}$ and $h^2_{N(HS)}$ are the heritabilities based on full-sib and half-sib family selection, respectively.

^yEarly yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.

^aScored 1 to 9 (1 = poor, 5 = good, 9 = excellent); except for color, which was scored 1 = white, 5 = med.-light green, 9 = very dark green).

^wSE.

variance. The medium base population had the largest dominance variance for percentage of culls, fruit shape, and seedcell size, and the wide base population had the largest dominance variance for fruit color and overall performance (Tables 3–5).

In the elite population, the estimate of additive genetic variance was negative or less than its SE for fruit color. The estimate of dominance variance was negative or less than its SE for percentage of culls, fruit shape, and overall performance. Additive variance was much greater than dominance variance for percentage of culls, shape, and overall performance. Dominance variance was greater than additive variance for the 3 yield traits (total, marketable, and early fruit number per plot) as well as for fruit color. Additive variance and dominance variance were nearly equal for seedcell size (Table 3).

In the medium base population, additive variance was negative or less than its SE for early fruit yield, percentage of culls, seedcell size, and overall performance; and dominance variance estimates were negative or less than their SEs for early yield and overall performance. Additive variance was larger than dominance variance for total yield, shape, color, and overall performance. Dominance variance was larger than additive variance for marketable and early yield and seedcell size (Table 4).

In the wide base population, additive variance was positive and greater than its SE for all traits, and the dominance variance was negative or less than its SE for all traits except fruit shape and color. Additive variance was larger than dominance variance for all traits (Table 5).

Heritability. Heritabilities based on full-sib family selection ranged from 0.00 to 0.30 among the 3 populations. Heritabilities

for total, marketable, and early fruit yield ranged from 0.18 to 0.25, 0.12 to 0.22, and 0.03 to 0.20 for the elite, medium base, and wide base populations, respectively (Tables 3–5). Those values were consistent with the estimates reported by Smith et al. (8) in a monoecious pickling cucumber population.

Heritabilities for fruit quality traits ranged from 0.00 to 0.30. These values were considerably lower than the estimates of 0.25 to 0.49 reported by Smith et al. (8). Heritabilities for fruit quality in all 3 populations were lower than expected and generally lower than heritabilities for the yield traits. In contrast, Smith et al. (8) reported that heritabilities for fruit quality traits were higher than those for yield traits in the population they studied.

Heritabilities in the wide base population were generally higher than those observed in the elite and medium base populations, except for fruit shape and overall performance, which were highest in the medium base population. Heritabilities for yield traits were much higher in the wide base population than in the elite or medium-base population (Tables 3–5).

Heritabilities based on half-sib family selection were low (0.00 to 0.25) for all traits. The wide base population had the highest heritabilities for all traits except for fruit shape and overall performance (Tables 3–5). Heritabilities for selection based on half-sib families were usually less than half as large as those based on full-sib family selection. Thus, if full-sib family selection can be carried out with less than twice the resources required for half-sib family selection, full-sib family selection would be the method of choice.

Correlations. Highly significant correlations, both genetic and phenotypic, existed among the 8 traits studied in the 3 popu-

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations of cucumber traits measured with full-sib families nested in half-sib families in a North Carolina Design I analysis.

Trait	Fruit yield (no./plot)				Fruit quality score ^y			
	Total	Market-able	Early ^z	Culls (%)	Shape	Color ^x	Seed-cell size	Overall performance
<i>Elite population</i>								
Total yield	---	0.93	0.71	0.31	-0.07NS	0.05NS	-0.40	--- ^x
Marketable yield	0.97	---	0.69	0.03NS	0.22	-0.12	-0.27	---
Early yield	0.60	0.62	---	0.18	1.58	-0.31	-0.03NS	---
Culls (%)	-0.50	-0.65	-0.38	---	-1.16	0.05NS	-1.12	---
Shape	0.54	0.59	0.35	-0.54	---	-0.03NS	1.12	---
Color	-0.19	-0.22	-0.23	0.17	0.08NS	---	0.79	---
Seedcell size	0.26	0.29	0.18	-0.26	0.36	-0.04NS	---	---
Overall performance	0.51	0.54	0.28	-0.47	0.82	0.12	0.41	---
<i>Medium-base population</i>								
Total yield	---	1.25	1.12	-0.30	-0.01NS	0.40	0.61	0.12
Marketable yield	0.95	---	0.65	-0.40	0.42	0.87	0.83	0.21
Early yield	0.56	0.59	---	-0.23	-0.07NS	-0.66	0.60	0.88
Culls (%)	-0.35	-0.51	-0.24	---	-0.02NS	-0.64	-0.53	-0.40
Shape	0.38	0.49	0.23	-0.40	---	0.65	1.49	-0.01NS
Color	-0.03NS	-0.10	-0.22	0.04NS	0.17	---	1.62	-0.24
Seedcell size	0.25	0.27	0.08NS	-0.16	0.15	-0.07	---	-0.40
Overall performance	0.17	0.19	0.09	-0.13	0.36	0.10	0.11	---
<i>Wide-base population</i>								
Total yield	---	0.72	0.61	0.37	0.24	0.21	-0.31	0.55
Market yield	0.89	---	0.77	-0.42	0.83	0.16	-0.18	0.68
Early yield	0.60	0.69	---	-0.58	0.61	0.34	0.31	0.63
Culls (%)	-0.43	-0.67	-0.45	---	-1.11	0.12	-0.03NS	-0.33
Shape	0.39	0.58	0.46	-0.56	---	0.14	-0.09NS	0.28
Color	0.14	0.12	-0.02NS	-0.05NS	0.15	---	0.13	0.58
Seedcell size	-0.02NS	-0.04NS	-0.07NS	0.02NS	0.04NS	0.04NS	---	0.41
Overall performance	0.26	0.35	0.19	-0.35	0.60	0.31	0.13	---

^zEarly yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.

^yScored 1 to 9 (1 = poor, 5 = good, 9 = excellent⁺; except for color, which was scored 1 = white, 5 = med.-light green, 9 = very dark green).

^xCorrelations not calculable due to negative genetic variance for overall performance.

^{NS}Not significant at the 1% level (all others significant at the 1% level).

lations (Table 6), with the genetic correlations being somewhat smaller than the phenotypic correlations in the elite population. As expected, total fruit yield had a large positive genetic correlation with marketable (0.72 to 1.25) and early (0.61 to 1.12) fruit yield in all 3 populations.

The percentage of culls had a negative genetic correlation with all traits in the 3 populations except for marketable fruit yield, total yield, early yield, and color in the elite population; and shape in the wide base population. In the medium base population, the correlation of the percentage of culls with fruit shape was nonsignificant (Table 6). In the elite and wide base populations, the percentage of culls had a large negative genetic correlation with shape (1.16 and 1.11, respectively). Shape in the elite and wide base populations had a large positive genetic correlation with early yield (1.58 and 0.83, respectively).

Gain from selection. The initial means (\bar{x}_0) and the predicted means for the 3 populations after 1 to 15 cycles of full-sib family selection were calculated to determine the best population for improving the 8 traits studied. A representative set of means is given in Table 7. After 5 cycles of full-sib family selection, the wide base population had the highest predicted mean for total

yield, the medium base population was highest for shape, and the elite population had the highest predicted means for all other traits (data not shown). After 6 cycles of selection, the wide base population had the highest predicted means for all 3 yield traits. After 7 cycles of selection, the wide base population had the highest predicted means for all traits except fruit shape, color, percentage of culls, and overall performance (data not shown). The predicted mean for fruit color in the wide base population surpassed the predicted means of other populations after 11 cycles of selection (data not shown). After 15 cycles of selection, the predicted means of the wide base population remained the lowest for shape and overall performance, but were at a relatively high level (a mean score of 8).

It is risky to predict population means based on data from a one-year study because estimates of gain from selection will usually be changed by the selection process. Thus, predicted gains are less likely to be accurate as more cycles of selection are involved. However, in order to determine which populations would be the most useful in short term and long term selection programs, it is necessary to use such predictions.

Predicted means above 9 (the upper limit of the fruit quality

Table 7. Initial and predicted means after full-sib family selection for 3 fruit yield and 5 fruit quality traits in 3 fresh-market cucumber populations.^z

Selection cycle	Fruit yield (no./plot)			Fruit quality score ^x				Overall performance
	Total	Market-able	Early ^y	Culls (%)	Shape	Color	Seed-cell size	
Elite population								
1	23.8	19.4	2.8	22.8	6.2	7.7	5.7	6.1
3	30.8	24.5	3.2	22.7	6.9	7.7	6.4	6.7
6	37.8	26.7	3.5	22.6	7.7	7.7	7.0	7.4
9	44.8	34.8	3.8	22.5	8.4	7.7	7.7	8.1
12	51.8	40.0	4.2	22.5	9.1	7.7	8.4	8.7
15	58.7	45.1	4.8	22.4	9.9	7.7	9.1	9.4
Medium base population								
0	21.9	17.4	2.5	24.5	5.9	7.2	5.8	5.6
3	29.5	21.3	3.1	24.5	7.6	7.8	6.0	6.7
6	37.2	25.1	3.6	24.5	9.2	8.5	6.1	7.8
9	44.9	29.0	4.2	24.5	11.4	9.3	6.3	9.2
12	52.6	32.8	4.7	24.5	12.5	9.5	6.4	10.0
15	60.3	36.7	5.3	24.5	14.2	10.4	6.5	11.1
Wide base population								
0	20.5	14.1	4.5	36.9	4.9	3.5	4.4	4.2
3	31.4	22.1	9.1	36.6	6.3	4.8	5.6	4.9
6	42.2	29.7	13.6	36.3	7.7	6.0	6.9	5.6
9	53.0	38.2	18.2	36.0	9.1	7.2	8.5	6.6
12	63.9	46.3	22.7	35.6	10.5	8.4	9.4	7.0
15	74.7	54.3	27.3	35.3	11.8	9.7	10.6	7.8

^zData are initial and predicted means after 0, 3, 6, 9, 12, and 15 cycles of full-sib family selection assuming no change in heritability or phenotypic variance, and selecting for only one trait at a time.

^yEarly yield is the number of oversized fruits (>60 mm in diameter) per plot at harvest.

^xScored 1 to 9 (1 = poor, 5 = good, 9 = excellent*; except for color, which was scored 1 = white, 5 = med.-light green, 9 = very dark green). Scores above 9 indicate improvement in fruit quality traits to levels not now observed.

scale used in this study) represent gains to levels in quality not now observed. If indeed those levels were reached, the rating system would have to be adjusted to account for the improved levels of quality.

The wide base population was predicted to be the best population for improving the traits measured in this study because, after 11 cycles of full-sib family selection, it had the highest predicted means for all traits except fruit shape and overall performance. Although the predicted means for the wide base population for fruit shape and overall performance were not the highest, they were at a relatively high level (a mean score of 8) after 15 cycles of selection.

The greatest gains in fruit yield (total and marketable) over the short term (<5 years) were achieved in the wide base population, with predicted means of 38.6 and 27.5 fruit per plot, respectively. That prediction represented a gain of 15 and 8 fruit per plot, respectively, over the highest initial means observed in the 3 populations studied. Thus, the wide base population was the best for both short term (<5 years) and long term (>5 years) breeding efforts for improved fruit yield, and for long-term breeding for improved fruit quality.

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