Cucurbit Genetics Cooperative

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2005 & 2006

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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 individuals who have an interest in cucurbit genetics and breeding. CGC membership is on a biennial basis. For more information on CGC and its membership rates, visit our website (*http://www.umresearch.umd.edu/cgc/*, or *http://cuke.hort.ncsu.edu/cgc/*) or contact Tim Ng at (301) 405-4345 or *cucurbit.genetics.cooperative@gmail.com*.

CGC Reports are issued on an annual basis. The Reports include articles submitted by CGC 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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NEWS & COMMENT

RESEARCH REPORTS

30th Annual CGC Business Meeting (2006)

Todd C. CGC Chair, North Carolina State University, Raleigh, NC

The Cucurbit Genetics Cooperative met with the Cucurbitaceae 2006 conference in Asheville, North Carolina at 6 pm on September 18. The idea of having CGC available only on the web was discussed. It was decided to continue the print version of CGC until there was a larger percentage of the membership online with high speed connections.

Linda Wessel-Beaver presented an overview of CGC membership. The membership list has been expanded and updated. Conference attendees were encouraged to register for CGC membership, and many took advantage of the offer.

Angela Davis presented summary statistics and cost analyses on the annual CGC Reports, as well as an update on the forthcoming CGC Report No. 29 (2006). After considering the options, there was a unanimous vote to increase CGC membership dues to $20/year starting with CGC 30 (2007). Dues will be $30 for all three CGC volumes: 27 (2004), 28 (2005), and 29 (2006). Back issues continue to be offered for sale (subject to availability) at $10 per volume.

The CGC website has been updated and expanded. Issues 1through 22 have been typed and placed on the web. Issues 1 through 6 have been proofed.

Announcements were made on the upcoming EUCARPIA meeting in Avignon, France, as well as plans for Cucurbitaceae 2010.

Comments from the CGC Coordinating Committee

The Call for Papers for the 2007 Report (CGC Report No. 30) has been sent out. Papers should be submitted to the respective Coordinating Committee members by 31 December 2006. The report will be published by June 2007. As always, we are eager to hear from CGC members regarding our current activities and the future direction of CGC.

- Todd C. Wehner, chair and website editor
- Angela Davis, associate chair and print editor
- Linda Wessel-Beaver, associate chair and membership coordinator
- Tim Ng, associate chair and treasurer
- Jack E. Staub, assistant editor (cucumber)
- Kevin Crosby, assistant editor (melon)
- Gabriele Gusmini, assistant editor (*Cucurbita* spp.)
- Mark G. Hutton, assistant editor (other genera)
- Stephen R. King, assistant editor (watermelon)

The coordinating committee would like to thank Amy Helms and Anamari Holcomb for technical assistance.

Comments from 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 choosing 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 which 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: Nischit V. Shetty (curator) and Todd C. Wehner (assistant curator)
- Melon: Michael Pitrat (curator) and James D. McCreight (assistant curator)
- Other Genera: Mark G. Hutton (curator) and Deena Decker-Walters (assistant curator)
- Cucurbita spp.: Harry Paris (curator) and Richard W. Robinson (assistant curator)
- Watermelon: Todd C. Wehner (curator) and Stephen R. King (assistant curator)

Comments from the CGC Gene Curators

CGC has appointed Curators for the four major cultivated groups: cucumber, melon, watermelon and *Cucurbita* spp.

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: Nischit V. Shetty (curator) and Todd C. Wehner (assistant curator)
- Melon: Michael Pitrat (curator) and James D. McCreight (assistant curator)
- Other Genera: Mark G. Hutton (curator) and Deena Decker-Walters (assistant curator)
- *Cucurbita* spp.: Harry Paris (curator) and Richard W. Robinson (assistant curator)
- Watermelon: Todd C. Wehner (curator) and Stephen R. King (assistant curator)

Pickling Cucumber Improvement Committee

The Pickling Cucumber Improvement Committee met with the Cucurbitaceae 2006 conference in Asheville, North Carolina at 5 pm on September 18. The committee developed a list of research priorities for cucumber. The next meeting will be with Pickle Packers International in Memphis, TN on October 2-4, 2007.

Proceedings from Cucurbitaceae 2006

Cucurbitaceae 2006 was held on 17-21 September 2006 in Asheville, North Carolina (USA), and was organized by G.J. Holmes, J.R. Schultheis, and T.C. Wehner at North Carolina State University, Raleigh, NC. The Proceedings are available as a 602 page book entitled *Cucurbitaceae Proceedings 2006* (81 papers). The cost of the book is $30 (includes mailing cost), and orders can be sent to T.C. Wehner. For more information, see: http://cuke.hort.ncsu.edu/cucurbit/meetings/ccrbtceae06mtg.html

2005 Watermelon Research and Development Working Group – 25th Annual Meeting

Stephen R. King
Texas A&M University, College Station, TX

The 25th annual meeting of the Watermelon Research and Development Working Group was held Sunday, February 6, 2005 in Little Rock, AR in conjunction with the Southern Association of Agricultural Scientists and the Southern Region of the American Society for Horticultural Sciences. Refreshments were sponsored by Syngena Seeds, so please let Xingping Zhang and the other Syngenta folks know that we really appreciate our sponsors!

The first item of business was seed company releases and updates. Xingping Zhang (Syngenta Seeds), Don Dobbs (Willhite Seed), Brenda Lanini (Harris Moran), Gary Elmstrom (Sunseeds), Glen Price (Sugar Creek Seeds) and Pete Suddarth (Abbott & Cobb) each gave updates on new products

and emerging problems facing the seed industry. These updates were followed by a talk by Tom Williams, Watermelon Consultant, on the success of the personal size seedless watermelon and then by P. Dittmar and J. Schultheis, North Carolina State University who talked about the characterization of the growth and development of commercially available watermelon cultivars. Statewide watermelon trial results were presented by Don Maynard, University of Florida who gave a review of Florida statewide watermelon trials and Steve King, Texas A&M University who reviewed Texas statewide watermelon trials for 2004. The morning session concluded with the topic of managing foliar diseases: John Damicon, Oklahoma State University, talked about controlling powdery mildew, anthracnose and downy mildew diseases in watermelon; Tony Keinath, Clemson University, talked about controlling gummy stem blight and preventing fungicide resistance in the greenhouse and field; and Kenny Seebold and Ron Gitaitis, University of Georgia talked about how to differentiate between *Acidovorax avenae* subsp. *citrulli* and *Acidovorax facilis*: why does it matter?

Following the lunch break, special presentations were provided by Steven Fore, Director of Research, National Watermelon Promotion Board, who talked about the watermelon consumer: what they know and how they respond in the retail market, and David Thompson, Rutgers University who gave an overview of the workshop on *Phytophthora capsici* in cucurbits that was held the previous day.

The afternoon session continued with the following research updates:

- G. Holmes, North Carolina State University. Forecasting long-distance movement of cucurbit downy mildew in 2005.
- W. Roberts, W. Fish and B. Bruton. Oklahoma State University and USDA-ARS. Grafted watermelon affects fruit quality.
- W. Roberts, W. Fish, B. Bruton and T. Popham. Oklahoma State University and USDA-ARS. Improving the fresh cut quality of watermelons through grafting and root stock selection.
- N. Guner and T. Wehner, North Carolina State University. Watermelon genes controlling fruit traits.
- A. Levi, C. Thomas, A. Davis, S. King, G. Gusmini, T. Wehner, Y. Xu, J. King and X. Zhang. USDA-ARS; Texas A&M University, North Carolina State University, Seminis, Inc, and Syngenta Seeds. Development of genetic linkage map and expressed sequence tag (EST) DNA library for watermelon.
- P. Perkins-Veazie, USDA-ARS. Lycopene, citruline, and low sugar watermelons for human health.
- A. Davis, T. Wehner, A. Levi and S. King. USDA-ARS, North Carolina State University and Texas A&M University. Update on powdery mildew resistance screening in watermelon.
- B. Bruton, P Roberts and R. Muchovej. USDA-ARS and University of Florida. Status of watermelon vine decline and fruit rot in Florida.

The meeting concluded with a discussion of Fusarium wilt differentials.

In addition to our refreshment sponsors, we are grateful to SAAS and SRASHS for providing support and a room for us to meet.

2006 Watermelon Research and Development Working Group – 26th Annual Meeting

Stephen R. King
Texas A&M University, College Station, TX

The 26th annual meeting of the Watermelon Research and Development Working Group was held Sunday, February 5, 2006 in Orlando, Florida in conjunction with the

Southern Association of Agricultural Scientists and the Southern Region of the American Society for Horticultural Sciences. Refreshments were sponsored by Harris Moran, so please let Brenda Lanini know that we really appreciate our sponsors!

Benny Bruton called the meeting to order and welcomed everyone and was followed by seed company reports. Brenda Lanini (Harris Moran), Fred McCuistion (Seminis, Inc), Gary Elmstrom (Sunseeds), Jamey Adams (Southwestern Vegetable Seed), Xingping Zhang (Syngenta Seeds), and Don Dobbs (Willhite Seed) gave updates and talked about new releases for their respective companies. These updates and discussions were followed by the following research topics: Don Dobbs, Willhite Seed, talked about Willhite's progress in wilt tolerance; Jonathan Schultheis, North Carolina State University talked about the upcoming Cucurbitaceae 2006 conference; Don Maynard, University of Florida talked about causes of occasional seediness in triploid watermelon; PJ Dittmar, DW Monks and JR Monks, North Carolina State University, talked about the effects of post-application halosufuron-methyl at various percents of coverage on watermelon.

The next topic was statewide watermelon trial reports for 2005, and included a review of Texas statewide watermelon trials by Juan Anciso, Larry Stein, Steve King and Bob Whitney of Texas A&M University; the 2005 Delaware seedless watermelon variety trial results was presented by Emmalea Ernest, Tracy Wootten and Ed Kee from the University of Delaware; an overview of the watermelon variety trials in Georgia was presented by George Boyhan from the University of Georgia; and the Seedless and mini-watermelon variety trials data for South Carolina was presented by Gilbert Miller of Clemson University.

Steven Fore, Director of Research for the National Watermelon Promotion Board, Orlando, FL presented the US watermelon consumer and market trends, which was followed by Bob Morrissey, Executive Director, National Watermelon Association, Plant City, FL, who presented the new outlook at the National Watermelon Association.

The following research reports were presented:

- P. Perkins-Veazie, USDA-ARS, Lane, OK. Changes in carotenoids and amino acids during processing of watermelons.
- J.A. Thies and A. Levi, USDA-ARS, Charleston, SC. Resistance to root-knot nematodes in watermelon plant introductions.
- M. Taylor, B. Bruton, W. Fish and W. Roberts. OSU and USDA-ARS, Lane, OK. Economic comparison between conventional versus grafted watermelon transplants.
- P. Roberts, S. Adkins and B. Bruton. University of Florida and USDA-ARS. Watermelon vine decline and fruit rot in Florida.
- A.Y. Tetteh and T.C. Wehner, North Carolina State University. Screening watermelon for resistance to powdery mildew race 2.
- A. Levi, A. Davis, P. Wechter and A. Hernandez, USDA-ARS. Developing and mapping expressed sequenced tags (ESTs) for watermelon.
- J. Schultheis and J. Anciso. North Carolina State University and Texas A&M University. Triploid watermelon yield as affected by spacing SP-1 at various plant intervals.
- W.R. Jester, M.L. Adams and G.J. Holmes, North Carolina State University. Comparison of cultural practices and fungicides for control of Phytophthora blight of watermelon
- K. Cushman, P. Roberts, R. Muchovej, J. Huan and T. Williams. University of Florida and Syngenta Seeds. Increased interest in grafted watermelons.

- R.L. Hassell, J. Schultheis, W.R. Jester, S.M. Olsen, D.N. Maynard and G. Miller. Clemson University, North Carolina State University and University of Florida. Yield and quality of mini triploid watermelon cultivars n diverse locations in the southeast.
- W. Roberts, B. Bruton, W. Fish and M. Taylor. Oklahoma State University and USDA-ARS. Effects of grafting on watermelon quality: year two.

U.S. Cucurbit Crop Germplasm Committee Update

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

The Cucurbit Crop Germplasm Committee met with the Cucurbitaceae 2006 conference in Asheville, North Carolina at 5:30 pm on September 19. The committee developed a list of research priorities for cucumber. The next meeting will be with Pickle Packers International in Memphis, TN on October 2-4, 2007.

Upcoming Meetings of Interest to Cucurbit Researchers

Cucurbit Crop Germplasm Committee
10 am, 19 July 2007, Westin-Kierland Hotel, Scottsdale, AZ, with the annual meeting of the American Society for Horticultural Science, James D. McCreight, USDA-ARS, Salinas, CA USA, Tel: 408-755-2864; Fax: 408-755-2866
http://www.ars-grin.gov/npgs/cgclist.html

Cucurbit Genetics Cooperative
9 am, 16 July 2007, Westin-Kierland Hotel, Scottsdale, AZ, with the annual meeting of the American Society for Horticultural Science, Todd C. Wehner, North Carolina State University, Raleigh, NC 27695-7609, Tel: 919-515-5363; Fax: 919-515-2505
http://cuke.hort.ncsu.edu/cgc/index.html

National Melon Research Group
21-24 May, 2008, Avignon, France, with EUCARPIA-Cucurbitaceae, James D. McCreight, USDA-ARS, Salinas, CA USA Tel: 408-755-2864; Fax: 408-755-2866

Pickling Cucumber Improvement Committee
21-24 May, 2008, Avignon, France, with EUCARPIA-Cucurbitaceae, Nischit V. Shetty, Seminis Vegetable Seeds, Tifton, GA 31793 USA, Tel: 229-386-8701; Fax: 229-386-8805

Cucurbita Research Group
21-24 May, 2008, Avignon, France, with EUCARPIA-Cucurbitaceae, Gabriele Gusmini, Syngenta Seeds, Naples, FL 34114 USA, Tel: 239-775-4090; Fax: 239-774-6852
http://cuke.hort.ncsu.edu/cgc/cgccucurbita/cgccucurbitamain.html

Watermelon Research Group
4 February 2007, Mobile, Alabama, with American Society for Horticultural Science, southern region. Benny Bruton, USDA-ARS, Lane OK 74555 USA, Tel: 580-889-7395
http://cuke.hort.ncsu.edu/cgc/wrg/wrgmain.html

EUCARPIA-Cucurbitaceae 2008
Under the aegis of EUCARPIA, the next meeting on Genetics and Breeding of Cucurbitaceae will be organized by INRA. It will be held in Avignon in the south of France on 21-24 May 2008. EUCARPIA-Cucurbitaceae 2008 intends to bring together all the researchers involved in cucurbit genetics and breeding to share new developments in all aspects of genetic resources, genetics and breeding, genomics and biotechnology. For more information, see http://www.inra.fr/cucurbitaceae2008

Upcoming Meetings & News of Interest

Organization/Meeting	Dates	Location	Contact
28th Annual Meeting of the Watermelon Research & Development Working Group	February, 2008	In conjunction with the 66th Annual Meeting of the Southern Region - American Society for Horticultural Science, Dallas, TX, USA	Stephen King srking@ag.tamu.edu
Cucurbit Crop Germplasm Committee Meeting	July 19, 2007 10:00-12:00 AM	In conjunction with American Society for Horticultural Science 2007, Scottsdale, AZ, USA	Jim McCreight jmccreight@pw.ars.usda.gov
Cucurbit Genetics Cooperative Report Business Meeting	July 16, 2007 9:00-10:00 AM	In conjunction with American Society for Horticultural Science 2007, Scottsdale, AZ, USA	Todd Whener todd_wehner@ncsu.edu
Pickle Packers International	Spring, 2008	Atlanta, GA, USA	1-800-240-3340 http://www.ilovepickles.org
***Cucurbita* Research Group**	May, 2008	In conjunction with IX EUCARPIA International Meeting on Cucurbitaceae Eucarpia 2008, Avignon, France	Gabriele Gusmini gabriele.gusmini@syngenta.com
IX EUCARPIA International Meeting on Cucurbitaceae Eucarpia 2008	May 21-24, 2008	Avignon, France	Nathalie Boissot Jean-Paul Bouchet Véronique Chovelon Catherine Dogimont Michel Pitrat http://www.eucarpia.org/index_euc_01.html

Control of Cucumber Grey Mold by Endophytic Bacteria

R. P. An and Q. Ma
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Abstract: Endophytic bacterial strains B12 and B13 isolated from cucumber leaves effectively controlled cucumber grey mold, *Botrytis cinerea*. Both culture broth and culture filtrates were effective in inhibiting spore germination and germtube elongation of *B. cinerea*. Preliminary studies on the effects of pH and temperature on stability of the culture filtrates in inhibition of the pathogen were made.

Introduction: Grey mold, *Botrytis cinerea*, is a widespread pathogen of economic importance in greenhouse and open-field cucumber cultivation. As chemical control is not always efficient, benign alternative methods of protection are becoming more attractive. The term endophyte refers to interior colonization of plants by microorganisms that do not have pathogenic effects on their hosts. Some bacterial endophytic species have been implicated in the promotion of plant growth and protection against pathogens (1-4, 12). Wilhelm et al. (13) demonstrated that *Bacillus subtilis* strains isolated from the xylem sap of healthy chestnut trees exhibited antifungal effects against *Cryphonectria parasitica* causing chestnut blight. *Neotyphodium* elevates host protection against pathogens, and improves survival of grasses under competition (5). Endophytic isolates of *Pezicula* were shown to produce fungicidally active metabolites that are toxic to pathogens of their hosts (9).

B12 and B13 are two bacterial strains that have been isolated from the leaves of cucumber. On PDA plates, they were observed to inhibit the growth of *Botrytis cinerea.* In the present study, the effects of culture broth and culture filtrates of these two endophytic strains against *Botrytis cinerea* on cucumber leaves and the effects of pH and temperature on stability of the culture filtrates in inhibition of the pathogen were studied.

Materials and Methods: *Endophytes, pathogen , and plant.* B12 and B13 are two endophytic bacterial strains that were isolated from the leaves of cucumber in Yangling, Shaanxi Province, China. The cucumber plants examined in this study were supplied by the Horticulture Department, Northwest A&F University. The pathogen, *Botrytis cinerea*, was obtained from Plant Pathology laboratory. The cultures were maintained on potato-dextrose agar (PDA) medium at 4°C; and fresh cultures were grown on PDA plates at 25°C before experimentation. Spore suspensions were prepared from ten-day-old PDA cultures by dislodging spores from the surface of the cultures with a sterile bacteriological loop in sterile distilled water. The concentration was adjusted to $5x10^6$ spores ml^{-1}.

Antagonist. Liquid cultures were grown in 250 ml flasks containing 100 ml of nutrient broth (NB) which had previously been added using four sterile bacteriological loops of the cultures. Flasks were then incubated on a rotary shaker (170rpm) at 28°C for 48 h. The concentration was adjusted to $5x10^9$ CFU/ml. Culture filtrates were subsequently prepared by filtering the supernatant of centrifuged cultures of antagonist through a 0.22 μm polycarbonate membrane filter.

Antagonism in vitro. To evaluate the effects of culture filtrates on control of grey mold on leaves of cucumber, 6-mm-diameter callus from three-day-old cultures of *Botrytis cinerea* grown on PDA plates were cut off and then placed on cucumber leaves that had been previously sprayed with 2ml of the culture filtrates under serial dilutions of 1x, 10x, 20x, 50x, and 100x, with sterile distilled water as control. Then the leaves were placed in Petri dishes at 25°C. There were three replicate trials of ten leaves arranged in a completely randomizated design. The lesion diameter was recorded after four days. This experiment was repeated three times.

The effects of liquid cultures on spore germination and germtube elongation of the pathogen were assessed in potato dextrose broth (PDB). One-hundred-microliter (100 µl) spores suspension of $5x10^6$ spores ml^{-1} culture broth containing bacteria at $5x10^7$, $5x10^8$, $5x10^9$ CFU/ml concentrations, and culture filtrates, plus sterile distilled water were added into 10 ml glass tubes containing 5 ml PDB. Then they were placed on a rotary shaker (140rpm) at 25°C for 20h. No fewer than 100 spores were observed microscopically per replicate to record germination and germtube length. This experiment was repeated twice (6).

The stability of culture filtrates. Twenty ml glass tubes that contained 10 ml culture filtrates were placed in water bathes for 20 min each at 50, 60, 70, 80, 90 and 100°C before experimentation. The pH of other culture broths were adjusted each at 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0, 10.0, 11.0 and 12.0 with HCl or NaOH. Subsequently, 6-mm-diameter callus from 3-day-old cultures of *Botrytis cinerea* on PDA plates were taken and placed on PDA plates which contained 1ml of culture broth containing bacteria of $5x10^9$ CFU/ml, culture filtrates, sterile distilled water, and 20ml PDA. The lesion diameter was measured 96 h later. This experiment, containing three replications, was repeated three times.

Results: *The effect of culture filtrates against Botrytis cinerea on detached leaves of cucumber.* Culture filtrates were effective in inhibiting the development of disease on detached leaves of cucumber (Table 1). The pathogen was controlled at the high concentrations, the inhibition rate of B12 and B13 were 83.2 (± 3.2) % and 81.4(± 3.1) %, respectively.

Effect of B12 and B13 against Botrytis cinerea in vitro. Spore germination of *Botrytis cinerea* in PDB was significantly inhibited as the concentration of cultures broth increased ($P<0.05$) (Table1). Spore germination rates treated with $5x10^9$ CFU/ml of B12 and B13 culture broths had the most pronounced effects; being 5.5(±0.2) % and 8.6 (±0.4) %, respectively. The germtube length of the pathogen also decreased significantly compared to the control ($P<0.05$). The germtube lengths treated with $5x10^9$ CFU/ml cultures broth of the strains B12 and B13 were 25.9 (± 2.7) µm and 33.4 (±3.1) µm, respectively. Spore germination and germtube elongation of the pathogen were also significantly inhibited by culture filtrates, suggesting that in the culture filtrates there might be some metabolites produced toxic to the pathogen. The inhibition effect was similar with cultures broth at $5x10^9$ CFU/ml. In general, B12 had a more pronounced effect than B13 did in inhibiting *B. cinerea*.

The stability of culture filtrates. Culture filtrates of the two strains were stable at high temperatures, and although the effects on inhibition rate of the pathogen decreased slightly, the biocontrol effect was stable (Figure 1).

Culture filtrates of the two strains were stable against the pathogen at pH values between 6.0 and 9.0 (Figure 2). The effects of pH in culture filtrates on inhibition rate of pathogen decreased with the increase of alkalinity or acidity.

Discussion: Microbial endophytes are typically defined as microorganisms that are detected after surface sterilization of a plant part (7), and are assumed to originate from seed and/or the surrounding growing environment. Van Buren et al. (11) demonstrated that 32% of 192 endophytic bacterial strains isolated from potato stems exhibited biocontrol activity against the bacterial ring rot pathogen. Results of the present study showed that endophytic bacterial strains isolated from cucumber leaves can effectively control *Botrytis cinerea*, and that both of culture broth and culture filtrate types examined were effective in inhibiting the spore germination and germtube elongation of *B. cinerea*. We agree with Reiter (8) that endophytes represent a promising source of biocontrol strains, and that their use may be more successful than that of rhizosphere bacteria due to less competition with other bacteria in the apoplast.

Seghers et al. (10) demonstrated that agricultural practices significantly influence certain populations of the root endophytic community. Results of Reiter et al. (8) suggest that similar phylogenetic groups and genera, but different species and strains, were present in the different plant varieties. Our preliminary investigation indicates that differing cultivars might contain different endophytic communities. Thus, biocontrol mechanisms need further study. It is likely from such studies that the interactions among plants, pathogens, and bacterial endophytic communities will be an active field of research in the future.

Acknowledgements:

We wish to thank Dr. Jack E. Staub for his excellent reviewing and correction for our manuscript. This project was financially supported in part by the Program for Changjiang Scholars and Innovative Research Team in the University (No.200558) and the Yangling Foundation of Sci-Tch Development of Agriculture.

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Table 1. The effect of culture endophytic bacterial filtrates (B12 and B13) against *Botrytis cinerea* on detached leaves of cucumber

Serial dilutions	Inhibition rate (%)	
	B12	B13
1x	83.2 (± 3.2) d	81.4 (± 3.1) c
10x	66.5 (± 2.9) c	62.6 (± 2.7) c
20x	46.8 (± 2.5) bc	39.4 (± 2.3) bc
50x	15.7 (± 2.1) b	13.5 (± 2.0) b
100x	2.5 (± 1.3) a	0 (± 0) a

Each value is the mean of three trials(±SE). Values followed by different letters are statistically different at P = 0.05 according to Duncan's multiple range test.

Table 2. The effects of endophytic bacterial strains on spore germination and germtube elongation of *Botrytis cinerea* spores

Treatments	Spore germination rate (%)		Germtube length (μm)	
	B12	B13	B12	B13
Cultures broth ($5x10^7$ CFU / ml)	34.0 (± 3.2) d	56.5 (± 3.5) d	39.2 (± 3.4) d	56.7 (± 3.7) d
Cultures broth ($5x10^8$ CFU / ml)	12.6 (± 2.5) c	21.5 (± 2.6) c	31.5 (± 3.1) c	44.5 (± 3.6) c
Cultures broth ($5x10^9$ CFU / ml)	5.5 (± 0.2) b	8.6 (± 0.4) b	25.9 (± 2.7) b	33.4 (± 3.1) b
Culture filtrates	9.8 (± 0) c	15.4 (± 2.3) b	28.7 (± 2.9) c	38.3 (± 3.4) b
Sterile distilled water	98.5 (± 0) a		164.5 (± 3.8) a	

Each value is the mean of three trials(±standard error). Values in each row followed by the different letter are significantly different at P = 0.05 according to Duncan's multiple range test.

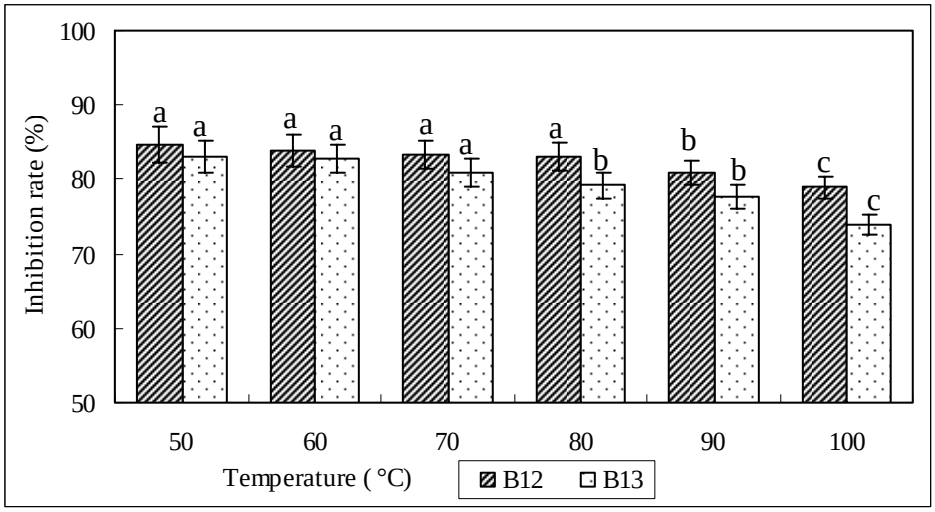

Fig. 1. The effects of temperature on inhibition rate of culture filtrates. Inhibition rates are the mean of three trials. Values followed by the different letters are statistically different at P = 0.05 according to Duncan's multiple range test.

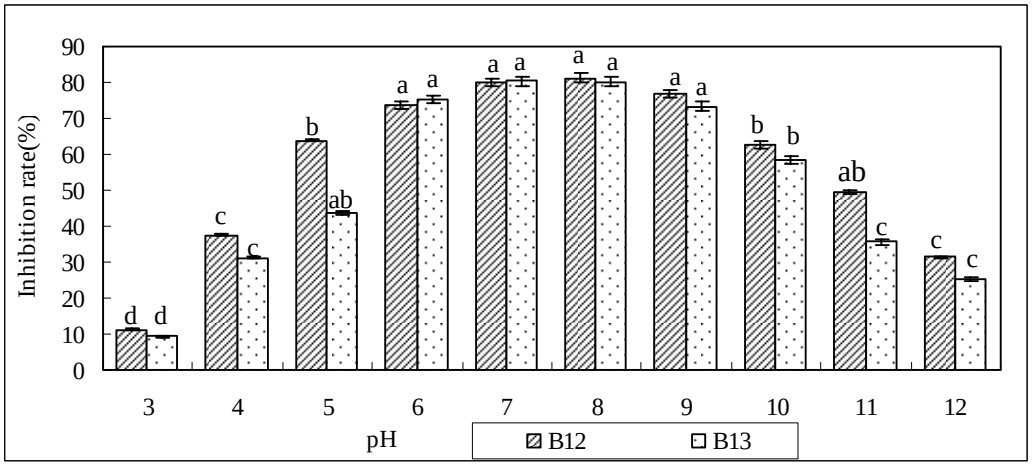

Fig. 2. The effects of pH on inhibition rate of culture filtrates. Bars represent standard deviations of the means. Values followed by the same letters are not statistically different at P =0.05 according to Duncan's multiple range test.

Systemic Resistance against *Sphaerotheca fuliginea* in Cucumber by Cell Fungal Fragments of *Flammulina velutipes*

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Abstract: Cellular fragments of the fungus *Flammulina velutipes* (JZGP), extraction of *F. velutipes* fermentation solution (JZG), Benzothiadiazoles (BTH, BION®), and KangDuFeng (KDF) were studied as candidates of SAR inducers in the cucumber-*Sphaerotheca fuliginea* system. The results demonstrated that the treatments of all candidate inducers placed on the first leaf of cucumber plants six days before challenging inoculation on the upper leaves with *S. fuliginea*, induced systemic resistance. Disease incidence and index were significantly lower when compared with the water-treated control. The systemic acquired resistance (SAR) levels induced by the JZGP solution diluted 500 times and the JZG treatment were higher than that elicited by KDF alone, but lower than the BTH treatment. Treatments with these inducers led to an increase in activities of chitinase and beta-1,3-glucanase in cucumber leaves compared with control plants, indicating that these inducers triggered SAR in the cucumber plants examined. The results of this study will assist in the exploitation of biological inducers of plant resistance in cucumber.

Introduction: Powder mildew, caused by *Sphaerotheca fuliginea*, is a widely distributed and destructive disease of greenhouse and field-grown cucumber plants. The disease is typically controlled by fungicide applications. As the problems of the fungicide resistance and the pollution to the environment have become increasingly serious, alternative methods of protection are essential. Resistance can be systemically induced in plants by abiotic or biotic elicitor(s) (1,4-6,11,12). Among the abiotic compounds, salicylic acid (SA) was found to induce systemic resistance (SAR) to fungal, bacterial and viral pathogens. Benzothiadiazole (BTH) mimics SA, and is capable of inducing SAR. In 1996, BTH was introduced in Germany, and is now available as the commercial product BION®. Resistance inducing effects of this product have been demonstrated in plants against different crop diseases(2,7).

Hijwegen and Verhaar demonstrated that three fungal culture filtrates were able to induce resistance to *Peronospora parasitica* in red cabbage reducing disease incidence by 52% (8). Based on our research investigating the active component of cellular fragment of *Flammulina velutipes* (JZGP), the active extracted component of *F. velutipes* fermentation is proteoglycan.

Biochemical changes associated with induced systemic resistance, including

enhancement of levels of chitinase and beta-1,3-glucanase in some plants, have been reported(2,3,10). However, the induction of systemic resistance to *S. fuliginea* by cell fragments of this fungus, however, has not been extensively investigated in cucumber. Therefore, the objectives of the research reported herein are to break the cells for releasing proteoglycan present in fungus cells, and to study the induced resistance in cucumber-*Sphaerotheca fuliginea* system.

In the present paper, four different resistance inducers were compared for their potential effect against powdery mildew (*S. fuliginea*) infection: 1) the synthetic inducer BTH (BION®); 2) biotic agents cellular fragment (JZGP); 3) biotic agents produced after extraction of fermentation (JZG) from *F. velutipes*, and; 4) a biotic product (KDF). We provide evidence for the effectiveness of fungal cell fragment's for inducing systemic protection against powdery mildew in cucumber plants. In addition, the levels of chitinase and beta-1,3-glucanase were investigated to evaluate their potential role in inducing systemic resistance against powdery mildew in the upper leaves of plants by foliar spray of fungal cell fragments.

Materials and Methods: *Pathogen.* *Sphaerotheca fuliginea* was obtained from cucumber plants grown in greenhouse. Inoculum was obtained from freshly infected leaves on which the fungus was sporulating. Conidia were gently brushed into distilled water resulting in a conidial suspension.

Inducers: For the JZGP solution, cell fragments of *Flammulina velutipes* (JZGP) was used at two concentrations (diluted with distilled water): 500 x and 1000 x. A solution of *F. velutipes* was designated JZG where a fermented solution was concentrated for about 1000 x as the base solution. The base solution was diluted 1000 x for experimentation. The benzothiadiazole (BTH, BION®) treatment was obtained from Novatis Agro-Chemistry Company Ltd. The concentration of BTH used in the experiment was 75 g/ml. The KangDuFeng treatment was produced by the Institute of Plant Protection, Beijing Academy of Agriculture and Forestry, Beijing, China.

Plants, inoculation, and induction of systemic resistance. Greenhouse grown cucumber plants (*Cucumis sativus* L. cv. Youza 8) were employed for experimentation when the sixth-true leaf was fully expanded. Treatment with inducers was made by daubing the third leaf from bottom into each treatment solution. Six days later, the upper three leaves of the plants were inoculated with the pathogen by spraying the conidial suspension of *S. fuliginea* onto non-infected leaves. Control plants were treated with tap water by spraying. Each treatment had nine replicates, and disease incidence and index were recorded.

Assay of enzyme activity. Sampling: The third cucumber leaf of each plant was treated with inducers JZGP, JZG, KDF and BTH. Control plants were treated with tap water. The 4th, 5th and 6th leaves were sampled at 2, 5, and 8 days after treatment and stored in refrigerator at -80°C for analysis.

The extraction of enzyme solution, preparation of colloidal chitin and detection of chitinase activity followed the methods of Boller(2). Total beta-1,3-glucanase activity was assayed by the method of Reuveni(8). For expression of chitinase, one unit of chitinase activity was defined as an amount capable of releasing 1 µg N-Acetylgucosamine (GlcNAc) from deacetyl glycol chitin in one hour, and was expressed as u g^{-1} fresh weight of tissue. The expression of beta-1,3-glucanase: was defined as the amount of enzyme required to release1µg glucose of reducing lamminarin in one minute, and is expressed herein as u g^{-1} fresh weight of tissue.

Results: *Systemic induced resistance in cucumber seedlings.* The upper leaves of cucumber seedlings were more resistant to the infection by *S. fuliginea* after being treated with different inducers on the third leaves (Table 1). Disease index and incidence were reduced greatly, showing significant difference from the control at $P<0.05$.

After the third leaves were treated with BTH, the upper leaves of cucumber plants were inoculated with *S. fuliginea*, inducing systemic resistance. In the treated plants, the disease incidence (21.5%) and index (15.3) were reduced by 67.6% and 81.7% respectively compared with the control (66.4% and 83.5, respectively).

The disease incidence of cucumber plants inoculated with *S. fuliginea* after spraying with JZG and JZGP (500 x)in the third leaf was 25% (JZG) and 25.2% [JZGP (500 x)] on the upper leaves. This was a reduction by 62.3% (JZG) and 62.0% [JZGP (500 x)] when compared with control. Likewise, the disease index was 30.4 (JZG) and 26.4 [JZGP (500 x)], being reduced by 63.6% and 68.4% respectively, when compared with control.

Treatments with KDF and JZGP (1000 x) also induced resistance in the upper leaves of cucumber plants. The intensities, however, were lower than those of other inducers. Of the four inducers, BTH was the most effective at controlling *S. fuliginea*, followed by JZGP (500 x̣) and JZG. Treatments JZGP (1000 x̣) and KDF were similar and less effective than other treatments.

In addition to the reduction of disease index and incidence, the appearance of disease symptoms in treated plants was postponed by 3-4 days compared with the non-treated control.

Activities of chitinase in leaves of treated plants. The chitinase activity in leaves treated with inducers was higher than that in control (Table 2). The chitinase activity increased beginning on the second day post-treatment. The enzymes activity continued to increase during the first eight days post-treatment. The chitinase activity was the highest in leaves treated with BTH. During the first five days, the chitinase activity in leaves treated with all agents was higher than control. These differences were significant ($P<0.05$) when compared to controls.

Activities of beta-1,3-glucanase in leaves of treated plants. There was a significant increase in beta-1,3-glucanase activity in cucumber leaves as a result of various treatments (Table 3). Only on the fifth day was the activity lower than control after foliar treatment with BTH. On the eighth day, the enzyme activities in all the treatments were dramatically ($P<0.05$) higher than controls.

Discussion: Four SAR inducer candidates were tested which included cell fragments of *F. velutipes* (JZGP), Benzothiadiazole (BTH), a fermented solution of *F. velutipes* (JZG) and KangDuFeng (KDF). Cucumber leaves treated with inducers systemically protected upper leaves against powdery mildew caused by *S. fuliginea*. Disease incidence and index were significantly reduced with all treatments. Of the four candidate inducers, JZGP (500 x̣) and JZG were higher than KDF in inducing resistance, but lower than BTH.

In order to find alternative resistance inducers, these treatments were selected from an array of about 20 potential agents (chemical and biological). Among the treatments, the effectiveness of the fermented solution of *F. velutipes* (JZG) was similar to cell fragments of *F. velutipes* (JZGP). However, the fungus solution producing procedure is time consuming, taking more than ten days to prepare. BTH has not been registered in China; and thus JZGP has the potential for practical application.

In the interaction between plant and fungus, beta-1,3-glucanase and chitinase are thought to play multiple roles in plant self-defense (9). The results of our study indicate that chitinase and beta-1,3-glucanase activity increased in inducer treated cucumber leaves, suggesting that the increased activity of chitinase and beta-1, 3-glucanase was related to induced resistance.

Time course of increased activity of chitinase and beta-1, 3-glucanase patterns indicated that the fungus-extract treatment probably is responsible for the triggering of defense responses, inducing the systemic resistance. Difficulties associated with the formulation of cell fragments of *F. velutipes* (JZGP) is an area that was addressed by this research. Thus, further research is necessary to define the action mode of the agents.

Acknowledgements:

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Table1. Effects of inducers on the resistance of cucumber to powdery mildew.

Inducers	Concentrations	Date of symptom appeared	Disease incidence (%)	Disease index
Contol	Water	27 Dec.	66.4 a	83.5 a[1]
BTH	75μg/ml	31 Dec.	21.5 d	15.3 f
JZG	1000 x	31 Dec.	25 c	30.4 d
JZGP-1	500 x	31 Dec.	25.2 c	26.4 e
JZGP-2	1000 x	30 Dec.	33.5 b	50.3 b
KDF	400 x	30 Dec.	34.0 b	40.63 c

[1]Different letters indicate significant differences among the treatments (P < 0·05).

Table 2. Chitinase activity in leaves at various times after inducers treatments as measured by fresh weight (FW) changes (U/g FW).

Inducers	Concentrations	Days after treatment		
		2	5	8
JZGP	500 x	20.4 c	108.5 bc[1]	125.2 a
BTH	75μg/ml	23.4 b	129.0 a	132.8 a
JZG	1000 x	28.3 a	113.0 b	128.2 a
KDF	400 x	22.6 b	99.1 cd	117.0 b
Control		19.2 c	86.9 d	107.0 b

[1]Different letters indicate significant differences among the treatments (P < 0·05).

Table 3. Activities of beta-1,3-glucanase in leaves at various times after inducers treatment as measured by fresh weight (FW) changes (U/g FW).

Inducers	Concentrations	Days after treatment		
		2	5	8
JZGP	500 x	339.8 b	473.0 a[1]	650.4 c
BTH	75μg/ml	320.7 c	320.2 c	595.8 c
JZG	1000 x	521.0 a	457.9 ab	856.9 a
KDF	400 x	290.6 d	527.4 a	802.9 a
Control		288.5 d	369.4 bc	433.7 d

[1]Different letters indicate significant differences among the treatments (P < 0·05).

Fruit Size in Melon in Monoecious and Andromonoecious Isolines

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Rosa (2), as early as 1928, noted the association of elongate fruit with pistillate flowers and globular fruit with perfect flowers among monoecious and andromonoecious cultivars, in an occasional pistillate fruit in a round-fruited andromonoecious cultivar, and in F_2 populations segregating for monoecious and andromonoecious flowering habits. Later, both Kubicki (1) and Wall (4) made a similar observation that in populations segregating for monoecious (A-) and andromonoecious (aa) flower types, elongate fruit shape was strongly associated with pistillate flowering, either through linkage or pleiotropy. Anecdotal observations by breeders suggest that the "A" allele also increases fruit size, and as a result, the "A" gene for monoecity has been incorporated into several large-fruited eastern cultivars of cantaloupe. The data presented here were obtained because the effect of pistillate versus perfect flower type on fruit size and other morphological traits had not, to my knowledge, been systematically examined in near isogenic progeny segregating for monoecious and andromonoecious flowering.

Methods: The present study employed two breeding lines, NH6414 and NH6888, segregating for monoecious and andromonoecious flowering habits in the F_6 generation. The breeding lines were grown in a melon breeding nursery at the Kingman Research Farm in Madbury, New Hampshire. On 8 June of 2000, 20 transplants of each breeding line were planted into raised beds spaced 1.8 m apart. Beds were covered with 1.25 mil black plastic and supplied with 8 mil drip irrigation tubing (emitter spacing 30 cm). Within-row spacing was 0.3 m. At harvest in August, data were taken on fruit weight, maximum fruit diameter (midpoint between stem and blossom end), fruit length (stem to blossom end), midpoint cavity diameter, and width of blossom scar.

Results and Discussion: Even though sample sizes were small in the fruit comparisons, differences in several fruit morphological traits between fruit derived from either pistillate or perfect flowers were large enough to be statistically significant (Table 1). In segregants from the F_6 population of NH6888, fruit from pistillate flowers averaged 130% larger than those from perfect flowers. Fruit size was larger in the population derived from NH6414, and although the absolute weight difference between ovary types (844 g) was similar to NH6888 (878 g), the percentage increase in size of fruit developed from pistillate as compared to perfect flowers was much smaller (68%). Both fruit length and fruit width were greater in pistillate than in perfect fruit. However, the ratio of fruit length to fruit width in pistillate fruit was higher (1.13 for NH6888 and 1.17 for NH6414) than in perfect fruit (0.91 for NH6888 and 0.89 for NH6414), and the ratios were similar for the two populations.

Observations of breeders suggest that two other traits appear to differ between fruit derived from pistillate or perfect flowers. Diameter of seed cavities and blossom scars appear to be smaller in fruit from pistillate than in fruit developed from perfect flowers. Rosa (1) reported that oblong fruits of melon generally had a higher density than oblate or globular fruit. Scott (3) found a similar association, but the coefficients of correlation were small. Fruit with small or tight seed cavities have greater density than open-cavity fruits, and tight seed cavity is generally considered a desirable trait. Based

on visual appearance, cavities appeared to be smaller in pistillate than in perfect fruits. Actual measurements did not reveal significant differences in cavity diameter (Table 1), but flesh was thicker in pistillate than in perfect fruit so the relative proportion of cavity area was smaller. Pistillate fruit have a longer seed cavity than perfect fruit, so overall fruit density may not have differed between the two fruit types. The effect of flower type on fruit blossom scar was likewise not statistically significant, but there was considerable variability in size of blossom scars in fruit derived from perfect flowers. The COVs for blossom scars were 0.15 and 0.28, respectively for pistillate and perfect fruit of NH6888, and 0.12 and 0.22, respectively, for pistillate and perfect fruit NH6414. Blossom scars are always small in fruit derived from pistillate flowers because the base of the hypanthium fused to the ovary is small. In perfect flowers, the size of the hypanthium base, and resulting blossom scar, can vary considerably both within a line, as was the case in this study, and between lines (personal observations, author).

The monoecious gene is therefore useful in a breeding program to achieve greater fruit size and a smaller blossom scar, but may cause fruit to be undesirably elliptical or oblong. Fruit shape in monoecious cultigens can be modified, however, by genes that are epistatic
to the elongating effect of pistillate flowers on fruit shape, so it is possible to breed globular fruit in monoecious strains. In addition, the effect of monoecity on fruit shape is incompletely dominant (Wall, 1967; author, unpublished data), so that F_1 hybrids produced from pistillate x perfect flowered lines show reduced elongation as compared to fruit from pistillate x pistillate crosses.

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Table 1. Morphological traits of fruit harvested from two breeding lines of *Cucumis melo* segregating in the F_6 generation for monoecious (pistillate + staminate) verses andromonoecious (perfect + staminate) flowering pattern. Replications are given in parentheses after flower type.

Breeding line and flower type	Fruit wt. (g)	Avg. fruit length (mm)	Ave. fruit width (mm)	Diameter cavity (mm)	Mesocarp diam. (mm)	Blossom scar diam. (mm)
NH6888						
pistillate (7)	1554	158	140	46	47	19
perfect (5)	676	101	110	47	32	25
$LSD_{0.05}$	**457**	**15**	**16**	**NS**	**7**	**NS**
NH6414						
pistillate (5)	2086	181	155	53	51	21
perfect (5)	1242	126	141	55	43	25
$LSD_{0.05}$	**389**	**13**	**12**	**NS**	**7**	**NS**

Genetic Diversity of Melon (*Cucumis melo* L.) Estimated by SSR Markers

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Introduction: SSRs are excellent markers, being PCR markers, co-dominant and highly polymorphic. In addition, SSR markers are known to be most useful anchor markers for map merging, and their usefulness in melon has been demonstrated (1, 2, 4, 5). Here we report the polymorphism detected by a set of 48 SSRs in a collection of 102 melon (*Cucumis melo* L.) genotypes. The information presented is valuable for the selection of SSRs for future applications.

Material and Methods: *Plant material.*: A collection of melon genotypes was obtained from the following seed companies (7-10 genotypes from each company): Rijk Zwaan, The Netherlands; De Ruiter Seeds, The Netherlands; Semillas Fito, Spain; Syngenta Seeds, France; Sakata Seed Corporation, Japan; Enza Zaden, The Netherlands; Hazera, Israel; Seminis Inc, USA; Nunhems Zaden, The Netherlands and Zeraim Gedera, Israel. DNA was extracted from a bulk of roots of 8-10 plants for each genotype, using the mini-procedure described by Fulton et al. (3). In addition, four parental lines of mapping populations from the Newe Ya'ar collection were included: PI414723; 'Dulce'; 'Vedrantais'; PI161375 (2, 5). Altogether, 102 genotypes belonging to different market types (e.g. Cantaloup, Charentais, Honey Dew, Ananas, Galia, Inodorus, and Oriental Melon) were scored.

SSR markers. Forty-eight SSR markers developed in our laboratory were chosen for this study. All of these markers were previously found to be polymorphic between the parental lines of at least one of the mapping populations mentioned above. Twenty-eight of the markers have already been published (1, 2, 4).

PCR amplification and polyacrylamide gel electrophoresis were performed as described by Danin-Poleg et al. (1).

Gene diversity. Allele frequencies, allele number and gene diversity were calculated. Gene diversity was calculated as:
Gene Diversity = $1 - \Sigma P^2_{ij}$, where P_{ij} is the frequency of the jth allele for ith SSR locus summed across all alleles for the locus, as described by Danin-Poleg et al. (1).

Results and Discussion: All 48 SSR markers amplified clear DNA fragments in all 102 genotypes (for illustration see Fig. 1). A total of 212 alleles were scored (Table 1). The highest number of alleles was detected using the marker CMATN89 (13 alleles) and the lowest number was found to be 2 alleles detected by each of 6 SSRs (CMAGN55, CMTAAN87, CMCAN90, CMGAN92, CMTGGN99, CMGA15). The selected SSR markers generated an average of 4.3 alleles per locus, and gene diversity varied between 0.04 and 0.82 (Table 1). The high level of polymorphism detected indicates that these SSR markers provide a useful tool for estimating genetic variation in melon**.**

Acknowledgements:

Contribution no. 109/2007 of the Institute of Plant Sciences, Agricultural Research Organization, Bet Dagan, Israel.

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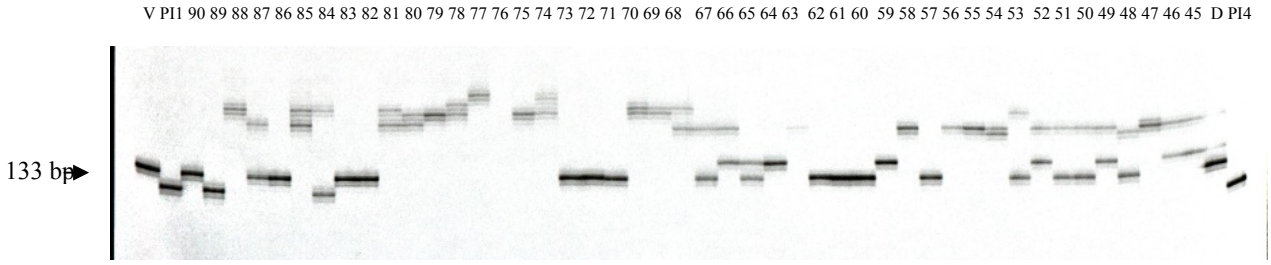

Figure 1. A group of melon genotypes scored using the marker CMATN89 on polyacrylamide gel. V – 'Vedrantais', PI1 – PI161375, D – 'Dulce', PI4 – PI414723, 45-90 melon genotypes from the collection. The arrow indicates the size of the allele of 'Dulce'.

Table1. The number of alleles and the gene diversity detected by 48 SSR markers in a collection of 102 melon genotypes.

Marker name	Number of alleles	Gene Diversity	Marker name	Number of alleles	Gene Diversity
CMGAN3**	3	0.27	CMTCN62**	3	0.5
CMCTN4**	3	0.54	CMTCN65**	4	0.45
CMCTN7**	3	0.44	CMTCN66**	7	0.65
CMTCN14**	3	0.61	CMCTN71**	7	0.63
CMATN22**	3	0.55	CMAGN73**	7	0.43
CMGAN24**	3	0.08	CMAGN75**	7	0.6
CMGAN25**	3	0.53	CMAGN79**	10	0.81
CMTCN30**	4	0.72	CMGAN80**	4	0.53
CMTCN34	6	0.66	CMGTN84	3	0.55
CMAG36*	8	0.7	CMCTN85	5	0.53
CMGAN37	4	0.57	CMCTN86	6	0.56
CMTCN40	4	0.33	CMTAAN87	2	0.05
CMTCN41**	4	0.42	CMATN89	13	0.82
CMCTTTN44	4	0.42	CMCAN90	2	0.13
CMAGN46	4	0.54	CMTTCN91	3	0.59
CMGAN48	4	0.05	CMGAN92**	2	0.04
CMAGN52**	6	0.6	CMTGGN99	2	0.39
CMCTN53**	4	0.13	CMATN101	5	0.08
CMAGN55	2	0.3	CMGA104*	6	0.68
CMTCN56**	4	0.55	CMGA15*	2	0.04
CMCTN57	3	0.15	CMCT44*	3	0.04
CMCTN58	3	0.11	CMGT108*	4	0.47
CMGAN59	7	0.35	CMTA134a*	5	0.66
CMAGN61**	3	0.51	CMGA120	5	0.43

* Primers published by Danin-Poleg et al. (1, 2).

** Primers published by Gonzalo et al. (5).

A Recessive Gene for Light Immature Exterior Color of Melon

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Introduction: Exterior appearance is an important aspect of fruit quality and consumer acceptance of cucurbits. However, as compared with *Cucurbita pepo* L., little is known concerning the mode of inheritance of various exterior fruit colors of *Cucumis melo* L. Thirteen loci affecting fruit color have been identified in *Cucurbita pepo* (2) and although eight are listed for *Cucumis melo* (3), it has not been possible to determine whether the duplicate factors listed for fruit mottling, *Mt* and *Mt-2*, and fruit striping, *st* and *st-2*, are one and the same gene. Information on possible gene interactions is scant, too, with a gene for yellow exterior color, *Y*, and a gene for fruit striping, *st*, considered to be epistatic to *Mt*, but mottling has higher contrast on a dark green background than on a light green or yellow background, and it is entirely possible that the mottling is visible on the two latter colors if the fruits are examined more carefully. Moreover, as shown in *Cucurbita pepo* (2), in order to obtain a clearer understanding of gene interactions, it is necessary to study fruit color as a function of fruit development. And melons do undergo changes in exterior color during their development.

Nonetheless, only two genes have been identified so far as affecting immature fruit color in melons (3). One, designated *Wi*, is a dominant factor for *white* color of the immature fruit (3). The other, designated *st-2*, is a recessive factor for striped immature fruit color. This gene was identified in the cross of 'Dulce' (striped) with PI 414723, an accession having intense (dark) green immature fruit color (1). We made a cross between 'Dulce' and an accession having light immature color, 'TAM-Dew'. We also crossed 'Krymka' which has dark-colored fruits, with 'Eshkolit Ha'Amaqim', which has light-colored fruits. Our objective is to describe and consider the results of these crosses.

Materials and Methods: The American muskmelon, *Cucumis melo* subsp. *melo* Reticulatus Group 'Dulce', which has striped, dark and light, immature fruit color was crossed with the American honeydew-type melon, *C. melo* subsp. *melo* Inodorous Group 'TAM-Dew', which has light immature fruit color. 'Krymka', a local cultivar from Crimea (Reticulatus Group) that has dark (intense) colored fruits throughout their development, was crossed with 'Eshkolit Ha'Amaqim.' The latter was derived in part from genetic material related to 'Ha'Ogen' (*C. melo* subsp. *melo* Cantalupensis Group) but the fruits of 'Eshkolit Ha'Amaqim' are light-colored throughout their development. Some F_1 plants from each cross were self-pollinated and/or backcrossed to their respective parents to obtain F_2 and BC_1 progenies. Seeds of the parental, familial, and backcross progenies were sown in the field in early August at Newe Ya'ar (Yizre'el Valley, northern Israel). Fruits were observed between 12 and 24 days after flowering, at which time they were scored for external color intensity.

Results and Discussion: 'Dulce' and 'TAM-Dew' bred true for exterior immature fruit color and all of the F_1 plants examined had striped exterior color, closely resembling that of the striped parent, 'Dulce' (Table 1). The F_2 segregated in accordance with a 3:1 ratio of striped to light and the backcross to 'TAM-Dew' segregated in accordance with a 1:1 ratio of striped to light. These results indicate that there is a single gene determining striped

young fruit exterior color, and that it is dominant to light fruit color.

'Krymka' and 'Eshkolit Ha'Amaqim' bred true for exterior immature fruit color and all of the F_1 plants examined had dark exterior color, closely resembling that of the dark parent, 'Krymka' (Table 2). The F_2 segregated in accordance with a 3:1 ratio of dark to light and the backcross to 'Eshkolit Ha'Amaqim' segregated in accordance with a 1:1 ratio of dark to light. These results indicate that there is a single gene determining dark young fruit exterior color, and that it is dominant to light fruit color.

The results of both crosses are compatible with the idea that there exists a recessive gene for light exterior immature fruit color in *Cucumis melo*. This gene for light fruit color apparently is not at the same locus as the heretofore reported dominant gene for light fruit color, *Wi*. However, it is not known what the genetic relationship is between the dominant gene for striped fruit, as in 'Dulce', and the dominant gene for dark fruit, as in 'Krymka'. To determine whether these two genes are at separate loci or in an allelic series, such as occurs in *Cucurbita pepo* (2), a testcross for allelism will need to be conducted.

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Table 1. Results of crossing 'Dulce' (striped fruit) with 'TAM-Dew' (light fruit).

Accession	Total	Striped rind	Light rind	Expected ratio	χ^2	*P*
P_1, Dulce	15	15	0			
P_2, TAM-Dew	15	0	15			
F_1, $P_2 \times P_1$	15	15	0			
F_2, $(P_2 \times P_1) \otimes$	244	188	56	3:1	0.546	0.46
BC_1, $P_2 \times (P_2 \times P_1)$	88	43	45	1:1	0.045	0.83

Table 2. Results of crossing 'Krymka' (dark fruit) with 'Eshkolit Ha'Amaqim' (light fruit).

Accession	Total	Dark rind	Light rind	Expected ratio	χ^2	*P*
P_1, Krymka	15	15	0			
P_2, Eshkolit Ha'Amaqim	15	0	15			
F_1, $P_2 \times P_1$	15	15	0			
F_2, $(P_2 \times P_1) \otimes$	203	148	55	3:1	0.475	0.48
BC_1, $P_2 \times (P_2 \times P_1)$	45	25	20	1:1	0.556	0.45
BC_1, $P_1 \times (P_2 \times P_1)$	40	40	0			

SNP Discovery and Mapping in Melon (*Cucumis melo* L.)

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Introduction: Several studies have applied various marker types (including RFLP, RAPD, AFLP and SSR) for mapping and assessing genetic variation within *C. melo* (1, 3, 6, 7). A partial linkage map of melon from a cross between PI 414723 (*C. melo* Group *Acidulus*) and 'Dulce' (C. *melo* Group *Reticulatus*) was previously described by us (2). Single nucleotide polymorphisms (SNPs) are an abundant form of genetic variation in the genome of various species that are extremely useful for gene mapping and phylogenetic studies. In recent years, SNPs have become important as genomic markers with numerous technical methods developed for their detection (4). In this study, SNP markers for genes belonging to major fruit metabolic pathways were developed. In order to link between these markers and fruit quality traits, these SNPs are currently being located on the PI 414723 × 'Dulce' map.

Materials and Methods: *Plant material.* The F_2 mapping population included 112 individuals derived from a cross between 'Dulce' and PI 414723 (2). The 'Dulce' fruit is aromatic, sweet, of high pH, with orange-colored flesh and a netted rind. The PI 414723 fruit is non-aromatic, non-sweet, and acidic, with salmon-colored flesh and no net.

SNP discovery. From the melon EST database (http://melon.bti.cornell.edu), three different methods were used for SNP detection: (i) comparative analysis of sequences of different genotypes, (ii) primers designed for the end sequences of interesting ESTs were used to amplify the genomic DNA of both parental lines ('Dulce' and PI 414723); this was followed by screening of the amplicons using either DHPLC (Denaturing High Performance Liquid Chromatography) or SSCP (Single Strand Conformational Polymorphisms), in order to find polymorphism between the parental amplicons. The polymorphic amplicons were re-sequenced in order to validate the SNPs, (iii) direct sequencing of parental amplicons.

Genotyping. SNP genotyping was conducted using the Sequenom MassARRAY® platform, by the high-throughput genotyping assays: hME and iPLEX. These assays allowed multiple PCR reactions in a single well (5). JoinMap 3.0 (Kyazma, Holland) was used for linkage analysis and map calculations.

Results: SNP Markers for ca. 100 genes belonging to major fruit metabolic pathways were developed (Table 1). These include genes encoding for key enzymatic and transport steps in carbohydrate, acid, volatile and carotenoid metabolism in melon and

other cucurbits. SNP frequency was found to vary between one in 5000 bp to ten in 300 bp. A search for linkages between SNPs and traits is underway using a RIL population derived from the F_2 population.

Acknowledgements:

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Table 1. Genes associated with carbohydrate, carotenoid and organic acid metabolism. SNPs were developed for all the listed genes. Stars mark the genes located on the melon map.

Carbohydrate genes		**Carotenoid genes**	**Organic acid genes**		
Alkaline alpha galactosidase I	Hexose transporter 1	* Geranylgeranyl Pyrophosphate reductase	Phosphoenol pyruvate carboxykinase	NAD malate dehydrogenase (mitochondria)	* Vacuolar pump V0-a subunit
* Alkaline alpha galactosidase 2	* Hexose transporter 6	Geranylgeranyl pyrophosphate synthase	* Phosphoenol pyruvate carboxylase (a)	NAD malate dehydrogenase (glyoxysome)	* Vacuolar pump V0-c' subunit
* Acid alpha galactosidase 1	* Acid invertase 1	* Phytoene synthase 1	* Phosphoenol pyruvate carboxylase (b)	* NADP malic enzyme (chloroplast)	* Vacuolar pump V0-c subunit
* Putative galactose kinase	* Acid invertase 2	* Phytoene synthase 2	* Citrate synthase (glyoxysome)	* NAD malate dehydrogenase (chloroplast)	* Vacuolar pump V0-d subunit
Galactose-1-phosphate uridyltransferase	*Alkaline/ neutral invertase 1	* Phytoene desaturase	* Citrate synthase (mitochondria)	* Malate synthase (glyoxysome)	* Vacuolar pump V0-e subunit
* UDP-glucose 4-epimerase 1	*Alkaline/ neutral invertase 2	* Zeta carotene desaturase	* Aconitase	* NADP Isocitrate lyase	* Vacuolar pump V1-a subunit
UDP-glucose 4-epimerase 2	* Sucrose synthase	* Lycopene beta-cyclase	* NAD Isocitrate dehydrogenase (β)	ATP citrate lyase (b)	* Vacuolar pump V1-b subunit
UDP-glucose 4-epimerase 3	Sucrose synthase 1	* Beta-carotene hydroxilase	* ą keto glutarate dehydrogenase (E2)	NADP malic enzyme (cytosol)	Vacuolar pump V1-C subunit
UDP-glucose pyrophosphorylase	* Sucrose cleavage protein-like	* Carotenoid isomerase	* Succinyl CoA synthetase (α)	* NAD Isocitrate dehydrogenase	* Vacuolar pump V1-d subunit
*Phosphoglucomutase (cytosol)	Hexokinase 2		* Succinyl CoA synthetase (β)	* Citrate transporter (mitochondria)	* Vacuolar pump V1-e subunit
* Sucrose-phosphate synthase 1	Fructokinase 3		* Succinate dehydrogenase (α)	*Citrate transporter (glyoxysome)	* Vacuolar pump V1-f subunit
Putative sucrose transporter			* Succinate dehydrogenase (β)		Vacuolar pump V1-G subunit
Sugar transporter superfamily			* Fumarase		Vacuolar H[+]-translocating inorganic pyrophosphatase

Construction of a RAPD Marker-Based Linkage Map in Ananas Melon

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Introduction: Melon (*Cucumis melo* L.) fruit flesh is a significant source of carbohydrates, ascorbic acid, beta-carotene, folic acid, and potassium. Sucrose is a major factor to determine mature melon fruit sweetness. Ascorbic acid and beta-carotene are major nutrients for human health. Due to consumer preference, these are highly important quality traits of different melon classes. The improvement of these traits is important to breeding programs of most melon types worldwide. Diseases of melon are primary constraints limiting melon production. A yellowing disease, caused by cucurbit yellow stunting disorder virus that is transmitted by *Bemisia tabaci*, is common in South Texas. Molecular tagging and mapping information for these fruit quality traits and disease resistance is expected to be useful to melon breeders because of the possibility to use molecular markers for marker-assisted selection in their breeding programs. Therefore, our initial objective was to construct a RAPD marker-based genetic linkage map in an F2 population derived from the melon cross of 'Deltex' x TGR1551 for conducting research on the genetics of melon fruit quality and disease resistance.

Materials and Methods: One hundred-eight F2 plants derived from the cross of 'Deltex' x TGR1551 were planted in a greenhouse at the Texas Agricultural Research and Extension Center-Weslaco in 2003. The 'Deltex' parent is a commercial ananas cultivar with high fruit quality, while the TGR1551 parent is a wild type with low fruit quality. Total genomic DNA was extracted from the leaf tissue of the 108 F2 plants along with their parents (4). A total of 360 random 10-mer primers (Operon Technologies, Alameda, Calif.) were used for the RAPD analysis (5). PCR was performed on 96-well plates in an MJ Research thermalcycler (model PTC-0100; MJ Research, Waltham, Mass.). Protocols for PCR and the composition of the final volume of reactants were the same as those described previously (4). A 100-bp DNA ladder (Life Technologies, Grand Island, N.Y.) was used to estimate the length of RAPD markers. The name of each RAPD marker is derived from an "O" prefix for Operon primers, the letters identifying the Operon kit, Operon primer number, and the approximate length (bp) of the marker (3). The 360 primers were used to screen between the parents 'Deltex' and TGR1551. Primers that generated marker polymorphisms between the parents were tested in the F2 population from the cross between 'Deltex' and TGR1551 to assess genetic linkage of RAPD markers to the traits of interest. To detect segregation distortion of markers, F2 population marker data were tested for goodness-of-fit to a 3:1 ratio using the chi-square test. The RAPD marker-based linkage map was constructed on the data for the 108 F2 plants of the 'Deltex' x TGR1551 cross using MAPMAKER version 3.0 (2). On the basis of a LOD score of 3.0 and a linkage threshold of 0.4, linkage groups were displayed using the Group command. To establish a linkage group, a subset of markers was initially selected based on LOD scores and pairwise linkages. The best linkage order within the subset was calculated using the Compare command and then, additional markers were inserted using the Try command. LOD scores of at least 2.0 were considered different between the most and second most likely position for the marker. The Ripple command was finally

used to check the marker order. Map distances (cM) between ordered loci of markers were calculated using recombination fractions and the Kosambi mapping function (1).

Results and Discussion: A total of 208 RAPD markers that segregated in the F2 population of the 'Deltex' x TGR1551 cross were scored for constructing the genetic linkage map (Table 1). All markers displayed an amplified DNA fragment in the 'Deltex' parent that was absent in the TGR1551 parent. An example of marker OE08.600 obtained from the 'Deltex' parent is shown in Figure 1. Of the 208 markers, 195 (94%) fit the expected 3:1 ratio in the F2 population on the basis of the chi-square goodness-of-fit test (Table 1). Thirteen markers (6%), however, deviated significantly from the expected 3:1 ratio ($P < 0.05$) in the genetic population. Thus, we excluded the 13 distorted markers in developing the linkage map.

One hundred and ninety-five RAPD markers were used for constructing the genetic map (Table 1). These non-distorted markers were divided into 12 linkage groups, three unlinked pairs (UP), and ten unassigned markers. We developed the molecular marker-based linkage map with 185 RAPD markers (Figure 2). The number of non-distorted markers per linkage group ranged from three on linkage group 12 to 36 on linkage group 6 (Table 1). An average of 14.9 markers were mapped per linkage group. Our linkage map included 157 marker loci spanning a total map distance of 1148 cM. The number of loci per linkage group varied from three on linkage group 12 with a length of 36 cM to 30 on linkage group 6 with a length of 178 cM. An average of 12.6 loci were located per linkage group. Each linkage group spanned an average length of 91 cM.

This genetic linkage map will be utilized to identify markers linked to QTL controlling mature melon fruit sweetness, quality, size, and shape traits as well as disease resistance, and to determine the genetic relationships among QTL for these important traits in the F2 population derived from the 'Deltex' x TGR1551 cross.

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Table 1. Illustration of the molecular marker-based linkage map on the basis of 208 RAPD markers segregating in 108 F2 plants derived from the 'Deltex' x TGR1551 cross.

Linkage group	No. of markers	No. of loci	Map distance (cM)	Mean distance (cM)	No. of distorted markers[z]
1	23	18	130	7.2	1
2	20	16	106	6.6	1
3	8	7	91	13.0	1
4	14	12	93	7.8	1
5	11	10	82	8.2	1
6	38	30	178	5.9	2
7	11	10	153	15.3	1
8	13	11	40	3.6	0
9	15	11	39	3.5	0
10	17	12	67	5.6	1
11	16	11	80	7.3	1
12	3	3	36	12.0	0
Unlinked pair 1	2	2	27	13.5	0
Unlinked pair 2	2	2	4	2.0	0
Unlinked pair 3	2	2	22	11.0	0
Unassigned markers	13				3
Total	208	157	1148	7.3	13

[z]Markers deviating from the expected 3:1 ratio ($P < 0.05$) were not included in the map.

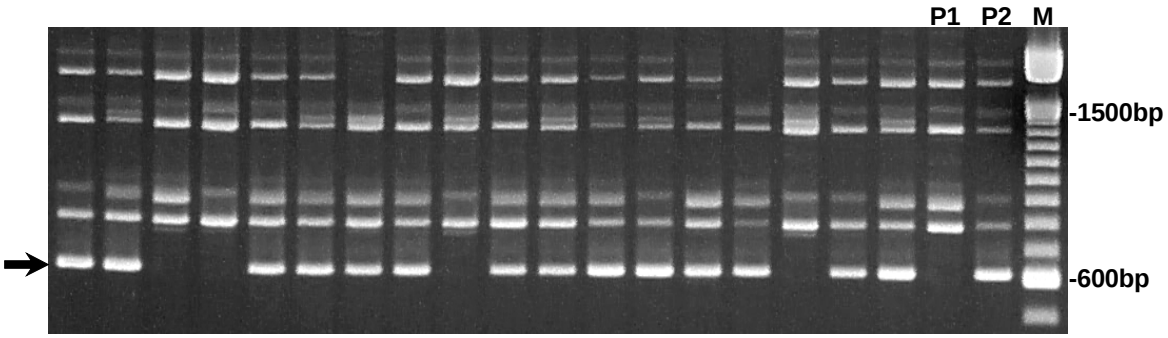

Figure 1. Segregation of RAPD marker OE08.600 amplified from 'Deltex' in an F2 population derived from the melon cross of 'Deltex' x TGR1551. Lines1-18=F2 plants of the cross, P1=TGR1551, P2='Deltex', and M=a 100-bp DNA marker ladder.

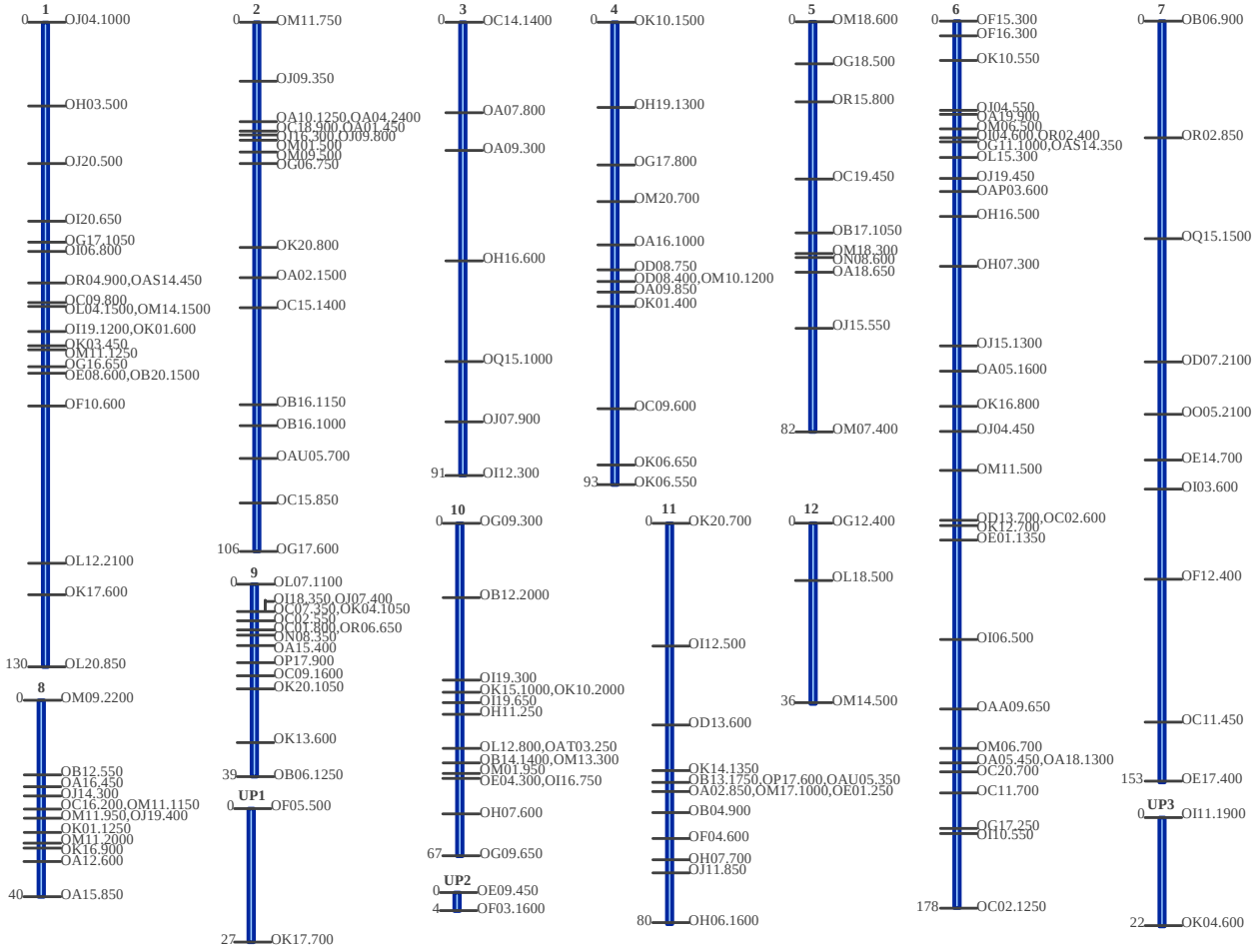

Figure 2. The RAPD marker-based linkage map constructed using an F_2 population of the 'Deltex' x TGR1551 cross. The marker names are given on the right and the length in cM is indicated on the left of each linkage group.

Mapping of QTL for Sugars in Ananas Melon

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Introduction: Sugar components such as sucrose, fructose, glucose, and total soluble solids are major factors influencing mature melon (*Cucumis melo* L.) fruit sweetness. Molecular markers linked to genes regulating synthesis of sugar components may improve the breeder's ability to recover high sugar genotypes and aid in the development of high sugar cultivars. Therefore, our objective was to identify RAPD markers associated with QTL for sucrose, glucose, fructose, total sugars (TS), and total soluble solids (TSS) in an existing molecular marker-based linkage map constructed by means of an F2 population derived from the melon cross of 'Deltex' (high sugars) x TGR1551 (low sugars).

Materials and Methods: One hundred-eight F2 plants from the cross of 'Deltex' x TGR1551 were planted in a greenhouse at the Texas Agricultural Research and Extension Center-Weslaco in 2003. The 'Deltex' parent is an ananas type with good fruit quality, while the TGR1551 parent is a wild type with poor fruit quality. Data for sucrose, glucose, fructose, and TS were obtained from the 108 F2 plants using HPLC. Total soluble solids data were also obtained from the F2 plants using a temperature corrected refractometer with digital readout. A RAPD marker-based linkage map was recently developed by Park and Crosby (3) using the 108 F2 plants of the same cross. MAPMAKER version 3.0 (2) was used for the linkage analysis of 208 RAPD markers. The name of each RAPD marker is derived from an "O" prefix for Operon primers, the letters identifying the Operon kit, Operon primer number, and the approximate length (bp) of the marker (3). Simple linear regression (SLR), for each pairwise combination of quantitative traits and marker loci, was used to analyze the data for detection of QTL affecting sucrose, glucose, fructose, TS, and TSS content. Significant differences in trait associations were based on F-tests ($P<0.05$) (1). Loci with the lowest P value per QTL were chosen and then were added in a stepwise multiple regression (SMR) to select the best set of markers ($P<0.05$) for prediction of the total trait phenotypic variation explained by the identified QTL (4). Pearson correlations of mature fruit sweetness traits including three sugars were also determined in our population. All statistical analyses were conducted using the Statistical Analysis System (SAS Inst., Cary, N.C.).

Results and Discussion: Continuous frequency distributions for sucrose, glucose, fructose, TS, and TSS were observed in the F2 population (Figure 1), indicating that the fruit sweetness traits were quantitatively inherited.

Twenty-four RAPD markers, located on several different linkage groups of the molecular marker-based melon map (Figure 2), were found to be significantly associated with QTL affecting sucrose, glucose, fructose, TS or TSS in the F2 population of

the 'Deltex' x TGR1551 cross in the greenhouse based on SLR (Table 2).

Two RAPD markers were significantly associated with QTL for sucrose content in our population on the basis of SLR (Table 2). The two markers on linkage groups 1 and 3 associated with QTL (Figure 2) were significant in a SMR analysis where the full model explained 10% of the total phenotypic variation for sucrose. Five markers were significantly associated with QTL regulating glucose content in this population by means of SLR. Particularly, three unlinked markers (OK10.1500, OJ09.800, and OG17.1050), amplified from 'Deltex', accounted for 10% to 12% of the variation for the trait. The five markers were significant in the SMR analysis with a total variation of 32% for the glucose trait. We identified significant associations of nine RAPD markers, located on different linkage groups, with QTL controlling fructose concentration in the population by SLR. Eight markers were significant in the SMR analysis with a total fructose variation of 41%. Four unlinked markers were associated with QTL affecting TS and TSS in the mapping population based on SLR, respectively. In the SMR analysis the two groups of the four markers were significant with total R^2 values of 18% and 23% for the TS and TSS traits, respectively.

These RAPD markers associated with the sugar synthesis QTL in the molecular linkage map detected here could be useful in melon breeding for improving the mature fruit sweetness.

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Table 1. Correlations of sucrose, glucose, fructose, total sugars, and total soluble solids in an F2 population derived from the melon cross of 'Deltex' x TGR1551.

Sweetness trait	Sucrose	Glucose	Fructose	Total sugars
Total soluble solids	0.63**	0.17	0.07	0.71**
Total sugars	0.79**	0.35**	0.26**	
Fructose	-0.30**	0.70**		
Glucose	-0.24*			

*,**Significant at $P \leq 0.05$ or 0.01, respectively.

Table 2. Simple linear regression (SLR) and stepwise multiple regression (SMR) analyses of marker and data for detection of QTL for three sugars, total sugars (TS), and total soluble solids (TSS) in an F2 population derived from the cross of 'Deltex' (high sugars) x TGR1551 (low sugars).

Sugar	RAPD	Linkage	SLR		SMR	
trait	marker	group	*P*	R^2	*P*	R^2
Sucrose	OJ07.900	3	0.009	6	0.009	6
	OG16.650	1	0.039	4	0.031	4
					Cumulative R^2	10
Glucose	OK10.1500	4	0.000	12	0.000	12
	OJ09.800	2	0.000	10	0.003	7
	OF05.500	unassigned	0.009	6	0.006	6
	OG17.1050	1	0.001	10	0.019	4
	OK04.600	unassigned	0.022	5	0.033	3
					Cumulative R^2	32
Fructose	OE08.600	1	0.001	10	0.001	10
	OR02.800	unassigned	0.005	7	0.007	6
	OK20.1050	9	0.013	6	0.010	5
	OE14.700	7	0.023	5	0.013	5
	OK17.600	1	0.007	7	0.018	4
	OK10.1500	4	0.036	4	0.020	4
	OI12.300	3	0.012	6	0.023	4
	OJ09.800	2	0.019	5	0.039	3
	OJ13.400	unassigned	0.031	4		
					Cumulative R^2	41
TS	OE14.700	7	0.012	6	0.012	6
	OC14.1400	3	0.030	4	0.021	5
	OM14.500	12	0.032	4	0.029	4
	OJ09.350	2	0.045	4	0.042	3
					Cumulative R^2	18
TSS	OK10.550	6	0.002	8	0.002	8
	OC18.900	2	0.008	6	0.009	6
	OB12.550	8	0.013	6	0.017	5
	OC14.1400	3	0.021	5	0.038	4
					Cumulative R^2	23

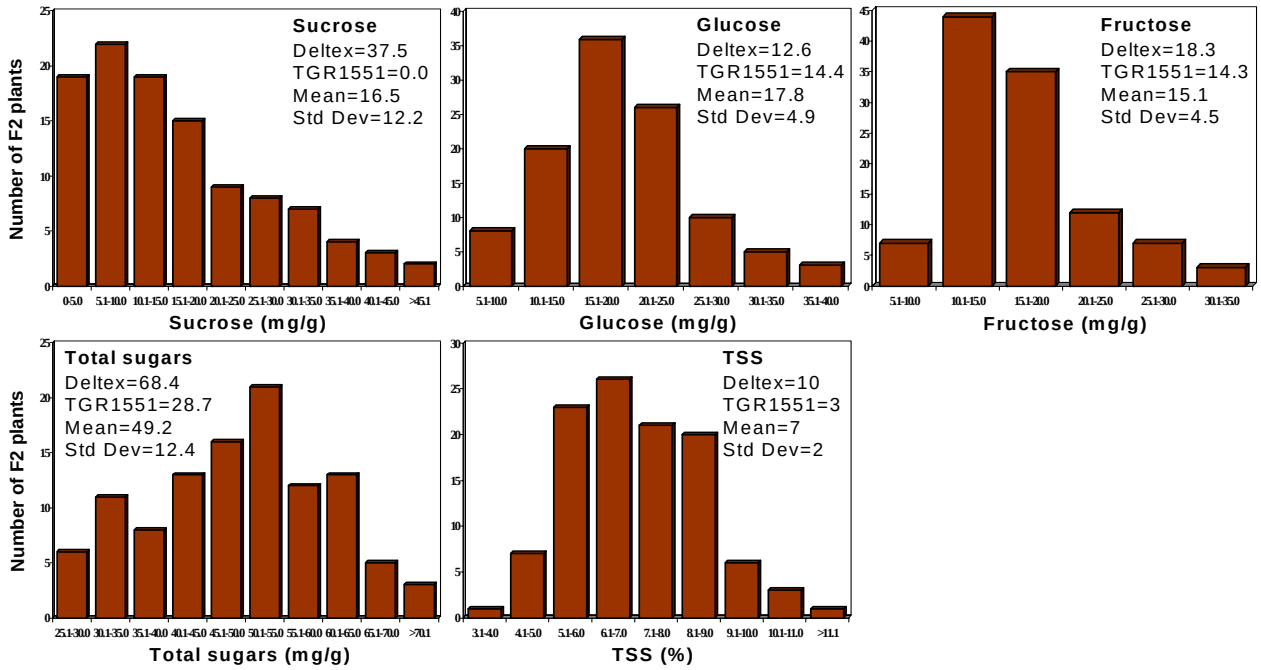

Figure 1. Frequency distributions for sucrose, glucose, fructose, total sugars, and total soluble solids (TSS) of F2 plants derived from the melon cross of 'Deltex' x TGR1551.

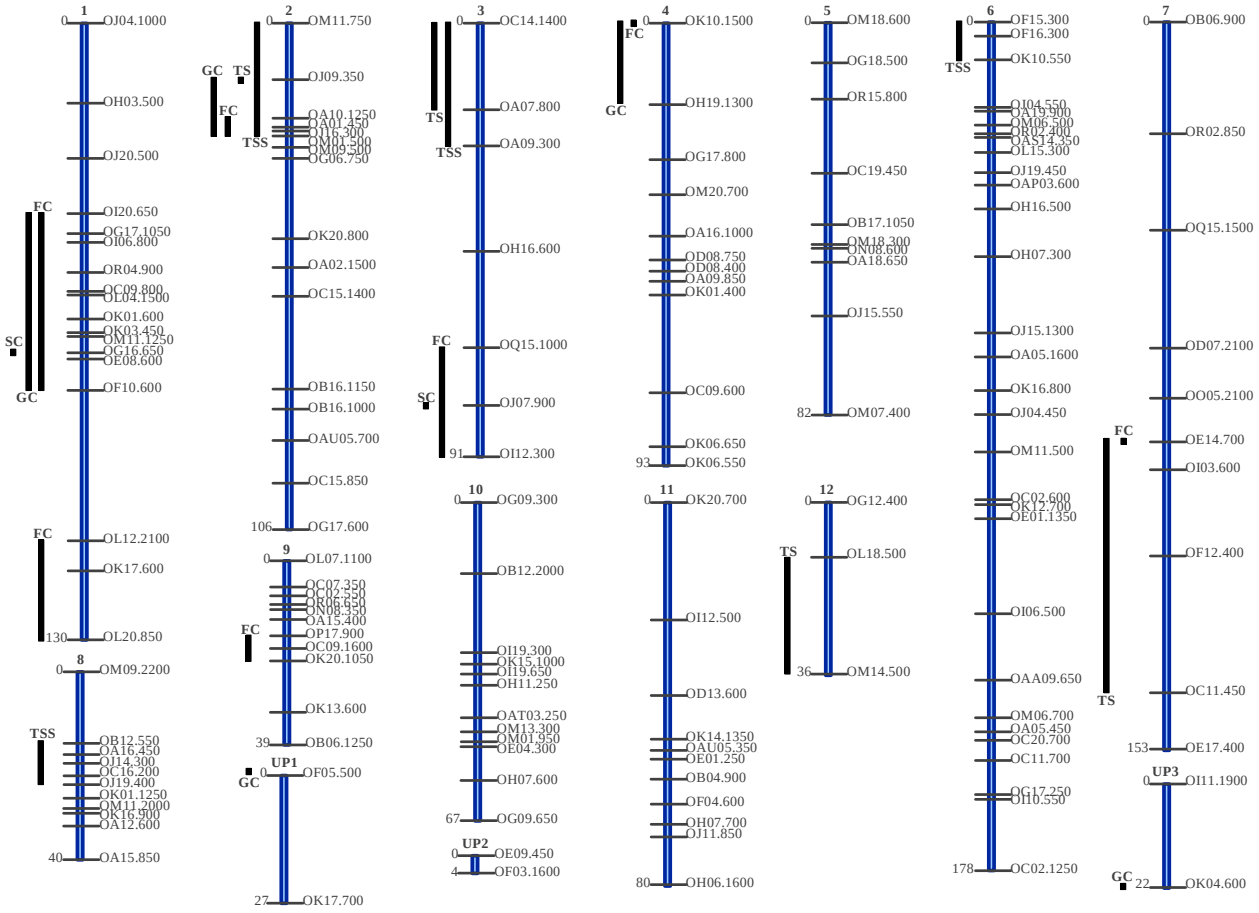

Figure 2. Linkage map for the 'Deltex' x TGR1551 mapping population with locations of QTL for mature melon fruit sweetness traits. Bars to the left of each linkage group indicate the intervals having significant trait associations ($P < 0.05$). For traits evaluated in the current study: SC = sucrose content; GC = glucose content; FC = fructose content; TS = total sugars; and TSS = total soluble solids.

Mapping of QTL for Fruit Size and Shape Traits in Ananas Melon

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Introduction: Mature fruit size and shape are important traits of most melon (*Cucumis melo* L.) types. The former is also an important component of yield in melon. Information on molecular markers linked to genes for these fruit traits may contribute to our understanding of the genetics of fruit size and shape and offer prospects for the use of molecular markers in modification or maintenance of fruit characteristics in melon breeding programs. Therefore, our objective was to identify RAPD markers linked to QTL for fruit weight, length, and diameter in an existing molecular marker-based linkage map constructed by means of an F2 population derived from the melon cross of 'Deltex' (larger fruit size) x TGR1551 (smaller fruit size).

Materials and Methods: One hundred-eight F2 plants from the cross of 'Deltex' x TGR1551 were planted in a greenhouse at the Texas Agricultural Research and Extension Center-Weslaco in 2003. The 'Deltex' parent is an ananas type with larger fruit size, while the TGR1551 parent is a wild type with smaller fruit size. Phenotypic data for fruit weight, length, and diameter were recorded from the 108 F2 plants along with their parents. A RAPD marker-based linkage map was recently developed by Park and Crosby (3) using the 108 F2 plants of the same cross. MAPMAKER version 3.0 (2) was used for the linkage analysis of 208 RAPD markers. The name of each RAPD marker is derived from an "O" prefix for Operon primers, the letters identifying the Operon kit, Operon primer number, and the approximate length (bp) of the marker (3). Simple linear regression (SLR), for each pairwise combination of quantitative traits and marker loci, was used to analyze the data for detection of QTL affecting fruit weight, length, and diameter. Significant differences in trait associations were based on F-tests ($P<0.05$) (1). Loci with the lowest P value per QTL were chosen and then were added in a stepwise multiple regression (SMR) to select the best set of markers ($P<0.05$) for prediction of the total trait phenotypic variation explained by the identified QTL (4). Pearson correlations of fruit size and shape traits were also determined in our population. All statistical analyses were conducted using the Statistical Analysis System (SAS Inst., Cary, N.C.).

Results and Discussion: Continuous frequency distributions for fruit weight, length, and diameter were observed in the F2 population (Figure 1), indicating that the fruit size and shape traits were quantitatively inherited. Mature fruit weight was found to be significantly and positively correlated with fruit length and diameter in the population (Table 1). We also noted a significant positive correlation between fruit length and diameter.

Twenty-two RAPD markers, located on several different linkage groups of the molecular marker-based melon map (Figure 2), were found to be significantly associated with QTL controlling fruit weight, length, or diameter in the F2 population of the 'Deltex' x TGR1551 cross in the greenhouse on the basis of SLR (Table 2).

A total of nine RAPD markers were identified to be significantly associated with QTL for fruit weight in our population based on SLR

(Table 2, Figure 2). Seven unlinked markers associated with QTL were significant in a SMR analysis where the full model explained 42% of the total phenotypic variation for fruit weight.

Five markers were detected to be significantly associated with QTL regulating fruit length in this population by means of SLR (Table 2, Figure 2). Particularly, marker OR02.850 on linkage group 7 amplified from 'Deltex' accounted for 20% of the phenotypic variation for the trait. The five markers were significant in the SMR analysis with a total phenotypic variation of 40% for the fruit length trait.

We found significant associations of eight RAPD markers, located on several different linkage groups of the molecular linkage map, with QTL affecting fruit diameter in the population on the basis of SLR (Table 2, Figure 2). Seven markers were significant in the SMR analysis with a total phenotypic variation of 37% for the fruit diameter trait.

Of the RAPD markers associated with nine QTL for fruit weight in the molecular marker-based linkage group detected here, four on linkage groups 3, 6, 7 and 9 and three on linkage groups 3, 7 and UP3 (Figure 2) were also observed to be significantly associated with QTL for fruit length and diameter, respectively (Table 2), suggesting that in this cross these fruit size and shape traits are controlled partially by the same QTL.

These RAPD markers associated with QTL controlling the mature fruit size and shape traits in the molecular linkage map identified here are expected to be useful in melon breeding programs for modifying fruit size.

These RAPD markers associated with the sugar synthesis QTL in the molecular linkage map detected here could be useful in melon breeding for improving the mature fruit sweetness.

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Table 1. Pearson correlations of fruit weight, length, and diameter in an F2 population derived from the melon cross of 'Deltex' x TGR1551.

Fruit weight and length	Fruit weight and diameter	Fruit length and diameter
0.79**	0.73**	0.24**

**Significant at $P \leq 0.01$.

Table 2. Simple linear regression (SLR) and stepwise multiple regression (SMR) analyses of marker and data for detection of QTL for fruit weight, length, and diameter in an F2 population derived from the cross of 'Deltex' (larger fruit weight) x TGR1551 (smaller fruit weight).

Fruit trait	RAPD marker	Linkage group	SLR		SMR	
			P	R^2	*P*	R^2
Weight	OB06.900	7	0.000	10	0.000	10
	OI03.600	7	0.001	9	0.001	9
	OP17.900	9	0.003	8	0.004	7
	OJ04.450	6	0.005	7	0.007	6
	OQ15.1000	3	0.008	6	0.026	4
	OG05.1050	unassigned	0.026	5	0.034	3
	OG09.300	10	0.038	4	0.045	3
	OK04.600	unassigned	0.028	4		
	OA10.1250	2	0.047	4		
					Cumulative R^2	42
Length	OR02.850	7	0.000	20	0.000	20
	OP17.900	9	0.001	9	0.001	9
	OJ04.450	6	0.017	5	0.015	5
	OQ15.1000	3	0.030	4	0.032	3
	OJ13.400	unassigned	0.040	4	0.043	3
					Cumulative R^2	40
Diameter	OI03.600	7	0.002	8	0.002	8
	OI11.1900	unassigned	0.004	8	0.004	8
	OM06.500	6	0.016	5	0.011	5
	OJ07.900	3	0.011	6	0.013	5
	OC15.1400	2	0.013	6	0.015	5
	OK20.700	11	0.028	4	0.033	3
	OL18.500	12	0.034	4	0.047	3
	OB16.500	unassigned	0.049	4		
					Cumulative R^2	37

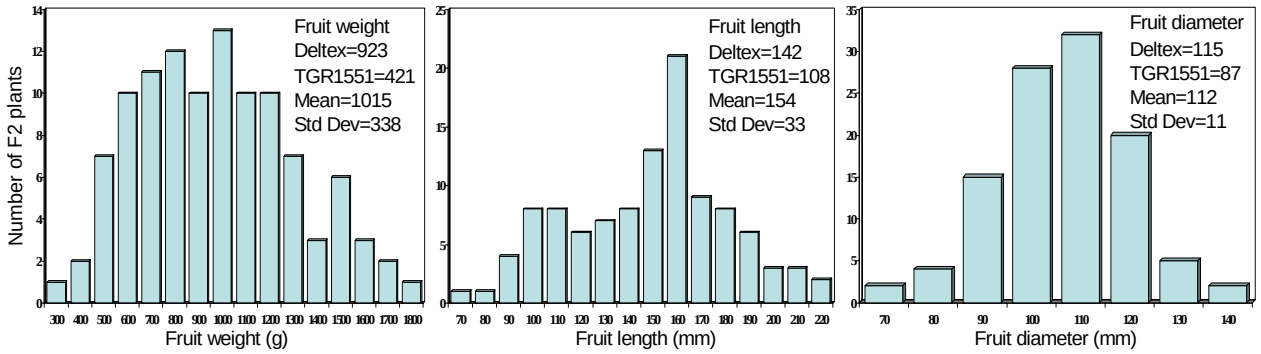

Figure 1. Frequency distributions for fruit weight, length, and diameter of F2 plants derived from the melon cross of 'Deltex' (larger fruit weight) x TGR1551 (smaller fruit weight).

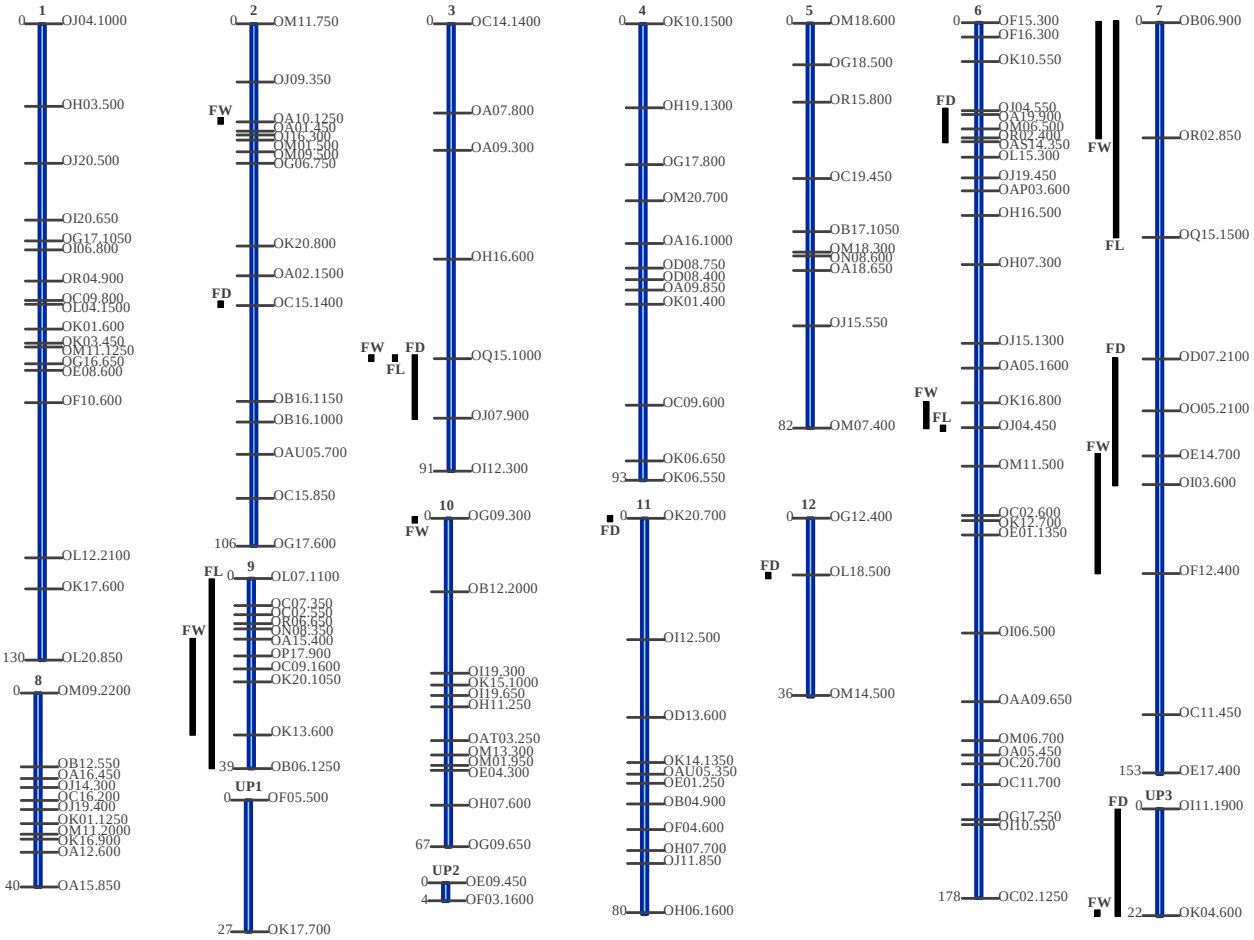

Figure 2. Linkage map for the 'Deltex' x TGR1551 mapping population with locations of QTL for melon fruit size and shape traits. Bars to the left of each linkage group indicate the intervals having significant trait associations ($P < 0.05$). For traits evaluated in the present study: FW=fruit weight; FL=fruit length; and FD=fruit diameter.

Grafted Watermelon Stand Survival After Transplant in a High-Wind Area

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Grafting of watermelon (*Citrullus lanatus* (Thunb.) Matsum. and Nakai) to disease resistant rootstocks is a common practice in many parts of the world but despite the reported advantages, such as resistance to soil-borne diseases and increased water use efficiency, the practice is not common in the U.S. The use of rootstocks has been shown to enhance the vigor of the scion through avoidance of soil pathogens, tolerance of low soil temperatures and/or salinity, and increased scavenging of soil nutrients (2). The type of rootstock has been shown to affect watermelon plant growth and yields (3). Yetisir et.al. (4) demonstrated that the survival rate of grafted plants was inversely correlated with the difference in diameters of scion and rootstock, and that the number of vascular bundles positively affected the growth rate of the grafted watermelon plants. Edelstein, M. et.al. (1) showed that stem diameter and number of vascular bundles of the rootstock did not correlate with scion plant fresh weight for *C. melo* scions and 22 *Cucurbita* spp. rootstocks.

Increases in soil born pathogens accompanied by the loss of effective pesticides such as methyl bromide may necessitate the use of alternative forms of disease control, such as the use of disease resistant rootstocks, in the U.S. One disadvantage that has been observed by growers in the U.S. is a high mortality of grafted watermelon plants. Despite the potential benefits of using grafted watermelon, little research has been done in the U.S. The purpose of this research was to investigate the feasibility of using grafted watermelon plants in high-wind areas.

Materials and Methods: *Plant material.* Watermelon scions included 'Royal Sweet' (diploid) and 'Sugar Time' (triploid), and the rootstock was 'Strongtosa' (an interspecific hybrid between *Cucurbita maxima* and *C. moschata*). Seeds were sown into 3.8 cm square x 6.3 cm deep Speedling flats (#F128A, Speedling, Inc., Sun City, FL) containing Redi-earth growth media (SunGro, Vancouver, BC). The watermelon cultivars were sown 5 d prior to sowing the rootstock. Watermelon plants were 10 to 12 days old at time of grafting.

Grafting. Scions were grafted using a modified tongue and grove method with or without the aid of a wooden pin. The tongue and grove method involved cutting a slit in the rootstock and cutting the scion to fit the grove made in the rootstock. The scion was then attached either with parafilm to hold the two together since clamps were unavailable, or with a toothpick (wooden-pin) inserted into both the scion and rootstock to align the two. This method was also held together with parafilm (Figure 1). Grafted plants were placed in flats in a warm environment for 48 hours. Temperatures ranged from 23^{o}C to 28^{o}C but the environment was not sufficiently humid and there was a high loss of plants shortly after grafting. Seedlings were planted in a Lane, Okla. field 3 weeks later in a randomized complete block design with four replications in a serpentine arrangement. The field had Bernow fine-loamy, siliceous, thermic,

glossic palendalf soil. There were no wind breaks in the field. Survival counts were taken prior to transplanting in the field, and at 3 d and 10 d after transplanting.

Statistics. Means were calculated for grafting frequency by dividing the number of graft attempts by successful grafts (prior to transplanting) for each variety and method. Three and ten day survival frequencies were calculated by dividing number of transplants surviving after 3 d or 10 d by the number of transplants for each treatment. Analysis of variance was performed using Proc GLM with mean separation by Duncan's multiple range test (SAS statistical software, Cary, NC).

Results and Discussion: The wooden-pin modification of the tongue and groove method did speed the grafting process compared to the non-modified method because the toothpick provided sufficient support. Survival of the tongue and groove and wooden-pin modified tongue and groove method were similar, ranging from 33 to 40% success (Table 1), which indicates that the wooden-pin modification did not hinder the healing process.

Both methods were similar for transplant survival after 3 days with a range from 70 to 83%. However, Sugar Time had a lower survival rate (24 to 37%) at day 10 than Royal Sweet (67 to 69%). This may be due to smaller seedling size at time of grafting compared to Strongtosa reducing graft acceptance. Survival of the grafted plants was significantly reduced when compared to the respective survival of non-grafted plants. The primary cause of transplant loss appeared to be tissue breakage at the graft union. Wind conditions in Lane following transplanting had gusts up to 32 mph (Table 2). Very few plants were lost after the 10 day stand count

The goals of any grafting modifications should be to reduce input costs and increase survivability in the field. The methods used here did not show significantly different changes in survivability, but the wooden-pin method did decrease the amount of time required to perform the grafts, which will result in lower costs. However, it appears the added support afforded by the wooden-pin modified method will not result in increased survival of grafted watermelon plants under high wind conditions. Further study is needed with multiple rootstock/ scion combinations and grafting techniques to determine optimal survival rates of grafted plants under high-wind conditions.

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Table 1. Comparison of grafting frequency and transplant survival frequency for the different cultivars and different grafting methods.

Variety	Method	% Graft survival*	Number of transplants	% 3d Survival**	% 10d Survival**
Royal Sweet	Parafilm	26	26	83b	69b
Royal Sweet	Toothpick	33	33	83b	67b
Royal Sweet	Non-grafted	NA	33	100a	91a
Sugar Time	Parafilm	30	30	70b	37b
Sugar Time	Toothpick	29	29	73b	24b
Sugar Time	Non-grafted	NA	33	98a	98a

*% Graft survival = (successful grafts/attempted grafts) x 100. One hundred graft attempts were made for each treatment. There were no significant differences at the $P_{0.05}$ level of probability.
**Percentage of plants surviving 3 and 10 days after transplanting. Means followed by the same letter are not significantly different at the $P_{0.05}$ level of probability.

Table 2. Wind speed weather data for 10 days following transplanting.

Days after transplant	Average (mph)	Gust (mph)
0	5	18
1	8	27
2	5	32
3	9	22
4	8	19
5	9	20
6	8	21
7	7	24
8	6	20
9	8	20
10	6	16

Figure 1. The toothpick modified tongue and groove graft procedure. A groove is made in the rootstock and a tongue is made in the scion to fit the groove. For the modification a toothpick is inserted into the rootstock and the scion is inserted onto the toothpick and pressed down to make contact with the rootstock. Parafilm was used to hold the graft in place.

Rootstock Effects on Plant Vigor and Watermelon Fruit Quality

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Abstract: Watermelon plants grafted onto rootstocks from squash or gourds were planted at Lane, Oklahoma. Weight, dimensions, and quality (SSC, firmness, lycopene content) of a seeded (Summer Flavor® 800) and a seedless (Summer Sweet® 5244) cultivar were measured. Watermelons from non-grafted plants weighed more than those from grafted plants. Fruit shape, determined by length, circumference, and their ratio, did not change significantly from fruit harvested from grafted and not grafted plants. Rind thickness was increased in fruits grafted to the gourd rootstock, '451'. Lycopene and firmness tended to be lower in non-grafted plants. Grafting decreased SSC in diploid fruit but had varying effect on the triploid fruit. The rootstock affected plant vigor in both triploid and diploid scion. These results show that fruit quality varies with both cultivar and rootstock and more vigorous plants tended to have better quality fruit.

Introduction: Grafting of cucurbits to rootstocks of different cucurbit species is a common practice in Asia, parts of Europe, and the Middle East. Use of rootstocks enhances the vigor of the plant through avoidance of soil pathogens, tolerance of low soil temperatures and/or salinity, and vigorous attainment of soil nutrients (Ruiz et al., 1997). The type of rootstock has been shown to affect watermelon plant growth and yields (Yetisir and Sari, 2003). In *Cucumis melo*, the type of rootstock determined yield and foliar phosphorous and magnesium content in the scions (Ruiz et al., 1997).

Watermelon production in the U.S. is increasingly challenged by soil pathogen pressure. Fields have to be rotated on a five to seven year cycle, or even abandoned, if fumigation treatment is unavailable. Grafting of differing cucurbit species to avoid soil pathogen problems is new to many U.S. producers but it promises to be an alternative to fumigation. In fact, some seed companies now offer watermelon transplants that are grafted onto squash or gourd rootstocks. Some literature indicates the rootstock used can alter the scion and resulting yield and quality attributes of the fruit. The purpose of this study was to determine rootstock effects on watermelon fruit quality, including size, sweetness, lycopene content, and firmness under Oklahoma growing conditions**.**

Materials and Methods: Watermelons of diploid and triploid cultivars Summer Flavor 800 (SF800) and Summer Sweet 5244 (SS5244) were obtained as grafted or non-grafted transplants from Abbott & Cobb (McAllen, TX). Plants were controls (no graft), grafted onto cushaw pumpkin (*Cucurbita argyrosperma* C. Huber) or hybrid squash (*C. pepo* L.) rootstocks. Plants were arranged in a randomized complete block design and fertility and care provided as outlined in Motes and Cuperus (1995). Watermelons were harvested, weighed, and length and circumference measured from blossom end to stem end. Fruits were cut lengthwise through the ground spot and rind thickness measured to 0.1 mm using calipers at the thinnest point near the blossom end. Color was taken at two locations in the heart and two locations in the locule areas with a Minolta CR200 colorimeter (Ramsey, NJ), using an 8 mm aperture and in CIE L*a*b*, using D65 illuminant. Firmness was measured in the heart and locule areas of both triploids and diploids, taking care to avoid seeds and seed traces, with a hand held gauge (Wagoner, fruit tester no. FDN20). Tissue in the heart and locule areas was measured for soluble solids content (SSC) by squeezing juice onto an Atago PR100 digital

refractometer (Bellevue, WA). About 50 g of tissue from heart and locule was combined and placed in 50 ml disposable centrifuge tubes and frozen at –80^{O}C. Tissue was homogenized with a Polytron about 2 days after harvest and lycopene determined using a Hunter scanning colorimeter calibrated to white and black plates to determine spectrophotometric concentrations of lycopene (Davis et al., 2003).

Vines were removed from the field, measured for length, number of nodes, and number of tendrils branching from the terminal tendril. A total of 4 to 5 vines per cultivar and graft treatment were used.

Data were subjected to analysis of variance, using a linear model (GLM) and SAS (ver. 8.0). Significant interactions of cultivar and rootstock led to separation of means within cultivars. Means were compared using Bonferroni, a mean comparison test that compares each mean to the overall mean.

Results and Discussion: *Fruit size and shape.* Diploid fruit (SF800) from the non-grafted controls were larger than those from grafted plants, as determined by weight and diameter (Table 1). Grafting did not affect the length, circumference, or diameter of seedless 'SS5244' fruit but grafting did decrease the weight of the fruit. The ratio of length to circumference indicates the degree of roundness in a variety, with 'SS5244' being more round (lower ratio) than 'SF800'. The ratio of length and diameter did not change for either cultivar when grafted, indicating no influence of rootstock on direction of expansion. Rind thickness increased for both seedless and seeded fruits when grafted to gourd rootstock '451' (Table 1).

Fruit quality. Firmness of the diploid and triploid watermelons was greater from plants grafted to rootstock '451' and '1330' (Table 2). Fruit SSC varied with the cultivar and rootstock but tended to be lower in grafted fruit. Grafting did not greatly affect the amount of red found in the fruit, but it did increase the amount of yellow in 3 of the 5 combinations. This may be an indication of increased ß-carotene and should be tested in future studies. Lycopene content was highest in 'SF800' fruit from the squash rootstock grafted plants, while fruit from grafted 'SS5244' plants had higher lycopene compared to control fruit. Nisini et al. (2002) found that both scion and rootstock affected fruit quality in muskmelon. In our experiment, genotype (seeded vs. seedless) may react differently to different rootstocks, warranting more study to find superior combinations. In our study, rootstock '451' produced higher quality seedless fruit when comparing lycopene content, firmness, and SSC than the other two rootstocks and the control. However, seeded fruit from plants grafted to 451 had less SSC than control fruit.

Vine characteristics. Vine vigor, measured as length of the terminal, number of laterals, and internode length on the terminal vine, was equal or greater from plants grafted to the '451' rootstock compared to control or '1330' rootstock (Table 3).

Our data suggest that gourd rootstock '451' is superior for vigor for both scions and for fruit quality of our seedless variety. However, due to high losses of plants, it was not possible to replicate triploid and diploid cultivars on the 1332 rootstocks. While this report requires a larger follow up study, it provides information on attributes to be considered when comparing grafted and non-grafted watermelons, and gives the first report on cultivars grown for typical U.S. markets for fruit quality and vine vigor between grafted and non-grafted watermelon plants.

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Table 1. Comparison of fruit size and shape from grafted and non-grafted watermelons.

									Rind thickness	
Cultivar	Rootstock	Type	number of fruit	wt (kg)	length (cm)	circumference (cm)	diameter (cm)	Length/ diameter ratio	Average	Blossom end (mm)
SF800	None	Control	18	9.0a	33.1a	70.0a	22.3a	1.5a	11.4b	8.9b
	1330	Squash	16	7.4b	31.3a	66.3b	21.1b	1.5a	11.8ab	9.9b
	451	Gourd	10	7.4b	31.0a	67.2ab	21.4b	1.4a	11.4b	11.8a
SS5244	None	Control	25	6.5a	25.7a	69.9a	22.2a	1.2a	12.0ab	9.1ab
(seedless)	1330	Squash	4	5.4a	24.2a	66.0a	21.0a	1.2a	11.1b	8.9b
	1332	Gourd	19	6.6a	25.8a	70.6a	22.5a	1.2a	12.8ab	10.8a
	451	Gourd	27	6.6a	25.1a	70.8a	22.2a	1.1a	13.5a	10.8a

Means separated within cultivar by Bonferoni, $P<0.05$.
Means followed by the same letter are not significantly different by the Bonferoni method at the P0.05 level of probability.

Table 2. Comparison of fruit quality from grafted and non-grafted watermelons.

Cultivar	Number of fruit	Rootstock	Type	SSC[Z]	Firmness (Pa)[Y]	L*	a*	b*	Hue	Chroma	Lyco-pene (ug/g)
SF800	18	None	Control	12.2a	7.9b	33.7b	24.4a	10.7b	23.4b	26.7b	63.7b
	16	1330	Squash	10.9b	10.5a	36.4a	25.6a	12.1a	25.2a	28.2a	65.8a
	10	451	Gourd	10.7b	11.8a	33.7b	27.1a	10.8b	22.9b	27.6ab	60.1b
SS5244	25	None	Control	11.7ab	7.5b	35.1b	25.9b	11.8c	24.3b	28.5b	56.0b
(seedless)	4	1330	Squash	10.7b	10.2a	36.7a	28.0a	14.1a	26.8a	31.3a	61.1a
	19	1332	Gourd	11.6ab	6.3b	34.8b	26.6b	12.9b	25.8ab	29.6b	64.2a
	27	451	Gourd	12.2a	10.5a	35.4b	26.6b	12.4c	23.9b	29.4b	65.4a

[Z] Average of 2 readings, one in the heart and one in the locule.
[Y] Average of 2 heart and 2 locule readings per fruit.
Means separated within cultivar by Bonferoni, P<0.05.
Means followed by the same letter are not significantly different by the Bonferoni method at the P0.05 level of probability.

Table 3. Comparison of vines from grafted and non-grafted watermelons.

Cultivar	**Number of plants**	**Rootstock**	**Type**	**Length of main vine (cm)**	**Number of nodes**	**Internode length (CM)**	**Number of laterals**
SF800	18	none	Control	430.8a	57.0a	7.6ab	16.0b
	16	1330	Squash	418.5a	60.0a	7.0b	16.8b
	10	451	Gourd	430.8a	48.3b	8.8a	18.3a
SS5244	25	none	Control	415.4ab	62.2a	6.7b	9.6b
	19	1332	Gourd	351.1b	54.5b	6.3b	9.3b
	27	451	Gourd	481.5a	62.0a	7.7a	13.4a

Means separated within cultivar by Bonferoni, P<0.05.

Pilot Survey Results to Prioritize Research Needs in the Watermelon Industry

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It is useful for researchers of any commodity to occasionally survey their clientele to monitor for any new developments and make sure their research is focused on major problems. A discussion at the Watermelon Research and Development Working Group meeting in Asheville, NC (2006) led to the development of a survey to solicit responses from a cross section of the watermelon industry. The survey was a list of closed-ended questions with ordered response categories so that respondents would be limited to problems that we felt could be addressed by research. Write-in space is provided in case someone felt that a major issue was left out. The original survey was sent out to watermelon breeders in the private industry, and to growers attending the Texas Watermelon Association Annual Meeting in January, 2007. The purpose of this initial survey was to sample a small subset of the industry, evaluate the results and decide if the survey was useful or whether it could be modified to create a useful survey for a nationwide evaluation.

The results were compiled by inverting the rankings by each respondent to where a ranking of 1 was assigned a value of 5, and ranking of 2 was assigned a value of 4 and so on so that the individual rankings could be added to provide an overall ranking. The results from the seed companies and growers were calculated separately, and because there were more growers responding than seed company representatives, the values from each group were weighted to provide equal representation from each group for the overall ranking.

The results from the seed company respondents separated into three groups (Table 1). The top priority was clearly gummy stem blight, since this one priority had more than twice as many points as any other topic. The second tier of priorities included molecular markers, powdery mildew, fruit quality (including hollow-heart and hard seed coats), and grafting/rootstocks. The third tier included watermelon fruit blotch, Fusarium wilt, post-harvest fruit quality (including fresh cut), triploid production, rootknot nematodes, squash vein yellowing virus, phytonutrients, Anthracnose, vine decline and whiteflies.

The grower respondents were a little more diverse with their responses compared to the seed company respondents. Grafting/ rootstocks was the top priority in need of research investment according to this group of respondents. Fusarium wilt was also a top priority for this group, followed by gummy stem blight, whiteflies, triploid production, and watermelon fruit blotch. Twelve other research topics received a small number of votes by this group which are listed in Table 1.

The weighted averages revealed that gummy stem blight was the number one problem in need of research by the total group of respondents, while grafting/rootstocks was a close second. The next 5 topics included Fusarium wilt, powdery mildew, fruit quality, molecular markers, and watermelon fruit blotch.

While this survey was limited to 5 major seed companies with watermelon breeding programs and only included growers attending the Texas Watermelon Association meeting in 2007, it still provides meaningful insight as to where public researchers should be committing a portion of their research to address needs of the watermelon industry in the U.S.

The original survey has been modified slightly by adding a heading to classify respondents and a few of the categories have been combined, resulting in the current version (Appendix 1). We propose to send this survey to all grower groups, public research and extension programs working on watermelon, as well as private companies working on watermelon. Suggestions on modifying the survey are welcome, and should be sent to Steve King at srking@tamu.edu. Current plans are to finalize the survey and send it out in the fall of 2007.

Acknowledgement:

The authors are grateful to the attendees of the Watermelon Research and Development Working Group meetings in Asheville, NC (2006) and Mobile, AL (2007) for their input and to Patrick Lillard for his revisions. This research was supported by USDA CSREES #2005-34402-16401, "Designing Foods for Health".

Table 1. Results of the research needs survey.

	Total Points[1]			Ranking		
Topic	Seed Co.	Grower	Weighted Ave.[2]	Seed Co.	Grower	Weighted Ave.[2]
Gummy stem blight	21	18	93	1	3	1
Grafting/rootstocks	7	36	75	5	1	2
Fusarium wilt	2	23	40	10	2	3
Powdery mildew	9	7	39	3	8	4
Fruit quality[3]	8	5	33	4	10	5
Molecular markers	10	0	32	2	18	6
Watermelon fruit blotch	4	10	27	6	6	7
White flies	0	16	23	13	4	8
Triploid production	2	11	22	10	5	9
Post harvest fruit quality[4]	4	4	19	6	12	10
Rootknot nematodes	3	3	14	8	14	11
Phytonutrients	1	7	13	12	8	12
Squash vein yellowing virus	3	2	13	8	15	12
Anthracnose	0	8	12	13	7	14
White fly gemini virus	0	5	7	13	10	15
Watermelon vine decline	1	2	6	12	15	16
Leaf miners	0	4	6	13	12	16
Seed transmission of diseases	0	3	4	13	14	18
Downy mildew	0	1	1	13	17	19
Phytopthera capsii	0	0	0	13	18	20
Spider mites	0	0	0	13	18	20

[1]Total points were calculated by inverting the 1 to 5 rating from each respondent and adding the points (e.g. a 1 rating received 5 points and a 5 rating received 1 point).
[2]Weighted averages were calculated by giving each group 50% of the total.
[3]Includes hollow-heart, hard seed coats in seedless rind necrosis and other factors that can be affected pre-harvest.
[4]Includes fresh cut, shelf-life, shipability and other factors that are affected post-harvest

Appendix 1. Copy of the proposed survey

Watermelon Research Needs Survey

Please Check:

_____Grower
_____Shipper
_____Retailer
_____Processor
_____Public Researcher
_____Industry Researcher

If Grower, Please Check (Optional):

Number of Acres Farmed:
_____Less than 100 acres
_____100 to 500 acres
_____More than 500 acres

Areas where you operate (check all that apply):

_____Southeast (FL, GA, SC, etc…)
_____Southwest (TX, NM, etc…)
_____Midwest (OK, MO, AR, IN, etc…)
_____West (CA, AZ, NM, etc…)
_____Mexico
_____Other:_____

Please Rank the top 5 topics that you think should be addressed by research (1 to 5 with 1 = top priority and 5 being lower priority):

Diseases:	**Insects**:
_____Fusarium wilt	_____Whiteflies
_____Why are seedless more susceptible to Fusarium?	_____Spider mites
_____Watermelon vine decline (IL vine decline)	_____Leaf miners
_____Squash vein yellowing virus (FL vine decline)	_____Other insect _____
_____White fly gemini virus	
_____Gummy stem blight	**Breeding/Cultural:**
_____Powdery mildew	_____Grafting/rootstocks
_____Downy mildew	_____Phytonutrients (health benefits)
_____Watermelon fruit blotch	_____Easier triploid production
_____Transmission of WFB by rootstocks	_____Different methods of seedless production
_____Anthracnose	_____Pre-harvest fruit quality (hollow heart, hard seed coats, etc…)
_____Seed transmission of diseases	_____Post-harvest fruit quality (shelf-life, fresh cut, etc…)
_____Phytothera capsii	_____Molecular markers
_____Rootknot nematodes	_____Molecular map
_____Fusarium wilt differentials	
	Rank Other Problems Not Listed:
_____Other Disease:_____	

Any other comments related to research needs (use back of form if necessary):

A New Male Sterile Mutant Identified in Watermelon with Multiple Unique Morphological Features

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Only a few genes controlling male sterility have been reported in watermelon (1). A new spontaneous male sterile mutant was identified in our breeding program from a cross between 'Yellow Doll' and 'Cream of Saskatchewan'. The original cross was made in 2005, and the F_1 was selfed and backcrossed in 2006. The F_2 were grown in the greenhouse in the fall of 2006 to collect phenotypic data. Eight out of 40 plants in the F_2 population showed the male sterile phenotype, which appears to fit a 3:1 segregating ratio suggesting a single recessive gene (χ^2=0.53). However, no mutants were observed in either parents or the F_1.

There were several other morphological features that were unique to the male sterile plants (Fig. 1). The number of leaf lobes was much fewer than normal plants. Seedlings appeared to grow much slower and had a spindly appearance compared to their non-male sterile counterparts. The male sterile mutants also had much longer internodes than non-male sterile plants, and the growth rate of the male sterile mutants appeared to be much slower than normal segregants. The leaf lobing was much less on mutant plants and appears to be less than that reported for the dwarf male-sterile watermelon (*ms-dw*) (2). The curvature of the leaf was also more convex compared to non-male sterile plants. The stem above the first node exhibited a mild fasciation in mature plants, which gradually returned to the normal angular stem above the second node. Microscopic evaluation of anthers from the male sterile mutants revealed that the pollen sac did not dehisce. The female flowering pattern appeared normal. Although we were not able to obtain pollinated fruit from this population, we suspect it is because the plants were old by the time we noticed the male sterility. Reserve seed from this population has been planted in the greenhouse and sib mating appears to be successful.

This mutant appears to be different from the other reported male sterile mutants because of the multiple morphological features that are affected. If this mutant is proven to be unique we will propose *ms-3* as the name for this new gene. This new mutant could be a valuable genetic source for watermelon breeding since it appears that seedlings can be identified that carry the male sterile trait. Progeny from the original cross, as well as fertile F2's have been planted for further evaluation of this unique trait in watermelon.

Acknowledgement:

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Figure 1. Male sterile mutant in watermelon showing anthers that failed to dehisce. Normal leaf lobing can be seen in a fertile sibling in the background.

Spontaneous Mutant Showing Pale Seedling Character in Watermelon [*Citrullus lanatus* (Thunb.) Matsum. and Nakai]

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The pale seedling character in watermelon was reported first in 1979 (1). The pale leaf trait was hypothesized to be controlled by a pair of recessive genes interacting with a single dominant gene (2). The name, delayed green, was proposed for this trait and the symbols *dg* and *I-dg* were proposed for the recessive and dominant genes, respectively (3). Until 1996, it was reported that the dominant allele *I-dg* inhibits the expression of the gene *dg*, since the F_2 populations fit a 13:3 ratio and backcross progeny fit 1:1 ratio (2, 3, 4). But in 1996, it was reported that delayed green is inherited as a single recessive nuclear gene (5).

In 1998, I found a spontaneous mutant which showed a pale seedling character. This study was undertaken to verify the inheritance.

Material and Methods: A spontaneous mutant that shows pale seedling character was found in a breeding line in 1998 in Korea. This line originated from a cross between a yellow-fleshed breeding line and red-fleshed one. In 1992, a cross between the yellow-fleshed line and red-fleshed line, and the backcross of this F_1 to red-fleshed line was made. From 1993, self-pollination was made twice per year to make inbred lines. In the spring of 1998, 5 mutants that showed the pale seedling character out of 10 progeny were found in F_{11} generation and seeds were obtained from all mutants. In the fall of 1998, the crosses were made between pale leaf plants and normal plant of 5 elite lines. In the spring of 2002, F_1 seeds were planted and pollinations were made to obtain backcross and F_2 progeny.

Results and Discussion: In the crosses between pale leaf plants and normal plant of 5 elite lines, the F_1 progeny did not show the trait. The results of the progeny test are recorded in Table 1. In the F_2, a total 488 of 1438 seedlings were scored as pale leaf. The F_1 plants backcrossed with the pale leaf male parent produced a total of 996 pale leaf seedlings were found in a population of 2021 plants. The F_2 population fit a 3:1 ratio (χ^2 = 0.117) and the backcross progeny fit 1:1 ratio (χ^2 = 0.416). These data suggest that the pale seedling character is inherited as a single recessive nuclear gene.

The name, delayed green, and the symbol, *dg*, for pale leaf trait were proposed first in 1986 by Rhodes (3). It is not certain whether the pale leaf trait described here shows the same phenotype with that of the delayed green trait or not. Further study is needed to clarify the relationship of both traits.

The pale leaf trait can be detected at the cotyledon stage by color (Figure 1a). The difference between pale cotyledon and normal one is sometimes not clear when the soil is dry. In the stage of second true leaf, the distinction is more obvious (Figure 1b). The old leaf of pale seedlings becomes more greenish after transplanting, but it is still less green than normal (Figure 1c).

The mutant was first observed in 5 of 10 plants in F_{11} generation. It is suggested that the pale leaf gene (tentatively marked as *pl*) occurred in the F_{10} generation and the mutation occurred in one of the two germ cells from a plant of the F_9 generation or as a somatic mutation from a plant of F_{10} generation (Figure 2). The first alternative could result from unequal crossing-over or

another type of minute chromatin loss, gain, or qualitative change at meiosis; the second could result from failure of minute chromatin duplication, loss of a minute chromatin fragment, or a qualitative change during meiosis.

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Table 1. Segregation for the pale seedling character in the F_2 and backcross populations

Generation	No. of observed plant		Expected ratio	χ^2	Probability
	Green	Pale			
F2					
Pale x Line A	294	102	3:1	0.121	0.750>P>0.500
Pale x Line B	405	135	3:1	0.000	P>0.950
Pale x Line C	264	90	3:1	0.034	0.900>P>0.750
Pale x Line D	277	95	3:1	0.057	0.900>P>0.750
Pale x Line E	198	66	3:1	0.000	P>0.950
Total	1438	488	3:1	0.117	0.750>P>0.500
BC					
(Pale x A) (Pale)	225	218	1:1	0.111	0.750>P>0.500
(Pale x B) (Pale)	290	284	1:1	0.063	0.900>P>0.750
(Pale x C) (Pale)	185	179	1:1	0.099	0.900>P>0.750
(Pale x D) (Pale)	192	185	1:1	0.130	0.750>P>0.500
(Pale x E) (Pale)	133	130	1:1	0.034	0.750>P>0.500
Total	1025	996	1:1	0.416	0.750>P>0.500

Figure 1. Comparison of pale green seedlings with normal one: (left) Top, pale leaf seedling at the cotyledon stage. Bottom, normal, (middle) Top, pale green seedling at the second true leaf stage. Bottom, normal, (right) Left, pale leaf seedling at the pollination stage. Right, normal.

Year	Season	Generation	Progeny-plant	Putative genotype
1992	spring	F_1		
1992	fall	BC_1		
1993	spring	F_2	HY477-3	+/+
			↙-sibs	+/+
1993	fall	F_3	HY477-3-11	+/+
			↙-sibs	+/+
1994	spring	F_4	HY477-3-11-7	+/+
			↙-sibs	+/+
1994	fall	F_5	HY477-3-11-7-11	+/+
			↙-sibs	+/+
1995	spring	F_6	HY477-3-11-7-11-2	+/+
			↙-sibs	+/+
1996	spring	F_7	HY477-3-11-7-11-2-4	+/+
			↙-sibs	+/+
1996	fall	F_8	HY477-3-11-7-11-2-4-1	+/+
			↙-sibs	+/+
1997	spring	F_9	HY477-3-11-7-11-2-4-1-3	+/+
			↙-sibs	+/+
1997	fall	F_{10}	HY477-3-11-7-11-2-4-1-3-2	+/*pl*
			↙-sibs	?/?
1998	spring	F_{11}	HY477-3-11-7-11-2-4-1-3-2-5	+/*pl*
			-1	*pl*/*pl*
			-3	*pl*/*pl*
			-8	*pl*/*pl*
			-9	*pl*/*pl*
			-10	*pl*/*pl*
			-sibs	?/?

Figure 2. The suggestive origin for the recessive allele (*pl*) responsible for the pale seedling character of mutant found in 1998 in Korea

Review of Watermelon Genetics for Plant Breeders

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In watermelon [*Citrullus lanatus* (Thunb.) Matsum. & Nakai var. *lanatus*] breeding, most of the useful traits subject to improvement or study have been either fruit characteristics or resistance to diseases of abiotic and biotic origin, often controlled by single genes. The genetics of watermelon have been studied extensively, and many genes have been characterized during the last 60 to 70 years (8, 9, 14, 15, 40).

Genetics of Plant Architecture and Sex Expression

Plant architecture traits have been minor objectives for watermelon breeders, often limited to the development of cultivars with short vines (dwarf type) to be used by home gardeners. The inheritance of dwarfism has been studied, and some genes producing the dwarf phenotype have been described (19, 23, 25). The dwarf type can be obtained using one of the four genes: *dw–1*, *dw–2*, *dw–3*, and *ms-dw*. Dwarfism in watermelon is caused by shortened internodes (*dw–1*) or reduced internode number (*dw–2*). The mechanism of action of the *dw-3* allele has not been reported.

Genes regulating sex expression in watermelon have not been described, with the exception of the *a* gene for andromonoecious plants, the dominant allele producing monoecious (*A*) (42). No gynoecious or parthenocarpic germplasm has been identified in watermelon, as opposed to cucumber (*Cucumis sativus* L.), where seedless fruit can be obtained from a gynoecious, parthenocarpic cultivar grown in isolation from cucumber pollen. Thus, seedless watermelons are produced only on sterile triploid plants, by inducing fruit formation with diploid pollen.

Male-sterility has been reported in several mutant lines, and four genes have been described to confer this trait. The *ms (ms-1)* gene causes the development of small anthers and pollen abortion (59, 60). In addition, the *ms-2* and *ms-dw* genes for male sterility have recently been identified. The *gms* gene, instead, induces male sterility due to chromosome desynapsis, accompanied by absence of trichomes on the leaves (glabrous male sterile) (53, 54). Technological application of these two genes has been pursued for the production of hybrid seed, even though hand-pollination and daily removal of male flowers are still the most common techniques, probably due to the low cost of labor in the countries of seed production (Asia and Central America) (24).

Genetics of Resistance

Little information is available on the genetics of resistance to abiotic stresses in watermelon, even though traits such as drought and heat tolerance would be useful traits. A single dominant gene (*Ctr*) was identified for tolerance of cold temperatures (<20°C at night) at the seedling stage (37, 38).

The primary nematode species attacking watermelon are the peanut [*Meloidogyne arenaria* (Neal) Chitw.], southern [*M. incognita*, (Kofoid and White) Chitw.], and Javanese [*M. javanica* (Treub) Chitw.] root-knot nematodes. Although losses to these parasites may be as much as 50% (24), the extensive use of fumigants has delayed the search for nematode resistant germplasm and the study of the genetics of resistance. Currently, as methyl bromide is phased out, interest is increasing in the development of nematode resistant cultivars.

Genetic resistance to insect pests does not have a very important role in the protection of watermelon crops. So far, insect control is mostly achieved chemically. Nevertheless, genes for resistance to the red pumpkin beetle (*Aulacophora foveicollis* Lucas), *Af*, and to the fruit fly (*Dacus cucurbitae* Coquillett), *Fwr*, have been identified. Resistance for both genes, *Af* and *Fwr*, was dominant to susceptibility (21, 51). Most insect pests in the United States are specific to each region of watermelon production, making it economically less advantageous to develop insect resistant cultivars. Nevertheless, some pests are common over different areas, i.e. the melon aphid (*Aphis gossypii* Glover) and the cucumber beetle species *Acalymma vittatum* Fabricius and *Diabrotica undecimpunctata howardi* Barber (24). In those cases, genetic resistance may be an efficient alternative to chemical control.

Various species of fungi, viruses, and bacteria cause destructive diseases of watermelon. In the United States, fungal diseases are a major limitation on the watermelon industry in the Southeastern region, while viruses are more damaging in Western production areas. The most important fungal diseases (with causal agent) are anthracnose (*Colletotrichum lagenarium* (Pass.) Ellis & Halst), downy mildew (*Pseudoperonospora cubensis* Berk. & M.A. Curtis), Fusarium wilt (*Fusarium oxysporum* Schlechtend.:Fr. f. sp. *niveum* (E.F. Sm.) W.C. Snyder & H.N. Hans), gummy stem blight (*Didymella bryoniae* (Auersw.) Rehm), Monosporascus root rot and vine decline (*Monosporascus cannonballus* Pollack & Uecker), Phytophthora blight (*Phytophthora capsici* Leonian), Pythium damping-off (*Pythium* spp.), and powdery mildew (*Podosphaera xanthii* (Castagne) U. Braun & N. Shishkoff). The main viral diseases are cucumber mosaic (CMV), papaya ringspot (PRSV type W, previously known as WMV), watermelon mosaic (WMV; previously known as WMV-2), squash mosaic (SqMV), zucchini yellow mosaic (ZYMV), and the watermelon vine decline virus. Bacterial fruit blotch, caused by *Acidovorax avenae* subsp. *citrulli* Schaad et al. is a serious disease that is seedborne. Despite the high number of biotic pathogens listed, the genetics of resistance have been described only for the control of Fusarium wilt, gummy stem blight, anthracnose, watermelon mosaic, and zucchini yellow mosaic (11, 57).

Seven races of anthracnose have been reported, but races 1, 2, and 3 appear to be the most important in watermelon (24). Most cultivars are resistant to races 1 and 3, and resistance sources to race 2 have been identified, with PI 512385 being the most resistant (3). Resistance to all three races was inherited as a dominant gene in multiple crosses: *Ar-1* conferred resistance to races 1 and 3 (22), and *Ar-2*[1] to race 2 (56).

Resistance has been found for three races (0, 1, and 2) of Fusarium wilt, and watermelon differentials have been identified. 'Black Diamond' and 'Sugar Baby' are susceptible to all races, 'Quetzali' and 'Mickylee' are resistant to race 0, 'Charleston Gray' is resistant to race 0 and moderately resistant to race 1, 'Calhoun Gray' is resistant to races 0 and 1, and PI 296341 and PI 271769 are resistant to all races (Table 1) (24). In addition, the inheritance of resistance to race 1 has been described. Resistance was inherited as a single dominant gene (*Fo-1*) in crosses of the resistant 'Calhoun Gray' or 'Summit' with the susceptible 'NH Midget' (16).

Resistance to gummy stem blight was found in PI 189225 and PI 271778 and deployed as a single recessive gene (*db*) to develop the resistant cultivars 'AU-Producer', 'AU-Golden Producer', 'AU-Jubilant', and 'AU-Sweet Scarlet' (28-31). Nevertheless, these cultivars were less resistant than their resistant parents, thus demonstrating the difficulty of transferring resistance to gummy stem blight.

Watermelon resistance to viruses has been identified for PRSV, WMV, and ZYMV (24). So far, two genes for resistance to zucchini yellow mosaic have been reported. Plants homozygous for *zym*-FL were resistant to a strain of ZYMV from Florida (36). More recently, resistance to a Chinese strain of the same virus was inherited as the single recessive gene *zym-CH* (57). In addition, Xu et al. (2004) estimated that tolerance to watermelon mosaic in two crosses was controlled by a minimum of two genes with high broad-sense heritability.

Finally, one recessive gene (*pm*) for the susceptibility to powdery mildew was reported (41). In addition, resistance to the isolates causing problems now has been reported, and research is in progress on the inheritance of resistance to this important new disease in watermelon.

Genetics of Fruit Characteristics

The watermelon fruit consists of the exocarp, mesocarp, and endocarp. The endocarp is the seed-containing part that is consumed as food, and the mesocarp (white crisp inner layer) and exocarp (thin green outer layer) are usually referred to as the rind. Fruit traits of interest in watermelon can be grouped into six categories: 1) yield, 2) shape, 3) weight, 4) rind, 5) flesh, and 6) seeds. Each of these categories includes characteristics that are important for successful cultivars. Yield may be determined by the number of fruit per unit of production and may be separated into marketable and non-marketable yield (culls), based on the overall external appearance of the fruit. The rind may differ in color, pattern, thickness, toughness, and flexibility. The flesh may differ in color, texture, sweetness (sugar or total soluble solids content), and resistance to hollowheart (internal voids). The seeds may differ for color, size, and resistance to formation of hard seed coats in triploid (seedless) watermelons.

The inheritance of yield components in watermelon was studied extensively in the 1960s and 1970s. Heterosis and general (GCA) and specific (SCA) combining ability were measured in many crosses (6, 7, 26, 27, 46-49). More recent studies of the effects of reciprocal crosses on yield components in watermelon have been contradictory (10, 39, 43). Heterosis was inconsistent over experiments, but the studies involved either diallel or top crosses of elite inbreds, and not a random set of lines from a population. Furthermore, the experiments included only a small number of non-randomly chosen elite cultivars as parents, so the results are valid only for those specific crosses and are not generally applicable.

Watermelon fruit can be round, oval, blocky, or elongate in shape (24). The inheritance of fruit shape has not been widely studied, but the round, oval, and elongate phenotypes were shown to be determined by the incomplete dominance of the *O* gene. The homozygous dominant plants had elongated fruit, the homozygous recessive fruit were round (spherical), and the heterozygous fruit were oval (33, 55). In addition, the shape of the fruit can be predicted by the shape of the ovary at anthesis, thus making ovary shape a useful marker for things such as hybrid seed production (52).

The fruit of the cultivated watermelon may vary in weight from 1 to 100 kg. In the United States, commercial fruit are usually classified into four categories: icebox (<5.5 kg), small or pee-wee (5.5-8.0 kg), medium (8.1-11.0 kg), large (11.1-14.5 kg), and giant (>14.5 kg) (24). Recently, the icebox category was divided into mini (<4 kg) and icebox (4-5.5 kg) fruit sizes. Fruit weight in watermelon production is a yield component, which contributes to total yield per unit of land. However, since fruit of different sizes are marketed in different categories, fruit weight should be regarded as a descriptor of fruit type. In two preliminary studies of inheritance of fruit weight, significant additive, dominant, and epistatic effects were reported, dominance and dominance-by-

dominance being the largest gene effects (4, 44). Nevertheless, single genes or quantitative trait loci have not been identified for the weight of watermelon fruit.

Both mechanical characteristics and color of the watermelon rind are of great importance to the development of cultivars with good shipping ability, long shelf-life, and attractive appearance. The only gene reported to influence the mechanical characteristics of the rind (toughness and flexibility) was the *t* gene for the thin, tender rind, bursting when cut, from 'California Klondike' (35), renamed *e* for explosive rind by Poole (1944). So far, no study has described the inheritance of rind toughness among watermelon families with non-explosive rind.

The inheritance of rind color and pattern has been studied since the 1930s. The most common rind colors are solid green (dark, medium, and light), striped (narrow, medium, and wide dark green stripes on a light green background), and gray (medium green lines on a light green background). The genes described for the different skin colors and patterns are part of a three-allele series at the *g* locus: *G* for dark green, g^s for striped, and *g* for light green (55). However, this model does not seem to apply in all watermelon cultivars. Furthermore, the inheritance of some rind colors such as gray or medium-green have not been published, even though these have been two common colors during the last century of watermelon breeding.

The genetics of the flesh color in watermelon have been studied and genes for the red, orange, salmon yellow, canary yellow, and white colors have been reported. A triple-allelic series was identified at the *y* locus to regulate red, orange, and salmon yellow flesh colors (*Y*, y^o, and *y*, respectively) (17, 18, 32, 35). The canary yellow color (*C* gene) was dominant to pink (*c*) and epistatic to red (*Y*) (18, 32). In addition, the red color was also recorded in individuals homozygous for *C*, where the production of the yellow pigment was inhibited by the *i-C* gene (inhibitor of canary yellow) (18, 40). A third gene for the yellow flesh (*B*) has also been described in a breeding line. The white flesh gene (*Wf*) was epistatic to *B* (15, 45). Nevertheless, breeding for specific flesh colors has often been challenging, due to frequent distortion of the inheritance of some of these genes, thus suggesting that a more complex model may determine flesh color in segregating populations of watermelon.

Sugar content of the flesh in watermelon is measured as total soluble solids (degrees Brix). It is the major component of taste, and may vary from 1 to 16° Brix (24). So far, no study of the genetics of total soluble solids based on a set of cultivars representative of a large range of watermelon germplasm has been reported. Furthermore, preliminary studies included parents that differed by only 2 to 3 °Brix in sugar content (2, 5). A study of crosses between cultivars at the extremes of the range of watermelon sweetness would be useful to the improvement of the organoleptic properties of the flesh of watermelon.

Genetics of Seed Characteristics

Watermelon seeds usually are classified according to their color and size, both traits being of great interest to breeders. Seed color may affect the appearance of cut fruit greatly (seed color that contrasts with flesh color are usually preferred), while their size can limit the edibility of the fruit itself. Large seeds usually are removed from the flesh when consumed, while tiny (tomato seed) seeds might be ingested. Most of the current commercial cultivars have short (small) or medium size seeds, rather than long (large) or tomato seed.

Commercially, watermelon seeds are categorized by size: long (or large), medium, short (or small) (approximately 10, 7, and 5 mm long), and tomato seed (watermelon seeds the size of tomato seeds). According to Poole et al. (1941), the *l* and *s* genes interact

to determine seed size for the long, medium, and short classes (*ll SS* for long, *LL SS* for medium, and *LL ss* or *ll ss* for short). The tomato seed size was studied in a cross between a 'Sugar Baby' mutant with tomato seed size and 'GN-1', with short seeds. The tomato seed size trait was inherited as a single recessive gene (*ts*) (58). The interaction of *ts* with *l* and *s* has not been described so far. In addition, a gene (*Ti*), dominant over medium seeds, has been described for the so-called "tiny" seed-size in 'Sweet Princess' (50). Tiny seeds have size similar to small seeds (Fig. 2).

The main colors of watermelon seeds are white, tan, brown, black, red, green, and dotted (24). In addition, seeds may have lighter or darker margins (ring), or may be covered by an additional layer of fleshy pericarp in Egusi cultivars, as controlled by the *eg* gene (Fig. 1) (12, 13).

The genes *r*, *t*, and *w* determine seed color. Black is given by triple dominant; mottled is homozygous recessive only for *w*; tan is homozygous recessive only for *t*; white with tan tip is homozygous recessive only for *t* and *w*; red is homozygous recessive only for *r* and *t*. Finally, triple recessive results in white seeds with pink tip (34). The dotted (renamed from mottled) seed type is determined by the *d* gene, acting as a modifier of black: *RR TT WW DD* gives solid black and *RR TT WW dd* gives dotted black seed-coat (20, 32, 34).

Seeds of certain cultivars show vertical cracks (parallel to the longest axis of the seed) of the seed-coat, usually less than one mm wide and about 50-75% of the seed length. The development of these cracks has been determined to be under the genetic control of *cr* (1). It is not known if this phenotype has any advantage in germination and whether growers would perceive seeds with cracks as defective, compared to normal seeds.

Other genes of minor interest to breeders have been studied and described, as reported in the current watermelon gene list (11). These include genes for green flower color (*gf*), golden leaf color (*go*), along with several genes coding for specific proteins. In addition, watermelon breeders have selected for many different characteristics, such as flesh color, rind pattern, plant architecture, and leaf shape, for which the inheritance is unknown so far. Efforts are under way to collect mutants for storage and distribution by the Cucurbit Genetics Cooperative watermelon gene curators (T.C. Wehner and S.R. King).

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Table 1. Watermelon differentials useful for identification of Fusarium wilt races 0, 1, and 2.

Cultivar	Race 0	Race 1	Race 2
'Black Diamond', 'Sugar Baby'	S	S	S
'Quetzali', 'Mickylee'	R	S	S
'Charleston Gray'	R	M	S
'Calhoun Gray'	R	R	S
PI 296341, PI 271769	R	R	R

S=susceptible, M=moderately resistant, R=resistant. Fusarium wilt is caused by *Fusarium oxysporum* Schlechtend.:Fr. f. sp. *niveum* (E.F. Sm.) W.C. Snyder & H.N. Hans.

Figure 1. Watermelon seeds covered by an additional layer of fleshy pericarp in Egusi cultivars, as controlled by the *eg* gene.

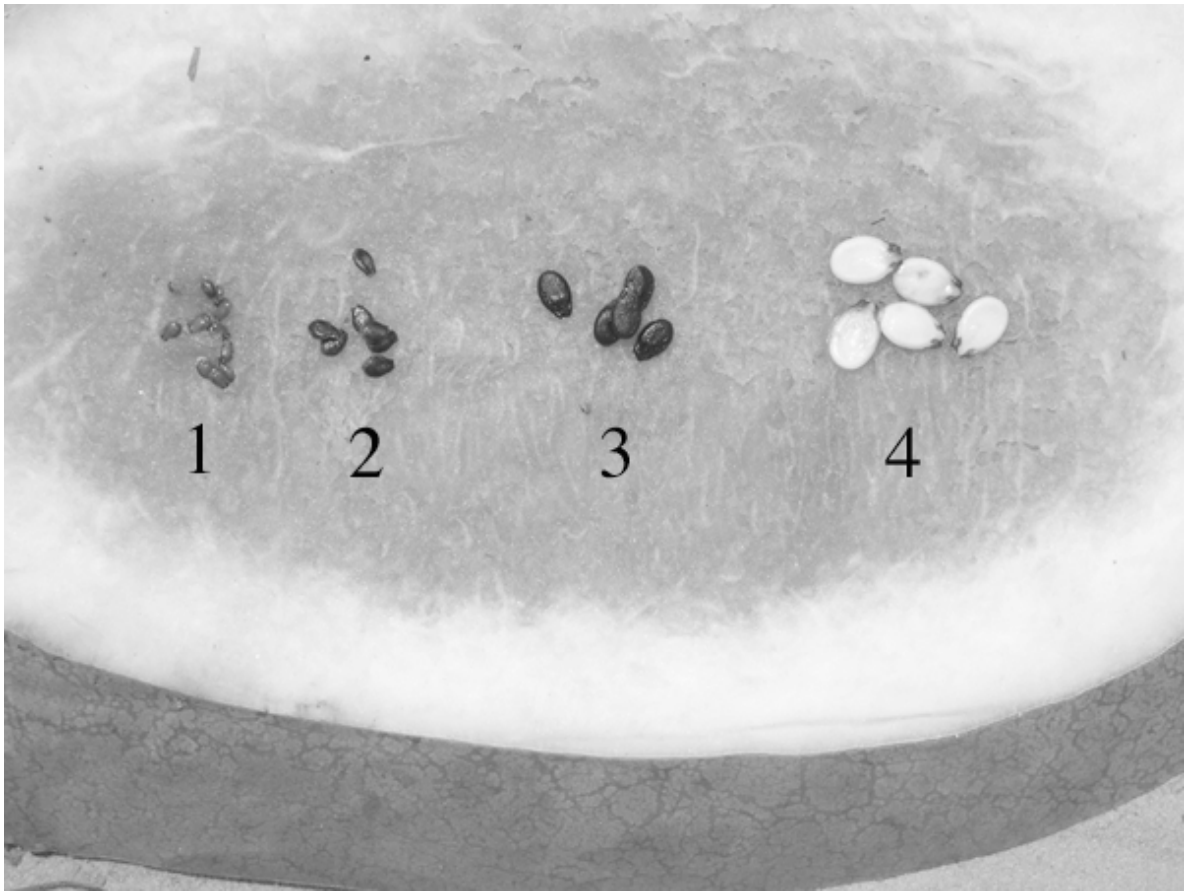

Figure 2. Watermelon seed size: 1 = tomato size (watermelon seeds the size of tomato seeds), *LL ss tsts* or *ll ss tsts*; 2 = short (or small, 5 mm long), *LL ss* or *ll ss*; 3 = medium (7 mm long), *LL SS*; and 4 = long (or large) (10 mm long), *ll SS*.

Milestones in Watermelon Cultivar Development

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Watermelon [*Citrullus lanatus* (Thunb.) Matsum. & Nakai var. *lanatus*] is a major vegetable crop in the United States. Total production from 1999 to 2002 was 1.67 million Mg•year^{-1} of marketable fruit, and the consumption *per capita* was 6.6 kg of fresh fruit (3-5, 7). During that time, the state with the highest production was Florida (ca. 380,000 Mg•year^{-1}), and the state with the largest cultivated area was Texas (ca. 18,000 ha•year^{-1}) (6).

Watermelon breeding has been going on for thousands of years, but science-based programs in the U.S. were not started until the late 1800s. By 1900, 'Angeleno', 'Chilean', 'Florida Favorite', 'Georgia Rattlesnake', 'Cole Early', 'Kleckley Sweet', and other open-pollinated cultivars had been released (8). Initially, many watermelon cultivars with different fruit types were available to growers. However, as the market became more established, the cultivars converged on a few types. In addition, the limits to production imposed by new diseases favored those cultivars having resistance.

In 1954, C.F. Andrus released 'Charleston Gray', with elongate fruit shape, gray rind, and red flesh (Fig. 1). It was resistant to Fusarium wilt, anthracnose, and sunburn. 'Charleston Gray' became the leading cultivar in the commercial market, although niche markets and home gardeners continued to use a diverse array of types. In 1970, C.V. Hall released 'Allsweet' (Fig. 2) with resistance similar to 'Charleston Gray', but improved fruit quality. 'Allsweet' had elongate fruit shape and rind with wide dark green stripes. The Allsweet fruit type is still popular, even though alternative types have been introduced to the consumers during the last thirty years. Examples of new types are 'Dixielee' and 'Crimson Sweet', both having round fruit with narrow dark green stripes on a light green background. Another type is 'Sugar Baby', with round fruit and solid dark green rind.

A major change in watermelon breeding in the United States occurred in 1962 with the release of the first seedless watermelon cultivar, 'Tri-X-313', by O.J. Eigsti. However, it was not until the 1990s that seedless watermelons became commercially important, due to the slow improvement in fertility of the tetraploid parents used as the female parent in the production of triploid (seedless) hybrids.

In addition to Andrus, Eigsti, and Hall, a few other major contributors have improved American watermelons in the last fifty years. In the 1950s and 1960s, J.M Crall (University of Florida, Leesburg) released 'Dixielee', a successful alternative to 'Allsweet' for its different fruit-type and superior quality, and 'Minilee' and 'Mickylee', the first icebox (<5.5 kg/fruit) cultivars adapted to the Southeastern United States. Since the 1980s, W.S. Barham improved the techniques for breeding and producing seedless cultivars. In the 1980s and 1990s, T.V. Williams developed the hybrids 'Fiesta', 'Mardi Gras', and 'Sangria', which dominated the market during that time.

In 2003, X. Zhang introduced the mini seedless watermelon type, having 1.5 to 4.0 kg fruit weight. They appeal to those in small families who do not want to store leftover watermelon that cannot be finished in one meal. The first two cultivars released were 'Petite Perfection' and 'Precious Petite' (Syngenta Seeds - Rogers Brand) (1, 2).

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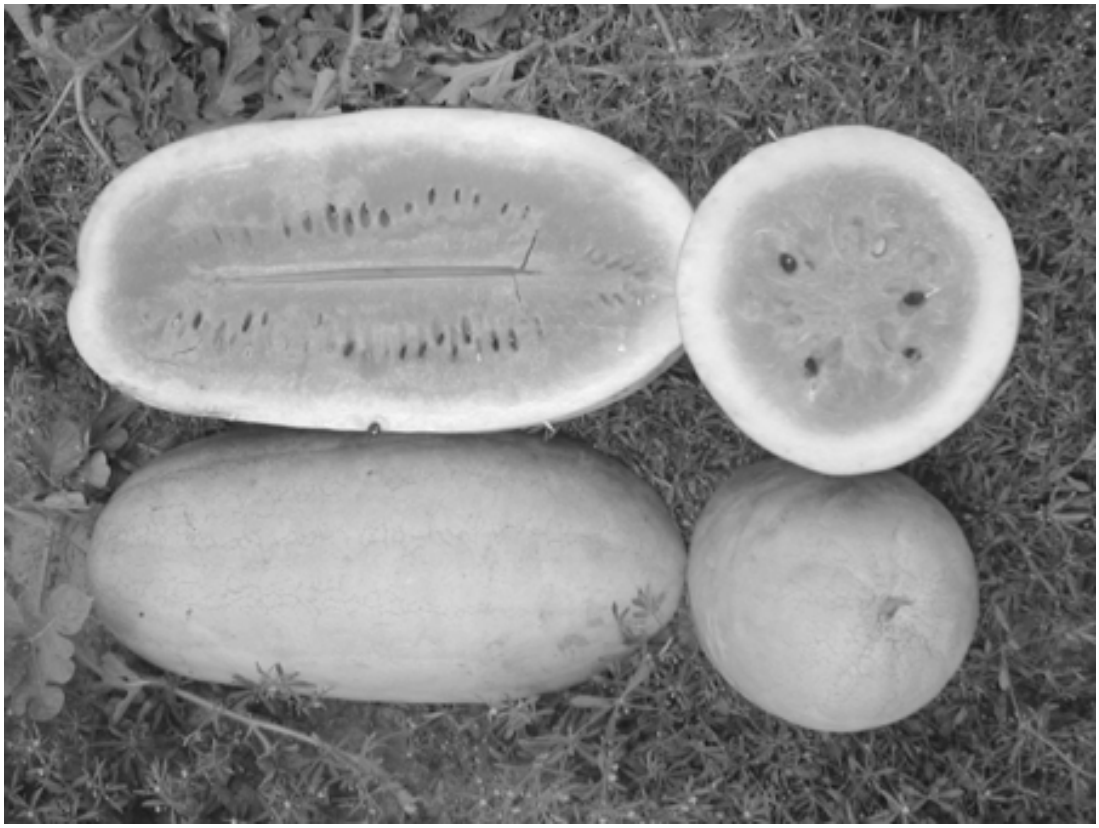

Figure 1. Cultivar Charleston Gray, released in 1954 by C.F. Andrus. Resistant to Fusarium wilt, anthracnose, and sunburn.

Figure 2. Cultivar Allsweet, released in 1970 by C.V. Hall. Resistance similar to 'Charleston Gray', but higher fruit quality.

Systematic Studies on the Family *Cucurbitaceae* of Eastern Bihar, India

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In India, the family *Cucurbitaceae* is represented by 36 genera and 100 species (2). *Cucurbitaceae* are a major family among economically important domesticated species, particularly those with edible fruits including cucumber (*Cucumis sativus*), melon (*Cucumis melo*), watermelon (*Citrullus lanatus*), squash and pumpkin (*Cucurbita* spp.), bitter melon (*Momordica charantia*), chayote (*Sechium edule*), loofah (*Luffa* spp.), bottle gourd (*Lagenaria siceraria*), snake gourd (*Trichosanthes cucumerina* var. *anguina*) and wax gourd (*Benincasa hispida*). Some of these represent the earliest cultivated plants. Some have medicinal and other uses. Those with hard- shelled fruits, particularly *Lagenaria*, have been used to manufacture containers and musical instruments since ancient times.

Bihar lies between 24°20'10'' N to 27°31'15" N and 83°19'50" E to 88°17'40" E. Its boundaries touch Nepal in the North , the SState of Jharkhand in the South, the State of West Bengal in the East, and the State of Uttar Pradesh in the West. Bihar State covers an area of 99,200 km^2 and is divided into 38 districts. In Bihar, the river Ganga flows from West to East. The Gangetic plain, created by the Ganga and its tributaries Kosi, Sone, Gandak, etc., forms almost a flat alluvial plain except for the Himalayan foot hills and the tarai regions in the extreme northwest. The eastern Bihar consists of 7 districts viz., Bhagalpur, Purnia, Katihar, Saharsa, Madhepura, Araria and Kishanganj. The rich vegetation and diversity of Bihar have attracted the attention of a number of explorers and botanists during history (1).

For this study, a total number of 11 genera and 24 species were collected from different areas is Eastern Bihar. The genera included *Benincasa, Coccinia, Cucumis, Cucurbita, Citrullus, Diplocyclos, Lagenaria, Luffa, Melothria*, *Momordica,* and *Trichosanthes.* The genera *Benincasa*, *Coccinia*, *Diplocyclos*, and *Lagenaria* were represented by one species each. *Citrullus*, *Melothria*, *Momordica* and *Cucumis* included two species, whereas *Cucurbita* and *Trichosanthes* included three species each. The genus *Luffa* was the largest genus represented by four species. It is evident from the study that the species collected during field surveys are found in all the districts of Eastern Bihar except a few species which are confined to a particular district. *Luffa echinata* and *Melothria heterophylla* are confined to Katihar, *Citrullus colocynthis* are confined to Kishnaganj, *Luffa hermaphrodita* and *Trichosanthes tricuspidata* are confined to Bhagalpur and *Melothria maderspatana* is confined to Purnia.

Cucurbitaceae in Eastern Bihar include both wild and cultivated taxa. The wild species collected during this study were *Coccinia grandis, Cucumis melo* var. *agrestis, Diplocyclos palmatus, Luffa echinata, Melothria maderspatana*, *M. heterophylla, Trichosanthes cucumerina,* and *T. tricuspidata*. Cultivated species were: *Benincasa hispida*, *Citrullus colocynthis, C. lanatus, Coccinia grandis, Cucumis melo,* var. *momordica, C. melo*. var *utillissimus, Cucumis sativus*, *Cucurbita maxima, C. moschata, C. pepo, Lagenaria siceraria, Luffa acutangula, L. cylindrica, L. hermaphrodita, Momordica charantia, M. dioica, T. cucumerina* var. *anguina*, and *T. dioica*. The cultivated taxa (*Benincasa hispida, Coccinia grandis, Cucurbita maxima, C. moschata, C. pepo, Lagenaria siceraria, Luffa acutangula, L. cylindrica, L.*

hermaphrodita, Momordica charantia, M. dioica, T. cucumerina var. *anguina,* and *T. dioica*.) are mainly grown in "*diara*" regions. *Citrullus lanatus, Cucumis melo,* var. *momordica, C. melo.* var *utillissimus, C. sativus* are cultivated for their edible fruits. *Luffa hermaphrodita* is cultivated mainly in Bhagalpur district. *Cucumis melo* var. *agrestis*, found growing in a wild condition in all the districts of eastern Bihar, is sold in the market as a vegetable crop.

Cucurbits are also used in the indigenous system of medicine. *Lagenaria siceraria*, *Trichosanthes dioica*, *T. cucumerina*, *T. cucumerina* var. *anguina*, and *Benincasa hispida* are rich in protein and vitamin C. Each and every part of pointed gourd has high nutritional value. The roots contain amorphous saponin. Species of *Momordica* are used in diabetes. The seeds of *Citrullus lanatus* are used as cooling medicine. Root, stem, and leaves of *Coccinia grandis* are used in indigenous medicine against skin diseases. Fruits of melons are eaten when ripe and are also used in chronic eczema. Bottle gourd (*Lagenaria siceraria*), ribbed gourd (*Luffa acutangula*), white gourd (*Benincasa hispida*), cucumber (*Cucumis sativus*), and pointed gourd (*Trichosanthes dioica*) are some of the most common vegetables (3).

Plants included in the study are extensive climbers, generally monoecious. The stem varies from slender to robust, sulcate, leaves are cordate to acute or, upper surface of the lamina is 3- lobed, lobes obtuse in *Diplocyclos palmatus*; 3-7 lobed in *Trichosanthes tricuspidata*; shortly trilobed or angular or apex acute or shortly acuminate, basal sinus broad, deep in *Lagenaria siceraria*; 5-lobed in *Trichosanthes cucumerina* var. *anguina*; deeply 5-lobed or obscurely 5-angled, apex round in *Luffa echinata*; 5-7 lobed in *Trichosanthes cucumerina* var. *anguina*; terminal lobe acute, others round in *Citrullus lanatus*; entire to palmately lobed in *Coccinia grandis*; basal lobes narrow round, 1.5-2.0 cm deep round on both surfaces in *Trichosanthes dioica.* The tendril bifid in *Citrullus lanatus*, *Cucurbita pepo*, *Diplocyclos palmatus*; 3-fid in *Trichosanthes tricuspidata*, *Luffa acutangula*, *L. cylindrica*; 2-6 fid in *Cucurbita maxima*; 2-3 fid in *T. cucumerina* var. *anguina*, *T. cucumerina*, many fids in *Cucurbita moschata*. The shape of tendril varies from slender to filiform. The male flowers fasiculate in *Cucumis melo, C. sativus*, *Melothria maderspatana*; solitary in *Momordica charantia*, *M. dioica*, *Cucurbita moschata*; racemose or paniculata; either solitary, robust in *Trichosanthes cucumerina* var. *anguina*; few to many - flowered in *Melothria heterophylla*; 5-12 flowered in *Luffa echinata*; 15-20 flowered in *Luffa cylindrica*; 17-20 flowered at the apex in *Luffa acutangula*. The female flower is solitary in *Cucurbita maxima, C. moschata*, *Trichosanthes cucumerina* var. *anguina*, *T. dioica*, *T. tricuspidata*, solitary, solitary or fasciculate in *Cucumis sativus*; solitary or sub fasciculate in *Melothria maderspatana*; solitary or with axillary male flowers in *Melothria heterophylla*. The fruit ovoid in *Momordica dioica*, *Luffa echinata*, *Benincasa hispida*; ovoid, conical tappering at both ends with a long sharp beak in *Trichosanthes cucumerina*; oblong in *Melothria heterophylla*; oblong, glaborous in *Cucumis sativus*; oblong, glabrous, smooth in *Trichosanthes dioica*; oblong-ellipsoidal, angular, smooth, compressed inconspicuously winged in *Luffa hermaphrodita*; oblong, muricate-tuberculate, trivalved in *Momordica charantia*; oblong, constricted at the middle in *Cucurbita moschata*; oblong-clavate, angular, acutely 10-angled in *Luffa acutangula*; globose in *Diplocyclos palmatus*; globose, slightly depressed in *Citrullus colocynthis*; globose, smooth, echinate in *Melothria maderspatana*; globose, glabrous, ellipsoid in *Trichosanthes tricuspidata*; subglobose or ellipsoid in *Citrullus lanatus*; fusiform, obtuse in *Luffa cylindrica*; cylindric often twisted/coiled in *Trichosanthes cucumerina* var. *anguina*;

subglabrous, round at both ends in *Coccinia grandis*; polymorphous in *Cucumis melo*; variable in shape in *Cucurbita pep*o; variously shaped in *Lagenaria siceraria*, dehiscent at apex in *Momordica charantia*. The seeds are oblong in *Citrullus lanatus*, *Coccinia grandis*, *Cucumis melo*, *C. sativus*, oblong, corrugated, finely rugulose; undulate in *Trichosanthes cucumerina* var. *anguina*; *Luffa acutangula*, *L. cylindrica*, *Cucurbita maxima*; ovate- oblong in *Citrullus colocynthis*, ovate-oblong, undulate, truncate or slightly in *Trichosanthes cucumerina*; ovate, beaked in *Luffa hermaphrodita*; ovate, broad, attenuate in *Diplocyclos palmatus*; ovate, slightly verrucosa in *Luffa echinata*; broadly or narrowly ovate in *Cucurbita moschata*, *C. pepo*; obovate-oblong or triangular in *Lagenaria* siceraria; ovoid in *Benincasa hispida*. The spermoderm pattern varies from rugulate to retico-rugulate in the family Cucurbitaceae. The majority of the taxa show rugulate pattern of spermoderm viz., *Benincasa hispida*, *Cucumis melo* var. *momordica*, *C. melo* var. *utillissimus*, *C. sativus Citrullus colocynthis*, *Cucurbita maxima*, *C. moschata*, *C. pepo Lagenaria siceraria*, *Luffa acutangula*, *Trichosanthes cucumerina*, *T. cucumerina* var. *anguina*, *T. tricuspidata*, *Momordica charantia*,. The spermoderm pattern varies from retico-rugulate (*Citrullus lanatus*, *Coccinia grandis*)*;* reticulate (*Cucumis melo* var. *agrestis*, *Diplocyclos palmatus*, *Luffa echinata*, *L. hermaphrodita Melothria heterophylla*, *M. maderspatana*, *Momordica dioica*, *Trichosanthes dioica*) to tuberculate (*Luffa cylindrica*).

Flowering and fruiting were observed throughout the year in *Coccinia grandis*; from June to October in *Benincasa hispida*; November to January in *Citrullus colocynthis*; March to July in *Citrullus lanatus*; July to September in *C. melo* var. *momordica;* March to June in *C. melo* var. *utilissimus;* May to October in *Cucumis melo* var. *agrestis;* March to October in *Cucumis sativus;* March to August in *Cucurbita maxima;* March to December in *Cucurbita moschata;* July to October in *Cucurbita pepo;* July to May in *Lagenaria siceraria;* June to October in *Luffa acutangula;* June to December in *Luffa cylindrica;* September to January in *Luffa echinata;* August to November in *Luffa hermaphrodita;* June to March in *Melothria heterophylla;* July to December in *Melothria maderspatana*; June to October in *Momordica charantia*; June to October in *Momordica dioica*, *Trichosanthes cucumerina*; May to August in *Trichosanthes cucumerina* var. *anguina*; March to September in *Trichosanthes dioica;* and June to November in *Trichosanthes tricuspidata*.

Coccinia grandis is one of the most common cucurbitaceous plants found throughout the State, spreading or climbing, rather vigorously on bushes, trees, walls and old buildings. *Cucumis melo* var. *agrestis* is common in waste places and cultivated fields. *Diplocyclos palmatus* are common in waste places, Ganga banks, road side bushes, trees and hedges. The species is conspicuous in the field due to bunches of globose, green or red, white striped fruits. *Trichosanthes cucumerina* is common during the rainy season on walls, old buildings, wayside bushes and trees.

Luffa hermaphrodita is cultivated throughout Bihar during the rainy season. However, cultivars vary in their fruit morphology (shape, size, number of fruits per inflorescence). One peculiar feature observed was that the number of female flowers in an inflorescence varies from 4-15 and all the ovaries do not develop into fruits. During our survey we have found that cultivars of *L. hermaphrodita* bear seven fruits in each inflorescence and this appears to be a constant feature of the cultivars. On the basis of development of seven fruits per inflorescences, *L. hermaphrodita* is locally known as "*Satputia*" meaning seven children. In *L. cylindrica* usually two different cultivars are being grown by the

local farmers. One has dark green fruits and other has light green fruits. In the former, the seeds are grey whereas in latter the seeds are ash coloured. The shape and size of the fruits are more or less similar. *L. acutangula* is also under cultivation. The cultivars can be distinguishable on the basis of their fruit morphology. The uniform character of all the cultivars is ridged fruits. *L. acutangula* is grows in the wild. The fruits are no doubt angular in the beginning but as the fruits attain maturity, their angular nature slowly disappears and fruit becomes shorter in length. It has been observed that fruits of some cultivars become bitter in taste. *L. echinata*, a wild species, is confined to North Bihar especially in Purnea and Katihar district. The genus *Trichosanthes* exhibits diversity at specific and infraspecific levels. This diversity needs to be conserved especially in *T. dioica* where varieties are known only under cultivation. Farmers prefer certain cultivars for large scale cultivation. Germplasm of less preferred varieties may vanish forever if conservation measures are not taken immediately (4).

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Cucumis SSR Markers Applied to the Study of Genetic Diversity in the *Cucurbita* Genus

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The genus *Cucurbita* L. includes five cultivated species. *C. pepo* L., *C. maxima* Duchesne, and *C. moschata* Duchesne are the three most economically important. A high level of morphological and agronomical variability exists within these species. Large collections of *Cucurbita* landraces with a high potential value for breeding are maintained elsewhere. The COMAV's Genebank at the Polytechnic University of Valencia holds the largest collection of Spanish *Cucurbita* landraces. This collection also includes many accessions from the areas of origin and diversification of the different species (3).

Molecular tools, and particularly molecular markers, are very useful for the management of large germplasm collections. However, although new biotechnologies are increasingly being applied in *Cucurbita* breeding, it is still in the early stages when compared to other major Cucurbits. Only a few linkage maps with a low marker density have been reported. These maps are mainly based on dominant molecular markers, such as RAPDs, ISSRs or AFLPs. This type of markers has been used mostly to study the genetic variation in *Cucurbita* (3, 7).

SSRs are locus-specific markers assumed to be high quality (codominant, highly informative, and evenly dispersed throughout genomes). Identification of SSR markers can be attempted by screening genomic or cDNA libraries or by searching DNA sequence databases. None of these genomic tools are available for *Cucurbita* species. SSR markers have been largely reported in the *Cucumis* L. genus, also belonging to the Cucurbitaceae family. Katzir et al. (5) demonstrated that primers specific to melon and cucumber SSRs also amplified DNA from the *Cucurbita* genus. Seven (14%) of the 50 SSRs *Cucumis* primers tested (1) were found to be functional and polymorphic among a collection of *C. pepo* accessions, but their utility in other species of *Cucurbita* was not tested (6, 7). Since these studies, the SSR density in the melon genetic map has been significantly increased (4), providing new SSRs which may be potentially useful in *Cucurbita*.

We have studied the cross homology of 60 *Cucumis* SSRs in the *Cucurbita* genus. These markers were selected from those mapped (from 3 to 10 per chromosome) in the last version of the Spanish genetic reference map (Piel de sapo x PI 161375) (4). These included both SSRs derived from genomic libraries (gSSRs) as well as from EST sequences (EST-SSR). Some of the *loci* are conserved across the two main species of the *Cucumis* genus. Accessions representative of the phenotypic diversity of each *Cucurbita* species (8, 12, and 15 for *C. maxima, C. moschata* and *C. pepo,* respectively) were used in the assays. This sample included Spanish landraces and some landraces from South and Central America. In the case of *C. pepo,* the eight edible cultivar groups were represented.

A high percentage (63.3%) of the SSRs assayed did not amplify in any species, even when the PCR conditions described for melon varied. Most of the amplified SSRs were monomorphic, but a small subset was polymorphic in one, two, or all three species. Of the 20 EST-SSRs assayed, 2 amplified in *C. pepo* (TJ2 and TJ31), 1 in *C. maxima* (TJ24), and 2 in the three species (CSWTA02 and CSTCC813), but only CSTCC813 was polymorphic in *C. moschata* and *C. pepo* (Table 1). Of the 40 gSSRs assayed, 28 were developed by Danin-Poleg, et al., (1) and the remaining 12 were among those recently described in Gonzalo, et al. (4). Of the first subset, 1 amplified in *C. pepo* (CSWCT01), 1

amplified in *C. moschata* and *C. maxima* (CMGA165), both of which being monomorphic, and 7 amplified in the 3 species. CMGA128 and CMGA15 were monomorphic, and the remaining five (CMTC51, CMTC123, CMAG59, CMGA172, CMTC168) were polymorphic within and between species (Table 1, Figure 1). The *loci* CSGA057, CMCT160a and CSTTT15a, previously reported as polymorphic in *C. pepo* (6), did not amplify in our assay. Of the second subset, 1 amplified in *C. pepo* and *C. maxima* (CMTCN56), being polymorphic between species, and 3 amplified in *C. pepo* and *C. moschata* (CMAGN75, monomorphic between and within species, and CMGAN21 and CMTAAN100, polymorphic between species). Three *loci* amplified in the 3 species, but only two were polymorphic within and between species (CMTGN17 and CMAGN73).

Results agree with previous studies in Cucurbitaceae and other families, indicating limited conservation of SSR *loci* between *Cucumis* and *Cucurbita*. Despite this limited success, the selected SSR markers were informative and allow us to reach certain conclusions about the analysed germplasm. In *C. maxima* a similar level of variation was detected among the Spanish landraces and the South American accessions. However, accessions of *C. moschata* from South and Central America displayed a higher level of variation than Spanish landraces. *C. pepo* was the most variable species and alleles unique to subspecies were detected.

The density of EST-SSR markers in the melon genetic map is currently being increased using a large collection of ESTs obtained in the Spanish Melon Genome Initiative (2). The usefulness of these EST-SSRs for genetic studies of *Cucurbita* is currently being investigated.

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Table 1. SSR loci, derived from two *Cucumis* species, which detected polymorphism between or within species in a collection of *Cucurbita* germplasm.

SSR *locus*	WS [z]			LG [y]	BS [x]	Origin	Cm/Cs [w]	Ref.
	C. maxima	*C. moschata*	*C. pepo*					
CSTCC813	1/nt	2/nt	2/ni	G12	NO	Cucumber cDNA library	ns/2	1,7,4
CMTC51	3/nt	4/nt	2/1-null	G4	YES	Non-coding region of EMBL CMACO1	1/2	1,6,7, 4
CMTC123	3/nt	1/nt	3/nt	G12	YES	Melon genomic library	2/1	1,4
CMAG59	1/1	1-null/1	2-null/3	G1	YES	Melon genomic library	5/ns	5,6,7, 4
CMGA172	1/nt	2/nt	1/nt	G9	NO	Melon genomic library	3/2	1,4
CMTC168	1/nt	1/nt	1-null/nt	G10	YES	Melon genomic library	4/ns	1,4
CMTGN17	1/ni	3/ni	2-null/ni	nm	YES	Melon genomic library	ni	7
CMAGN73	1/ni	1/ni	3/ni	G10	YES	Melon genomic library	ni	6,4

[z] Variability within species, the first number indicates the number of alleles identified in our assay (null, null allele), and the second number the alleles previously reported (nt: not previously tested, ni: previously reported as polymorphic, but without information about the number of alleles)
[y] Linkage group according to Gonzalo et al. (4), nm: not mapped
[x] Variability between species
[w] Number of alleles reported in *Cucumis melo* and *Cucumis sativus*, ns: no signal, ni: no information

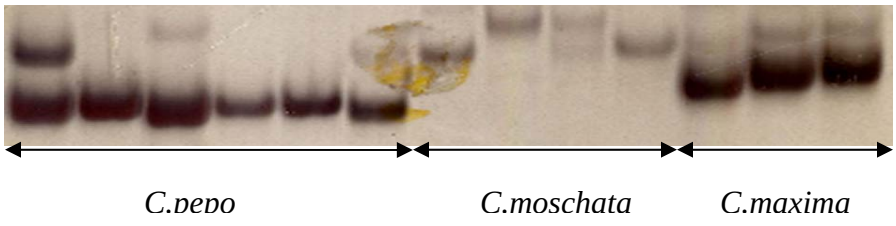

Figure 1. Example of the SSR locus CMTC51 that detects different alleles in *C. maxima*, *C. moschata* and *C. pepo.*

Inheritance of Yellow Seedling Lethal in *Cucurbita maxima* Duch.

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Introduction: Within the genus *Cucurbita*, the presence of lethal yellow seedlings, lacking chlorophyll, was previously observed in *C. pepo* (1). Our objective was to further investigate the inheritance of this trait in *C. maxima*.

Material and Methods: In a F2 progeny from a normal green seedling plant of *Cucurbita maxima* var. *zapallito* (Carrière) Millán, cultivar 'Zapallito Redondo' (Ferry Morse Seed Company), a segregation of 132 normal green to 48 yellow seedlings was observed in the field of the Universidad Nacional de Rosario, Zavalla, Argentina, in spring of 2003. This ratio fitted a 3:1 expected segregation ratio (χ^2=0.26; P=0.5-0.8). All yellow seedlings were lethal, dying at a cotyledonar stage, approximately two weeks after emergence. The normal green seedlings were grown and self-pollinated. Eighteen F3 families were obtained. Each of these families was planted in the field in 2004 and normal green and yellow seedlings were counted.

Results and Discussion: Segregation of F3 families derived from normal green seedling plants are reported in Table 1. A 3:1 normal green to yellow seedling ratio fitted in all segregant families. A 2:1 segregant to non-segregant ratio was observed among families. These results, as in *C. pepo*, are indicative of a single recessive gene being responsible for the yellow lethal seedlings. Yellow seedlings manifested only in F2 plants or in F3 families derived from normal green seedling (heterozygous) plants. All non-segregant selfed progenies were derived from normal green seedling homozygous dominant plants. The ratio heterozygous to dominant homozygous plants in the first selfed progeny that were advanced in selfings fitted the expected 2:1 segregation ratio. Following the rules for gene nomenclature, we propose to name this gene, as in *C. pepo, ys*. Finally, during the 2005 season, this trait was also observed in a sibbed progeny from accession Max 90 of the IPK Institute Genetic Bank, Gatersleben, Germany.

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Table 1. Goodness of fit Tests for normal green and yellow seedlings observed in selfed progenies derived from normal green seedling plants of *C. maxima*.

F3 families	Number of seedlings		Expected ratio	X^2	P-value
	Normal	Yellow			
			Segregant		
1	8	2	3:1	0.13	0.5-0.8
3	22	4	3:1	1.28	0.2-0.5
6	20	11	3:1	1.81	0.1-0.2
8	32	7	3:1	1.02	0.2-0.5
9	23	9	3:1	0.16	0.5-0.8
10	48	22	3:1	1.54	0.2-0.5
11	21	9	3:1	0.40	0.5-0.8
13	7	1	3:1	0.67	0.2-0.5
14	21	3	3:1	2.00	0.2-0.5
15	34	14	3:1	0.44	0.5-0.8
16	6	4	3:1	1.20	0.2-0.5
18	20	8	3:1	0.19	0.5-0.8
			Non-segregant		
2	44	0	1:0		
4	43	0	1:0		
5	34	0	1:0		
7	11	0	1:0		
12	27	0	1:0		
17	48	0	1:0		
Segregant:Non-segregant F3 families			2:1	0.001	0.95-0.99

Another Relationship between Stem and Fruit Color in *Cucurbita pepo*

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Introduction: Thirteen loci affecting fruit color have been identified in *Cucurbita pepo* L. (2). One of these loci, *D*, affects both, the color of the stem and the color of the intermediate-age and mature fruit (3). Plants of the recessive *d/d* genotype have light green stems. The dominant allele, *D*, causes the plant stem to become dark green at a young age, making it a useful phenotypic marker for estimating hybrid seed purity in crosses using a *d/d* female parent and a *D/D* male parent. The dominant *D* allele also results in darkening of the color of fruits that would otherwise be light in color, beginning about a week after anthesis and attaining full intensity by a week to 10 days later, at 15—18 days after anthesis. Thus, in intermediate-age and mature fruits, the dominant *D* allele is epistatic to the genes conferring light fruit color, *l-1* and *l-2*. Ordinarily, plants having dark stems also have dark intermediate-age and mature fruits. Most cultivars of pumpkin and acorn squash serve as very numerous examples. On the other hand, there are a few exceptions. One of them is the scallop squash cultivar 'White Bush Scallop', which has light-colored fruit, conferred by the dominant allele *W*. This allele prevents darkening of intermediate-age fruit color and is epistatic to *D* in the fruit (1). However, this cultivar segregates for stem color (dark vs. light yellow-green stems).

Materials and Methods: Two plants of 'White Bush Scallop', one having dark stems and one having light stems, were self-pollinated. Each bred true for stem and fruit color and their progeny were crossed with a near-isogenic *D/D* accession of 'Vegetable Spaghetti'. The F_1 plants from both crosses had light intermediate-age fruits, with the F_1 plants from the dark-stem inbred having dark stems, whilst the F_1 plants from the light-stem inbred had light stems. Thereafter, donor-parent stem and intermediate-age fruit colors were backcrossed for six generations into a near-isogenic *D/D* inbred of 'Vegetable Spaghetti' that was designated 540a-1-1-2-4. Sixth backcross-generation plants were self-pollinated and selected for donor-parent stem and fruit colors, this being repeated until true-breeding, new *D/D* lines were obtained, one having dark stems and light fruits and the other having light stems and light fruits. These three inbreds, 540a-1-1-2-4 and its two derivatives, were then intercrossed, with the ultimate purpose of elucidating the genetic basis of their differing fruit and stem colors. The plants were grown in the field at Newe Ya'ar Research Center, Ramat Yishay, Israel, in the summer and fall of 2004 and 2005.

Results and Discussion: All three inbreds bred true. The light intermediate-age fruit color of 1278-2-12-3, conferred by *W* from 'White Bush Scallop', was dominant to the dark intermediate-age fruit color of 540a-1-1-2-4 (Table 1). Likewise, the light fruit color of 1243-4-4-20 was dominant to the dark fruit color of 540a-1-1-2-4. The light stem of 1243-4-4-20 was dominant to the dark stem of both 540a-1-1-2-4 and 1278-2-12-3. The backcrosses to the recessive parent fit reasonably well the expected 1:1 ratio in each respective case, and the one F_2 population, of dark-fruited crossed with light-fruited, fit the 1:3 ratio of dark:light, as expected. Light stem color was inherited together with light fruit color, except for one plant out of the 400 in the backcross to the dark-stem, dark-fruit inbred 540a-1-1-2-4. This exceptional plant had a dark stem but a light fruit. The dark stem, light fruit phenotype, observed and checked in the field, was not misclassified.

There are several possibilities which could account for the co-inheritance (in all but 1 of 400 plants) of light fruit and light stem color,

as exhibited by accession 1243-4-4-20. There may exist a gene for light stem color that is separate from but tightly linked to gene *W*. This could account for the one exceptional plant in the backcross but proof would require finding the opposite exception, that is, a plant having a light stem and a dark fruit. Another possibility is that there may be duplicate, tightly linked genes for light fruit color, one of which, *W*, affects fruit color only and another, heretofore unidentified, which affects both fruit and stem color. To test this, a much larger population of the testcross (Table 1) is needed. A third possibility is that the *W* locus is a tri-allelic series, with a heretofore unidentified allele affecting both stem and fruit color being the top dominant of the three; the one exceptional plant would then have to be attributed to an error in pollination or seed harvest. Or, it could be attributable to a mutation of the top-dominant allele. The yellow-green hue of the light-stem plants of this material is not suggestive of vitality.

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Table 1. Results of crossing among near-isogenic accessions differing in color of stem and intermediate-age (15-18 days past anthesis) fruit.

	Number of plants						
Accession	Total	Dark stem, Dark fruit	Dark stem, Light fruit	Light stem, Light fruit	Expected ratio	χ^2	*P*
P_1, 540a-1-1-2-4	26	26	0	0			
P_2, 1278-2-12-3	24	0	24	0			
F_1, $P_1 \times P_2 + P_2 \times P_1$	21	0	21	0			
BC_1, $(P_2 \times P_1) \times P_1$	28	18	10	0	1:1	2.286	0.13
P_3, 1243-4-4-20	9	0	0	9			
F_1, $P_1 \times P_3 + P_3 \times P_1$	20	0	0	20			
F_2, $(P_1 \times P_3) \otimes$	86	21	0	65	1:3	0.016	0.90
BC_1, $P_1 \times (P_1 \times P_3)$	167	93	0	74	1:1	2.162	0.14
BC_1, $(P_1 \times P_3) \times P_1$	233	120	1	112	1:1	0.348	0.55
BC_1, Total	400	213	1	186	1:1	1.960	0.16
F_1, $P_2 \times P_3 + P_3 \times P_2$	16	0	0	16			
Test, $P_1 \times (P_3 \times P_2)$	80	0	38	42	1:1	0.200	0.64

Diversity within *Cucurbita maxima* and *C. moschata* for Resistance to RNA Viruses

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Introduction: Pumpkin, *Cucurbita* L. spp., is a major vegetable crop grown in almost all regions, from cool temperate to tropical. In addition, some *Cucurbita* are used as rootstocks for other cucurbit crops. Zucchini yellow mosaic virus (ZYMV), Papaya ringspot virus-W (PRSV-W), Cucumber fruit mottle mosaic virus (CFMMV), Cucumber mosaic virus (CMV), Cucumber vein yellowing virus (CVYV), and Melon necrotic spot virus (MNSV) are serious and destructive viral RNA pathogens of cucurbit crops (1, 2, 3). As some of the viruses are soil-borne and some pumpkins are resistant to them, such pumpkin rootstocks can protect susceptible scions. Hence, pumpkin plant introductions were surveyed for virus resistance.

Materials and Methods: In this study, new diagnostic tools, both molecular and immunological, have been developed for identifying the RNA viruses infecting cucurbits. Israeli isolates of PRSV-W, CMV, CVYV and MNSV were sequenced, cloned, and the sequences were compared to other described isolates. In addition, a Real-Time PCR (Q-RT PCR) assay was calibrated to detect ZYMV, PRSV-W and CFMMV. Nine *Cucurbita maxima* Duchesne and two *C. moschata* Duchesne accessions from different geographical regions were screened for resistance and tolerance to mechanical infection with the viruses. Together with symptom screening, we measured the accumulated virus level in different accessions through RNA-hybridization and Q-RT PCR.

Results and Discussion: The severities of symptoms were evaluated on a scale from 0 to 5 (Table 1). Inoculation with the potyviruses ZYMV and PRSV-W caused leaf deformation, acute mosaic and significant damage in most of the accessions. The level of accumulated virus for most of the accessions was high, but not homogenous. Furthermore we found an S_3 inbred of *C. maxima* PI 458139 that was slightly tolerant to these two potyviruses. Plants that were inoculated with CFMMV displayed chlorotic mosaic, yellowing and developmental damage, except for two *C. maxima* accessions, 73115 and the PI 458139 S_3 inbred. In most of the accessions, plants infected with CMV showed initial chlorotic spots on the inoculated cotyledons, but no sign of systemic viral movement. No symptoms were detected in any of the accessions mechanically infected with CVYV and MNSV, which may indicate immunity.

Although most of the accessions tested were found to be susceptible to ZYMV, PRSV-W and CFMMV, all were resistant to CVYV and MNSV. Interestingly, CMV infection was expressed as necrotic lesions on the cotyledons of plants of most accessions while systemic infection was observed in few accessions. Further efforts are expected to be

focused on *C. maxima* PI 458139 because of its resistance to CFMMV and lower susceptibility to ZYMV and PRSV-W, for use in classical breeding as well as for investigating the mode of inheritance of its resistance to CFMMV

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Table 1. Severity of symptoms in eleven accessions infected with ZYMV, PRSV-W, CFMMV, CMV, CVYV, and MNSV.

Cucurbita sp.	IGB[z] Number	ZYMV	PRSV-W	CFMMV	CMV[y]	CVYV	MNSV
C. maxima	73079	4[x]	4	4	co	0	0
C. moschata	59329	5	5	1	3-sy	0	0
C. maxima	73085	3	3	3	1	0	0
C. maxima	73088	3	3	3	co	0	0
C. maxima	59319	3	3	2	co	0	0
C. maxima	73112	3	3	3	1	0	0
C. maxima	73115	3	3	0	0	0	0
C. maxima	73081	4	4	5	1	0	0
C. moschata	73082	5	4	2	0	0	0
C. maxima	73113	4	3	4	co	0	0
C. maxima	PI [w]	2	2	0	co	0	0

[z] IGB = Israel Gene Bank (www.agri.gov.il/Depts/GeneBank/Genebank.html)
[y] co = symptoms on cotyledons only; sy = systemic infection
[x] 0 = none to 5 = severe symptoms
[w] PI = S_3 inbred of PI 458139

Precocious Yellow Rind Color in *Cucurbita moschata*

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Introduction: In a recent review, Paris and Brown (2) described 18 loci affecting fruit skin color in *Cucurbita.* Of this total, 14 loci are found in either *C. pepo*, or in both *C. pepo* and *C. maxima.* Only three loci controlling fruit color have been described in *C. moschata*: *Gr, Mldg* and *B*. Dominant *Gr* results in green fruit, versus the recessive buff color (5). Dominant *Mldg* causes mottled immature fruit color, while *mldg* results in a non-mottled rind (1). The *B* (*Bicolor)* gene, which confers a "precocious yellow" color to the ovaries as soon as they are differentiated, is not found naturally in *C. moschata,* but has been crossed into this species from *C. pepo*, and functions as in the latter species (3). This gene is designated *Bicolor* because it was first described in bicolor (yellow/green) gourds (6). The *B* locus and its interactions with other loci are well studied in *C. pepo* and reviewed by Paris and Brown (2). The "precociousness" of color conferred by the *B* gene differentiates it from *Y*, the incompletely dominant gene for yellow fruit color (rather than green) in intermediate age fruit. The recessive *bb* genotype produces normal green ovaries. Depending on the type and number of alleles present at two modifier loci (*Ep-1* and *Ep-2*), the degree of color can range from bicolor yellow/green to fully yellow ovaries. The yellow color remains until maturity or can be further enhanced by other modifiers. Furthermore, color can extend to the peduncle, calyx, stems, male flowers and foliage. A modifier gene, *Ses-1* suppresses the expression of yellow foliage (7). Precocious yellowing of ovaries is also found in *C. maxima,* but the locus, B^{max}, is not allelic to *B* in *C. pepo* (8).

Yellow rind colors are observed among many cultivars and landraces of both *C. pepo* and *C. maxima*; however, we found no published reports of yellow rind color in *C. moschata.* In the early 1990's, Wessel-Beaver observed bicolor fruits of *C. moschata* in a photograph taken of harvested fruits near Guayaquil, Ecuador. The fruits were of varying size and shape, suggesting that they were from a local landrace. The photograph was taken by Dr. D. Maynard (University of Florida), and he indicated that these types of fruit were quite common in the area (D. Maynard, personal communication). Wessel-Beaver grew out a sample of seed from these fruits and observed that the plants produced precocious yellow ovaries, usually bicolor. She was unable to maintain this seed stock. A few years later, Wessel-Beaver grew out seed from a single yellow-orange fruit from a farmer's market in Colombia. The fruit appeared to be from a landrace, rather than improved cultivar, as suggested by its somewhat warty skin. Like the Ecuadorian landrace, this fruit produced progeny with precocious yellow bicolor fruit. Some of the progeny had fully yellow fruit. At maturity the fruit had a golden yellow-orange color. Our objective was to study the inheritance of precocious yellow fruit color in *C. moschata.*

Materials and Methods: A selfed (S_2) line produced from the original fruit from Colombia was used for this research. This material was designated 'Colombian Golden.'

In Puerto Rico. 'Colombia Golden' was crossed with Colombia 5 (a Colombian landrace with green ovaries and green mottled fruit at maturity) and 'Soler' (a Puerto Rican

cultivar with green ovaries and dark green fruit at maturity). The F_1 cross 'Colombia Golden' x 'Colombia 5' was selfed and backcrossed to both 'Colombia Golden' and 'Colombia 5'. Only an F_2 population was produced for the cross 'Colombia Golden' x 'Soler'. Fifty plants each of the 'Colombia Golden' x 'Colombia 5' F_2 and backcross populations were planted in April 2005 at the Isabela Substation of the University of Puerto Rico. Before anthesis, plants were classified as having (i) precocious yellow and/or bicolor ovaries or (ii) green ovaries. Plants were also classified as (i) having yellow leaves, stems, peduncles, and/or staminate flowers or (ii) all green. At maturity, plants were classified as carrying (i) yellow, bicolor and/or spotted yellow fruit or (ii) normal (green, mottled, or buff) fruit. One hundred plants of the F_2 population 'Colombia Gold' x 'Soler' were planted at the Fortuna Substation (near Juana Díaz, PR). Plants were classified as having (i) precocious yellow and/or bicolor ovaries (pre-anthesis) or (ii) green ovaries. Plants were also classified as (i) having yellow leaves, stems, peduncles, and/or staminate flowers or (ii) all green. No mature fruit data was taken in this population.

In Wisconsin. 'Waltham' (Jung Seed Company, Randolf, WI; a butternut type with green ovaries at anthesis and buff-colored fruit at maturity) was crossed to five individual S_2 plants of 'Colombian Golden'. The resulting F_1 plants were self-pollinated and five populations were independently evaluated. Twenty five plants from each F_2 population were grown in the summer of 2005 at the Arlington Agricultural Experiment Station, Arlington, WI. Conventional farming practices and no irrigation was used. Data on pigmentation was collected during anthesis. Plants were classified as described above.

Data were analyzed by chi-square at $\alpha = 0.05$ using software found at http://www.quantpsy.org (4). The null hypothesis was the model for a single recessive gene controlling precocious yellow color (a 3:1 model for the F_2 populations, a 1:1 model for the backcross to 'Colombia Golden' and a "all green" model for the backcross to 'Colombia 5'). The five Wisconsin F_2 populations were analyzed individually and then in a pooled analysis.

Results and Discussion: Probabilities in all chi-square tests were greater than $\alpha = 0.05$ for data collected during anthesis. Thus, there was no evidence to reject the null hypothesis that a single recessive gene controls precocious yellow coloring in *C. moschata.* In Puerto Rico, all plants with yellow foliage at eight weeks also had yellow foliage at 16 weeks. More plants developed yellow color (including leaves, stems, peduncles and staminate flowers, as well as ovaries) as the season progressed. Although some plants did not set fruit before the conclusion of the trial, plants with yellow vegetative parts always produced fruit that were either bicolor or completely yellow. The reverse was also true: plants producing yellow or bicolor fruit always had some other plant parts, usually leaves, with yellow sectors. In Wisconsin, a significant increase in the number of plants with yellow fruit pigmentation was observed as the season progressed, although formal data was not collected. In fact, it appeared that the 3:1 (non-yellow:yellow) segregation changes substantially as fruit mature. We did not observe this in the Puerto Rico populations. The non-golden parent used in crosses in Wisconsin (Waltham) has a genetic background very different from the parents used in Puerto Rico (Soler and Colombia 5), both of which are of tropical origin. While mature fruit color in the populations tested in Puerto Rico varied from bright or dull orange to green, fruit colors in the Wisconsin populations included bright orange, dull orange, green, tan and even white (a color not reported in the literature for *C. moschata,* but previously observed by Wessel-Beaver in germplasm from Colombia) (Figure 1).

Contrary to what has been reported in both *C. pepo* and *C. maxima*, we observed the precocious yellow trait to be recessive in *C. moschata*,. *B* (in *C. pepo*) and B^{max} (in *C. maxmima*) genes are known to be non-allelic (8), and it seems likely that the gene we observed in *C. moschata* is also non-allelic to these two previously known genes. We propose that the gene for precocious yellow in *C. moschata* be known as b^{mos}. However, genetic control of orange color in mature fruits of *C. moschata* appears to be more complex than that of precocious yellow.

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Table 1. Chi-square values and probabilities associated with segregations of F_2 and backcross populations used to test a single recessive gene model for the inheritance of the precocious yellow trait in *C. moschata.*

Cross	Plant part[1]	Observed segregation[2]		Model tested	$\chi 2$ value	Probability
		Green	Yellow/ Bicolor			
			Wisconsin			
Col Golden x Waltham - A	Fruits/ovaries at anthesis	17	6	3:1	0.014	0.901
Col Golden x Waltham – B	Fruits/ovaries at anthesis	21	2	3:1	3.261	0.071
Col Golden x Waltham – C	Fruits/ovaries at anthesis	14	6	3:1	0.267	0.606
Col Golden x Waltham – D	Fruits/ovaries at anthesis	12	8	3:1	2.400	0.121
Col Golden x Waltham - E	Fruits/ovaries at anthesis	21	3	3:1	2.000	0.157
Pooled	Fruits/ovaries at anthesis	85	25	3:1	0.303	0.582
			Puerto Rico			
Col Gold x Col 5 (F2)	Plant at 8 weeks	39	11	3:1	0.240	0.624
	Plant at 16 weeks	33	17	3:1	2.160	0.142
	Fruits at 20 weeks	27	13	3:1	1.200	0.273
(Col Gold x Col 5) x Gold (BC)	Plant at 8 weeks	28	22	1:1	0.720	0.396
	Plant at 16 weeks	25	25	1:1	0.000	1.000
	Fruits at 20 weeks	18	16	1:1	0.118	0.732
(Col Gold x Col 5) x Col 5 (BC)	Plant at 8 weeks	50	0	All green	---	---
	Plant at 16 weeks	50	0	All green	---	---
	Fruits at 20 weeks	49	1	All green	---	---
Col Gold x Soler (F2)	Plant at 16 weeks	75	25	3:1	0.000	1.000

[1] Eight and 16 week old plants were classified as "yellow/bicolor" if yellow sectors appeared on all or some of the following plant parts: immature ovaries, leaves, stems, peduncles and/or staminate flowers. Plants with yellow sectors on vegetative parts always had yellow (or bicolor) ovaries.

[2] Not all plants set fruit in the populations tested in Puerto Rico.

Figure 1. Range of mature fruit color observed in F_2 populations of Colombia Golden x Waltham planted in Arlington, Wisconsin. Note the all white (arrow) and bicolor fruits.

Diversity of Cucurbit Species Cultivated in Côte d'Ivoire for Edible Seeds

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Introduction: Cucurbits are cultivated worldwide, in extremely diverse environments and are important economic crops, particularly in the Americas, Europe, and Asia. In sub-Saharan Africa, the indigenous species are prized for their oleaginous seeds consumed as soup thickener, preferentially during popular celebrations and important ceremonies (1, 2, 3). The African cultivated cucurbits are reported to be rich in nutrients (3, 4), well adapted to extremely divergent agro-ecosystems and low-input agriculture (5, 6). Despite their agronomic, cultural, and culinary importance, these plants lack attention from research and development and are thus categorized as orphan crops (4, 5). Promoting the production and use of such crops can result in securing food and increasing income for poor farmers.

To address these issues, a collaborative project between the Agronomic University of Gembloux (Belgium) and the University of Abobo-Adjamé (Côte d'Ivoire) has been implemented using the main edible-seeded cucurbit species cultivated in Côte d'Ivoire as plant models. Specifically, three topics were defined for the project: collection and genetic characterization of the *Cucurbitaceae*, agronomic evaluation of the most common species, and implementation of improved cropping systems for their cultivation. We report herein preliminary results obtained from investigations on inter- and intra-species diversity of the target plant materials.

Materials and Methods: Investigations were made in 2000-2004 throughout three zones (South, East, and Centre), based on agro-ecology and food habits of local populations. A total of 40 villages were selected (10 in South, 10 in East, and 20 in Centre), the number of villages per zone being based on the results of a preliminary survey of the target sites. In each zone, a participatory rural appraisal-based method (7) was used to gather local community knowledge of traditionally cultivated cucurbit species, namely their vernacular names, diversity, relative cultural and social importance, and uses. To check if morphological variations observed within a species were not due to environmental conditions prevailing in the original sites, representative samples of each plant introduction (PI) accession were grown at our experiment station in multiple seasons (2-4), two replicates, and 20-50 seeds per plot (25 m x 25 m). Within each species, morphological differences between cultivars were examined considering the following features: mature fruit shape and color, seed shape, seed size (estimated as height x width), and 100-seed weight. The estimates of seed size and 100-seed weight were then used to compare cultivars using Student *t*-test (for two cultivars) or one-way analysis of variance (for more than two cultivars) using the Newman-Keuls test if necessary (8). Statistical analysis was performed using StatsDirect™ 2.4 statistical package for Windows (9).

Results: A total of 176 PI accessions composed of five species in five genera were collected throughout the three zones: *Citrullus lanatus* var. *citroides* (Thumb.) Matsum. & Nakai. (90 PI accessions), *Cucumeropsis mannii* Naudin (43 PI accessions), *Cucumis melo* var. *agrestis* L. (25 PI accessions) *Cucurbita moschata* L. (5 PI accessions), and *Lagenaria siceraria* (Molina) Standl. (13 PI accessions). All are cultivated mainly by women as intercrops with staples in fields or backyard gardens. Intraspecies diversity based on fruit and seed traits was observed in the five species.

C. lanatus var. *citroides.* This species is monoecious, yellow flowered, and has creeping annual vines, with leaves deeply divided into 5-7 more or less subdivided lobes. Locally called "wlêwlê", the species is the most common edible-seeded cucurbit cultivated in Côte d'Ivoire. The fruits are round or oval (Figure 1), uniformly light green or mottled light and dark green and have white bitter flesh surrounding the seeds. The mature dried seeds are yellowish in color (Figure 1). Two groups were reported for this species. The first group, including three cultivars (defined on the basis of seed size) has smooth seeds that are tapered to the point of attachment. Fruits of the second group, including one cultivar, are round and narrow or wide striped. The seeds are ovoid and flattened, with a thickened and roughened margin. Statistical analysis indicated significant differences between and within groups for seed weight (hundred-seeds) and size (Table 1). Note that a type which presents slightly colored-flesh fruit, with brown seeds are often observed on permanent rubbish piles or empty lots in urban areas. This form could be a weedy type probably derived from the edible-fleshed *C. lanatus* var. *lanatus* that is widely consumed in towns.

C. mannii. This species is a monoecious annual climbing vine, locally called "n'viêlê". The leaves are embossed, with three notched lobes. Fruit are uniformly slight green or yellowish and blocky. Seeds are whitish, flattened, and tapered to the point of attachment (Figure 2). Vertical training of the vines is believed to be important to maximize yield of this species. For this reason in the target zones, *C. mannii* is systematically intercropped with yam (*Dioscorea* spp.), since the latter also needs to be grown on trellis. Three cultivars defined on the basis of seed size were found for this species (Figure 2 and Table 1).

C. melo var. agrestis. Two andromonoecious types with dark green leaves, yellow flowers, and small oval fruit (3-5 cm length) were collected in the target zones. The most common type (Figure 3) is cultivated and locally called "lomi n'gatê". Seeds of this type are toasted, ground, and used as soup thickener. The flesh of fruits is light green, lacks aroma, and has bitter taste. The second type, uncultivated, is often found along roads, on permanent rubbish piles or empty lots in villages and cities. Its mature fruits are orange in color (Figure 3), are aromatic, and are exclusively used as a vegetable. Fruit are cut into slices and added to soup. In addition to mature fruit color, the other differences between the two types are related to seed size and seed weight (Table 1).

C. moschata. Two open-pollinated cultivars, identified as *C. moschata* and locally named "n'gando" were collected. These cultivars have yellow flowers and blocky fruits with orange flesh. This species is found in backyard gardens or empty lots in villages and cities. The main differences between these two cultivars are color of the mature fruit that can be mottled light and dark green, or yellow, and seed size (Figure 4 and Table 1).

L. siceraria. This is a species of the monoecious white flowered gourds locally called "bebou". The local name is related to the manually shelling of the seeds, due to their hard coat. Two cultivars, different in fruit shape (blocky or round), were

collected. Fruit and seed shape and size are reported to be highly variable in *Lagenaria* (11). In our case, seeds from the round-fruited cultivar are characterized by the presence of a cap on the distal side (Figure 5). With regard to seed size and weight, significant differences were observed between these two cultivars (Table 1).

Acknowledgments:

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Table 1. Sample size (*n*) and mean (±SD) for two seed traits analyzed to test differences between cultivars of edible-seeded cucurbits from Côte d'Ivoire

Species	Cultivar / Type	Seed size (mm^2) (n = 100)	100-seed weight (mg) (n = 10)
Citrullus lanatus			
	Big seeds	120.41±16.94[c]	11.50±0.61[a]
	Medium seeds	58.81±9.76[b]	5.49±0.23[b]
	Small seeds	42.07±7.17[a]	4.26±0.26[c]
	Thickened margin seeds	179.06±26.11[d]	17.45±0.60
Cucumeropsis mannii			
	Big seeds	138.31±12.90[c]	11.87±0.59[a]
	Medium seeds	96.80±10.79[b]	10.73±0.33[b]
	Small seeds	49.44±7.68[a]	4.47±0.15[c]
Cucumis melo var. *agrestis*			
	Green-fruited	19.16±2.59[b]	1.11±0.04[a]
	Orange-fruited	13.24 ±1.48[a]	0.58±0.11[b]
Cucurbita moschata	Green-fruited	79.59±9.12[a]	7.54±0.34[a]
	Yellow-fruited	123.92±11.48[b]	7.87±0.53[a]
Lagenaria siceraria			
	Round-fruited	159.08±19.43[a]	25.08±0.70[a]
	Blocky-fruited	190.78±26.88[b]	21.60±2.80[b]

NB: For each trait and species, means within a column followed by different superscripts were significantly different ($P \leq 0.01$), based on Student *t* or Newman-Keuls test.

Figure 1. Fruit and seed of *Citrullus lanatus* var. *citroides*. Left to right, top row, fruit shape and color: round and light green; oval and light green; and round and wide striped. Bottom row, seed shape, color, and size: tapered, yellowish, and large; tapered, yellowish, and medium; tapered, yellowish, and small; ovoid, flattened, yellowish, and large.

Figure 2. Fruit and seed of *Cucumeropsis mannii*. Bottom row, left to right, seed size: large, medium, and small.

Figure 3. Fruit and seed of *Cucumis melo* var. *agrestis*. Top row, left to right: cultivated type; wild type. Bottom row, left to right: seed of the cultivated type; seed of the wild type.

Figure 4. Fruit and seed of *Cucubita moschata*. Top row, left to right: yellow cultivar; green cultivar. Bottom row, left to right: seed of the yellow cultivar; seed of the green cultivar.

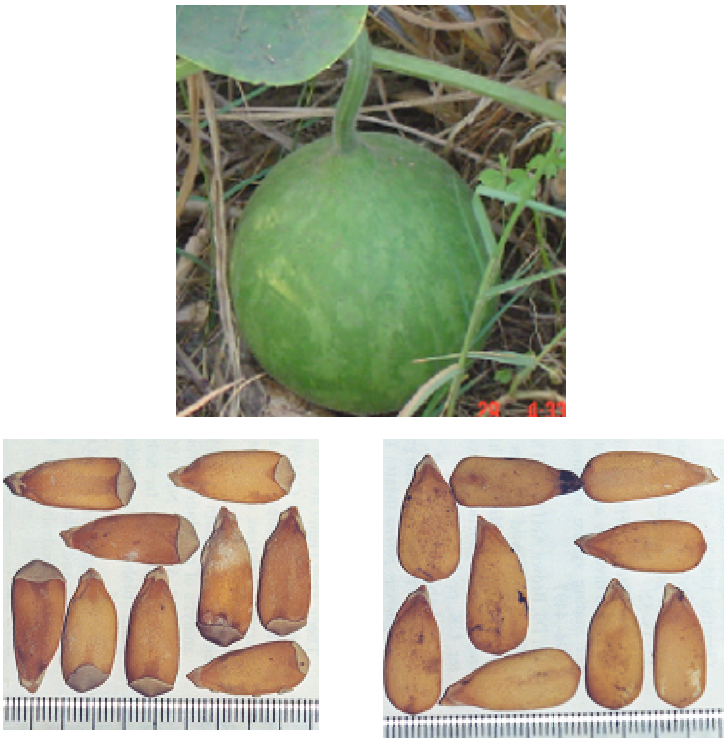

Figure 5. Fruit and seed of *Lagenaria siceraria*. Bottom row, left to right: seed of the round cultivar, seed of the blocky cultivar.

Genetic Variability in Ascorbic Acid and Carotenoids Content in Indian Bitter Gourd (*Momordica charantia* L.) Germplasm

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Bitter gourd (*Momordica charantia* L.) is one of the important vegetables among the cultivated cucurbits. The crop is widely cultivated through out the tropics. The origin of this important crop is probably India with a secondary centre of diversity in China (2). India is endowed with a wide range of diversity in this crop; hence, there is a vast opportunity for genetic improvement. The immature fruits are good source of iron, vitamin A, B, C, and inexpensive source of proteins and minerals (7) and the nutritive values of bitter gourd fruits vary with the varieties. The small-fruited (*Momordica charantia* var. *muricata*) types are found to be more nutritious than the large-fruited (*Momordica charantia* var. *charantia*) types (6). The systematic evaluation of bitter gourd genotypes based on ascorbic acid and carotenoids content in bitter gourd is either lacking or scanty. Therefore, a study was made to evaluate bitter gourd germplasm with high ascorbic acid and total carotenoids content besides several other traits.

A total of thirty eight accessions of bitter gourd collected and maintained at the Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi were grown in a randomized block design with three replications during March to July 2004. The recommended agronomic practices were adopted for optimum growth of the crop. Most of the economically important fruit and plant characters were also observed during the cropping period. The predominant sex form was monoecious; however, two very promising gynoecious lines and two predominantly female flowering types were included in this study. Number of fruits per plant varied from 7.07 to 47.07 and weighted from 10.47g to 136.41g each. Fruit length ranged from 3.26 cm to 28.72 cm with diameter from 2.55 cm to 5.98 cm and flesh thickness of 0.31 cm to 2.08 cm. The color of the fruit was from milky white to dark green. Fruit surface also showed different conformations i.e. continuously ridged to almost smooth. For analysis of ascorbic acid and carotenoids, fruits were picked at commercial edible stage. Ascorbic acid was determined by titrating a known weight of sample with 2,6-dichlorophenol-indophenol dye using metaphosphoric acid as stabilizing agent (1). Total carotenoids were determined by a modified method of one described by Ranganna (5).

Data were averaged and statistically analysed. The analysis of variance indicated highly significant differences among the genotypes for ascorbic acid and carotenoid content. This suggests that there is a considerable amount of variation among the genotypes. Mean, range, phenotypic (PCV) and genotypic (GCV) coefficient of variation is presented in Table 1. The variability estimate revealed that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all quantitative characters studied but the difference between PCV and GCV for ascorbic acid and total carotenoid content was insignificant which indicated that these quality traits are least affected by environment. The above findings were in agreement with the results obtained by Jaiswal *et.al.* (3). The range of ascorbic acid content was 60.20 mg to 122.07 mg/100 g of fresh weight with a population mean of 82.14mg/100g of fresh weight (Fig. 1). Similarly, total carotenoid content ranged from 0.205mg to 3.2mg with a population mean of 1.6mg/100g of fresh weight (Fig. 2). The highest amount of ascorbic acid was found in genotype DBTG-3 (122.07mg) followed by DBTG-8 (120.53mg), DBTG-6

(115.13mg), DBTG-9 (108.43mg), DBTG-7 (100.67mg) and DBTG-4 (92.15mg). The genotype, DBTG-8 recorded maximum total carotenoids content (3.2mg) followed by DBTG-9 (3.0mg), DBTG-101 (2.9mg), DBTG-6 (2.8mg), DBTG-4 (2.7mg) and DBTG-2 (2.6mg). Among the above mentioned genotypes, DBTG-3, DBTG-8, DBTG-6 and DBTG-101 were small fruited genotypes ((*Momordica charantia* var. *muricata*) those were found superior with respect to nutritional property. Among the small-fruited genotypes, DBTG-8 was found to be highly promising for its better nutritional qualities long with higher fruit yield. In large fruited group ((*Momordica charantia* var. *charantia*), the genotype DBTG-4 was observed to be most promising with respect to fruit yield, fruit length, fruit diameter, flesh thickness and high ascorbic acid and total carotenoid content. It was very interesting to note that some of the white-fruited genotypes like, Pusa Do Mausami (White), Preethi and DBTG-10 contain very less amount of total carotenoids (less than 0.5mg/100g). It might be due to the fact that, these genotypes contain less chlorophyll, which may have contributed to less carotenoid synthesis (4). It is concluded that genotypes with higher ascorbic acid and carotenoid content may be utilized for quality improvement of bitter gourd. These materials are now being utilized for the genetic study and the inbreds are maintained in the Institute.

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Table 1.Total carotenoid and ascorbic acid content of 6 most important genotypes based on average values

Characters	Ascorbic acid (mg/100g)	Total carotenoids (mg/100g)
Range	92.15-122.07	2.6-3.2
Population mean	82.14	1.6
GCV	19.75	48.62
PCV	19.87	48.64
CD at 5%	2.99	0.03
High value genotypes	DBTG-3, DBTG-8, DBTG-6, DBTG-9, DBTG-7, DBTG-4	DBTG-8, DBTG-9, DBTG-101, DBTG-6, DBTG-4, DBTG-2

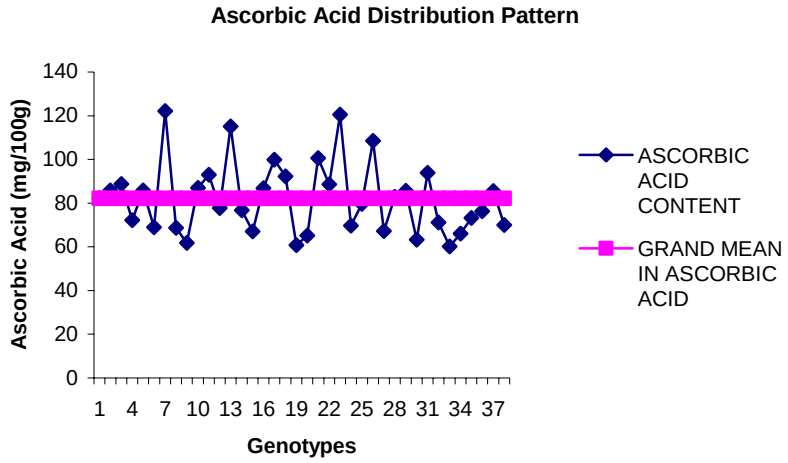

Fig1. Ascorbic acid distribution pattern among the 38 genotypes based on average values

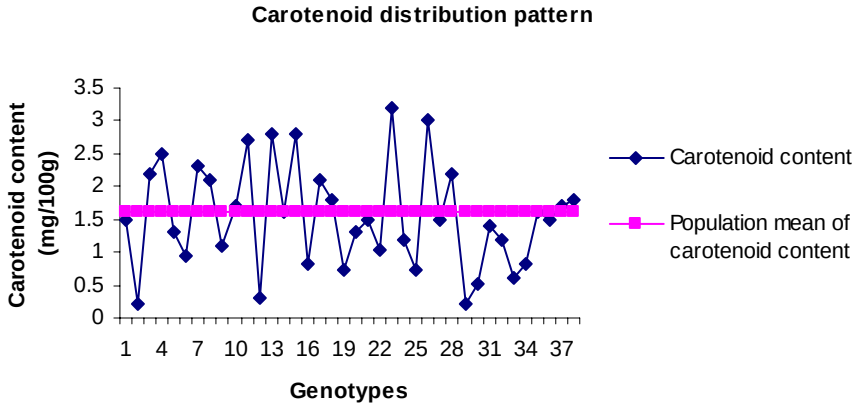

Fig2. Total carotenoid distribution pattern among the 38 genotypes based on average values

Graphical Analysis (Wr-Vr) and Numerical Approach for a Diallel analysis of Yield Components in Bottlegourd (*Lagenaria siceraria* (Mol.) standl.)

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Introduction: Detailed information concerning the genetic control of the characters under selection is important if plant breeders are to conduct their programme efficiently by the choice of appropriate parents and selection methodology. Moreover, it is highly desirable that the information is obtained under the same conditions where selection is to take place. A breeding effort was initiated at Pantnagar in 2003 and 2004 to complement exiting programme, with the aim of producing hybrids of bottle gourd (*Lagenaria siceraria* (Mol). standl.) with particular emphasis as production problems and consumer preference including high yielding varieties having greater fruit number, weight ,earliness, non fibrous flesh at edible stage. The present diallel study was conducted to assist the breeding of high yield cultivars. A considerable number of diallel studies have been reported in bottlegourd. Most have been heterosis and combining ability analysis (9, 10) since the development of commercial F_1 hybrids cultivar is a major aim of cucurbit breeders (8). Some studies (7, 11, 12) have employed the Jinks Hayman method of analysis (3, 4, 5, 6).

This study investigated whether the genetic control of the commercially important characters which are subjected to selection was different at Pantnagar bred material, and what additional genetic resources, if any, were present in the available germplam to allow further progress to be made. The merits of diallel analysis in plant breeding have been hotly debated (16) but it remains a popular technique for combining a detailed genetic analysis of a small fixed set of genotypes (usually commercial cultivars) with the production of the hybrid seed for further breeding work. While other designs in themselves may require less labour and be able to test a larger number of genotypes (13) they do not produce all possible hybrids. This means that after analysis a further round of hybridization and seed production may be needed before the hybrids with the greatest potential can be exploited. In addition, the accumulation of information in the literature is of considerable assistance with planning, executing and analyzing diallel experiments.

Materials and Methods: The eight diverse genotypes of bottle gourd (*Lagenaria siceraria* (Mol.) standl.) were chosen as representing a fixed sample of the best germplam available for a range of characters of commercial importance, including yield and other related components. The parents were crossed by hand, reciprocal hybrids were excluded. The parental (8 lines) and F1 (28lines)was grown in a furrow irrigated experiment at Vegetable Research Centre of G.B. Pant Uni. of Agric. and Technology, Pantnagar, UA ,India, at an altitude of 243.84m above mean sea level and 29^0 N altitude and 79.3^0 longitude in the kharif, 2003 and summer, 2004. The experiment received standard agronomic practices. The experiment consisted of three randomized complete blocks with 36 treatments consisting of 8 parents and $28F_1$ hybrids. Each treatment had one rows of 5 meter length with plant to plant distance of 1 meter and row to row distance of 3meter. There were 5 hills per entry. The sowing of seeds was done directly in the field. The parental lines were PBOG 13 (round fruit), PBOG22,

PBOG 54, PBOG 61, PBOG 76, PBOG 117, PBOG 119and Pusa Naveen. The data obtained from half diallel with eleven characters viz., days to first female flower, node number to first male flower, days to first fruit harvest, main vine length, number of nodes on main vine, internodal length, fruit length, fruit diameter, pedicel length, number of fruit per plant and fruit yield (q/ha). Genetic analysis of diallel data for graphical approach (Wr-Vr graph) as well as genetic components of variation was according to method of Hayman (2,6) .Plotting of Wr-Vr graph was done with the help of sigma plotting package The first three assumptions of the additive/ dominance genetic model underlying an analysis of the diallel cross (3) were tested as follows:

(1) diploid segregation; (2) homozygous parents each parent was maintained by inbreeding and was assumed to be homozygous; and (3) no reciprocal differences. The remaining assumptions of the simple additive dominance genetic model 14) are (4) independent effect of non- allelic genes (i.e. no epistasis); (5) no multiple allelisam and (6) genes independently distributed between parents.

Results and Discussions: Graphical analysis of the experimental data recorded was done in order to get information about allelic constitution of the parents used in the diallel cross. In the present study, regression coefficient values (b, wr, vr) for eleven characters viz; days to first female flower, node number to first male flower, days to first fruit harvest, main vine length, number of nodes on the main vine, inter nodal length, fruit length, fruit diameter, pedicel length, number of fruit per plant and fruit yield (q/ha) did not differ significantly from unity indicating the absence of epistasis. This indicated the fulfilment of the assumption that epistasis is absent for these characters. The Wr-Vr graphs for these characters have been presented in Figures (Fig.1-11).But for the rest characters regression value differs significantly. So, for these characters epistatic gene action may be present. For almost all the characters, the parental array points were scattered all along the regression line in the Wr-Vr graph. This indicates the genetic diversity among the parents for all the traits studied. Distribution of array points in Wr-Vr graph also decides relative proportions of dominant and recessive alleles present in parent. For days to first female flower regression coefficient did not differ significantly from unity, suggesting absence of epistasis. The regression line passed above the origin indicating the presence of partial dominance. The parent PBOG117 had more number of dominant alleles while PBOG 22 which was located at the opposite end of regression line had maximum number of recessive alleles. For node number to first male flower regression line passed below the origin indicating that this trait was conditioned by over dominance, confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was more than unity (1.42). PBOG 54 had the maximum number of dominant alleles, being nearest to the origin. However, PBOG22, PBOG119 and Pusa Naveen carried maximum number of recessive alleles being farthest from the origin. For days to first fruit harvest, regression coefficient value was 1.15. The regression line intercepted the Wr axis below the origin. This confirmed that over dominance was involved in the expression of days to first fruit harvest in the parents. Pusa Naveen exhibited maximum frequency of dominant alleles being nearest to the origin, while PBOG 22 and PBOG 13 had the maximum recessive alleles, being farthest from origin. Parent PB0G22 had maximum frequency of dominant alleles for main vine length while PBOG 119, PBOG 61, Pusa Naveen and PB0G 54 had high number of recessive alleles. The line of regression intercepted Wr axis below the origin indicates the presence of over dominance in the inheritance of main vine length. Rest of the parents PB0G13, PB0G76 and PBOG117 possessed an almost

equal proportion of dominant and recessive alleles for main vine length. For number of nodes on the main vine, complete dominance was found as the regression line passed close to the origin; distribution of parental arrays along the regression line showed that parents PB0G13 had maximum number of dominant alleles while maximum frequency of recessive alleles was in parent PB0G 76. For internodal length, over dominance was found as regression line passed below the origin. Parent PBOG 76 had maximum frequency of dominant alleles. However, parent PBOG 61 and PBOG 119 had number of recessive alleles. For fruit length, partial dominance was found, as the regression line passed above the origin. The result confirmed by the estimated value of $(H_1/D)^{1/2}$, where it was less than unity i.e. (0.56) . Distribution of the parental arrays along the regressions line showed that PB0G61 exhibited maximum frequency of dominant alleles, while PB0G13 had maximum frequency of recessive alleles. The parents with the balanced proportion of dominant and recessive alleles were, PB0G22, PB0G 54, PB0G119 and Pusa Naveen. Regression coefficient was 1.14 and regression line intercepted the Wr axis below the origin, indicating the involvement of over dominance in the inheritance of fruit diameter. This result was in conformity with the value of $(H_1/D)^{1/2}$, where it was more than unity (1.37). The distribution of parental arrays along the regression line suggested that PB0G22, PB0G54, PB0G61, PB0G117, PB0G 119 and Pusa Naveen had the maximum number of dominant alleles and parent PBOG 13 had maximum number of recessive alleles. The parent, PB0G76 had the equal proportion of dominant and recessive alleles for fruit diameter. For pedicel length regression line passed above the origin, indicating almost partial dominance to control the inheritance of pedicel length. This results was confirmed by the estimated value of $(H_1/D)^{1/2}$; where it was less than unity (0.87).The parent PB0G117 possessed maximum number of dominant alleles and maximum recessive alleles was shown by PB0G 13. Parent PB0G22, PB0G54, PB0G 61, PB0G76 PB0G119 and Pusa Naveen had balanced proportion of dominant and recessive alleles. For number of fruits per plant, parents PBOG 117 and PusaNaveen had maximum frequency of dominant alleles, where as the parent with maximum frequency of recessive alleles was PB0G22. The parents PB0G 13, PB0G54, PB0G61, PB0G76 and PB0G119 had the intermediate proportion of dominant and recessive alleles. Due the regression line passed below the origin indicating over dominance to control the expression of number of fruits per plant. For fruit yield (q/ha) over dominance was found to control the inheritance of fruit yield; as the regression line passed below the origin. The result was in conformity with the estimated value of $(H_1/D)^{1/2}$ where it was more than unity. The parents Pusa Naveen and PB0G 117 had maximum frequency of dominant alleles. However, PB0G13 and PB0G 54 had a greater number of recessive alleles. Parent PBOG 22, PB0G 61, PB0G 76 and PB0G 119 showed a balanced proportion of dominant and recessive alleles. Genetic components of variation are presented in Table1. Additive genotypic variance (D) was significant for the characters viz., days to first female flower, node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length and fruit yield. Dominance component (H_1) was significant for the character viz., node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield (q/ha). Thus, the additive and dominance both the variances were pre dominance component governing the expression of yield (q/ha) and other yield components. The mean squares due to gca and sca both were also found to be significant/ highly significant of most of the character except fruit weight indicating the presence of both additive and non-additive gene action. Involvement of both additive and non-

additive gene action in the inheritance of yield and related traits were also reported by (1, 7)

The contradiction between the approaches of as genetic component of variation and Wr-Vr graph analysis could be ascribed to the presence of correlated gene distribution (2). Ratio of dominant and recessive alleles $(4DH_1)^{1/2}+F/ (4DH_1)^{1/2}-F$ was more than unity for days to first female flower, node number to first female flower, days to first fruit harvest, fruit length, fruit diameter, pedicel length, number of fruits per plant and fruit yield (q/ha). The higher proportions of dominant genes observed in most of the characters are in agreement with the findings of (9 and 15).The proportion of genes with positive and negative effects $(H_2/4H_1)$ in the parents was less than 0.25 days to first female flower, node number to first female flower, days to first fruit harvest, fruit diameter and pedical length consistently over both the seasons. This suggested asymmetrical distribution of dominant genes with positive and negative effects.

Since the distribution of array points reflects the parental diversity, it is suggested that the crosses of Pusa Naveen with other potential lines should be the potential ones to derive high yielding genotypes. The parents for making crosses could be selected on the basis of gca effects. However, selecting the parents on the basis of genetic diversity can not be ignored. The crosses between the diverse parents shall be the potential ones for throwing out desirable segregants. So, the crosses should preferably between the parents located away from the origin in Wr-Vr graph analysis, subject to fulfilment of other criteria, namely good gca effect and the desirable mean values for the important traits. Wr-Vr graphical analysis indicated the involvement of dominant genes for earliness and recessive genes for fruit diameter i.e. the round shape fruit was conditioned by recessive genes. In bottle gourd, increasing attention is being paid towards breeding of superior cultivars with greater focus on development of hybrids. This segment of research has gained momentum due to enactment of New Seed Policy Act-1998 where in among other things, the vegetable hybrid seed and those of the parental lines are allowed to be imported under open general license (OGL). A large number of private sector seed companies have entered in hybrid seed research and marketing. There is pressure on public sector institutions to contribute substantially on hybrid breeding on commercial scale. Along with this, it is also to be recognized that on bottle gourd, the local germplasm/inbred lines should be prominently used in breeding programmes. In this context the diallel analysis using the inbred from the local indigenous germplasm of bottle gourd assumes significance.

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Table 1: Genetic components of variation and their proportions for yield and yield attributing traits in bottlegourd (kharif, 2003 and summer, 2004).

Components / proportions	Days to first female flower		Node number to first male flower		Days to first fruit harvest		Main vine length		Number of nodes on main vine	
	kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	172.60**	42.66**	34.26**	0.89**	245.05**	67.75**	7.58	4.03**	292.82*	27.42
	±34.22	± 7.55	±8.36	± 0.30	±13.30	±5.25	±4.00	±0.81	±81.44	±74.38
F	70.44	4.28	37.50	0.78	202.68	21.77*	5.85	8.09**	144.38*	100.19*
	±80.86	± 17.83	±19.75	± 0.71	±31.43	±12.41	±9.46	±1.91	±192.44	±175.75
H_1	181.36	77.55**	69.25*	2.45**	235.42**	63.66**	24.87*	19.86**	738.02**	633.57**
	±78.67	± 17.35	±19.21	±0.69	±30.58	±12.07	±9.21	±1.85	±187.22	±170.98
H_2	139.21	64.19**	55.46*	1.85**	128.91**	59.65**	22.18*	14.67**	684.02**	463.19**
	±68.44	± 15.09	±16.71	±0.60	±26.60	±10.50	±8.01	±1.61	±162.89	±148.75
h^2	3.05	1.01	-1.21	0.10	10.37	-0.43	-0.06	1.60	47.92	292.40**
	±45.90	± 10.12	±11.21	± 0.40	±17.84	±7.04	±5.37	±1.08	±109.24	±99.76
E	7.07	3.11	2.77	0.23	11.93*	1.71	0.33	0.54	5.82	2.80
	±11.41	± 2.52	±2.79	±0.10	±4.43	±1.75	±1.33	±0.27	±27.15	±24.79
$(H_1/D)^{1/2}$	1.03	1.35	1.42	1.66	0.98	0.97	1.81	2.22	1.59	4.81
$(H_2/4H_1)$	0.19	0.21	0.20	0.19	0.14	0.23	0.22	0.18	0.23	0.18
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$	1.50	1.08	2.25	1.71	2.45	1.40	1.54	2.65	1.37	2.23

Components / proportions	Internodal length (cm		Fruit length (cm)		Ftuit diameter (cm)		Pedicel length (cm)		No. of fruits/plant		Fruit yield (q/ha)	
	Kharif	Kharif	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	7.71** ±1.10	119.21** ±4.31	75.40** ±3.55	59.12** ± 3.14	5.02** ±0.75	7.52** ±0.80	108.50** ±9.69	5.07 ±3.69	9.55 ±4.16	3.21* ±0.72	16401.57** ±4934.65	6882.54** ±2058.49
F	10.51** ±2.59	28.84* ±10.19	75.84** ±8.38	53.15** ± 7.43	8.17** ±1.76	5.41** ±1.89	28.94 ±22.91	11.67 ±8.71	6.83 ±9.83	1.00 ± 1.71	19025.57 ±11660.12	5394.12 ±4864.01
H_1	10.68** ±2.52	37.29** ±9.92	56.72** ±8.15	45.13** ±7.23	9.44** ±1.71	7.68** ±1.84	70.55* 22.29	37.41** ±8.48	42.07** ±9.57	8.79** ±1.67	53769.82** ±11344.03	24632.14** ±4732.16
H_2	6.55* ±2.19	33.63** ±8.63	32.20** ±7.09	29.42** ± 6.29	5.21** ±1.49	5.95* ±1.60	64.65* ±19.39	28.15** ±7.37	38.24** ±8.32	6.65** ±1.45	47663.43** ±9869.3	20058.39** ±4116.97
h^2	4.82* ±1.47	8.73 ±5.79	-0.15 ±4.76	-0.17 ± 4.22	0.08 ±1.00	0.35 ±1.07	7.28 ±13.0	7.18* ±4.98	23.22** ±5.58	2.73* ±0.97	19778.62* ±6618.77	7946.55** ±2761.02
E	0.76 ±0.37	4.83 ±1.44	0.71 ±1.18	0.53 ± 1.05	0.45 ±0.25	0.17 ±0.27	2.52 ±3.23	0.74 ±1.23	0.38 ±1.39	0.07 ±0.24	138.93 ±1644.88	47.76 ±686.16
$(H_1/D)^{1/2}$	1.18	0.56	0.87	0.87	1.37	1.01	0.81	2.72	2.10	1.65	1.81	1.89
$(H_2/4H_1)$	0.15	0.23	0.14	0.16	0.14	0.19	0.23	0.19	0.23	0.19	0.22	0.20
$\frac{(4DH_1)^{1/2}+F}{(4DH_1)^{1/2}-F}$	3.75	1.55	3.76	3.12	3.19	2.10	1.40	2.47	1.41	1.21	1.94	1.52

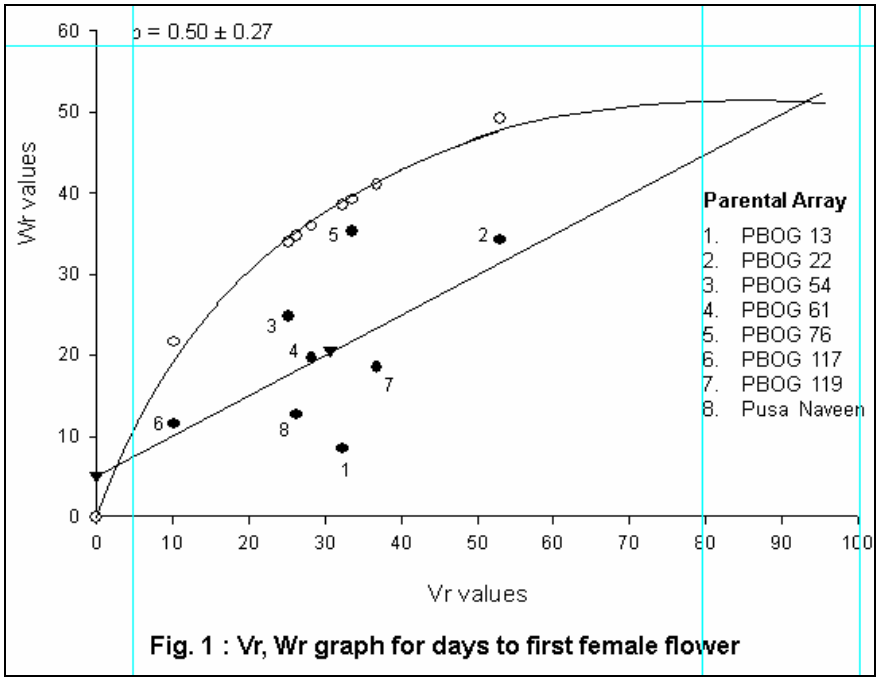

Fig. 1 : Vr, Wr graph for days to first female flower

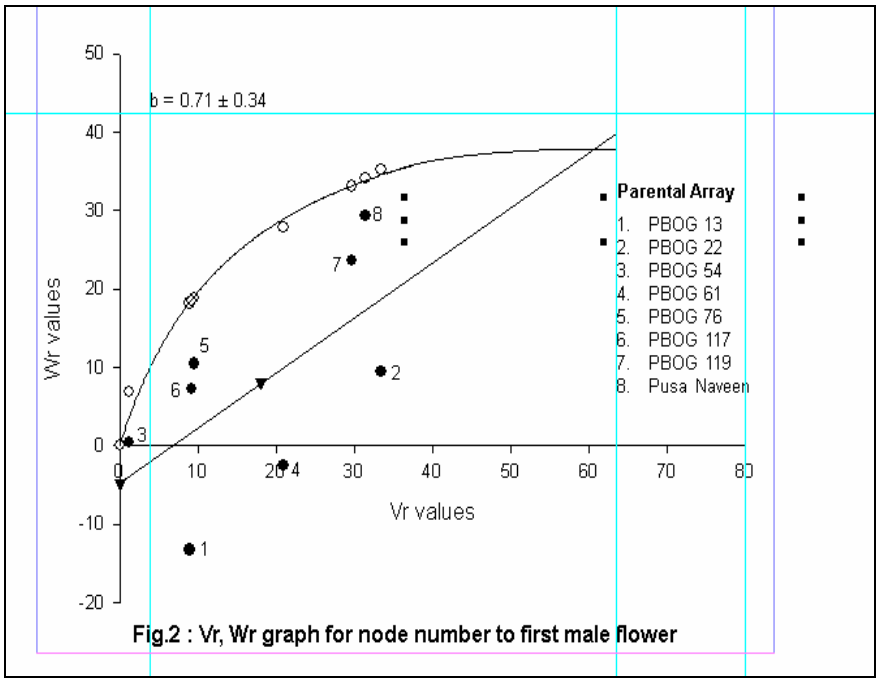

Fig.2 : Vr, Wr graph for node number to first male flower

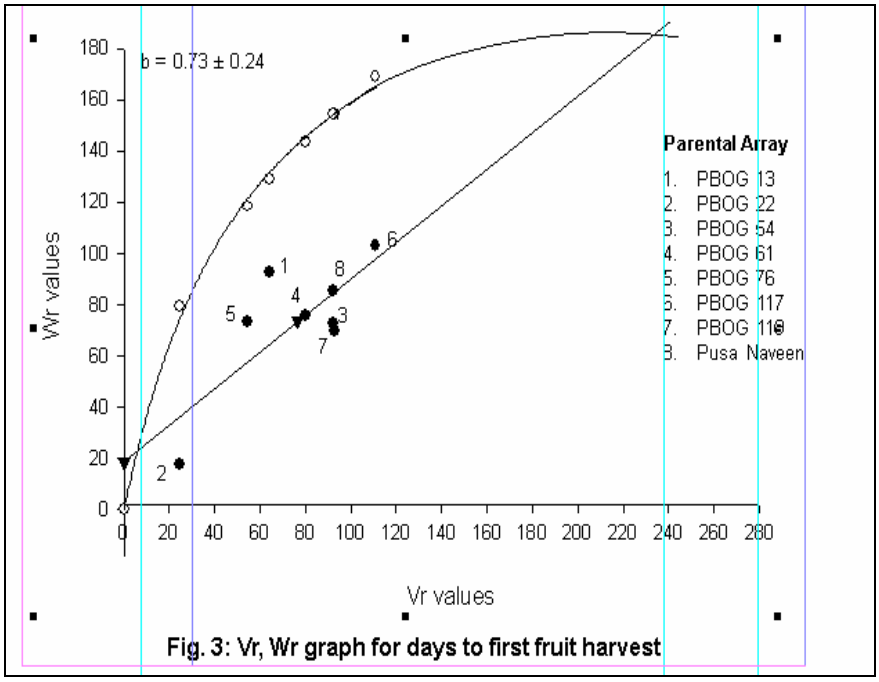

Fig. 3: Vr, Wr graph for days to first fruit harvest

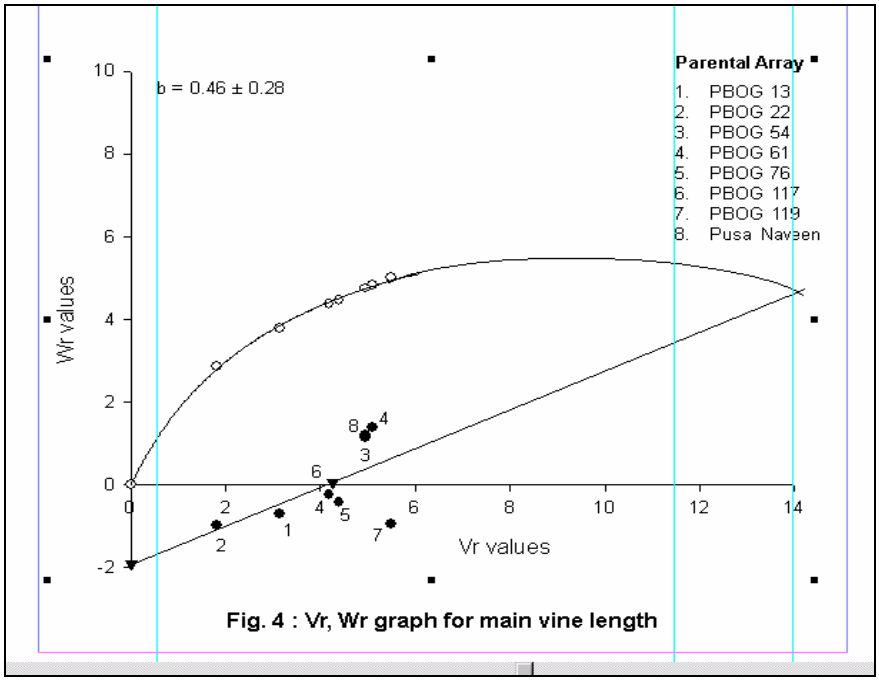

Fig. 4 : Vr, Wr graph for main vine length

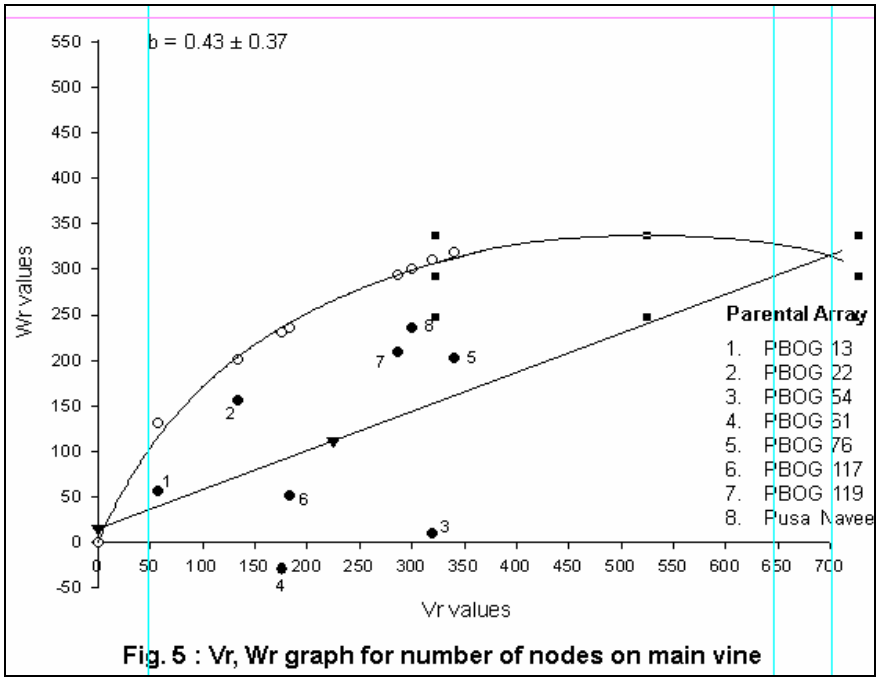

Fig. 5 : Vr, Wr graph for number of nodes on main vine

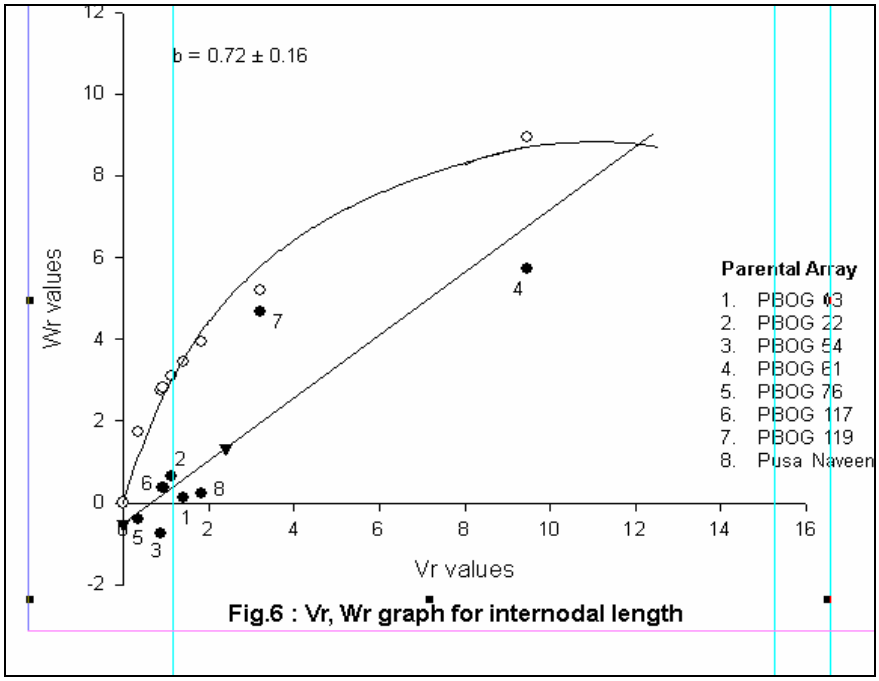

Fig.6 : Vr, Wr graph for internodal length

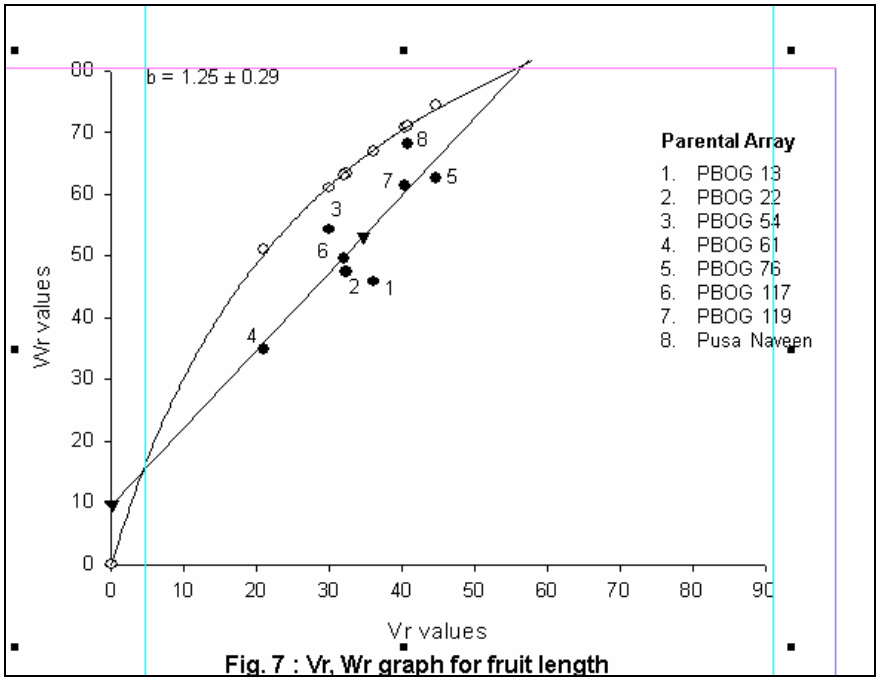

Fig. 7 : Vr, Wr graph for fruit length

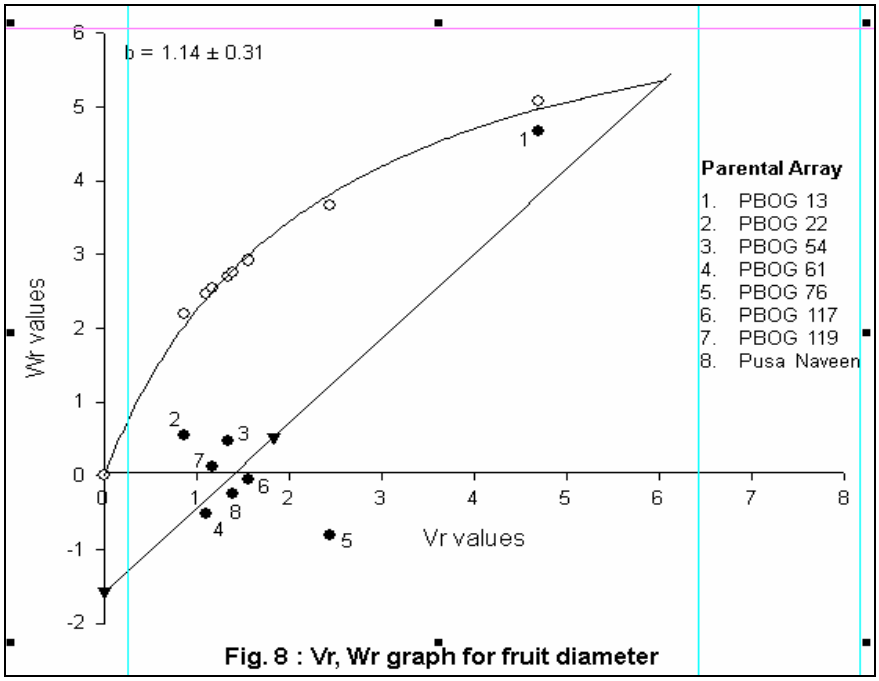

Fig. 8 : Vr, Wr graph for fruit diameter

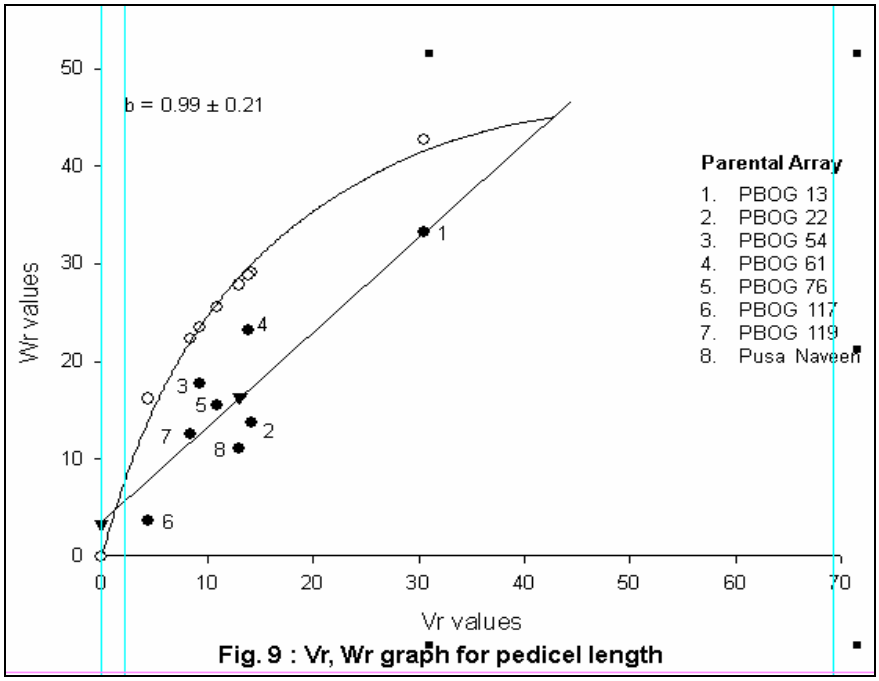

Fig. 9 : Vr, Wr graph for pedicel length

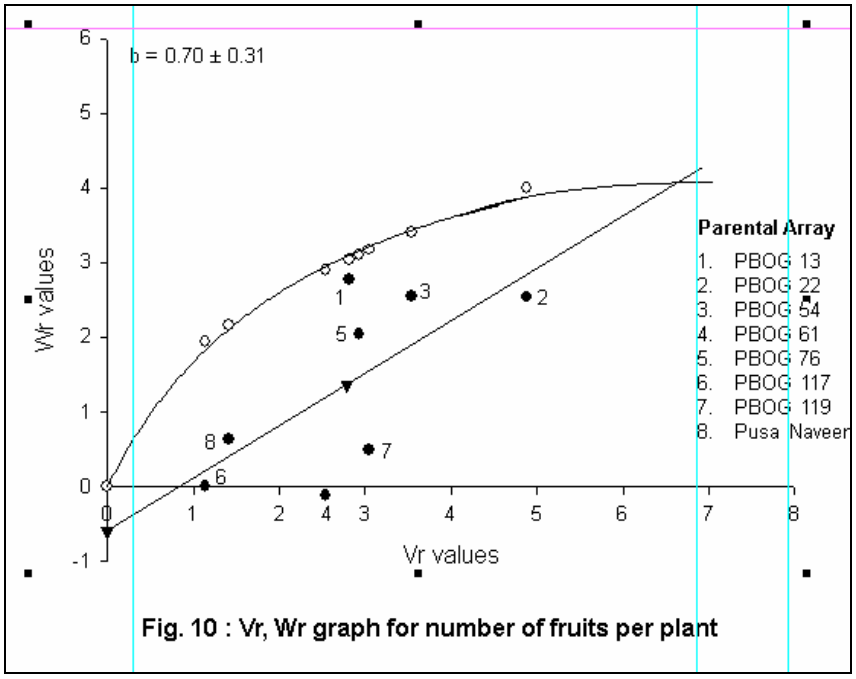

Fig. 10 : Vr, Wr graph for number of fruits per plant

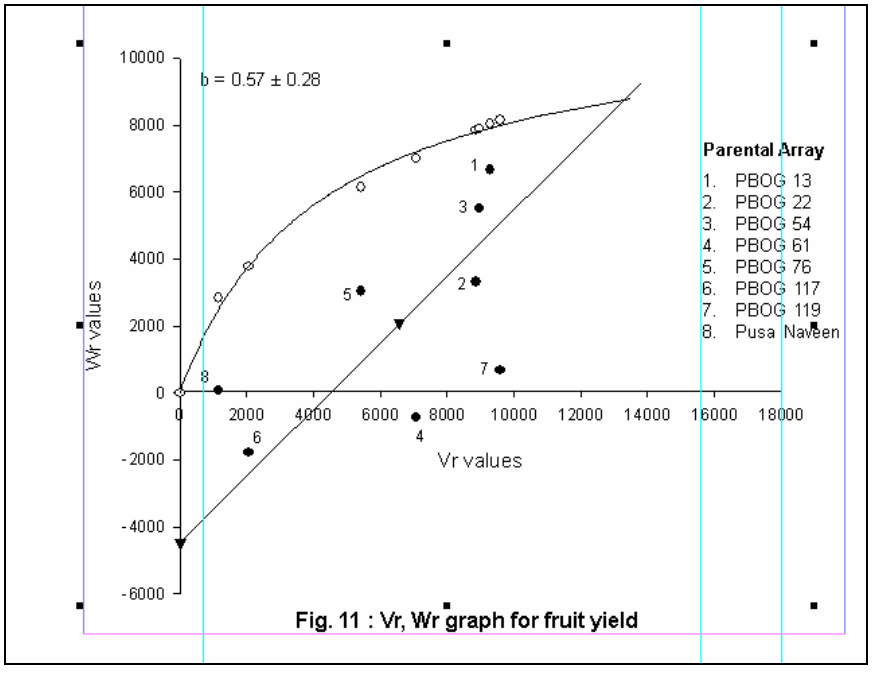

Fig. 11 : Vr, Wr graph for fruit yield

Gene List 2005 for Cucumber

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This is the latest version of the gene list for cucumber (*Cucumis sativus* L.). In addition to morphological and resistance genes, this list includes genes that have been cloned from different plant tissues of cucumber. The genes in the list have been grouped into ten categories as follows: seedling markers, stem mutants, leaf mutants, flower mutants, fruit type mutants, fruit color mutants, resistance genes (mostly to diseases), protein (isozyme) variants, DNA (RFLPs and RAPDs) markers (Table 1), and cloned genes (Table 2). There is also a review of linkage of the morphological and resistance genes. Complete lists and updates of genes for have been published previously, as follows:

Previous Lists
- Robinson et al., 1976
- Robinson et al., 1982
- Pierce and Wehner, 1989
- Wehner, 1993
- Wehner and Staub, 1997
- Xie and Wehner, 2001

Revisions to the 2005 cucumber gene list include the addition of *Psm* for paternal sorting of mitochondria (Havey et al., 2004).

Researchers are encouraged to send reports of new genes, as well as seed samples to the cucumber gene curator (Nischit V. Shetty), or to the assistant curator (Todd C. Wehner). Please inform us of omissions or errors in the gene list. Scientists should consult the list as well as the rules of gene nomenclature for the Cucurbitaceae (Robinson et al., 1976; Robinson et al., 1982) 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 Mutants

Seedling Mutants

One of the advantages of using the cucumber in genetic research is the availability of seedling markers. To date, five non-lethal color mutants [virescent (*v*) (Poole, 1944; Tkachenko, 1935), variegated virescence (*vvi*) (Abul-Hayja and Williams, 1976), yellow cotyledons-1 (*yc-1*) (Aalders, 1959), yellow cotyledons-2 (*yc-2*) (Whelan and Chubey, 1973; Whelan et al., 1975), yellow plant (*yp*) (Abul-Hayja and Williams, 1976)] and 4 lethal, color mutants [chlorophyll deficient (*cd*) (Burnham et al., 1966), golden cotyledon (*gc*) (Whelan, 1971), light sensitive (*ls*) (Whelan, 1972b), pale lethal (*pl*) (Whelan, 1973)] have been identified.

Six seedling traits which affect traits other than color include bitterfree (*bi*) (Andeweg, 1959), blind, (*bl*) (Carlsson, 1961), delayed growth (*dl*) (Miller and George, 1979), long hypocotyl (*lh*) (Robinson et al., 1982), revolute cotyledons (*rc*) (Whelan et al., 1975) and stunted cotyledons (*sc*) (Shanmugasundarum and Williams, 1971; Shanmugasundarum et al., 1972).

Stem Mutants

Seven genes have been identified which affect stem length: bush (*bu*) (Pyzenkov and Kosareva, 1981), compact (*cp*) (Kauffman and Lower, 1976), determinate (*de*) (Denna, 1971; Kooistra, 1971; Odland and Groff, 1963b), dwarf (*dw*) (Robinson and Mishanec, 1965), tall height (*T*) (Hutchins,

1940) and *In-de* which behaves as an intensifier for *de* (George, 1970). Rosette (*ro*) which also affects height is characterized by muskmelon-like leaves (de Ruiter et al., 1980).

Unlike these genes, fasciated (*fa*) (Robinson, 1978b; Shifriss, 1950) affects stem confirmation, not length.

Leaf Mutants

Several genes have been shown to control leaf or foliage characteristics. Eight in particular are responsible for leaf shape: blunt leaf apex (*bla*) (Robinson, 1987a), cordate leaves-1 (*cor-1*) (Gornitskaya, 1967), cordate leaves-2 (*cor-2*) (Robinson, 1987c), crinkled leaf (*cr*) (Odland and Groff, 1963a), divided leaf (*dvl*) (den Nijs and Mackiewicz, 1980), ginko leaf (*gi*) (John and Wilson, 1952), little leaf (*ll*), (Goode et al., 1980; Wehner et al., 1987) and umbrella leaf (*ul*) (den Nijs and de Ponti 1983). Note that ginko leaf is a misspelling of the genus *Ginkgo.*

The original cordate leaf gene identified by Gornitskaya (1967) differs from *cor* proposed by (Robinson, 1987c) which also had calyx segments which tightly clasp the corolla, hindering flower opening and insect pollination. Therefore, we propose that the first gene identified by Gornitskaya be labeled *cor-1* and the second identified by Robinson be labeled *cor-2*.

It should be noted that plants with stunted cotyledon may look similar to those with ginko at the younger stages but the cotyledons of *sc* mutants are irregular and *gi* mutants are sterile.

Opposite leaf arrangement (*opp*) is inherited as a single recessive gene with linkages to *m* and *l*. Unfortunately, incomplete penetrance makes the opposite leaf arrangement difficult to distinguish from normal plants with alternate leaf arrangement (Robinson, 1987e).

Five mutants which affect color or anatomical features of the foliage are golden leaves (*g*) (Tkachenko, 1935), glabrous (*gl*) (Inggamer and de Ponti, 1980; Robinson and Mishanec, 1964), glabrate (*glb*) (Whelan, 1973), short petiole (*sp*) (den Nijs and Boukema, 1985) and tendrilless (*td*) (Rowe and Bowers, 1965).

Flower Mutants

Sex expression in cucumber is affected by several single-gene mutants. The *F* locus affects gynoecy (femaleness), but is modified by other genes and the environment, and interacts with *a* and *m* (androecious and andromonoecious, respectively) (Galun, 1961; Kubicki, 1969; Rosa, 1928; Shifriss, 1961; Tkachenko, 1935; Wall, 1967). Androecious plants are produced if *aa* and *ff* occur in combination, otherwise plants are hermaphroditic if *mm FF*, andromonoecious if *mm ff*, gynoecious if *MM FF* and monoecious if *MM ff*. The gene *F* may also be modified by an intensifier gene *In-F* which increases the femaleness (Kubicki, 1969b). Other genes that affect sex expression are *gy* for gynoecious (Kubicki, 1974), *m-2* for andromonoecious (Kubicki, 1974) and *Tr* for trimonoecious expression (Kubicki, 1969d).

Cucumbers, typically considered day-neutral plants, have occasionally been shown to express sensitivity to long days. Della Vecchia et al. (1982) and Shifriss and George (1965) demonstrated that a single gene for delayed flowering (*df*) is responsible for this short-day response.

Another gene which may give the impression of eliciting daylength sensitivity by causing a delay in flowering is *Fba*. In reality, *Fba* triggers flower bud abortion prior to anthesis in 10 to 100% of the buds (Miller and Quisenberry, 1978).

Three separate groups have reported single genes for multiple pistillate flowers per node. Nandgaonkar and Baker (1981) found

that a single recessive gene *mp* was responsible for multiple pistillate flowering. This may be the same gene which Fujieda et al. (1982) later labeled as *pf* for plural pistillate flowering. However, they indicated that 3 different alleles were responsible, with single pistillate being incompletely dominant over multiple pistillate: pf^{+} for single pistillate, pf^{d} for double pistillate and pf^{m} for multiple pistillate (more than 2 flowers per node).

Thaxton (1974), reported that clustering of pistillate flowers is conditioned by a single dominant gene (we propose the symbol, *Mp-2*), and that modifier genes influence the amount of clustering. Thaxton (1974) also determined that clustering of perfect flowers is controlled by genes different from clustering of gynoecious flowers.

Several genes for male sterility have been reported for cucumber, but because of the ease of changing sex expression with growth regulators, little commercial use has been made of them. Five genes, *ms-1*, *ms-2*, *ap*, *cl* and *gi* have been identified. The genes *ms-1* and *ms-2* cause sterility by pollen abortion before anthesis; *ms-1* plants are also partially female sterile (Robinson and Mishanec, 1965; Shanmugasundarum and Williams, 1971; Whelan, 1972a). Apetalous mutants (*ap*) on the other hand have infertile anthers which appear to have been transformed into sepal-like structures (Grimbly, 1980). Ginko (*gi*), mentioned earlier as a leaf mutant, also causes male sterility (John and Wilson, 1952).

One of these male steriles may be of little use except as a genetic marker. Closed flower (*cl*) mutants are both male and female sterile, so seed production must be through the heterozygotes only (Groff and Odland, 1963). With this mutant, the pollen is inaccessible to bees because the buds remain closed.

Three genes alter floral characteristics: green corolla (*co*) (Currence, 1954; Hutchins, 1935), orange-yellow corolla (*O*), negative geotropic peduncle response (*n*) (Odland and Groff (64). Green corolla (*co*), named because of its green petals, has enlarged but sterile pistils (Currence, 1954; Hutchins, 1935), and has potential for use as a female sterile in hybrid production.

Fruit Mutants

Because the fruit is the most important part of the cucumber economically, considerable attention has been given to genes affecting it. One such gene is Bitter fruit, *Bt*, (Barham, 1953) which alters fruit flavor by controlling cucurbitacin levels. The gene *Bt* is different from *bi* because it consistently alters only the fruit cucurbitacin levels compared to *bi* which affects the whole plant.

Five genes conditioning skin texture are *Tu*, *te*, *P*, *I* and *H*. Smooth (*Tu*) and tender (*te*) skin are usually associated with European types, while American types are generally warty and thick skinned (Poole, 1944; Strong 1931). Heavy netting, *H*, which occurs when fruit reach maturity may be tightly linked or pleiotropic with *R* and *B* (discussed later).

In *Cucumis sativus* var. *tuberculatus*, Tkachenko (1935) found that gene *P*, causing fruit with yellow rind and tubercles, was modified by gene *I*, an intensifier which increases the prominence of the tubercles (Tkachenko, 1935).

There are 3 genes which affect internal fruit quality, each identified by viewing transections of fruits; Empty chambers-1 (*Es-1*), Empty chambers-2 (*Es-2*) and locule number (*l*) (Youngner, 1952).

Hutchins (1940) proposed that 2 genes controlled spine characteristics, with *f* producing many spines and being tightly linked with *s* which produced small spines. Poole (1944) used the data of Hutchins (1940) to suggest that *s* and *f* were the same gene and proposed the joint symbol *s* for a

high density of small spines. Tkachenko (1935) who used the same symbol for control of less dense spines, did not look at spine size, and the same gene might have been involved. However, Fanourakis (1984) and Fanourakis and Simon (1987) reported 2 separate genes involved, and named them *ss* and *ns* for small spines and numerous spines, respectively.

These may differ from those that led Carruth (1975) to conclude that 2 genes act in a double recessive epistatic fashion to produce the dense, small spine habit. We propose that these genes be labeled *s-2* and *s-3* and *s-1* be used instead of *s* proposed by Poole (1944).

Carruth (1975) and Pike and Carruth (1977) also suggested that carpel rupture along the sutures was inherited as a single recessive gene that was tightly linked with round, fine-spined fruits. This may be similar to what Tkachenko (1935) noted in the 'Klin mutant' as occasional deep-splitting flesh. We suggest the symbol *cs* for carpel splitting, but note that because penetrance of the trait may be lower under certain environmental conditions (Carruth, 1975) this trait may be related to the gooseberry (*gb*) fruit reported by Tkachenko (1935). Another character not found in commercial cultivars was protruding ovary (*pr*) reported by Youngner (1952).

There is dispute over the inheritance of parthenocarpy, a trait found in many European cucumbers (Wellington and Hawthorn, 1928). Pike and Peterson (1969) suggested an incompletely dominant gene, *Pc*, affected by numerous modifiers, was responsible. In contrast, de Ponti and Garretsen (1976) explained the inheritance by 3 major isomeric genes with additive action.

A modifier of fruit length, *Fl*, was identified by its linkage with scab resistance (*Cca*) (Henry Munger, personal communication; Wilson, 1968). Expressed in an additive fashion, fruit length decreases incrementally from heterozygote to homozygote (*fl fl*).

Fruit Color

Twelve mutants have been identified which affect fruit color either in the spines, skin, or flesh and a few of these appear to act pleiotropically. For example, *R* for red mature fruit color is very closely linked or pleiotropic to *B* for black or brown spines and *H* for heavy netting (Hutchins, 1935; Tkachenko, 1935; Wellington, 1913). It also interacts with *c* for cream colored mature fruit in such a way that plants which are (*RR CC*), (*RR cc*), (*rr CC*) and (*rr cc*) have red, orange, yellow and cream colored fruits, respectively (Hutchins, 1940).

The *B* gene produces black or brown spines and is pleiotropic to or linked with *R* and *H* (Wellington, 1913). The homozygous recessive plant is white spined with cream colored mature fruit and lacks netting. Other spine color genes are *B-2*, *B-3* and *B-4* (Cowen and Helsel, 1983; Shanmugasundarum et al., 1971a).

White immature skin color (*w*) is recessive to the normal green (Cochran, 1938), and yellow green (*yg*) is recessive to dark green and epistatic with light green (Youngner, 1952). Skin color may also be dull or glossy (*D*) (Strong, 1931; Tkachenko, 1935) and uniform or mottled (*u*) (Andeweg, 1956; Strong, 1931).

Kooistra (1971) reported 2 genes that affect fruit mesocarp color. White flesh (*wf*) and yellow flesh (*yf*) gene loci interact to produce either white (*WfWf YfYf* or *wfwf YfYf*), yellow (*WfWf yfyf*), or orange (*wfwf yfyf*) flesh color.

Insect Resistance

Bitterfree, *bi*, is responsible for resistance to spotted and banded cucumber beetles (*Diabrotica* spp.) (Chambliss, 1978; Da Costa & Jones, 1971a; Da Costa & Jones, 1971b) and two-spotted spider mites (*Tetranychus urticae* Koch.) (Da Costa &

Jones, 1971a; Soans et al., 1973). However, this gene works inversely for the 2 species. The dominant allele which conditions higher foliage cucurbitacin levels incites resistance to spider mites by an antibiotic affect of the cucurbitacin. The homozygous recessive results in resistance to cucumber beetles because cucurbitacins are attractants.

In the 1989 Cucurbit Genetics Cooperative Report the authors labeled the gene for resistance to *Diabrotica* spp. *di*, but wish to retract it in light of recent evidence.

Disease Resistance

Currently there are 15 genes known to control disease resistance in *C. sativus*. Three of these condition virus resistance. Wasuwat and Walker (1961) found a single dominant gene, *Cmv*, for resistance to cucumber mosaic virus. However, others have reported more complex inheritance (Shifriss et al., 1942). Two genes condition resistance to watermelon mosaic virus, *Wmv* (Cohen et al, 1971) and *wmv-1-1* (Wang et al., 1984). Most recently, resistance to zucchini yellow mosaic virus (*zymv*) has been identified (Provvidenti, 1985).

Both resistance to scab, caused by *Cladosporium cucumerinum* Ell. & Arth., and resistance to bacterial wilt caused by *Erwinia tracheiphila* (E. F. Smith) Holland are dominant and controlled by *Ccu* (Abul-Hayja et al., 1978; Andeweg, 1956; Bailey and Burgess, 1934) and *Bw* (Nuttall and Jasmin, 1958; Robinson and Whitaker, 1974), respectively. Other dominant genes providing resistance are: *Cca* for resistance to target leaf spot (*Corynespora cassiicola*) (Abul-Hayja et al., 1978), *Cm* for resistance to Corynespora blight (*Corynespora melonis*) (Shanmugasundarum et al., 1971b), *Foc* for resistance to Fusarium wilt (*Fusarium oxysporum* f. sp. *cucumerinum*) (Netzer et al., 1977) and *Ar* for resistance to anthracnose [*Colletotrichum lagenarium* (Pars.) Ellis & Halst.] (Barnes and Epps, 1952). In contrast, resistance to *Colletotrichum lagenarium* race 1 (Abul-Hayja et al., 1978) and angular leaf spot (*Pseudomonas lachrymans*) (Dessert et al., 1982) are conditioned by the recessive genes *cla* and *psl*, respectively.

Several reports have indicated that more than one gene controls resistance to powdery mildew [*Sphaerotheca fuliginea* (Schlecht) Poll.] with interactions occurring among loci (Hujieda and Akiya, 1962; Kooistra, 1968; Shanmugasundarum et al., 1971b). The resistance genes *pm-1* and *pm-2* were first reported by Hujieda and Akiya (1962) in a cultivar which they developed and named 'Natsufushinari'. Kooistra (1968) using this same cultivar, later confirmed their findings and identified one additional gene (*pm-3*) from USDA accessions PI200815 and PI200818. Shimizu et al. (1963) also supported 3 recessive genes which are responsible for resistance of 'Aojihai' over 'Sagamihan'.

Several genes with specific effects have been identified more recently (Shanmugasundarum et al., 1971b) but unfortunately, direct comparisons were not made to see if the genes were identical with *pm-1*, *pm-2* and *pm-3*. Fanourakis (1984) considered a powdery mildew resistance gene in an extensive linkage study and proposed that it was the same gene used by Shanmugasundarum et al. (1971b) which also produces resistance on the seedling hypocotyl. Because expression is identified easily and since it is frequently labeled in the literature as '*pm*' we believe that this gene should be added to the list as *pm-h* with the understanding that this may be the same as *pm-1*, *pm-2* or *pm-3*.

Currently, one gene, *dm*, has been identified which confers resistance to downy mildew [*Pseudoperonospora cubensis* (Berk. & Curt.) Rostow] (van Vliet and Meysing, 1974). Inherited as a single recessive gene, it also appeared to be linked with *pm* (van Vliet, 1977). There are, however, indications that more than one gene may be involved (Jenkins, 1946).

Environmental Stress Resistance
Presently, only 2 genes have been identified in this category; resistance to sulfur dioxide air pollution conditioned by *Sd* (Bressan et al., 1981) and increased tolerance to high salt levels conditioned by major gene, *sa*, Jones (1984).

Other Traits
The dominant allele, *Psm*, induces paternal sorting of mitochondria, where *Psm* is from MSC 16 and *psm* is from PI 401734 (Havey et al., 2004).

Molecular and Protein Markers
Isozyme variant nomenclature for this gene list follows the form according to Staub et al. (Staub et al., 1985), 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. For example, an allele at locus 1 of FDP (fructose diphosphatase) which has a mobility 4 mm less that of the most common allele would be assigned the designation *Fdp(1)*-96.

RFLP marker loci were identified as a result of digestion of cucumber DNA with *Dra*I, *Eco*RI, *Eco*RV, or *Hind*III (Kennard et al., 1994). Partial-genomic libraries were constructed using either *Pst*I-digested DNA from the cultivar Sable and from *Eco*RV-digested DNA from the inbred WI 2757. Derived clones were hybridized to genomic DNA and banding patterns were described for mapped and unlinked loci (CsC482/H3, CsP314/E1, and CsP344/E1, CsC477/H3, CsP300/E1).

Clones are designated herein as CsC = cDNA, CsP = *Pst*I-genomic, and CsE = *Eco*RI-genomic. Lower-case a or b represent two independently-segregating loci detected with one probe. Lower-case s denotes the slowest fragment digested out of the vector. Restriction enzymes designated as DI, *Dra*I; EI, *Eco*RI; E5, *Eco*RV; and H3, *Hind*III. Thus, a probe identified as CsC336b/E5 is derived from a cDNA library (from 'Sable') which was restricted using the enzyme *Eco*RV to produce a clone designated as 336 which displayed two independently segregating loci one of which is b. Clones are available in limited supply from Jack E. Staub.

RAPD marker loci were identified using primer sequences from Operon Technologies (OP; Alameda, California, U.S.A.) and the University of British Columbia (Vancouver, BC, Canada). Loci are identified by sequence origin (OP or BC), primer group letter (e.g., A), primer group array number (1-20), and locus (a, b, c, etc.) (Kennard et al., 1994). Information regarding unlinked loci can be obtained from Jack E. Staub.

Because of their abundance, common source (two mapping populations), and the accessibility of published information on their development (Kennard et al., 1994) DNA marker loci are not included in Table 1, but are listed below.

The 60 RFLP marker loci from mapping cross Gy 14 x PI 183967 (Kennard et al., 1994): CsP129/E1, CsC032a/E1, CsP064/E1, CsP357/H3, CsC386/E1, CsC365/E1, CsP046/E1, CsP347/H3, CsC694/E5, CsC588/H3, CsC230/E1, CsC593/D1, CsP193/H3, CsP078s/H3, CsC581/E5, CsE084/E1, CsC341/H3, CsP024/E1, CsP287/H3, CsC629/H3, CsP225s/E1, CsP303/H3, CsE051/H3, CsC366a/E5, CsC032b/E1, CsP056/H3, CsC378/E1, CsP406/E1, CsP460/E1, CsE060/E1, CsE103/E1, CsP019/E1, CsP168/D1, CsC560/H3, CsP005/E1,

CsP440s/E1, CsP221/H3, CsC625/E1, CsP475s/E1, CsP211/E1, CsP215/H3, CsC613/E1, CsC029/H3, CsP130/E1, CsC443/H3, CsE120/H3, CsE031/H3, CsC366b/E5, CsC082/H13, CsP094/H3, CsC362/E1, CsP441/E1, CsP280/H3, CsC137/H3, CsC558/H3, CsP037a/E1, CsP476/H3, CsP308/E1, CsP105/E1, and Csc166/E1.

The 31 RFLP marker loci from mapping cross Gy 14 x PI 432860 (Kennard et al., 1994): CsC560/D1, CsP024/E5, CsP287/H3, CsC384/E5, CsC366/E5, CsC611/D1, CsP055/D1, CsC482/H3, CsP019/E1, CsP059/D1, CsP471s/H13, CsC332/E5, CsP056/H3, CsC308/E5, CsP073/E5, CsP215/H3, CsC613/D1, CsP266/D1, CsC443/H3, CsE031/E1, CsE120/H3, CsE063/E1, CsP444/E1, CsC612/D1, Cs362/E1, CsP280/H3, CsC558/H3, CsP008/D1, CsP308/E1, CsC166/E1, and CsP303/H3.

The 20 RAPD marker loci from mapping cross Gy 14 x PI 432860 (Kennard et al., 1994): OPR04, OPW16, OPS17, OPE13a, OPN06, OPN12, OPP18b, BC211b, OPN04, OPA10, OPE09, OPT18, OPA14b, OPU20, BC460a, OPAB06, OPAB05, OPH12, OPA14a, and BC211a.

In addition to the isozymes, RFLPs and RAPDs, nearly 100 cloned genes are listed here (Table 2).

Possible Allelic or Identical Genes

Several of the genes listed may be either pleiotropic, closely linked, or allelic. Additional research is needed to compare the sources of the various similar genes to ensure that they are not duplicates. In some instances this may be difficult because many of the earlier publications did not list the source of the genes or the methods used to measure the traits, and many of these authors are deceased.

An example of this is the two-locus model (*R c*) for fruit color. We have been unable to locate any plants with red or yellow colored mature fruits. All plants evaluated in other studies have color inherited as a single gene. Hutchins may have separated fruit with cream color into 2 groups, yellow and cream, and fruits with orange color into two groups, orange and red. However, those distinctions are difficult to make using available germplasm. Situations like these may be impossible to resolve.

In the future, researchers should use the marker lines listed here, or describe and release the marker lines used so that allelism can be checked by others. Currently, groups of similar genes that need to be checked to determine how they are related include the following: the chlorophyll deficiency mutants (*cd, g, ls, pl, v, vvi, yc-1, yc-2,* and *yp*), the stem mutants (*bu, de, dw, In-de,* and *T*), the leaf shape mutants (*rc* and *ul*), the sex expression mutants (*a, F, gy, In-F, m, m-2,* and *Tr*), the male sterility genes (*ap, cl, ms-1,* and *ms-2*), the flowering stage mutants (*df* and *Fba*), the flower color mutants (*co* and *O*), the powdery mildew resistance mutants (*pm-1, pm-2, pm-3* and *pm-h*), the fruit spine color mutants (*B, B-2, B-3*, and *B-4*), the fruit skin color mutants (*c, R,* and *w*), the spine size and density mutants (*s, s-2*, and *s-3*) and the seed cell mutants (*cs* and *gb*).

Two groups of associated traits, one from 'Lemon' cucumber (*m, pr,* and *s*) and the other involving fruit skin color, surface texture, and spine type (*R, H,* and *B*), need to be checked using large populations to determine whether they are linked or pleiotropic. Recent gains have been made in this area by Robinson (1978a) who demonstrated that the *m* gene is pleiotropic for fruit shape and flower type, producing both perfect flowers and round fruits, and Abul-Hayja et al. (1975) and Whelan (1973) who determined that *gl* and *glb* are independent genes.

New information indicates that comparisons also need to be made between resistance to

scab (*Ccu*) and Fusarium wilt (*Foc*) and between resistance to target leaf spot (*Cca*) and *Ulocladium cucurbitae* leafspot. Mary Palmer (personal communication) found a fairly consistent association between resistances to scab and Fusarium wilt, which suggests that they might be linked or using the same mechanism for defense against the pathogen.

Similar defense mechanisms might also be responsible for similarities in resistance to target leaf spot (*Cca*) and *Ulocladium cucurbitae* leafspot (Henry Munger, personal communication).

Genetic Linkage

Since cucumber has just 7 chromosome pairs and over 100 known genes, it would seem that linkage maps would be fairly complete by now. Unfortunately, we know of few references reporting linkages of more than 2 gene loci, and this is the first review to summarize the literature for linkages and attempt to describe different linkage groups.

Many difficulties were encountered and should be considered when reading this review. First, a portion of the nomenclature is still unclear and some of the genes may be duplicates of others since common parents were not compared. This problem was discussed in the previous section. Secondly, some of the linkage relationships analyzed in previous studies did not involve specific genes. Linkages in several reports were discussed for plant traits that might have been inherited in multigenic fashion, or if a single gene were involved, it was not specifically identified.

Therefore, in this review linkages for traits without genes will be omitted and a '?' will follow each gene which has a questionable origin. Six linkage groups could be determined from the current literature (Fig. 1). The order in which the genes were expressed in each group does not necessarily represent the order in which they may be found on the chromosome.

Linkage Group A

The largest linkage group in cucumber has 12 genes, composed of *wmv-1-1, gy, gl, dl, dvl, de, F, ms-2, glb, bi, df* and *B-3* or *B-4*. In contributing to this grouping, Whelan (1974) noted that *ms-2* is linked with *glb* (rf=.215±.029) and *de* (rf=.335±.042) while being independent of *bi, gl, yc-1, yc-2,* and *cr*. Gene *de* is linked with *F* (Odland and Groff, 1963b; Owens and Peterson, 1982) which in turn is linked with *B-3* or *B-4* (Cowen and Helsel, 1983), *gy* (rf=.04) (Kubicki, 1974), *bi* (rf=.375) and *df* (rf=34.7) (Fanourakis, 1984; Fanourakis and Simon, 1987). Gene *de* is also weakly linked with *dl* (Miller and George, 1979), strongly linked with *dvl* (Netherlands, 1982), and independent of *cp* (Kauffman and Lower, 1976). Gene *wmv-1-1* is linked with bitterfree (*bi*) but independent of *Ccu, B, F* or *pm*? (Wang et al., 1987).

Two reports show that *dvl* is weakly linked with *gl* (rf=.40) and independent of *bi* and *Ccu* (Netherlands, 1982; den Nijs and Boukema, 1983), while Robinson (1978f) originally indicated that *gl* was linked with *yc* and independent of *B, m, l,* and *yg* as well as *bi* (Netherlands, 1982) and *sp* (den Nijs and Boukema, 1985), but more recently he indicated that *gl* was independent of *yc* (Robinson, 1987d).

Completing linkage group I, Cowen and Helsel (1983) demonstrated that the spine color genes (*B-3* and *B-4*) were independent of the genes for bitterness, and Whelan (1973) found that *pl* was independent of *glb* and *bi*, while *glb* was independent of *gl, bi, ls, yc,* and *cr*. The last clarifies that *gl* and *glb* must indeed be separate loci.

Linkage Group B

Group II is composed of 9 genes (*n, pr, l, m, opp, m-2, Bw, s*? and *ms*?) unless *s*? (Robinson, 1978) is the same as *s* from Hutchins (1940) and Poole (1944). If these are the same, then linkage groups II and III will be joined for a total of 12 genes. Of the first 7, two pairs have been defined with

recombination values. Youngner (1952) determined that *m* and *l* were linked with a recombination frequency of .326 ± .014 and Robinson determined that *opp* was linked to both (Robinson, 1987e). Iezzoni and Peterson (1979, 1980) found that *m* and *Bw* were separated by only one map unit (rf=.011±.003). Iezzoni et al. (1982) also determined that *m-2* was closely linked with both *m* and *Bw*, and that *Bw* was independent of *F* from linkage group I (Iezzoni and Peterson, 1980).

Robinson (1978c, 1978d), and Youngner (1952) found that linkages existed between *m, l, n, pr* and spine number (*s*?) with the possibility of pleiotropy being responsible for the *m*/*pr* relationship. They also demonstrated that *B, yg*, and *pm*? were independent of the same genes (Robinson, 1978c; Youngner, 1952).

Rounding out the linkage group is one of the male sterility genes (*ms*?). Robinson (1978d) found that it was linked with both *m* and *l*, but did not identify which male sterile gene it was.

Linkage Group C

Group III is the oldest and most mystifying linkage group. It is currently composed of *R* for red or orange mature fruit color, *H* for heavy netting, *B* for black or brown spine color, *c* for cream mature fruit color and *s* for spine frequency and size (Hutchins, 1940; Poole, 1944; Strong, 1931; Tkachenko, 1935). However, there is speculation on the nature of this linkage group. Since very few recombinants of the *R, H, B* and *c, h, b* linkage groups have been reported, it is also felt that these characteristics may be the response of 2 alleles at a single pleiotropic gene. There is also speculation that *R* and *c* are different alleles located at the same locus (see earlier discussion).

Hutchins (1940) found that *s* was independent of *B* and *H* while *s* was linked with *R* and *c*. If he was correct, then pleiotropy of *H* and *B* with *R* and *c* is ruled out. His report also indicated that *B* and *s* were independent of *de* as was *de* of *R, c* and *H*.

A possibility exists that this linkage group may be a continuation of group II through the *s* gene. Poole (1944) used the data of Hutchins (1940) to determine that *c* and *s* are linked with a recombination frequency of .163 ± .065. The question that remains is whether *s* (Hutchins, 1940; Poole, 1944) is the same as the gene for spine number in the findings of Robinson (1978c). If Cowen and Helsel (1983) are correct in their finding that a linkage exists between *F* and *B* then groups I and III may be on the same chromosome. However, in this text they will remain separated based on conclusions of Fanourakis (1984) which indicate that errors may be common when attempting to distinguish linkages with *F* since classification of *F* is difficult. This difficulty may also explain many conflicting reports.

Linkage Group D

Twelve genes (*ns, ss, Tu, Pc, D, U, te, cp, dm, Ar, coca* and *pm*? or *pm-h*) are in group IV, but the identity of the specific gene for powdery mildew resistance is elusive. Van Vliet and Meysing (1947, 1977) demonstrated that the gene for resistance to downy mildew (*dm*) was either linked or identical with a gene for resistance to powdery mildew (*pm*?), but because the linkage between *pm*? and *D* was broken while that of *dm* and *D* was not, *pm*? and *dm* must be separate genes. The problem lies in the lack of identity of *pm*? because Kooistra (1971) also found that a gene for powdery mildew resistance (*pm*?) was linked to *D*.

Further complicating the identity of *pm*, Fanourakis (1984) found that *pm-h* was linked to *te* and *dm*, yet *cp*, which must be located at approximately the same locus, was independent of *te*. He suggested that there were either 2 linkage groups, *ns, ss, Tu, Pc, D, U, te* and *cp, dm, Ar*, located at

distal ends of the same chromosome with *pm-h* at the center, or the 2 groups are located on different chromosomes with a translocation being responsible for apparent cross linkages. However, evidence for the latter which suggested that *F* was associated with the 7-gene segment is not probable since there are few other supportive linkages between genes of this segment and linkage group I. A more likely explanation is the occurrence of 2 or more genes conditioning resistance to powdery mildew being found on this chromosome.

More recently Lane and Munger (1985) and Munger and Lane (1987) determined that a gene for resistance to powdery mildew (*pm*?) was also linked with *coca* for susceptibility to target leaf spot but that linkage, though fairly tight, was breakable.

The last 4 genes in this group are *Tu, D, te* and *u* (Strong, 1931). Until recently it was believed that each in the recessive form were pleiotropic and consistent with European type cucumbers and each in the dominant form were pleiotropic and consistent with American type cucumbers. Fanourakis (1984) and Fanourakis and Simon (1987) reported that crossing over (R=23.7) occurred between *te* and the other 3 genes which still appeared to be associated. However, using triple backcrosses they demonstrated that there is a definite order for *Tu, D* and *u* within their chromosome segment and that the *Tu* end is associated with the *ns* and *ss* end.

Linkage Group E

Group V is currently composed of 3 genes *lh, sp* and *ul*. The gene *sp* was strongly linked with *lh* and weakly linked with *ul* (Zijlstra and den Nijs, 1986). However Zijlstra and den Nijs (1986) expressed concern for the accuracy of the *sp* and *ul* linkage data since it was difficult to distinguish *ul* under their growing conditions.

Linkage Group F

Group VI is comprised of 2 genes, *Fl* and *Ccu* which appear to be tightly associated. Wilson (1968) concluded that pleiotropy existed between scab resistance and fruit length because backcrossing scab resistance into commercial varieties consistently resulted in reduced fruit length. However, Munger and Wilkinson (1975) were able to break this linkage producing varieties with scab resistance and longer fruit (Tablegreen 65 and 66, Marketmore 70 and Poinsett 76). Now when these varieties are used to introduce scab resistance long fruit length is consistently associated.

Unaffiliated Genes

Independent assortment data are as important in developing linkage maps as direct linkage data and several researchers have made additional contributions in this area. One of the most extensive studies, based on the number of genes involved, is by Fanourakis (1984). He indicated that *Ar* was independent of *df, F, ns, B, u, mc, pm, Tu,* and *D*; *dm* was independent of *bi, df, F, ns, ss, B, te, u, mc, Tu* and *D*; *bi* was independent of *cp, df, B, pm-h, te, u, mc* and *Tu*; *cp* was independent of *df, F, ns, ss, te, u, Tu,* and *D*; *F* was independent of *sf, B, pm-h, te, u, mc, Tu* and *D*; *df* was independent of *te, u, Tu*, and *D*; *ns* was independent of *B, pm-h* and *mc*; *ss* was independent of *B* and *mc*; and *B* is independent of *pm-h, te, u, Tu* and *D*.

Two other extensive studies indicated that *yc-2* was not linked with *rc, yc-1, de, bi, cr, glb, gl*, and *m*, (Whelan et al., 1975) and both *Ccu* and *Bw* were independent of *bi, gl, glb, ls, rc, sc, cr, mc, gy-1* and *gy-2* (Abul-Hayja et al., 1975). Meanwhile, white immature fruit color (*w*) was inherited independently of black spines (*B*), and locule number (*l*) (Cochran, 1938; Youngner, 1952).

Whelan (1973) found that light sensitive (*ls*) was not linked with nonbitter (*bi*?) but did not indicate which bitter gene he used.

Zijlstra (1987) also determined that *bi* was independent of *cp, gl* is independent of *lh* and *ccu* is independent of *lh, ro* and *cp*.

Powdery mildew has been the subject of several linkage studies. Robinson (1978e) indicated that resistance in 'Ashley' which contains 3 recessive factors was independent of *B, l, pr, yg, fa, s,* and *H*. Kooistra (1971) found that powdery mildew resistance was not linked with *yf* or *wf* and Barham (1953) determined that the resistance genes in USDA PI 173889 were independent of *Bt*.

Like linkage data, independent assortment data may be very valuable in developing gene maps, but care must be taken when utilizing them. For example, resistance to powdery mildew was demonstrated in the previous paragraph but none of the researchers were able to identify the particular gene involved.

Table 1. The non-molecular genes of cucumber.

Gene	Synonym	Character	References[z]	Supplemental references[z]	Available[y]
a	-	*androecious*. Produces primarily staminate flowers if recessive for *F*. *A* from MSU 713-5 and Gy 14; *a* from An-11 and An-314, two selections from 'E-e-szan' of China.	Kubicki, 1969		P
Ak-2	-	*Adenylate kinase* (E.C.# 2.7.4.3). Isozyme variant found segregating in PI 339247, and 271754; 2 alleles observed.	Meglic and Staub, 1996		P
Ak-3	-	*Adenylate kinase* (E.C.# 2.7.4.3). Isozyme variant found segregating in PI 113334, 183967, and 285603; 2 alleles observed.	Meglic and Staub, 1996		P
al	-	*albino cotyledons*. White cotyledons and slightly light green hypocotyl; dying before first true leaf stage. Wild type Al from 'Nishiki-suyo'; *al* from M_2 line from pollen irradiation.	Iida and Amano, 1990, 1991		?
ap	-	*apetalous.* Male-sterile. Anthers become sepal-like. *Ap* from 'Butcher's Disease Resisting'; *ap* from 'Butcher's Disease Resisting Mutant'.	Grimbly, 1980		L
Ar	-	*Anthracnose resistance.* One of several genes for resistance to *Colletotrichum lagenarium. Ar* from PI 175111, PI 175120, PI 179676, PI 183308, PI 183445; *ar* from 'Palmetto' and 'Santee'.	Barnes and Epps, 1952		P
B	-	*Black or brown spines*. Dominant to white spines on fruit.	Strong, 1931; Tkachenko, 1935; Wellington, 1913	Cochran, 1938; Fujieda and Akiya, 1962; Hutchins, 1940; Jenkins, 1946; Youngner, 1952	W
B-2	-	*Black spine-2*. Interacts with *B* to produce F_2 of 15 black: 1 white spine. *B-2* from Wis. 9362; *b-2* from PI 212233 and 'Pixie'.	Shanmugasundarum et al., 1971a		?
B-3	-	*Black spine-3*. Interacts with *B-4* to produce an F_2 of nine black: 7 white spine. *B-3* from LJ90430; *b-3* from MSU 41.	Cowen and Helsel, 1983		W
B-4	-	*Black spine-4*. Interacts conversely with *B-3*. *B-4* from LJ90430; *b-4* from MSU 41.	Cowen and Helsel, 1983		W
bi	-	*bitterfree*. All plant parts lacking	Andeweg and	Cantliffe, 1972;	W

		cucurbitacins. Plants with *bi* less preferred by cucumber beetles. Plants with *Bi* resistant to spider mites in most American cultivars; *bi* in most Dutch cultivars.	DeBruyn, 1959	Da Costa and Jones, 1971a, 1971b; Soans et al., 1973	
bi-2		*bitterfree-2*. Leaves lacking cucurbitacins; *bi-2* from NCG-093 (short petiole mutant).	Wehner et al., 1998a		W
bl	*t*	*blind.* Terminal bud lacking after temperature shock. *bl* from 'Hunderup' and inbred HP3.	Carlsson, 1961.		L
bla	-	*blunt* leaf. Leaves have obtuse apices and reduced lobing and serration. *bla* from a mutant of 'Wis. SMR 18'.	Robinson, 1987a		W
Bt	-	*Bitter fruit*. Fruit with extreme bitter flavor. *Bt* from PI 173889 (Wild Hanzil Medicinal Cucumber).	Barham, 1953		W
bu	-	*bush.* Shortened internodes. *bu* from 'KapAhk 1'.	Pyzenkov and Kosareva, 1981		L
Bw	-	*Bacterial wilt resistance.* Resistance to *Erwinia tracheiphila. Bw* from PI 200818; *bw* from 'Marketer'.	Nutall and Jasmin, 1958	Robinson and Whitaker, 1974	W
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*.	Kubicki et al., 1986a		?
c	-	*cream mature fruit color*. Interaction with *R* is evident in the F_2 ratio of 9 red (*RC*) : 3 orange (*Rc*) : 3 yellow (*rC*) : 1 cream (*rc*).	Hutchins, 1940		L
Cca	-	*Corynespora cassiicola resistance.* Resistance to target leaf spot; dominant to susceptibility. *Cca* from Royal Sluis Hybrid 72502; *cca* from Gy 3.	Abul-Hayja et al., 1975		W
Ccu	-	*Cladosporium cucumerinum resistance*. Resistance to scab. *Ccu* from line 127.31, a selfed progeny of 'Longfellow'; *ccu* from 'Davis Perfect'.	Bailey and Burgess, 1934	Abul-Hayja and Williams, 1976; Abul-Hayja et al., 1975, Andeweg, 1956	W
cd	-	*chlorophyll deficient*. Seedling normal at first, later becoming a light green; lethal unless grafted. *cd* from a mutant selection of backcross of MSU 713-5 x 'Midget' F1 to 'Midget'.	Burnham, et al., 1966		L
chp	-	*choripetalous.* Small first true leaf; choripetalous flowers; glossy ovary; small fruits; few seeds. Wild type *Chp* from 'Borszczagowski'; *chp* from chemically induced mutation.	Kubicki and Korzeniewska, 1984		?
cl	-	*closed flower*. Staminate and pistillate flowers do not open; male-sterile (nonfertile pollen).	Groff and Odland, 1963		W
cla	-	*Colletotrichum lagenarium resistance*. Resistance to race 1 of anthracnose; recessive to susceptibility. *Cla* from Wis. SMR 18; *cla* from SC 19B.	Abul-Hayja et al., 1978		W
Cm	-	*Corynespora melonis resistance*. Resistance to *C. melonis* dominant to susceptibility. *Cm* from 'Spotvrie'; *cm* from 'Esvier'.	van Es, 1958		?
Cmv	-	*Cucumber mosaic virus resistance*. One of several genes for resistance to CMV. *Cmv* from 'Wis. SMR 12', 'Wis. SMR 15', and 'Wis. SMR 18'; *cmv* from 'National Pickling' and 'Wis. SR 6'.	Wasuwat and Walker, 1961	Shifriss et al., 1942	W

co	-	*green corolla*. Green petals that turn white with age and enlarged reproductive organs; female-sterile. *co* from a selection of 'Extra Early Prolific'.	Hutchins, 1935	Currence, 1954	L
cor-1	-	*cordate leaves-1*. Leaves are cordate. *cor-1* from 'Nezhinskii'.	Gornitskaya, 1967		L
cor-2	*cor*	*cordate leaves-2*. Leaves are nearly round with revolute margins and no serration. Insect pollination is hindered by short calyx segments that tightly clasp the corolla, preventing full opening. *cor-2* from an induced mutant of 'Lemon'.	Robinson, 1987c		?
cp	-	*compact*. Reduced internode length, poorly developed tendrils, small flowers. *cp* from PI 308916.	Kauffman and Lower, 1976		W
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.	Kubicki et al., 1986b		?
cr	-	*crinkled leaf*. Leaves and seed are crinkled.	Odland and Groff, 1963a		?
cs	-	*carpel splitting*. Fruits develop deep longitudinal splits. *cs* from TAMU 1043 and TAMU 72210, which are second and fifth generation selections of MSU 3249 x SC 25.	Caruth, 1975; Pike and Caruth, 1977		?
D	*g*	*Dull fruit skin*. Dull skin of American cultivars, dominant to glossy skin of most European cultivars.	Poole, 1944; Strong, 1931; Tkachenko, 1935		W
de	*I*	*determinate habit*. Short vine with stem terminating in flowers; modified by *In-de* and other genes; degree of dominance depends on gene background. *de* from Penn 76.60G[*], Minn 158.60[*], 'Hardin's PG57'[*], 'Hardin's Tree Cucumber'[*], and S_2-1 (and inbred selection from Line 541)[**].	Denna, 1971[*]; George, 1970[**]; Hutchins, 1940	Nutall and Jasmin, 1958	W
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'.	Soltysiak et al., 1986		?
df	-	*delayed flowering*. Flowering delayed by long photoperiod; associated with dormancy. *df* from 'Baroda' (PI 212896)[*] and PI 215589 (*hardwickii*)[**].	Della Vecchia et al., 1982[*]; Shifriss and George, 1965[**].		W
dl	-	*delayed growth*. Reduced growth rate; shortening of hypocotyl and first internodes. *dl* from 'Dwarf Marketmore' and 'Dwarf Tablegreen', both deriving dwarfness from 'Hardin's PG-57'.	Miller and George, 1979		W
dm	*P*	*downy mildew resistance*. One of several genes for resistance to *Pseudoperonospora cubensis*. *Dm* from Sluis & Groot Line 4285; *dm* from 'Poinsett'.	van Vliet and Meysing, 1977	Jenkins, 1946; Shimizu, 1963	W
dm-1	*dm*	*downy mildew resistance-1*. One of three genes for resistance to downy mildew caused by *Pseudoperonospora cubensis* (Berk &	Doruchowski and Lakowska-Ryk, 1992		?

		Curt). Wild type *Dm-1* from Wisconsin SMR 18; *dm-1* from WI 4783. Not checked for allelism with *dm*.			
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*.	Doruchowski and Lakowska-Ryk, 1992		?
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*.	Doruchowski and Lakowska-Ryk, 1992		?
dvl	*dl*	*divided leaf*. True leaves are partly or fully divided, often resulting in compound leaves with two to five leaflets and having incised corollas.	den Nijs and Mackiewicz, 1980		W
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'.	Rucinska et al., 1992b		?
dw	-	*dwarf*. Short internodes. *dw* from an induced mutant of 'Lemon'.	Robinson and Mishanec, 1965		?
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 M_2 line from pollen irradiation.	Iida and Amano, 1990, 1991		?
dwc-2	-	*dwarf cotyledons-2*. Small cotyledons; late germination; small first true leaf. Wild type *Dwc-2* from 'Nishiki Suyo'; *dwc-2* from M_2 line from pollen irradiation.	Iida and Amano, 1990, 1991		?
Es-1	-	*Empty chambers-1*. Carpels of fruits separated from each other, leaving a small to large cavity in the seed cell. *Es-1* from PP-2-75; *es-1* from Gy-30-75.	Kubicki and Korzeniewska, 1983		?
Es-2	-	*Empty chambers-2*. Carpels of fruits separated from each other, leaving a small to large cavity in the seed cell. *Es-2* from PP-2-75; *es-2* from Gy-30-75.	Kubicki and Korzeniewska, 1983		?
F	*Acr*, *acr*^{F}, *D*, *st*	*Female*. High degree of pistillate sex expression; interacts with *a* and *M*; strongly modified by environment and gene background. *F* and *f* are from 'Japanese'.	Galun, 1961; Tkachenko, 1935	Kubicki, 1965, 1969a; Poole, 1944; Shifriss, 1961	W
fa	-	*fasciated*. Plants have flat stems, short internodes, and rugose leaves. *fa* was from a selection of 'White Lemon'[*].	Robinson, 1987b[*]; Shifriss, 1950		?
Fba	-	*Flower bud abortion*. Preanthesis abortion of floral buds, ranging from 10% to 100%. *fba* from MSU 0612.	Miller and Quisenberry, 1978		?
Fdp-1	-	*Fructose diphosphatase* (E.C.# 3.1.3.11). Isozyme variant found segregating in PI 192940, 169383 and 169398; 2 alleles observed.	Meglic and Staub, 1996		P
Fdp-2	-	*Fructose diphosphatase* (E.C.# 3.1.3.11). Isozyme variant found segregating in PI 137851, 164952, 113334 and 192940; 2 alleles	Meglic and Staub, 1996		P

		observed.			
Fl	-	*Fruit length*. Expressed in an additive fashion, fruit length decreases incrementally with each copy of *fl* (H. Munger, personal communication).	Wilson, 1968		W
Foc	*Fcu-1*	*Fusarium oxysporum f. sp. cucumerinum resistance*. Resistance to fusarium wilt races 1 and 2; dominant to susceptibility. *Foc* from WIS 248; *foc* from 'Shimshon'.	Netzer et al., 1977; Vakalounakis, 1993, 1995, 1996		W
G2dh	-	*Glutamine dehydrogenase* (E.C.# 1.1.1.29). Isozyme variant found segregating in PI 285606; 5 alleles observed.	Knerr and Staub, 1992		P
g	-	*golden leaves*. Golden color of lower leaves. *G* and *g* are both from different selections of 'Nezhin'.	Tkachenko, 1935		?
gb	*n*	*gooseberry fruit*. Small, oval-shaped fruit. *gb* from the 'Klin mutant'.	Tkachenko, 1935		?
gc	-	*golden cotyledon*. Butter-colored cotyledons; seedlings die after 6 to 7 days. *gc* from a mutant of 'Burpless Hybrid'.	Whelan, 1971		W
gi	-	*ginkgo*. Leaves reduced and distorted, resembling leaves of Ginkgo; male- and female-sterile. Complicated background: It was in a segregating population whose immediate ancestors were offspring of crosses and backcrosses involving 'National Pickling', 'Chinese Long', 'Tokyo Long Green', 'Vickery', 'Early Russian', 'Ohio 31' and an unnamed white spine slicer.	John and Wilson, 1952		L
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.	Rucinska et al., 1992b		?
gig	-	*gigantism*. First leaf larger than normal. Wild type *Gig* from 'Borszczagowski'; *gig* from chemically induced mutation.	Kubicki et al., 1984		?
gl	-	*glabrous*. Foliage lacking trichomes; fruit without spines. Iron-deficiency symptoms (chlorosis) induced by high temperature. *gl* from NCSU 75* and M834-6**.	Robinson and Mishanec, 1964*	Inggamer and de Ponti, 1980**; Robinson, 1987b	W
glb	-	*glabrate*. Stem and petioles glabrous, laminae slightly pubescent. *glb* from 'Burpless Hybrid'.	Whelan, 1973		W
gn	-	*green mature fruit*. Green mature fruits when *rr gngn*; cream colored when *rr GnGn*; orange when *R_ __*. Wild type *Gn* from 'Chipper', SMR 58 and PI 165509; *gn* from TAMU 830397.	Peterson and Pike, 1992		W
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.	Knerr and Staub, 1992		P
Gr-1	-	*Glutathione reductase-1* (E.C.# 1.6.4.2). Isozyme variant found segregating in PI 109275; 5 alleles observed.	Knerr and Staub, 1992		P
gy	-	*gynoecious*. Recessive gene for high degree of pistillate sex expression.	Kubicki, 1974		W
H	-	*Heavy netting of fruit*. Dominant to no netting and completely linked or pleiotropic with	Hutchins, 1940; Tkachenko, 1935		W

		black spines (*B*) and red mature fruit color (*R*).			
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*.	Vakalounakis, 1992		W
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.	Iida and Amano, 1990, 1991		?
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.	Iida and Amano, 1990, 1991		?
I	-	*Intensifier of P*. Modifies effect of *P* on fruit warts in *Cucumis sativus* var. *tuberculatus.*	Tkachenko, 1935		?
Idh	-	*Isocitrate dehydrogenase* (E.C.# 1.1.1.42). Isozyme variant found segregating in PI 183967, 215589; 2 alleles observed.	Knerr and Staub, 1992		P
In-de	*In(de)*	*Intensifier of* de. Reduces internode length and branching of *de* plants. *In-de* and *in-de* are from different selections (S_5-1 and S_5-6, respectively) from a determinant inbred S_2-1, which is a selection of line 541.	George, 1970		?
In-F	*F*	*Intensifier of female sex expression.* Increases degree of pistillate sex expression of *F* plants. *In-F* from monoecious line 18-1; *in-F* from MSU 713-5.	Kubicki, 1969b		?
l	-	*locule number*. Many fruit locules and pentamerous androecium; five locules recessive to the normal number of three.	Youngner, 1952		W
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.	Iida and Amano, 1990, 1991		?
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.	Iida and Amano, 1990, 1991		?
lh	-	*long hypocotyl.* As much as a 3-fold increase in hypocotyl length. *lh* from a 'Lemon' mutant.	Robinson and Shail, 1981		W
ll	-	*little leaf.* Normal-sized fruits on plants with miniature leaves and smaller stems. *ll* from Ark. 79-75.	Goode et al., 1980; Wehner et al., 1987		W
ls	-	*light sensitive.* Pale and smaller cotyledons, lethal at high light intensity. *ls* from a mutant of 'Burpless Hybrid'.	Whelan, 1972b		L
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'.	Whelan, 1971, 1972		?
m	*a, g*	*andromonoecious.* Plants are andromonoecious if (*mf*); monoecious if (*Mf*); gynoecious if (*MF*) and hermaphroditic if (*mF*). *m* from 'Lemon'[*].	Rosa, 1928[*]; Tkachenko, 1935	Shifriss, 1961; Wall, 1967; Youngner, 1952	W

m-2	*h*	*andromonoecious-2.* Bisexual flowers with normal ovaries.	Iezzoni, 1982; Kubicki, 1974		?
Mdh-1	-	*Malate dehydrogenase-1* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 171613, 209064, 326594; 3 alleles observed.	Knerr and Staub, 1992		P
Mdh-2	-	*Malate dehydrogenase-2* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 174164, 185690, 357835, 419214; 2 alleles observed.	Knerr and Staub, 1992		P
Mdh-3	-	*Malate dehydrogenase-3* (E.C.# 1.1.1.37).	Knerr et al., 1995		P
Mdh-4	*Mdh-3*	*Malate dehydrogenase-4* (E.C.# 1.1.1.37). Isozyme variant found segregating in PI 255236, 267942, 432854, 432887; 2 alleles observed.	Knerr and Staub, 1992		P
mj		A single recessive gene for resistance to the root-knot nematode (*Meloidogyne javanica*) from *Cucumis sativus* var. *hardwickii*; *mj* from NC-42 (LJ 90430).	Walters et al., 1996; 1997	Walters and Wehner, 1998	W
mp	pf^{+}, pf^{d}, pf^{p}	*multi-pistillate.* Several pistillate flowers per node, recessive to single pistillate flower per node. *mp* from MSU 604G and MSU 598G.	Nandgaonkar and Baker, 1981	Fujieda et al., 1982	W
Mp-2	-	*Multi-pistillate-2.* Several pistillate flowers per node. Single dominant gene with several minor modifiers. *Mp-2* from MSU 3091-1.	Thaxton, 1974		?
Mpi-1	-	*Mannose phosphate isomerase* (E.C.# 5.3.1.8). Isozyme variant found segregating in PI 176954, and 249562; 2 alleles observed.	Meglic and Staub, 1996		P
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.	Knerr and Staub, 1992		P
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'.	Pyzhenkov and Kosareva, 1981		?
ms-1	-	*male sterile-1.* Staminate flowers abort before anthesis; partially female-sterile. *ms-1* from selections of 'Black Diamond' and 'A & C'.	Shifriss, 1950	Robinson and Mishanec, 1967	L
ms-2	-	*male sterile-2.* Male-sterile; pollen abortion occurs after first mitotic division of the pollen grain nucleus. *ms-2* from a mutant of 'Burpless Hybrid'.	Whelan, 1973		?
$ms\text{-}2^{(PS)}$	-	*male sterile-2 pollen sterile.* Male-sterile; allelic to *ms-2*, but not to *ap*. $ms\text{-}2^{(PS)}$ from a mutant of Sunseeds 23B-X26.	Zhang et al., 1994		?
mwm	-	Moroccan watermelon mosaic virus resistance single recessive gene from Chinese cucumber cultivar 'TMG-1'	Kabelka and Grumet, 1997		W
n	-	*negative geotropic peduncle response.* Pistillate flowers grow upright; *n* from 'Lemon'; *N* produces the pendant flower position of most cultivars.	Odland, 1963b		W
ns	-	*numerous spines.* Few spines on the fruit is dominant to many. *ns* from Wis. 2757.	Fanourakis, 1984; Fanourakis and Simon, 1987		W
O	*y*	*Orange-yellow corolla.* Orange-yellow dominant to light yellow. *O* and *o* are both from 'Nezhin'.	Tkachenko, 1935		?
opp	-	*opposite leaf arrangement.* Opposite leaf arrangement is recessive to alternate and has	Robinson, 1987e		W

		incomplete penetrance. *opp* from 'Lemon'.			
P	-	*Prominent tubercles.* Prominent on yellow rind of *Cucumis sativus* var. *tuberculatus*, incompletely dominant to brown rind without tubercles. *P* from 'Klin'; *p* from 'Nezhin'.	Tkachenko, 1935		W
Pc	*P*	*Parthenocarpy.* Sets fruit without pollination. *Pc* from 'Spotvrie'*; *pc* from MSU 713-205*.	Pike and Peterson, 1969; Wellington and Hawthorn, 1928; Whelan, 1973	de Ponti and Garretsen, 1976	?
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.	Fanourakis and Simon, 1987		W
Pep-gl-1	-	*Peptidase with glycyl-leucine* (E.C.# 3.4.13.11). Isozyme variant found segregating in PI 113334, 212896; 2 alleles observed.	Meglic and Staub, 1996		P
Pep-gl-2	-	*Peptidase with glycyl-leucine* (E.C.# 3.4.13.11). Isozyme variant found segregating in PI 137851, 212896; 2 alleles observed.	Meglic and Staub, 1996		P
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.	Knerr and Staub, 1992		P
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.	Knerr and Staub, 1992		P
Per-4	-	*Peroxidase* (E.C.# 1.11.1.7). Isozyme variant found segregating in PI 215589; 2 alleles observed.	Knerr and Staub, 1992		P
Pgd-1	-	*Phosphogluconate dehydrogenase-1* (E.C.# 1.1.1.43). Isozyme variant found segregating in PI 169380, 175692, 222782; 2 alleles observed.	Knerr and Staub, 1992		P
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.	Knerr and Staub, 1992		P
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.	Knerr and Staub, 1992		P
pl	-	*pale lethal.* Slightly smaller pale-green cotyledons; lethal after 6 to 7 days. *Pl* from 'Burpless Hybrid'; *pl* from a mutant of 'Burpless Hybrid'.	Whelan, 1973		L
pm-1	-	*powdery mildew resistance-1.* Resistance to *Sphaerotheca fuliginia*. *pm-1* from 'Natsufushinari'.	Fujieda and Akiya, 1962; Kooistra, 1971	Shanmugasundarum et al., 1972	?
pm-2	-	*powdery mildew resistance-2.* Resistance to *Sphaerotheca fuliginia*. *pm-2* from 'Natsufushinari'.	Fujieda and Akiya, 1962; Kooistra, 1971	Shanmugasundarum et al., 1972	?
pm-3	-	*powdery mildew resistance-3.* Resistance to *Sphaerotheca fuliginia*. *pm-3* found in PI 200815 and PI 200818.	Kooistra, 1971	Shanmugasundarum et al., 1972	W
pm-h	*s, pm*	*powdery mildew resistance expressed by the hypocotyl.* Resistance to powdery mildew as noted by no fungal symptoms appearing on seedling cotyledons is recessive to	Fanourakis, 1984; Shanmugasundarum et al., 1971b		W

		susceptibility. *Pm-h* from 'Wis. SMR 18'; *pm-h* from 'Gy 2 *cp cp*', 'Spartan Salad', and Wis. 2757.			
pr	-	*protruding ovary*. Exerted carpels. *pr* from 'Lemon'.	Youngner, 1952.		W
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'.	Wang et al., 1984		
Prsv-2		Resistance to papaya ringspot virus; *Prsv-2* from TMG-1.	Wai and Grumet, 1995	Wai et al., 1997	W
psl	*pl*	Pseudomonas lachrymans *resistance.* Resistance to *Pseudomonas lachrymans* is recessive. *Psl* from 'National Pickling' and 'Wis. SMR 18'; *psl* from MSU 9402 and Gy 14.	Dessert et al., 1982		W
Psm	-	*Paternal sorting of mitochondria.* Mitochondria sorting induced by dominant gene *Psm*, found in MSC 16; *psm* from PI 401734.	Havey et al., 2004.		W
R	-	*Red mature fruit.* Interacts with *c*; linked or pleiotropic with *B* and *H.*	Hutchins, 1940		W
rc	-	*revolute cotyledon.* Cotyledons are short, narrow, and cupped downwards; enlarged perianth. *rc* from 'Burpless Hybrid' mutant.	Whelan et al., 1975		L
rc-2		recessive gene for revolute cotyledons; rc-2 fro NCG-0093 (short petiole mutant)	Wehner et al., 1998b		W
ro	-	*rosette*. Short internodes, muskmelon-like leaves. *ro* from 'Megurk', the result of a cross involving a mix of cucumber and muskmelon pollen.	de Ruiter et al., 1980		W
s	*f, a*	*spine size and frequency*. Many small fruit spines, characteristic of European cultivars is recessive to the few large spines of most American cultivars.	Strong, 1931; Tkachenko, 1935	Caruth, 1975; Poole, 1944	W
s-2	-	*spine-2*. Acts in duplicate recessive epistatic fashion with *s-3* to produce many small spines on the fruit. *s-2* from Gy 14; *s-2* from TAMU 72210.	Caruth, 1975		?
s-3	-	*spine-3*. Acts in duplicate recessive epistatic fashion with *s-2* to produce many small spines on the fruit. *S-3* from Gy 14; *s-3* from TAMU 72210.	Caruth, 1975		?
sa	-	*salt tolerance*. Tolerance to high salt levels is attributable to a major gene in the homozygous recessive state and may be modified by several minor genes. *Sa* from PI 177362; *sa* from PI 192940.	Jones, 1984		P
sc	*cm*	*stunted cotyledons*. Small, concavely curved cotyledons; stunted plants with cupped leaves; abnormal flowers. *Sc sc* from Wis. 9594 and 9597.	Shanmugasundarum and Williams, 1971; Shanmugasundarum et al., 1972.		W
Sd	-	*Sulfur dioxide resistance*. Less than 20% leaf damage in growth chamber. *Sd* from 'National Pickling'; *sd* from 'Chipper'.	Bressan et al., 1981		W
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'.	Soltysiak and Kubicki 1988		?

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.	Iida and Amano, 1990, 1991		?
Skdh	-	*Shikimate dehydrogenase* (E.C.# 1.1.1.25). Isozyme variant found segregating in PI 302443, 390952, 487424; 2 alleles observed.	Meglic and Staub, 1996		P
sp	-	*short petiole*. Leaf petioles of first nodes 20% the length of normal. *sp* from Russian mutant line 1753.	den Nijs and de Ponti, 1983		W
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.	Rucinska et al., 1992a		?
ss	-	*small spines*. Large, coarse fruit spines is dominant to small, fine fruit spines. *Ss* from 'Spartan Salad', 'Wis. SMR 18' and 'GY 2 *cp cp*'; *ss* from Wis. 2757.	Fanourakis, 1984; Fanourakis and Simon, 1987		W
T	-	*Tall plant.* Tall incompletely dominant to short.	Hutchins, 1940		?
td	-	*tendrilless*. Tendrils lacking; associated with misshapen ovaries and brittle leaves. *Td* from 'Southern Pickler'; *td* from a mutant of 'Southern Pickler'.	Rowe and Bowers, 1965		W
te	-	*tender skin of fruit*. Thin, tender skin of some European cultivars; recessive to thick tough skin of most American cultivars.	Poole, 1944; Strong, 1931		W
Tr	-	*Trimonoecious*. Producing staminate, perfect, and pistillate flowers in this sequence during plant development. *Tr* from Tr-12, a selection of a Japanese cultivar belonging to the Fushinari group; *tr* from H-7-25. MOA-309, MOA-303, and AH-311-3.	Kubicki, 1969d		P
Tu	-	*Tuberculate fruit.* Warty fruit characteristic of American cultivars is dominant to smooth, non-warty fruits characteristic of European cultivars.	Strong, 1931; Wellington, 1913	Andeweg, 1956; Poole, 1944	W
u	*M*	*uniform immature fruit color*. Uniform color of European cultivars recessive to mottled or stippled color of most American cultivars.	Strong, 1931	Andeweg, 1956	W
ul	-	*umbrella leaf.* Leaf margins turn down at low relative humidity making leaves look cupped. *ul* source unknown.	den Nijs and de Ponti, 1983		W
v	-	*virescent.* Yellow leaves becoming green.	Strong, 1931; Tkachenko, 1935		L
vvi	-	*variegated virescent.* Yellow cotyledons, becoming green; variegated leaves.	Abul-Hayja and Williams, 1976		L
w	-	*white immature fruit color*. White is recessive to green. *W* from 'Vaughan', 'Clark's Special', 'Florida Pickle' and 'National Pickling'; *w* from 'Bangalore'.	Cochran, 1938		W
wf	-	*White flesh*. Intense white flesh color is recessive to dingy white; acts with *yf* to produce F_2 of 12 white (*WfWf YfYf* or *wfwf YfYf*) : 3 yellow (*WfWf yfyf*) : 1 orange (*wfwf yfyf*). *Wf* from EG and G6, each being dingy	Kooistra, 1971		?

		white (*WfWf YfYf*): *wf* from 'NPI ' which is orange (*wfwf yfyf*).			
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.	Iida and Amano, 1990, 1991		?
Wmv	-	*Watermelon mosaic virus resistance.* Resistance to strain 2 of watermelon mosaic virus. *Wmv* from 'Kyoto 3 Feet'; *wmv* from 'Beit Alpha'.	Cohen et al., 1971		P
wmv-1-1	-	*watermelon mosaic virus-1 resistance.* Resistance to strain 1 of watermelon mosaic virus by limited systemic translocation; lower leaves may show severe symptoms. *Wmv-1-1* from Wis. 2757; *wmv-1-1* from 'Surinam'.	Wang et al., 1984	Provvidenti, 1985	?
wmv-2	-	*watermelon mosaic virus resistance.* Expressed in the cotyledon and throughout the plant; *wmv-2* from TMG-1.	Wai et al., 1997		W
wmv-3	-	*watermelon mosaic virus resistance.* Expressed only in true leaves; *wmv-3* from TMG-1.	Wai et al., 1997		W
wmv-4	-	*watermelon mosaic virus resistance.* Expressed only in true leaves; *wmv-4* from TMG-1.	Wai et al., 1997		W
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.	Iida and Amano, 1990, 1991		?
yc-1	-	*yellow cotyledons-1.* Cotyledons yellow at first, later turning green. *yc-1* from a mutant of Ohio MR 25.	Aalders, 1959		W
yc-2	-	*yellow cotyledons-2.* Virescent cotyledons. *yc-2* from a mutant of 'Burpless Hybrid'.	Whelan and Chubey, 1973; Whelan et al., 1975		W
yf	*v*	*yellow flesh.* Interacts with *wf* to produce F_2 of 12 white (*Wf Yf* and *wf Yf*) : 3 yellow (*Wf yf*) : 1 orange (*wf yf*). *Yf* from 'Natsufushinari', which has an intense white flesh (*Yf wf*); *yf* from PI 200815 which has a yellow flesh (*yf Wf*).	Kooistra, 1971		P
yg	*gr*	*yellow-green immature fruit color.* Recessive to dark green and epistatic to light green. *yg* from 'Lemon'.	Youngner, 1952		W
yp	-	*yellow plant.* Light yellow-green foliage; slow growth.	Abul-Hayja and Williams, 1976		?
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.	Rucinska et al., 1991		?
zym-Dina	-	zucchini yellow mosaic virus resistance; *zym-Dina* from Dina-1.	Kabelka et al., 1997	Wai et al., 1997	P
zym-TMG1	*zymv*	*zucchini yellow mosaic virus resistance.* Inheritance is incomplete, but usually inherited in a recessive fashion; source of resistance is 'TMG-1'.	Provvidenti, 1987; Kabelka et al., 1997	Wai et al., 1997	W

[z] Asterisks on cultigens and associated references indicate the source of information for each.

[y] W = Mutant available through T.C. Wehner, cucumber gene curator for the Cucurbit Genetics Cooperative; P = mutants are available as standard cultivars or accessions from the Plant Introduction Collection; ? = availability not known; L = mutant has been lost.
* Isozyme nomenclature follows a modified form of Staub et al. (1985) previously described by Richmond (1972) and Gottlieb (1977).

Table 2. The cloned genes of cucumber and their function.[z]

Gene accession	Tissue source	Function	Clone type	Reference
Genes involved in seed germination or seedling development				
X85013	Cotyledon cDNA library	Encoding a T-complex protein	cDNA	Ahnert et al., 1996
AJ13371	Cotyledon cDNA library	Encoding a matrix metalloproteinases	cDNA	Delorme et al., 2000
X15425	Cotyledon cDNA library	Glyoxysomal enzyme malate synthase	Genomic DNA fragment	Graham et al., 1989; 1990
X92890	Cotyledon cDNA library	Encoding a lipid body lipoxygenase	cDNA	Höhne et al., 1996
L31899	Senescing cucumber cotyledon cDNA library	Encoding an ATP-dependent phosphoenolpyruvate carboxykinase (an enzyme of the gluconeogenic pathway)	cDNA	Kim and Smith, 1994a
L31900	Cotyledon cDNA library	Encoding microbody NAD(+)-dependent malate dehydrogenase (MDH)	cDNA	Kim and Smith, 1994b
L44134	Senescing cucumber cDNA library	Encoding a putative SPF1-type DNA binding protein	cDNA	Kim et al., 1997
U25058	Cotyledons	Encoding a lipoxygenase-1 enzyme	cDNA	Matsui et al., 1995; 1999
Y12793	Cotyledon cDNA library	Encoding a patatin like protein	cDNA	May et al., 1998
X67696	Cotyledon cDNA library	Encoding the 48539 Da precursor of thiolase	cDNA	Preisig-Muller and Kindl, 1993a
X67695	Cotyledon cDNA library	Encoding homologous to the bacterial dnaJ protein	cDNA	Preisig-Muller and Kindl, 1993b
X79365	Seedling cDNA library	Encoding glyoxysomal tetrafunctional protein	cDNA	Preisig-Muller et al., 1994
X79366	Seedling cDNA library	Encoding glyoxysomal tetrafunctional protein	cDNA	Preisig-Muller et al., 1994
Z35499	Genomic library	Encoding the glyoxylate cycle enzyme isocitrate lyase	Genomic gene	Reynolds and Smith, 1995
M59858	Cotyledon cDNA library	Encoding a stearoyl-acyl-carrier-protein (ACP) desaturase	cDNA	Shanklin and Somerville, 1991
M16219	Cotyledon cDNA library	Encoding glyoxysomal malate synthase	cDNA	Smith and Leaver, 1986
Genes involved in photosynthesis and photorespiration activities				
M16056	Cotyledon cDNA library	Encoding ribulose bisphosphate carboxylase/oxygenase	cDNA	Greenland et al., 1987
M16057	Cotyledon cDNA library	Encoding chlorophyll a/b-binding protein	cDNA	Greenland et al., 1987
M16058	Cotyledon cDNA library	Encoding chlorophyll a/b-binding protein	cDNA	Greenland et al., 1987
X14609	cotyledon cDNA library	Encoding a NADH-dependent hydroxypyruvate reductase (HPR	cDNA	Greenler et al., 1989
Y09444	Chloroplast genomic	tRNA gene	Chloroplast	Hande and

	library		DNA fragment	Jayabaskaran, 1997
X75799	Chloroplast genomic library	Chloroplast tRNA (Leu) (cAA) gene	Genomic DNA fragment	Hande et al., 1996
D50456	Cotyledon cDNA library	Encoding 17.5-kDa polypeptide of cucumber photosystem I	cDNA	Iwasaki et al., 1995
S69988	Hypocotyls	Cytoplasmic tRNA (Phe)	cytoplasmic DNA fragment	Jayabaskaran and Puttaraju, 1993
S78381	Cotyledon cDNA library	Encoding NADPH-protochlorophyllide oxidoreductase	cDNA	Kuroda et al., 1995
D26106	Cotyledon cDNA library	Encoding ferrochelatase	cDNA	Miyamoto et al., 1994
U65511	Green peelings cDNA library	Encoding the 182 amino acid long precursor stellacyanin	cDNA	Nersissian et al., 1996
AF099501	Petal cDNA library	Encoding the carotenoid-associated protein	cDNA	Ovadis et al., 1998
X67674	Cotyledon cDNA library	Encoding ribulosebisphosphate carboxylase/oxygenase activase	cDNA	Preisig-Muller and Kindl, 1992
X58542	Cucumber genomic library	Encoding NADH-dependent hydroxypyruvate reductase	Genomic DNA fragment	Schwartz et al., 1991
U62622	Seedling cDNA library	Encoding monogalacto-syldiacylglycerol synthase	cDNA	Shimojima et al., 1997
D50407	Cotyledon cDNA library	Encoding glutamyl-tRNA reductase proteins	cDNA	Tanaka et al., 1996
D67088	Cotyledon cDNA library	Encoding glutamyl-tRNA reductase proteins	cDNA	Tanaka et al., 1996
D83007	Cotyledon cDNA library	Encoding a subunit XI (psi-L) of photosystem I	cDNA	Toyama et al., 1996
Genes expressed mainly in roots.				
AB025717	Root RNA	Lectin-like xylem sap protein	cDNA	Masuda et al., 1999
U36339	Root cDNA library	Encoding root lipoxygenase	cDNA	Matsui et al., 1998
AB015173	Root cDNA library	Encoding glycine-rich protein-1	cDNA	Sakuta et al., 1998
AB015174	Root cDNA library	Encoding glycine-rich protein-1	cDNA	Sakuta et al., 1998
Flower genes				
AF035438	Female flower cDNA library	MADS box protein CUM1	cDNA	Kater et al., 1998
AF035439	Female flower cDNA library	MADS box protein CUM10	cDNA	Kater et al., 1998
D89732	Seedlings	Encoding 1-aminocyclo-propane-1-carboxylate synthase	cDNA	Kamachi et al., 1997
AB003683	Seedlings	Encoding 1-aminocyclo-propane-1-carboxylate synthase	cDNA	Kamachi et al., 1997
AB003684	Seedlings	Encoding 1-aminocyclo-propane-1-carboxylate synthase	cDNA	Kamachi et al., 1997
AB035890	Fruit RNA	Encoding polygalacturonase	cDNA	Kubo et al., 2000
AF022377	Floral buds	Encoding agamous-like putative transcription factor (CAG1) mRNA	cDNA	Perl-Treves et al., 1998
AF022378	Floral buds	Encoding agamous like putative transcription factor (CAG2) mRNA	cDNA	Perl-Treves et al., 1998
AF022379	Floral buds	Encoding agamous-like putative transcription factor (CAG3) mRNA	cDNA	Perl-Treves et al., 1998

U59813	Genomic DNA	Encoding 1-aminocyclo-propane-1-carboxylate synthase	Genomic DNA fragment	Trebitsh et al., 1997
X95593	Corolla cDNA library	Encoding carotenoid-associated protein	cDNA	Vishnevetsky et al., 1996
AB026498	Shoot apex RNA	Ethylene-receptor-related gene	cDNA	Yamasaki et al., 2000
Genes involved in fruit development and maturation				
AB010922	Fruit cDNA library	Encoding the ACC synthase	cDNA	Mathooko et al., 1999
J04494	Fruit cDNA library	Encoding an ascorbate oxidase	cDNA	Ohkawa et al., 1989; 1990
AB006803	Fruit cDNA library	Encoding ACC synthase	cDNA	Shiomi et al., 1998
AB006804	Fruit cDNA library	Encoding ACC synthase	cDNA	Shiomi et al., 1998
AB006805	Fruit cDNA library	Encoding ACC synthase	cDNA	Shiomi et al., 1998
AB006806	Fruit cDNA library	Encoding ACC oxidase	cDNA	Shiomi et al., 1998
AB006807	Fruit cDNA library	Encoding ACC oxidase	cDNA	Shiomi et al., 1998
AB008846	Pollinated fruit cDNA library	Corresponding genes preferentially expressed in the pollinated fruit	cDNA	Suyama et al., 1999
AB008847	Pollinated fruit cDNA library	Corresponding genes preferentially expressed in the pollinated fruit	cDNA	Suyama et al., 1999
AB008848	Pollinated fruit cDNA library	Corresponding genes preferentially expressed in the pollinated fruit	cDNA	Suyama et al., 1999
Genes involved in cell wall loosening and cell enlargement				
AB001586	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK1.1)	cDNA	Chono et al., 1999
AB001587	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK1.2)	cDNA	Chono et al., 1999
AB001588	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK2.1)	cDNA	Chono et al., 1999
AB001589	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK2.2)	cDNA	Chono et al., 1999
AB001590	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK3)	cDNA	Chono et al., 1999
AB001591	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK4.1)	cDNA	Chono et al., 1999
AB001592	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK4.2)	cDNA	Chono et al., 1999
AB001593	Hypocotyl RNA	Encoding homologous to serine/threonine protein kinases (for CsPK5)	cDNA	Chono et al., 1999
U30382	Hypocotyl cDNA library	Encoding expansins	cDNA	Shcherban et al., 1995
U30460	Hypocotyl cDNA library	Encoding expansins	cDNA	Shcherban et al., 1995
Genes induced or repressed by plant hormones				
D49413	Hypocotyl cDNA library	Corresponding to a gibberellin-responsive gene encoding an extremely hydrophobic protein	cDNA	Chono et al., 1996

AB026821	Seedling RNA	Encoding IAA induced nuclear proteins	cDNA	Fujii et al., 2000
AB026822	Seedling RNA	Encoding IAA induced nuclear proteins	cDNA	Fujii et al., 2000
AB026823	Seedling RNA	Encoding IAA induced nuclear proteins	cDNA	Fujii et al., 2000
M32742	Cotyledon cDNA library	Encoding ethylene-induced putative peroxidases	cDNA	Morgens et al., 1990
D29684	Cotyledon cDNA library	Cytokinin-repressed gene	cDNA	Teramoto et al., 1994
D79217	Genomic library	Cytokinin-repressed gene	Genomic DNA fragment	Teramoto et al., 1996
D63451	Cotyledon cDNA library	Homologous to Arabidopsis cDNA clone 3003	cDNA	Toyama et al., 1995
D63384	Cotyledon cDNA library	Encoding catalase	cDNA	Toyama et al., 1995
D63385	Cotyledon cDNA library	Encoding catalase	cDNA	Toyama et al., 1995
D63386	Cotyledon cDNA library	Encoding catalase	cDNA	Toyama et al., 1995
D63387	Cotyledon cDNA library	Encoding lectin	cDNA	Toyama et al., 1995
D63388	Cotyledon cDNA library	Encoding 3-hydroxy-3-methylglutaryl CoA reductase	cDNA	Toyama et al., 1995
D63389	Cotyledon cDNA library	Encoding 3-hydroxy-3-methylglutaryl CoA reductase	cDNA	Toyama et al., 1995
D63388	Cotyledon cDNA library	Encoding a basic region/helix-loop-helix protein	cDNA	Toyama et al., 1999
Resistance genes				
M84214	Genomic library	Encoding the acidic class III chitinase	cDNA	Lawton et al., 1994
M24365	Leave cDNA library	Encoding a chitinase	cDNA	Metraux et al., 1989
D26392	Seedling cDNA library	Encoding FAD-Enzyme monodehydroascorbate (MDA) reductase	cDNA	Sano and Asada, 1994
Somatic embryo gene.				
X97801	Embryogenic callus cDNA library	MADS-box gene	cDNA	Filipecki et al., 1997
Repeated DNA sequences				
X03768	Genomic DNA	Satellite type I	Genomic DNA fragment	Ganal et al., 1986
X03769	Genomic DNA	Satellite type II	Genomic DNA fragment	Ganal et al., 1986
X03770	Genomic DNA	Satellite type III	Genomic DNA fragment	Ganal et al., 1986
X69163	Genomic DNA	Satellite type IV	Genomic DNA fragment	Ganal et al., 1988a
X07991	rDNA	Ribosomal DNA intergenic spacer	Genomic DNA fragment	Ganal et al., 1988b
X51542	Cotyledons	Ribosomal DNA intergenic spacer	Genomic DNA fragment	Zentgraf et al., 1990

[z] Only the sequences published in both journals and the genebank database are listed.

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2006 Gene List for Melon

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Gene lists of melon have been published previously, the last one in 2002 (18, 19, 106, 109, 111, 112, 120). They included different types of genes: disease and pest resistance genes, isozymes, leaf, stem, flower, fruit and seed characters... The 2007 list includes a total number of 174 loci, QTLs for 15 disease resistance or fruit related traits, and one cytoplasmic mutant (*cyt*-*Yt*) (Table 1).

Genes have also been cloned in melon (mRNA or complete gene with eventually intron…). Only genes with complete sequences are listed in table 2. Most of them are related to fruit maturation. Many partial clones, for instance Resistance Gene Homologues, are also available in databases.

Genetic maps using different types of molecular markers have been published (4, 12, 25, 27, 93, 99, 132). Linkages between isozymes (124) and between phenotypic mutants (107) have also been reported. These maps have been constructed using different melon genotypes as parents and some markers cannot be transferred easily from one map to another or are not polymorphic between all the parents (Table 3). There is not yet a reference saturated map of melon. Moreover very few phenotypic traits have been mapped.
The name of some pathogens has changed: for instance the two causal agents of powdery mildew are now *Podosphaera xanthii* and *Golovinomyces cichoracearum*, instead of respectively *Sphaerotheca fuliginea* and *Erysiphe cichoracearum*.

Allelism tests have often not been performed, inflating the number of described genes. This is particularly clear for *Powdery mildew resistance* but also for many other traits. This could be because accessions previously described with this trait are not (or no more) available. It is strongly recommende to send seed samples along with reports of new genes to the melon gene curators. They should consult the lists and the rules of gene nomenclature for the *Cucurbitaceae* (18, 119) before proposing a gene name and symbol.

Table 1. Gene list of melon. In **bold characters** are the genes which are maintained by the curators or which are very common in collections (like *andromonoecious* or *white testa*). In light characters are genes which either have been apparently lost, are not yet maintained by curators, or have uncertain descriptions. In the second part of the table are QTL and in the third part one cytoplasmic factor.

Gene symbol		Character	LG[z]	References
Prefered	Synonym			
a	***M***	***andromonoecious*. Mostly staminate, fewer perfect flowers; on *A*_ plants, pistillate flowers have no stamens; epistatic to *g*.**	**4, II**	**113, 121, 131**
ab	-	*abrachiate*. Lacking lateral branches. Interacts with *a* and *g* (*e.g. ab ab a a G*_ plants produce only staminate flowers).		40
Ac	**-**	***Alternaria cucumerina* resistance (in MR-1).**		**127**
Aco-1	***Ac***	***Aconitase-1*. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224769.**	**A**	**124**

Acp-1	*APS-1*^{1}, *Ap-1*^{1}	*Acid phosphatase-1*. Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has two bands.		37
Acp-2	***Acp-1***	***Acid phosphatase-2*. Isozyme variant with two alleles, each regulating one band, in PI 194057, PI 224786. Relationship with *Acp-1* is unknown.**		**124**
Acp-4	**-**	***Acid phosphatase-4*. Isozyme variant with two alleles, each regulating one band, in PI 183256, PI 224786. Relationship with *Acp-1* unknown, different from *Acp-2*.**		**124**
Af	-	*Aulacophora foveicollis* resistance. Resistance to the red pumpkin beetle.		129
Ag	**-**	***Aphis gossypii* tolerance. Freedom of leaf curling following aphid infestation (in PI 414723).**		**11**
Ak-4	**-**	***Adenylate kinase*. Isozyme variant with two alleles, each regulating one band, in PI 169334.**		**124**
Ala	-	*Acute leaf apex*. Dominant over obtuse apex, linked with *Lobed* leaf. (*Ala* in Maine Rock, *ala* in PV Green).		45
alb	**-**	***albino*. White cotyledons, lethal mutant (in Trystorp).**		**5**
Al-1	Al_1	*Abscission layer-1*. One of two dominant genes for abscission layer formation. See *Al-2*. (*Al-1 Al-2* in C68, *al-1 al-2* in Pearl).		125
Al-2	A_{l2}	*Abscission layer-2*. One of two dominant genes for abscission layer formation. See *Al-1*.		125
Al-3		***Abscission layer-3*. One dominant gene for abscission layer formation (in PI 161375). Relationship with *Al-1* or *Al-2* is unknown**	**VIII**	**101**
Al-4		***Abscission layer-4*. One dominant gene for abscission layer formation (in PI 161375). Relationship with *Al-1* or *Al-2* is unknown**	**IX**	**101**
Al-5	**-**	***Abscission layer-5*. One dominant gene for abscission layer formation (Full-slip in TAM Uvalde)**		**137**
bd	-	*brittle dwarf*. Rosette growth with thick leaf. Male fertile, female sterile (in TAM-Perlita45).		21
Bi	**-**	***Bitter*. Bitter seedling (common in honeydew or in Charentais type while most American cantaloupes are *bi*).**		**73**
Bif-1	*Bif*	*Bitter fruit-1*. Bitterness of tender fruit in wild melon. Relations with *Bi* are unknown.		95
Bif-2	-	*Bitter fruit-2*. One of two complementary independent genes for bitter taste in young fruit: *Bif-2_ Bif-3_* are bitter. (Relationships with *Bi* and *Bif-1* are unknown).		77
Bif-3	-	*Bitter fruit-3*. One of two complementary independent genes for bitter taste in young fruit: *Bif-2_ Bif-3_* are bitter. (Relationships with *Bi* and *Bif-1* are unknown).		77
cab-1	**-**	***cucurbit aphid borne* yellows virus resistance-*1*. One of two complementary independent genes for resistance to this polerovirus: *cab-1 cab-1 cab-2 cab-2* plants are resistant. (in PI 124112).**		**29**

cab-2	**-**	***cucurbit aphid borne* yellows virus resistance-*2*. One of two complementary independent genes for resistance to this polerovirus: *cab-1 cab-1 cab-2 cab-2* plants are resistant. (in PI 124112).**		**29**
cb	*cb*$_1$	*cucumber beetle* resistance. Interacts with *Bi*, the nonbitter *bi bi cb cb* being the more resistant (in C922-174-B).		90
cf	**-**	***cochleare folium*. Spoon-shaped leaf with upward curling of the leaf margins (spontaneous mutant in Galia)**		**72**
cl	-	*curled leaf*. Elongated leaves that curl upward and inward. Usually male and female sterile.		21
Cys	-	*Cucurbit yellow stunting* disorder virus resistance. One dominant gene for resistance to this crinivirus in TGR-1551.		74
dc-1	-	*Dacus cucurbitae-1* resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See *dc-2*.		122
dc-2	-	*Dacus cucurbitae-2* resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See *dc-1*.		122
dl	**-**	***dissected leaf* (in URSS 4). Highly indented leaves.**	**10**	**32**
***dl*^{v}**	***cl***	***dissected leaf Velich*. First described as *cut leaf* in Cantaloup de Bellegarde. Allelic to *dl*.**	**10**	**130**
dl-2	-	*dissected leaf-2*. First described as « hojas hendidas ».		36
dlet	*dl*	*delayed lethal*. Reduced growth, necrotic lesions on leaves and premature death.		141
Ec	**-**	***Empty cavity*. Carpels are separated at fruit maturity leaving a cavity. *Ec* in PI 414723, *ec* in Védrantais.**	**III**	**98**
ech	**-**	***exaggerated curvature of the hook*. Triple response of seedlings germinating in darkness in presence of ethylene. *ech* in PI 161375, *Ech* in Védrantais.**	**I**	**101**
f	**-**	***flava*. Chlorophyl deficient mutant. Growth rate reduced (in K 2005).**	**8**	**105**
fas	**-**	***fasciated* stem (in Vilmorin 104).**		**42**
Fdp-1	**-**	***Fructose diphosphate-1*. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224688.**		**124**
Fdp-2	**-**	***Fructose diphosphate-2*. Isozyme variant with two alleles, each regulating one band, in PI 204691, PI 183256.**		**124**
fe	**-**	***fe* (iron) inefficient mutant. Chlorotic leaves with green veins. Turns green when adding iron in the nutrient solution.**		**91**
Fn	**-**	***Flaccida necrosis*. Semi-dominant gene for wilting and necrosis with F pathotype of *Zucchini yellow mosaic virus* (*Fn* in Doublon, *fn* in Védrantais).**	**2, V**	**118**
Fom-1	***Fom*$_1$**	***Fusarium oxysporum melonis* resistance. Resistance to races 0 and 2 and susceptibility to races 1 and 1,2 of Fusarium wilt (*Fom-1* in Doublon, *fom-1* in Charentais T).**	**5, IX**	**117**

Fom-2	***Fom*$_{1.2}$**	***Fusarium oxysporum melonis* resistance. Resistance to races 0 and 1 and susceptibility to races 2 and 1,2 of Fusarium wilt. (*Fom-2* in CM 17187, *fom-2* in Charentais T).**	**6, XI**	**117**
Fom-3	**-**	***Fusarium oxysporum melonis* resistance. Same phenotype as *Fom-1* but segregates independently from *Fom-1*. (*Fom-3* in Perlita FR, *fom-3* in Charentais T).**		**139**
g	**-**	***gynoecious*. Controls the presence of one (*g*) or two (*G*) types of flowers on one plant. Epistatic to *a* : *A_ G_* monoecious; *A_ g g* gynoecious; *a a G_* andromonoecious; *a a g g* hermaphrodite.**		**113**
gf	**-**	***green flesh* color. Recessive to salmon. (*gf* in honeydew, *Gf* in Smiths' Perfect cantaloupe).**	**IX**	**54**
gl	**-**	***glabrous*. Trichomes lacking (in Arizona glA).**	**3**	**39**
gp	-	*green petals*. Corolla leaf like in color and venation.		85
Gpi	**-**	***Glucosephosphate isomerase*. Isozyme variant with two alleles, each regulating one band, in PI 179680.**		**124**
Gs	-	*Gelatinous sheath* around the seeds. Dominant to absence of gelatinous sheath.		46
Gsb-1	***Mc***	***Gummy stem blight* resistance-1. High degree of resistance to *Didymella bryoniae = Mycosphaerella citrullina* (in PI 140471).**		**41, 114**
Gsb-2	*Mc-3*	*Gummy stem blight* resistance-2. High level of resistance to *Didymella bryoniae = Mycosphaerella citrullina* in PI 157082, independent from *Gsb-1*, *Gsb-3*, *Gsb-4* and *gsb-5*.		41, 142
Gsb-3	***Mc-4-***	***Gummy stem blight* resistance-3. High level of resistance to *Didymella bryoniae = Mycosphaerella citrullina* in PI 511890, independent from *Gsb-1*, *Gsb-2*, *Gsb-4* and *gsb-5*.**		**41, 142**
Gsb-4	**-**	***Gummy stem blight* resistance-4. High level of resistance to *Didymella bryoniae = Mycosphaerella citrullina* in PI 482398, independent from *Gsb-1*, *Gsb-2*, *Gsb-3* and *gsb-5*.**		**41**
gsb-5	**-**	***gummy stem blight* resistance-5. High level of resistance to *Didymella bryoniae = Mycosphaerella citrullina* in PI 482399, independent from *Gsb-1*, *Gsb-2*, *Gsb-3* and *Gsb-4*.**		**41**
gyc	**-**	***greenish yellow corolla*.**		**140**
gy	***n, M***	***gynomonoecious*. Interacts with *a* and *g* to produce stable gynoecious plants (*A_ g g gy gy*) (in WI 998).**		**63, 65**
h	**-**	***halo* cotyledons. Yellow halo on the cotyledons, later turning green.**	**4, II**	**89**
Idh	**-**	***Isocitrate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 224688.**	**A**	**124**
Imy	-	*Interveinal mottling and yellowing* resistance. Resistance to a complex of viruses in PI 378062.		52
jf	-	*juicy flesh*. Segregates discretely in a monogenic ratio in segregating generations.		14

L	-	*Lobed* leaf. Dominant on non lobed, linked with *Acute leaf apex*. (*L* in Maine Rock, *l* in P.V. Green).		45
lmi	**-**	***long mainstem internode*. Affects internode length of the main stem but not of the lateral ones (in 48764).**	**8**	**80**
Liy	**-**	***Lettuce infectious yellows* virus resistance. One dominant gene for resistance to this crinivirus in PI 313970.**		**82**
Lt	**-**	***Liriomyza trifolii* (leafminer) resistance (in Nantais Oblong).**		**30**
M-Pc-5	-	*Modifier of Pc-5*. Gene *Pc-5* for downy mildew resistance (see *Pc-5*) is dominant in presence of *M-Pc-5*, recessive in the absence of *M-Pc-5*.		2
Mc-2	*Mc*^{i}	*Mycosphaerella citrullina* resistance-2. Moderate degree of resistance to gummy stem blight (in C-1 and C-8)		114
Mca	-	*Macrocalyx*. Large, leaf like structure of the sepals in staminate and hermaphrodite flowers (*Mca* in makuwa, *mca* in Annamalai).		44
Mdh-2	**-**	***Malate dehydrogenase-2*. Isozyme variant with two alleles, each regulating one band, in PI 224688, PI 224769.**	**B**	**124**
Mdh-4	**-**	***Malate dehydrogenase-4*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923.**	**B**	**124**
Mdh-5	**-**	***Malate dehydrogenase-5*. Isozyme variant with two alleles, each regulating one band, in PI 179923, PI 180283.**	**B**	**124**
Mdh-6	**-**	***Malate dehydrogenase-6*. Isozyme variant with two alleles, each regulating one band, in PI 179923, PI 180283.**	**B**	**124**
Me	-	*Mealy* flesh texture. Dominant to crisp flesh. (*Me* in *C. callosus*, *me* in makuwa).		46
Me-2	**-**	***Mealy* flesh texture-2 (in PI 414723).**		**98**
Mnr-1	***Mnr1***	***Melon necrotic resistance 1*. One of two dominant genes for resistance to *Melon necrotic spot virus* (MNSV) located at 19 cM from *nsv*. *Mnr-1* in Doublon, *mnr-1* in ANC-42.**	**XII**	**78**
Mnr-2	***Mnr2***	***Melon necrotic resistance 2*. One of two dominant genes for resistance to *Melon necrotic spot virus* (MNSV) independent from *Mnr-1*. *Mnr-2* in Doublon, *mnr-2* in ANC-42.**		**78**
Mpi-1	**-**	***Mannosephosphate isomerase-1*. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.**	**A**	**124**
Mpi-2	**-**	***Mannosephosphate isomerase-2*. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.**	**A**	**124**
ms-1	***ms*^{1}**	***male sterile-1*. Indehiscent anthers with empty pollen walls in tetrad stage.**	**3**	**6**
ms-2	***ms*^{2}**	***male sterile-2*. Anthers indehiscent, containing mostly empty pollen walls, growth rate reduced.**	**6, XI**	**9**
ms-3	***ms-L***	***male sterile-3*. Waxy and translucent indehiscent anthers, containing two types of empty pollen sacs.**	**12**	**81**
ms-4	**-**	***male sterile-4*. Small indehiscent anthers. First male flowers abort at**	**9**	**75**

		bud stage (in Bulgaria 7).		
ms-5	**-**	***male sterile-5*. Small indehiscent anthers. Empty pollen (in Jivaro, Fox).**	**13**	**71**
Mt	-	*Mottled* rind pattern. Dominant to uniform color. Epistatic with *Y* (not expressed in *Y_*) and *st* (*Mt_ st st* and *Mt_ St_* mottled; *mt mt st st* striped, *mt mt St_* uniform). (*Mt* in Annamalai, *mt* in makuwa).		46
Mt-2	**-**	***Mottled* rind pattern (in PI 161375). Relationship with *Mt* unknown.**	**II**	**98**
Mu	-	*Musky* flavour (olfactory). Dominant on mild flavour (*Mu* in *C. melo callosus*, *mu* in makuwa or Annamalai).		46
Mvd	-	*Melon vine decline* resistance. Semi-dominant gene for partial resistance to *Acremonium cucurbitacearum* and *Monosporascus cannonballus* (in Pat 81 *agrestis* melon)		55
My	-	*Melon yellows* virus resistance. Semi-dominant gene, in Nagata Kin Makuwa, for partial resistance to this crinivirus.		38, 88
n	**-**	***nectarless*. Nectaries lacking in all flowers (in 40099).**		**7**
Nm	**-**	***Necrosis* with *Morocco* strains of *Watermelon mosaic virus*, a potyvirus (*Nm* in Védrantais, *nm* in Ouzbèque).**		**115**
nsv	**-**	**Melon *necrotic spot virus* resistance. One recessive gene for resistance tothis carmovirus in Gulfstream, Planters Jumbo.**	**7, XII**	**20**
O	**-**	***Oval* fruit shape. Dominant to round; associated with *a*.**		**131**
Org-1	-	*Organogenic* response for *in vitro* shoot regeneration. Partially dominant. Interacts with an additive model with *Org-2*.		86
Org-2	-	*Organogenic* response for *in vitro* shoot regeneration. Partially dominant. Interacts with an additive model with *Org-1*.		86
Org-3	-	*Organogenic* response for *in vitro* regeneration. Dominant allele for high response in BU-12/3, recessive allele in PMR 45 or Ananas Yokneam. Probably different from *Org-1* and *Org-2*.		43
p	**-**	***pentamerous*. Five carpels and stamens; recessive to trimerous (in Casaba).**	**XII**	**121**
Pa	**-**	***Pale* green foliage. *Pa Pa* plants are white (lethal); *Pa pa* are yellow (in 30567).**	**3**	**79**
Pc-1	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See *Pc-2*.**		**17, 126**
Pc-2	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See *Pc-1*.**		**17, 126**
Pc-3	**-**	***Pseudoperonospora cubensis* resistance. Partial resistance to downy mildew (in PI 414723).**		**35**
Pc-4	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary genes for downy mildew resistance in PI 124112. Interacts with *Pc-1* or *Pc-2*.**		**66**

Pc-5	-	*Pseudoperonospora cubensis* resistance. One gene in Line 5-4-2-1 which interacts with *M-Pc-5* in the susceptible line K15-6 (*Pc-5* is dominant in presence of *M-Pc-5*, recessive in the absence of *M-Pc-5*).		2
Pep-gl	**-**	***Peptidase with glycyl-leucine*. Isozyme variant with two alleles, each regulating one band, in PI 218070.**	**B**	**124**
Pep-la	**-**	***Peptidase with leucyl-alanine*. Isozyme variant with two alleles, each regulating one band, in PI 183256.**		**124**
Pep-pap	**-**	***Peptidase with phenylalanyl-proline*. Isozyme variant with two alleles, each regulating one band, in PI 183256.**		**124**
Pgd-1	*6-PGDH-2*[1] *Pgd-2*[1]	*Phosphoglucodehydrogenase-1*. Isozyme variant with two alleles, each regulating one band.The heterozygote has one intermediate band.		37
6-Pgd-2	**-**	***6-Phosphogluconate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 161375, Védrantais. Relationship with *Pgd-1* is unknown.**	**IX**	**4**
Pgd-3	**Pgd**	***6-Phosphogluconate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 218070. Relationship with *Pgd-1* and *6-Pgd-2* is unknown.**	**A**	**124**
Pgi-1	*PGI-1*[1]	*Phosphoglucoisomerase-1*. Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		37
Pgi-2	*PGI-2*[1]	*Phosphoglucoisomerase-2*. Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		37
Pgm-1	*PGM-2*[1] *Pgm-2*[1]	*Phosphoglucomutase-1*. Isozyme variant with two alleles, each regulating two bands. The heterozygotes has three bands.		37
Pgm-2	***Pgm***	***Phosphoglucomutase*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923. Relationship with *Pgm-1* is unknown.**	**A**	**124**
pH	**-**	***pH* (acidity) of the mature fruit flesh. Low pH value in PI 414723 dominant to high pH value in Dulce**	**VIII**	**27**
pin	**-**	***pine-seed* shape (in PI 161375).**	**III**	**99**
Pm-1	***Pm*[1] *Pm-A ?***	***Powdery mildew* resistance-1. Resistance to race 1 of *Podosphaera xanthii* (in PMR 45).**		**58**
Pm-2	***Pm*[2] *Pm-C ?***	***Powdery mildew* resistance-2. Interacts with *Pm-1*. Resistance to race 2 of *Podosphaera xanthii* (in PMR 5 with *Pm-1*).**		**8**
Pm-3	***Pm*[3]**	***Powdery mildew* resistance-3. Resistance to race 1 of *Podosphaera xanthii* (in PI 124111).**	**7**	**50, 51**
Pm-4	***Pm*[4]**	***Powdery mildew* resistance-4. Resistance to *Podosphaera xanthii* (in PI 124112).**		**50, 51**
Pm-5	***Pm*[5]**	***Powdery mildew* resistance-5. Resistance to *Podosphaera xanthii* (in PI 124112).**		**50, 51**
Pm-6	**-**	***Powdery mildew* resistance-6. Resistance to *Podosphaera xanthii* race 2 (in PI 124111).**		**64**

Pm-7	**-**	***Powdery mildew* resistance-7. Resistance to *Podosphaera xanthii* race 1 (in PI 414723).**		**1**
Pm-E	**-**	***Powdery mildew* resistance-E. Interacts with *Pm-C* in PMR5 for *Golovinomyces cichoracearum* resistance.**		**34**
Pm-F	**-**	***Powdery mildew* resistance-F. Interacts with *Pm-G* in PI 124112 for *Golovinomyces cichoracearum* resistance.**		**34**
Pm-G	**-**	***Powdery mildew* resistance-G. Interacts with *Pm-F* in PI 124112 for *Golovinomyces cichoracearum* resistance.**		**34**
Pm-H	**-**	***Powdery mildew* resistance-H. Resistance to *Golovinomyces cichoracearum* and susceptibility to *Podosphaera xanthii* (in Nantais oblong).**		**34**
Pm-w	***Pm-B ?***	***Powdery mildew* resistance in WMR 29. Resistance to *Podosphaera xanthii race 2***	**2, V**	**107**
Pm-x	**-**	***Powdery mildew* resistance in PI 414723. Resistance to *Podosphaera xanthii.***	**4, II**	**107**
Pm-y	**-**	***Powdery mildew* resistance in VA 435. Resistance to *Podosphaera xanthii.***	**7, XII**	**107**
Pm-z		***Powdery mildew* resistance in PI 313970. Resistance to *Podosphaera xanthii* races 1 and 2US.**		**83**
PmV.1	**-**	***Powdery mildew* resistance in PI 124112. Resistance to *Podosphaera xanthii* races 1, 2 and 3.**	**V**	**97**
PmXII.1		***Powdery mildew* resistance in PI 124112. Resistance to *Podosphaera xanthii* races 1, 2 and 5 and to *Golovinomyces cichoracearum* race 1**	**XII**	**97**
***Prv*^{1}**	***Wmv***	***Papaya Ringspot virus* resistance. Resistance to W strain of this potyvirus (formerly *Watermelon mosaic virus 1*) (in B 66-5, WMR 29, derived from PI 180280). Dominant to *Prv*^{2}.**	**5, IX**	**103, 133**
***Prv*^{2}**	**-**	***Papaya Ringspot virus* resistance. Allele at the same locus as *Prv*^{1} but different reaction with some strains of the virus (in 72-025 derived from PI 180283). Recessive to *Prv*^{1}.**	**5, IX**	**60, 103**
`Prv-2`	**-**	***Papaya Ringspot virus* resistance-2 (in PI 124112). Relationship with *Prv* is unknown.**		**84**
Px-1	*PRX-1*^{1}	*Peroxidase-1*. Isozyme variant with two codominant alleles, each regulating a cluster of four adjacent bands. The heterozygote has five bands.		37
Px-2	*Px*$_{2A}$ *Prx2*	*Peroxidase-2*. Isozyme variant with two codominant alleles, each regulating a cluster of three adjacent bands. The heterozygote has 4 bands.		15, 23
r	**-**	***red* stem. Red pigment under epidermis of stems, especially at nodes; tan seed color (in PI 157083).**	**3**	**10, 79**
ri	-	*ridge*. Ridged fruit surface, recessive to ridgeless. (*ri* in C68, *Ri* in Pearl).		125
s	-	*sutures*. Presence of vein tracts on the fruit (« sutures »); recessive to ribless.		3
s-2	**-**	***sutures-2* on the fruit rind (in PI 161375). Relationship with *s* is**	**XI**	**98**

		unknown.		
Sfl	*S*	*Subtended floral leaf*. The floral leaf bearing the hermaphrodite flowers is sessile, small and encloses the flower. (*Sfl* in makuwa, *sfl* in Annamalai).		44
si-1	***b***	***short internode-1*****. Extremely compact plant habit (bush type) (in UC Topmark bush).**	**1**	**28**
si-2	**-**	***short internode-2*****. Short internodes from 'birdnest' melon (in Persia 202).**		**94**
si-3	**-**	***short internode-3.*** **Short internodes in Maindwarf.**		**68**
Skdh-1	-	*Shikimate dehydrogenase-1*. Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has three bands.		15, 47
slb	*sb*	*short lateral branching*. Reduction of the elongation of the lateral branches, in LB		92
So	-	*Sour* taste. Dominant to sweet.		69
So-2	**-**	***Sour*** **taste-2 (in PI 414723). Relationship with *So* is unknown.**		**98**
sp	-	*spherical* fruit shape. Recessive to obtuse; dominance incomplete.		3, 76
spk	**-**	***speckled*** **fruit epidermis (*spk* in PI 161375 or PI 414723, *Spk* in Védrantais).**	**VII**	**99**
st	-	*striped* epicarp. Recessive to non-striped.		49
st-2	***st***	***striped epicarp-2*****. Present in Dulce, recessive to non-striped in PI 414723. Relationship with *st* is unknown.**	**XI**	**27**
suc		***sucrose*** **accumulation. Low sucrose level in Faqqous (*suc*), high sucrose in Noy Yizre'el (*Suc*). Incomplete recessivity.**		**13**
v	**-**	***virescent.*** **Pale cream cotyledons and hypocotyls; yellow green foliage (mainly young leaves).**	**11**	**53**
v-2	**-**	***virescent-2.***		**33**
v-3	**-**	***virescent-3.*** **White cotyledons which turn green, light green young leaves which are normal when they are older.**		**110**
Vat	**-**	***Virus aphid transmission*** **resistance. Resistance to the transmission of several viruses by *Aphis gossypii* (in PI 161375).**	**2, V**	**102**
w	**-**	***white*** **color of mature fruit. Recessive to dark green fruit skin. (*w* in honeydew, *W* in Smiths' Perfect cantaloupe).**		**54**
wf	**-**	***white flesh*****. Recessive to salmon. *Wf* epistatic to *Gf_*.**		**16, 56**
Wi	-	White color of *immature* fruit. Dominant to green.		69
Wmr	**-**	***Watermelon mosaic virus*** **(formerly *Watermelon mosaic virus 2*) resistance (in PI 414723).**	**II**	**48**
Wt	**-**	***White testa*****. Dominant to yellow or tan seed coat color.**		**49**
Wt-2	**-**	***White testa-2*** **(in PI 414723). Relationship with *Wt* unknown.**	**IV**	**98**

Y	**-**	***Yellow* epicarp. Dominant to white fruit skin.**		**49**
yg	**-**	***yellow green* leaves. Reduced chlorophyll content.**	**6, XI**	**134**
***yg*^{w}**	***lg***	***yellow green Weslaco*. First described as *light green* in a cross Dulce x TAM-Uvalde. Allelic to *yg*.**		**22**
yv	**-**	***yellow virescence*. Pale cotyledons; yellow green young leaves and tendrils; bright and yellow petals and yellow stigma; etiolated; older leaves becoming green.**	**1**	**138**
yv-2	***yv-X***	***yellow virescence-2*. Young leaves yellow green, old leaves normal green**	**5, IX**	**108**
Zym	***Zym-1***	***Zucchini Yellow Mosaic* virus resistance. Resistance to pathotype 0 of this potyvirus (in PI 414723).**	**4, II**	**104**
Zym-2	**-**	***Zucchini Yellow Mosaic* potyvirus resistance. One of three complementary genes (see *Zym* and *Zym-3*) for resistance to this potyvirus (in PI 414723)**		**24**
Zym-3	**-**	***Zucchini Yellow Mosaic* potyvirus resistance. One of three complementary genes (see *Zym* and *Zym-2*) for resistance to this potyvirus (in PI 414723)**		**24**
cmv	-	*cucumber mosaic virus* resistance. Three recessive genes have been described in the cross Freemans's cucumber x Noy Amid. Seven QTLs are involved in resistance to three different strains of this cucumovirus in the cross Védrantais x PI 161375.		31, 61
ea	-	*earliness*. Nine QTLs described in the cross Piel de Sapo x PI 161375.		87
ecol	-	*external color of the fruit*. Four QTLS described in the cross Piel de Sapo x PI 161375.		87
eth		*ethylene* production in fruit (climacteric crisis). Four QTLs described in the cross Védrantais x PI 161375.		101
fl	-	*fruit length*. Four QTLs described in the cross Védrantais x PI 161375 and 4 QTLs in the cross Védrantais x PI 414723, one is common to both crosses.		100
fom	-	*Fusarium oxysporum* f.sp. *melonis* race 1.2 resistance. Nine QTLs described in the cross Védrantais x Isabelle.		96
fs	-	*fruit shape* (ratio fruit length/fruit width). Six QTLs described in the cross Védrantais x PI 161375 and 2 QTLs in the cross Védrantais x PI 414723, which are common to both crosses. Eight QTLs described in the cross Piel de Sapo x PI 161375.		100 87
fw	-	*fruit width*. Five QTLs described in the cross Védrantais x PI 161375 and 1 QTLs in the cross Védrantais x PI 414723.		100
fw	-	*fruit weight*. Six QTLs described in the cross Piel de Sapo x PI 161375.		87
ofc	-	*orange flesh color*. Three QTLs described in the cross Piel de Sapo x PI 161375.		87
ovl	-	*ovary length*. Six QTLs described in the cross Védrantais x PI 161375.		100

ovs	-	*ovary shape* (ratio ovary length/ovary width). Six QTLs described in the cross Védrantais x PI 161375.	100
ovw	-	*ovary width*. Eight QTLs described in the cross Védrantais x PI 161375.	100
pc	-	*Pseudoperonospora cubensis* resistance. Nine QTLs for resistance to downy mildew described in the cross Védrantais x PI 124112.	97
ssc	-	*soluble solid content*. Five QTLs described in the cross Piel de Sapo x PI 161375.	87
cyt-Yt	-	*cytoplasmic yellow tip*. Chlorophyll deficient mutant with yellow young leaves, turning green when becoming older. Maternally inherited.	116

z Linkage group to which this gene belongs: Letters correspond to 124, arabic numbers to 107 and roman numbers to 99. See Table 3.

Table 2. List of cloned genes in melon and their function. Sequences can be submitted directly to databases or can be published in journals (Reference). A few genes have been mapped (Linkage Groups)

Gene symbol	**Gene accession**	**(Putative) Function**	**Author**	**LG** [z]	**Ref.** [y]
Cm-AAT	AB075227	Alcohol acetyltransferase GeAAT	Ishimaru M.		
Cm-AAT2	AF468022	Putative alcohol acyltransferase (AT2)	El Yahyaoui F. *et al*		
Cm-AAT3	AY859053	putative alcohol acyl-transferases	El-Sharkawy *et al*		
Cm-AAT4	AY859054	putative alcohol acyl-transferases	El-Sharkawy *et al*		
Cm-Aco	X82840	Acotinase	Peyret *et al*		
Cm-ACO1	X95551	1-aminocyclopropane-1-carboxylate (ACC) oxidase 1	Lasserre E. *et al*		70
Cm-ACO2	X95552	1-aminocyclopropane-1-carboxylate (ACC) oxidase 2	Lasserre E. *et al*	VIII	70
Cm-ACO3	X95553	1-aminocyclopropane-1-carboxylate (ACC) oxidase 3	Lasserre E. *et al*		70
Cm-ACS1	AB025906	1-aminocyclopropane-1-carboxylate (ACC) synthase 1	Yamamoto M. *et al*	XI	136
Cm-ACS1	AB032935	1-aminocyclopropane-1-carboxylate (ACC) synthase	Shiomi S. *et al*	XI	
Cm-ACS2	AB032936	1-aminocyclopropane-1-carboxylate (ACC) synthase 2	Shiomi S. *et al*		
Cm-ACS2	D86242	1-aminocyclopropane-1-carboxylate (ACC) synthase 2	Ishiki Y. *et al*		57
Cm-ADH1	DQ288986	putative alcohol dehydrogenases (ADH1)	Manriquez *et al*		
Cm-ADH2	DQ288987	putative alcohol dehydrogenases (ADH2)	Manriquez *et al*		
Cm-AGPP-mlf2	AF030383 AF030384	ADP-glucose pyrophosphorylase large subunit (mlf2)	Park S.-W. *et al*		
Cm-AGPP-msf1	AF030382	ADP-glucose pyrophosphorylase small subunit (msf1)	Park S.-W. *et al*		
Cm-AO1	AF233593	Ascorbate oxidase AO1	Sanmartin M. *et al*		
Cm-AO3	Y10226	Ascorbate oxidase AO3	Pateraki *et al*		

Cm-AO4	AF233594	Ascorbate oxidase AO4	Sanmartin M. *et al*		
Cm-AOS	AF081954	Allene oxide synthase (AOS)	Tijet N. *et al*		
Cm-ASR1	AF426403 AF426404	Abscisic acid response protein (Asr1)	Hong S.-H. *et al*		
Cm-At1	AY066012	Aminotransferase 1	Taler D. *et al*		
Cm-At1	AY354206	Aminotransferase 1 (Ananas Yokneam)	Taler *et al*		
Cm-At1	AY354208	Aminotransferase 1 (Hemed)	Taler *et al*		
Cm-At2	AF461048	Aminotransferase 2	Taler D. *et al*		
Cm-At2	AY354207	Aminotransferase 2 (Ananas Yokneam)	Taler *et al*		
Cm-At2	AY354209	Aminotransferase 2 (Hemed)	Taler *et al*		
Cm-CCM	D32206	Cucumisin (serine protease)	Yamagata H. *et al*		135
Cm-CHI1	AF241266	Chitinase 1	Zou X. *et al*		
Cm-CHI2	AF241267 AF241538	Chitinase 2	Zou X. *et al*		
Cm-DREB1	AB125974	DREB-like protein	Mizuno *et al*		
Cm-E8	AB071820	Regulator of ethylene synthesis, similar to *Le-E8*	Fujimori A. *et al*		
Cm-EFE	X69935	ethylene-forming enzyme	Balagué *et al*		
Cm-EGase1	AB271851	Endoglucanase	Kubo *et al*		
Cm-eIF4E (nsv)	DQ393830	Eukaryotic translation initiation factor 4E from PI 161375	Nieto *et al*	XII	
Cm-eIF4E (Nsv)	DQ393831	Eukaryotic translation initiation factor 4E from cv Védrantais	Nieto *et al*	XII	
Cm-eIF4E (Nsv)	DQ393832	Eukaryotic translation initiation factor 4E from cv WMR 29	Nieto *et al*	XII	
Cm-EIL1	AB063191	Transcription factor Ethylene Insensitive 1 for At-EIN3-like protein	Sato T. *et al*		
Cm-EIL2	AB063192	Transcription factor Ethylene Insensitive 2 for At-EIN3-like protein	Sato T. *et al*		
Cm-ERF1	AB125975	ERF-like protein	Mizuno *et al*		
Cm-ERF2	AB125976	ERF-like protein	Mizuno *et al*		
Cm-ERS1	AB049128	Ethylene receptor ERS1	Furukawa H.		
Cm-ERS1	AF037368	Putative ethylene receptor ERS1	Sato Nara K. *et al*	I	123
Cm-ETR1	AB052228	Ethylene receptor (ETR1)	Furukawa H.		
Cm-ETR1	AF054806	Putative ethylene receptor (ETR1)	Sato Nara K. *et al*		123
Cm-EXP1	DQ914793	Ripening-related expansin (EXP1)	Rose and Bennett		
Cm-Fom2	DQ287965	*Fusarium oxysporum melonis*-2 resistance gene	Joobeur *et al*		
Cm-GAS1	AY077642	Galactinol synthase (GAS1)	Volk G.M. *et al*		
Cm-GAS2	AY077641	Galactinol synthase (GAS2)	Volk G.M. *et al*		
Cm-GLD	AF252339	L-galactono-1,4-lactone dehydrogenase	Pateraki I. and Kanellis A.K.		
Cm-GPU1	DQ445484	Galactose-1-phosphate uridyltransferase	Dai *et al*		
Cm-GS	AY773090	glutamine synthetase	Zhang *et al*		
Cm-HMG-CoA	AB021862	3-hydroxy-3-methylglutaryl	Kato-Emori S. *et al*		62

		coenzyme A reductase		
Cm-HPL	AF081955	Fatty acid 9-hydroperoxide lyase (HPL)	Tijet N. *et al*	128
Cm-ITS1	AF006802	Internal Transcribed Spacer 1	Jobst J. *et al*	59
Cm-ITS2	AF013333	Internal Transcribed Spacer 2	Jobst J. *et al*	59
Cm-Lec17	AF520577	17 kDa phloem lectin (Lec17)	Dinant S. *et al*	
Cm-Lec17-1	AF517156	17 kDa phloem lectin Lec17-1	Dinant S. *et al*	
Cm-Lec17-3	AF517157	17 kDa phloem lectin Lec17-3 mRNA	Dinant S. *et al*	
Cm-Lec26	AF517154	26 kDa phloem lectin (Lec26)	Dinant S. *et al*	
Cm-LOX1	DQ267934	13S-lipoxygenase (LOX1)	Whitaker *et al*	
Cm-m2	AJ565931	profilin (cuc m 2 gene).	Lopez-Torrejon *et al*	
Cm-m2	AY271295	profilin (m2) reticulatus	Sankian *et al*	
Cm-m2	AY292385	profilin (m2) reticulatus	Sankian *et al*	
Cm-m2	AY292386	profilin (m2) mashadi	Sankian *et al*	
Cm-m2	AY292387	profilin (m2) mashadi	Sankian *et al*	
Cm-m2	AY879597	profilin (m2)	Sankian *et al*	
Cm-mirk	DQ116940	inward rectifying potassium channel (mirk)	Zhang *et al*	
Cm-MPP	AF297643	Mitochondrial processing peptidase beta subunit	He C. *et al*	
Cm-PAL	X76130	phenylalanine ammonia-lyase	Diallinas and Kanellis	
Cm-Per	AY373372	Netting associated peroxidase	Keren-Keiserman *et al*	67
Cm-PG1	AF062465	Polygalacturonase precursor (MPG1)	Hadfield K.A. *et al*	
Cm-PG2	AF062466	Polygalacturonase precursor (MPG2)	Hadfield K.A. *et al*	
Cm-PG3	AF062467	Polygalacturonase precursor (MPG3)	Hadfield K.A. *et al*	
Cm-PLDa1	DQ267933	phospholipase D-alpha (PLDa1)	Whitaker *et al*	
Cm-Pro	E08267	Protease	Yamagata and Iwasaki Patent: JP 1994284890-A 1 11-OCT-1994	
Cm-ProETR1	E51774	Promoter of melon ethylene receptor	Ezura H. *et al* Patent JP 2001037484-A 14 13-FEB-2001	
Cm-PSY1	Z37543	Phytoene synthase	Karvouni *et al*	
Cm-SPS	DQ364058	sucrose phosphate synthase	Hou *et al*	
Cm-SPS	DQ521271	sucrose phosphate synthase	Yu *et al*	
Cm-TCTP	AF230211	Translationally controlled tumor protein-related protein	Gomez-Lim M.A. *et al*	
Cm-UGGP	DQ399739	UDP-galactose/glucose pyrophosphorylase	Dai *et al*	
Cm-UGP	DQ445483	UDP-glucose pyrophosphorylase	Dai *et al*	
Cm-Vat	CQ859491 CQ859490 CQ859488 CQ859487	*Aphis gossypii* resistance	Dogimont *et al* Patent WO 2004072109-A 5 26-AUG-2004	
Cm-XTH1	DQ914794	Xyloglucan endotransglucosylase/ hydrolase 1 (XTH1)	Rose and Bennett	

Cm-XTH2	DQ914795	Xyloglucan endotransglucosylase/ hydrolase 2 (XTH2)	Rose and Bennett
Cm-XTH3	DQ914796	Xyloglucan endotransglucosylase/ hydrolase 3 (XTH3)	Rose and Bennett

[z] Linkage group to which this gene belongs according to 99.
[y] Bibliographical references

Table 3. Genes and QTLs localization and correspondance between linkage groups using common markers such as phenotypic traits or molecular markers (mainly SSR according to 26).

109[z]	4[z]	132[z]	124[z]	12[z]	93[z]	99[z]	27[z]	Genes	QTLs
1	-	-	-	-	-	-	-	*si-1, yv*	
2	2+K	-	-	6	4	V	-	**Cm-ACO1, Fn, Pm-w, Vat, PmV.1**	*fl5.1, fw5.2, fw4.1, ssc4.1, ssc4.2, fomV.1, fomV.2*
3	-	-	-	-	-	-		*gl, ms-1, Pa, r*	
4	D	-	-	3	8	II	IV	*a, h, mt-2, Pm-x, Zym*	*cmv2.1, cmv2.2, eth2.1, fl2.1, fs2.1, fs2.2, fw2.1, ovl2.1, ovl2.2, ovs2.1, ovs2.2, ovw2.1, ssc8.1, pcII.1*
5	5	-	-	11	7	IX	II	*Al-4, Fom-1, gf, 6-Pgd2, Prv, yv-2*	*cmv9.1, fw9.1, ovl9.1, ovs9.1, fs7.1, ecol7.1*
-	-	-	A	-	-	-	-	*Aco-1, Idh, Mpi-1, Mpi-2, Pgd-3, Pgm-2*	
6	6	III	-	1	5	XI	III	*Cm-ACS1, Fom-2, ms-2, s-2, yg*	*eth11.1, fs11.1, fw5.1, fw5.2, fs5.1, fomXI.1, pcXI.1*
7	7	-	-	3	11	XII	-	*nsv, p, Pm-Y, PmXII.1*	*cmv12.1, cmv12.2, fs12.1, fw12.1, ovs12.1, ovw12.1, fs11.1, fomXII.1, pcXII.1*
8	-	-	-	-	-	-	-	*f, lmi*	
9	-	-	-	-	-	-	-	*dl*	
10	-	-	-	-	-	-	-	*ms-3*	
11	-	-	-	-	-	-	-	*ms-4*	
12	-	-	-	-	-	-	-	*ms-5*	
13	-	-	-	-	-	-	-	*v*	
-	C	-	-	10	10	IV	-	*Wt-2*	*fl4.1, fw4.1, ovl4.1, ecol10.1, ea10.1, pcIV.1*
-	E	-	-	3+8+13 (+17?)	1	VIII	I	*Al-3, Cm-ACO2, pH*	*cmv8.1, fl8.1, fl8.2, fs8.1, fs8.2, ovl8.1, ovs8.1, ovs8.2, ovw8.1, ea1.1, ea1.2, ea1.3, fs1.1, scc1.1, gfc1.1, pcVIII.1*
-	F	-	-	-	3	VII	VI	*spk*	*fw7.1, ovl7.1, ovs7.1, fs3.1, ecol3.1, fw3.1, ofc3.1*
-	G	-	-	3+12	6	I	VIII	*ech, Cm-ERS1*	*eth1.1, fl1.1, fs1.1, ovs1.1, fs6.1, fs6.2*
-	J	-	-	-	2	III	V	*Cm-ACS5, Ec, pin*	*cmv3.1, cmv3.2, eth3.1, ofc2.1, ssc2.1, ea2.1, fomIII.1, fomIII.2, fomIII.3*
-	-	-	B	-	-	-	-	*Mdh-2, Mdh-4, Mdh-5, Mdh-6, Pep-gl*	
-	A	-	-	4+7	9	X	-		*ovw10.1, ea9.1, ea9.2,*

-	B	-	-	9	12	VI	-	*ecol9.1, fs9.1 fl6.1, fw12.1, fw12.2, ofc12.1, ea12.1, ea12.2, fomVI.1, fomVI.2, pcVI.1*

N.B. If *6-Pgd-2* (4) and *Pgd-3* (124) correspond to the same locus, which is probable but not yet demonstrated, lines 5 and 6 of this table can be merged.
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Gene Nomenclature for the Cucurbitaceae

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,. All letters of the symbol and name are in lower case if the mutant gene is recessive, with the first letter of the symbol capitalized for the dominant or normal allele. (Note: For CGC *research articles*, the normal allele of a mutant gene may be represented by the symbol "+", or the symbol of the mutant gene followed by the superscript "+", if greater clarity is achieved for the manuscript.)
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 re-occurrences 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.
10. 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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Lin, Depei. Sichuan Acad. Agric. Science No. 20 Jingjusi Road ; Chengdu 610066 P.R. China. Email: pyplin@126.com; Ph: 86-28-84590018; Fax: 86-28-84504177; Interests: watermelon, melon and cucurbit breeding.

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Neill, Amanda. The Botanical Research Inst. of Texas 509 Pecan St., Fort Worth, TX 76102-4060, USA. Email: aneill@brit.org; Interests: *Gurania* and *Psiguria*.

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Price, Glen. 201 Lena Lane, Anadarko, OK 73005, USA. Email: angusstars@netride.net; Ph: 405-247-3220; Interests: seedless watermelon: polyploidy, genetics, breeding, cytogenetics, germplasm.

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Saito, Takeo. National Research Institute Vegetables., Ornamentals & Tea, Ano, Mie 514-2392, Japan. Email: romario@nivot.affrc.go.jp; Ph: 81-59-268-1331; Fax: 81-59-268-1339; Interests: breeding melons resistant to diseases and insects, use of DNA markers for melon breeding.

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Wehner, Todd. Dept. Horticultural Science Box 7609 North Carolina State Univ., Raleigh, NC 95616, USA. Email: todd_wehner@ncsu.edu; Ph: 919-515-5363; Fax: 919-515-2505; Interests: pickling/slicing cucumber, watermelon, luffa gourd, selection, disease resistance, yield, genetics and breeding.

Wessel-Beaver, Linda. Dept. Agronomy & Soils P.O. Box 9030 Univ. of Puerto Rico, Mayaguez PR 27695-7609, USA. Email: lbeaver@uprm.edu; lwesselbeaver@yahoo.com; Ph: 787-832-4040 x 2383; Fax: 787-265-0220; Interests: squash breeding and genetics; disease and insect resistance; cucurbit evolution and domestication.

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Yorty, Paul. Qualiveg Seed Production 3033 E., 3400 N., Twin Falls, ID 83301,

USA. Ph: 208-733-0077; Fax: 208-733-0077; Interests: cucurbit breeding.

Zhang, Xingping. Syngenta Seeds 21435 Co. Rd. 98, Woodland, CA 95695, USA. Email: xingping.zhang@syngenta.com; Ph: 530-666-0986; Fax: 530-666-5273; Interests: watermelon and melon genetics & breeding.

Zhang, Jiannong. Melon Research Institute Gansu Univ. of Agriculture, Lanzhou, Gansu 730070, P.R. of China.

Zhou, Ihichen. Xinjiang XiYu Seeds Co., LTD. No. 32 Eastern Ningbian Road, Changji Xingiang 831100 P.R. of China. Email: xiyuseedsxj@hotmail.com; Ph: +86-994-2893011; Fax: +86-994-2892415; Interests: breeding watermelon, melon, squash and other cucurbits.

Zitter, Thomas A. Cornell University Dept. Plant Pathology 334 Plant Science Bldg, Ithaca, NY 14853-5908, USA. Email: taz1@cornell.edu; Ph: 607-255-7857; Fax: 607-255-4471; Interests: fungal, bacterial & viral diseases; disease resistance.

Zoro Bi, Irie A. Universite Abobo-Adjame UFR des sciences de la nature, 02 BP 801 Abidjan 02 Cote d'Ivoire. Email: zorobi@ua.bobo.ci; Interests: germplasm collection and classification for *Cucumis melo* var. *argrestis*, *Citrullus lanatus* ssp. *lanatus*, *Citrullus* ssp. *Cucumeropsis mannii*, & *Lagenaria siceraria*.

CGC Members in the United States

Alabama
Dane, F

Arkansas
Morelock, T
Thompson, GA

Arizona
Navazio, JP
Ray, D

California
Barham, WS
Chung, P
Elmstrom, G
Gabor, B
Himmel, P
Huan, J
Humaydan, H
Johnson, B
Juarez, B
King, JJ
Knerr, LD
Lanini, B
McCreight, JD
Nadel, M
Ouyang, W
Owens, K
Peterson, PS
Poulos, JM
Randhawa, P
Randhawa, L
Tolla, G
Zhang, X

Colorado
Carle, RB
Hollar, LA
Walters, T

Florida
Guner, N
Gusmini, G
Maynard, DN
Pettit, F
Taurick, G
Williams, TV
Wolff, DW

Georgia
Boyhan, GE
Groff, D

Iowa
Block, C
Drowns, G
Merrick, LC
Reitsma, K
Summers, WL

Idaho
Love, SL
Yorty, P

Illinois
Frobish, M

Indiana
Martyn, R

Kansas
Carey, EE

Maryland
Kirkbride, Jr., JH
Ng, TJ

Maine
Hutton, M
Johnston, R

Michigan
Grumet, R

North Carolina
Denlinger, P
Schultheis, JR
Wehner, T

New Hampshire
Loy, JB

New Jersey
Wang, G

New York
Andres, TC
Goldman, AP
Munger, HM
Provvidenti, R
Robinson, RW
Whitwood, T
Zitter, TA

Ohio
Bell, D

Oklahoma
Bruton, BB
Davis, AR
Price, G

Oregon
Di Nitto, LV
Gabert, AC
Myers, JR
Reiten, J

Pennsylvania
Stephenson, AG

Puerto Rico
Wessel-Beaver, L

Rhode Island
Brown, R

South Carolina
Levi, A
Ling, K-S
Rhodes, BB
Thies, J
Thomas, C

Texas
Coffey, R
Crosby, K
King, SR
Kuti, JO
Lester, G
Neill, A

Wisconsin
Havey, MJ
Jahn, M
Lower, RL
Simon, PW
Staub, JE

International CGC Members

Argentina
Lopez-Anido, F

Australia
Blazey, D
Herrington, M
Martin, H
McGrath, DJ

Austria
Lelley, T
Pachner, M
Teppner, H
Winkler, J

Brazil
Della Vecchia, PT
Maluf, WR
Oliveira de Paiva, W

Costa Rica
Ramirez, M del P

Cote d'Ivoire
Zoro Bi, IA

Czech Republic
Holman, B
Křístková, E
Lebeda, A

Denmark
Kampmann, HH

Egypt
Aboul-Nasr, M H
Hassan, A
Kapiel, T

France
Baudracco-Arnas, S
Boissot, N
De Lancen, F
Gautier, J
Ignart, F
Kol, B
Legg, E
Oliver, M
Picard, F
Pitrat, M
Robledo, C
Rocherieux, J
Sipeyre, B

Germany
Tatlioglu, T
Theurer, C

Greece
Vakalounakis, D

India
Aurangabadkar, L
Ganapathi, A
Jain, J
Peter, KV
Sanghani, A

Indonesia
Rokhman, F

Israel
Burger, Y
Cohen, E
Cohen, R
Cohen, Y
Haim, D
Herman, R
Karchi, Z
Katzir, N
Paris, H
Perl-Treves, R
Vardi, E

Italy
de Groot, E
Gatto, G
Stravato, VM
Vecchio, F

Japan
Ezura, H
Furuki, T
Hagihara, T
Hirabayashi, T
Ito, K
Kanda, M
Kato, K
Konno, Y
Kuginuki, Y
Matsuura, S
Mochizuki, T
Saito, T
Shindo, E
Sugiyama, K
Yamanaka, H

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Cho, M-C
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Om, Y-H
Kwack, SN
Yang, D-H

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Van Kooten, HC

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China, People's Republic of
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Ma, Q
Wu, M
Bao, HQ
Chen, JF
Cui, H
Li, H
Lin, D
Zhang, J
Zhou, I

Peru
Holle, M

Philippines
Beronilla, R

Poland
Halaj, W
Niemirowicz-Szczytt, K

Serbia
Berenji, J
Sušić, Z

South Africa
Swanepoel, C
Lee, D-H
Lee, SY

Spain
Ayuso, MC
Den Hertog, M
Fito, L
Gómez-Guillamón, ML
Kraakman, P
Nuez Viñales, F
Palomares, G
Peiro Abril, JL
Roig, LA

Sudan
Omara, SK
Sultanate of Oman
Khan, IA

Sweden
Lehmann, LC

Taiwan
Chen, F-C
Sun, Z

Thailand
Asavasena, S
Chuanchai, V
de Hoop, SJ
Duangsong, U
Iamsangsri, S
Mekiyanon, S

Turkey
Çaglar, G
Dogan, R

United Kingdom
Poostchi, I

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

1. 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.
2. 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.
3. 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 at least 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.
2. 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.
3. 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 for at least the most recent five years, 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.