Cucurbit Genetics Cooperative

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The **Cucurbit Genetics Cooperative** (CGC) was organized in 1977 to develop and advance the genetics of economically important cucurbits. Membership to CGC is voluntary and open to workers who have an interest in cucurbit genetics. Membership is on a biennial basis.

CGC Membership and Subscription Rates

Biennium	Member	Library
1993-94	$14.00 US*	$24.00 US

*Payment must be by a check drawn on a U.S. bank, or by a U.S. or International Postal Money Order. Checks and Money Orders should be made payable to "Cucurbit Genetics Cooperative." Airmail subscription rates for the CGC Report are also available upon request.

CGC Reports are issued on an annual basis. The Reports include articles submitted by members for the use of CGC members. None of the information in the annual report may be used in publications without the consent of the respective authors for a period of five years.

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Comments from the CGC Coordinating Committee

The Call for Papers for the 1994 Report (CGC Report No. 17) will be mailed in August 1993. Papers should be submitted to the respective Coordinating Committee members by 31 December 1993. The Report will be published by June 1994. As always, we are eager to hear from CGC members regarding our current activities and the future direction of CGC.

Gary W. Elmstrom (melon)
Mark G. Hutton (other genera)
J. Brent Loy (*Cucurbita* spp.)
Dennis T. Ray (watermelon)
Jack E. Staub (cucumber)
Timothy J Ng, Chair

Comments from the CGC Gene List Committee

Lists of known genes for the Cucurbitaceae have been published previously in HortScience and in reports of the Cucurbit Genetics Cooperative. CGC is currently publishing complete lists of known genes for cucumber (*Cucumis sativus*), melon (*Cucumis melo*), watermelon (*Citrullus lanatus*), and *Cucurbita* spp. on a rotating basis.

It is hoped that scientists will consult these lists as well as the rules of gene nomenclature for the Cucurbitaceae before selecting a gene name and symbol. Thus, inadvertent duplication of gene names and symbols will be prevented. The rules of gene nomenclature were adopted in order to provide guidelines for the naming and symbolizing of genes previously reported and those while will be reported in the future. Scientists are urged to contact members of the Gene List Committee regarding questions in interpreting the nomenclature rules and in naming and symbolizing new genes.

Cucumber:	Todd C. Wehner
Melon:	Michel Pitrat
Watermelon:	Warren R. Henderson
Cucurbita spp.:	Mark G. Hutton & Richard W. Robinson
Other genera:	Richard W. Robinson

Comments from the CGC Gene Curators

CGC has appointed curators for the four major cultivated groups: cucumber, melon, watermelon and *Cucurbita* spp. A back-up Curator for the "Other genera" category is needed; anyone wishing to take on this responsibility should contact the Chair.

Curators are responsible for collecting, maintaining and distributing upon request stocks of the known marker genes. CGC members are requested to forward samples of currently held gene stocks to the respective Curator.

Cucumber:	Todd C. Wehner	Watermelon:	Gary W. Elmstrom
	Jack E. Staub		E. Glen Price
Melon:	J.D. McCreight		Billy B. Rhodes
	Michel Pitrat	*Cucurbita* spp.:	Mark G. Hutton
Other genera:	Richard W. Robinson		Richard W. Robinson

16th Annual CGC Business Meeting

The 16th annual CGC Business Meeting was held on 21 December 1992 in conjunction with the 1992 Cucurbit Conference in Raleigh, North Carolina. Todd Wehner chaired the meeting in Tim Ng's absence, and 21 members and guests (representing six different countries) were in attendance.

An update of CGC Report and CGC membership statistics was presented. Jack Staub was nominated and elected as CGC Coordinating Committee member for cucumber (Cucumis sativus). Jack replaces Todd Wehner, who had completed his ten year term as a member of the Coordinating Committee.

Two amendments to the CGC By-laws were proposed by the CGC Chair: (1) to change the By-laws to allow for more than five members on the CGC Gene List Committee, and (2) to limit guaranteed availability of back issues of the CGC Report to only the most recent five issues. The first proposed amendment reflects both the increasing complexity of maintaining gene lists and the willingness of CGC members to volunteer their services in this activity. The second proposed amendment addresses the physical difficulty of storing and maintaining increasing stocks of back issues, the costs of mechanical reproduction of exhausted back issues, and the plans for storing older reports as digitized images.

There was little discussion of the first issue. However, with the second proposed amendment there was concern expressed that CGC should keep all back issues available until a concerted effort was made to get libraries to pick up the entire set for future reference. As CGC By-laws require that any amendments to the By-laws must be approved by a mail ballot of the membership, these proposed amendments will be discussed further at the 1993 CGC Business Meeting and mail ballots will be included in the August "Call for Papers for CGC Report No. 17" mailing to the membership.

1992 Cucurbit Conference

The 1992 Cucurbit Conference was held 20-23 September 1992 in Raleigh, North Carolina. Participating organizations included the National Cucumber Conference (NCC), the Pickling Cucumber Improvement Committee (PCIC), the Cucurbit Genetics Cooperative (CGC), the Watermelon Research Group (WRG), the Cucurbit Crop Advisory Committee (CCAC), the National Melon Research Group (NMRG), and the Squash & Pumpkin Research Group (SPRG). Tom Monaco coordinated the Cucumber Field Day.

There was an informal decision to have a US Cucurbit Conference in even years alternating with EUCARPIA, beginning in 1994. Many of the commodity groups present at the conference agreed to combine into a single cucurbit organization for coordination of the meetings.

1993 Watermelon Research Group Meeting

Gary Elmstrom, University of Florida, Leesburg, FL USA

The 12th annual meeting of the Watermelon Research Group (WRG) was held in Tulsa, Oklahoma, on 31 January 1993. Attendance was up due to a number of plant pathologists who were attending the watermelon fruit blotch workshop. Glen Price (American Sunmelon) made local arrangements and provided watermelon for all. Gary Elmstrom announced that he would be stepping down as WRG Chair after 12 years of service in this capacity, and Ray Martyn (Texas A&M) will be assuming these duties.

US Cucurbit Crop Advisory Committee 1992-93 Update

J.D. McCreight, USDA-ARS, Salinas, CA USA

On September 23 1992, the US Cucurbit Crop Advisory Committee (CCAC) met in Raleigh, North Carolina in conjunction with the Cucurbit Conference organized by the Department of Horticultural Science, North Carolina State University.

The CORE Concept and its applicability to cucurbits was further discussed and it was decided to construct core collections for each species based on geographic origin and proven value for one or more specific characters.

The National Seed Storage Laboratory (NSSL) is now accepting samples for long- term storage. NSSL has specific requirements for numbers of seeds and germination percentage that must be met. There were discussions on various aspects of deleting duplicates of accessions; ensuring entry of valuable breeding lines and varieties from scientists either prior to or upon retirement when their program will not be continued; obtaining correct species identification for USDA taxonomists in a timely manner, conditioning acceptance of HortScience Cultivar & Germplasm Release manuscripts upon submission of samples to the National Plant Germplasm System (NPGS); germplasm exchange with Russia, The Netherlands and India; availability of accessions in NPGS; and increase of accessions outside of the US on a contract basis. The CAC Report is approximately four years old and needs to be updated for various reasons including the transfer of the melon collection from Georgia to Iowa, retirements, and progress in evaluating germplasm collections.

Two germplasm evaluation proposals were recommended for funding in FY1993: Evaluation of the U.S. plant introduction collection of melon (Cucumis melo) and squash (Cucurbita moschata and C. pepo) for resistance to gummy stem blight (Didymella bryonia Auersw.) Rehm (M.A. Kyle and T.A. Zitter), and Genetic diversity in cucumber (Cucumis sativus L.) and melon (Cucumis melo L.) accessions as measured by morphological and biochemical genetic markers (J.E. Staub and J.D. McCreight).

The 1993 meeting is scheduled for July 24 in Nashville, Tennessee, in conjunction with the Annual Meeting of the American Society for Horticultural Science.

Upcoming Meetings of Interest to Cucurbit Researchers

Groups meeting in conjunction with the **1993 Annual Meeting of the American Society for Horticultural Science** in Nashville, Tennessee (24-29 July 1993):

Cucurbit Crop Advisory Committee	Saturday, 24 July 8:00 a.m. - 12:00 p.m.	James D. McCreight USDA-ARS Salinas, CA USA Tel: 408/755-2864 FAX: 408/755-2866
National Melon Research Group	Saturday, 24 July 1:00 p.m. - 3:00 p.m.	James D. McCreight USDA-ARS Salinas, CA USA Tel: 408/755-2864 FAX: 408/755-2866
Squash Breeders	Saturday, 24 July 3:30 p.m. - 5:00 p.m.	Laura Merrick University of Maine Orono, ME USA Tel: 207/581-2950 FAX: 207/581-2999
Cucurbit Genetics Cooperative	(to be announced)	Timothy J Ng University of Maryland College Park, MD USA Tel: 301/405/4345 FAX: 301/314-9308

Other meetings:

The 13th annual meeting of the Watermelon Research Group will be held in conjunction with the 1994 annual meeting of the Southern Association of Agricultural Scientists (SAAS) and the Southern Region of the American Society for Horticultural Science (SRASHS) during the week of 5-9 February 1994 in Nashville, Tennessee.

Cucurbitaceae '94

Cucurbitaceae '94 will be held in the lower Rio Grande Valley of Texas in either October or early November and will be hosted by the the Texas Agricultural Experiment Station, Weslaco, and the USDA-ARS Subtropical Agricultural Research Laboratory, Weslaco. Jim Dunlap (TAES) and Gene Lester (USDA, ARS) will be the hosts for this meeting. The first announcement and call for papers is forthcoming.

Correlations Between Years for Foliar Gummy Stem Blight Disease Ratings on Field Grown Cucumbers

Paul C. St. Amand and Todd C. Wehner

Department of Horticultural Science, North Carolina State University, Raleigh, NC 27695-7609

It is often desirable to know if resistance data from one test is positively and highly correlated with other tests. A high positive correlation indicates that testing once in any year is a good measure of resistance and a low correlation indicates that multi-year tests are necessary to determine the resistance of a cultigen (breeding lines, cultivars, and plant introduction accessions). The objective of this study was to calculate correlations among years for foliar ratings of gummy stem blight in field-grown cucumbers.

Field tests were conducted in 1981, 1982, 1983, and 1986 to determine the resistance of diverse cucumbers to gummy stem blight. Each test was conducted at the Horticultural Crops Research Station at Clinton, N.C. with 3 (1982) or 6 (1983, 1986) replications, except for the 1981 test, which was conducted at the Horticultural Crops Research Station at Castle Hayne, N.C. without replication. Field plots were rated for foliar lesions using a 0 to 9 scale (0 = no foliar symptoms, 9 = plant dead). The rating system was modeled after the categories developed by Thompson and Jenkins (2). Plots were inoculated with equal numbers of spores from 12 isolates of *Didymella bryoniae*. Plants were sprayed at the vine-tip-over stage (4 to 6 true leaves) to run-off using a Solo back-pack sprayer at 15 to 20 psi. Overhead irrigation was used (25 to 38 mm·week-1) to spread the inoculum and encourage uniform disease development. Every 3rd row (4th row for 1986) was planted with susceptible 'Wisconsin SMR 18' to enhance the uniformity of disease spread. Plots were 6 m long (1981) with 40 plants each, or 3 m long (1982, 1983, 1986) with 30 plants each and were planted on raised, shaped beds 1.5 m apart (center to center) separated at each end by 1.5 m alleys. Standard cultural practices were used for crop production (1). A randomized complete block design was used for all tests. One rating was given for each plot 7, 14 and 21 days after inoculation, except in 1981 which was rated only 7 days after inoculation. Data were analyzed using PROC REG of SAS (SAS Institute, Cary, N.C.).

Disease ratings were greatest in 1982 and the mean rating was very similar for years 1981, 1983, and 1986 (Table 1). The range of disease ratings was greatest in 1981 and was smallest in 1983 and 1986. Pearson product-moment correlations and Spearman rank correlations between years were moderate to high (Table 2); however, the highest correlations are based on small numbers of cultigens and the correlations tended to decrease as cultigen number increased. Rankings of cultigens were usually less correlated than were actual ratings, indicating that changes in rank often occurred. Wyszogrodzka et al. (3) calculated the Pearson correlation coefficient between gummy stem blight field tests conducted in Florida and Wisconsin. That correlation (r=0.42) was moderate and similar to those reported here for tests involving larger numbers of cultigens.

Table 1. The mean, standard deviation, median, minimum, and maximum of foliar disease ratings of cucumber for gummy stem blight for four field tests conducted in different years. Also shown is the number of cultigens rated in each test[z].

Year	Number of cultigens	Mean	Standard deviation	Median	Minimum	Maximum
1981	31	5.6	3.1	8.0	1.5	9.0
1982	46	6.3	2.0	6.6	1.7	9.0
1983	45	5.1	0.8	5.1	2.9	8.2
1986	36	5.5	0.9	5.5	3.6	7.2

[z]Foliar symptoms were rated from no symptoms (0) to complete necrosis (9).

Table 2. Correlations between years for foliar disease ratings of cucumber cultigens inoculated with gummy stem blight. Pearson product-moment correlation coefficients are above the diagonal and Spearman rank correlation coefficients are below the diagonal[z].

	Year			
Year	1981	1982	1983	1986
1981	--	0.57 (31) ***	0.68 (10) *	0.93 (6) **
1982	0.56 (31) ***	--	0.73 (14) ***	0.73 (8) *
1983	0.82 (10) **	0.84 (14) ***	--	0.66 (32) ***
1986	0.70 (6) NS	0.64 (8) NS	0.48 (32) **	--

[z]The symbols NS, *, **, and *** indicate not significant, or significant at the 0.05, 0.01, or 0.001 levels, respectively. Numbers in parenthesis indicate the number of cultigens shared between tests.

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Turgid flowers are essential for good fruit and seed set in cucumber

R. Szegedi, I. Cserni and P. Milotay
Vegetable Crops Research Institute, 6000 Kecskemet, P.O.B. 116, Hungary

Fruit number per unit area and shape is generally a good predictor of seed cucumber yield. In short-fruited varieties most of the available ovules are fertilized under optimum conditions resulting in high seed set throughout the ovary (3). However, late setting fruits, or fruits developed under dry field conditions often remain small and deformed containing a reduced number of seeds when compared to fruits grown under optimal conditions.

Pollination is successful up to 24 hours after anthesis under glasshouse conditions (5), and a minimum two-week irrigation period is sufficient to produce viable seeds (4). However, since drip irrigation significantly affects fruit size, shape and seed yield in a large containers study (1), an experiment was designed to evaluate the influence of withholding water during pollination on fruit and seed set.

Plants of the monoecious pickling line K 4599 were trellised during the summer of 1990 under an isolating net. The planting was drip irrigated every 6 hours with fixed doses. Before pollination and after pollination irrigation was withheld in one of two rows (waterstress treatment) resulting in flagging during the noon hours, while plants in the second row remained turgid (control). 30-30 flowers were hand pollinated using two turgid male flowers on plants without previous fruit set on both rows between 12:00 and 13:00 hours. Daily temperature during pollination and the days of early fruit development ranged from 18 to 31C. After harvest the seed number, seed weight, germination %, radicle and hypocotyl elongation (4 days at 25C) were recorded to compare treatment and control.

Pollinated flowers set fruit on 93% of the control plants, while only 57% of the pollinations were successful on tagging plants. Fruits of the control plants were regular in shape with an average length of 17.6 cm, while 12 of the 17 fruits developed from non-turgid flowers were pear shaped with an average length of 16.3 cm. Seed number from fruit harvested from control and treatment (water withheld) plants ranged from 124 to 289 and 45 to 168 respectively. Averages calculated from 10-10 randomly chosen fruits show that fruits from water withheld plants had a significantly reduced seed number and seed weight per fruit, but withholding water did not affect thousand seed weight and germination % (Table 1). Radicle and hypocotyl elongations did not show treatment differences (data not shown).

Because pollen germinates on the stigma within 30 minutes, pollen treatment tubes reach the ovary in 12 hours and fertilize ovules enlarge within 30-36 hours (2). Our results indicate that water status of the pistillate flower during this period appears to be a significant factor in determining the quantity and quality of fruit and seed set.

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Table 1. Seed yield of cucumber fruits developed from turgid and non-turgid flowers at pollination.

Pollination of	Number of fruit set	Seed number per fruit	Seed weight per fruit (g)	Thousand seed weight (g)	Germination at 25C (%)
Turgid flowers	28	213.2	4.31	21.3	99.0
Non-turgid flowers	17	90.3	1.94	21.6	100.1
LSD 5%		30.8	0.48	NS*	NS

*NS = not significant

Vine Rolling vs. Conventional Multiple Harvest of Cucumbers in North Carolina

Todd C. Wehner and Conrad H. Miller

Department of Horticultural Science, North Carolina State University, Raleigh, NC 27695-7609

Most cucumbers (*Cucumis sativus* L.) in North Carolina are harvested 2 to 3 times per week for 2 to 4 weeks in two production seasons (spring and summer). Fruits are harvested by searching through the vines for marketable sizes. Since it is difficult to see fruits in the canopy, some fruits are not harvested each time. Those that become oversized before they are picked in the next harvests are unmarketable, resulting in lost yield.

Ease of harvest has been improved using machines, new cultivar types, and more efficient techniques. Harvest machines reduce the labor input where they can be adapted to the production system (Haffar and Van Ee, 1984). New cultivar types such as gynoecious flowering permit fewer harvests for the same yield as monoecious types (Wehner and Miller, 1985). Techniques for improved harvest efficiency such as vine training can reduce vine damage, and provide a longer production period for the crop. We were interested in vine rolling for improved recovery of fruits hidden near the base of the plant.

The objective of this study was to determine if harvest was faster and easier if the vines were rolled over as they were picked.

Methods. The experiment was run at the Horticultural Crops Research Station near Clinton, NC. Seeds were planted in rows 1.5 m apart on raised beds. Plots were 9 m long with 1.5 m alleys at each end. Fertilizer was incorporated before planting at a rate of 90-39-74 kg·ha^{-1} (N-P-K), and a side dressing of N (34 kg/ha) was applied at vine tip-over stage. Irrigation was applied as needed up to three times a week for a minimum of 25 mm of water per week. Recommended cultural practices were used (Hughes et al., 1983).

Plots were planted 22 July, 1982, and thinned 2 August to a density of 86,450 plants·ha^{-1}. Harvests were made Mondays and Thursdays 26 August to 7 September for pickling and 30 August to 10 September for slicing cucumbers. Cultivars tested were 'Calypso' pickle and 'Slicemaster' slicer, both gynoecious hybrids. Pollen was supplied with border rows of 'Sumter' pickle or 'Poinsett 76' slicer, both monoecious inbreds.

The experiment design was a randomized complete block with 5 replications and 2 harvest methods (conventional vs. vine rolling). The pickling and slicing crops were kept separate in harvest and grading operations. Plots were harvested 4 times (twice weekly), and the fruits graded and weighed. Grades were the NC grades for pickles and USDA grades for slicers. NC grades were based on fruit diameter as follows: No. 1=0-26 mm, No. 2=27-38 mm, No. 3=39-50 mm, No. 4>50 mm. USDA grades were based on quality as specified by federal guidelines (USDA, 1958). Harvests were timed for each of the methods, conventional and vine rolling. Vines were rolled over on one side as a worker harvested that side, then rolled back the other way by the second worker. Vines were left in their rolled-up state after harvest, and were not laid back out over the soil. That resulted in the exposure of the base of the plant to sun and wind, and some stems and leaves were upside down.

Data were collected on fruit weight by grade, and summarized using analysis of variance. Treatment comparisons were essentially t-tests for conventional vs. vine rolling harvest methods.

Results. Differences in yield between conventional and vine rolling were significant for fruit weight in pickling cucumbers, but not for fruit value of pickling (Table 1) or for yield of slicing cucumbers (Table 2). Where the differences were significant, the vine rolling treatment resulted in lower yields (68% as much for pickles), and took longer (18% more for pickles, 2% more for slicers) than conventional plots. Vine rolling did, however, result in a significantly higher percentage of No. 1, and lower percentage No. 3 and 4 grade pickles than the conventional method (Table 1). In slicers, the vine rolling treatment produced fewer Fancy and No. 1 grade fruits than conventional, indicating more stress or less effective pollination (Table 2).

Vine rolling required more time to perform than conventional harvest, and resulted in lower yield. In the case of pickling cucumbers, vine rolling did shift the distribution of fruit sizes toward grade 1 and 2, and away from 3 and 4. That may be advantageous for producing small pickling cucumber sizes, but more frequent harvest would probably have the same effect without reducing the yield. Although there was less damage to the vines in the vine rolling treatment compared with conventional (data not shown), the effect was not translated into increased yield in the short harvest period (2 weeks). Vine training probably would have reduced vine damage by the harvest crew, and improved the recovery of small grade pickles in the same way that vine rolling did. However, vine training would avoid the increased exposure of the base of the vine without leaving some vines turned upside down.

Table 1. Comparison of 2 multiple-harvest methods for yield and harvest time in pickling cucumbers[z].

Harvest method	Fruit yield ($/ha)	Fruit yield (Mg/ha)	Harvest time (sec/plot/harv)	Mean size grade[y]	% size grades 1	2	3	4
Conventional	2477	23.9	128	2.7	9	34	38	19
Rolled[x]	2186	16.1	151	2.4	17	39	33	10
LSD (5%)	NS	2.2	-	0.2	4	6	1	6
CV (%)	15	6	-	3	15	9	2	24

[z]Data are means over 5 replications and 4 harvests. NS indicates F ratio not significant (5%).
[y]Grades are 1 to 4 for the NC sizes.
[x]Vines were flipped over the row while harvesting each side.

Table 2. Comparison of 2 multiple-harvest methods for yield and harvest time in slicing cucumbers[z].

Harvest method	Yield (Mg/ha) Fancy & No. 1	Yield (Mg/ha) Market-able	Harvest time (sec/plot/harv.)	Mean size grade[y]	Fancy+ No. 1 (%)	Culls (%)
Conventional	20.4	27.7	120	1.1	66	10
Rolled[x]	11.3	18.7	122	1.5	50	19
LSD (5%)	NS	NS	-	0.3	12	NS
CV (%)	50	41	-	14	12	50

[z]Data are means over 5 replications and 4 harvests. NS indicates F ratio not significant (5%).
[y]Grades are 0 to 3 for the 4 USDA sizes, where 0=Fancy, 1=No. 1, 2=No. 2, 3=cull.
[x]Vines were flipped over the row while harvesting each side.

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Observations on Fruit Netting in Cucumber

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Several fruit surface (skin) types have been identified in cucumber (*Cucumis sativus* L.), including warty (American), smooth (middle-eastern), ridged (greenhouse), and netted (wild). Hutchins (1940) identified the netted trait as a single gene (*H*) linked with black spines and red mature fruit color, and also mentioned the occurrence of intermediate netting. That trait was assigned to linkage group III by Pierce and Wehner (1990). More recently, Peterson and Pike (1992) suggested the netted skin characteristic was quantitatively inherited.

Cucumber accessions PI 197086 and PI 165509 were reported to be resistant to belly rot caused by *Rhizoctonia solani* Kuhn (AG-4) by Clark and Block (1984) and also have netted skin. Since that skin type is not horticulturally acceptable, belly rot resistance must be controlled by separate genes for those cultigens to be useful parents in a program aimed at breeding belly rot resistance. In muskmelon, it has been suggested that fruit netting provides enhanced disease resistance by acting as a physical barrier (Webster and Craig, 1976). In cucumber, it is not known whether netted skin provides a physical barrier, or whether some other mechanism is responsible for resistance.

During the summer of 1992, a study was conducted to determine whether netted skin was responsible for belly rot resistance. Both PI 197086 and PI 165509 have highly netted skin on the mature fruits. Young fruits (less than five days after pollination) do not have netted skin. Netting develops over the next few days, often starting at the ends of the fruit. At about that time, it appears that the epidermal layer stops expanding with the rest of the fruit. That phenomenon has been reported in *Cucumis* fruits (Webster and Craig, 1976). In the plant introduction accessions we observed, the result was corky tissue developing between pieces of the epidermis. The amount of netting increased slowly, and fruits became completely netted as they matured. In muskmelon, the skin netting was a combination of lenticellar tissue derived from a subepidermal periderm, and cork cells which were complementary tissue of lenticels (Webster and Craig, 1976). It appeared that the netting phenomenon in cucumber may be a result of the same mechanisms operating in muskmelon.

The two plant introduction accessions studied each had slightly different netting. In the case of PI 165509, the netting left the fruit with a red color, with cream colored veins (netting) over the surface. In the case of PI 197086, the netting was an obvious result of the dark, reddish-black epidermis becoming cracked, and then flaking to reveal a cream colored second layer. If the fruits were rubbed, most of the outer cracked skin layer was easily removed. It appeared that "netting" was the cracking the epidermal layer, which was red to dark maroon in color. That trait developed slowly, and resulted in what appeared to be an intermediate amount of netting on immature fruit.

The importance of this finding is that care must be taken when studying netted skin. Immature fruits may appear to be without netting, or intermediately netted, when in fact those fruits will develop complete netting if left in the field until maturity. This is a problem when ratings are made on immature fruits, and correlations to the netted skin phenotype are desired.

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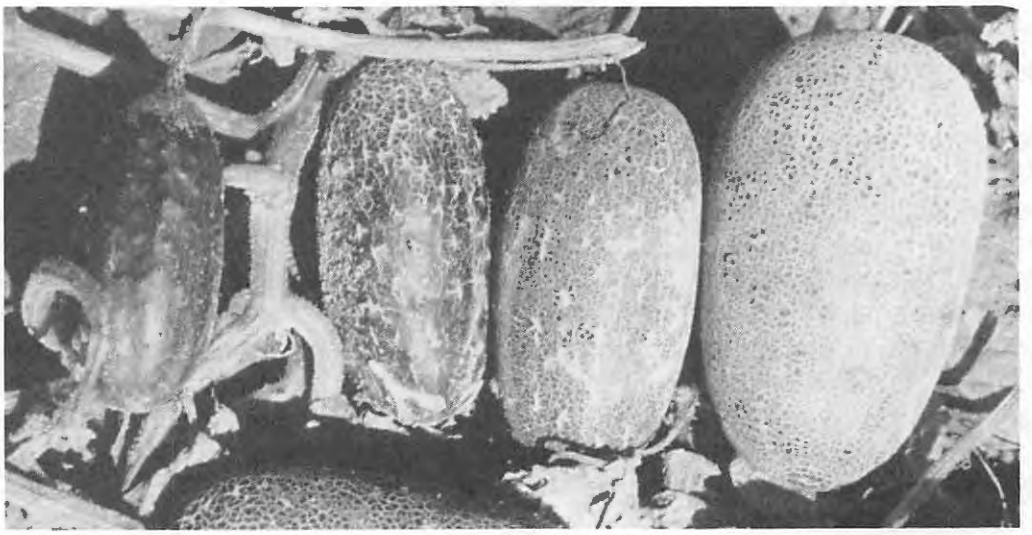

Figure 1. Four fruits of different ages from the same plant. Maturity and netting increase from left to right. The plant is from the F_2 generation of a cross between Wis. SMR 18 x PI 197086.

Leaf Structure and Photosynthetic Relationships in *Cucumis sativus* var. *sativus* and *Cucumis sativus* var. *hardwickii*

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Cucumis sativus var. *sativus* L. (cucumber) is widely cultivated in many parts of the world. *Cucumis sativus* var. *hardwickii* (R.) Alef. is a fully cross-compatible botanical variety of var. *sativus.* Variety *hardwickii* is of potential economic importance since it possesses a multiple lateral branching and sequential fruiting habit not found in var. *sativus.*

We have been using var. *hardwickii* as a source of genes for increasing yield potential in commercial cucumber. We have reported that there are morphological differences between these botanical varieties (Schuman et al., 1985). Three morphological plant characteristics and leaf anatomy were evaluated in two different seasons in the greenhouse for each of five var. *sativus* and five var. *hardwickii* cultigens. We found inter- and intravarietal differences which were, in the main, consistent acrossed growing environments.

Because leaf anatomy and morphology could be important factors associated with productivity differences between var. *hardwickii* and var. *sativus*, we designed a series of studies to more completely define varietal leaf variation and photosynthetic response.

We used the var. *hardwickii* accessions PI 215589, PI 462369, PI 486336, PI 183967, PI 273648, and LJ 91176, and the var. *sativus* breeding lines WI 1983 and WI 2238. In addition, we also evaluated the var. *sativus* x var. *hardwickii* derived (F_7) line WI 2963. Accessions and lines were grown in a field nursery and leaf thickness, maximum photosynthetic potential and chorophyll content measurements were taken from each of four plants arranged in a randomized complete block design grown on a m^2 spacing. Samples were taken during first flowering, but before the fruits had developed beyond approximately 1 cm in diameter (approximately 45 to 50 days after planting). Maximum photosynthetic rate was estimated from leaf slices (discs) prepared from the fourth leaf from the terminal whorl using the technique of Jones and Osmond (1973).

Matings were also made between the var. *sativus* (P_2) breeding line WI 1606 and the var. *hardwickii* (P_1) PI 215589 to produce reciprocal F_1 and BC_1 progeny. Studies were conducted in a greenhouse and field nursery. Maximum photosynthetic potential and chorophyll content measurements of these cultigens and their cross-progeny were taken from each of four plants arranged in a randomized complete block design on a m^2 spacing. Parents, F1

and BC1 plants were flowering and fruits were enlarging (approximately 2 to 2.5 cm in diameter) on the sampling days.

The results of comparisons between var. *hardwickii* accesssions, var. *sativus* lines and a derived line are given in Table 1 and Figure 1. Microscopic measurements indicate that leafs of the var. *sativus* lines examined were thicker than var. *hardwickii*, and the cells of var. *sativus* were larger with a more open arrangement. Maximum photosynthetic rates was greater in var. *hardwidkii* when compared to var. *sativus.* Likewise, the dry weight of chlorophyll (mg/g) of var. *hardwickii* was often higher (three of five cases) than that of var. *sativus.* The derived line was usually closer to var. *sativus* for the traits examined.

Cross-progeny comparisons indicated that measurements taken in the field were higher than those in the greenhouse (Table 2). Reciprocal F_1 differences ($P_1 \times P_2 > P_2 \times P_1$) were also observed in the BC_1 indicating the cytoplasmic nature of this trait. There appears to be a relationship between the compressed leaf structure of var. *hardwickii* and its high maximum photosynthetic rate.

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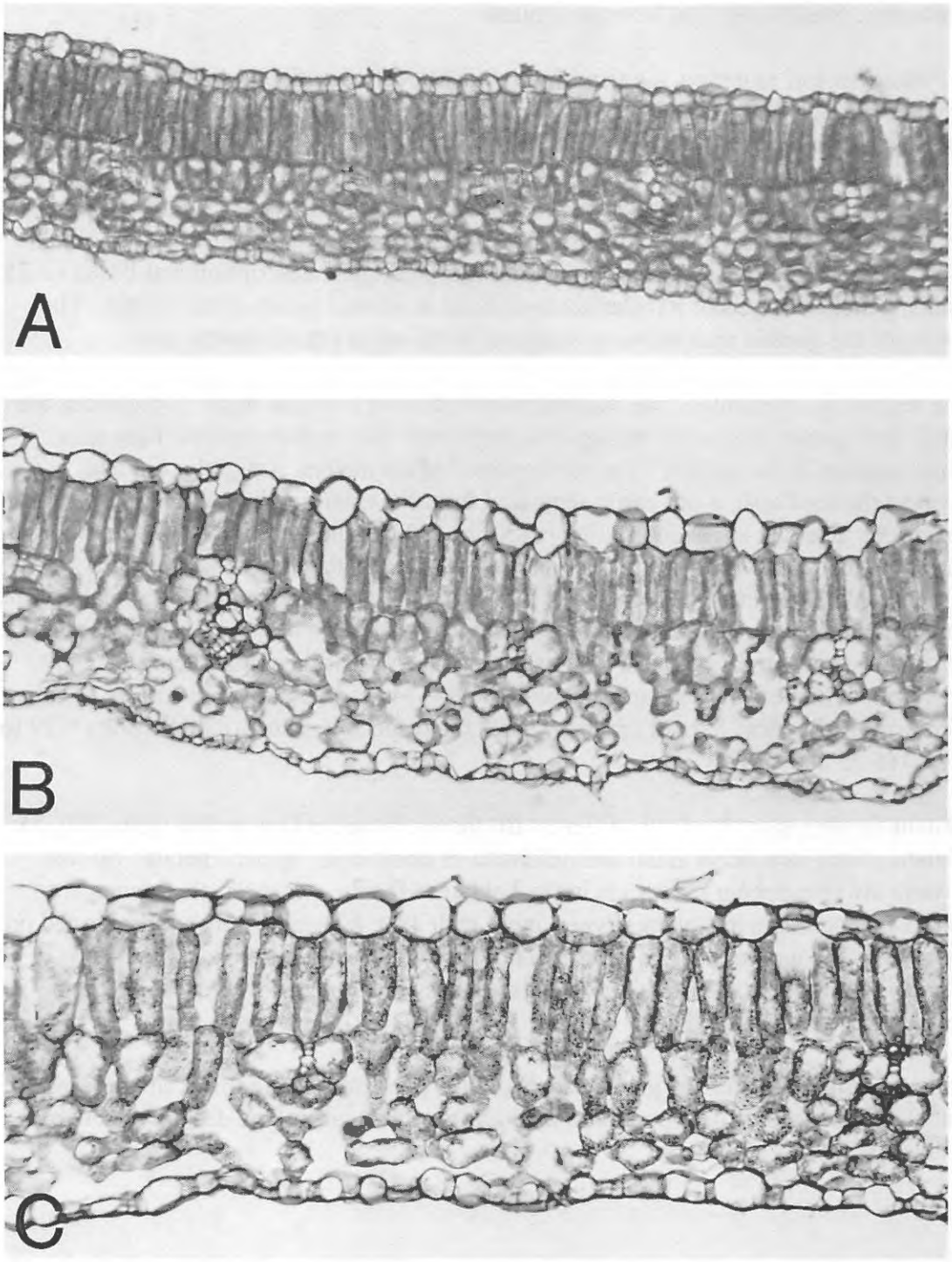
Table 1. Means ($\bar{X}$) and standard errors (Sx) of leaf thickness, maximum photosynthesic rate (μmO_2 evolved/mg chlorophyll/hr), and chlorophyll concentration of several *Cucumis sativus* var. *sativus* and var. *hardwickii* cultigens and a var. *sativus* x var. *hardwickii* derived line [(WI 1606 x PI 215589) F_7].

Botanical variety	Line or PI	Thickness (mm)		Photosyn. rate		Chlorophyll (mg/g dry wt.) a		b		a+b	
		$\bar{X}$	Sx	$\bar{X}$	Sx	$\bar{X}$	Sx	$\bar{X}$	Sx	$\bar{X}$	Sx
hardwickii	215589	8.0	0.17	56.50	4.50	8.71	1.36	1.56	0.23	10.27	0.38
	462369	9.3	0.26	51.30	4.27	8.37	0.67	3.11	0.30	11.48	0.21
	LJ 91176	11.9	0.26	48.94	4.54	8.50	0.36	2.16	0.61	10.66	0.07
	486336	10.6	0.06	45.65	2.10	7.20	1.33	1.61	0.77	8.81	0.42
	183967	11.2	0.46	58.80	5.29	10.7	0.04	3.44	0.60	14.14	0.17
	273648	9.6	0.14	46.65	4.14	---	---	---	---	---	---
sativus	WI 1983	16.2	0.55	36.56	3.60	8.60	0.14	1.86	0.02	10.46	0.05
	WI 2238	13.5	0.32	28.30	0.75	7.59	0.65	2.75	0.14	10.36	0.19
Derivative	WI 2963	18.2	0.40	37.96	4.00	8.27	0.83	2.10	0.11	10.37	0.72

Table 2. Field and greenhouse mean maximum photosynthetic rates (μmO_2 evolved/mg chlorophyll/hr) of *Cucumis sativus* var. *hardwickii* (PI 215589) and var. *sativus* line WI 1606 and their F_1 and BC_1 progeny.

	Maximum photosynthetic rate							
	Parents		Cross-progeny					
Days from plant	P_1 215589	P_2 1606	F_1a $P_1 \times P_2$	F_1b $P_2 \times P_1$	BC_1 ($P_2 \times F_1a$)	BC_1 ($F_1a \times P_2$)	BC_1 ($F_1b \times P_1$)	BC_1 ($F_1b \times P_2$)
Field								
55	54.24	39.10	105.41	56.28	35.63	31.41	38.45	54.24
56	59.00	36.86	80.77	41.84	32.46	29.30	27.49	39.00
Greenhouse								
42	97.14	34.62	---	---	98.26	162.59	86.75	123.50
43	62.17	42.59	91.64	71.52	112.78	143.39	47.04	75.57
50	68.42	39.26	83.78	31.27	126.36	141.07	---	---

Figure 1. A comparison of the leaf structure of *Cucumis sativus* var. *hardwickii* (A; PI 486336), *Cucumis sativus* var. *sativus* (B; WI 2238), and a derivative (C; F_7) of the a cross between var. *hardwickii* (PI 215589) and var. *sativus* (WI 1606) (10 X).


A
B
C

Cucumber (*Cucumis sativus* L.) induced mutations: A *Phaseolus* leaf mutant

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A *Phaseolus* leaf mutation, along with other previously described cucumber mutants produced in our laboratory (1,2,3), was obtained by chemical mutagenesis. As far as we know no similar mutation has been described or listed in the CGC cucumber gene list.

This mutant has been generatively reproduced in our laboratory for several years and since it was derived from inbred Borszczagowski line, this was the line used to obtain subsequent generations. While the mutant's morphological description was based on 25 plants, genetic analysis of its inheritance utilized as several hundred individuals. The results of the genetic analysis were analyzed by chi-square contingency tests.

The mutant is detectable at the cotyledons and the first true leaf stage. Cotyledons are small, dark green with violet endings and frequently have a characteristic light spot which appears in the middle. The development of cotyledons is slightly retarded, because the seed coat is not easily separated from the emerging hypocotyl. Mutant plants are smaller than the standard (mutant = 83.5 to 152 cm and standard = 225 to 366 cm) with a smaller number of internodes (mutant = 9-26 and standard = 32-40) (Fig. 1). Mutant leaves are delicate, wrinkled at the end of the main vine, and the leaf margins are undulating and curled (Fig. 2). In most cases leaf blades are not serrated and as such deformations make them appear heart-shaped. The size of the mutant leaf is slightly smaller than that of the standard (mutant leaves = 14 to 16 cm long, and 13 to 17 cm wide with leaf petiole 8 to 12 cm long, while the respective standard dimensions = 19 to 26, 20 to 25 and 12 to 15 cm).

Mutant flowers are remarkably different fro those of standard cucumber types (Fig. 3). Mutant plants bare either small and deformed or completely reduced petals. Mutant flowers are reminiscent of flowers in the Labiateae family. Most female flowers are sterile. As common in standard types, more male than female flowers are developed on the plant. The mutant usually sets fruits but they are often deformed and seedless (Fig. 4). As in the standard, mature fruits are brown in color, however the epidermis is not netted.

Following the results of the genetic analysis, it is possible to state that a single recessive gene (*phl* - phaseolus leaf) condition the morphological phenotype described above (Table 1).

Table 1. Inheritance of phaseolus-type leaf (phl)

Generation	No. observed		No. expected		Ratio tested ratio	X^2	P
	Normal	Mutated	Normal	Mutated			
P1 (normal)	30	0	30	0	1:0	--	--
P2 (mutated)	0	25	0	25	0:1	--	--
F1	40	0	40	0	1:0	--	--
F2	335	101	327	109	3:1	0.78	0.50-0.80
F1 x P1	83	0	83	0	1:0	--	--
F1 x P2	124	116	120	120	1:1	0.26	0.50-0.80

Figure 1. Cucumber plant possessing *Phaseolus* leaf mutant.
Figure 2. Comparison of a *Phaseolus* mutant and standard leaf.
Figure 3. Comparison of female and male flowers from *Phaseolus* mutant (left) and standard (right) cucumber plants.
Figure 4. A deformed fruit from a *Phaseolus* mutant (left) compared to the typical fruit from Borszczagowski.

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Figure 1. Chemically-induced *Phaseolus* leaf mutant of cucumber.

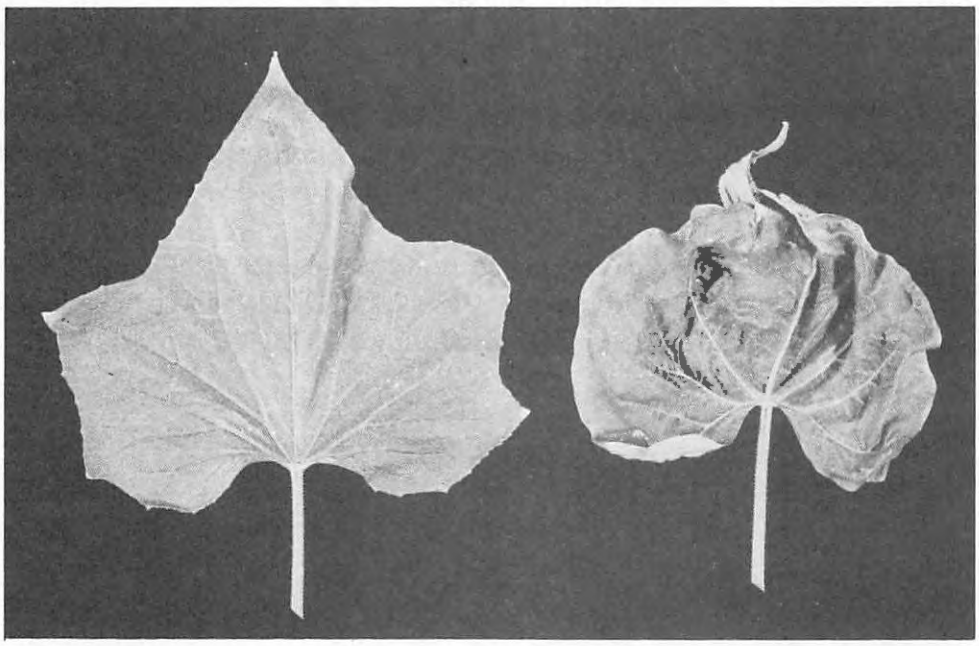

Figure 2. Morphology of leaves from normal and mutant plants.

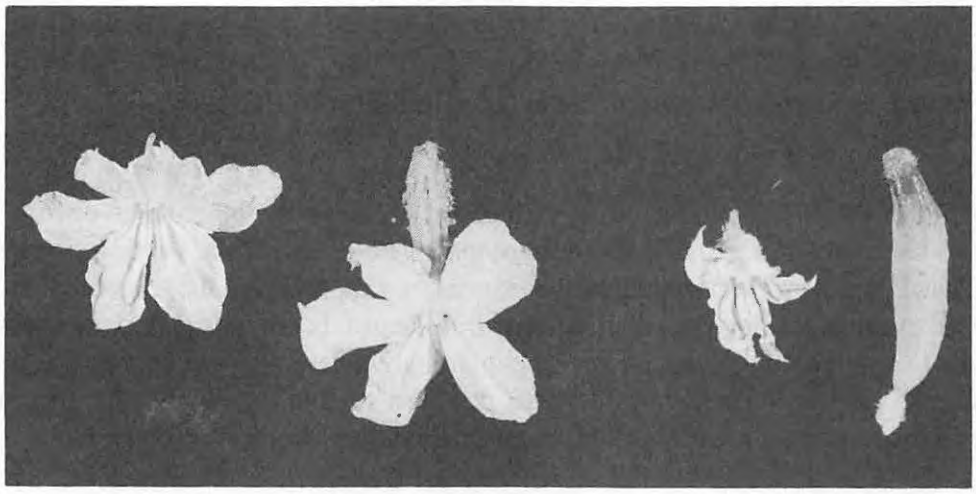

Figure 3. Morphology of flowers from normal and mutant plants.

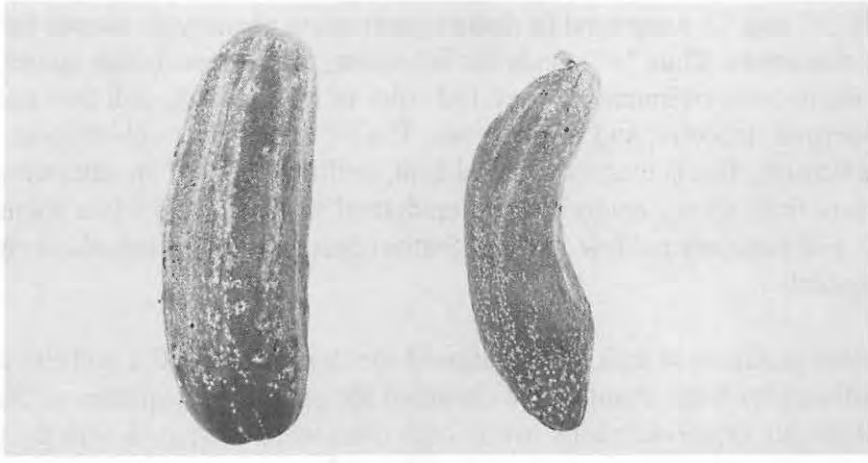

Figure 4. Morphology of fruits from normal and mutant plants.

Independence of fruit length and 10 other characters in cucumber.

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Fruit length of cucumber exhibits great variability. Although the inheritance of fruit length has been investigated, data are not comparable because of the varying germplasm sources used and the collection and analysis measures applied (2,3,4,5). Limited agreement exists regarding the inheritance of fruit length, however most researchers agree that it is a quantitative character. The quantitative nature of the inheritance of fruit length and its association with the fruit neck has been studied (1). We report here the linkage relations of fruit length with 10 other qualitative characters of cucumber.

The long fruited line 791 from our cucumber breeding program was crossed with the non-necked American variety SMR-18 and F 2 and BC progeny were produced. Parents, F1, F2, BCP1 and BCP2 progeny were evaluated for fruit length and the following characters: bitterness (bi), powdery mildew resistance (pm), female sex expression (F), spine size (ss), warted fruit (Tu), uniform fruit color of immature fruit (u), mature fruit color (R), glossy fruit (D), structure of epidermis (pe), and spine color (B). Evaluation and classification was made as previously described (1).

The symbols "+" and "-" were used to denote contrasting phenotypic classes for the segregating characters. Thus "+" stands for bitterness, femaleness, rough spines, warted fruit, nonuniform color of immature fruit, red color of mature fruit, dull fruit epidermis, palisade epidermal structure, and black spines. The "-" stands for nonbitterness, monoecious flowers, fine spines, nonwarted fruit, uniform color of immature fruit, cream color of mature fruit, glossy epidermis, flat epidermal structure, and white spines respectively. For powdery mildew "R" designates resistance, "I" intermediate resistance and"S"susceptibility.

The continuous variation of fruit length allowed for separation of F 2 and BC generations in classes differing by 8 cm. Plants were classified for other characteristics within each class of fruit length. Observed ratios within each class were compared with the total ratio of the characteristic over the classes by X^2 analysis. Thus the deviation of the partial ratios from the total ratio of the characteristic indicates linkage associations of any characteristic with the fruit length.

Partial phenotypic segregations and X^2 analysis for each particular character are generally indicated in Tables 1 and 2. Observed ratios within each class of fruit length do not indicate significant deviations from the total phenotypic character ratios. Significant deviations were, however, found in one F 2 class for female sex expression, and in some classes of the BC1P2 generation for spine size, warted fruit, uniform color of immature fruit, dull fruit epidermis, and structure of epidermis. The rest of the partial BC ratios for these characters follow the expected segregation. Moreover, the respective partial ratios in the F2 generation segregate according to the expectation. Thus, it is hard to accept the

observed deviation as indicative of any linkage relationships. Therefore, we propose that the segregation of the fruit length and the characteristics evaluated is independent.

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Table 1. Phenotypic F 2 segregation and X^2 values of the 10 characters within each class of fruit length of cucumber.

Trait		Total ratio	Fruit length (cm) 12-19.99 Ratio	X^2	20-27.99 Ratio	X^2	≥28.00 Ratio	X^2
bi	+:	151	12	0.10	94	1.64	47	3.34
	-:	49	3		37		7	
pm	R:	14	0	1.54	11	0.49	3	1.85
	I:	22	1		13		9	
	S:	164	14		108		42	
F	+:	81	9	2.36	43	3.20	29	3.91*
	-:	119	6		88		25	
ss	+:	157	12	0.02	95	2.33	40	1.09
	-:	43	3		35		15	
Tu	+:	157	12	0.02	106	0.43	39	1.88
	-:	43	3		24		16	
u	+:	157	12	0.02	106	0.43	39	1.88
	-:	43	3		24		16	
R	+:	156	13	0.59	102	0.01	41	0.51
	-:	44	2		28		14	
D	+:	157	11	0.24	106	0.43	40	1.09
	-:	43	4		24		15	
pe	+:	156	12	0.02	106	0.43	38	2.89
	-:	44	3		24		17	
B	+:	155	13	0.59	101	0.06	41	0.51
	-:	45	2		29		14	

*significant difference at 0.05 level.

Table 2. Segregation and X^2 values of the BC1P2 generation for the 10 characters of cucumber within each class of fruit length.

Trait		Total ratio	Fruit length (cm) 0-27.99 Ratio	X^2	28-35.99 Ratio	X^2	≥36.00 Ratio	X^2
bi	+:	81	4	0.25	60	0.02	17	0.35
	-:	88	6		67		15	
	R:	33	2	0.28	27	0.80	4	2.40
pm	I:	46	4		30		12	
	S:	97	7		74		16	
F	+:	125	7	1.86	94	0.03	24	0.24
	-:	51	6		37		8	
ss	+:	55	9	8.74**	43	0.15	3	7.13**
	-:	121	4		88		29	
Tu	+:	72	9	4.31*	59	0.92	4	10.68**
	-:	104	4		72		28	
u	+:	73	8	2.16	61	1.40	4	11.06**
	-:	103	5		70		28	
R	+:	92	7	0.01	69	0.01	16	0.03
	-:	81	6		60		15	
D	+:	74	9	3.93*	61	1.14	4	11.45**
	-:	102	4		70		28	
pe	+:	72	9	4.15*	59	1.01	4	11.00**
	-:	102	4		70		28	
B	+:	92	7	0.01	69	0.01	16	0.07
	-:	84	6		62		16	

*, **: significant differences at 0.05 and 0.01 levels, respectively.

Diallel analysis of cucumber germination at optimum and suboptimal temperatures

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Germination of cucumber seeds under cool weather conditions is frequently erratic resulting in poor, or non-uniform emergence. Cucumber seeds germinate rapidly between 20-30C, however there is a sharp reduction in germination percentage and initial seedling development below 15C (3). Although laboratory selection of a genetically broad-base cucumber population for improved germinability at suboptimal temperature resulted in better and faster emergence in the field (4), heritability for this character is low (6). To study the nature of genetic effects controlling germination under optimum and suboptimal temperatures a laboratory experiment was conducted utilizing seeds produced from a set of diallel crosses.

Five F5 to F7 generation parthenocarpic pickling cucumber lines of different origin and their hybrids were used. Seeds were produced during the spring in a plastic house. One hundred seeds (four replications of 25 seeds) of parents and crosses were placed into the folding of moistened filter papers. Each row of seeds (one replication) were placed into the cut foldings to allow for unconstrained radicle and hypocotyl growth. The filter papers were then rolled up, placed in plastic bags, and held in incubators in a vertical position at 17 and 25C. After 4 and 7 days at 17C and 4 days at 25C percentages of radicle protrusion, radicle and hypocotyl elongations were recorded.

Statistical analysis was carried out according to the model 2, method 1 of Griffing (2). Before the analysis percentage data were angularly transformed. Maternal effects were estimated by the method of Topham (5).

At 25C all seed lots germinated over 95% (Table 1), and the average heterosis of hybrids was 1.02. At 17C germination proceeded slower and the average performance of hybrids over the mean of the parents was 0.89 at day four and 0.92 at day seven. At seven days the poorest seed lots germinated near 50%, while the best parents and hybrids showed maximum germination. Keeping lagging lots seeds at 17C to day 12 resulted in only a slight improvement.

Radicle elongations showed relatively small, but significant differences at optimum temperature (Table 2). More marked differences were detected at 17C resulting in an average heterosis of 1.22 and 1.06 at day four and day seven respectively. Variability increased within the seed lots at suboptimal temperature also. Hypocotyl development followed radicle protrusion by 1.5 days at optimum temperature and about 3 days at suboptimal temperature (data not shown).

The Griffing analysis resulted in significant general combining ability (gca) and specific combining ability (sca) effects for all characters at both temperatures. Reciprocal effects were also significant except for germination percentage at 25C. According to the variances

(Table 3), dominance and non-allelic effects were much more important than additive effects at suboptimal temperature both for germination percentage and seedling growth. The average degree of dominance for these characters refers to over-dominance. At 25C, over-dominance was found only for germination percentage and radicle elongation was conditioned by additive genetic effects.

When analyzing gca effects, line KP exhibited significantly positive values, and line 17K significantly negative values for percent germination at 17C. In case of radicle growth, lines Ac18 and KP produced significantly positive gca values at the same temperature (data not shown).

Narrow-sense heritability values obtained for percent germination were not significant at both temperatures and radicle elongation gave only higher heritability at 25C ($h^2 = 0.62$). Significant maternal effects in this study were obtained at sub-optimal temperature for percent germination (0.68) and radicle length growth (0.77). At optimum temperature only for radicle length (0.61) was significant. The nature of this effect should be studied further (1).

The parthenocarpic pickling cucumber lines involved in this study do not provide sufficient genetic base for improving germinating ability at suboptimal temperature.

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Table 1. Germination of cucumber seeds at 25C after 4 days, at 17C after 7 days, and at 17C after 4 days (transformed data).

Parents	Temp/ days	S750	Ac18	M72	KP	17K	Mean
S750	25/4	87.1	90.0	90.0	85.9	90.0	88.6
	17/7	85.9	82.0	70.7	47.3	52.4	67.6
	17/4	83.3	75.4	56.6	31.4	42.3	57.8
Ac18	25/4	90.0	90.0	90.0	87.1	90.0	89.4
	17/7	87.1	72.6	82.6	80.0	51.7	74.9
	17/4	83.3	66.5	70.7	72.6	42.4	67.1
M72	25/4	90.0	87.1	77.1	87.1	81.8	84.8
	17/7	87.1	75.6	60.5	81.3	47.9	70.5
	17/4	82.0	67.1	53.8	78.5	35.9	63.5
KP	25/4	90.0	87.1	90.0	90.0	90.0	89.4
	17/7	90.0	90.0	87.1	90.0	56.9	82.8
	17/4	90.0	85.9	83.3	80.4	35.0	74.9
17K	25/4	90.0	87.1	90.0	90.0	90.0	89.4
	17/7	83.0	84.1	66.9	86.4	90.0	78.1
	17/4	55.6	75.7	62.8	82.1	84.2	72.1
Mean	25/4	89.4	88.3	87.4	88.0	88.4	88.3
	17/7	82.6	80.9	73.5	77.0	59.8	74.8
	17/4	78.8	74.1	65.4	69.0	48.0	67.1

Critical differences at 25C after 4 days, 17C after 7 days and 4 days = 3.9, 8.8 and 10.7, respectively.

Table 2. Radicle length (mm) of cucumber seedlings at 25C after 4 days, at 17C after 7 days and at 17C after 4 days.

Parents	Temp/ days	S750	Ac18	M72	KP	17K	Mean
S750	25/4	93.8	103.6	100.3	90.2	93.5	96.3
	17/7	48.7	58.4	54.5	35.1	35.6	46.5
	17/4	9.1	12.4	11.4	2.9	6.3	8.4
Ac18	25/4	105.2	105.1	106.9	102.1	93.8	103.8
	17/7	81.3	49.9	56.0	64.0	38.6	54.0
	17/4	12.3	5.9	7.2	10.6	4.4	8.1
M72	25/4	99.2	105.1	93.1	99.4	80.5	95.5
	17/7	60.8	53.0	44.9	63.1	43.4	53.0
	17/4	15.1	10.2	4.1	11.5	5.8	9.3
KP	25/4	104.7	106.2	106.3	97.4	85.8	100.1
	17/7	65.2	68.6	64.8	53.2	34.1	57.2
	17/4	16.3	17.3	15.6	11.8	7.0	13.7
17K	25/4	89.6	95.6	97.5	96.9	85.3	95.0
	17/7	42.2	51.9	53.8	50.4	53.6	50.4
	17/4	11.0	11.0	12.4	10.4	12.3	11.4
Mean	25/4	98.5	103.1	100.8	87.2	91.0	98.1
	17/7	55.8	56.4	54.8	53.2	41.4	52.2
	17/4	12.9	11.4	10.1	9.4	7.2	10.2

Critical differences at 25C after 4 days, 17C after 7 days and 4 days = 3.4 5.5 and 2.6, respectively.

Table 3. Variances and genetic components of germination and seedling growth analyzed by Griffing's method 1.

Character	Mg	Ms	Mr	Me	$\sigma^2 g$	$\sigma^2 s$	h^2	a
OPTIMUM TEMPERATURE								
Germination %	16.25**	10.79*	5.44 ns	4.46	0.58	3.77	0.12	1.81
Radicle length	139.70***	21.50***	36.30***	4.85	23.80	9.33	0.62	0.65
SUBOPTIMUM TEMPERATURE								
Germination % day 4	236.93***	260.96***	428.47***	33.58	0.00	135.00	0.02	—
Germination % day 7	194.22***	204.21***	235.63***	24.87	2.15	106.76	0.02	6.81
Radicle length day 7	159.16***	98.12***	78.99***	6.61	6.54	54.43	0.18	2.04

*, **, *** = significant at 5, 1 and 0.1% level, respectively.

Application of factor analysis to cucumber breeding

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Cucumber breeding objectives suggested by the "Chinese Cucumber Breeding Cooperation Team" include the development of a early maturing, high yielding cucumber which is resistant to anthracnose, fusarium wilt and downy mildew disease, and which possesses good commodity characters for Chinese markets. These objectives require the incorporation of many quantitatively inherited traits.

It is necessary to develop a comprehensive selective method for reaching these objectives. Studies which identify genetic relationships among traits (correlations) is a prerequisite for any comprehensive selection method. There are certain limitations inherent in traditional correlation analysis. Factor analysis, however, can be used to overcome some problems which are inherent in correlation analysis. The aim of this study was to investigate genetic relationships among several traits in cucumber using factor analysis.

An experiment was conducted at the Horticulture Station, of the Northwestern Agricultural University. Twenty-four varieties and inbreds were evaluated in a randomized block design with 3 replications. Ten plants of each cultigen were randomly chosen to evaluate 26 quantitative traits during the growth period. Traits included: 1) the node position of the first pistillate flower (x_1); 2) the days from sowing to the first pistillate flowering plant in the population (x_2); 3) the days from sowing to pistillate flowering of 50% of the plants (x_3); 4) the days from sowing to first male flowering plant in the population (x_4); 5) the days from sowing to staminate flowering in 50% of the plants (x_5); 6) leaf area per plant in the early stage (x_6); 7) fruit length (x_7); 8) fruit diameter (x_0); 9) leaf number in the early stage (x_8); 10) pistillate flower density (main vine) in the early stage (x_9); 11) number of pistillate flowers (main vine) in the early stage (x_{10}); 12) number of staminate flowers (main vine) in the early stage (x_{11}); 13) number of harvested fruit per plant in the early stage (x_{12}); 14) average fruit weight in the early stage (x_{13}); 15) early yield per plant (x_{14}); 16) total number of branches (x_{15}); 17) average length between two close nodes (x_{16}); 18) total number of leaves (x_{17}); 19) the highest fruit setting node (x_{18}); 20) number of harvested fruits per plant (x_{19}); 21) total fruit weight per fruit (x_{20}); 22) total yield per plant (x_{21}); 23) downy mildew resistance in the early stage (x_{22}); 24) downy mildew resistance in the late stage (x_{23}); 25) fusarium wilt disease incidence (percentage; x_{24}) and; 26) anthracnose disease incidence severity (x_{25}). Resistance to anthracnose was identified by an *in vitro* leaf method.

Original data of x_9, x_{23} and x_{24} underwent anti-sine transformation and the variance was analyzed in a randomized block design. Genotype values (g_{ij}) of traits were estimated according to Chui-Yu Liu (1981) and then genotype correlation coefficients were calculated on the basis of genotypic value.

The main factor solution (factor analysis) was calculated using the genotype correlation matrix. The orthogonal factor load matrix was calculated by orthogonal rotation and transformation of the initial maximum variance using the BLQMIN oblique rotation method. The oblique factor load matrix and oblique factor correlation matrix were also analyzed.

Variance analysis detected significant differences among all observed traits, except for fruit diameter (x_0). Results show that the difference between model parameters was caused by genetic factors. Therefore, the genetic analysis could be evaluated in 25 x 25 matrix (25 traits).

Most of the trait loads centralized on a factor ($F_{1\text{-}5}$; Table 1). A biological explanation of all factors can be given: In factor F_1, x_6, x_8, x_7, x_{13}, x_{14}, x_{16}, x_{19}, x_{20}, x_{21}, x_{23}, x_{24} and x_{25} traits occupied the higher load. These traits centralized all yields and component factors, except the x_{12} trait. Therefore, F_1 factor is named the "Yield factor". Three kinds of disease (anthracnose, fusarium wilt and downy mildew) had a higher load, which indicated that there was close association between plant resistance disease level and yield. All of the susceptible parameters were negatively loaded, which indicated that they are negative factors for yield.

Higher traits loads in factor F_2 included x_1, x_3, x_9, x_{10}, x_{11}, x_{12} and x_{14} which were associated with traits of earliness, and F_2 was named the "early - mature factor". The node of first female flower, pistillate flower density (main vine) in the early stage, and number of pistillate flowers (main vine) in early stage had very high loads. Results indicate that these traits had the greatest effects on earliness.

Higher trait loads in factor F_3 included x_6, x_8, x_{17} and x_{18} which reflected plant nutrient level and plant growth vigor. Therefore, this factor was named the "Yield physiology factor". The load of total average fruit weight was high and average fruit weight at early stage also had a positive load. These data indicate physiological factors had a direct positive effect on fruit weight.

The load of x_2, x_3, x_4 and x_5 was higher than other traits in factor F_4 and was named the "flowering season factor". In addition, x_6, x_8, x_7 and x_{12} traits also had a certain load. The number of harvested fruit was the only positive value. Results show that components of this factor could result in delayed growth and development, while influencing yield by increasing fruit weight and reducing the number of fruit.

High trait loads were observed for x_4, x_5, x_{11}, x_{15}, x_{22} and x_{23} in factor F_5. This factor was named the "male flower development factor". The time of male flowering and the number of male flowers (increase) during the early part of the season was closely associated with downy mildew susceptibility.

Table 1. Factor loading matrix after orthogonal rotation transformation (genotype).

Traits	F_1	F_2	F_3	F_4	F_5
X_1	0.0909	-0.7137	0.3977	0.2239	0.1267
X_2	0.3323	-0.3775	-0.0021	0.7427	0.2136
X_3	0.1331	-0.5830	0.1883	0.5687	0.1845
X_4	0.2033	0.0274	-0.0219	0.8166	-0.3887
X_5	0.3820	-0.0692	-0.1084	0.7453	-0.3660
X_6	0.7670	-0.0303	0.5123	0.3280	-0.1242
X_7	0.8639	-0.0504	0.1894	0.3222	0.1484
X_8	0.5668	-0.0169	0.6095	0.3367	-0.1954
X_9	0.0943	0.9708	-0.0675	0.0824	0.1457
X_{10}	0.1077	0.8622	0.0986	-0.0330	0.1400
X_{11}	0.0516	-0.4363	0.3967	-0.0462	0.5504
X_{12}	0.3366	0.7722	-0.1883	-0.3558	0.0500
X_{13}	0.8306	-0.0427	0.2732	0.3145	0.1383
X_{14}	0.8109	0.5093	-0.0292	0.0283	0.0666
X_{15}	0.0012	-0.3291	0.1474	0.1302	-0.695
X_{16}	0.7747	-0.1202	0.2234	0.0804	0.0307
X_{17}	0.2910	-0.2044	0.8847	-0.136	0.0929
X_{18}	0.4830	-0.1631	0.8038	-0.0436	0.1051
X_{19}	0.8934	0.2664	0.1526	0.0530	-0.2160
X_{20}	0.8191	-0.0834	0.4010	0.1978	-0.1020
X_{21}	0.9173	0.0603	0.1689	0.1056	-0.2768
X_{22}	-0.4571	0.2414	0.3065	-0.2842	0.5540
X_{23}	-0.7594	-0.0988	0.1045	-0.1685	0.4936
X_{24}	-0.8134	-0.1482	-0.2374	-0.2374	-0.1266
X_{25}	-0.5227	-0.1296	0.1039	0.2561	0.3375

Factor analysis may be useful for describing and clarifying interrelationships among traits. As such this technique may be an important guide for selection during cucumber breeding.

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Application of narrow sense canonical characters to cucumber breeding

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Previous studies have shown that the correlation between heterosis of early yield in F_1 hybrids and its associated component (ACT) traits was near 1.0. Early maturity of F_1 hybrids is closely related to the trait constitution of parental lines. In order to develop a hybrid which possesses early maturity heterosis, parental lines must have both early maturity and ACT. Thus, the establishment of a reliable and effective selection scheme is essential. Such a scheme should possess the following: 1) a means for overcoming complicated correlations among important agronomic characteristics and unfavorable traits; 2) a means for overcoming low heritabilities often associated with quantitative characters, and; 3) a means for overcoming interference of non-additive effects in the early generations. A selection scheme which incorporates independent multiple characters with maximum narrow sense heritabilities may be reliable and effective during the course of pedigree breeding. Such a scheme is described below.

The additive variance and covariance of traits were separated from the genetic variance and covariance using analysis of combining ability covariance with eight parental inbred lines and 16 F_1 hybrids. This produced a narrow sense correlation heritability matrix (H_N). The H_N was used to construct two narrow sense canonical multiple characters with maximum narrow sense heritabilities. Four inbred lines, Changmi-1, Zangqiu-m, Pinli-m, and Hei235 were used as male parents and four inbred lines, Yue82, Jing4-3-1, Xilong58-5, and 7742 were used as female parents to produce an incomplete diallel.

The resulting F_1 hybrids were evaluated in a randomized complete block design with three replications. The narrow sense correlation heritability for two traits Xi and Xj (h^2_{Nij}) was estimated by means of variance and covariance of combining ability according to a random model.

The narrow sense correlation heritability matrix:

$$H_N = \begin{matrix} h^2_{N1} & h^2_{N12} & h^2_{N1m} \\ h^2_{N21} & h^2_{N2} & h^2_{N2m} \\ h^2_{Nm1} & h^2_{Nm2} & h^2_{Nm} \end{matrix}$$

The concepts of narrow sense canonical character were expressed as:

$P^*_{Ni} = b_i' p$ $(i = 1, 2.....s, s<m)$;

Such that P^*_N must satisfy the following two terms: 1) $p^2 (b'p, b'A) = \max$ and 2) $D(b'p) = 1$,

The phenotypic random vector $P = (p_1, p_2, ...p_m)'$, and

The additive random vector $A = (a_1, a_2, ...a_m)'$ constituting P^*_{Ni} is calculated by solving matrix equation $(H_n - \hat{p}^2 R_p)\beta = 0$.

The following traits were chosen as objective traits for the comprehensive selection scheme: 1) early yield per plant (S1); 2) number of early fruit (S2); 3) number of early female flowers on the main stem (S3); 4) total number of branches (S4); 5) number of leaves at the time of first flowering (S5); 6) the node position at which the first female flower appeared (S6).

H_N was estimated by means of combining ability using covariance analysis. Six eigenvalues and six eigenvectors of H_N for Rp were obtained by solving the matrix equation $(H_N - {}^2R_p)\beta = 0$ (Table 1).

Table 1. The broad sense eigenvalues and eigenvectors of HN for Rp.

Eigenvalues		0.998 $\hat{p}_1$	0.773 $\hat{p}_2$	0.258 $\hat{p}_3$	-0.895 $\hat{p}_4$	-2.520 $\hat{p}_5$	-5.306 $\hat{p}_6$
Adjusted eigenvalues		0.998	0.773	0.258	0.000	0.000	0.000
	s_1	0.449	0.492	-1.187	0.356	0.081	-2.382
	s_2	-0.315	0.074	-0.094	0.328	0.099	4.179
eigenvectors	s_3	-0.353	-0.251	0.385	0.482	-2.259	-1.538
	s_4	0.062	0.640	1.106	1.452	-0.164	1.025
	s_5	0.192	-0.904	-0.610	0.788	0.765	-1.482
	s_6	0.490	0.077	-0.963	-0.902	-2.457	0.818

Eigenvalues ($\hat{p}$) reflect the narrow sense heritabilities of corresponding canonical characters in biological sense (Table 2). For example, $\hat{p}^2_3 = 0.2583$, it is very low as a heritability, $\hat{p}^2_4$, $\hat{p}^2_5$, $\hat{p}^2_6$ are negative numbers and can be regarded as zero.

Table 2. The heritabilities ($\hat{p}^2_1$) and their corresponding eignevectors for the broad sense and narrow sense canonical characters $\hat{p}^2_1$, $\hat{p}^2_2$, $\hat{p}^2_3$ used to structure canonical characters.

Heritabilities			Bigenvectors					
			s1	s2	s3	s4	s5	s6
$\hat{p}^2_1$	Broad sense	0.999	-1.640	2.184	0.194	0.836	-1.984	1.283
	Narrow sense	0.998	0.449	-0.315	-0.353	0.062	0.192	0.490
$\hat{p}^2_2$	Broad sense	0.999	0.517	-1.290	1.450	0.092	0.782	-0.823
	Narrow sense	0.773	0.492	0.074	-0.251	0.640	-0.904	0.077
$\hat{p}^2_3$	Broad sense	0.928	0.382	-0.743	-1.508	-0.906	0.113	-1.542
	Narrow sense	0.258	-1.187	-0.094	0.385	1.106	-0.610	-0.963
$\hat{p}^2_4$	Broad sense	0.897	1.118	-1.364	0.473	1.109	0.167	-0.990
	Narrow sense	0.000	0.356	0.328	0.482	1.452	0.788	-0.902
$\hat{p}^2_5$	Broad sense	0.785	1.600	-2.837	1.800	-1.416	0.143	1.515
	Narrow sense	0.000	0.081	0.099	-2.259	-0.164	0.765	-2.457
$\hat{p}^2_6$	Broad sense	0.724	-0.863	-0.896	0.405	0.244	-0.143	0.847
	Narrow sense	0.000	-2.382	4.179	-1.538	1.025	-1.482	0.818

The broad sense canonical heritabilities is much larger than those of the narrow sense canonical characters. These results indicate that genes controlling each objective trait have many non-additive effects. There is a large difference between broad sense and narrow sense canonical characters in eigenvalues and weighting coefficients for objective traits.

The first canonical character (P^*_{N1}). In accordance with the quantity and direction of weighting coefficient of each target trait, we used a reverse P^*_{N1} selection. That is, selecting the lineage with small P^*_{N1} value (i.e., the lineage with low node position at which the first female flower appeared, more female flowers in main stem and early fruits harvested, fewer branches and leaves at first flowering). These characteristics are all important in early maturity.

The second canonical character (P^*_{N2}). We employed a positive P^*_{N2} selection. That is, the lineage with fewer leaves at first flowering and high early fruit yield were selected. Nevertheless, P^*_{N2} selection was ineffective in reducing the number of branches.

Table 3. The narrow sense canonical character values of 8 parental and 16 hybrids (F1)

	Narrow sense canonical character 1 (P^*_{N1})	Narrow sense canonical character 2 (P^*_{N2})
Yue 82(M1)	1.0757	-3.7898
Jing 4-3-1(M2)	1.6548	-0.8218
Xilong 58-5(M3)	1.6158	-1.9314
7742(M4)	3.8848	-3.5500
Changmi-1(F1)	1.3303	-1.4092
Zhangqiu-m(F2)	7.2461	-6.9080
Pinli-m(F3)	1.9358	-1.9746
Hei235(F4)	3.4756	-1.5404
H_1	0.3051	-2.2553
H_2	2.2231	-2.7390
H_3	2.3907	-1.7190
H_4	1.6023	-1.4923
H_5	1.2318	-0.3444
H_6	2.5815	-1.1398
H_7	2.0961	-0.5351
H_8	2.8573	-0.0409
H_9	2.2798	-0.9479
H_{10}	3.1833	-1.6005
H_{11}	2.4834	0.0571
H_{12}	3.1118	-1.1334
H_{13}	2.7619	-2.2661
H_{14}	3.5662	-2.1424
H_{15}	3.1481	-1.3824
H_{16}	3.0969	-1.3155

F_1, M_1, M_2, and M_3 (Table 3) were selected in P^*_{N1} reverse selection and F_1, F_4, M_2, and M_3 were selected in P^*_{N2} positive selection. F_1, M_2, and M_3 were all chosen in the selection of P^*_{N1} and P^*_{N2}. Data indicate that all inbred lines F_1(Changmi-1), M_2 (Jing4-3-1) and M_3(Xilung 58-5) possess better characteristics for early maturity. However, in the course of P^*_{N2} selection, none of the inbred lines were outstanding and thus all lines tested have shortcomings in this regard.

Maximum heritabilities and independence of canonical characters embody the advantages of this breeding method [1][2]. Yang De and DaiJunti (1983) reported on canonical character selection in the offspring of wheat populations [3]. Canonical analysis of early maturing cucumber lines overcame serious interferences with non-additive effects and thus is viewed as a reliable comprehensive selection scheme for early generations. As an overall appraisal, it can also define the best combinations from which unique early-mature diphyletic lines can be synthesized during the course of pedigree selection. Nevertheless,

only the use of lines with maximum broad sense heritabilities of canonical characters can avoid the serious interferences with broad sense canonical selection in early generations. In order to overcome such defeats, new breeding methods should be developed which allow for the establishment of narrow sense canonical characters with maximum narrow sense heritabilities. Such methods will increase the accuracy and reliability of canonical selection and thus overall appraisal of parental lines and F_1 hybrids.

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Cucumis Germplasm: 1992 Collection Expedition in India

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The Governments of India and the United States of America recently joined in a cooperative effort for: 1) the construction of modern germplasm storage facilities and establishment of a computerized germplasm database in India; 2) joint germplasm explorations in the two countries; and 3) the training of Indian scientists in the U.S. Most of the U.S. portion of the funding of this cooperative effort is from the U.S. Agency for International Development (USAID) through the USDA, Office of International Cooperative Development (OICD), a sister agency of USDA, ARS. The first cooperative effort of this program was a sunflower germplasm collection trip in the U.S. in 1992. The second cooperative effort was a *Cucumis* exploration trip in India which we undertook in October and November, 1992.

The primary objective of the *Cucumis* expedition was the collection of landraces of cucumber (*Cucumis sativus* L.) and melon (*Cucumis melo* L.). Other cucurbits were also collected during the expedition. Collections were made in three states (Rajasthan, Madhya Pradesh, and Uttar Pradesh) immediately following the rainy season (July through September). Seeds were collected from cultivated and non-cultivated areas, vegetable markets (subji mundi), and from seed dealers. Though many samples were collected as fruit we were not always able to observe the plants or the growing areas. Wherever possible, notes were taken at the collection site about the origin, description, and use of the collections.

The expedition provided several surprises. Cucumber landraces were difficult to find due to 1) the timing of the expedition (i.e. too late in the year), 2) a five-year drought that had completely eliminated the stocks of landraces in some areas (e.g., Sri Ganganagar), and 3) the slow adoption of open-pollinated varieties available through local seed dealers. An overwhelming number of melons were found in fields and markets. There were differences in botanical nomenclature of melon between the Indian and U.S. scientists (1). All melons including *Cucumis melo agrestis* are used as fresh (salad), cooked (vegetable) or dried preparations in India.

Approximately 677 samples were collected. Of these, 665 were cucurbits (Table 1) and 12 were non-cucurbits. There were approximately 186 cucumber and 447 melon collections, and they fell into several sub-groups (Table 2). Exact numbers of each will be known after discrepancies in the records have been resolved, and plants of some accessions have been observed.

These seeds will be available after they have been increased and properly documented (phenotypic and genotypic characterization) in the U.S. Germplasm Resources Information Network (GRIN) database. To that end, tentative 1993 plans call for an increase of a portion of these cucumber and melon collections in the U.S. and a substantial parallel increase of the collections in India. Based on the success and cooperation of the 1992 exploration, a proposal has been submitted to USAID through ARS, OICD, for a second joint *Cucumis* collection exploration in southern India and the Himalayan foothills in the 1994 summer season (May-June).

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Table 1. Numbers of cucurbit and non-cucurbit species collected in India during October and November, 1992.

Species	By State			Total
	Rajasthan	Madhya Pradesh	Uttar Pradesh	
Cucurbit				
Citrullus sp.	7			7
Cucumis melo	301[ZY]	146[X]		447
Cucumis sativus	104	63[YW]	18	185
Cucurbita maxima	1			1
Cucurbita moschata	4			4
Cucurbita pepo	3	2	1	6
Lagenaria siceraria	4			4
Luffa acutangula	1	2		3
Luffa cylindrica	1			1
Momordica charentia	2	1		3
Momordica dioca		1		1
Praecitrullus sp.	2			2
Triconsanthes bracteata	1			1
Non-Cucurbit				
Abelmoschus esculentus, okra		6		6
Cyamopsis tetragonoloba, cluster bean	1			1
Raphanus sativus, radish	1			1
Vigna unguiculata, cowpea	1			1
Zea mays, maize		3		3

[Z]Five samples obtained in Rajasthan were collected by D. C. Bhander, Central Arid Zone Research Institute, Jodhpur, Rajasthan in Gujarat.

[Y]One sample could be a mixture of *C. melo* and *C. sativus*.

[X]Five samples could be mixtures of *C. melo* and *C. sativus*.

[W]Four samples grown in Madhya Pradesh were purchased at a market in Rajasthan.

Table 2. Sub-groups of melon and cucumber collections from India during October and November, 1992.

Species	By State			Total
	Rajasthan	Madhya Pradesh	Uttar Pradesh	
Cucumis melo				
agrestis	88[Z]	73		161
flexuosus	7	12		19
momordica	194[Z]	53[Y]		247
not designated	12	8[X]		20
Cucumis sativus				
land races	80	43[YW]	14	138
open-pollinated varieties	23	21	4	48

[Z]Five samples obtained in Rajasthan were collected by D. C. Bhander, Central Arid Zone Research Institute, Jodhpur, Rajasthan in Gujarat.

[Y]One sample could be a mixture of *C. melo* and *C. sativus*.

[X]Four samples could be mixtures of *C. melo* and *C. sativus*.

[W]Four samples grown in Madhya Pradesh were purchased at a market in Rajasthan.

Resistance to Melon Dieback in Spanish Landraces of Melon

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Melon dieback is a serious vine decline disease of melon in Spain (2,3). The primary origin of this disease has been attributed to several ground fungus [*Rhizoctonia solani* (1), *Acremonium* sp. (4) and *Monosporascus cannoballus* (6)]. Melon dieback etiology associated with *Acremonium* sp. has been smartly by the Department of Plant Production of UPV (5). Inoculation with this fungus in hydroponic culture conditions produces root rot on melon seedlings (4). Nevertheless this technique seems not to be effective to carry out a screening of resistant genotypes to melon dieback. While these difficulties persist, a possible way to localize sources for resistance is to work in field conditions.

We have evaluated the response of 47 melon accessions to melon dieback in field conditions during spring-summer season of 1992. The trials were carried out in two locations (Puzol and Romani) in Valencia (Spain). In both places plants were grown in plots where the disease had previously been noted during 1991. The majority of evaluated accessions are Spanish landraces belonging to 'Amarillo', 'Rochet' and 'Piel de Sapo' types. The number of replicates was four per each accession of 'Amarillo' type and three for the rest of the accessions (Table 1). The number of plants per replicate was variable. It was sown in May. Affected plants during July and August were registered. The end of the trial was in the middle of August.

The following data summarize the incidence of melon dieback in this trial:

- Number of accessions with an incidence higher than 50% in both locations: 21.
- Number of accessions with an incidence higher than 50% in one location: 19.
- Number of accessions with an incidence lower than 50% in both locations: 7.

The accession No. 6 ("Cantaloupe" type) stand out among the accessions with an incidence lower than 50% in both locations (Table 1). This accession showed a consistent response although it did not escape completely to the disease. This could indicate that this accession has a notable degree of resistance to melon dieback and it could have interest as source for resistance. This should be confirmed in further trials. The accessions No. 12 and No. 18 ("Amarillo" type) could be employed as direct use materials. On the other hand the use of plots where the disease had previously been noted could be feasible as previous trial for the screening of sources for resistance, according to the results of this work.

Table 1. Accessions with an incidence lower than 50% in both locations.

		Location*							
		Puzol				Romani			
Accession	Incidence**	R1	R2	R3	R4	R1	R2	R3	R4
6	a	4	4	4	4	4	3	2	3
6	b	0	0	0	0	0	0	2	0
7	a	3	4	4	4	4	3	3	4
7	b	1	0	1	0	1	2	0	4
12	a	4	4	4	4	3	3	4	3
12	b	0	3	1	0	0	1	3	0
18	a	1	4	4	6	3	4	4	4
18	b	0	0	0	4	2	0	1	0
43	a	4	5	4	-	4	4	2	-
43	b	2	1	0	-	2	3	0	-
28	a	4	5	3	-	4	5	6	-
28	b	3	1	0	-	2	2	2	-
30	a	5	2	1	-	1	2	2	-
30	b	0	1	0	-	0	2	0	-

*R: replicate
**a: tested plants
b: affected plants

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Club Mildew: Working Group on Resistance of Melon to Powdery Mildew

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Determinations of races of powdery mildew and resistance genes in melon are confusing. For instance, plants resistant to "race 2" and susceptible to "race 1" have been observed in the F_2 families from crosses of PI 124111F or PI 124112 with a susceptible line inoculated with Israeli isolates. This characterization was not observed using a French "race 2" isolate on the same families or on a collection of more than 400 accessions. Apparently these two "race 2" isolates do not have the same virulence genes.

At the 5th EUCARPIA Symposium on Cucurbitaceae in Skiernierwice and Warsaw, Poland, in July 1992, a group of melon breeders and pathologists (Table 1) formed a working group to clarify the relationships between the genes for resistance and the powdery mildew races. This cooperative research includes three objectives: First, obtain melon lines possessing only one gene for powdery mildew resistance. Second, test these lines with different isolates of powdery mildew at different locations around the world. Third, conduct allelism tests among the powdery mildew resistance genes.

The first and third objectives will be done by the current Club Mildew members and should be accomplished by 1995. For the second objective we welcome new members particularly from South America, Africa, Australia, Far East, India, and the Middle East in order to have a better sample of the variability in melon powdery mildew.

Table 1. Club Mildew members, affiliation, and country.

J. M. Alvarez INIA Zaragoza (Spain)	D. Gabillard Royal Sluis France Nîmes (France)	M. Pitrat INRA Montfavet (France)
F. Bertrand VRED Nîmes (France)	M. L. Gómez-Guillamón CSIC Malaga (Spain)	C. Robledo VRED Nîmes (France)
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Downy Mildew (*Pseudoperonospora cubensis* B & C) Resistance in Melon (*Cucumis melo* L.)

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Downy mildew has become a major threat to commercial cucurbits including melon and cucumber in India (5). In the sub-tropical parts during the premonsoon rains and in other humid and high rainfall areas, it is a devastating disease. In several trials conducted during rainy season by Dr. T. A. More at Delhi he noted almost 100 percent losses in cucumber and melon (4). He also observed that 'Phoot' or snapmelon (*Cucumis melo* var. *momordica*), a non-dessert type of Indian origin and FM 1 of U.S. origin hold resistance to downy mildew. 'Phoot' was reported to be resistant to downy mildew from South India (6). Hence, efforts were made to screen advanced progenies (F6 and F7) of 'Phoot' (R) x Monoecious-4 (S) and FM 1 (R) x Pusa Madhuras (S) crosses for resistance to downy mildew thrice under natural epiphytotic conditions (Table 1) as per the procedure of Bonnet and Blancard (1) and also to study their performance in two replicated yield trials.

Results indicated that lines VRM 1-3, 5-10, 7-12, and 16-5 # B-1 of FM 1 x Pusa Madhuras cross and only one line VRM 31-1-2 of 'Phoot' x Monoecious-4 cross were highly resistant to downy mildew (Table 1). Combining these results with two replicated yield trials, two lines namely VRM 5-10 and 31-1-2 showed promise for downy mildew resistance and high productivity. These lines have attained homozygosity for major horticulturally important characters and now are in F9 generation.

Detailed study on inheritance of downy mildew resistance under artificial inoculation conditions in three resistant x susceptible crosses using six generations - P1, P2,F1, F2,BC 1 and BC 2 (2,3) was conducted. Inheritance of downy mildew resistance is governed by two dominant genes in 'Phoot' x Monoecious-3 and 'Phoot' x Pusa Madhuras crosses and two recessive genes are responsible for the same in 'Phoot' x Lucknow Safeda cross. Duplicate type of epistasis was evidenced in all the crosses.

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Table 1. Downy mildew resistance (PDI %) in advanced breeding lines.*

Breeding lines	F_6	F_7		Average
	Rainy season - 1990	Summer season - 1991	Rainy season - 1991	
VRM-1-3	NT	12.5	20.8	16.7
VRM-5-10	8.3	31.3	42.9	27.5
VRM-7-12	12.5	33.9	21.9	22.8
VRM-16-5 # B-1	5.6	17.5	NT	11.6
VRM-31-1-2	7.1	22.3	21.9	17.8
Phoot(R)-Check	3.1	9.4	17.9	10.1
Monoecious-4(S)-Check	71.6	62.5	NT	67.1
Total no. of lines tested	33	18	10	-

R = Resistant, S = Susceptible, NT = Not tested

*All these lines are in F9 generation at the present

Gene for Resistance to Fusarium Wilt Race 1 in Oriental Pickling Melon

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Several races of *Fusarium oxysporum* f. sp. *melonis* afflict melons. The dominant genes *Fom-1*, carried by 'Doublon', and *Fom-3*, carried by 'Perlita', confer resistance to races 0 and 2, whereas the dominant gene *Fom-2*, carried by 'CM 17187', confers resistance to races 0 and 1. 'Charentais T' is susceptible to races 0, 1, and 2 (2,3).

Resistance to Fusarium wilt races 0 and 1 was found in a number of Oriental pickling melon (*Cucumis melo* L. var. *conomon* Makino) accessions and breeding lines, including 'Freeman's Cucumber' (R. Cohen and H. Nerson, unpublished observations). The objective of this investigation was to determine the mode of inheritance of resistance and identify the gene(s) responsible. For this purpose, 'Freeman's Cucumber' (seed sample kindly provided by H. M. Munger, Cornell Univ., U.S.A.) was crossed with 'Charentais T' and 'CM 17187' (seed samples kindly provided by G. Risser, Station d'Amélioration des Plantes Maraîchères, France) to obtain filial, backcross, and testcross generations. The plants used for crossing had resulted from one or two generations of self-pollination of the original samples. Inoculation of melon seedlings with Fusarium wilt race 1 was as described previously (1); identification of the pathogen as race 1 was confirmed by using 'Hemed' (seed sample obtained from Hazera' Seed Co., Israel), which is resistant to races 0 and 2, as a control. The results presented in Table 1 are based on inoculations made in May 1991 and in November of the following year.

All plants of 'Charentais T' and 'Hemed' were, as expected, susceptible to Fusarium wilt race 1 (Table 1). All plants of 'CM 17187' and 'Freeman's Cucumber' were resistant. All plants of all possible F_1s between 'Charentais T', 'CM 17187', and 'Freeman's Cucumber' were also resistant. Therefore, the resistance to race 1 in 'Freeman's Cucumber', is dominant.

The F_2 of 'Charentais T' and 'Freeman's Cucumber', with the former the female parent, fit the expected 3:1 ratio of a single dominant gene conferring resistance. Although the reciprocal cross did not fit this ratio, having an excess of susceptible individuals, the overall F_2 population of this cross had a reasonable fit. In addition, the backcross to the susceptible 'Charentais T' fit reasonably well the expected 1:1 ratio for a single dominant gene conferring resistance. Therefore, it would appear that 'Freeman's Cucumber', like 'CM 17187', carries a single gene for resistance to Fusarium wilt race 1. All plants of the backcross to 'Freeman's Cucumber' were, as expected, resistant.

No susceptible individuals out of 176 were found in the F_2 of the cross of the two resistant accessions. Likewise, no susceptible individuals were found in the testcross for allelism: 'Charentais T' crossed with the F_1 of the two resistant accessions. As stated above, 'Freeman's Cucumber' was found to be resistant to race 0. These results and observations suggest that 'Freeman's Cucumber' carries the same gene for resistance as 'CM 17187', *Fom-2*.

Table 1. Segregation for resistance to Fusarium wilt race 1 in crosses involving Charentais T, CM 17187, and Freeman's Cucumber

Generation	Description	Number of plants			Expected ratio	X^2	P
		Total	R	S			
P_1	Charentais T	48	0	48			
P_2	CM 17187	17	17	0			
P_3	Freeman's Cucumber	52	52	0			
P_4	Hemed	81	0	81			
F_1	$P_1 \times P_2$	32	32	0			
F_1	$P_2 \times P_1$	40	40	0			
F_1	$P_1 \times P_3$	56	56	0			
F_1	$P_3 \times P_1$	49	49	0			
F_2	$(P_1 \times P_3)\otimes$	127	96	31	3:1	0.024	0.87
F_2	$(P_3 \times P_1)\otimes$	87	53	34	3:1	9.199	<0.01
F_2	Total	214	149	65	3:1	2.472	0.12
BC_1	$P_1 \times (P_1 \times P_3)$	220	100	120	1:1	1.818	0.18
BC_1	$P_3 \times (P_3 \times P_1)$	104	104	0			
F_1	$P_2 \times P_3$	16	16	0			
F_1	$P_3 \times P_2$	13	13	0			
F_2	$(P_2 \times P_3)\otimes$	40	40	0			
F_2	$(P_3 \times P_2)\otimes$	136	136	0			
Test	$P_1 \times (P_3 \times P_2)$	224	224	0			

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Contribution No. 3701-E from the Agricultural Research Organization, Bet Dagan, Israel.

Breeding and Development of Cucumber Green Mottle Mosaic Virus (CGMMV) Resistant Lines in Melon (*Cucumis melo* L.)

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In sub-tropical parts of India around Delhi, CGMMV has been found more common and dangerous than any other virus on melon (5,6). A research project on breeding for CGMMV resistance in melon was started in 1984. An extensive research carried out enabled to identify the 'Phoot' or snap-melon (*C. melo* var. *momordica*), 'Kachri' (both non-dessert Indian types) and FM 1 as resistant to CGMMV (1,3,4). Back inoculation and transmission electron microscopic studies confirmed that they posses symptomless carrier nature of CGMMV resistance. 'Phoot' and FM 1 were utilized to incorporate the CGMMV resistance into Monoecious 4 (M4) and Pusa Madhuras (PM) respectively (Fig. 1).

The crosses 'Phoot' x M4 and FM 1 x PM were advanced to F2 by selfing. Progeny of the two crosses were studied independently. In F2 and F3 generations, sibbing between the selected CGMMV resistant plants was done in order to pool the resistant genes, keeping in view the polygenic recessive nature of inheritance of CGMMV resistance (2). From F4 to F8 generations selected plants were selfed to advance the generations. From F2 to F5 screening for CGMMV resistance was done in two stages. The seedling at cotyledonary stage was inoculated with pure isolate of CGMMV under artificial inoculation conditions in insect-proof nethouse (in January-February) and selected resistant plants were transplanted in the field in the first week of March. They were again screened for CGMMV resistance under natural epiphytotic conditions and simultaneously selection was made for better horticultural characters and selected plants were sibbed in F2 and F3) or selfed (in F4 to F5). From F6 to F8, generations were advanced by selfing. In F6 and F7 generations screening for CGMMV resistance was done under natural epiphytotic conditions. During F6 and F7 generations, performance for better horticultural characters was evaluated in the replicated yield trials. In F8, the level of CGMMV resistance was ascertained by employing the direct antigen coating ELISA technique after artificial inoculation with pure isolate of CGMMV.

Finally lines VRM 5-10, 29-1, 31-1, 31-2, 42-4, and 43-6 were selected from F5 to F10 which are highly resistant or resistant to CGMMV and possess better horticultural characters of economic importance (Table 1).

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Fig. 1. Breeding procedure, screening technique for CGMMV resistance and yield trials.

'PHOOT' x M4 (R) (S)		FM1 x PM (R) (S)
F1		F1
⊕		⊕
F2	Artificial screening - field screening - selection for better horticultural traits.	F2
#		#
F3	-do-	F3
#		#
F4	-do-	F4
⊕		⊕
F5	-do-	F5
⊕		⊕
F6	Field screening and yield trial.	F6
⊕		⊕
F7	-do-	F7
⊕		⊕
F8	Artificial inoculation with CGMMV-screening by direct antigen coating ELISA technique. Selection of lines having CGMMV resistance and better horticultural traits.	F8

⊕ = Selfed, # = Sibbed

Artificial inoculation was done with pure isolate of CGMMV.

Table 1. Evaluation of melon cultigens to CGMMV.

Cultigens[z]	CGMMV reaction PDI (%)[y]		Reaction[z,x]	Yield/plant (kg)[w]	T.S.S. (%)[v]
	Field	Inoculation			
VRM-5-10	11.5	16.1	HR	1.165	9.2
VRM-29-1	12.3	20.9	HR	3.020	6.9
VRM-31-1-2	14.7	8.8	R	3.475	6.7
VRM-42-4	21.1	26.3	HR	1.880	7.7
VRM-43-6	33.5	21.5	R	1.626	7.4
Phoot(R)-Check	21.9	13.5	R	2.135	5.2
FM 1 (R)-Check	0.0	16.0	NT	1.090	8.9
Pusa Madhuras (S)-Check	67.5	62.6	HS	1.085	9.5
Monoecious-4 (S)-Check	80.1	81.6	HS	1.155	7.1

[z]R = resistant, S = susceptible, HS = highly susceptible, NT = not tested.

[y]PDI = percent disease index. Field results of avg. of 1 yr and inoculation results are from avg. of 3 separate screenings.

[x]Direct antigen coating ELISA technique was employed after artificial inoculation with pure isolate of CGMMV.

[w]Average of 2 replicated yield trials.

[v]T.S.S. = total soluble solids.

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The Role of Viruses in Sudden Wilt of Melons in New York

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It is now 50 years since I saw melons near Geneva, N.Y. wilt and die just as the first fruits were ripening. This was in a field in which W. D. Enzie was breeding for improved horticultural features and was typical of what came to be called "sudden wilt". Over the years since than, horticulturists and plant pathologists studying the problem in New York have implicated low soil temperatures, fusarium, pythium, and cucumber mosaic virus (CMV). However, the disorder has been so difficult to duplicate experimentally that there has been no consensus about the cause except that it is probably complex and can involve more than one agent.

In occasional years when sudden wilt is severe, differences have appeared in variety trials and breeding plots which offer some clues. The most frequent observation has been the superior survival of breeding lines and hybrids selected for cucumber mosaic resistance (CMR). On the other hand, these have so often failed to show superiority that other factors must have been more important or the level of CMR has been inadequate.

One contributing factor may be powdery mildew. Over the past 30 years there have been three occasions when susceptible lines wilted while their PMR counterparts remained turgid. Even though mildew did not appear to be severe, it apparently reduced the ability of the roots to supply water. Low soil temperature likewise reduces water uptake but by itself has not been shown to cause the wilting and death so often observed.

There have been two recent incidents in which viral resistance made a great difference in the survival of melons late in the season. In 1990, progenies segregating for WMV resistance (WMR), and with three backcrosses to Topmark, Honeydew, TAM Uvalde, and Cornell CPM339, were inoculated as seedlings with WMV and set in the field along with the susceptible recurrent parents. During pollination, the superiority of resistant segregates in all four backcrosses over the corresponding recurrent parents was evident, but it was also clear that CMV had come into the planting because CPM339, which has a moderate level of resistance, was the only recurrent parent to set fruit. Then in early September as fruit was about half developed, the CPM339 plants collapsed and died, as did most of the WMR segregates except for those with backcrosses to CPM339. In short with both CMV and WMV present, resistance to either virus kept plants alive long enough to set fruit, and in most cases viable seed, but only those with resistance to both produced edible fruit.

In 1992, resistance to papaya ringspot virus (PRR) made a large difference in survival in a planting of diverse melons which we hoped would remain disease-free. One purpose was to compare fruit type of PR resistant Cornell PPM339 and its hybrids with its recurrent parent PM339 and its hybrids. PM339 has a low level of cucumber mosaic resistance and is also the recurrent parent of CPM339 mentioned above. Soon after transplanting, a few plants with virus symptoms were removed from the field, and PRV and CMV were both found to be present. Spread did not appear to be rapid through the flowering period, but plants began to die as fruit developed slowly in the cold wet season. In

September the superior survival of PPM339 and its hybrids as compared with their near-isogenic counterparts became evident and Table 1 gives the proportion of live plants just before frost.

Table 1. Proportion of live plants on September 22.

Row No.	Identity	-PRR	+PRR
68, 69	PM339	2/24	
70, 71	PPM339		15/24
607	PM339 X MR324	0/6	
608	PPM339 X MR324		3/6
615	PM339 X TAM Uvalde	1/6	
616	PPM339 X TAM Uvalde		2/6
638	PM339 X Gulfcoast	1/6	
639	PPM339 X Gulfcoast		3/6
	Total	4/42	23/42

It is doubtful that anyone would have suspected PRV as a cause of death had it not been for the isogenic comparisons. While we did not follow symptoms closely in this case, we have often seen in the past that when CMV infection occurs late in the season, there may be only a few days between the appearance of typical mosaic symptoms on the vine tips and their death, leaving little or no indication of the cause.

Screening of Melons for Sweetpotato Whitefly Resistance: 1992

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Sweetpotato whitefly, *Bemisia tabaci* Genn. (SPWF) B strain virtually destroyed the Fall 1991 melon crop in the lower desert valleys of Arizona and California (4). SPWF-B does not appear to be an important vector of lettuce infectious yellows virus (LIYV, 1). In 1991, 17 of 150 PIs from India appeared to have some level of resistance to SPWF-B (3). In 1992, these 17 PIs were retested for SPWF-B resistance along with 108 previously untested PIs from India plus 27 standard varieties, breeding lines, and F_1, F_2 and backcross families from crosses among LIYV and SPWF-B resistantand susceptible parents.

A field test to evaluate SPWF-B resistance was planted on August 5 at the USDA, Irrigated Desert Research Station, Brawley, California. Plots were planted on 80 inch centers and consisted of five two-plant hills spaced 30 inches apart; there were two replications. Plots were treated once with Thiodan shortly after emergence for flea beetle control. The test was evaluated on a plot basis four weeks (September 2 and 3) and eight weeks (September 30) later for number of live plants, plant size, plant condition, yellowing, leaf necrosis (burn) and flowering.

The SPWF-B population at Brawley during the test period was high. Four weeks after planting (September 2-3), mean number of plants per plot, and plant size and condition varied among the entries (Table 1). Because little foliar yellowing was observed, yellowing data are not presented. A few entries had begun to flower, and as expected none of the entries was large enough to completely cover the bed. Plant condition was in general very good at this time. After an additional four weeks (8 weeks after planting) the plots had deteriorated. Many plants died; the proportion of plants surviving ranged from zero for 41 entries to 85% for one entry (F_1 Freeman Cucumber x Snakemelon); nine other entries had survival rates ≥ 50% (PI 271329 < PI 370021 < PI 381775 < PI 277281 < BC Snakemelon (Freeman Cucumber x Snakemelon) < BC Freeman Cucumber (Freeman Cucumber x Snakemelon) < F_2 Freeman Cucumber x Snakemelon < PI 145594 < PI 210542). Despite the higher survival rates, these lines were comparable to lines with lower (<50%) survival rates for plant size and condition. It is, however, significant to note that Snakemelon had a 42.1 % survival rate and that F_1, F_2 and BC families from crosses of Snakemelon with Freeman Cucumber comprised four of the 10 entries with survival rate ≥ 50%. Snakemelon, and BC Snakemelon (Freeman Cucumber x Snakemelon) were among the best five entries for plant condition after eight weeks. Five entries had a mean plant condition > 3.0 (PI 212895 < Snakemelon < BC Snakemelon (Freeman Cucumber x Snakemelon) < F_2 (90625 x Top Mark) < PI 370021). Snakemelon was previously identified as a potential source of LIYV resistance and has very large vines in the presence of high levels of LIYV (2).

In 1991, a single plant of PI 164825 appeared to be resistant to SPWF-B feeding. Self-pollinated seed from that individual was not obtained, but crosses were made with WMR 29 and I5. PI 164825 was retested in this test but none of the plants were as outstanding as the individual observed in 1991. The two F_1 families made with PI 164825 were not remarkable (Table 1). PI 145594 was the only PI identified in 1991 as a potential source of SPWF-B resistance that performed well in this test (Table 1). Five PIs tested for the first time in 1992 were among the best entries for survival, and plant size and condition after eight weeks. These will be retested.

None of the entries in this test was superior for survival, and plant size and condition. Snakemelon from the Middle East and families from crosses of Snakemelon were among the best entries in 1992 for plant survival, size and condition after eight weeks exposure in the field to SPWF-B. Five previously untested wild melon introductions from India (PI 210542, PI 271329, 277281, 370021, PI 381775) were identified in 1992 as having some potential as sources for SPWF-B resistance. The better lines for these characteristics will be

examined in subsequent field tests exposed to natural populations of SPWF-B. They should also be compared with Top Mark and other varieties in controlled greenhouse tests for response to SPWF-B feeding and reproduction.

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Table 1. Mean number of plants per plot[z], plant size[y] and condition[x] on September 2-3, 1992 and changes in these parameters on September 30 in response to sweetpotato whitefly feeding.

Group and Entry	September 2-3			September 30		
	Live	Size	Cond	% Surv	Δ Size	Δ Cond
Varieties and Parental Lines						
90625	9	2	9	16.7	1	-8
AR 5	8	1.5	8	37.5	-0.5	-7
Freeman Cucumber	9	2	8.5	16.7	-1	-7.5
PMR Honeydew	8	1.5	7	6.2	-0.5	-6
Snakemelon	9.5	2.5	6.5	42.1	2	-3
Top Mark	7.5	1.5	7	40	-0.5	-6
WMR 29	9.5	1	6	21.0	0	-4
Snakemelon x Freeman Cucumber						
F_1 FC x Snake	10	2	7.5	85	1	-4.5
F_2 FC x Snake	10	2.5	6	75	1.5	-4.5
BC FC (FC x Snake)	10	2	7	70	0.5	-5
BC Snake (FC x Snake)	8.5	3	6.5	58.8	2	-3
90625 x AR 5						
F_1 90625 x AR 5	10.5	2.5	7.5	0		
F_2 90625 x AR 5	9	1.8	6.8	27.8	-0.5	-4.2
BC (90625 x AR 5) x AR 5	8	2	7	31.2	-0.5	-6
90625 x Top Mark						
F_1 90625 x Top Mark	9.8	2	7.5	12.8	-0.3	-6.5
F_1 Top Mark x 90625	9.5	2.2	7.8	34.2	0	-6.2
F_2 90625 x Top Mark	9.5	1.8	7	5.3	3.2	-3
F_2 Top Mark x 90625	9.5	2.5	7.5	31.6	2.5	-5
BC Top Mark x 28377	9.5	2	6.5	13.2	-1	-5.5
BC 28380 x Top Mark	10.2	2	7	9.8	-1	-6
BC 28380 x 90625	9.2	2.2	7.8	13.5	0.8	-6.4
BC Top Mark x 28380	10	2	7	17.5	-1	-5.8
90625 x PMR Honeydew						
F_1 PMR HD x 90625	9.5	2.5	8	15.8	0.5	-7
F_2 PMR HD x 90625	7.8	1.8	7.5	25.8	-0.5	-5.5
PI 164825 crosses						
F_1 PI 164825 x WMR 29	1	2	7.5	0		
F_1 PI 164825 x 15	7.5	2.5	6.5	26.7	-0.5	-5
Plant Introductions tested in 1991						
123682	7	1	5.5	7.1	0	-4.5
124092	8.5	2	5.5	0		
124103	10	1.5	5.5	5	-0.5	-4.5
124106	6.5	1.5	5	15.4	1.5	-3
124109	9.5	2.5	6.5	0		

Group and Entry	September 2-3			September 30		
	Live	Size	Cond	% Surv	Δ Size	Δ Cond
124431	7	2	5	0		
124440	10	2	5	0		
124447	6.5	2	5	0		
124550	9.5	2.5	7	10.5	1.5	-6
145594	9	2	9	77.8	1	-6.5
164749	8	2	7.5	12.5	0	-6.5
164825	8.5	2	5.5	11.8	1	-4.5
165515	9	2	5.5	5.6	3	-4.5
165525	7.5	1	6.5	13.3	0	-5.5
179669	9.5	2	7	26.3	1	-6
179671	6	2	6	0		
179890	10	2	6.5	0		
Plant Introductions tested in 1992						
179901	9.5	2	6.5	10.5	0	-5.5
179902	8.5	2	6.5	17.6	1	-5
179903	10	3	6.5	45	0	-5.5
179904	8	2	6.5	0		
179905	9.5	2	6.5	10.5	0	-4.5
179906	8.5	2	6.5	11.8	0	-5.5
179909	8	3	8	25	0	-6.5
179911	6	2	6.5	25	0.5	-5.5
179913	10	2.5	6.5	0		
179915	10	2.5	7.5	35	-1.5	-6
179916	10	2	5.5	5	-1	-4.5
179917	10	3	7.5	5.5	1.5	-6
179919	10.5	2	6.5	9.5	1	-5.5
179920	9.5	2.5	6.5	15.9	0.5	-5.5
179922	6.5	1	8.5	15.4	0	-6.5
179923	6	1	9	0		
180280	6	1	6.5	8.3	0	-3.5
180281	7.5	1.5	7	13.3	-0.5	-5
180283	5	1	7.5	30	0	-5.5
181051	9.5	2	6	10.5	2	-3
182937	6.5	2	8.5	0		
182938	9.5	2	6.5	0		
182943	9	1.5	5	5.6	-0.5	-4
182949	8.5	2	6	17.6	0	-5
182952	10	2	6	5	-1	-5
182959	9	2	6.5	22.2	-0.5	-5
182964	5	1.5	9	20	0.5	-8
183025	7.5	2	5.5	6.7	-1	-4.5
183029	9.5	2	6	0		
183031	10	2	5.5	0		
183032	8	1.5	5	0		
183036	10	1.5	5	0		
183040	10	1.5	6	0		
183045	8.5	1	6	11.8	0	-5
183048	7	2	6	0		
183049	6	1	4	8.3	0	-3
183051	8.5	2.5	6	5.9	0.5	-5
183052	6.5	2	6.5	15.4	-1	-5.5
183054	5.5	2	8	9.1	1	-6
183055	9	2	7	27.8	2	-4.5
183128	9.5	2.5	7.5	0		
183303	10	2.5	6	10	-1.5	-5
183305	10	3.5	7	30	-0.5	-6
183307	9.5	2	6	10.5	2	-3
183311	3.5	1	8.5	0		
183397	9.5	2.5	6	5.3	-1.5	-4
183444	10	2.5	7	15	0.5	-6
210077	9.5	1.5	6.5	26.3	1	-5
210541	10.5	1.5	7	14.3	0.5	-5
210542	8	1	8.5	81.2	1	-5.5
212803	8	2	7	25	1.5	-6
212895	8.5	2.5	7	29.4	1	-3.5
213247	8.5	2	6	5.9	1	-5
214048	8.5	2.5	7	0		

Group and Entry	September 2-3			September 30		
	Live	Size	Cond	% Surv	Δ Size	Δ Cond
214154	9.5	2	6.5	0		
214318	9.5	2	7	0		
216030	9	2	6	22.2	-0.5	-4.5
217599	8.5	2	6.5	11.8	0	-5
271329	10	2	8	50	1.5	-7
271335	10	2	6.5	10	0	-5.5
275633	8.5	2	6.5	17.6	-1	-5
277281	9.5	2.5	8	57.9	2	-6.5
277282	8	2	6.5	6.2	-1	-5.5
277283	9	2	6	0		
277284	9	2	5.5	0		
279367	9	2	6	0		
288330	9	2	6.5	16.7	0	-5
288333	10	2	7	20	1	-5.5
302445	10	3	6.5	25	1	-5
302446	9	1.5	7	0		
323316	8.5	2.5	7	5.9	-1.5	-5
358942	8.5	2	7	17.6	0	-5.5
370020	9	2	6	0		
370021	10	3	7.5	50	0.5	-3.5
381758	9.5	2.5	6.5	0		
381760	7.5	2	7	26.7	-1	-6
381761	9.5	1.5	6	10.6	-0.5	-4
381762	8.5	1.5	6	11.8	0	-5
381765	7	1.5	6.5	21.4	0	-5.5
381766	8.5	2	7	0		
381770	7.5	2	6.5	0		
381771	7.5	1.5	5.5	6.7	-0.5	-4.5
381772	9.5	1.5	6	10.5	-0.5	-4
381773	10	1	5.5	10	0	-4.5
381774	9.5	2	7	5.3	-1	-6
381775	8.5	2	9	52.9	1.5	-7
381779	10.5	2	7	19.0	0.5	-6
381781	10	2.5	7.5	5	-0.5	-6.5
381782	10	1.5	6.5	10	-0.5	-3.5
381783	9	2	7.5	38.9	0.5	-6.5
381784	8.5	2	6	5.9	0	-4
381786	10	1.5	6.5	15	-0.5	-5
381787	10	2	7.5	20	-0.5	-6.5
381788	9.5	2	7	21.0	-1	-6
381790	7.5	2	8	6.7		-7
381792	10	2	7	0		
381794	10	1.5	6	10	-0.5	-5
381797	7	2	8	42.8	0.5	-6.5
381800	9.5	2	8	0		
381802	10	2	6	30	1	-4.5
381803	8	1.5	5.5	6.2	-0.5	-2.5
401731	8	1.5	7	12.5	-0.5	-6
431581	10	1.5	6.5	0		
504523	5.5	1.5	6.5	0		
504524	8.5	1.5	4.5	0		
504525	10	2.5	6.5	5	-1.5	-5.5
504526	7.5	2.5	6.5	0		
504527	9.5	2	5.5	0		

[z]Number of live plants is the mean; Surv is the Percentage plants remaining on September 30.
[y]Size was rated on a 1 (very small, only a few true leaves) to 9 (completely covering the bed) scale.
[x]Condition was rated on a 1 (dead) to 9 (vigorous, flowers) scale.

Genotypic Control of Regeneration Potential in *Cucumis melo*

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Present study was undertaken to outline the genotypic control of regeneration potential in *C. melo*. Three sex forms viz. andromonoecious (Pusa Madhuras), gynoecious (GM-5D, GM-6C-4, GM-7 and GM-6E-7) and monoecious M_4 were utilized in regeneration studies to find out the genotypic control of regeneration potential of different sex forms.

Materials and Methods. In vitro regeneration studies were carried out in Pusa Madhuras, GM-5D, GM-6C-4, GM-7, GM-6E-7 and M_4. Both epicotyl and cotyledonary explants were used. Pre-standardized de-differentiation medium of MS + 0.5 mg/l (MB) and differentiation medium of MS + 1.0 mg/l IAA and 5.0 mg/l Kinetin (MIK) were used following the usual procedure of regeneration (1). Callus obtained on MB medium was transferred to MIK medium after 2-3 weeks, for differentiation of shoot buds.

Results. Among the various sex forms of *C. melo*, andromonoecious sex form (Pusa Madhuras) has been found to be highly responsive to regeneration on pre-standardized de-differentiation and differentiation medium (Table 1). The four gynoecious forms showed no response to callus formation on MB medium. Similarly neither any direct regeneration nor callus induced regeneration was observed on MIK medium. In monoecious sex form (M_4), cotyledonary leaf explants were found to be equally responsive to differentiation medium than explants of Pusa Madhuras. In epicotyl explants of M_4, 23.82 (± 10.80) per cent callus induced regeneration was observed in comparison to 66.66 (± 7.21) per cent callus induced regeneration observed in Pusa Madhuras epicotyl explants.

Discussion. Various sex forms of *Cucumis melo* differ in two genes *A* & *G*. The andromonoecious form (Pusa Madhuras) is homozygous recessive for *a* and homozygous dominant for *G* whereas the monoecious form M_4 has a genotype of *A-G* (3,4,5). The gynoecious sex form is designated as *A-g g* plus modifiers at *g* locus (5). The high regeneration potential observed in Pusa Madhuras (1) and M_4 (2) may be governed by dominant *G*. Dominant *A* has a repressing effect on regeneration.

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Table 1. Regeneration response of various sex forms of *C. melo*[1]

Various sex forms	Explant	Explants forming callus (%)	Explants with shoots (%)	No response (%)
Andromonoecious (Pusa Madhuras)	Epicot.	33.33 ± 7.21	66.66 ± 7.21	0
	Cot. leaf	83.33 ± 28.86	16.66 ± 8.86	0
Monoecious (M_4)	Epicot.	75.18 ± 12.30	23.82 ± 10.80	0.98 ± 0.67
	Cot. leaf	56.10 ± 20.30	30.49 ± 6.76	13.39 ± 4.20
Gynoecious				
GM-5D	Epicot	0	0	100
	Cot. leaf	0	0	100
GM-6C-4	Epicot.	0	0	100
	Cot. leaf	0	0	100
GM-7	Epicot.	0	0	100
	Cot. leaf	0	0	100
GM-6E-7	Epicot.	0	0	100
	Cot. leaf	0	0	100

[1]Epicotyl and cotyledonary explants were incubated on de-differentiation medium (MS + 0.5 mg/l BA) for 2-3 weeks before transfer to shoot bud differentiation medium (MS + 1.0 mg/l IAA and 5.0 mg/l Kinetin).

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Genetic Parthenocarpy in *Cucurbita Pepo* L.

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Fruit set of summer squash can be very poor when conditions are unfavorable for pollination. Many F_1 hybrid cultivars have been bred to have a high ratio of female to male flowers and they may not have sufficient male flowers for good pollination at all times. The problem of poor fruit set is especially acute early in the season when prices are highest, but production may be limited because the low temperature, long day length, and high light intensity of that season promotes female sex expression and reduces male flower formation. Genetic parthenocarpy would be of value in situations where male flower production is insufficient and could also increase yield when there are insufficient bees for good pollination, when bee activity is restricted by wet weather, and when pollinating insects are kept away from squash blossoms by plastic tunnels or other row coverings. If row covers did not need to be opened or removed for pollination, they could be left on squash plants longer to improve growth and early yield by increasing the temperature around the squash plants, and also reduce losses from insects and insect-transmitted virus diseases.

Genetic differences in *Cucurbita pepo* for ability to set parthenocarpic fruit were reported by den Nijs and Veldhuyzen den Zanten (1982). They found that early production of parthenocarpic fruit ranged from none for some cultivars to 42% for 'DG-4'. Previously, Rylski (1972) noted that 'Zucchini Elite' had a stronger parthenocarpic characteristic than 'Bushy White'.

For the past three years we have been selecting for genetic parthenocarpy in the summer squash breeding program at Geneva, NY. Several CMV resistant breeding lines, including 82-138 and 82-141, compared favorably with 'DG-4' for parthenocarpic fruit set. Preliminary tests this past season, however, indicated that there may already be commercially available cultivars with even better parthenocarpic fruit set than the best of our breeding lines selected for parthenocarpy.

Thirty-three *C. pepo* cultivars and breeding lines were grown in the field and the first female flowers to develop on each plant were enclosed in paper bags before anthesis to prevent insect pollination. The number of female flowers closed for each cultivar or line is given in Table 1. Only fruit that developed to a marketable stage were recorded as being set parthenocarpically, and fruit that had some ovary enlargement, then turned brown and ceased development were not recorded as set. The fruit that were considered parthenocarpic had normal size and shape, and at maturity contained no seeds.

Two thirds of the entries in the trial set parthenocarpic fruit, the best being 'Chefini Hybrid' with 82% fruit set (Table 1). It is not known if the unusually cool and wet season of 1992 in New York was a factor in the extraordinary set of parthenocarpic fruit by some cultivars.

Many summer squash cultivars with the same fruit color have a similar gene background and may have similar incidence of parthenocarpy. It was previously reported (1, 2) that zucchini-type cultivars have better parthenocarpic fruit set than yellow- or white-fruited cultivars. That was generally true in our test, but there were exceptions. Green-fruited 'Ambassador', for example, was relatively poor in parthenocarpic fruit set in our trial and also in Holland (1), and none of the five female flowers we tested for 'Dark Green Zucchini' set fruit, but the yellow-fruited cultivar Gold Strike had excellent set of parthenocarpic fruit. Results from our breeding program and cultivar tests indicate that it should be possible to breed parthenocarpic squash of different fruit colors and types.

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Table 1. Parthenocarpic fruit set of squash cultivars and lines.

Cultivar or Line	Type	No. female flowers tested	% Parthenocarpy
Chefini Hybrid	zucchini	11	82
Gold Strike	yellow straightneck	8	75
Black Beauty	zucchini	7	71
Black Magic	zucchini	9	67
NY-82-138	zucchini	2	50
NY-92-728	zucchini	7	43
Green Magic	zucchini	12	42
NY-82-141	zucchini	8	38
Gold Slice	yellow straightneck	6	33
Cocozelle	striped straightneck	7	29
Goldie Hybrid	yellow crookneck	17	29
President	zucchini	14	29
Black Jack	zucchini	16	25
Gold Rush	precocious yellow straightneck	10	20
Caserta	striped straightneck	17	18
Golden Girl	yellow straightneck	12	17
Onyx	zucchini	7	14
Senator	zucchini	14	14
NY-92-727	zucchini	14	14
Hyrific	yellow straightneck	9	11
White Scallop	white scallop	9	11
Ambassador	zucchini	10	10
Yellow Crookneck	yellow crookneck	8	0
Gold Bar	yellow straightneck	10	0
Honey Boat	Delicata winter squash	4	0
Multi Pik	precocious yellow straightneck	12	0
Peter Pan	green scallop	11	0
Royal Acorn	green acorn winter squash	5	0
Scallopini	green scallop	9	0
Slendergold	yellow straightneck	6	0
Early Prolific Straightneck	yellow straightneck	5	0
Dark Green Zucchini	zucchini	5	0
NY-92-730	zucchini	6	0

Productivity of Naked Seed Squash, Cucurbita pepo L.

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The naked-seed squash has been reported by Curtis (2,3). The seed lacks the lignified seed coat. Whitaker (5) referred to studies on this mutation by several Austrian and German investigators. Abak et al. (1) started a breeding project in 1985 for seed production in Turkey. Percent oil in naked seed strains of the present study is 35.4% as reported by Farag (4).

Seeds of naked seed Kurbis squash were kindly provided by Dr. L. Tanasch of University of Austria in 1988. S_0 plants were grown in Hermosillo at the University of Sonora Experiment Station from seeds planted in April 1991 at a 0.5 x 3.0 m spacing. Fourteen plants were self pollinated in June 1991 and the fruits were harvested in August. S_1 seeds were extracted and segregation for seed type, normal or naked, was observed. All but two of the selfed plants produced fruits having naked seeds. S_1 naked seeds were planted in September 1991 under isolation, and harvested in December for observation. The plants exhibited normal growth, and produced open-pollinated fruits having naked seeds, confirming homozygosity of the naked trait.

Another planting of S_1 seed was made in March 1991 under isolation. The growth of S_1 plants was normal and they partially recovered from viral infection by spraying with Dithane M-45. Vigorous, spiny vines with profuse male and female flowering, and normal set of fruits by open pollination were observed. Mature fruits were harvested in July 1992. Data were recorded on 74 fruit from 31 plants. These were cut cross-wise and seeds were extracted and dried at ambient temperature. Fruits were morphologically described, and data were recorded on number and weight of fruits per plant. Fruit and seed traits were correlated on a single fruit basis. Simple and partial correlations were computed for fruit weight, number and weight of seeds, and seed size (mg/seed).

Results. There was no segregation for seed type. Fruits of all S_1 plants contained naked seeds. However, the green color of the exposed cotyledons (inner seed coat) varied in intensity from medium green to dark green. The mature fruit was round, oblate in shape. The pedicel end was spiny, solid, rather soft and ridged with 8 angles and inconspicuous flaring. The color of fruit skin (rind) was orange and splashed green. The rind was smooth and not hard. The flesh had a creamy color and fibrous texture. The placenta was gelatinous and orange.

The number of fruits per plants varied from 1 to 9 and averaged 3.3. Total fruit weight per plant ranged from 0.47 to 12.67 kg with a mean weight of 4.64 kg. Among the 74 individual fruits, the range of fruit weight was 0.47 to 3.17 kg, and the average was 1.55

kg. Number of seeds per fruit ranged from 16 to 393 and averaged 136. The average seed weight per fruit was 18.2 g and ranged from 1.4 to 64.1 g. Seed size averaged 134 mg and varied from 46 to 223 mg.

A strong association existed between number and weight of seeds per fruit, as evidenced from simple and partial correlation values (0.921 - 0.925) that were positive and highly significant (Tables 1 and 2). The values of the coefficient of determination indicated that 85 to 86 percent of the variation in seed weight can be ascribed to number of seeds. Seed size showed a strong, positive association with fruit weight (r = 0.488). Twenty-four percent of the variation in seed size can be attributed to fruit size.

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Table 1. Simple correlation between fruit characters of naked seed squash (n=74 fruits).

Characters correlated	Coefficient of Correlation r	Coefficient of Determination r^2
Fruit wt. vs Number of seeds	0.207 ns	0.043
Fruit wt. vs Weight of seeds	0.346 **	0.120
Number of seeds vs Weight of seeds	0.921 **	0.848
Fruit wt. vs Seed size	0.488 **	0.238

Table 2. Partial correlation between fruit characters of naked seed squash (n=74 fruits).

Characters correlated	Coefficient of Correlation r	Coefficient of Determination r^2
Fruit wt. vs Number of seeds (fixing Wt. of seeds)	-0.306 *	0.094
Fruit wt. vs Wt. of seeds (fixing Number of seeds)	0.408 **	0.166
Number of seeds vs Wt. of seeds (fixing Fruit wt.)	0.925 **	0.856

The Chromoplast Ultrastructure of Two Isogenic Lines of *Cucurbita pepo* Fruits at Different Developmental Stages

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Introduction: Many agriculturally important processes take place in the various developmental states of plastids. Chroloplasts are extensively studied due to their photosynthetic process. Chromoplasts, the principal carotenoid-bearing organelles in higher plants, are the major sites of vitamin A precursors for fruits and vegetables. In most of higher plants, chloroplasts are much alike in morphology, but chromoplasts are found to be in a great diversity of shapes and sizes, especially during plastid differentiation (5).

The understanding of plastid differentiation and interconversion is of fundamental biological interest. We chose *Cucurbita pepo*, for they display a fascinating array of colors during fruit development. The biochemical aspects of carotenoid accumulation in the chromoplast of different squash varieties were studied by Schafer et al. (6). We reported restriction site and genetic maps of chloroplast DNA of *Cucurbita pepo*, which corresponds to 153 kb in size (3).

Changes in plastid ultrastructure from two genotypes affecting fruit pigment (*YY* B^+B^+: fruits is initially green, then yellow) & *YY BB* : precociously yellow) of squash with isogenic backgrounds were compared at different stages of fruit development.

Materials and Methods: Fruits of two isogenic lines of squash (c.v. Early Prolific) were harvested at five developmental stages: 2 days postpollination, at pollination, 3 days postpollination, 10 days postpollination, and 20 days postpollination. We also used other squash varieties which display distinct green and yellow colors representing chloroplasts and chromoplasts, respectively. Small pieces of squash fruits were cut from the pericarp of fruits at five progressive stages, fixed in 3% glutaraldehyde in a 0.06 M phosphate buffer (pH 7.3) in ice for 3 hrs, and post-fixed in 2% OsO_4 for 2 hrs. The samples were dehydrated through a graded series of acetone and propylene oxide and then embedded in Epon resin. Thin sections were stained with 6% uranyl acetate for 90 min and lead citrate for 6 min (4) and observed with an electron microscope (Phillips) at 80 V.

Results and Discussions: Longitudinal section of chloroplast of green zucchini fruits showed the granal and stomatal thylakoid network similar to that observed in leaf tissue of Early Prolific squash.

Appearance of plastoglobuli and internal membrane structure in prochromoplasts paralleled the disappearance of thylakoid membranes of chloroplasts in *YY* B^+B^+ fruits. Therefore, we assume that thylakoid materials in chloroplasts may be used for the formation of internal membranes and plastoglobuli during chromoplast differentiation (Fig.1.a-e).

According to their structure and pigment composition of *YY* B^+B^+ fruits and of tomato fruits (2), we suggest that chromoplasts undergo structural changes from the membranous chromoplasts to the globular chromoplasts (Fig.1.d-e).

Chromoplasts in fruits were indeed derived directly from proplastids in precocious (*YY BB*) fruits (Fig. 1.f-h). It was reported that chromoplasts of the precociously pigmented yellow portion of bicolor ornamental gourd were differentiated directly from proplastids (1).

Very similar fine structure of plastids was observed in mature fruits of both genotypes. Based on previous hypothesis (6) and our results, we suggest that *B* and *Y* genes control the timing of chromoplast or chloroplast appearance rather than structure or content of plastids.

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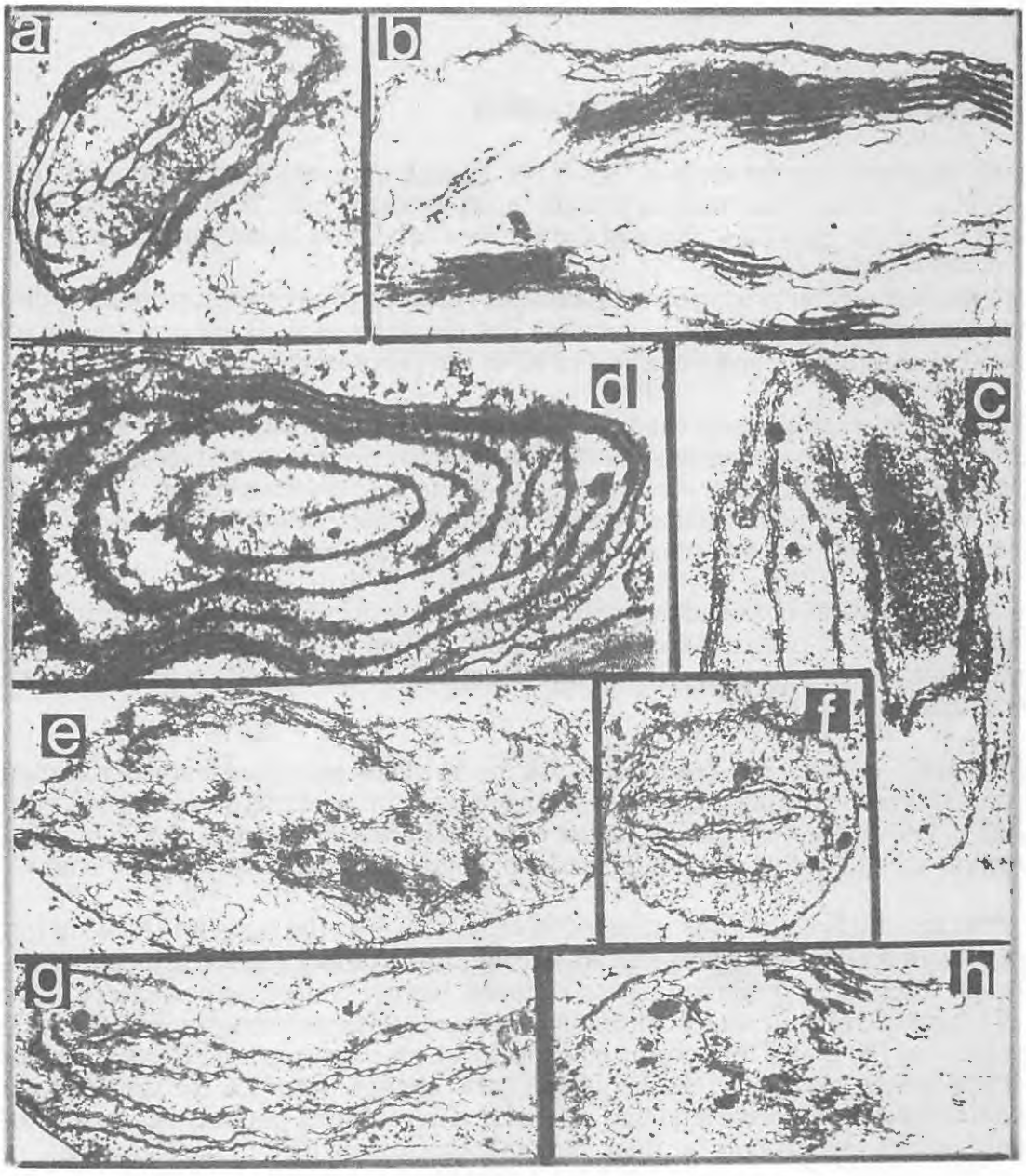

Fig.1.a. Proplastid of *YY* B^+B^+ ovary 2 days before anthesis. 1.b. Chloroplast of *YY* B^+B^+ fruit at anthesis. 1.c. Prochromoplast of *YY* B^+B^+ fruit 3 days postanthesis. 1.d. Cross section of membraneous chromoplast from *YY* B^+B^+ fruits 10 days postanthesis. 1.e. Longitudinal sectioned globular chromoplast of *YY* B^+B^+ fruit 20 days postanthesis. 1.f. Prochromoplast of *YY BB* fruit at anthesis. 1.g. Membraneous chromoplast of *YY BB* fruit 10 days postanthesis. 1.h. Globular chromoplast of *YY BB* fruit 20 days postanthesis.

A Case of Extremely Low Expressivity of Gene B2 in C. moschata.

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An F_2 population of the cross IL-B x NJ-B, C. moschata, was grown in the fall of 1989 in Naples, Florida. According to present interpretation (1, 2), IL-B is B1+B1+ B2B2 and NJ-B, B1B1 B2+B2+. Each of the B genes conditions chlorophyll deficiency.

Both parents exhibit precocious depletion of chlorophyll in ovaries, prior to anthesis, and their fruits are uniformly pigmented. But the stems of IL-B are persistently golden, devoid of chlorophyll, and the stems of NJ-B are persistently green.

One of the F_2 segregates, plant 807-34, produced bicolor fruits and persistently green stems. Although its ovaries were uniformly green, at pre-anthesis stages, they later on turned into bicolor fruits at some point during the post-anthesis stages. The fact that the bicolor design was first visible sometime during the post-anthesis stages indicated, according to present interpretation, that 807-34 carried gene B2.

An F_3 progeny was obtained from 807-34 and this progeny was grown in spring of 1990. It consisted of 110 plants, 106 of which were classified with a high degree of confidence. And analysis of this F_3 progeny suggested that 807-34 was B1+B1+ B2B2+ (see test 5, Table 2, in reference 1).

Of the 106 F_3 plants, 56 were bicolor. All the 56 plants produced fruits that turned bicolor sometime during the post-anthesis stages, and were therefore considered to be B2B2+. However, these bicolor individuals greatly varied in size of the chlorophyll deficient area in their fruits and in extent of chlorophyll deficiency in their stems.

A program of inbreeding was initiated in order to clarify the basis for the wide range of variation in the above F_3 progeny. As a result, two phenotypically distinct lines evolved through selection and inbreeding two different bicolor-fruited individuals: (a) plants that produced fruits in which chlorophyll deficiency effected about one-half of their surface, and (b) plants that produced fruits in which chlorophyll deficiency was confined to a few golden spots or a relatively small area (about 1.0 cm^2) at the proximal end. The data for case (b) are presented and interpreted here. Three phenotypic classes were identified and the symbols for these phenotypes are described in the following.

Symbols for three phenotypic classes (Table 1):

I. PDC-UO, PDC-SL = precocious depletion of chlorophyll uniformly affects ovaries prior to anthesis; fruits are uniformly golden; chlorophyll deficiency clearly affects the stems early in plant development, the basal portion of the plant being golden, but later on the expressivity level of chlorophyll deficiency is low, fluctuating between golden and green.

Unlike the PDC-UO, PDC-S phenotype of IL-B whose petioles are golden (tests 10-11, Table 1, in reference 1), the petioles of PDC-UO, PDC-SL are green.

II. GOT-VL, GS = ovaries are uniformly green at pre-anthesis stages; chlorophyll deficiency becomes visible late in post-anthesis stages and is confined to a small area, often inconspicuous, at the proximal end of the fruit (late turning); stems are persistently green.

This phenotype represents a very low expressivity level of chlorophyll deficiency. And significantly, some fruits of a given plant may be uniformly green.

III. GO, GS = ovaries, fruits and stems are persistently green.

It should be emphasized that unless a large number of fruits is carefully examined in each plant, a potentially phenotype of class II may be placed mistakenly in class III. Furthermore, there is evidence suggesting that the environment can transform some or all plants of class II into class III (e.g., see the offspring of plant 3 in the present Table 1).

Interpretation

The analysis of the data in Table 2 does not disagree with either the 3:1 or the 13:3 hypothesis. However, the 3:1 hypothesis is favored with some elaboration. The present contention is (i) that the PDU-UO, PDC-SL phenotype of this line is B2B2; (ii) that the GOT-VL, GS phenotype is B2B2+; (iii) that the GO, GS class consists of either B2+B2+ exclusively or a combination of B2+B2+ and B2B2+ in various proportions; (iv) that the genetic background of this line is homozygous for certain regulators of B2; (v) that said regulators attenuate or partially suppress the action of B2; (vi) that the degree of suppression is especially high in the heterozygotes; and (vii) that the environment can further intensify this suppression. Consequently, in some environments, B2 can operate as recessive rather than as dominant or codominant gene.

If the 13:3 hypothesis were applicable, one would have expected (a) that the GOT-VL, GS phenotype was heterozygous for both B2 and its partial suppressor, and (b) that the offspring of such double heterozygote would have consisted of some bicolor individuals in which chlorophyll deficiency effected a large portion of the fruit. No such individuals were observed in the present experiment.

Acknowledgement:

I thank Rogers NK Seed Co. for enabling me to conduct this study.

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Table 1. Offspring of self-pollinated plants that manifested extremely low expressivity of gene B2 (see text)

Parents[z]			Offspring				
				Phenotypic Classes			
				I	II	III	
Plants[y]	Pedigree	Growing Season	Growing Season	PDC-UO PDC-SL	GOT-VL GS	GO GS	Total
1	807-34-110[x]	Spring, '90	Fall, '90	10	18	12	40
			Fall, '92	8	11	13	32
2	807-34-110-2	Fall, '90	Spring, '91	4	8	8	20
			Fall, '92	2	12	18	32
3	807-34-110-2-10	Spring, '91	Fall, '91	12	11	8	31
			Spring, '92	4	0	27	31
4	807-34-110-2-10-13	Fall, '91	Spring, '92	7	0	25	32
			Fall, '92	4	8	11	23
5	807-34-110-2-10-30	Fall, '91	Spring, '92	4	0	28	32
			Fall, '92	3	0	4	7
			Grand Total	58	68	154	280

z All parental plants exhibited extremely low expressivity (phenotype GOT-VL, GS) of gene B2 (see text).

y Two samples of each parental plant were tested. The two samples were drawn from the same seed packet.

x F_3 segregate of the cross IL-B (phenotype PDC-UO, PDC-S) X NJ-B (phenotype PDC-UO, GS). See reference 1.

Table 2. Analysis of the data presented in Table 1.

Parental Plants	Offspring: Phenotypic Classes II + III	Offspring: Phenotypic Classes I	Total	Hypothesis #1 3:1 X^2	Hypothesis #2 13:3 X^2
1	54	18	72	0.0000	1.8462
2	46	6	52	5.0256	1.7751
3	46	16	62	0.0699	2.0265
4	44	11	55	0.7333	0.0564
5	32	7	39	1.0341	0.0442
	222	58	280	6.8629	5.7484
				2.7428	0.7092
				4.1201	5.0392

		X^2	df	P
Hypothesis #1:	Deviation	2.74	1	0.05 - 0.10
	Heterogeneity	4.12	4	0.30 - 0.50
Hypothesis #2:	Deviation	0.71	1	0.30 - 0.50
	Heterogeneity	5.04	4	0.20 - 0.30

INHERITANCE OF IMMATURE FRUIT COLOR IN *C. MOSCHATA*

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Bush types of *C. moschata* with field resistance to Papaya Ring Spot Virus-W were developed in Brazil, as an alternative to *C. pepo* for the production of immature fruits (1). Lines were obtained for different immature fruit color such as: Mottled Light and Dark Green, Uniform Dark Green and Precocious Yellow. Several studies have been reported on the inheritance of immature fruit color in *C. pepo* (2, 3, 4, 5, 6). However, no report was found in the literature on the inheritance of this train in *C. moschata*. The present paper reports on the inheritance of immature fruit color in a cross between two *C. moschata* lines which produce Mottled Light and Dark Green (P1) and Uniform Dark Green (P2) immature fruits, respectively.

Parental lines were selfed for seven generations before being crossed to produce the F1, F2, BCP1 and BCP2 populations. Parents F1, F2, BCP1 and BCP2 populations were grown under field conditions at Sao Manuel-SP, Brazil, during the Summer season of 1992. Plants were scored for immature fruit color 3 to 5 days after the anthesis of the female flowers.

The results are presented in Table 1. Chi-square analysis revealed a good fit for a single completely dominant gene hypothesis for the Mottled Light and dark Green immature fruit color. It is proposed the use of the symbol *Mldg* for this gene in *C. moschata*.

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Table 1. Inheritance of immature fruit color in *C. moschata*

Population	Number of Plants			Expected Ratio	X^2	P
	Mottled Light and Dark Green	Uniform Dark Green	Total Plants			
P1	90	0	90	1:0		
P2	0	89	89	0:1		
F1	0	0	83	1:0		
F2	283	96	379	3:1	0.014 >	0.99
BCP1	189	0	189	1:0		
BCP2	90	95	185	1:1	0.135 >	0.99

BREEDING BUSH TYPES OF *C. MOSCHATA* WITH FIELD RESISTANCE TO PRSV-W

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Immature fruits of *C. pepo* and *C. moschata* are used in Brazil for raw or steamed salads. The market preference is towards *C. pepo* cultivars which bear slightly tapered, cylindrical fruits. However, the available *C. pepo* cultivars in Brazil are very susceptible to Papaya Ring Spot Virus-W which makes difficult their production, particularly during the late Spring and Summer periods. Some cultivars of *C. moschata* show good field resistance to PRSV-W, but they are late, produce plants with long vines and fruits that resemble the straightneck Butternut types. The present paper relates to the development of novel types of *C. moschata* with bush growth habit, good PRSV-W field resistance, earliness and which produce slightly tapered cylindrical fruits, similar to those of *C. pepo*.

METHOD. The lines were obtained through pedigree and backcross selection as shown in Fig. 1 and Fig. 2. Selections for field resistance to PRSV-W were practiced in all generations, under natural field infection conditions, using spread rows and plants of *C. pepo* cv. Caserta as a standard immature squash type. Cv. Piramoita contributed the bush growth habit and PRSV-W resistance (1,2),F1 hybrid Seaulmadi the slightly tapered cylindrical fruit shape and PPI 165561 the precocious yellow fruit colour (3).

RESULTS. The main characteristics of the novel *C. moschata* breeding lines developed by the program are presented in Table 1.

CONCLUSIONS. Preliminary commercial field trials have indicated a good acceptance of the novel breeding lines among farmers in main production areas of Brazil. We believe that these novel types of *C. moschata* will be interesting to other tropical countries besides Brazil.

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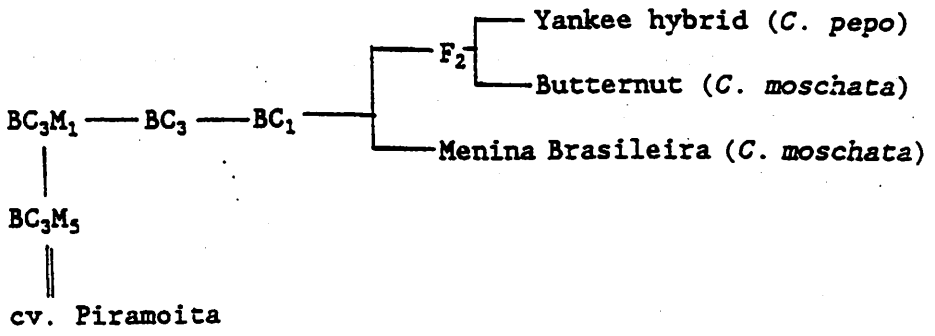

Fig. 1 Pedigree of the bush type, PRSV-W field resistant *C. moschata* cv. *Piramoita*.

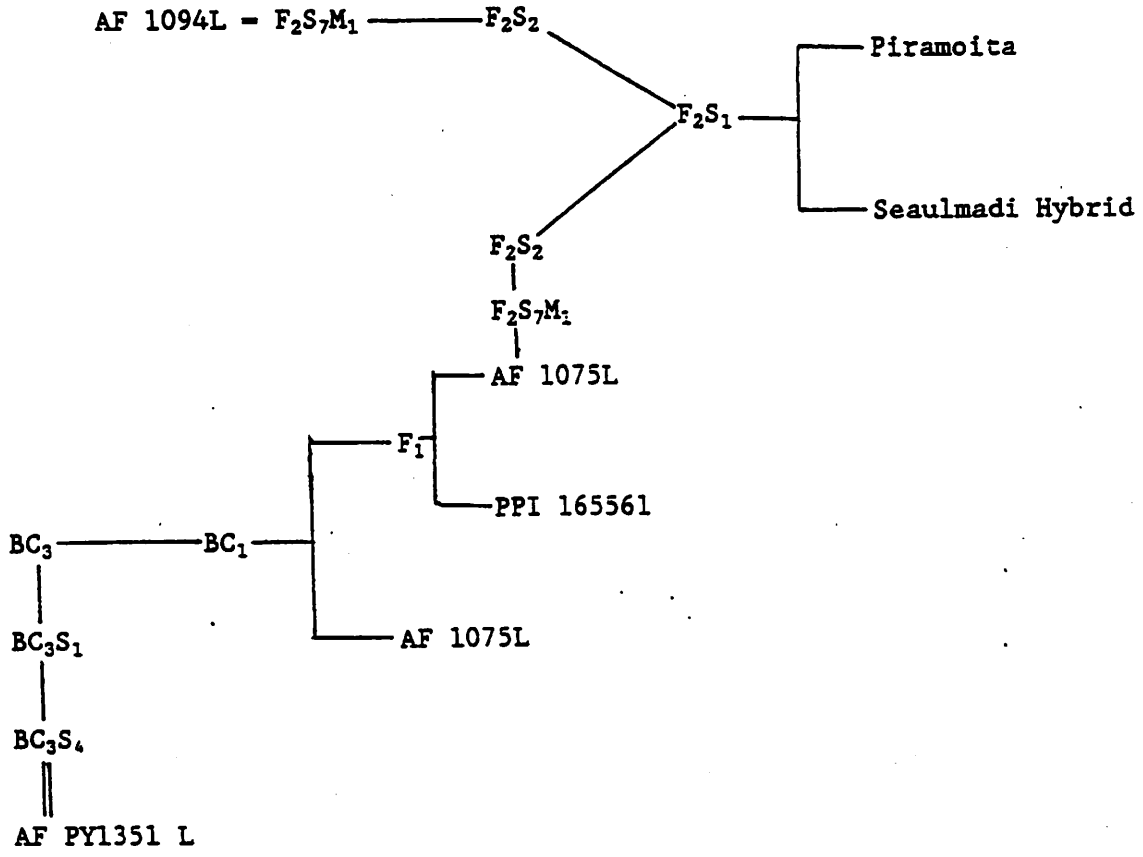

Fig. 2 Pedigrees of the bush type PRSV-W field resistant *C. moschata* breeding lines AF 1075 L, AF 1094 L and AF PY1351 L.

Table 1. Characteristics of some *C. moschata* breeding lines with bush growth habit and PRSV-W field resistance.

Characteristics	Breeding Lines/Cultivar			
	AF1075 L	AF1094 L	AF1351 L	Piramoita
Plant diameter (m)	1,50	1,20	1,50	1.80
Days for flowering	55	50	55	55
Sex of the 1st flower	female	male	female	female
Fruit length/diameter (cm)	15/7	15/5	15/7	--
Fruit colour	mottled light and dark green	uniform dark green	precocious yellow	mottled light and dark green
Fruit shape	tapered cylidr.	tapered cylindr.	tapered cylindr.	long straightneck
Fruit gorwth[1] (days)	5	5	6	5
Productivity[2] (fruits/plant)	20-30	20-30	20-30	15-20

[1] Fruit growth - days from anthesis to the commercial harvesting size.

[2] Productivity - fruit/plant for a 40 days harvest period.

Powdery and Downy Mildew Resistance in *Cucurbita moschata* Accessions

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Powdery mildew is a disease found wherever cucurbit crops are grown. Two organisms are reported as the causal agents of this disease: *Erysiphe cichoraceatum* DC ex. Merat and *Sphaerotheca fuliginea* (Schlecht. ex Fr.) Poll. (3). In Puerto Rico *E. cichoraceatum* is the most prevelant pathogen (based on germ tube studies (2)) although *S. fuliginea* is occasionally found (1). With the introduction of drip irrigation and plastic mulches in Puerto Rico, pumpkins are now grown on a commercial scale during the cool dry season. These conditions favor powdery mildew. Downy mildew (*Psuedoperonospora cubensis*) prefers somewhat warmer and wetter conditions than does powdery mildew (3). In the Caribbean and Central America where *C. moschata* is often grown with few or low-cost imputs, farmers traditionally plant in the warm rainy season because of lack of irrigation equipment. In Puerto Rico downy mildew can limit production during the summer months or whenever unseasonable rains fall.

In this study all available accessions of *C. moschata* from the Southern Regional Plant Introduction Station, Experiment, Georgia were tested for powdery mildew resistance in the field and greenhouse and for downy mildew resistance in the field at Isabela, PR (18 N latitude, elevation 131 m). For the field test accessions were direct-seeded on 5 December 1991 in plots consisting of single 3.9 m-wide rows with 4 plants spaced 1.2 m apart. Two replications (blocks) of each of the 343 accesions were planted. Eighteen of the 343 accessions did not germinate, 8 accessions had poor germination (fewer plants were tested and these accessions were not grown in the greenhouse), and 27 accessions were clearly not *C. moschata* or included mixtures of other *Cucurbita* spp. Powdery and downy mildew field ratings were taken on 23 January and 12 to 14 February, 1992. Conditions were excellent for the development of both diseases since a warm, rainy period (28 C day/24 C night) accompanied the planting, followed by cooler, dry weather (25 C day/22 C night). A 0 to 5 scale was used: 0 = no mildew; 1 = less than 1 lesion per leaf; 2 = 1 lesion per leaf; 3 = several sporulating lesions per leaf, some mildew on petioles or stems; 4 = many sporulating lesions on leaves, petioles and stems; 5 = most leaves, petioles and stems completely mildewed, leaves dessicated or dead. The greenhouse evaluation for powdery mildew consisted of two single-plant replications (blocks) of each accession. Block 1 was planted on 17 March and block 2 on 21 April 1992. Plants were inoculated by dusting with infected leaf tissue and rated as in the field.

Accessions having a mean powdery mildew rating of ≤ 1.5 on the second field evaluation date are included in Table 1. Field ratings over all accessions ranged from 0 to 5 with a mean rating of 2.7, an LSD of 1.06 , and a CV of 19.8%. Almost half of the resistant accessions appeared to be something other than *C. moschata*. The resistant accessions came from very diverse origins. In the greenhouse most accessions were highly susceptible (Table 1). An exception was PI 438811 from Mexico.

Fourty-five accessions showed field resistance (a mean rating of 0) to downy mildew (Table 2). Field ratings over all accession ranged from 0 to 5 with a mean of 2.2, an LSD of 1.3 and a CV of 54.6%. Again, some of the resistant accessions appear to not be *C. moschata*. All resistant accessions are from Central America (mainly Mexico) with the exception of two PI's from India. Most accessions collected in temperate regions were highly susceptible to powdery mildew.

A rather large amount of phenotypic variation was observed within many accessions. Correlation between field and greenhouse powdery mildew ratings was very low. Larger numbers of plants from accessions showing some resistance are currently being evaluated.

Table 1. Field and greenhouse powdery mildew ratings for *C. moschata* PI's with a mean field rating of ≤ 1.5.

PI Num.	Origin	Field	Greenhouse	PI Num	Origin	Field	Greenhouse
193499	Ethiopia[1]	1.0	3.0	379295	Yugoslavia[1]	0.0	0.0
201254	Mexico[1]	1.5	---	414906	India[1]	1.0	5.0
234251	Japan	1.5	4.0	438811	Mexico	1.5	2.0
249565	Thailand	1.5	5.0	482490	Zimbabwe	1.0	4.0
298036	Australia[1]	0.0	0.0	482523	Zimbabwe[1]	1.5	2.5
357916	Yugoslavia	1.5	3.0	540906	Unknown	1.5	4.0
369346	Costa Rica	1.5	3.5				

[1] Accession appears to be misclassified as *C. moschata*

Table 2. *C. moschata* accessions with a mean field rating of 0 for downy mildew.

PI Number	Origin	PI Number	Origin	PI Number	Origin
168547	Mexico	190185	Mexico[1]	196923	Mexico[1]
200736	El Salvador	201254	Mexico[1]	201471	Mexico
201473	Mexico	326184	Mexico[1]	381810	India
381815	India	438577	Guatemala	438578	Guatemala
438723	Mexico	438726	Mexico	438731	Mexico
438747	Mexico	438748	Mexico	438756	Mexico
438760	Mexico	438772	Mexico	438775	Mexico
438776	Mexico	438781	Mexico	438784	Mexico
438787	Mexico	438790	Mexico	438792	Mexico[1]
438794	Mexico	438824	Mexico	442248	Mexico
442249	Mexico	442250	Mexico	442251	Mexico
442253	Mexico	442256	Mexico	442257	Mexico
442258	Mexico	442272	Mexico	442274	Mexico
442276	Mexico	442281	Mexico	442284	Mexico
451836	Guatemala	451837	Guatemala	451845	Guatemala

[1] Accession appears to be misclassified as *C. moschata*

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Leaf Silvering of Squash: A Brief Review

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Leaf silvering is an important malady of squash and pumpkins in the Middle East, Puerto Rico, the southern United States, and possibly other regions (1,2,3,9,11,12,13). Leaf silvering was first recognized and reported as a serious disorder of squash in Israel (1,2,3,4). The symptoms were illustrated and described by Paris et al. (10) in Israel and by Simons et al. (13) and Maynard and Cantliffe (9) in Florida. The symptoms, in mild cases, are silvering in and parallel to the veins in the upper surface of the leaves; in severe cases, the entire upper leaf surface is silvered and the petioles, stems, flowers, and fruits are pale in color (10). The rate of photosynthesis is about 30% lower in completely silvered than in green leaves (5).

Leaf silvering is induced by the sweetpotato whitefly, Bemisia tabaci Genn., especially by the nymphs (11,14) of what is sometimes referred to as the poinsettia or IV-90 strain (6). Efforts to find a pathogenic organism, such as a virus or viroid, associated with silvering have failed, leading to the conclusion that silvering is a systemic phytotoxemia (6,14). Silvering is exacerbated by drought stress in the broad sense (i.e. plant water deficit) and its components (low soil moisture, high temperatures, high light intensity, long days, etc.) (3,4,10). Chemical control of the whitefly (8) and cultural practices which reduce plant water deficit (3,4) have been reported to reduce the severity of the disorder. Silvering was reduced in a cultivar that was less susceptible to silvering when grown on reflective mulch with full irrigation (7).

Differential susceptibility to silvering occurs among cultivar groups, cultivars, and even among different strains of the same cultivar in Cucurbita pepo (H.S. Paris, P.J. Stoffella, and C.A. Powell, manuscript in preparation). Whilst genetic material immune to silvering has not been found, the cocozelle and vegetable groups of C. pepo have been found to contain some less susceptible cultivars.

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Inheritance of Resistance to Races 0, 1, and 2 of *Fusarium oxsporum* f. sp. *niveum* in Watermelon (*Citrullus* sp. PI 296341)

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Martyn and Netzer (1) reported Citrullus sp. PI 296341-FR to be 100% resistant to races 0 and 1 of *Fusarium oxsyporum* f. sp. *niveum* but segregating for resistance to race 2. We report here inheritance studies with this PI.

Materials and Methods. Seeds of parents, PI 296341-FR, New Hampshire Midget (NHM) and F_1, F_2 and BC_1 generations were surface sterilized and germinated. Eight-day seedlings with fully expanded cotyledons were used for inoculation. Roots of the seedlings were rinsed with water and then dipped in a spore suspension for 10 min. Inoculation concentration of each race of fusarium was 10^6 spores ml^{-1}. Inoculated plants were single planted in styrofoam trays and moved into the greenhouse. Plants were watered daily and fertilized weekly. The temperature in the greenhouse was 26 +/- 2 ^oC. Wilting began 5-7 days after inoculation. Data collected before transplanting (18 days post inoculation) and after planting (50 days after inoculation) are shown in Table 1. A set of crosses were made in the summer using resistant PI 296341 and F_1 individuals. Resistant F_1 plants were selfed or backcrossed in each case to produce F_2 and backcross progeny.

Results. The data support Martyn and Netzer's observation that the resistance genes in the resistant parent PI 296341-FR were not fixed. Inheritance to each race in this PI will be discussed separately.

Race 0 Resistance: F_1 progeny from reciprocal crosses with NHM are segregating 1:1 resistant to susceptible, indicating heterozygosity of one or more dominant genes for resistance in PI 296341. Segregation in the F_2 population from a selfed resistant F_1 plant fits a 9:7 ratio, suggesting an interaction between nonallelic genes. Segregation of the backcross population with NHM also indicates modifier(s) which overcome the dominant gene for resistance.

Race 1 Resistance: Dominance for resistance to race 1 in PI 2996341 is indicated. This result is in agreement with Netzer and Weintall (2). However, the presence of a susceptible class in the F_1 indicates other modifer gene(s). The susceptible class from the testcross to the recessive parent is much higher than expected, also indicating segregation of modifier gene(s). At 18 days, the F_2 progeny segregate 3:1 R:S as expected, but the susceptible class has increased by 50 days.

Race 2 Resistance: Both resistant and susceptible individuals exist in the parent PI 296341. The cross of a resistant individual with the susceptible NHM parent results in predominantly, but not exclusively, susceptible individuals. Thus, it is clear that resistance to race 2 is governed by at least one recessive pair of genes. If a 13:3 model is hypothesized for the F_2 generation, i.e., a dominant gene from NHM is epistatic over a recessive gene for resistance in PI 296341, then the data fit the model perfectly. If the backcross to the susceptible parent is assumed to be AaBb x aaBB, then all the backcross progeny will carry the B gene that is epistatic over a. If the few progeny scored as resistant in the F_1 and backcross populations were actually susceptible, the hypothesis that one or more recessive genes is interacting with a dominant gene is consistent with the data.

Our data suggest epistasis between resistance genes in PI 296341 and the susceptible cultivar New Hampshire Midget.

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Table 1. Resistance/susceptible distribution in different families inoculated with races 0, 1 and 2 of *Fusarium oxysporum* f. sp. *niveum.*

Races of the Pathogen	Families	Resistant:Susceptible 18 days	50 days	Hypothesis	p
Race 0	PI 296341	15:0	15:0	1:0	1.00
	NHM	0:15	0:15	0:1	1.00
	296341xNHM	9:11	9:11	1:1	0.70-0.50
	NHMx296341	13:7	10:10	1:1	0.99-0.95
	(296341xNHM)NHM	9:27	4:32	0:1	0
	296341xNHM) F_2	70:24	52:42	9:7	0.90-0.75
Race 1	PI 296341	15:0	15:0	1:0	1.00
	NHM	0:15	0:15	0:1	1.00
	296341xNHM	16:4	15:5	3:1	0.99-0.95
	NHMx296341	17:3	16:4	3:1	0.75-0.50
	(296341xNHM)NHM	12:23	6:29	1:3	0.25-0.10
	(296341x296341) F_2	67:28	61:34	2:1	0.75-0.50
Race 2	PI 296341	10:5	8:7	1:1	0.75-0.50
	NHM	2:13	0:15	0:1	1.00
	296341xNHM	4:14	1:17	0:1	0
	NHMx296341	3:17	2:18	0:1	0
	(NHMx296341)NHM	1:39	1:39	0:1	0
	(NHMx296341) F_2	20:72	18:77	3:13	>0.90

Male Sterile, *ms*, in Watermelon not Linked to Delayed Green, *dg* and *I-dg*

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The genetic male-sterile, *ms,* from China (1) has been reported to be unlinked to *gms* (1) and *Sp* (2). Data are reported here on its relationship to the two genes that determine delayed green - *dg* and *I-dg*.

To transfer *dg* (and its eptistatic gene, *I-dg*) into the male-sterile line, the following cross was made in 1990: *ms ms Dg Dg i-dg i-dg* and *Ms Ms dg dg I-dg I-dg* .

The fertile, normal green F_1 (*Ms ms Dg dg I-dg i-dg*) was selfed in the spring of 1991. The F_2 population was tested in the greenhouse in the fall of 1991. An F_2 population of 111 individuals was selected first for delayed green and then male sterility. The F_2 seedling population consisted of 88 normal: 23 delayed green (13:3 ratio, X_2=0.283). The 23 delayed green plants were grown out for fertility testing and seed. Seven (7) male-sterile recombinants were found among the 23 delayed green progeny, consistent with a 61:3 segregation of male sterile, delayed green ($X^2 = 0.651$).

Finally, the delayed green, male fertile class was obtained by subtracting the 7 delayed green, male sterile from the 23 delayed green total in the population. Thus, there were 16 delayed green, male fertile individuals in the F_2, consistent with a 55:9 segregation of delayed green, male sterile (X^2=0.011).

These preliminary data suggest that *ms* is assorting independently.

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Fertility Shift in an *In Vitro* Regenerated Male-sterile Line in Watermelon

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Regeneration of a male-sterile line was begun in November of 1991. Cotyledons from 20-day old fruit (*ms ms* x *Ms ms*) were inoculated on 10 µM BA regeneration medium (Adelberg and Rhodes (1). Regenerated shoot buds were subcultured on 10 µM BA during January and early February, 1992. The shoot buds were inadvertently subjected to a severe heat shock (over 37 °C) for a period of 2 days during the subculture when an air conditioner motor failed. The subcultured shoot buds were transferred to 5 µM IBA for rooting in late February, 1992. Rooted plantlets were transplanted into the greenhouse in early March, 1992. A total of 249 plantlets were transplanted into the greenhouse, and 230 plantlets survived (92.4% survival).

Two hundred regenerated plants were transplanted into the field at Edisto Research and Education Center, Blackville. A great range of pollen sizes were observed in this population - from 1673 μm^2 to 5419 μm^2. Only two putative tetraploids, identified by morphology, were observed. No visible somaclonal variation was obtained in the first generation other than the fertility segregation ratio.A 1:1 fertile:sterile ratio was expected, but 146 fertile:54 sterile were actually found.

Why did the fertile:sterile ratio change so drastically? One possibility was that the *Ms ms* tissue generated more plants than the *ms ms* tissue without any effect of temperature. The other possibility is that, under the conditions of this regeneration trial, the *ms* gene reverted to *Ms*. Perhaps the heat shock was responsible for this reversion. The mechanism responsible for this effect is being investigated. Nearly one hundred individuals were either selfed or sib crossed. If some of the fertile plants are transiently fertile because of temperature, their selfed progeny may be sterile.

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Protoplast Isolation and Culture of Watermelon Cotyledons

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Protoplast culture and subsequent regeneration could lead to more rapid genetic progress with watermelon. Experiments were conducted to define conditions for protoplast culture of cotyledons.

Effects of Mannitol, Cellulase and Pectinase on Protoplast Isolation from Watermelon Cotyledons.
A factorial experiment was performed to determine effects of mannitol, cellulase and pectinase on protoplast isolation. Three levels of mannitol (0.3, 0.4 and 0.5 M), three levels (0.5, 1.0, 1.5, and 2.0 %) of cellulase (E. C. 3.2.1.4, C-9422, Sigma) and two levels (0 and 0.4%) of pectinase (E.C. 3.2.1.15, P-4625, Sigma) were dissolved in the following buffer: 0.1 M glycine, 10 mM $CaCl_2 \cdot 2H_20$, 0.7 mM KH_2P04 at pH 5.7. Enzyme solutions were sterilized by filtration. Cotyledons of 1 week old seedlings grown in the greenhouse were used as the explant source. Cotyledons were first washed with tap water one hour, then surface-disinfected with 10% Clorox for 10 min., then rinsed four times in sterile distilled water. Lower epidermis of the cotyledon was peeled off with fine curved forceps, cut into 0.4 x 0.4 mm segments and put into a sterile enzyme solution. The tissue was incubated in darkness at 28°C for 4-6 hr. At the end of digestion, the cotyledon tissue and enzyme solution was shaken gently by hand to release the protoplasts. Enzyme solution and protoplasts were filtered through a nylon mesh (45 µM pore size), and filtrate was transferred to a centrifuge tube and spun at 200 RCF (Microcentrifuge Model 5-9A, Fisher Scientific) for 3-5 min. Protoplasts were resuspended in 0.5 ml of buffer solution with different concentrations of mannitol but without cellulase and pectinase. Density of protoplasts was determined with a hemocytometer, and viability of the protoplasts was examined after staining with 0.1% phenosafranin.

The optimal concentration of enzyme solution for isolating watermelon cotyledon protoplasts was 0.4 M mannitol, 1.5% cellulase and 0.4% pectinase (Table 1). Large standard errors indicate that all three factors are important for watermelon protoplast isolation. Sorbitol at 0.4 M was an equally effective osmoticum for isolation of osmoticum in trials not presented here.

Effect of Temperature and Time during the Enzyme Digestion on Protoplast Density and Viability.
Materials and procedures were same as in the first trial. Enzyme solution consisted of 0.4 M mannitol, 1% cellulase, 0.4% pectinase, 0.1 M glycine, 10 mM $CaCl_2 \cdot H_20$ and 0.7 mM K_2H_2P04 at pH 5.7. Three temperatures and digestion times were tested. Every treatment had three replications. In order to obtain a high intact protoplast density in a short time, we selected a suitable digestion period of 4-6 h at 29°C (Table 2).

Effect of Calcium Concentration in Enzyme Solution
It is known that Ca^{+2} can stabilize the protoplast membrane and enhance the survival of protoplasts. Four levels of Ca^{+2} in enzyme solution were evaluated: 0, 10, 15 and 20 mM. Enzyme solution consisted of 1% cellulase, 0.4% pectinase and 0.4 M mannitol at pH 5.7. In this experiment, immature cotyledons were used to isolate protoplasts. First, proximal portion of cotyledons were dissected from the embryo, cut

in half lengthwise and transferred to MS medium with 10 mM BA, 3% sucrose, and 0.7% agar at pH 5.7. These were maintained at 25±2°C, with a 16 h light period produced by cool white fluorescent lamps at 30 μmol m^{-1} sec^{-2}. After 10-14 days of culture, green, expanding cotyledons were cut into 0.1 cm strips and put into sterile enzyme solution kept in darkness at 26° C for 4 h. Every treatment had three replicates. The results are shown in Table 3.

Protoplast viability was highest at 20 mM Ca^{+2} although the protoplast density was lower at 15 mM Ca^{+2}. Unless a high density is desired, 20 mM Ca^{+2} is suitable for protoplast isolation (Table 3).

Effect of Cotyledon Source on Protoplast Isolation

Because harvested watermelon seeds are often difficult to decontaminate prior to tissue culture, protoplast isolation from cotyledons of harvested (dried) seed and cotyledons of seed from the intact fruit were compared.

1. Fresh seed from mature fruit. Mature fruit harvested in the greenhouse were surface disinfected with 95% ethanol, and seeds were removed asepticaly. Embryos were removed from seed coats. Cotyledon explants were dissected from embryos and transferred to MS salts medium with 0.7% agar, 3% sucrose, 10 uM BA, 100 mg l^{-1} myo-inositol, 2 mg l^{-1} glycine, 0.2 mg l^{-1} nicotinic acid at pH 5.7. Tissue was maintained at 25 ±2°C under light. After 8-15 days the cotyledons were cut into 0.1 cm strips and put into the enzyme solution.

2. Aseptic seed from mature fruit were dried in the laminar flow hood and kept in sterile bottles. Seeds were soaked in sterile distilled water before use. After 24-48 h, embryos were removed from seed coats and cultured as above.

In a second test with dried seeds, aseptic mature seeds were soaked in sterile distilled water and shaken on a platform shaker at 150 rpm for 24 hours. Seeds were transferred to a Magenta GA7 vessel with a layer of wet filter paper and kept in the dark at 30° C. After 2 days embryos with ca. 1 cm radicle were removed from seed coats and transferred to the same medium used in test 1, but without BA. Cotyledons 8-14 days old were cut into 0.1 cm strips and put into the enzyme solution.

Cotyledons of fresh seeds from mature fruit were the best explant source for isolation and culture of protoplasts. The density of the protoplasts was 1.0-1.3 x 10^5 ml^{-1} and protoplast viability was 68-74%.

Protoplasts were cultured on liquid and agar gelled B5 medium (Gamborg, et al., 1968) with different levels of growth regulators. Protoplasts became more oval after 2-3 days, indicating the synthesis cell wall. The protoplasts survived 15 days. However, protoplasts from dried seeds died in 2-3 days although the density and viability was not significantly different from protoplasts of fresh seeds. Results indicate that cotyledons from fresh seeds of mature fruit should be explants for protoplast isolation.

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Table 1. Effect of 3 levels of mannitol, 2 levels of pectinase and 4 levels of cellulase on watermelon cotyledon protoplast density and variability.

Ingredient	Density (x 10^4)	Variability (%)
Mannitol		
0.3 M	14.5±12.4[a]	46.9±28.3
0.4 M	14.7±13.8	58.6±15.6
0.5 M	13.7±18.7	51.6±22.3
Pectinase[b]		
none	2.6±2.2	55.2±15.2
0.4%	26.0±8.7	47.0±25.6
Cellulase[c]		
0.5%	15.2±14.90	48.5±16.0
1.0%	14.5±15.3	47.1±21.0
1.5%	16.6±14.1	60.2±10.4
2.0%	10.9± 6.2	48.7±30.4

[a]Standard errors.

[b,c]Pectinase was E.C. 3.2.1.15, P-4625; Cellulase, E.C. 3.2.1.4, C-9422, both Sigma.

Table 2. Effect of temperature and digestion time on watermelon cotyledon protoplast density and variability.

	20		25.5		29	
	D(x10^4)[a]	V	D (x10^4)	V	D (x10^4)	V
digestion (h)						
4	8.2	85.4	12.3	92.4	19.4	88.2
6	12.0	87.8	16.0	83.8	20.0	82.2
8	12.8	78.9	22.3	75.8	27.4	72.5
10	19.0	69.0	26.2	77.9	23.8	61.0

[a]D = density; V = viability

Table 3. Effect of Ca^{+2} in enzyme solution on density and viability of protoplasts from immature watermelon cotyledons.

	Ca^{+2} (mM)[a]			
	0	10	15	20
Density(x10^4)	1.9	3.9	2.5	2.2
Viability(%)	64.7	80.8	88.7	94.1

[a]$CaCl_2 \cdot 2H_2O$

Crossability between *Momordica charantia* and *Momordica dioica*

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Bittergourd (*Momordica charantia*) is an important fruit vegetable in the warm humid tropics, grown throughout the year. Preference for this vegetable varies highly with the extent of bitterness. In the present study an attempt was made to cross *M. charantia* with *M. dioica*, the bitterless, small fruited, tuberous perennial to seek possibilities of transferring desirable attributes of the latter to the former.

Both direct and reciprocal crosses were made between *M. charantia* and *M. dioica*. Anthesis in *M. charantia* is between 4:00 and 10:00 a.m. while that in *M. dioica* is between 5:30 a.m. and 12:00 p.m. Therefore, pollens from both species were collected at anthesis time, stored at 10°C and hand pollinated at the corresponding time of anthesis in both species.

The results (Table 1) indicated that the cross *M. charantia* x *M. dioica* or its reciprocal failed to set fruit when normal pollens were used as reported earlier (Trivedi and Roy, 1972; Dutt and Pandey, 1982). The ovary did not grow further; it shriveled and dried in three days. However, when crosses were made using pollens collected and stored at 10°C, the percentage of success was above 90. The fruits and F_1 seeds resembled their respective female parents in both direct and reciprocal crosses (Fig. 1 and 2). The number of chaffy seeds was more in crossed fruits than in selfed fruits. Further studies are in progress.

This is the first report of success of crossing between *M. charantia* and *M. dioica*. The study indicated the possibility of utilizing the bitterless, perennial tuberous *M. dioica* in transferring the desirable attributes to the commercially cultivated large fruited bittergourd. The study also shows the possibility of identifying the progenitor of bittergourd through genome analysis. The failure in earlier studies could be attributed to nonsynchronization of anthesis in two species, which is solved through storing pollens at low temperature and pollinating at anthesis in both species.

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Table 1. Crossability between *M. charantia* and *M. dioica*.

Crosses/selfs	Number of				
	Crosses or selfs	Fruit set	Seeds/ fruit	Bold seeds	Chaffy seeds
M. charantia x *M. dioica* (using pollens stored at 10°C)	50	46	23	14	9
M. dioica x *M. charantia* (using pollens stored at 10°C)	50	47	21	11	10
M. charantia (selfed)	25	24	22	19	3
M. dioica (selfed)	25	23	20	18	2
M. charantia x *M. dioica* (using normally collected pollens)	50	0	-	-	-
M. dioica x *M. charantia* (using normally collected pollens)	50	0	-	-	-

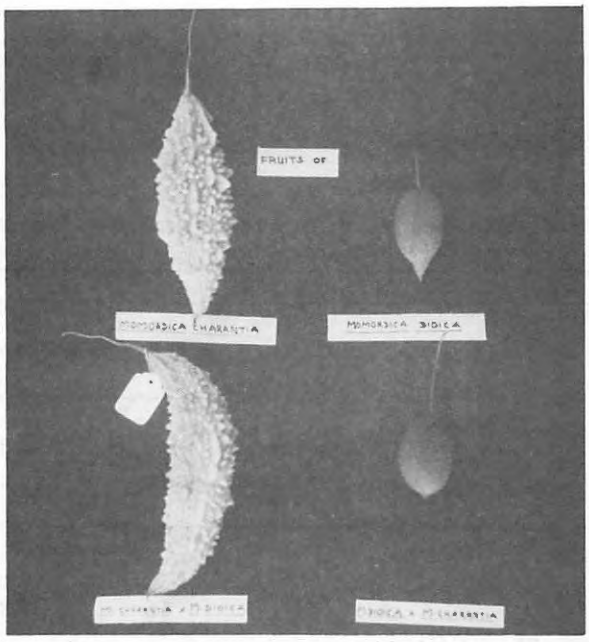

Figure 1. Fruits of selfs and reciprocal crosses between *Momordica charantia* and *M. dioica*.

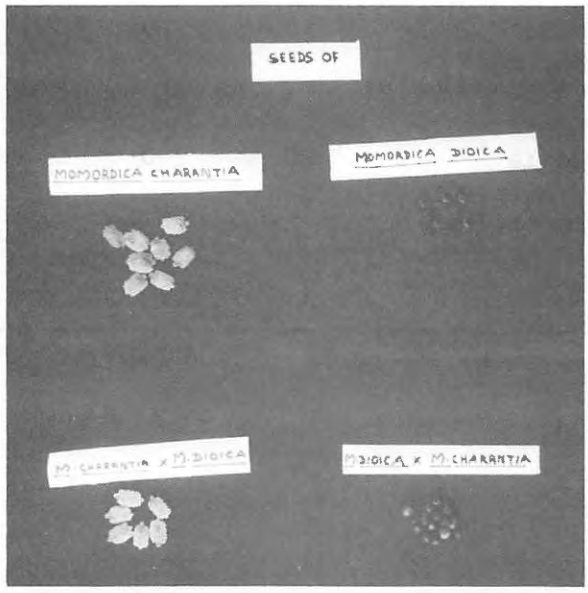

Figure 2. Seeds from selfs and reciprocal crosses between *Momordica charantia* and *M. dioica*.

Preliminary screening of cucurbits species for *Bemisia tabaci* Genn. whitefly resistance

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The majority of the Spanish production of early cucurbits dedicated to the foreign markets is being produced in greenhouses in Almería, Southern Spain. In the last few years, one of the most important problems in the culture of melon in this area was the yellowing virus disease (1,2,3) transmitted by the greenhouse whitefly *Trialeurodes vaporiarorum* W. (4). A systematic investigation of sources for resistance to this disease led to the discovery of resistance in several wild species of *Cucumis* and *Citrullus* (1,5) as well as in *Cucumis melo* var *agrestis* (6).

More recently, a progressive substitution of *Trialeurodes* by another whitefly *Bemisia tabaci* Genn. was detected in that geographic area. In 1991 this was responsible for the severe loses in production of melon cultured in the greenhouses of Almeria. This fact seems to be similar to those previously described in the lower desert valleys of California, Arizona and Mexico fall melon production between 1978 and 1991 (7), and in the United Arab Emirates with both melon (8) and watermelon (9).

The acquisition of new sources of resistance to whitefly could represent the first step in the fight against the direct as well indirect damages which whitefly produces. Interestingly, preliminary screening of accesions in agrestis-type melon for resistance to SPWF-P opened up hopeful results (7). In this paper we present the response versus *Bemisia* of a series of 30 entries belonging to genera *Cucumis* (including melon, cucumber and wild relatives), *Citrullus* (watermelon and the wild relative C. *colocynthis*), *Lagenaria*, *Momordica*, *Trichosanthes*, *Benincasa*, *Cucurbita*, *Ecballium* and *Luffa*, grown in greenhouse in Almería, Spain.

The enormous population of whitefly in that area permitted us to evaluate the resistance to *Bemisia* feeding and reproduction in natural conditions. The 30 entries (12-15 plants per accession) of the 18 species were cultivated in the same greenhouse in sandy soil with drip irrigation in the period July-October 1992. Adult population as well as eggs which settled on the leaves were scored and evaluated in a range 0-5. The aspect of the whole plant and production of fruits were also scored. Table 1 shows the results of whitefly attack on the different entries studied.

All the melon cultivars and the cucumber line were severely affected by whitefly while the *agrestis* -type melon used in this experiment showed low susceptibility. This observation confirms the results reported by MacCreight (7) in a study made in another geographic area with a series of *agrestis*-type melons in which he found a certain degree of resistance to *Bemisia* in some entries.

We have also observed a different response within the entries of the wild relatives *Cucumis africanus*, *C. anguria*, *C. myriocarpus*, *C. dipsaceus* and *C. zeyheri*, but all of them showed several degrees of susceptibility to whitefly. On the contrary, the three accesions of the other wild relative, *Cucumis metuliferus*, were completely resistant to the pest. Since resistance to other plagues and diseases have been described in this species (see a revision in 10) its behavior versus *Bemisia* is very interesting and we will try to evaluate and corroborate these results in subsequent experiments.

Citrullus lanatus (watermelon) plants were completely devastated as a consequence of *Bemisia* attack. The three accessions of their wild relative *Citrullus colocynthis* were susceptible but not as seriously damaged.

Benincasa hispida was as susceptible as melon, cucumber and watermelon. The two entries of *Lagenaria siceraria* were affected by whitefly although at a different level. However, the two species of *Luffa* showed completely different response: *L. acutangula* was susceptible while *L. cylindrica* appeared resistant and free of whitefly. Similarly, all the entries of *Ecballium elaterium*, *Momordica balsamina* and *Trichosanthes cucumerina* appeared permanently free of insects throughout the culture cycle in spite of being cultivated in the same greenhouse together with the other starved species and with a very high population of *Bemisia* in the environment.

Although the real resistance to *Bemisia* should be confirmed in additional cycles of culture and under different culture conditions, these results can be useful for successive breeding programs. The lesser susceptibility of some lines of *C. melo* var. *agrestis* (7) (see also Table 1) could be relevant since, in this case, there is not any cross ability barriers with the cultivars of melon. On the other hand, to profit from the sources of resistance present in the wild relative *Cucumis metuliferus* or in the genera *Ecballium, Luffa, Momordica* or *Trichosanthes*, it would be necessary to apply a program of somatic hybridization by protoplast fusion. At present, our group is carrying out a wide program of this kind doing symmetric as well as asymmetric hybridizations between melon as recipient species and several of the wild species as donors of desirable genes.

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Table 1. Susceptibility of different cucurbits to the whitefly *Bemisia tabacci* .

Species and line	Source and accession	Whitefly Population	
		Adults	Eggs
Cucumis melo 'Cant. Charentais'	Clause	+++++	+++++
Cucumis melo 'Valenciano Tardío'	Intersemillas	+++++	+++++
Cucumis melo 'Tokio Early'	J. Abadía (CEBAS, Murcia)	+++++	+++++
Cucumis sativus 'Marketer'	Clause	+++++	+++++
Cucumis melo var. *agrestis*	Gatersleben CuM 190/1982	+	+
Cucumis africanus L5	IVT Gbnr.1984	++	-
Cucumis anguria var. longipes L1	Pretoria, 71113	+	+
Cucumis anguria var. longipes L3	IVT Gbnr. 1790	+++	+++
Cucumis dipsaceus	Gatersleben Ha 408/1981	++	++
Cucumis metuliferus L1	IVT Gbnr.1802	-	-
Cucumis metuliferus L4	Gatersleben CuC 16/1981	-	-
Cucumis metuliferus L3	Pretoria, 78263	-	-
Cucumis myriocarpus L1	IVT Gbnr. 1979	+++++	+++++
Cucumis myriocarpus L2	IVT Gbnr. 1051	++	++
Cucumis zeyheri L1	IVT Gbnr. 1786	++++	+++
Cucumis zeyheri L2	IVT Gbnr. 1785	++	+
Cucumis zeyheri L3	Pretoria, 77048	+++	++
Citrullus lanatus 'Dulce Maravilla'	F1 Hybrid Sluis&Groot	+++++	+++++
Citrullus colocynthis 'Rhodes'	Edisto R-309	++	+++
Citrullus colocynthis 'Argelia'	UPV-87 (Argelia)	+	+++
Citrullus colocynthis 'Canarias'	UPV-85 (Gran Canaria)	++	+++
Benincasa hispida	Gatersleben BEN 14/1982	+++++	+++++
Cucurbita martinezii	INRA, Montfavet, 1981	++	-
Ecballium elaterium	UPV-EE87	-	-
Lagenaria siceraria 'Murcia'	UPV.ETSIA, 87	++++	++++
Lagenaria siceraria 'Gatersleben'	Gatersleben LAG 41/1986	++	+++
Luffa cylindrica	Gatersleben LUF 25/1985	-	-
Luffa acutangula	Gatersleben LUF 19/1982	+++	+++
Momordica balsamina	Gatersleben MOM 16/1985	-	-
Trichosanthes cucumerina	Gatersleben TCH 4/1982	-	-

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GATERSLEBEN: Zentralinstitut für Genetik und Kulturpflanzenforschung (ZIGuK), DDR-4325 Gatersleben.
INRA-Montfavet: Institut National de la Recherche Agronomique. Station d'Amelioration des Plantes Maraicheres, Domaine Sainte Maurice, 84140, Montfavet, France.
INTERSEMILLAS: Intersemillas, S.A. Quart de Poblet, Valencia, Spain.
CLAUSE: Clause Graines d'Elite.91221 Bretigny-sur-Orge. Cedex. France
CEBAS: Centro de Edafología y Biología Aplicada del Segura, Murcia, Spain.
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Cucumber, Melon and Squash Germplasm from the Cornell Collection

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A number of accessions and breeding lines representing H.M. Munger's *Cucumis* and *Cucurbita* germplasm collection have been increased in recent years and are available to interested workers. This work was supported in part by Hortinnova and Petoseed Co.

Cucumis

Cucumber

Tokyo Long Green
Yomaki Source of high level PMR
Hawaii 60G-10 " " " " bred by Gilbert
Denna's Dwarf Tablegreen type
Marketmore 80 *Bw* (Bacterial Wilt Resistance)
Albion (PMR551) *Bw* " "
additional cucumber germplasm listed in Munger (1985)

Melon

Iroquois
PMR Iroquois
PMR Monoecious Iroquois
Delicious 51
PMR Delicious 51 (typical Delicious 51)
PD 23 selection 23, PMR Delicious 51, male parent of 'Progress' hybrid
PB 13 Minn 90-36, Fusarium resistant, similar to PB12 (Minn 99-36), the resistant parent of Iroquois
MR 324, 335 Eastern type with low level cucumber mosaic (CM) resistance
M (= MMR) 324, 328, 339 Eastern type with low level CM resistance + monoecious
PM (= PMM) 324, 328, 339 " " " " " " " " + PMR
PPM 339 Monoecious, PMR + papaya ringspot resistance
ZPPM 339 PPM 339 + ZYM resistance
PMR Charentais
Siberian Honeydew
C. melo conomon 'Freeman cucumber' source of CM resistance (Enzie 1943)
C. melo dudaim Source of monoecious (Wall 1967) and WM resistance
PI 414723-4 S_3 Source of WMV and ZYM resistance

Cucurbita

Genic male sterility in Eskandarany Egyptian squash (*C. pepo*)
Male sterile EPS type derived from Eskandarany
Male sterile Caserta type " " "
CMR 469 CMV-resistant yellow *C. pepo* derived from *C. martinezii*
W225 " " " " " " " (viny)
PI 174186 selected for scab resistance
Early Prolific Straightneck x PI 174186 F_2 and backcrosses
PI 174183 selected for scab resistance
C. martinezii Source of powdery mildew resistance (Contin and Munger 1977), CMV resistance and gummy stem blight resistance
C. pepo x *C. moschata* bush butternut populations (Munger 1990)
C. mixta Variant, silver skin gourd

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Gene List Update for Cucumber

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Lists of the genes for cucumber (*Cucumis sativus* L.) have been published previously (12, 16). However, in the interest of updating the information, following is a list of the 43 genes introduced or modified since the last report (13). That makes a total of (105 plus 43 minus 2 renamed) 146 reported gene mutants.

A wild type cultivar has not been proposed for cucumber as the reference for all "+" alleles. 'Marglobe' tomato has been chosen as the normal type for genetic studies in that crop. Perhaps 'Wisconsin SMR 18' should be the choice for cucumber, since it is an inbred that is used widely in genetic studies. In addition, it has many dominant and wild-type alleles.

The genes on the following list are of four categories, seedling markers, virus resistance, isozymes, and fruit mutants (Table 1). The seedling markers include a reclassification of *gc* as *ls* (25, 26), and a new group produced using gamma rays on pollen (4, 5). The fruit mutants are green mature fruit, *gn* (11), and palisade epidermis, *Pe* (2). Isozyme mutants now include 14 markers, many of which are linked (6). One virus resistance gene should be renamed according to the revised taxonomy of watermelon mosaic virus. Watermelon mosaic virus-1 was renamed papaya ringspot virus-watermelon strain (PRSV-W), so *wmv-1-1* should be renamed *prsv*, retaining *wmv-1-1* as a synonym. Watermelon mosaic virus-2 is renamed watermelon mosaic virus (WMV). Thus, the dominant gene for resistance to WMV does not change its symbol, remaining *Wmv*.

Isozyme variant nomenclature for this gene list follows the form according to Staub et al. (22), such that loci coding for enzymes (e.g. glutamine dehydrogenase, G2DH) are designated as abbreviations, where the first letter is capitalized (e.g. G2dh). If an enzyme system is conditioned by multiple loci, then those are designated by hyphenated numbers, which are numbered from most cathodal to most anodal and enclosed in parentheses. The most common allele of any particular isozyme is designated 100, and all other alleles for that enzyme are assigned a value based on their mobility relative to that allele.

Researchers are encouraged to send reports of new genes, as well as seed samples to the cucumber gene curators (Todd C. Wehner, Jack E. Staub and Richard W. Robinson). Please let me know of any omissions or errors in the following list.

Table 1. The 43 new or revised genes of cucumber*.

Gene	Synonym	Character	Reference
al		*albino cotyledons.* White cotyledons and slightly light green hypocotyl; dying before first true leaf stage. Wild type *al+* from 'Nishiki-suyo'; *al* from M2 line from pollen irradiation.	4,5
by	*bu*	*bushy.* Short internodes; normal seed viability. Wild type *by+* from 'Borszczagowski'; *by* from induced mutation of 'Borszczagowski'. Linked with *F* and *gy*, not with *B* or *bi*.	9
chp		*choripetalous.* Small first true leaf; choripetalous flowers; glossy ovary; small fruits; few seeds. Wild type *chp+* from 'Borszczagowski'; *chp* from chemically induced mutation.	7
cp-2		*compact-2.* Short internodes; small seeds; similar to *cp*, but allelism not checked. Wild type *cp-2+* from 'Borszczagowski'; *cp-2* from induced mutation of 'Borszczagowski' called W97. Not linked with *B* or *F*; interacts with *by* to produce super dwarf.	10
de-2		*determinate-2.* Main stem growth ceases after 3 to 10 nodes, producing flowers at the apex; smooth, fragile, dark-green leaves; similar to *de*, but not checked for allelism. Wild type *de-2+* from 'Borszczagowski'; *de-2* from W-sk mutant induced by ethylene-imine from 'Borszczagowski'.	21
dm-1	*dm*?	*downy mildew resistance-1.* One of three genes for resistance to downy mildew caused by Pseudoperonospora cubensis (Berk & Curt). Wild type *dm-1+* from Wisconsin SMR 18; *dm-1* from WI 4783. Not checked for allelism with *dm*.	1
dm-2		*downy mildew resistance-2.* One of three genes for resistance to downy mildew caused by Pseudoperonospora cubensis (Berk & Curt). Wild type *dm-2+* from Wisconsin SMR 18; *dm-2* from WI 4783. Not checked for allelism with *dm*.	1
dm-3		*downy mildew resistance-3.* One of three genes for resistance to downy mildew caused by Pseudoperonospora cubensis (Berk & Curt). Wild type *dm-3+* from Wisconsin SMR 18; *dm-3* from WI 4783. Not checked for allelism with *dm*.	1
dvl-2	*dl-2*	*divided leaf-2.* Divided leaves after the 2nd true leaf; flower petals free; similar to *dvl*, but allelism not checked. Wild type *dvl-2+* from 'Borszczagowski'; *dvl-2* from mutant induced by ethylene-imine from 'Borszczagowski'.	19
dwc-1		*dwarf cotyledons-1.* Small cotyledons; late germination; small first true leaf; died after 3rd true leaf. Wild type *dwc-1+* from 'Nishiki-suyo'; *dwc-1* from M2 line from pollen irradiation.	4,5
dwc-2		*dwarf cotyledons-2.* Small cotyledons; late germination; small first true leaf. Wild type *dwc-2+* from 'Nishiki-suyo'; *dwc-2* from M2 line from pollen irradiation.	4,5
G2dh		*Glutamine dehydrogenase* (E.C.# 1.1.1.29). Isozyme variant found segregating in PI 285606; 5 alleles observed.	6
gi-2		*ginkgo-2.* Spatulate leaf blade with reduced lobing and altered veins; recognizable at the 2nd true leaf stage; similar to gi, fertile instead of sterile. Wild type *gi-2+* from 'Borszczagowski'; *gi-2* from mutant in the Kubicki collection.	19
gig		*gigantism.* First leaf larger than normal. Wild type *gig+* from 'Borszczagowski'; *gig* from chemically induced mutation.	8

gn		*green mature fruit.* Green mature fruits when *R+R+ gngn*; cream colored when *R+R+ gn+gn+*; orange when *R_*. Wild type *gn+* from 'Chipper', SMR 58 and PI 165509; *gn* from TAMU 830397.	11
Gpi-1		*Glucose phosphate isomerase* (E.C.# 5.3.1.9). Isozyme variant found segregating (1 and 2) in PI 176524, 200815, 249561, 422192, 432854, 436608; 3 alleles observed.	6
Gr-1		*Glutathione reductase-1* (E.C.# 1.6.4.2). Isozyme variant found segregating in PI 109275; 5 alleles observed.	6
hl		*heart leaf.* Heart shaped leaves. Wild type *hl+* from Wisconsin SMR 18; *hl* from WI 2757. Linked with *ns* and *ss* in the linkage group with *Tu-u-D-pm*.	23
hn		*horn like cotyledons.* Cotyledons shaped like bull horns; true leaves with round shape rather than normal lobes; circular rather than ribbed stem cross section; divided petals; spineless fruits; pollen fertile, but seed sterile. Wild type *hn+* from 'Nishiki-suyo'; *hn* from M_2 line from pollen irradiation.	4,5
hsl		*heart shaped leaves.* Leaves heart shaped rather than lobed; tendrils branched. Wild type *hsl+* from 'Nishiki-suyo'; *hsl* from M_2 line from pollen irradiation.	4,5
Idh		*Isocitrate dehydrogenase* (E.C.# 1.1.1.42). Isozyme variant found segregating in PI 183967, 215589; 2 alleles observed.	6
lg-1		*light green cotyledons-1.* Light green cotyledons, turning dark green; light green true leaves, turning dark green; poorly developed stamens. Wild type *lg-1+* from 'Nishiki-suyo'; *lg-1* from M_2 line from pollen irradiation.	4,5
lg-2		*light green cotyledons-2.* Light green cotyledons, turning dark green (faster than lg-1; light green true leaves, turning dark green; normal stamens. Wild type *lg-2+* from 'Nishiki-suyo'; *lg-2* from M_2 line from pollen irradiation.	4,5
ls	*gc*	*light sensitive.* Yellow cotyledons, lethal in high light. Abstract gave *gc* as symbol; article that followed gave *ls* as symbol. Mutant *ls* from a selection of 'Burpless Hybrid'.	25,26
Mdh-1		*Malate dehydrogenase-1* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 171613, 209064, 326594; 3 alleles observed.	6
Mdh-2		*Malate dehydrogenase-2* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 174164, 185690, 357835, 419214; 2 alleles observed.	6
Mdh-3		*Malate dehydrogenase-3* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 255236, 267942, 432854, 432887; 2 alleles observed.	6
Mpi-2		*Mannose phosphate isomerase* (E.C.# 5.3.1.8). Isozyme variant found segregating in PI 109275, 175692, 200815, 209064, 263049, 354952; 2 alleles observed.	6
mpy	*mpi*	*male pygmy.* Dwarf plant with only staminate flowers. Wild type *mpy+* from Wisconsin SMR 12; *mpy* from Gnome 1, a selection of 'Rochford's Improved'.	14
Pe		*Palisade epidermis.* Epidermal cells arranged perpendicular to the fruit surface. Wild type *Pe* from 'Wisconsin SMR 18', 'Spartan Salad' and Gy 2 compact; *pe* from WI 2757.	2
Pep-la		*Peptidase with leucyl-leucine* (E.C.# 3.4.13.11). Isozyme variant found segregating in PI 169380, 175692, 263049, 289698, 354952; 5 alleles observed.	6

Pep-pap		*Peptidase with phenylalanyl-L-proline* (E.C.# 3.4.13.11). Isozyme variant found segregating in PI 163213, 188749, 432861; 2 alleles observed.	6
Per-4		*Peroxidase* (E.C.# 1.11.1.7). Isozyme variant found segregating in PI 215589; 2 alleles observed.	6
Pgd-1		*Phosphogluconate dehydrogenase-1* (E.C.# 1.1.1.43). Isozyme variant found segregating in PI 169380, 175692, 222782; 2 alleles observed.	6
Pgd-2		*Phosphogluconate dehydrogenase-2* (E.C.# 1.1.1.43). Isozyme variant found segregating in PI 171613, 177364, 188749, 263049, 285606, 289698, 354952, 419214, 432858; 2 alleles observed.	6
Pgm-1		*Phosphoglucomutase* (E.C.# 5.4.2.2). Isozyme variant found segregating in PI 171613, 177364, 188749, 263049, 264229, 285606, 289698, 354952; 2 alleles observed.	6
prsv	*wmv-1-1*	*watermelon mosaic virus 1 resistance.* Resistance to papaya ringspot virus (formerly watermelon mosaic virus 1). Wild type *prsv+* from WI 2757; *prsv* from 'Surinam'.	24
sh		*short hypocotyl.* Hypocotyl of seedlings 2/3 the length of normal. Wild type *sh+* from 'Borszczagowski'; *sh* from khp, an induced mutant from 'Borszczagowski'.	20
shl		*shrunken leaves.* First and 2nd true leaves smaller than normal; later leaves becoming normal; slow growth; often dying before fruit set. Wild type *shl+* from 'Nishiki-suyo'; *shl* from M_2 line from pollen irradiation.	4,5
sp-2		*short petiole-2.* Leaf petioles shorter, darker green than normal at 2-leaf stage; crinkled leaves with slow development; short hypocotyl and stem; little branching. Not tested for allelism with *sp*. Wild type *sp-2+* from 'Borszczagowski'; *sp-2* from chemically induced mutation.	18
wi		*wilty leaves.* Leaves wilting in the field, but not in shaded greenhouse; weak growth; no fruiting. Wild type *wi+* from 'Nishiki-suyo'; *wi* from M_2 line from pollen irradiation.	4,5
wy		*wavy rimed cotyledons.* Wavy rimed cotyledons, with white centers; true leaves normal. Wild type *wy+* from 'Nishiki-suyo'; *wy* from M_2 line from pollen irradiation.	4,5
ys		*yellow stem.* Yellow cotyledons, becoming cream-colored; cream-colored stem, petiole and leaf veins; short petiole; short internode. Wild type *ys+* from 'Borszczagowski'; *ys* from chemically induced mutation.	17

*Isozyme nomenclature follows a modified form (22) previously described by Richmond (15) and Gottlieb (3).

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Scientists should consult the above list as well as the rules of gene nomenclature for the Cucurbitaceae (16) before choosing a gene name and symbol. That will avoid duplication of gene names and symbols. The rules of gene nomenclature were adopted in order to provide guidelines for naming and symbolizing genes. Scientists are urged to contact members of the Gene List committee regarding rules and gene symbols.

Gene List Committee:

Cucumber	T. C. Wehner
Cucurbita spp.	R. W. Robinson
	M. G. Hutton
Melon	M. Pitrat
Watermelon	W. R. Henderson
Other genera	R. W. Robinson

Gene Nomenclature for the Cucurbitaceae

[From: **Robinson, R.W., H.M. Munger, T.W. Whitaker and G.W. Bohn. 1976. Genes of the Cucurbitaceae. HortScience 11:554-568.**]

1. Names of genes should describe a characteristic feature of the mutant type in a minimum of adjectives and/or nouns in English or Latin.
2. Genes are symbolized by italicized Roman letters, the first letter of the symbol being the same as that for the name. A minimum number of additional letters are added to distinguish each symbol.
3. The first letter of the symbol and name is capitalized if the mutant gene is dominant, and all letters of the symbol and name are in lower case if the mutant gene is recessive to the normal type. The normal allele of a mutant gene is represented by the symbol "+", or where it is needed for clarity, the symbol of the mutant gene followed by the superscript "+". The primitive form of each species shall represent the + allele for each gene, except where long usage has established a symbol named for the allele possessed by the normal type rather than the mutant.
4. A gene symbol shall not be assigned to a character unless supported by statistically valid segregation data for the gene.
5. Mimics, i.e. different mutants having similar phenotypes, may either have distinctive names and symbols or be assigned the same gene symbol, followed by a hyphen and distinguishing Arabic numeral or Roman letter printed at the same level as the symbol. The suffix-1 is used, or may be understood and not used, for the original gene in a mimic series. It is recommended that allelism tests be made with a mimic before a new gene symbol is assigned to it.
6. Multiple alleles have the same symbol, followed by a Roman letter or Arabic number superscript. Similarities in phenotype are insufficient to establish multiple alleles; the allelism test must be made.
7. Indistinguishable alleles, i.e. alleles at the same locus with identical phenotypes, preferably should be given the same symbol. If distinctive symbols are assigned to alleles that are apparent reoccurrences of the same mutation, however, they shall have the same symbol with distinguishing numbers or letters in parentheses as superscripts.
8. Modifying genes may have a symbol for an appropriate name, such as intensifier, suppressor, or inhibitor, followed by a hyphen and the symbol of the allele affected. Alternatively, they may be given a distinctive name unaccompanied by the symbol of the gene modified.
9. In cases of the same symbol being assigned to different genes, or more than one symbol designated for the same gene, priority in publication will be the primary criterion for establishing the preferred symbol. Incorrectly assigned symbols will be enclosed in parentheses on the gene lists.

[From: **CGC Gene List Committee. 1982. Update of cucurbit gene list and nomenclature rules. CGC 5:62-66.**]

The same symbol shall not be used for nonallelic genes of different *Cucurbita* species. Allelic genes of compatible species are designated with the same symbol for the locus.

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James M. Gaggero
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M. Allen Stevens
Paul Thomas
Anna Trulson
Jon Watterson
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Larry A. Hollar

Florida
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Gary Elmstrom
Larry D. Knerr
Mike Meadows
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Deena Decker Walters
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Tom V. Williams
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Covenant and By-Laws of the Cucurbit Genetics Cooperative

ARTICLE I. **Organization and Purposes**

The Cucurbit Genetics Cooperative is an informal, unincorporated scientific society (hereinafter designated "CGC") organized without capital stock and intended not for business or profit but for the advancement of science and education in the field of genetics of cucurbits (Family: Cucurbitaceae). Its purposes include the following: to serve as a clearing house for scientists of the world interested in the genetics and breeding of cucurbits, to serve as a medium of exchange for information and materials of mutual interest, to assist in the publication of studies in the aforementioned field, and to accept and administer funds for the purposes indicated.

ARTICLE II. **Membership and Dues**

The membership of the CGC shall consist solely of active members; an active member is defined as any person who is actively interested in genetics and breeding of cucurbits and who pays biennial dues. Memberships are arranged by correspondence with the Chairman of the Coordinating Committee.

The amount of biennial dues shall be proposed by the Coordinating Committee and fixed, subject to approval at the Annual Meeting of the CGC. The amount of biennial dues shall remain constant until such time that the Coordinating Committee estimates that a change is necessary in order to compensate for a fund balance deemed excessive or inadequate to meet costs of the CGC.

Members who fail to pay their current biennial dues within the first six months of the biennium are dropped from active membership. Such members may be reinstated upon payment of the respective dues.

ARTICLE III. **Committees**

1. The Coordinating Committee shall govern policies and activities of the CGC. It shall consist of six members elected in order to represent areas of interest and importance in the field. The Coordinating Committee shall select its Chairman, who shall serve as a spokesman of the CGC, as well as its Secretary and Treasurer.
2. The Gene List Committee, consisting of five members, shall be responsible for formulating rules regulating the naming and symbolizing of genes, chromosomal alterations, or other hereditary modifications of the cucurbits. It shall record all newly reported mutations and periodically report lists of them in the Report of the CGC. It shall keep a record of all information pertaining to cucurbit linkages and periodically issue revised linkage maps in the Report of the CGC. Each committee member shall be responsible for genes and linkages of one of the following groups: cucumber, *Cucurbita* spp., muskmelon, watermelon, and other genera and species.
3. Other committees may be selected by the Coordinating Committee as the need for fulfilling other functions arises.

ARTICLE IV. **Election and Appointment of Committees**

1. The Chairman will serve an indefinite term while other members of the Coordinating Committee shall be elected for ten-year terms, replacement of a single retiring member taking place every other year. Election of a new member shall take place as follows: A Nominating Committee of three members shall be appointed by the Coordinating Committee. The aforesaid Nominating Committee shall nominate

candidates for an anticipated opening on the Coordinating Committee, the number of nominees being at their discretion. The nominations shall be announced and election held by open ballot at the Annual Meeting of the CGC. The nominee receiving the highest number of votes shall be declared elected. The newly elected member shall take office immediately.

In the event of death or retirement of a member of the Coordinating Committee before the expiration of his/her term, he/she shall be replaced by an appointee of the Coordinating Committee.

Members of other committees shall be appointed by the Coordinating Committee.

ARTICLE V. **Publications**

1. One of the primary functions of the CGC shall be to issue an Annual Report each year. The Annual Report shall contain sections in which research results and information concerning the exchange of stocks can be published. It shall also contain the annual financial statement. Revised membership lists and other useful information shall be issued periodically. The Editor shall be appointed by the Coordinating Committee and shall retain office for as many years as the Coordinating Committee deems appropriate.
2. Payment of biennial dues shall entitle each member to a copy of the Annual Report, newsletters, and any other duplicated information intended for distribution to the membership. The aforementioned publications shall not be sent to members who are in arrears in the payment of dues. Back numbers of the Annual Report, available indefinitely, shall be sold to active members at a rate determined by the Coordinating Committee.

ARTICLE VI. **Meetings**

An Annual Meeting shall be held at such time and place as determined by the Coordinating Committee. Members shall be notified of time and place of meetings by notices in the Annual Report or by notices mailed not less than one month prior to the meeting. A financial report and information on enrollment of members shall be presented at the Annual Meeting. Other business of the Annual Meeting may include topics of agenda selected by the Coordinating Committee or any items that members may wish to present.

ARTICLE VII. **Fiscal Year**

The fiscal year of the CGC shall end on December 31.

ARTICLE VIII. **Amendments**

These By-Laws may be amended by simple majority of members voting by mail ballot, provided a copy of the proposed amendments has been mailed to all the active members of the CGC at least one month previous to the balloting deadline.

ARTICLE IX. **General Prohibitions**

Notwithstanding any provisions of the By-Laws or any document that might be susceptible to a contrary interpretation:

1. The CGC shall be organized and operated exclusively for scientific and educational purposes.
2. No part of the net earnings of the CGC shall or may under any circumstances inure to the benefit of any individual.

3. No part of the activities of the CGC shall consist of carrying on propaganda or otherwise attempting to influence legislation of any political unit.
4. The CGC shall not participate in, or intervene in (including the publishing or distribution of statements), any political campaign on behalf of a candidate for public office.
5. The CGC shall not be organized or operated for profit.
6. The CGC shall not:
   (a) lend any part of its income or corpus without the receipt of adequate security and a reasonable rate of interest to;
   (b) pay any compensation in excess of a reasonable allowance for salaries or other compensation for personal services rendered to;
   (c) make any part of its services available on a preferential basis to;
   (d) make any purchase of securities or any other property, for more than adequate consideration in money's worth from;
   (e) sell any securities or other property for less than adequate consideration in money or money's worth; or
   (f) engage in any other transactions which result in a substantial diversion of income or corpus to any officer, member of the Coordinating Committee, or substantial contributor to the CGC.

The prohibitions contained in this subsection (6) do not mean to imply that the CGC may make such loans, payments, sales, or purchases to anyone else, unless authority be given or implied by other provisions of the By-Laws.

ARTICLE X. **Distribution on Dissolution**

Upon dissolution of the CGC, the Coordinating Committee shall distribute the assets and accrued income to one or more scientific organizations as determined by the Committee, but which organization or organizations shall meet the limitations prescribed in sections 1-6 of Article IX.

Approvals:

W. Bemis

J. D. Norton

R. W. Robinson

W. R. Henderson

M. L. Robbins

R. L. Lower

Cucurbit Genetics Cooperative

Financial Statement

31 December 1992

Balance (31 December 1991)			**$4,026.69**
Receipts:			
	Dues & CGC back issue orders	$2,971.00	
	Interest on savings	$164.28	
	Total receipts		$3,135.28
Expenditures:			
	CGC Report No. 15 (1992)		
	Printing	$1,874.17	
	Mailing	$542.46	
	Call for papers (Report No. 16)	$108.35	
	Miscellaneous (envelopes, postage, etc.)	$135.92	
	U.S. FDIC bank fees	$9.90	
	Total expenses		$2,670.80
Balance (31 December 1992)			**$4,481.27**