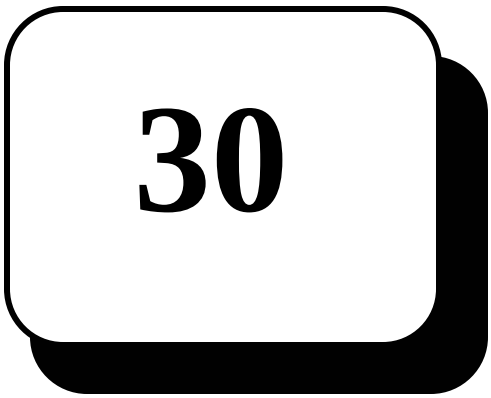
Cucurbit Genetics Cooperative



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The **Cucurbit Genetics Cooperative** (CGC) was organized in 1977 to develop and advance the genetics of economically important cucurbits. Membership to CGC is voluntary and open to 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 contact Tim Ng at (301) 405-4345 or *tn5@umail.umd.edu*.

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

Cucumber (Cucumis sativus)

Melon (*Cucumis melo*)

Pumpkin, Squash (*Cucurbita* spp.)

31st Annual CGC Business Meeting (2007)

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

The cucurbit genetics cooperative met with the annual conference of the American Society for Horticultural Science conference in Scottsdale, Arizona at 9 am in the Rainmaker A room on July 16, 2007. The following issues were discussed at the **meeting**.

We will be voting to change the by-laws to add three associate chair positions, one each for the print edition, membership, and treasurer. They will assist the chair, who will also be the website editor. That will keep CGC running smoothly without overloading any one person. **Angela Davis** is the associate chair for the printed journal, **Linda Wessel-Beaver** is the associate chair for membership, and **Tim Ng** is the associate chair for treasurer. For more information, see the current leadership list.

Todd Wehner will continue as CGC chair and website editor.

Jack Staub has resigned as assistant editor for cucumber after 15 years of dedicated service in that role to CGC. A nominating committee was established to identify a replacement. The committee consisted of assistant editors: Kevin Crosby, Mark Hutton, Gabriele Gusmini, and Stephen King (chair). They drafted **Rebecca Grumet** to serve as the new assistant editor for cucumber.

The **website** is on a server at NC State University. We have obtained the short address of http://cgc.ncsu.edu/ for the site.

CGC volumes 1 through 6 have been typed and proofed and are now on the website. **CGC volumes 7 through 22** have been typed and are being proofed. We are typing volumes 23 to 29 now.

Angela Davis is finishing CGC volume 29 (2006) and having it printed

We are now calling for papers for CGC volume 30 (2007); assistant editors will be looking for reports of interest in their crop areas.

Linda Wessel-Beaver is updating the membership list. Please contact her to make sure she has your correct mailing address. We have about 160 members and would like to invite previous members to become active in CGC again.

You can now pay your membership dues on line at **Google Checkout** using most major credit cards.

The **vegetable improvement newsletter** volumes 1 through 24 have been typed and proofed and are now on the website.

The **next meeting** of the cucurbit genetics cooperative will at the EUCARPIA cucurbit conference in Avignon, France in the summer of 2008.

The cucurbit genetics cooperative met with the Cucurbitaceae 2006 conference in Asheville, North Carolina at 6 pm on September 18. The following issues were discussed:

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 American Society for Horticultural Science has agreed to handle the funds for the annual membership dues for CGC. They will set up an account for us.

The **membership list** was expanded and updated. Conference attendees were encouraged to register for CGC membership, and many took advantage of the offer.

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.

Cucurbit Genetics Cooperative Report Call for Papers

The call for papers for **CGC 31** (2008) is open, and we are **accepting papers** for the volume now. If you do not receive your copy, contact Linda Wessel-Beaver.

Comments from the CGC Coordinating Committee

The Call for Papers for the 2008 Report (CGC Report No. 31) has been sent out. Papers should be submitted to the respective Coordinating Committee members by 31 December 2008. The report will be published by June 2009. 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 Jesy Cochran 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.

2007 Watermelon Research and Development Working Group – 27th Annual Meeting

Stephen R. King[1], Chair and Elizabetta Vivoda[2], Vice-chair

[1]Texas A&M University, College Station, TX; [2]Harris-Moran Seed Co., Davis, CA

The Watermelon Research and Development Group had some changes beginning in 2007. Benny Bruton announced at the beginning of the 27th annual meeting of the WRDG in Mobile, AL that he would be stepping down as chair after eight years of devoted service to the group. The group discussed how we wanted to be organized, and it was decided that we would develop a set of bylaws to better organize our group. Previous chairs of the WRDG have served an average of eight years, and these chairs have been solely responsible for organizing the annual meetings and conducting any other business of the WRDG. In order to alleviate some of this responsibility, it was decided to have the chair serve two year terms, and to elect a vice chair to assist with the business of the WRDG. It was also decided that a secretary position be created to assist with website maintenance and other communications for the WRDG. Stephen King was elected the chair, and Elizabetta Vivoda was elected the vice-chair to serve from 2007-2009. Todd Wehner (North Carolina State University) was elected the secretary.

A new website was developed by the secretary where information can be posted and easily accessed by the membership (http://cuke.hort.ncsu.edu/cgc/wrg/wrgmain.html). A set of bylaws was developed to organize the group, and an updated membership directory was developed. (both available on the website). The new bylaws outline that the chair and vice chair each serve two-year terms, and the vice-chair assumes the duties of the chair at the end of his/her two year term, so that we will elect a new vice-chair every two years. Also, it is specifically noted that an effort will be made to alternate these positions between industry and academic professionals.

The 27th annual meeting of the Watermelon Research and Development Working Group was held Sunday, February 4, 2007 in Mobile, Alabama in conjunction with the Southern Association of Agricultural Scientists and the Southern Region of the American Society for Horticultural Sciences. Refreshments were sponsored by Sakata Seed America, so please let Nihat Guner know that we really appreciate our sponsors!

Highlights included a presentation by Mark Arney, CEO of the National Watermelon Promotion Board. Mark discussed ways of developing closer ties between the NWPB and WRDG. The morning session included

seed company updates and variety trial reports. The afternoon session centered on research reports. Research topics presented included:

- Utilization of commercially available pollenizers for optimizing triploid watermelon production. P.J. Dittmar, D.W. Monks and J.R. Schultheis.
- Management of whitefly populations for the control of watermelon vined decline in Florida. P.D. Roberts, P.A. Stansly, S.A. Adkins, C.S. Kousik and B. Bruton.
- Assessment of methods to graft watermelon onto squash and gourd rootstocks for improved soil-borne disease tolerance. R.L. Hassell and V.B. DuBose.
- Carotenoid analysis using the puree absorbance method for germplasm screening. A.R. Davis, W.W. Fish, P. Perkins-Veazie, A. Levi and S.R. King.
- Broad mite (*Polyphagotarsonemus latus*) infestation and injury in watermelon and potential sources of resistance. C.S. Kousik, A. Levi, A.M Simmons, R. Hassell and B.M. Shepard.
- Tolerance of select watermelon plant introductions (PI) to watermelon vine decline in Florida. C.S. Kousik, S. Adkins and P.D Roberts.
- Evaluation of commercial watermelon rootstocks for tolerance to phytopthora blight and watermelon vine decline. C.S. Kousik, S. Adkins, P.D. Roberts and R. Hassell.
- Value to grafted watermelon: novel benefits and potential pitfalls. B. LaMolinare, T. Isakeit, A. Davis, W. Liu and S. King.
- Resistance of *Citrullus colocynthis* to whiteflies and spidermites. A. Levi, A. Simmons. R. Lopez, C. Kousik, M. Shepard, M. Jackson, H. Harrison, M. Edelstine, E. Palevski and K. Tadmor.
- Developing expressed sequenced tags (ESTs) for watermelon fruit. A. Levi, A. Davis, P. Wechter, A. Hernandez and J. Thimmapuram.
- Hot topics for watermelon research: a survey of the industry. S. King and A. Davis.

A total of nine abstracts from this meeting were published in HortScience (Vol. 42(3) June 2007, pages 453-454).

U.S. Cucurbit Crop Germplasm Committee Update

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

This group operates under the auspices of the USDA-ARS National Plant Germplasm System (NPGS), is composed of ARS, university and industry scientists, and provides guidance to NPGS on matters relating to cucurbit crops and wild related species. Committee membership and species-specific crop reports are accessible through the NPGS website: (http://www.ars-grin.gov/npgs/). The committee receives, reviews and recommends germplasm evaluation proposals annually for funding by NPGS, and also reviews and recommends proposals for germplasm collection and exchange. Contact James D. McCreight, USDA-ARS, Salinas, Calif., U.S.A., james.mccreight@ars.usda.gov for more information.

National Melon Research Group

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

2006 Meeting

The National Melon Research Group met on September 20, 2006 in conjunction with Cucurbitaceae 2006 hosted by North Carolina State University in Asheville, N.C.

Focus of the meeting was on powdery mildew, particularly the proliferation of races and differential melon cultigens. A committee organized to address the many research needs surrounding this international problem.

2008 Meeting

A session on powdery mildew was held on May 24 in conjunction with the IXth Eucarpia meeting, Cucurbitaceae 2008, held in Avignon, France. Discussion centered on powdery mildew, specifically establishment of a standard set of *P. xanthii* race pathotype and race differentials, and an objective system for designating pathotypes and races.

2010 Meeting

The next meeting will be held in conjunction with Cucurbitaceae 2010, which will be held in Charleston, S.C. Contact James D. McCreight, USDA-ARS, Salinas, Calif., U.S.A., james.mccreight@ars.usda.gov for more information.

Upcoming Meetings of Interest to Cucurbit Researchers

Cucurbit Crop Germplasm Committee

The next meeting will be held in conjunction with Cucurbitaceae 2010, which will be held in Charleston, S.C. Contact James D. McCreight, USDA-ARS, Salinas, Calif., U.S.A., james.mccreight@ars.usda.gov for more information.

Cucurbit Genetics Cooperative

The cucurbit genetics cooperative mets with the annual conference of the American Society for Horticultural Science conference. The next ASHS meeting will be 25th – 28th of July, 2009, at the Millennium Hotel, St. Louis, Missouri.
http://www.ashs.org/index.php?option=com_content&view=article&id=449&Itemid=193

Cucurbita Research Group

Meeting to be held at the next Cucurbitaceae meeting. Contact Gabriele Gusmini for details, gabriele.gusmini@syngenta.com

Watermelon Research Group 29th Annual Meeting

Atlanta, GA, February 1, 2009, Stephen R. King, Chair, Vegetable & Fruit Improvement Center, Department of Horticultural Sciences, Texas A&M University, College Station, TX 77843-2133, srking@tamu.edu, Phone: 979-845-2937, Cell: 979-229-8746, Elisabetta Vivoda, Vice-Chair, Harris Moran Seed Co., Davis, CA, e.vivoda@harrismoran.com, http://cuke.hort.ncsu.edu/cgc/wrg/wrgreport2009.html

ISHS, the 4th International Cucurbit Symposium

September 2009 in Changsha, Hunan, China, cucurbit2009@188.com, cucurbit2009@hunau.net, http://www.cucurbit2009.org/

Cucurbitaceae 2010

Location: Charleston, South Carolina, Date: Fall, 2010, Organizing committee: Judy Thies (chair), Amnon Levi, Shaker Kousik, Registration coordinator: Mike Neff, Amer. Soc. Hort. Sci., Contact: Judy Thies, U.S. Vegetable Laboratory, Charleston, SC 29414-5334, Tel: 843-402-5317, Fax: 843-573-4715

EUCARPIA-Cucurbitaceae 2012

Under the aegis of EUCARPIA, the next European meeting on Genetics and Breeding of Cucurbitaceae will be organized Dr. Sari. It will be held in May 2012 in either Adana or Antalya Turkey. Both are important cucurbit growing regions. EUCARPIA-Cucurbitaceae 2012 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, contact Dr. Nebahat Sari in Adana Turkey; Cukurova University, Department of Horticulture, Faculty of Agriculture; 01330 Adana-Turkey; Phone: 90.322.338 64 97 and Fax: 90.322.338 63 88 e-mail: nesari@cu.edu.tr

Upcoming Meetings & News of Interest

Organization/Meeting	Dates	Location	Contact
28th Annual Meeting of the Watermelon Research & Development Working Group	February, 2008 & 2009	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
Cucurbitaceae 2010	TBA	Charleston, SC.	Amnon Levi, Amnon.Levi@ARS.USDA.GOV Judy Thieves, Judy.Thies@ars.usda.gov Shaker Kousik, Shaker.Kousik@ars.usda.gov
X EUCARPIA International Meeting on Cucurbitaceae Eucarpia 2012	TBA	Turkey	Nebahat Sari, nesari@cu.edu.tr

Effects of Benzothiadiazole on Induction of Resistance in Cucumber to Infection by *Cladosporium cucumerinum*

Q. Ma and C. F. Wang
College of Plant Protection, Shaanxi Key Laboratory of Molecular Biology for Agriculture, Key Laboratory of Plant Protection Resources and Pest Management, Ministry of Education, Northwest A&F University, Yangling, Shaanxi 712100, P.R. China;
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Abstract: Tests of induction of resistance by benzothiadiazole (BTH) against scab disease, caused by *Cladosporium cucumerinum*, were conducted on etiolated cucumber (*Cucumis sativus* L.) seedlings. The results showed that 0.05-0.7mmol/L BTH could induce resistance of seedlings to the disease, with the concentration of 0.5mmol/L BTH being the best. The disease index decreased from 90.58 (Control) to 28.43, while the disease incidence decreased from 100% (Control) to 58.82%. However, BTH has no direct inhibition effect on the spore germination and mycelial growth at concentrations from 0.05 to 0.7mmol/L.

Introduction: Cucumber scab, caused by *Cladosporium cucumerinum*, is a worldwide disease on cucumber (*Cucumis sativus* L.), especially in greenhouse cucumber plants. Currently, the disease is controlled mainly by fungicide applications. As the problems of residues and pollution have been becoming increasingly serious, alternative protection methods are essential.

Systemic acquired resistance （SAR） can be induced in plants by abiotic or biotic elicitor(s) (4,6-7,9-10). Among the abiotic compounds, salicylic acid (SA) was found to induce systemic resistance to fungal, bacterial, and viral pathogens. Benzothiadiazole (BTH), a mimic of SA, is capable of inducing SAR. In 1996, BTH was introduced in Germany and is now available as a commercial product BION®. Resistance inducing effects of this product have been demonstrated in plants against different crop diseases (1-3), but for the cucumber plants against *C. cucumerinum*, the reports are rare.

Methods: The pathogen, *C. cucumerinum*, was obtained from our Plant Pathology Laboratory. The cultures were maintained on potato-dextrose agar (PDA) medium at 4°C; and fresh cultures were grown for 10 days on PDA plates at 22°C before experimentation.

The cucumber (*Cucumis sativus* L. cv. Jingyan 4) seeds examined in this study were purchased from a local seed company. The culturing method of etiolated cucumber seedlings followed Li (5). The benzothiadiazole (BTH, BION®) was obtained from Novartis Agro-Chemistry Co., Ltd.

The concentrations of BTH used in the experiment were 0.05， 0.1， 0.3， 0.5 and 0.7 mmol/L diluted in water. Etiolated cucumber seedlings of five days were sprayed with different concentrations of BTH. Three days later, the etiolated cucumber seedlings were inoculated with the pathogen by spraying with conidial suspensions of *C. cucumerinum*. 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 2×10^5 spores mL^{-1}. Control plants were treated by spraying tap water. There were at least 30 etiolated seedling in each treatment, and three replicates

per treatment. The plants were maintained in a dark growth chamber at 22°C and disease incidence and index were recorded after 4 days.

The effects of BTH on spore germination of the pathogen were assessed on concave slides. The spore suspension of $1x10^6$ spores ml^{-1} was kept at 22°C for 24h with BTH concentrations of 0.05, 0.1, 0.3, 0.5, 0.7 mmol/L. Five fields of vision were observed microscopically to record germination rate.

Four-mm-diameter callus from 10-day-old cultures of *C. cucumerinum* on PDA plates were taken and placed on PDA plates, which contained different concentrations of BTH. The mycelial diameters were measured every other day. This experiment was repeated three times. Disease assessment followed Li (5).

Results: Etiolated seedlings were sprayed with different concentrations of BTH (0.05, 0.1, 0.3, 0.5, and 0.7mmol/L) 3 days before inoculation with *C. cucumerinum*. Four days after inoculation, black brown lesion appeared both on the cotyledons and the hypocotyls. Some etiolated seedlings shrank and perished. The disease developed very quickly; only one to two days were needed from lesion appearance to death for the seedlings.

Table 1 shows that BTH with concentrations varying from 0.05 to 0.7 mmol/L had different effects, with 0.3-0.7 mmol/L better than others. The incidence and index of disease on the etiolated seedlings treated with 0.5 mmol/L BTH decreased dramatically, from 100% and 90.58 (control) to 58.82% and 28.43. The effects treated with 0.05 and 0.1 mmol/L BTH were not as good as with 0.3-0.7 mmol/L BTH, but also showed significant difference compared with control. Table 2 shows that no inhibitory activity was observed on conidial germination of *C. cucumerinum* at different concentrations of BTH. Fig. 1 shows that BTH has no direct inhibition to the mycelial growth of the pathogen at the concentrations from 0.05 to 0.7 mmol/L.

Discussion: In order to reduce pollution and strive for a cleaner environment, efforts are being made to develop alternatives to pesticides for the control of plant diseases. BTH has been found to be active in inducing systemic resistance against a wide range of pathogens in a diverse group of plants(8,11). This paper investigates the potential of this chemical for inducing systemic resistance in cucumber plants against *C. cucumerinum*. The results showed that 0.05-0.7 mmol/L BTH expressed effects on induced resistance, among which the induced resistance in seedlings treated with 0.3-0.7 mmol/L BTH had better effects.

According to Li(5), spray inoculation on etiolated seedlings for resistance identification is equally accurate for comparing with that on true leaf inoculation, and has advantages of time saving and symptom distinctiveness。BTH has no direct inhibition to the spore germination and mycelial growth at concentrations from 0.05 to 0.7 mmol/L, which means that the decreases of disease index and incidence are due to the resistance induction. As for the effect of BTH on the field plants, further research is needed.

Acknowledgements: This project was financially supported by the "National Science & Technology Pillar Program in the 11th Five-year Plan" (No. 2006BAD07B02), PCSIRT from Education Ministry of China (No.200558), the 111 Project from Education Ministry of China (No. B07049) and the Yangling Foundation of Sci-Tech Development of Agriculture.

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Table 1. Effects of BTH with various concentrations upon cucumber resistance induction to scab

Treatment (mmol/L)	Disease incidence (%)	Disease index	Disease severity
Control	100a	90.58a	5.43
0.05	100a	65.63bc	3.94
0.1	87.50a	46.88cd	2.81
0.3	75.00ab	32.50d	1.95
0.5	58.82b	28.43d	1.71
0.7	77.78ab	36.11d	2.17

Note: Significant difference at P=0.05.

Table 2. Effects of BTH on the spore germination of *C. cucumerinum*

Treatment (mmol/L)	Germination rate (%)
CK	76.85a
0.05	77.88a
0.1	80.35a
0.3	72.22a
0.5	72.08a
0.7	78.57a

Note: Significant difference at P=0.05.

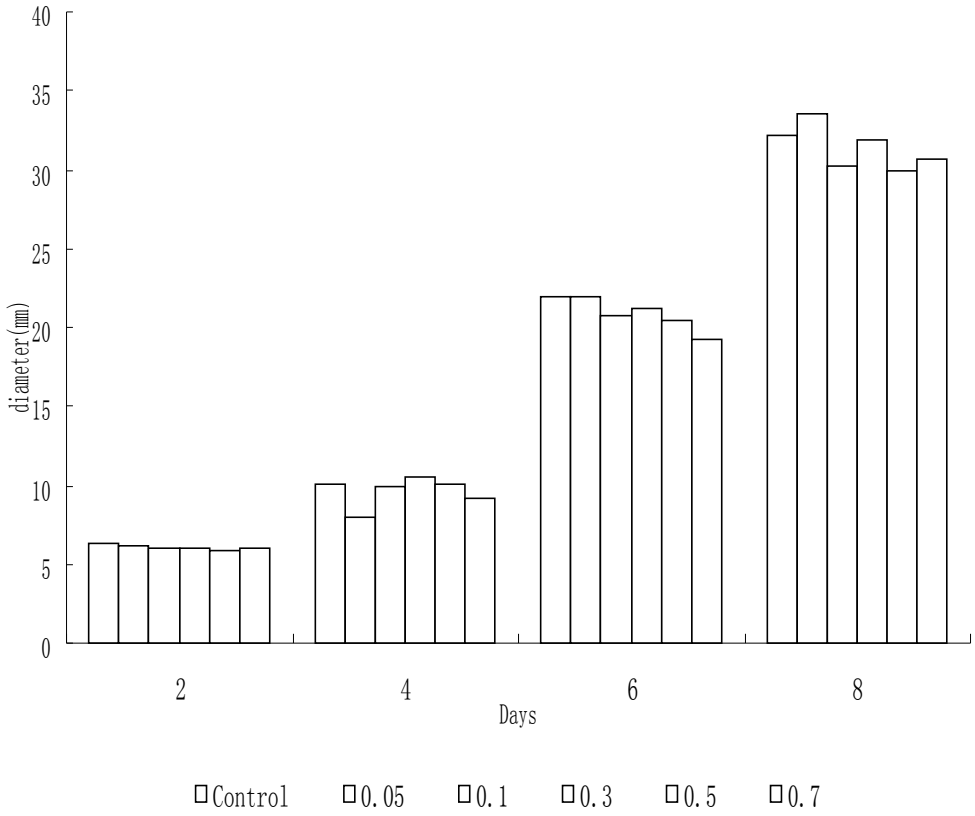

Fig.1 Effects of BTH upon the growth of *C. cucumerinum*

Genetic variability in *Cucumis sativus* var. *hardwickii* R. (Alef.) germplasm

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Abstract: Thirty-one accessions of a wild and feral form of cucumber *Cucumis sativus* var. *hardwickii* collected from different regions of India were evaluated for days to first fruit set and first picking, fruit weight, fruits per plant, fruit length:diameter (L:D ratio), and yield per plant. Highly significant variation was observed among the genotypes for all the characters studied. Mean fruit weight of *C. sativus* var. *hardwickii* was 57.3 g with a range of 33.0 to 99.1 g. Mean fruit number per plant was 18.7 with a range of 11.0 to 27.9 and the mean fruit yield per plant was 1010.9 g with a range of 663.7 to 1839.3 g. All the fruits were highly bitter in taste. The highest genotypic coefficient of variation was found for fruit weight (28.2) followed by fruits per plant (25.5), indicating the high selection response in respect of these traits. High genetic advance coupled with high heritability was obtained for fruit weight (56.5%, 94.5%), fruits per plant (47.4%, 81.4%), hence individual plant selection could be effective for isolation of superior genotypes for these traits. Since, there is no report on the genetic parameters of wild cucumber; the investigation highlighted the potential utilization of these germplasms for future breeding programmes.

Key words: Variation, morphology, *Cucumis sativus*

Rapid development of elite cultivars has hastened the displacement of old varieties and landraces and thus, in many species the broad genetic base needed for crop improvement continues to shrink (Staub et al. 1997). *Cucumis sativus* var. *hardwickii* (Royle) Alef. ($2n = 2x = 14$) is a wild, sympatric botanical variety of *C. sativus* that grows in the Himalayan foothills of India (Deakin et al. 1971). It is considered as wild progenitor of cucumber as it is easily crossable with cultivated cucumber. It possesses multiple and sequential fruiting habit and bears more than 40 fruits per plant (Horst and Lower 1978), while in India an average of 6-10 fruits per plant is obtained from the existing commercial cucumber cultivars under optimum growing conditions. Because *C. sativus* var. *hardwickii* possesses a sequential fruiting and multiple branching habit not present in *C. sativus* var. *sativus*, it has potential for increasing fruit yield in commercial cucumber (Staub et al. 1993).

In spite of Indian origin, no systematic attempt has been made to study the genetic variability of this wild species. The present investigation was conducted to gather information on the extent of variability available in the local cultivars and land races of *C. sativus* var. *hardwickii* collected from different regions of India which can be utilized in cucumber improvement programmes.

Materials and methods: The materials for the present investigation was comprised of thirty-one diverse accessions of *C. sativus* var. *hardwickii* (Table 1; Fig 1) collected from various parts of India through the National Bureau of Plant Genetic Resources, New Delhi. The accessions were selfed five times before evaluation at the Experimental Farm, Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi. These accessions were evaluated on the basis of yield and its related traits in the field during June to

December, 2004. The experiment was laid out in a randomized block design with three replications. Each accession was grown in a row with ten plants per replication. The pH of the soil was 7.2 at 20 cm below the surface. Twenty tons per 1 hectare of farmyard manure was drilled in shallow grooves before transplanting. The seedlings were transplanted on both sides of the channel with a spacing of 2 m between channel and 45 cm between plants with 90 cm irrigation channels. The recommended NPK fertilizer doses and cultural practices along with plant protection measures were followed. The observations were recorded for six characters: days to first fruit set, days to first picking, fruit weight (g), fruits per plant, fruit length:diameter (L:D ratio), and yield per plant (g). The analysis of variation was carried out as suggested by Snedecor and Cochran (1967). Genotypic and phenotypic coefficients of variation were calculated as per the formulae suggested by Comstock and Robinson (1952). Heritability in broad sense and expected genetic advance were calculated as per the formulae given by Allard (1960) and Johnson et al. (1955) respectively.

Results: The mean squares due to genotypes for all the characters were highly significant (data not presented). This result clearly indicated that there was significant (P=0.05) variation between the genotypes for all the characters under observations. Mean performance of all genotypes for different traits is given in Table 1. Days to first fruit set varied from 75.5 (IC-331445) to 111.5 (IC-277029) and the general mean observed for this character was 88.8 days. The mean value of days to first picking was 105.7 days, ranging from 91.0 (IC-277048) to 124.0 (IC-277029). The fruit weight ranged from 33.0g (IC-331628) to 99.1g (IC-331443) with general mean of 57.27 g. Number of fruits per plant ranged from 11.0 (IC-331443) to 29.2 (IC-331628) with a general mean of 18.7. The L:D ratio ranged from 1.2 (IC-277035) to 1.7 (IC-331443). Mean value for total yield per plant was 1010.9 g, ranging from 663.7 g (IC-202055) to 1839.3 g (IC-331620). All the fruits were highly bitter and non-edible. The highest heritability (94.5 %) was observed for fruit weight followed by L:D ratio (93.3 %), and yield per plant (81.6 %). while Days to first picking (72.0 per cent) showed the lowest heritability**.** The highest genetic advance expressed as percentage of mean was exhibited by fruit weight (56.5 %) followed by L:D ratio (50.2 %). The lowest genetic advance as percentage of mean was found in days to first picking (14.0 %) followed by days to first fruit set (20.3 %). The highest genotypic coefficient of variation was found for fruit weight (28.2) followed by fruits per plant (25.5) and L:D ratio (25.2), which indicated the possibility of obtaining high selection response for these traits. The data presented in Table 2 revealed high heritability estimates for all the traits ranging from 72.0 per cent (days to first picking) to 94.5 per cent (fruit weight).

Discussion: The data in present study revealed highly significant (P=0.05) differences among the genotypes for all the traits studied, indicating genetic variability among the genotypes. These might be due to natural crossing and existence of free gene flow between *C. sativus.var hardwickii* and cultivated cucumber (Bisht et al. 2004). Fruit weight (57.3 g) was much lower in *C. sativus* var. *hardwickii* germplasm than cultivated cucumber lines (~ 150 g). While number of fruits per plant (18.7) was very high in *C. sativus* var *hardwickii* compared to cultivated cucumber (~ 8 fruits per plant). Yield per plant was 1010.9 g, but all the fruits were highly bitter in taste. Similar findings on *C. sativus* var *hardwickii* germplasm had been reported by Horst and Lower (1978), Schuman et al. (1985), Staub (1985), Yang (1992), Bisht et al. (2004). Smith and Lower (1978) have suggested that the incorporation of genes for sequential fruiting from *C. sativus* var *hardwicki*, into commercial cucumber might be used to increase genetic diversity and the fruit setting potential of pickling cucumber.

Estimates of genetic parameters for various characters *viz*., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance in percentage of mean for all the characters of *Cucumis sativus* var *hardwickii* are presented in Table 2. The phenotypic coefficients of variation (PCV) were higher than their

corresponding genotypic coefficients of variation (GCV), for all the traits. However, a very narrow difference between them indicated less influence of environment in the expression of these traits. In this condition effective selection can be made on the basis of phenotype alone with a good probability of success. Liu and Staub (1999), Horton et al. (1980) and EI-Hafez et al. (1997) also reported high heritability with a range of 60% to 80% for most of the characters in cultivated cucumber.

Heritability estimates together with genetic advance provides better response during selection than either of the parameters alone (Johnson et al. 1955). In the present study, high genetic advance coupled with high heritability was obtained for fruit weight, fruits per plant and L:D ratio, indicating individual plant selection could be effectively utilized for isolation of superior genotypes for these traits. Similar results were also reported by Das et al. (2003) in cucumber and Rakhi and Rajamony (2005) in culinary melon. High heritability and moderate genetic advance was observed for days to first fruit set, days to first picking, and yield per plant, indicating the preponderance of additive gene action. On the other hand, traits like days to first fruit harvest which exhibited high heritability with low genetic advance can be improved through heterosis breeding by effectively utilizing non additive gene action.

Evaluation of the collections indicated that *C. sativus* var. *hardwickii* possesses important and useful characters such as prolific fruit bearing with high numbers of laterals (10-15; data not presented) which are of interest to breeders. The data presented suggest that variability for fruit characteristics within the *C. sativus* var. *hardwickii* germplasm collection is somewhat representative of the diversity within this species, and that variability for fruit morphologic characteristics is likely sufficient to provide the basis for the improvement of the cucumber crop.

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Table 1 Mean performance of *C. sativus* var. *hardwickii* accessions for different quantitative traits.

Accession[a]	Source[b]	Days to 1st fruit set	Days to 1st picking	Fruit weight (g)	Fruits/ plant	L:D ratio	Yield per plant (g)
IC-202049	Dehradun, Uttaranchal	99.5	115.0	52.3	17.2	1.3	897.2
IC-202055	Dehradun, Uttaranchal	104.7	120.4	53.7	12.4	1.3	663.7
IC-202058	Mussourie, Uttaranchal	90.8	106.4	65.9	11.3	1.3	742.4
IC-202060	Mussorie, Uttaranchal	99.1	113.9	51.0	19.8	1.4	1011.8
IC-202063	Kotwar, Uttaranchal	91.0	102.9	65.6	16.1	1.3	1059.9
IC-253909	Mt. Abu, Rajasathan	94.5	105.9	46.6	18.7	1.4	864.8
IC-253915	Mt. Abu, Rajasathan	99.6	113.4	58.7	15.9	1.3	931.7
IC-253916	Mt.Abu, Rajasathan	99.2	111.3	55.9	17.6	1.2	980.9
IC-277000	Melghat, Maharastra	87.8	98.3	50.7	19.1	1.3	965.0
IC-277017	Khandlaghat, Maharastra	94.5	108.6	39.9	26.4	1.3	1047.3
IC-277029	Raigdh Fort, Maharastra	108.5	124.0	57.0	16.1	1.3	911.4
IC-277030	Raigdh, Maharastra	92.6	109.2	61.7	15.3	1.3	939.6
IC-277035	Ratnagiri, Maharastra	104.4	121.7	64.9	15.6	1.2	1008.5
IC-277048	Ratnagiri, Maharastra	75.6	91.0	46.5	24.9	1.2	1151.5
IC-277054	Panhala, Orissa	85.3	100.0	53.9	15.0	1.4	796.2
IC-331444	Jeypore, Orissa	83.7	100.0	46.3	22.8	1.3	1052.8
IC-331446	Jeypore, Orissa	83.0	102.9	59.8	15.2	1.2	898.4
IC-331459	Bilaspur, Chhattisgarh	82.3	101.0	63.3	22.5	1.4	811.3
IC-331465	Shehdol, Madhya Pradesh	93.7	114.1	59.8	15.7	1.2	934.5
IC-331609	Pantnagar,Uttaranchal	76.6	95.4	33.9	27.9	1.4	938.0
IC-331616	Solan, Himachal Pradesh	83.2	104.5	89.0	15.9	1.5	1419.3
IC-331619	Solan, Himachal Pradesh	79.5	99.4	41.9	25.5	1.4	1070.8
IC-331620	Sirmur, Himachal Pradesh	86.3	107.1	88.5	20.9	1.6	1839.3
IC-331626	Sirmur, Himachal Pradesh	85.2	107.8	64.7	19.8	1.2	1273.3
IC-331627	Dehradun,Uttaranchal	74.4	94.1	87.7	14.2	1.5	12498.0
IC-331628	Rishikesh, Uttaranchal	81.6	100.9	33.0	19.2	1.4	964.0
IC-331629	Bhowali, Uttaranchal	77.7	96.6	42.4	24.1	1.3	1015.6
IC-331631	Pauri Gharwal, Uttarancha	75.7	92.4	56.8	16.0	1.3	9.7.7
IC-331443	Koraput, Orissa	83.5	101.4	99.1	10.9	1.7	1082.4
IC-331445	Jeypore, Orissa	75.5	96.0	45.3	23.3	1.3	1050.4
ASR-2092	Bhowali, Uttaranchal	105.2	121.2	66.5	13.1	1.4	859.1
Mean	-	88.8	105.7	57.3	18.6	1.3	1010.9
Range	-	75.5-108.5	91.0-124.0	33.0-99.1	10.9-27.8	1.2-1.7	663.7-1839.3
CV (%)	-	5.33	4.98	6.83	12.18	0.45	9.83
CD (P=0.05)	-	7.74	8.60	6.38	3.70	0.24	162.30

[a]Accessions were collected and conserved in gene bank of NBPGR, New Delhi.
[b]Place (State) of origin of these accession.

Table 2 Estimates of genetic parameters for various traits in *C. sativus* var. *hardwickii* genotypes.

Character	GCV	PCV	H_b (%)	GA	GA as (%) of mean
Days to 1st fruit set	10.9	12.1	80.7	17.9	20.3
Days to 1st picking	8.0	9.4	72.0	14.8	14.0
Fruit weight	28.2	29.1	94.5	32.4	56.5
Fruits per plant	25.5	28.2	81.4	8.8	47.4
L:D ratio	25.2	26.1	93.3	2.7	50.2
Yield per plant	20.7	22.9	81.6	38.1	38.4

GCV-Genotypic coefficient of variation; PCV-Phenotypic coefficient of variation; H_b- Heritability in broad sense; GA-Genetic Advance.

Cucumber accession PI308916, noted for compact plant habit and poor seedling emergence, exhibits poor apical hook formation.

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Cucumber (*Cucumis sativus* L.) accession PI308916 is characterized by very short internodes and vine length resulting in a compact plant habit (Table 1). The compact plant form, which is conferred by a single recessive allele, *cp*, was of interest to breeders as a way to increase planting density, and thereby increase yield per unit land area. Breeding lines derived from PI308916 were shown to have significant yield advantage (Kauffman and Lower, 1976; Edwards and Lower, 1982a). Efforts to produce finished cultivars were curtailed, however, as the PI308916-derived lines exhibited poor seedling emergence which could not be segregated away from the compact plant trait (Edwards and Lower, 1981, 1982b, 1983).

Subsequent studies in our lab, directed toward reducing incidence of *Phytophthora capsici* fruit rot, again led to PI308916 as a potentially useful germplasm (Ando and Grumet, 2006). Cucumber fruit rot, caused by the soil-borne oomycete *P. capsici*, is a significant problem affecting cucumber production in the midwest (Hausbeck and Lamour, 2004). Since screening cucumber germplasm for resistance to *P. capsici* did not yield a reproducible source of resistance useful for breeding efforts (Gevens et al., 2006), we screened cucumber germplasm for architectural types that might reduce disease incidence, either by reduced canopy density to allow for increased air movement (reduced temperature and humidity), increased accessibility of the fruit to chemical sprays, or reduced fruit contact with the soil In these studies PI308916 showed greatly reduced disease occurrence (1% vs. 20% for standard cultivars at the time of harvest (Ando and Grumet, 2006). The short internode length of the PI308916 plants resulted in a tendency to hold young fruit at an upright angle and off the ground. Direct inoculation tests showed that the reduced disease occurrence was not due to resistance of the fruit per se, suggesting that architecture which allows less contact of fruit with the soil led to reduced *P. capsici* infection (Ando and Grumet, 2006).

Given the potential usefulness of this the compact plant habit for both increased yield and reduced *P. capsici* infection, we sought to investigate the cause of the seeding emergence problem. Short internode length can be caused by reduced levels of plant hormones, such as gibberellins or brassinosteroids (BRs) (Clouse and Sasse 1998; Hooley 1994). Gibberellins can be associated with seed germination and BRs are associated with proper formation of the apical hook that allows the tightly folded germinating seedling to push through the soil surface (Li and Chory, 1999). Effects on either germination or apical hook formation could influence seedling emergence.

Tests of seed germination suggest that poor seedling emergence does not result from poor germination, per se, at least in laboratory conditions. Although PI308916 seeds were a bit slower to germinate (2 days instead of 1), all showed 100% radical emergence when germinated on moist filter paper (Table 1). On the other hand, examination of apical hook formation showed a distinct difference between the genotypes (Figure 1, Table 1). With only a few exceptions, Wautoma and Vlaspik seeds showed uniform, 100-180 hook angle, as is typical of a germinating dicot seed. In contrast, PI308916 failed to exhibit a uniform hook. Angles were highly variable, ranging form 0-180, suggesting that poor seedling emergence may result from poor apical hook formation.

Analysis of F_1 and F_2 progeny of reciprocal crosses of PI308916 with cv. Wautoma indicate that the loss of apical hook formation is Inherited as a recessive, single gene trait (Table 2). Almost all F_1 seedlings showed angles of 100-180, and F_2 progeny separated 3:1 for

angles of 100-180 vs. random angle size. While it remains to be verified that the short internode and poor apical hook formation co-segregate, a pleiotropic effect of the *cp* gene on apical hook formation would explain the inability to genetically separate the compact plant habit from effects on seedling emergence.

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Table 1. Internode and vine length, germination rate, and apical hook formation for PI308916 and cultivar Wautoma.

	Internode length (node 4-5) cm ± S.E.	Vince length (at 6 weeks) cm ± S.E.	Time to 100% germination	Apical hook angle (at 5 days)	
				Mean angle (± S.E.)	Range
PI 308916	1.1±0.3 n=62	8.3+4.6 n=58	2 days	95+19.7 n=132	20-180
Wautoma	3.3±0.7 n=98	55.1±8.6 n=44	1 day	130±15.5 n=120	65-180

Data are pooled from two (vine length) or three (internode, apical hook) experiments. Seedlings were germinated in the growth room in the dark for five days, then transferred to soil in the greenhouse after apical hook measurement.

Table 2. Observed and expected ratios for apical hook angle of 5-day old seedlings for Wautoma, PI308916 and their F_1 and F_2 progeny.

Genotype	Observed		Expected ration[1]		Chi square
	0-100	101-180	0-94	95-180	
Wautoma (W)	7	113			
PI308916 (PI)	66	63			
F1 (W x PI, PI x W)	21	165	10	90	0.21 ns
F1 (W x PI)	7	97			0.90 ns
F1 (PI x W)	14	68			3.81 ns
F2 (W x PI, PI x W)	150	680	20	80	1.80 ns
F2 (W x PI)	68	341			2.70 ns
F2 (PI x W)	82	339			0.04 ns

The expected ratios for segregating populations in a single recessive gene model, were calculated based on hook angle distributions of the parental phenotypes where approximately 10% of W and 50% of PI have angles <100. In the F_2 generation, it is expected that 25% will resemble PI and 75% W. With a segregation ratio of 3:1, 10% of 75% (7.5%) and 50% of 25% (12.5%), or 20%, will have hook angles less than 100.

Figure 1. Apical hook formation for Wautoma and PI308916. Seedlings were germinated for five days in the dark on moist filter paper.

Heritability of Chilling Resistance in Seedlings Tested from Two Diverse Cucumber Populations

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Additional index words: *Cucumis sativus*, cold shock resistance, low-temperature tolerance, vegetable breeding

Cucumber (*Cucumis sativus*) is a major vegetable crop in North Carolina, with the second largest production of pickling cucumber, and the third largest production of slicing cucumber in the U.S. (United States Department of Agriculture, 2001). Spring and summer crops are grown, with the spring crops planted around 15 April (Schultheis, 2000). Early planting of cucumber is used by growers interested in extending the production season. Usually, cucumbers are seeded when soil temperatures are low. Often, there is a long period of time between seeding and emergence, and this length of time may result in differences in stand establishment and seedling size as a result of differences in genetic response to temperature. In addition, low temperature may injure or kill seedlings, causing partial or complete stand reduction.

The previously mentioned circumstances require both cold germination ability and chilling resistance. Combining low-temperature germination ability with cold tolerance at the seedling stage may extend the growing season by allowing earlier planting in the spring season. Previous studies indicated that sufficient genetic variability exists for low-temperature germination ability in a germplasm collection, and that progress could be made by selection based on families rather than on single plant selections as there was low or moderate heritability for the trait (Nienhuis and Lower 1981; Wehner 1982). Genetic differences in the ability of cucumber seeds to germinate at suboptimal conditions have been reported (Aoki et al., 1988, 1989; Cabrera et al., 1992; Liu et al., 1984; Saczynska et al., 1993). Also, a method for testing the chilling resistance of cucumber seedlings (Smeets and Wehner, 1997) has been developed and explored for measurement of the heritability of the trait.

Although some research has been done on the genetics of low temperature germination of cucumber seeds (Wehner, 1982; Wehner, 1984; Smith et al., 1978), there is only one report on the inheritance of chilling resistance of cucumber seedlings (Chung et al., 2003). This study found evidence of cytoplasmic inheritance for the trait. Cucumber cultivars with rapid and uniform emergence followed by uniform growth at low temperatures would be desirable to minimize germination problems and to establish uniform stands.

Thus, the objective of this study was to estimate the heritability of chilling resistance in cucumber seedlings using two populations of cucumber at the seedling stage using offspring-parent regression.

Methods: Two cucumber populations were used for the study, the North Carolina wide base pickle (NCWBP; Wehner 1997) and the North Carolina elite slicer 1 (NCES1; Wehner 1998). The two populations were chosen because they represented pickling (processing) and slicing (fresh market) types, and had a wide genetic base, and a narrow, elite genetic base

respectively, and good germination ability. For each population, 416 parental plants were tested for chilling, then each plant was transplanted to an isolation block for random mating. Of the 416 parental plants, more than 350 survived to seed harvest. From those, 256 offspring families from each of the NCWBP and NCES1 populations were evaluated for chilling and provided complete data, testing three plants per family. Experiments were conducted under controlled environment conditions in the growth chambers of the phytotron of the Southeastern Plant Environment Laboratory at North Carolina State University (Thomas et al., 2005). Seeds were sown in peat pots (57 mm square, 100 ml volume) filled with a standard substrate of gravel and peat in a 1:1 ratio and placed in flats. Three seeds were sown in each pot, and thinned to one plant just after emergence.

After seeding the families, the flats were placed in growth chambers set at 26/22°C (day/night) temperatures under long days, consisting of nine hours of combined fluorescent and incandescent light (from 8 AM to 5 PM) and three hours of incandescent light (from 11 PM to 2 AM). Light intensity (PPFD) was 650 and 44 mmol m^{-2} s^{-1} respectively. Plants were watered with the standard phytotron nutrient solution (Thomas et al., 2005).

After the plants reached the first true leaf stage, they were moved from the main growth chamber to the chilling chamber for treatment at 4°C under a light intensity of 500 mmol m^{-2} s^{-1} PPFD for a duration of 7 hr. After the chilling treatment, they were returned to the main growth chamber and placed under the same light regime as before. Plants were rated 5 days after chilling, reading both the cotyledons and the first true leaf. The scale was 0 = no damage, 1-2 = trace of damage, 3-4 = slight damage, 5-6 = moderate damage, 7-8 = advanced damage, 9 = plant dead. Plants from classes 0, 1 and 2 were considered resistant (R), those from classes 3, 4, 5 and 6 were considered moderate (M), and those from classes 7, 8, 9 were considered susceptible (S). Data were collected as means over all cotyledons and/or leaves on the three plants that constituted the plot.

Plants of the two populations were given chilling treatments in the phytotron in early April, rated for chilling damage in mid-April, then transplanted to isolation blocks in the field in late April. Plants were random-mated during the summer, and seeds harvested in early July.

The experiment was a split-plot treatment arrangement in a randomized complete block design with three replications. Each flat constituted of one replication and contained 18 progeny rows of three plants each. Data were analyzed using the procedure GLM in SAS. Range was calculated as best minus worst cultigen for each treatment. Range/LSD was used to determine which treatments provided the best separation of cultigens.

Offspring-parent regression was used to estimate narrow-sense heritability. Ratings were corrected for position in the phytotron chamber and log transformations were used to normalize the data. Progeny means were regressed on parent performance and the narrow-sense heritability estimated as twice the regression coefficient (Hallauer and Miranda, 1981).

Results: The mean chilling injury ratings in the parent plants for the two populations (NCWBP and NCES1) were similar for cotyledon and first true leaf stage (Table 1). The NCWBP appeared to be slightly more resistant than the NCES1 population (mean values 4.6 and 5.0, respectively). Values for the offspring for each population were higher than for the parents. That result is not unusual since offspring and parent generations were tested at different times

to meet the assumption of no genotype x environment covariance between the generations. Variability for cotyledon and first true leaf ratings was similar for the parents and offspring in the two populations.

Mean chilling injury in this study was similar to other studies of chilling injury in commercial cultivars of cucumber, where mean ratings were between 4.8 and 6.5 for resistant cultigens and 5.5 to 7.1 for susceptible ones (Smeets and Wehner 1997). The two populations were developed by crossing a large array of genotypes differing in resistance to chilling, so it is interesting that both populations were fairly tolerant to chilling.

The parent generation of the two populations had chilling injury ratings for individuals of 0.0 to 8.0 and the offspring generation ranged from 1.3 to 9.0 (family means) for cotyledon and first true leaf ratings in the two populations, indicating a wide range of responses to the treatment (Table 1). The standard deviation for parents was the same for the two populations. The standard deviation for the offspring was lower than for the parents as expected since offspring data represented families means rather than single plant values as for the parents. The offspring of NCWBP had a larger standard deviation than the offspring of NCES1, as expected from the fact that the NCWBP population had a wider genetic base than the NCES1 population.

Narrow-sense heritability estimated by the parent-offspring regression gave low values (Table 1). Heritability estimates for cotyledon ratings ranged from 0.09 for NCWBP to 0.12 for NCES1. Scaling the data improved the heritability estimates to 0.10 and 0.18, respectively. Transformation (log or arc sine) did not have much effect on the estimates. Most of the values for the first true leaf were negative, indicating heritability for chilling resistance in the two populations for that trait was near zero.

The heritability of low temperature stress has been studied more for low temperature germination ability than for chilling injury at a seedling stage. Heritability estimates differed with germination trait and temperature used in the studies. At lower temperatures, heritabilities were lower (Nienhuis and Lower, 1981; Wehner, 1981; Wehner, 1982) than at higher temperatures (Smith et al., 1978). It is evident that test conditions are important and can affect plant response during chilling.

Low heritability and a large effect of some environmental factors (Lyons, 1973; Lyons et al., 1979; Smeets and Wehner, 1997) indicates that chilling resistance may be controlled by several genes. Low heritability indicates that effective selection for improved resistance should be done using replicated progeny rows rather than single-plant hills. Also, it may be desirable to identify accessions that exhibit higher cold tolerance or resistance during all early stages of plant growth, including germination. Finally, it would be useful to screen the USDA cucumber germplasm collection for chilling resistance to identify accessions superior to current breeding materials such as the NCWBP and NCES1 populations.

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Table 1. General statistics and heritabilities for chilling resistance in cucumber seedlings from two populations.z

Statistic		Population NCWBP	NCES1
Performance (cotyledon, 5 days after chilling)			
N	Parents	416	416
	Offspring	256	256
Mean	Parents	4.6	5.0
	Offspring	6.1	6.7
SD	Parents	1.5	1.5
	Offspring	1.2	0.9
Low	Parents	0.0	0.0
	Offspring	1.4	3.0
High	Parents	8.0	8.0
	Offspring	8.0	9.0
h^2N	Not scaled - Actual	0.09	0.12
	Not scaled - Log transformed	0.07	0.06
	Not scaled - Arc sine transformed	0.09	0.11
	Not scaled - Location corrected	0.00	0.12
h^2N	Scaled - Actual	0.10	0.18
	Scaled - Log transformed	0.12	0.14
	Scaled - Arc sine transformed	0.11	0.18
Performance (first true leaf, 5 days after chilling)			
N	Parents	416	416
	Offspring	256	256
Mean	Parents	4.6	5.0
	Offspring	5.3	6.6
SD	Parents	1.5	1.5
	Offspring	1.3	0.9
Low	Parents	0.0	0.0
	Offspring	1.3	3.9
High	Parents	8.0	8.0
	Offspring	8.0	8.2
h^2N	Not scaled - Actual	-0.10	-0.09
	Not scaled - Log transformed	0.05	-0.04
	Not scaled - Arc sine transformed	-0.10	-0.10
	Not scaled - Location corrected	0.02	-0.01
h^2N	Scaled - Actual	-0.11	-0.21
	Scaled - Log transformed	-0.08	-0.18
	Scaled - Arc sine transformed	-0.11	-0.19

z Data are for plants rated 5 days after chilling at 4°C; plants were rated 0 to 9 (0=no damage, 9=plant killed).

Study of Natural Variation in Root Structure within *Cucumis melo* L. using in vitro culture.

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Natural variation in root systems is being exploited in many crops, such as maize (6), rice (5), lettuce (2), etc. In these cases, wild taxa have been useful sources of variation for root architecture, since their roots usually exploit more unpredictable and stressful soil environments than the cultivated taxa (4).

The species *C. melo* includes two subspecies, *melo* and *agrestis* (3). Most cultivated melons are included in the subspecies *melo*. The subspecies *agrestis* includes wild, semi-wild and weedy germplasm that can be used as the donor of valuable genes for breeding cultivated melons, as both taxa are fully interfertile. In previous studies performed in fields and greenhouses, we found that the accessions belonging to the two subspecies display different root structures (1). However, the study of root systems recovered from soil substrate is not an easy task. *In vitro* culture techniques facilitate *in vivo* studies of root development.

In this study we have used *in vitro* culture to evaluate the root development of three accessions, *C. melo* subsp. *melo* cv Piel de sapo (PS), which is the most cultivated type in Spain, *C. melo* subsp. *agrestis* PI 161375 (PI), both PS and PI being used as parents for the Spanish map of melon, and *C. melo* subsp. *agrestis* Pat 81, which has been reported as being resistant to *Monosporascus* root rot (1)

Fifteen seeds of the three accessions (PS, PI 161375, and Pat 81) were surface sterilized for 20 min in 50% bleach with Tween-20, and rinsed 3 times with sterile water. Tubes with standard MS medium (pH 5.7), including 30 g/l of sucrose, vitamins, and 200mg/l of cefotaxime, were prepared and used to sow the sterilized seeds. After growing in the dark for two days, the germinated seeds were transferred into transparent plates (23x19x1cm) filled with 300 ml of the same medium. The plates were grown in a growth chamber (25ºC, 16/8 h light/ dark). Once a day for 15 days a digital image was taken of each root with a scanner. The digital images were analyzed with the specific software for roots WinRhizo-Pro 2003b (Regent Instruments Inc. Canada). The evaluated traits were: the total root length (the sum of the lengths of all of the roots), L (cm); the root projected area, PA (cm^2); the average root diameter, D (mm); the length of the primary root (cm), the number of laterals emerging from the primary root, NL; and the root width (the maximum horizontal distance between the root tips of the furthest lateral roots), W (cm).

PS developed roots with greater projected area (PA) and greater total length (L) than PI 161375 or Pat 81 (Fig 1). However, a higher PA or L does not necessarily imply an enhanced capacity for soil exploration and water/nutrient absorption. Another parameter such as L/PA could provide more information seeing as it measures the root investment in exploring more soil volume. L/PA was higher in PI 161375 and Pat 81 than in PS (Fig1). This parameter was negatively correlated to the root diameter (D). PS developed thicker roots than PI 161375 and Pat 81 (Fig 1). Generally, the absorptive roots are those which are thinner and of a higher order than the structural roots. Therefore, our results indicate that the accessions of the subspecies

agrestis are more efficient at producing absorptive length per unit of projected area.

The number of lateral roots (NL) was highest in PS, followed by Pat 81 and PI (Fig. 1). In general, the number of lateral roots is restricted by the length of the primary root. In our study, PS showed a higher density of lateral roots (4.8 lateral roots/cm of primary root at 15 days after sowing) in comparison with Pat 81 or PI (3.8 roots/cm and 2.0 roots/cm respectively). In PS the third order laterals appear quickly (at 4-5 days after sowing) and continuously. On the contrary, the few laterals of Pat 81 and PI 161375 do not branch till the 8th day after sowing on average, and the tertiary roots appear scattered on the secondary laterals. This *in vitro* culture assay also provided the opportunity of following the spatial distribution of the roots in the medium. The lateral roots of PS grew more horizontally (W of 14 cm), while Pat 81 and PI tended to grow more vertically (W of 8.5 and 6.8 cm respectively). Our results indicate that these wild accessions have priority in penetrating the soil with the minimum carbon investment (few and thin roots), while PS used a larger resource input to explore the topsoil layer rapidly.

Additionally, when we studied the root systems of these accessions in adult plants grown in different soil environments, we observed a higher length and branching level (number of laterals and root orders) in the wild taxa in comparison with PS (1). This discrepancy seems to suggest that wild taxa save resources in less stressful conditions, such as the *in vitro* culture in an artificial medium. However, they have a higher plasticity and can react dramatically by modifying their root architecture in stressful soil environments (6).

The methodology used has allowed the study of the main differences between the root systems of cultivated melons *vs* wild melons. Further studies could help to select accessions for their improved root systems according to our needs.

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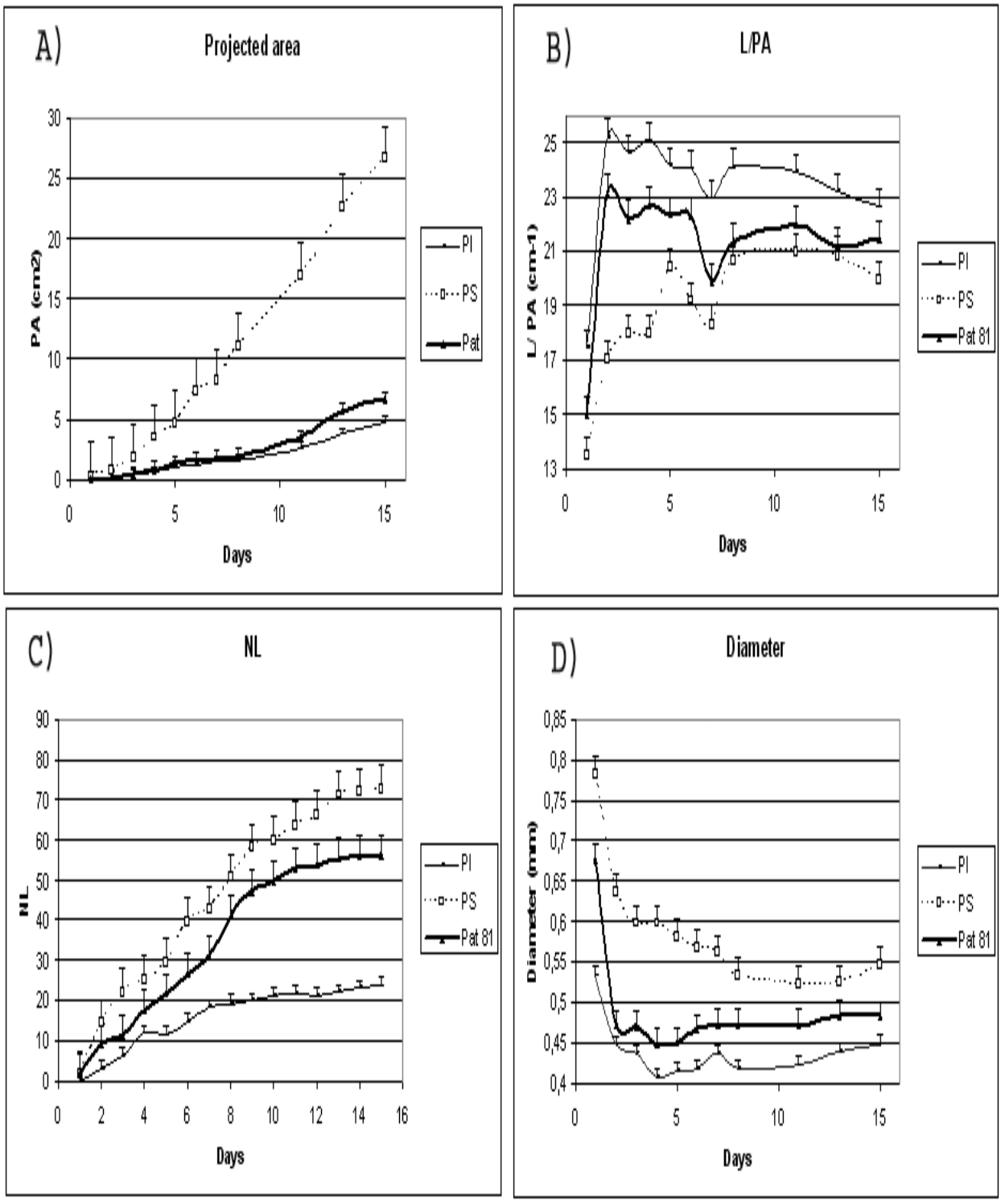
Figure 1. Evolution of the different parameters measured in the roots of *C. melo* subsp. *Melo* cv Piel de sapo (PS), *C. melo* subsp. *Agrestis* Pat 81, and *C. melo* subsp. *agrestis* PI 161375 during 15 days after sowing (DAS). A) Root projected area (PA, cm^2), B) root length per unit of projected area (L/PA) (cm^{-1}), C) number of laterals derived from the primary root (NL), D) average diameter of the root (D, mm).



Evaluation of non-preference of melon plants by *B. tabaci*

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The sweetpotato whitefly, *Bemisia tabaci* (Gennadius), is one of the most important pests affecting melon crops in the Mediterranean basin (Boubourakas et al. 2006) and other melon growing areas (Chu et al, 2007). Infestation levels greater than 2,6 larvae per 10 cm^2 have been reported to be responsible for 30% yield losses in melon (Riley and Palumbo, 1996); *B. tabaci* is also a vector for important viruses like CYSDV (*Cucurbit Yellow Stunting Disorder Virus*) or CVYV (*Cucurbit Vein Yellowing Virus*). Although tolerant accessions to this pest have been described, there are not breeding programs established, probably due to the lack of knowledge of the resistance genetics, the difficult management of whiteflies in a laboratory and the non-existence of an efficient selection method for resistance. We report the attempts to adapt and to examine the feasibility of the method described and tested with aphids by Martin and Fereres (2003) to evaluate resistance to *B. tabaci*.

Materials and Methods: To evaluate the preference or non-preference of different melon genotypes by *B. tabaci*, an adapted free-choice assay following Martin and Fereres (2003) has been carried out. The melon genotypes tested were 'TGR-1551', 'PI-161375', 'PI-414723', 'Nagata kin Makuwa', 'Doublon', 'Ananas', 'AR5' and 'Hale's best Jumbo'. The Spanish cultivar 'Bola de Oro' was used as whitefly susceptible control. Plants used in all the experiments were at 8-10 true leaf stage. Four leaf disks (2 cm diam.) of the second and third leaf from apex of each genotype together with four leaf disks of 'Bola de Oro' were alternately placed in Petri plates of 14 cm diam. The bottoms of each plate were covered with a layer of moistened filter paper and, over it, a layer Parafilm "M" (Pechiney, Chicago, IL. 60631) in order to avoid whitefly sticking. Eight Petri dishes (replications) by genotype were used and 3 Petri dishes were used as control using the combination 'Bola de Oro' vs 'Bola de Oro'. Fifty whiteflies were introduced into each Petri dish through an upper lid hole (0,5 cm diameter) using a Falcon tube. Petri dishes were then covered by black cloth (Thome et al., 1996) to avoid any phototropism effect (Blackmer and Byrne, 1993) and placed in climatic chamber at 25 ºC. Whiteflies settled on each leaf disk were counted at 15 min, 30 min, 1 h, 1.5 h, 3 h and 6 h after the whiteflies were released inside Petri dishes.

Synchronized whiteflies of "Q" biotype (48 h old) reared on whitefly susceptible melon plants were used in all the experiments.

The whole number of whiteflies settled on leaf disks at each time was statistically analyzed by a binomial statistic test in order to estimate preference for one genotype. All statistical tests were performed using the SPSS for windows v.14.0.1 (SPSS for Windows, Rel. 11.0.1. 2001. Chicago: SPSS Inc).

Results and Discussion: The percentage of whiteflies settled on each genotype based on the total whiteflies settled on leaf disks at different observation times is shown in Table 1.

A clear preference of *B. tabaci* towards 'Bola de

Oro' leaf disks was observed when this cultivar was evaluated together with 'PI-414723'. This preference was maintained until the end of the experiment.

When 'TGR-1551' was the tested genotype, differences in the whitefly preference were observed at 30 min, these differences increased and were maintained until 3 hours after the experiment began.

Whiteflies did not show differences between 'Bola de Oro' and most of the tested genotypes: 'Ananas', 'Hale's best Jumbo', 'Nagata Kin Makuwa', 'PI-161375', 'AR-5' and 'Doublon'. However, some differences in whitefly preference were punctually observed for 'Hale's best Jumbo' (3 h), 'Nagata Kin Makuwa' (1.5 h) and AR-5 (3 h) (Table 1).

'PI-414723' leaf disks were rejected in a short time, 15 min after the experiment began, which could indicate the existence of antixenotic mechanisms additional to the antibiotic mechanisms described by Sauvion et al. (2005). *B. tabaci* also showed preference towards 'Bola de Oro' leaf disks when 'TGR-1551' was the alternative, which may confirm the existence of antixenotic mechanisms as described by Soria et al. (1999). In both cases, these results at such early times may indicate the existence of constitutive antixenotic effects on the leaf surface.

'PI-161375' was tested by Boissot et al (2003) in field conditions, showing a low level of adult whitefly presence on leaves. However, in the free-choice test we carried out, whiteflies could not differentiate between 'Bola de Oro' and 'PI-161375'.

This bio-assay has allowed the evaluation of *B. tabaci* preference for several genotypes in a short time and small space. However, unknown factors could be involved in the behaviour of the whitefly in punctual observations in some susceptible genotypes. This method should be contrasted with other laboratory preference tests in order to evaluate its efficiency. Probably, this method could only differentiate strong differences in whitefly preference.

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Table 1. Percentage of whiteflies settled on leaf disks of each tested genotype over the total of settled whiteflies

Genotype vs 'Bola de Oro'	**Time after releasing**					
	15 min	**30 min**	**1 h**	**1,5 h**	**3 h**	**6 h**
TGR	42.65	40.86*	38.50**	34.43**	34.80**	44.44
AR5	55.13	47.62	48.31	48.30	41.04*	45.63
Ananas	53.03	54.26	47.20	45.54	50.41	51.66
Nagata Kin Makuwa	41.09	47.37	42.26	39.43*	47.39	46.80
Doublon	44.36	48.47	48.78	49.11	50.58	49.38
PI-161375	45.68	52.80	51.13	49.40	50.93	51.02
PI-414723	28.57*	30.67**	32.63**	32.50**	27.84**	29.88**
Hale's best Jumbo	56.48	48.25	45.03	43.35	42.71*	45.56
BO	55.73	52.36	50.90	52.62	52.29	51.84

* Signiticant deviation ($P<0.05$) using Binomial test at 0.5 probability

** Significant deviation ($P<0.001$) using Binomial test at 0.5 probability

High density of Type I trichomes related to tolerance to *Aphis gossypii* in primitive melon accessions

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Aphis gossypii Glover causes considerable direct and indirect damages to many crops and is considered a serious pest in melon, *Cucumis melo* L. Growing resistant or tolerant genotypes is the most effective and environmentally safe control strategy. The presence of glandular trichomes, because of the substances they produce and store, has been related to the rejection of plants as hosts by insects and spider-mites in several plant species (9, 10, 11). The presence of glandular trichomes in melons was first described by Gómez-Guillamón et al. (2006) according to the classification made by Kolb and Müller (2004) and the relation of Type I glandular trichomes to non-preference of plants by *A. gossypii* is under study.

In this work, the density of glandular trichomes (Type I) and the tolerance against Type I trichomes were counted on the second leaf from the plant apex in the area circumscribed to secondary veins. Two leaf disks (27 mm^2 area) per plant were immersed in absolute ethanol and heated to 80 ºC for three minutes. Then, samples were stained by their immersion in a 0.05 % toluidine blue O solution during 5 min (7).
A. gossypii infestation have been evaluated in several melon genotypes: four of them carried the gene *Vat*, three were aphid susceptible, and the behavior against *A. gossypii* of two more accessions was unknown (Table 1). The relationship between this trait and the tolerance against *A. gossypii* is discussed.

Aphid tolerance was tested in all genotypes. Twenty plants per genotype were infested with 10 aphids per plant, following Ivanoff (1945). Aphids were reared on plants of 'ANC-57'(Spanish melon accession) and adult aphids recently emerged were used in the experiments. Plants and aphid colonies were maintained in a growth chamber at 25ºC (day) and 20ºC (night) with a 16:8 hours (L:D) photoperiod.

Trichome density numbers were log-transformed before the statistical analyses that were made through one-way ANOVA ($P < 0.05$) and post hoc comparisons were done by Tukey b test.

A high density of glandular trichomes was found in the wild accessions carrying the *Vat* gene ('TGR-1551', 'PI 414723', and 'PI 161375') while a significantly lower density was observed in the three aphid susceptible accessions (Table 1); therefore the high density of these trichomes seems to be related to tolerance against *A. gossypii*. The results for genotypes 'Nagata kin Makuwa' and 'Ananas', whose response against *A. gossypii* was unknown supported this relationship; 'Nagata kin Makuwa' showed resistance to aphids and also had a high density of Type I trichomes; 'Ananas', with a low density of these trichomes, showed an aphid susceptible response (Table 1). Thus, the high density of Type I trichomes could be used as a morphological marker to select for aphid resistance when screening melon landraces or primitive accessions. 'AR 5', showed a glandular trichomes density similar to that observed in susceptible genotypes in spite of its tolerance to *A. gossypii*. Since this genotype is a bred line, we could assume that a

high density of glandular trichomes could be related to undesirable melon characters lost in the breeding program. The evaluation of the effect of these trichomes and related substances in the host selection by aphids should be encouraged, since this character could be an additional resistance factor in the aphid tolerance controlled by the *Vat* gene, and they should be taken into account in melon breeding.

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Table 1. Evaluation of melon genotypes for aphid infestation and glandular trichomes (Type I) density.

Genotype	Behavior against *A. gossypii*		Type I trichomes · cm^{-2} (mean ± SE)	Plants showing curled leaves (%)
'Nagata kin Makuwa'	U	-	320 a[z] ± 65	0
PI 161375	R	Pitrat and Lecoq, 1980	318 a ± 40	0
TGR-1551	R	Garzo et al., 2002	263 ab ± 44	0
PI 414723	R	Bohn et al., 1972	216 b ± 75	0
'AR 5'	R	McCreight et al., 1984	90 c ± 33	0
'Hale's Best Jumbo'	S	McCreight et al., 1984	69 cd ± 16	100
'Doublon'	S	Pitrat and Lecoq, 1980	61 cde ± 15	100
'Bola de Oro'	S	Soria et al., 2000	43 de ± 13	100
'Ananas'	U	-	41 e ± 20	100

U: unknown; R: resistant; S: susceptible; [z]significant differences through Tukey b test.

New Source of Resistance in *Cucumis melo*

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In spring-summer 2007 some new wild *Cucumis* accessions coming from Cabo Verde were sown in a greenhouse in order to regenerate and classify them.

Material and Methods: Accessions were cultivated in sandy soil with drip irrigation during the period April-July of 2007. Data related to plant habit, leaf and fruit characteristics were recorded.

Results and Conclusions: The accession from Cabo Verde, C-835 (registration number at the EELM germplasm collection), was classified as *C. africanus* Lindl attending Kirkbride (1993). Plants were of low vigour, with leaves 5-palmately lobed, 12-13 cm long and 9-10 cm wide. Fruits were small, 8 cm long and 3 cm wide, cylindrical shaped, fruit skin was mainly white color, with longitudinal purplish brown stripes; fruits had aculei of 0,4 cm long. Flowers of this accession were found to be very aromatic.

The accession C-836 was classified as *C. melo* subsp. *agrestis* (Naudin) Pangalo based on the character of pubescence type on the female-flower hypantium (Kirkbride, 1993). Plants were vigorous, monoecious, with shallowly ovate leaves of 10-12 cm long and 7-8 cm wide. Fruits were very small, 4-5 cm long and 3-4 cm wide, smooth skinned, green coloured with dark green longitudinal stripes (Picture 1).

During the season, observations under natural infestation conditions were also recorded. C-836 showed scarce presence of *Bemisia tabaci* in spite of the high whitefly population observed in the greenhouse. This accession was also tested for tolerance to *A. gossypii* in the laboratory, following the methodology described by Ivanoff (1945). Experiments were carried out in climatic chamber at 25 ºC (light) and 20 ºC (dark) and 16:8 h (L:D) photoperiod.

Each plant of fifteen was infested with 10 recently emerged aphids at the emerging first true leaf stage. No curled leaves were observed seven days after infestation, so the accession was considered aphid tolerant. Non-choice tests are in progress to evaluate its possible resistance against whitefly.

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Picture 1. Fruit of C-836 accession

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

New Plant Variety Protection (PVP) Forms for Pumpkin/Squash/Gourd

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The Plant Variety Protection Office administers the Plant Variety Protection Act by issuing Certificates of Protection in a timely manner. The Act provides legal intellectual property rights protection to developers of new varieties of plants which are sexually reproduced (by seed) or tuber-propagated. Proof of the distinctness, uniformity, and stability of the new variety lies with the owner and is required for obtaining a PVP certificate.

The Plant Variety Protection Office provides upon request application forms for protection of a plant variety with instructions on how to file applications. A PVP application consists of a completed and signed Form S&T-470 accompanied by a number of "exhibits", among which is Exhibit C, Objective Description of the variety. The goal of this exhibit is to allow the owner to describe how the new variety differs from all other known varieties of the crop, to indicate which group of varieties or market type the variety is most closely related, and to indicate the single variety that the owner believes is the one most similar to the new variety and describe how the new variety differs from it.

The Objective Description of Variety form (Exhibit C) for Pumpkin/Squash/Gourd (*Cucurbita* spp.) has not been substantially updated since the 1970s. The authors found that this form was inadequate to achieve the goal of this exhibit. We gathered at the George Washington Carver Center in Beltsville, MD in late February 2007, as a team effort of the PVP Office, industry, and public research toward devising a new, readily applicable and practical form.

All of us agreed that the characteristics listed on the form should be clearly defined, quickly and readily distinguishable or measurable, and expressed over a wide range of environments. Measurements of length or width of various plant parts are subject to wide variation due to irrigation, fertilization, and other factors, however relative measurements, for example length-to-width ratio, are much less so. The old Exhibit C form calls for measurements of cotyledons, petioles, laminae, fruits, peduncles, and seeds. The new form constituting exhibit C calls instead for ratios of length-to-width of these plant parts.

Moreover, the old form contains a number of characteristics, such as leaf pubescence, that differentiate *Cucurbita* species rather than varieties (cultivars) within a species and hence are not useful for distinguishing a new cultivar within its particular species. This, together with the overwhelming economic importance and intensive breeding of *Cucurbita pepo* as opposed to other *Cucurbita* spp. and other gourd taxa, led us to the conclusion that there should be two separate forms for Pumpkin/Squash/Gourd, one for *C. pepo* and one for all of the other species of *Cucurbita* and other taxa generally referred to as gourds, such as *Lagenaria* and *Luffa*.

On the *Cucurbita pepo* form, the first descriptor of the new variety is fruit shape, a familiar polygenic characteristic which has been used to establish edible-fruited variety groups (1), thereby focusing and facilitating the assessment of distinctness of the new variety; this basic descriptor is supplemented with an illustration.

On the other form, the first descriptor of the new variety is the full species name with botanical authority, again focusing and facilitating assessment of distinctness.

Photographic evidence of the distinctness of the new cultivar is also encouraged.

The two new forms constituting Exhibit C, one for *Cucurbita pepo* and one for all of the other species of *Cucurbita* and other taxa generally referred to as gourds, such as *Lagenaria* and *Luffa*, are appended below.

To obtain a PVP application by mail, please send an inquiry to:

Plant Variety Protection Office
National Agricultural Library, Room 401
10301 Baltimore Boulevard
Beltsville, MD 20705-2351
or phone: 301-504-5518, fax: 301-504-5291, or
e-Mail: pvpomail@usda.gov
Web site:
http://www.ams.usda.gov/science/pvpo/apply.htm#proof

Acknowledgements: We thank Ted Superak of Harris Moran Seed Co., Davis, Calif., for his comments.

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Comparison of Some Flower Characteristics of *Cucurbita pepo* Accessions

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It is well-known that *Cucurbita pepo* L. is extremely diverse in fruit characteristics. This diversity has been depicted and described in many publications and cultivar-groups have been categorized on the basis of fruit shape (1). In addition to the extreme diversity in fruit size, shape, and color, there is also a great diversity in seed size and relative dimensions (2), in vegetative characteristics and in characteristics of the flowers (4).

Squash flowers have been a culinary item for centuries (3), albeit far less important than the fruits. As part of a preliminary experiment to compare cultivars for suitability for the production and marketing of the flowers, we observed a number of characteristics of the flowers that appear to be relevant: number produced per plant of each, male and female, corolla length and corolla texture.

Seeds were obtained from various commercial outlets and herein are presented the results obtained from 21 accessions. Seeds were sown in flats in a commercial nursery and seedlings were transplanted on 14 April 2004 to the field at the Besor Experiment Station (southwestern Israel). Cultural conditions were as recommended for the season and location and included drip irrigation and fertilization, with a plant population of 15 per $10m^2$. Six plants of each cultivar were observed and flowering began on 15 May. Flowers were picked and counted every other day. On 02 June, corolla length was measured from the base of the corolla to the tip and a tactile evaluation of texture was conducted. The experiment was concluded after approximately five weeks, on 19 June.

The results in Table 1 indicate that large differences occurred among the accessions for number of flowers produced over the period of the experiment. The straightneck, crookneck, and scallop cultivars (all *C. pepo* subsp. *texana*) produced the most flowers, with the one pumpkin tested, one vegetable marrow and one cocozelle not far behind. Plant sexuality also differed greatly, ranging from accessions producing mostly male flowers and to others producing mostly female flowers.

The accessions also differed greatly in the length of the corolla. Generally, the accessions of subspecies *texana* (Acorn, Scallop, Straightneck, and Crookneck Groups) produced smaller corollas than those of subsp. *pepo* (Pumpkin, Vegetable Marrow, Cocozelle, and Zucchini Groups) (Table 1). Furthermore, the flowers, both male and female, of the subsp. *texana* accessions were softer, noticeably less firm than those of the subsp. *pepo* accessions. Nonetheless, great variability was found for these traits within subsp. *pepo*, especially within

the Cocozelle Group. Overall, in this observation plot, corolla length of male flowers was larger than that of female flowers.

The results indicate that a number of cocozelle and zucchini cultivars produce large, firm flowers, which should be well-adapted for culinary use. These cultivars are not as prolific producers of flowers as the subsp. *texana* cultivars that we observed. A replicated trial employing a wider representation of accessions is needed in order to determine if the differences that we observed among subspecies and groups is a general phenomenon.

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Table 1. Number of flowers produced and corolla length and texture of 21 accessions of *Cucurbita pepo*, Besor Experiment Station, southern Israel.

Accession	Group (ovary shape)	No. flowers			Corolla length (cm)		Corolla texture[z]	
		Male	Female	Total	Male	Female	Male	Female
Taybelle	Acorn	16.8	19.3	36.1	10.5	8.0	1.0	1.0
Jersey Golden Acorn	Acorn	16.0	13.2	29.2	8.8	8.0	1.0	1.0
Sunburst	Scallop	24.3	31.6	55.9	10.8	9.5	1.0	1.0
Early Prolific Straightneck	Straightneck	39.9	26.4	66.3	10.5	8.0	1.0	1.0
Ranger	Crookneck	23.4	34.4	57.8	10.3	9.0	1.0	1.0
Ronde de Nice	Pumpkin	31.5	23.0	54.5	12.8	11.5	1.5	2.0
Blanche non-coureuse	Veg. marr.	7.0	20.6	27.6	12.8	11.0	2.0	2.0
PI 288241	Veg. marr.	35.0	15.4	50.4	14.0	10.0	2.0	2.5
Romanesco	Cocozelle	5.7	20.4	26.1	16.5	8.8	2.5	2.5
Lungo Fiorentino	Cocozelle	38.8	10.7	49.5	13.3	9.5	1.5	1.5
Non-coureuse d'Italie	Cocozelle	15.1	17.8	32.9	12.3	9.3	2.0	2.0
Arlika	Cocozelle	11.3	19.8	31.1	13.0	9.5	2.0	1.8
Striato d'Italia	Cocozelle	19.6	8.2	27.8	11.8	8.5	2.2	2.0
PI 177370	Cocozelle	23.4	7.4	30.8	12.8	11.5	2.5	2.5
Gladio	Cocozelle	--[y]	--[y]	--[y]	14.8	13.8	2.5	2.5
Italiano Largo	Cocozelle	--[y]	--[y]	--[y]	15.8	12.5	2.5	2.5
Goldy	Zucchini	19.3	15.9	35.2	9.5	9.3	1.5	2.2
Nano Verde di Milano	Zucchini	15.7	10.8	26.5	10.8	10.3	2.2	2.5
Fordhook Zucchini	Zucchini	18.8	9.8	28.6	10.5	10.0	2.2	2.3
Raven	Zucchini	13.9	20.1	34.0	11.8	10.3	2.0	2.0
Mikonos	Zucchini	24.1	19.1	43.2	12.8	11.2	2.5	2.5
RSQ7049	Zucchini	8.9	17.3	26.2	11.3	9.0	2.5	2.5
Noche	Zucchini	13.2	31.2	34.4	12.3	10.3	3.0	2.5

[z]Scale of 1=soft, 2=fairly firm, 3=firm

[y]Flowers not counted

Extrafloral Nectaries in *Cucurbita maxima* Sub. *andreana* (Naudin) Filov

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Introduction: Nectaries, from a functional point of view, are easily defined as plant secreting structures that produce nectar (6). They can be situated in vegetative (extrafloral nectaries) or reproductive organs (floral nectaries), and may have different morphologies and anatomical origins (1). Extrafloral nectaries (*efns* hereafter) are usually small protuberances, which may be covered by protecting non secretory hairs (2, 11). Regardless of their position or origin, the function is to reward animals that provide the mobility that plants lack, that is: vector for pollen dispersal and physical defense (8). Structural nectaries were distinguished from non structural ones, (i.e. without any special differentiated nectariferous tissue) (12), which are more frequent among *efns* (1). Some *efns* are also devoid of vascularization and lack the anatomical organization typical of nectaries, while the most frequent vascular bundles may consist of phloem and xylem or phloem only (1). A continuous thick cuticle covers the epidermal cells of *efns* and nectar release generally takes place through cuticle rupture.

Based on ecological and morphological evidence (4, 5 and 9) and on mitochondrial gene single-base substitutions (10), *Cucurbita maxima* subsp. *andreana* has been recognized as the wild (agrestis) form of domesticated *C. maxima* Duch. However suggestions have been presented to maintain the wild taxon at the specific level, supported by the fact that *efns*, which are present in the abaxial side of leaves of domesticated forms of *Cucurbita*, were absent in subsp. *andreana*; and this overlooked feature should have taxonomic and evolutionary importance (3). These findings were based on herbaria specimens collected in the Córdoba province of Argentina. Due to the viny and vigorous growing habit of subsp *andreana*, it is probably that each exsiccatum was taken from only one or few plants in each provenance. In order to confirm Hunziker and Subilis (3) findings we extended the study to accessions from all the provinces reported by these authors to conform the natural distribution area (Buenos Aires, Entre Ríos, Santa Fe, Córdoba and San Luis), plus Santiago del Estero province; and considered at least five living plants from each provenance.

Materials and Methods: Twelve accessions of *C. maxima* subsp. *andreana* and two cultivated forms of *C. maxima* subsp. *maxima* were grown for assessing the presence or absence of *efns* (Table 1). Plants were seed planted in the spring of 2005 at the Experimental Field of the Agronomy Faculty, Rosario´s National University, located at Zavalla (33º 01' S; 60º 53' W), Santa Fe. The plantation grid was of 1.4 m and 0.8 m between rows and hills in the row respectively. Each accession was set in a non-replicated single row plot of eight hills. After emergence each hill was thinned to two plants. Due to a severe wind storm right after emergence, some plants were cut-off, leaving many plots with less than the optimal sixteen plants. During plant growth leaves were cut (between the fifth and the tenth node), and observed under stereomicroscope in order to determine the presence or absence of *efns*. Each plant was assessed in at least three leaves. In the accessions where *efns* were present, samples were collected, fixed in FAA, conserved in ethanol 70, and further dehydrated in an ethanol series and embebbed in Tecnovit 7100 (Heraeus

Kulzer GmbH). Semi-thin sections (0.5-1µm) were obtained using glass knives and stained with toluidine blue as general stain (7).

Results and Discussion: Ten out of the 12 surveyed accessions of *C. maxima* subsp *andreana* presented plants showing *efns* (Table 1). The two accessions where *efns* were completely absent in all assessed plants were from Córdoba and Santa Fe provinces. The two accessions from Santiago del Estero showed *efns* in all plants. The rest of the provenances of subsp *andreana* presented both plants showing and not showing *efns*. As expected, all the plants of the two cultivated accessions presented *efns.* Moreover, during the 2006 season, the search for *efns* was extended to a set of 72 domesticated *C. maxima* accessions (six plants per entry, data not shown), and the glands were present in all instances.

Morphologically, *efns* were observed as small protuberances with a columnar body and a head with a secreting surface (Figure 1). They showed a great variation in size (from 0.4 to 1 mm in length), and were more or less conical or cylindrical; those growing on higher order veins were more or less flattened. The column of long nectaries was covered by hairs, while shorter ones were deprived. This feature (hairy nectaries column) was not depicted by (3) in the cultivated forms of *Cucurbita*. In relation to the anatomical organization, sectioned material also showed a wide variation in size and complexity. The main structure was: in the column, complete vascular bundles with phloem and xilem, cells hold big vacuoles and were photosynthetic, the head contains the secretory tissue, typically constituted of medium sized cells with large nuclei. There is an evident layer of one or two cells dividing the column and the head, where the cell walls and maybe the intercellular space take the coloration of the non living cells of the xylem. No stomata, neither homologous way for nectar release were found. We propose that the mechanism should be holocrine secretion as expected for this kind of nectaries. No insect were observed visiting the *efns* when leaves were surveyed for their presence.

It is evident that the presence of *efns* is a feature of the domesticated forms of *C. maxima*, but not necessarily of the wild ancestral subsp. *andreana*. Some provenances completely lack these glands, while others (especially those from Santiago del Estero), showed, as the cultivated forms, *efns* in all surveyed plants. Two possibilities can explain their presence in cultivated forms, one is that domestication was conducted from populations not segregating for their presence; or, that the attribute of showing *efns* in originally domesticated *C. maxima* was fixed by chance. Inferred from the low percentage of plants with *efns* in some provinces, apparently, their presence is not an ecological important attribute for the survival of subsp. *andreana* in the actual area of distribution, and may be a relic structure from a primitive ancestor. Moreover, in comparison with the great amount of allocations devoted to vegetative and reproductive organs, the reduced resources that these glands involve does not seem to confer a disadvantage.

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Table 1. Number of plants with extrafloral nectaries by accession, and percentage of presence by provenance.

Accesion	Subspecies	Provenance[a]	Source [b]	Number of plants		Presence % by Provenance
				Presence	Absence	
UNR-132	*andreana*	Córdoba	UNR	0	15	
UNR-134	" "	Córdoba	UNR	2	3	12
UNR-133	" "	Córdoba	UNR	1	6	
UNR-138	" "	Santa Fe	UNR	0	13	
UNR-135	" "	Santa Fe	UNR	3	4	15
MAX-81	" "	Entre Ríos	IPK	3	2	60
UNR-141	" "	Santiago del Estero	UNR	11	0	
UNR-140	" "	Santiago del Estero	UNR	5	0	100
UNR-137	" "	San Luis	UNR	3	3	
MAX-66	" "	San Luis	IPK	4	1	64
UNR-139	" "	Buenos Aires	UNR	10	3	
PI 458659	" "	Buenos Aires	NE-9	1	6	55
PI 244702	*maxima*	Brasil	NE-9	6	0	
Zapallito	" "	Argentina	Ferry Morse	8	0	100

[a] For subsp *andrean*a Argentinian provinces as provenances are considered, otherwise country of origin is detailed.

[b] UNR, Rosario´s National University; IPK, Leibniz-Institute of Plant Genetics and Crop Plant Research, Germany ; NE-9, USDA-ARS, Northeast Regional PI Station, Cornell University, Geneva, USA; Ferry Morse Seed Company.

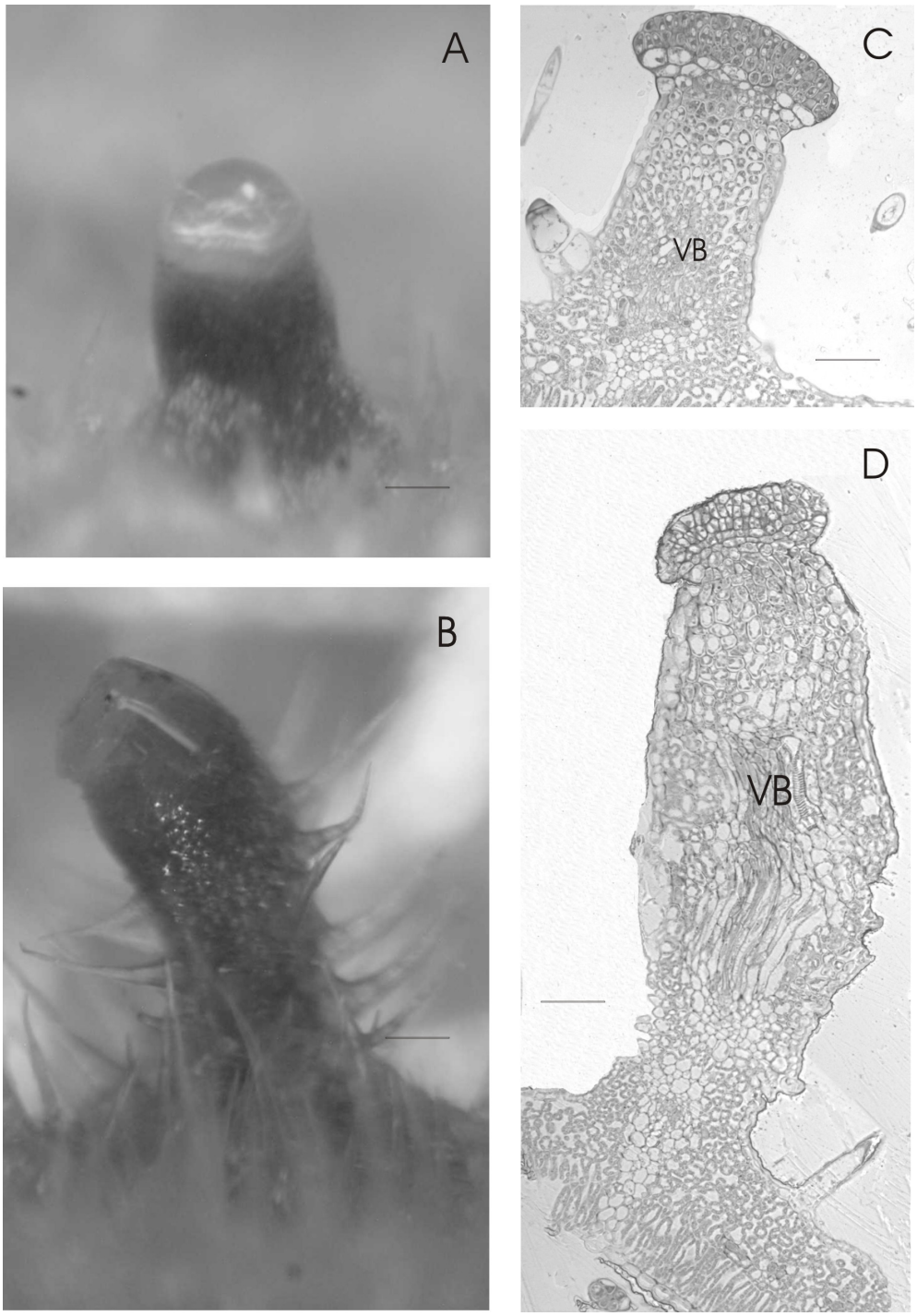

Figure 1. Extrafloral nectaries in *C. maxima* subsp. *andreana*. Bars = 100 µm. (A) Stereomicroscope photograph showing a short nectary with a secreted droplet visible on the head. (B) Stereomicroscope photograph showing a long hairy nectary, the secreted droplet is poured along the column. (C) and (D) Longitudinal sections showing the secreting head and column. In the column a vascular bundle is evident (VB), photosynthetic cells holding big vacuoles are present. The head contains the secretory tissue, typically constituted of medium sized cells with large nuclei.

Viable Seed Production of Temperate *Cucurbita moschata* Germplasm When Pollinated by *C. argyrosperma*.

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Cucurbita moschata Duchesne and *C. argyrosperma* Huber are closely related squash species and are known to be partially inter-fertile. These species commonly produce viable hybrid seed when *C. argyrosperma* is the maternal parent. This cross has been manually made via hand pollination by several researchers (3,4,9,10). A natural pollination experiment also showed that *C. argyrosperma* could set a high percent of fruit and viable seed in a field with only *C. moschata* as a pollen source (7). Gene flow between the species has also been demonstrated using isozyme and DNA techniques (1,2,5). Viable seed production with *C. moschata* as a maternal parent has very rarely been produced using tropical *C. moschata* germplasm (Wessel-Bever pers comm.). It is thought that the majority of *C. moschata* cytoplasm is incompatible with *C. argyropserma* nuclear genes (8). Embryo rescue techniques have also been used to produce viable F1 hybrids with *C. moschata* as the maternal parent (6). Here reported is the apparently easy production of viable seed by a temperate *C. moschata* variety when pollinated by *C. argyropserma*.

In January 2008, seed of *C. moschata* 'Butterbush' and *C. argyrosperma* 'Green Striped Cushaw' were planted in the pollinator free University of Connecticut Ecology and Evolutionary Biology department greenhouse. No other *C. moschata* cultivars were planted at this time in the greenhouse. The intent was to pollinated 'Green Striped Cushaw' with pollen from 'Butterbush' to begin a breeding project to create a bush cushaw type with higher beta carotene content for use by the urban Latino community in the northeastern U.S. The sequence of flowers initially did not allow for the intended cross but the reciprocal did present itself, though the literature did not support the chances of viable seed production. The 'Butterbush' was pollinated with the 'Green Striped Cushaw' on April 6, 2008. Two flowers were pollinated one in full anthesis and one bud pollinated the day before complete maturation. Both fruits set and developed normally. The lack of pollinators and other *C. moschata* cultivars eliminate the possibility of these fruits and the subsequent seeds being a product of an accidental self or cross. Later in May the 'Green Striped Cushaw' did eventually produce a female flower and was pollinated with 'Butterbush'. The fruits were harvested approximately 70 days after pollination. Surprisingly the 'Butterbush' seeds appeared mostly developed and viable. The fruit produced from bud pollination contained 88 seeds of which 55 appeared viable. The normally pollinated fruit contained 80 seed with 43 apparently viable. In July the 'Green Striped Cushaw' fruit was harvested and it had three very plump viable seeds and over 100 empty seed coats. Eight seeds from each 'Butterbush' fruit were planted, 5 germinated from the bud pollination, and 6 from the normal pollination. All three seeds from the 'Green Striped Cushaw' fruit germinated. The F1's produced with *C. moschata* as the maternal were immediately recognizable as hybrids, with cotyledons that were approximately twice as long as pure 'Butterbush' seedlings, the plants at fruiting have vines approximately 8ft long with

silver streaked leaves also indication *C. argyrosperma* parentage. When the F1's flowered they were sibbed or selfed. The male flowers produced abundant pollen and the hand pollinations have produced fruit but are not yet mature. These fruit are green striped and at approximately 10 pounds are about two to three times larger then typical 'Butterbush' fruits. These F1's have also been backcrossed to *C. argyrosperma* and have produced fruit.

Hybridization of these two species with *C. moschata* as the maternal parent may be useful in two ways: 1) increasing the chances of making F1 hybrids between the species in breeding programs and 2) introducing novel cytoplasmic genes into *C. argyrosperma* which could have an agronomic benefit. Additionally this cross may give us insight into biological isolation barriers between the species. The negative interaction between the tropical *C. moschata* cytoplasm and the *C. argyrosperma* nuclear genes may be an effective mechanism that allows C. *moschata* to remain distinct where the two species are commonly interplanted. *Vice versa* the acceptance of temperate *C. moschata* germplasm of *C. argyrosperma* pollen may represent a barrier breakdown in plants that have not generally been interplanted with the other species perhaps for generations. Additional investigation is needed to determine if 'Butterbush' is unique in its ability to easily accept *C. argyrosperma* pollen or if this is a common widespread trait in temperate *C. moschata* varieties.

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An Austrian Cucumber Mosaic Virus isolate is causing severe symptoms on resistant *Cucurbita pepo* cultigens

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Introduction: In 2005, we discovered some plants of a zucchini yellow mosaic virus (ZYMV)-tolerant oil-pumpkin breeding line (*Cucurbita pepo*), severely affected by a virus. Our first assumption was that ZYMV might have overcome the resistance, but ELISA tests revealed that most likely cucumber mosaic virus (CMV) caused the symptoms, although ZYMV was detected in very low concentrations as well. Using fruit flesh of such infected plants for inoculation of pumpkin seedlings lead to immediate death of all plants, independent of whether the plants were ZYMV-tolerant or susceptible. Therefore, we decided to isolate the CMV for further investigation.

Materials and methods: *Artificial inoculation:* An Austrian isolate of CMV was established as follows. Fruit flesh from oil-pumpkin with multiple virus infestation was collected in fall 2005 and used to inoculate tobacco plants. Tobacco, *Nicotiana tabacum*, is not susceptible to zucchini yellow fleck potyvirus (ZYFV) and squash mosaic comovirus (SqMV) (Plant Viruses Online: http://image.fs.uidaho.edu/vide/famly124.htm#Nicotiana%20tabacum). Tobacco is also not known to be susceptible to ZYMV, the most common virus in oil-pumpkin. Leaves of tobacco plants showing severe mosaic were tested with ELISA for CMV, ZYMV, WMV2 and SqMV. The presence of any virus other than CMV was excluded. Then CMV was increased on plants of the susceptible *C. pepo* variety Gleisdorfer Ölkürbis, because inoculations on *Cucurbita moschata*, using infected leaves of tobacco, failed. The Hungarian isolate (HI), provided to us by István Tóbiás (Plant Protection Institute, Hung. Acad. Sci., Budapest, Hungary), was purified and tested in the same way as the Austrian isolate (AUTI). The French isolate (FI), received from Muriel Archipiano (Clause Tézier, Domaine de Maninet, Route de Beaumont, Valence, France) was treated in the same way. The inoculum for the experiments was prepared from 1.0 g of infected leaves, ground in a mortar on ice, in 10ml inoculation buffer containing 1% K_2HPO_4. Finally, 1.0 g Celite® 545 was added. Seedlings were inoculated twice: first the two cotyledons, when the first true-leaf just appeared, and three days later the first true-leaf itself. Inoculation was carried out by gently rubbing the leaf surface with a finger in rubber gloves. The leaves were rinsed with water immediately after rubbing. Simultaneously the Hungarian and French isolates of CMV were tested.

Plant material: Nine *C. pepo* and nine *C. moschata* cultigens (Table 1) were grown in pots in the greenhouse at 23°-25°C day and 20°-22°C night temperatures at 50-70% RH. Natural illumination was supplemented with a combination of mercury and sodium vapor lamps (ca. 10,000 lux), maintaining a day-length of 14 hours during the whole experiment.

Evaluation: Plants were observed 14 and 24 days after the first inoculation. Leaf symptoms (LS) were rated from 0 (no symptoms) to 9 (severe mosaic). A rating of 10 was introduced for dead plants. Additionally, the approximate growth

reduction (GR), in relation to normal growth, was scored in percent. For further evaluation a total rating (TR), using the formula TR=LS+GR*0.05, was calculated. Plants with a TR=0 to 5 were classified as tolerant, such with TR>5 as susceptible. TR-values greater than 10 were limited to 10. To verify the TR-value, we applied the 0 to 5 rating system described by Walkey and Pink (4), who combined leaf symptoms and stunting in one score. After the last evaluation the experiment was terminated and the plant material was autoclaved.

Results and Discussion: A comparison of results obtained by the infection experiment (Table 1), shows that AUTI is the most aggressive isolate. The symptoms caused by HI were half as severe as those caused by AUTI, those caused by FI were still somewhat milder. Comparisons of results obtained with *C. pepo* and *C. moschata*, revealed that, except against AUTI, most of the *C. moschata* cultigens showed a high level of CMV resistance. 'Nigerian Local', however, developed severe symptoms when inoculated with AUTI, although we had hoped that it could be the source of a high level of resistance, as was reported by Brown et al. (1). Nigerian local was found to be resistant against a number of viruses and was therefore used in many breeding programs (1). We obtained a similar result with 'Menina 15' (received from Michael Pitrat, INRA, Montfavet, France), which is, analog to Nigerian Local, highly resistant against ZYMV (2). Only 'Zhou', a Chinese, hull-less *C. moschata* cultivar named by us according to its discoverer Zhou Xianglin (5) and Soler, (kindly provided by L. Wessel-Beaver, USDA-ARS, Puerto Rico), seemed to have resistance against AUTI (Fig. 1). All *C. pepo* cultigens, including 'Linda', an American zucchini F1 variety from Harris Moran Seed Company (Modesto, California) described as CMV-resistant, showed high susceptibility to AUTI. The zucchini variety True French (kindly provided by Harry Paris, Newe Ya`ar Res. Center, Ramat Yishay, Israel), developed clearly less leaf symptoms than most of the other *C. pepo* cultigens. 1997, for the first time, a ZYMV-epidemic destroyed half of the oil-pumpkin harvest in Austria (3). We are alarmed by the fact that, in our first experiment, CMV in combination with ZYMV killed all our test plants. We are wondering, why CMV in the field so far occurs only on single plants. One possibility could be that AUTI lost its aphid transmissibility. A sequencing of the virus genome is in progress. Further investigations will have to be carried out to determine the potential danger posed by this isolate.

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Yield of *Cucurbita moschata* Lines and Hybrids Grown in Sonora, Mexico.

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Introduction: *Cucurbita moschata* Duchesne is widely cultivated in Mexico, mainly under rain-fed conditions. In Northwest Mexico, landraces of this species are known as Cehualca (or Segualca) and are grown for mature fruit consumption mostly during the summer-fall season. In the coastal valley of Hermosillo, Sonora, improved varieties of winter squash are grown for the export markets mainly to the USA and Japan. Kabocha squash (*C. maxima*), Acorn and Spaghetti (*C. pepo*), and Butternut (*C. moschata*) are typically sown in August and picked in November and December. Landraces of *C. moschata* and *C. argyrosperma* are grown in the state of Sonora in elevated areas with higher rainfall than the valleys, and are sown in July and picked in October and November.

The yields of winter squash are highly variable; 'El Dorado', a tropical hybrid of *C. moschata* reached 90 ton.ha-1 grown under drip irrigation and plastic mulch (6). In another work with C. moschata, a high yield of 85 ton.ha-1 was obtained for the tropical hybrid C-42 x La Segunda by transplanting and using mulching and row cover in a favorable year, but the yield decreased to 43 ton.ha-1 by direct seeding without mulching and row cover in the same year. The previous year (1998) was humid and the yield under the last method was 28 ton.ha-1 (11). Experimental yields of *C. moschata* landraces obtained in the Department of Agriculture and Animal Science of the University of Sonora (DAG) during the summer-fall season under furrow irrigation, changed from 7.9 to 17.8 ton.ha-1 (3), and from 1.2 to 24.6 ton.ha-1 for the winter-spring season (10). The yield was improved by increasing the plant population reaching 30.3 ton.ha-1 for the summer-fall season of 1988 using 0.33 plants per square meter (8).

Halloween types of winter squash were evaluated and it was found that the yield increased significantly by setting pollinators. The cultivar Libby´s Select (*C. moschata*) had the highest yield (74.8 ton.ha-1) while the *C. pepo* cultivars Appalachian and Mammoth Gold had yields of 54.3 and 30.6 ton.ha-1 respectively (13). Similar results were reported with other cultivars of *C. pepo* of the same type with a high yield of 51.9 ton.ha-1 (1). The commercial yields of Kabocha grown in Sonora usually fluctuate from 12 to 18 ton.ha-1 (personal communication, Ing. Ricardo Navarro) while in Australia high experimental yields, around 43 ton.ha-1, may be reached with an average of 21.1 ton.ha-1. The interspecific hybrid 'Tetsukabuto' (*C. maxima x C. moschata*) had a yield of 66 ton.ha-1 (7). C. argyrosperma germplasm evaluated at DAG had yields between 3.2 and 38.8 ton.ha-1 for the spring season and from 4 to 28 ton.ha-1 for the fall season (9). Some germplasm had very low fruit set during the spring season and for the fall season the yield limiting factor was infection with squash leaf curl virus (SLCV), a whitefly-transmitted geminivirus (2). Feeding of immature stages of the biotype B of Bemisia tabaci, induces the squash silverleaf (SSL) disorder in squash (12).

The objective of this work was to evaluate the yield of five C. moschata lines of the round fruit type obtained at DAG and 15 hybrids obtained between these lines, and to make observations

about their reaction to SSL and SLCV during the summer-fall season.

Materials and Methods: The experiment was conducted at the experimental farm of DAG during the summer-fall season of 2000. The material tested consisted of five C. moschata, round-type lines obtained at DAG. The previous season these lines were selfed and sibbed, and direct and inverse crosses were done between them obtaining enough seed to conduct a yield trial for 15 hybrids. Lines 301 and 303 are resistant to SSL while lines 101 and 102 are susceptible, and line 282 shows tolerance exhibiting only mild silvering. All the lines show field resistance to SLCV.

The soil was conventionally prepared by plowing and disking, and was irrigated twice before planting to allow annual and perennial weeds to grow and then to be sprayed with glyphosate. Melon beds were formed with 4 m center to center and fertilized with N-P-K (17-17-17) at a rate of 400 kg.ha-1. Seeds were sown on August 25 in moist soil with two lines per bed and two seeds per hill which were 50 cm apart. Seedlings were later thinned leaving one plant per hill. The experiment was furrow irrigated weekly or as needed depending on the weather. No pesticides were used during the whole growing period despite insect and disease pressure.

Fruits were picked once on December 21 and 22, they were weighed in groups of three to five, and immature and off-shape fruits were discarded. The experimental plots measured 7 m and a completely randomized design with two replicates was used for ANOVA and a Tukey test was used for mean separation. A contrast test was used to compare the individual yield of each hybrid with their parents.

Results and Discussion: The fruit yield changed from 17.1 to 42.6 ton.ha-1 with an average of 32.5 ton.ha-1 (Table 1). Hybrids had an average yield of 35.6 ton.ha-1 while lines produced 23.2 ton.ha-1. Despite these differences in yield, only two groups of significance were obtained (Tukey 0.05). However, when each hybrid was compared to both parents, it was observed that hybrids 102 x 301, 282 x 101, 282 x 102, 282 x 301, 301 x 102, 301 x 282, 303 x 101 and 303 x 282 had highly significant yields (P>0.01) and hybrids 102 x 303 and 301 x 101 had a significantly higher yield (P>0.05). Similarly, C. moschata hybrids obtained from tropical varieties produced higher yields than their parents (6, 11). Our results are also similar to those reported by Rulevich et al. (11) when they used direct seeding without mulching and polyester cover in a year with high rainfall conditions under which they had a yield of 28 ton.ha-1. In October, during fruit development, we had high rainfall, conditions which favored the presence of foliar diseases such as Alternaria leaf spot.

These yields are typical of C. moschata grown in our area with very low or without pesticide applications and show that hybrid vigor shows up in our materials developed from local landraces. In a very similar experiment with C. argyrosperma, hybrid vigor was not so evident (9).

It was observed (results not shown) that only lines 301 and 303 were resistant to SSL and that line 282 showed slight silvering. All hybrids obtained from SSL resistant x susceptible crosses were susceptible. Also, hybrids derived from crosses using line 282 as a parent showed slight silvering, and hybrids between the two resistant lines were resistant showing dominance of SSL, a condition previously reported (5). All lines and hybrids showed field resistance to SLCV; only line 301 had two

plants (from 10 readings) with slight symptoms. No sampling for virus identification was done in this experiment, but a neighboring C. moschata plot of the butternut type was positive for both SLCV-restricted and SLCV-extended host range (4). All lines and hybrids developed yellowing of basal leaves before maturity but its origin could not be determined.

These results show that it is possible to grow C. moschata lines or hybrids during the summer-fall season in our area and perhaps in other locations without using pesticides and have a reasonable yield. These materials may be grown organically as well. In comparison, commercial varieties of the acorn, spaghetti, butternut, and kabocha squash have to be sprayed for insect and disease control.

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Table 1. Fruit weight and yield for 5 lines and 15 hybrids of *Cucurbita moschata* evaluated in Sonora, Mexico in year 2000.

Line or hybrid	Fruit weight (kg)	Fruit yield ($ton.ha^{-1}$)	Groups (Tukey 0.05)
303 x 301	4.3	42.6	a
102 x 303	3.3	42.4	a
303 x 282	3.4	39.5	ab
102 x 301	3.1	39.2	ab
282 x 101	4.1	38.8	ab
282 x 102	4.9	38.0	ab
301 x 102	3.2	37.7	ab
301 x 282	2.7	36.6	ab
282 x 301	3.6	36.4	ab
102 x 101	3.0	35.4	ab
301 x 101	3.4	35.1	ab
301 x 303	2.7	30.1	ab
303 x 301	2.7	30.0	ab
101 x 301	2.6	29.9	ab
303	1.9	28.8	ab
102	4.3	28.1	ab
101	3.0	24.4	ab
102 x 282	3.1	22.8	ab
301	1.6	17.4	b
282	2.8	17.1	b

Yield and Quality of the Interspecific Cross *Cucurbita argyrosperma* x *C. moschata*

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Introduction: In northwest Mexico, the mature fruit quality of *Cucurbita argyrosperma* Huber (ARG) fruits is lower than other winter squashes such as Kabocha and 'Waltham Butternut' (Waltham) (1,5,8). Merrick (7) found, working with landraces from northwest México, that fruit flesh color varies from pale to deep orange. She also found that there is high genetic compatibility between ARG and *C. moschata* (MOS). Wessel-Beaver et al (9) reported that desirable traits could be transferred between these two species, for example, using MOS to improve the sugar and carotene content in ARG. Interspecific, commercial F_1 hybrids within this genus such as 'Tetsukabuto' (*C. maxima* □ *C. moschata*) that are cultivated nowadays, have high yield and good quality and are also used as rootstocks for grafting melons. They are grown in fungi-infested soils and are useful in reducing applications of soil fumigants (3). The objective of this work was to study crosses of ARG x MOS in order to find out whether desirable traits such as high soluble solids content (SSC), intense orange flesh color and thus high carotenoid content, could be introduced to our ARG material. We also wanted to explore whether F_1 hybrids of acceptable quality could be obtained for commercial growing by crossing these species.

Materials and Methods: ARG (A-43, A-52, and A-71), six MOS breeding lines, and Waltham, were grown during the summer-fall season of 2005. Seventy-four crosses were performed from October 7 to 21 using ARG as the female parent. Forty-five fruits were picked on December 5 and seeds extracted from December 15 to 23. The number of sound (at least half-filled) seeds per fruit of hybrids and their female parent were counted and weighed. F_1 hybrids and male and female parents were established by direct seeding in August 18 and 19 of 2006 and selfing of hybrids and backcrossing to ARG was performed. However, it was noticed early during fruit development that all of the hybrids obtained using the six MOS breeding lines mentioned above as male parents had bitter fruits. Thus, they were discarded after fruit maturity. Bitterness was reported in F_1 individuals from ARG × *C. pepo* crosses (2). Selfed fruits from hybrids A-52 × Waltham and A-71 × Waltham were non-bitter and their seeds were saved. Also, seeds from backcrosses to ARG using these hybrids were obtained and then were direct-seeded along with parents on August 15, 2007. The accessions tested are listed in Table 1. Fruits were picked 51 days after flowering and a sample of 6 fruits was taken at random, weighed, and analyzed two days after harvest for SSC and flesh color. SSC was determined in fruit juice using an ABBE Leica Mark II refractometer model 10459 and flesh color was determined with a portable Minolta CR-300 tristimulus colorimeter.

Additional ARG × MOS crosses for F_1 seed were performed during the summer-fall season

of 2006 using ARG breeding lines A-30 and A-22 and the landrace San Pedro Ho:l purchased at Search Seeds, Tucson, AZ. Waltham was also used as pollinator. The ARG breeding lines have an elongated fruit shape similar to Waltham but have larger fruit and have an obviously inferior fruit quality in comparison to Waltham. The landrace produced mostly elongated fruits (used for pollination) but also pear and round shape fruit in lower proportion. Fruits were picked 47 days after flowering and analyzed 36 days after harvest. Fruit weight of the F_1 hybrids was recorded using a 10 kg balance, SSC was measured with an Atago hand refractometer, and flesh color was measured with a portable ColorTec PCM colorimeter. Seven randomly selected fruits were used for statistical analysis. Analyses of variance of data for fruit characteristics for both experiments were done as completely randomized designs and Duncan´s multiple range test was used for mean separations using the NCSS (Number Cruncher Statistical Systems) 2000 program.

Results and Discussion. Fruit set from the ARG × MOS pollinations performed in 2005 was 61% and the average number of F_1 seeds per fruit was 127 (1-402). Seeds had a weight per fruit of 19.4 g (0.2-75) (Results not shown). In comparison, the female parents had an average of 294 open-pollinated seeds per fruit (50-410) with a weight per fruit of 55.4 g (11.5-79.5). Merrick (7) obtained 55% fruit set from 13 ARG × MOS crosses and an average of 82 seeds per fruit while Wessel-Beaver et al., (9) reported 41% fruit set in 24 pollinations and acceptable seed formation. Table 1 shows the results for SSC and flesh color measured two days after harvest for lines A-52 and A-71 and crosses with Waltham. While fruit weight had a significant increase when compared with Waltham, SSC and flesh color did not. However, in a group of fruits from both F_2 populations that were self-pollinated and de-seeded 42 days after harvest (data not statistically analyzed), there were single SSC readings of 13.0 and 13.5% for two selections of A-71 × Waltham F_2 while Waltham had 13.0%. High readings for flesh color as well (analyzed with the ColorTec PCM colorimeter) were observed in a few fruits for the A-52 × Waltham F_2 (8410 and 8060) while Waltham had a score of 8470. Five fruits from A-71 × Waltham F_2 also had scores higher than 8020. Fruits with acceptable color usually had values higher than 7500. Scores for fruits of lines A-71 and A-52 were 6730 (pale yellow) and 6320 (almost white), respectively. It is well known that the sugar and carotene content increase in winter squash after harvest (1,6). The SSC of an ARG breeding line increased from 7% at harvest to 10% at 56 days after harvest, and then decreased significantly by 98 days after harvest (5).

Table 2 shows results for fruit weight, SSC, and flesh color measured 36 days after harvest for F_1 hybrids obtained in 2006. The SSC of Waltham reached 12.8% and was similar only in the hybrid A-22 × Waltham. Waltham had also a high score for flesh color and two hybrids, San Pedro × Waltham and A-22 □ Waltham were within the same group of significance. An estimate of yield was done considering the average fruit number and fruit weight. Line A-30 had a yield of 44.1 ton.ha^{-1} while Waltham produced 10.6 ton.ha^{-1}. Hybrids A-30 × Waltham, San Pedro × Waltham, and A-22 × Waltham had yields of 40.1, 23.4, and 23.3 ton ha^{-1} respectively. Intraspecific F_1 hybrids obtained using MOS breeding lines crossed with Waltham had larger fruits than Waltham but had lower yields than the female breeding lines (4).

Even though at harvest time *C. argyrosperma* × *C. moschata* fruits taken from small samples had low SSC and flesh color, single fruits from the F_2 generation from larger samples analyzed

several weeks after harvest may have quality comparable to an improved cultivar of winter squash. Therefore, it seems possible to develop *C. argyrosperma* cultivars with better fruit quality. It is also concluded that is possible to grow F_1 hybrids from this cross.

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Table 1. Fruit weight, soluble solids content (SSC), and flesh color (b or yellow color) of interspecific crosses of *Cucurbita argyrosperma* *C. moschata*

Plant material	Weight (kg)	SSC (%)	Flesh color (b)
A-52	2.0 b	5.6 b	60.8 b
A-52×W F_1	1.9 b	7.5 b	60.4 bc
A-52×W F_2	1.2 c	5.2 b	55.9 c
A-52× (A-52xW) R_1	1.6 bc	5.6 b	57.7 bc
Waltham (W)	1.0 c	10.2 a	72.3 a
A-71	2.5 a	6.9 b	44.2 c
A-71×W F_2	1.5 bc	5.9 bc	53.8 b
A-71× (A-71xW) R_1	1.4 bc	4.5 c	41.0c

Means within a column not followed by the same letter are significantly different (P<0.05).

Table 2. Fruit weight, soluble solids content (SSC), and flesh color according to colorimeter yellow index observed 36 days after harvest from interspecific crosses of *Cucurbita argyrosperma* *C. moschata* and parents.

Plant material	Weight (kg)	SSC (%)	Y (yellowness)
Waltham (W)	0.9 c	12.8 a	8366 a
A-22	2.2 b	8.3 cd	5897 c
A-30	3.6 a	8.0 cd	6694 b
San Pedro Ho:l	2.2 b	6.6 d	6529 bc
A-22 × W	1.9 b	11.5 ab	7810 a
A-30 × W	3.0 ab	7.6 cd	7164 b
San Pedro × W	2.4 b	9.8 bc	8069 a

Means within a column not followed by the same letter are significantly different (P<0.05).

New Source of Male Sterility in Ridge Gourd (Luffa acutangula (L.) Roxb.) and its Maintenance Through In Vitro Culture

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Introduction

Ridge gourd (*Luffa acutangula* (L.) Roxb.) is an important warm-season vegetable crop, having a long history of cultivation in tropical countries of Asia and Africa (Seshadri, 1990). Though cultivars of ridge gourd are monoecious, different sex forms were reported in this species, and the genetics of inheritance have been studied extensively (Choudhary and Thakur, 1966). So far, no male sterility has been reported in ridge gourd. An offtype was detected in a population of ridge gourd which was characterized by the production of rudimentary male flowers in racemes. Like muskmelon (Rudich *et al*., 1970), male sterility can be used to produce hybrids to capitalize on heterosis in a breeding program. Maintenance of the male sterile line is a major challenge. In order to study the genetics of male sterility, the line must be crossed with a different pollen parent to produce F_1, F_2 and backcross generations. Micro-propagation is the best approach we have found to maintain this unique source, since the genotype can be fixed without any genetic change.

Methods

The male flowers of the suspected male sterile line were subjected to microscopic analysis using a stereo microscope. and the fertility of the pollen was tested by staining with acetocarmine. Pistillate flowers of the male sterile offtype were crossed using pollen from 'Haritham'. The F_1 was generated and evaluated for pollen fertility. Micro-propagation was attempted to maintain male sterile plants. In order to standardize the establishment medium, explants were collected from two week old seedlings of monoecious 'Haritham' plants and cultured on Murashige and Skoog (1962) medium. Auxin (IAA) and cytokinin (BAP) were used individually or in combination at concentrations of 0, 0.5, 1.0, 1.5 and 2.0 mg l^{-1}.

Promising establishment media identified for monoecious plants were used for tissue culture of field-grown male sterile plants. The established shoots were used as the mother stock. For further multiplication, shoot tips and nodal portions were excised from the mother stock and cultured on MS medium supplemented with different BAP concentrations (0, 0.5, 1, 1.5 and 2 mg l^{-1}). The *in vitro* derived shoots were rooted on Murashige-Skoog medium using half strength fortified with IBA at 1.0 mg l^{-1} and charcoal at 200 mg l^{-1}. Plants were acclimatized for 30 days before they were transferred to the field.

Results

The male sterile line had rudimentary male flowers in racemes, but no fruit set after self-pollination. However fruit set was observed when pollinated using staminate flowers of the monoecious cultivar Haritham. The anthers of the suspected male sterile line were compared to those of 'Haritham' and had a marked difference with respect to the appearance of anther lobes. In the experimental line the lobes were flat and more pubescent whereas in 'Haritham', they

were was plump and filled with large fertile microspores. The microspores of the suspected male sterile line were shrunken, small and

sterile compared to those from the normal flowers. All plants in the F_1 population obtained by crossing with 'Haritham' had the male sterile character indicating its heritability.

Micropropagation has been applied successfully in cucurbits for maintenance of elite plant types (Barnes *et al*., 1978). Auxin:cytokinin ratio plays a pivotal role in determining the *in vitro* response of most of the cucurbits (Trulson and Shahin, 1986). Among the combinations, the highest explant response was observed using Murashige-Skoog medium with IAA at 1.5 mg l^{-1} + BAP at 2.0 mg l^{-1}. IAA:BAP combinations with the highest level of BAP (2 mg l^{-1}) induced profuse callus formation. Single shoots with short internodes were observed in all cultures developed from axillary meristems. The longest shoot was observed on Murashige-Skoog medium with BAP at 0.5 mg l^{-1} (9.0 cm) and with IAA at 1.5 mg l^{-1} + BAP at 2.0 mg l^{-1} (9.1 cm).

These two media were used for inoculating nodal cuttings of male sterile line collected from the field. Explant response was average, with 60% establishment in the medium, Murashige-Skoog medium with IAA at 1.5 mg l^{-1} + BAP at 2.0 mg l^{-1} (Fig. 2a) and 45% on Murashige-Skoog medium with BAP at 0.5 mg l^{-1}. Here also callus formation was observed from the base of the nodes. Shoot length after 45 days was maximum on Murashige-Skoog medium with IAA at 1.5 mg l^{-1} + BAP at 2.0 mg l^{-1} (7.5 cm) followed by BAP at 0.5 mg l^{-1} (5.3 cm). Cuttings (2 to 3 nodes) from *in vitro* shoots were used for inoculating in the multiplication medium. The highest number of shoots and nodes were observed in the medium with BAP at 1.0 mg l^{-1}.

Incorporation of BAP at 1.5 and 2.0 mg l^{-1} gave a diminishing effect on shoot multiplication. Callus formation was observed from the multiplication clumps which later transformed into shoots. The shoots from multiplication stage were used for rooting in MS medium (half strength) fortified with IBA at 1.0 mg l^{-1} and charcoal at 200 mg l^{-1} (Fig. 2c). A high percentage of rooting (95%) and continued shoot growth were observed in this medium (Fig. 2d). The rooted plants were transferred to a mist house in polyethylene bags where they were kept for one month before transplanting to the field (Fig. 2e). Tissue culture plants took 50 days after transplanting in the field for flowering and were all male sterile. Male sterility of the plants can be confirmed only after flowering and at this stage, chemical application for induction of male flowers as in cucumber and muskmelon will not be effective. This protocol can be used for maintenance and multiplication of male sterile ridge gourd plants.

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2a
RIDGE GUARD GYNOECIOUS LINE - ELONGATION
2b
2c
2d 2 division = 1 cm
2e

Genetics of Seed Yield and its Components in Bottle gourd (*Lagenaria siceraria* (Mol.) Standl.)

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Introduction: Bottlegourd [*Lagenaria siceraria* (Mol.) Standl.] is the cultivated species among the six species of *Lagenaria* having a diploid chromosome number of 22. The plants are annual viny pubescent herb with large white flower borne on slender peduncles. Breeding objectives of bottlegourd are based on seed production problems and consumer preference. In bottle gourd increasing attention is being paid towards breeding of superior cultivars with greater focus on development of hybrid seeds. F_1 hybrid breeding is prominent among the methods used in the improvement of bottle gourd. Diallel analysis helps in estimating the genetic components of variation, the degree of dominance, the proportion of dominant and recessive genes, the distribution of genes with positive and negative effects governing the expression of a particular trait. Diallel analysis using the inbreds from the local indigenous germplasm of bottlegourd assumes significance .With this viewpoint eight divergent genotypes were mated in a diallel fashion to study the genetics of seed yield and its component traits into bottlegourd.

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/ advanced line 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, UK, 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 fruited), PBOG22, PBOG 54 (segmented leaf), PBOG 61, PBOG 76, PBOG 117, PBOG 119 and Pusa Naveen. The data obtained from half diallel with seven characters viz., days to first male flower, node number to first female flower, number of primary branches per vine, fruit weight, pedicel diameter, number of seeds per fruits and 100 seed weight. Genetic analysis of diallel data for genetic components of variation was according to method of(3,9). The first three assumptions of the additive/ dominance genetic model underlying an analysis of the diallel cross (4) were tested as (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 (12) are (4) independent effect of non- allelic genes (i.e. no epistasis) ; (5) no multiple allelisam and (6) genes independently distributed between parents. Estimation of Genetics Components were done as follows:

The expected values of main components of genetic variance were estimated by solving the above equations for F_1 generation (3). In F_1 generation the expected values of main components are

$$\hat{D} = V_0L_0 - \hat{E}$$

$$\hat{F} = 2V_0L_0 - 4W_0L_{01} - 2(n-2)\hat{E}/n$$

$$\hat{H}_1 = V_0L_0 - 4W_0L_{01} + 4V_1L_1 - 3(n-2)\hat{E}/n$$

$$\hat{H}_2 = 4V_1L_1 - 4V_0L_1 - 2\hat{E}$$

$$\hat{h}^2 = 4(ML_1 - ML_0)^2 - 4(n-1)\hat{E}/n^2$$

$$E = M'e$$

Where,

N = number of parents

D = variance component due to additive gene effects

F = mean of the covariance of additive and dominance effects over all the arrays

H_1 = variance component due to dominance deviation

H_2 = dominance indicating asymmetry of positive and negative effect of genes

$$H_2 = H_1[1-(\mu-v)^2]$$

Where,

μ = proportion of positive genes in parents

v = proportion of negative genes in parents

h^2 =dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses)

V_0L_0 = variance of parents

V_r = variance of all the progenies in each parent of array

V_1L_1 = mean of all the V_r values

Wr = co-variance between parents and their off springs in one array

W_0L_{01} = mean of all W_r values

$(ML_1 - ML_0)^2$ = dominance relationship i.e. difference between the mean of the parents and the mean of their n(n-1) progenies.

V_0L_1 = variance of the means of arrays

E = the expected environmental component of variation

In order to test the significance of the main component: D, F, H_1, H_2, h^2 and E, the standard errors (SE) are calculated for each of mean as follows:

$$S_E(D) = (S^2 \times CD)^{1/2}$$

$$S_E(F) = (S^2 \times CF)^{1/2}$$

$$S_E(H_1) = (S^2 \times CH_1)^{1/2}$$

$$S_E(H_2) = (S^2 \times CH_2)^{1/2}$$

$$S_E(h^2) = (S^2 \times Ch^2)^{1/2}$$

$$S_E = (S^2 \times CE)^{1/2}$$

The above genetic components were used in computation of following genetic ratios :

1. Mean Degree of Dominance was calculated as $(H_1D)^{1/2}$. If the ratio obtained is equal to 1, this indicated presence of complete dominance; if more than 1, it indicates presence of over dominance and if less than 1, it reveals presence of partial dominance.
2. The proportion of dominant genes with positive or negative effects in parents is determined by the ratio : $H_2/4H_1$ with the maximum theoretical value of 0.25, which arises when p = q = 0.5 at all loci. A deviation from 0.25 would seem when $p \neq q$. Thus, $H_2/4H_1 \approx 0.25$ would means symmetrical distribution of positive and negative dominant genes in parents; and when $H_2/4H_1 \neq 0.25$ it means asymmetrical distribution (p = proportion of dominant alleles and q = proportion of recessive alleles).
3. The proportion of dominant and recessive genes in parents. It was calculated as $\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$. When this ratio is equal to 1 it indicates nearly equal proportion of dominant and recessive alleles in parents (i.e. p = q = 0.5). If the ratio is greater than 1 it refers to excess of dominant alleles and minority of recessive alleles (p > q). When this ratio is less than 1, it means minority of dominant alleles and excess of recessive alleles (p < q).

4. Number of dominant gene blocks is estimated by h^2/H_2 ratio.

Result and Discussions: The analysis of variance revealed highly significant differences among progenies indicating that the parents were diverse for the characters studied and diversity was transmittable to the offspring. The component analysis data is given in table 1.For days to first male flower in the kharif season experiment, only additive (D) variance was

significant, signifying the involvement of additive gene action in the inheritance of days to first male flower. The $(H_1/D)^{1/2}$ estimate was 1.17 which was greater than unity, and suggested the presence of over dominance. The proportion of dominant and recessive alleles pooled over parents $(4\ DH_1)^{1/2} + F\ /(4DH_1)^{1/2}–F$ was 1.11, suggesting almost equal proportion of dominant and recessive alleles. The proportion of dominant genes with positive and negative effects was 0.18, which was less than the theoretical maximum value of 0.25 which arises when u (alleles with positive effects) and V (alleles with negative effects) = 0.5. This indicating asymmetrical distribution of positive and negative dominant genes in the parents. In the summer season, the degree of dominance $(H_1/D)^{1/2}$ was found to be greater than one (1.85) indicating over dominance. The proportion of dominant and recessive alleles pooled over was 0.79 suggesting unequal preparation of dominant and recessive alleles. The proportion of dominant genes with positive and negative effects was 0.17 indicating asymmetrical distribution of positive and negative dominant genes in the parents. For node number to first female flower in both the seasons, the significant D and H_1 variances were observed. This indicated the role of both additive and dominance gene action in the inheritance of node number to first female flower. The estimate of $(H_1/D)^{1/2}$ was more than unity i.e. 1.90 in the kharif and 1.81 in the summer, indicating the over dominance. An asymmetrical distribution of positive and negative dominant genes for this trait was seen in the parents as $H_2/4H_1$ was 0.16 and 0.19 in the kharif and summer season, respectively. The value of relative frequency of dominant and recessive alleles in the parents was 3.35 in the kharif season and 2.42 was in the summer season, suggesting an excess of dominant alleles. For number of primary branches per vine dominance (H_1 and H_2) of genetic variance were significant in both the seasons. Mean degree of dominance $(H_1/D)^{1/2}$ was greater than unity (3.60 in the kharif season and 3.09 in the summer season) and thus suggested the presence of over dominance. The values $H_2/4H_1$ (0.22) were almost equal to the maximum theoretical value of 0.25 indicating symmetrical distribution of u (alleles with positive effects) and v (alleles with negative effects) in both the seasons. Proportion of dominant and recessive alleles was 0.86 in the kharif season and 1.29 in the summer season, suggesting almost equal proportion of dominant and recessive alleles in the parents. For fruit weight additive genetic component of variance (D) was non-significant. Dominance components (H_1 and H_2) were found to be significant. The $(H_1/D)^{1/2}$ estimate was (3.60 in the kharif season and 3.84 in the summer season) more than unity implying over dominance. The estimate of $H_2/4H_1$ (0.21) were almost equal to its maximum value of 0.25, indicating symmetrical distribution of dominant genes. Proportion of dominant and recessive alleles was more than one, suggesting excess of the dominant alleles. For pedicel diameter in both the seasons, none of the estimates was significant. For number of seeds per fruits, the analysis of variance component indicated that in both the season experiments, additive (D) and dominance variances (H_1) were significant. That follows that the expression of number of seeds per fruits was conditioned by both additive and dominance gene action. However, dominance component was predominant than the additive component. $(H_1/D)^{1/2}$ was 3.65 (kharif season) and 1.72 (summer season) and showed over dominance. $(H_2/4H_1)$ (0.17) was less than its maximum theoretical value. 0.25 showing asymmetrical distribution of positive and negative alleles over both the seasons. The value of $(4DH_1)^{1/2} + F/(4DH_1)^{1/2}-F$ was 2.31 and 2.84 during the kharif and summer seasons, respectively, indicating the excess of dominant alleles over both the seasons. For 100 seed weight dominance variances (H_1) was significant, signifying the involvement of dominance gene action to govern 100 seed weight. However, h^2 was significant in the both season. This indicated that there was presence of overall dominance effect. The $(H_1/D)^{1/2}$ estimate was more than unity i.e. (3.35 in the kharif season and 3.56 in the summer season), suggesting the presence of over dominance for 100 seed weight. An asymmetrical distribution

of positive and negative dominant genes for 100 seed weight was reflected in the parents as $H_2/4H_1$ was 0.18 (kharif season) and 0.16 (summer season). The proportion of dominant and recessive alleles pooled over parents $(4DH_1)^{1/2}$ + $F/(4DH_1)^{1/2}$-F was 2.64 (kharif season) and 3.21 (summer season) suggesting an excess of dominant alleles. It is worth nothing that bottle gourd like several other cucurbits does not respond to inbreeding (16). The cost of production of hybrid seed in bottle gourd is substantially low, as the F_1 seeds can be produced on commercial scale by the removal of male buds from the female parent and allowing insect pollination. The breeding methods for the improvement of crop depend on nature and magnitude of the components of genetic variances, combining ability of the parents and crosses and the extent of heterosis for quantitative traits. Choice of the parents is considered an important aspect in bottle gourd breeding programme aimed at improving yield and its components because superior parents may not necessarily transfer their superiority to the progenies (1). The theory of diallel crosses and the usefulness of diallel cross technique in genetic analysis of population have received sufficient attention in the past. Several diallel cross techniques have been proposed and applied to diverse problems. For example (2,6,13,17) have considered the utility of diallel crosses. The theory of diallel crosses and procedures for estimating certain genetic parameters in terms of gene models in varying degrees of complexity, have been discussed by (2,3,7,8,9,10). In addition to have an understanding of the combining ability and the genetic components of variation one gets information on the average degree of dominant and recessive alleles in the parents. Therefore, diallel cross analysis in totality is a useful biometrical technique in bottle gourd breeding. The higher proportion of dominant genes observed in most of the characters are in agreement with the findings of (14,15).The proportion of genes with positive and negative effects ($H_2/4H_1$) in the parents was less than 0.25 for days to first male flower, node number to female flower, number of seeds per fruit and 100 seed weight consistently over both the seasons. This suggested asymmetrical distribution of dominant genes with positive and negative effects. It is in accordance with the findings of (11, 15). The parents for making crosses could be selected on the basis of gca effects. Overall, both additive and non additive components of variation were found to play important roles in the inheritance of economic traits in bottle gourd as it evident from component analysis. The t^2 values were non-significant for the traits in the F_1, indicating the validity of assumptions underlying the diallel analysis. However, presence of non-additive interaction for the same traits was intriguing but, as suggested by (3) even if a traits exhibits a partial failure of assumptions, analysis could be carried out for such characters, though the results would not be as reliable as they would have been had all assumptions been fulfilled. In a cross-pollinated crop like bottle gourd, exploitation of non-additive genetic variance as such would be practical worth. However, conventional selection, is likely to lead to substantial trait improvement.

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Estimation of Genetics Components Example.

between crosses with both parents different	Genetic interpretation (expectations) F_1					
	D	F	H_1	H_2	h^2	E
V_0L_0 (Vp)	1					1
V_0L_1 (V_m)	1/4	-1/4	1/4	1/4		$1+(n-2)/2n^2$
V_1L_1 ($\overline{V}_r$)	1/4	-1/4	1/4			[1+(n-2)/2n]
W_0L_{01} ($\overline{W}_r$)	½	-1/4				1/n
$(ML_1\text{-}ML_0)^2$					1/4	$(n-1)/n^2$
V_r	¼	-1/4				1
W_r	½					1/n

Table 2. Mean Squares for Seed Yield and its Components in Bottle gourd.

Source of variation	Degree of freedom	Season	Days to first male flower	Node no. to first female flower	Number of primary branches /vine	Fruit weight (Kg)	Pedicel diameter (Cm)	Number of seeds per fruits	100 seed weight (g)
Replication	**2**	**Kharif**	**6.68**	**2.25**	**24.45**	**0.0098**	**0.0025**	**11797.8**	**12.61**
		Summer	**4.52**	**6.34**	**23.58**	**0.0168**	**0.0186**	**13980.2**	**21.84**
Genotypes	**35**	**Kharif**	**302.5****	**57.83***	**100.51****	**0.037***	**0.06***	**33953.3****	**16.67***
		Summer	**107.3***	**46.77***	**96.51***	**0.040***	**0.04***	**179051.2***	**21.43***
Error	**70**	**Kharif**	**11.63**	**9.36**	**2.07**	**0.0079**	**0.005**	**4062.1**	**2.15**
		Summer	**14.07**	**11.24**	**1.48**	**0.0039**	**0.018**	**4171.1**	**2.91**

* **Significant at 0.05 level of probability**
**** Significant at 0.01 level of probability**

Table 1.Genetic Components of Variation and their Proportions for Seed Yield and its Components in Bottle gourd

Components / proportions	Days to first male flower		Node no. to first female flower		Number of primary branches/vine		Fruit weight (kg)		Pedicel diameter (Cm)		Number of seeds per fruits		100 seed weight (g)	
	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer	Kharif	Summer
D	123.50* ± 30.7	15.8 ±8.0	26.1* ±7.9	10.1** ±2.9	8.4 ±1.1	5.5 ±3.5	0.0 ±0.01	0.01 ±0.01	0.00 ±0.03	0.00 ±0.00	3376.4* ±4542.4	8110.7** ±191.82	2.45 ±3.0	3.18 ±3.72
F	15.7 ±12.6	6.9 ±9.1	53.4* ±18.6	15.2 ±6.3	4.4 ±2.2	4.3 ±2.8	0.00 ±0.02	0.01 ±0.02	0.00 ±0.06	0.00 ±0.01	9747.0 ±1033.4	13337.8* ±4515.9	7.40 ±7.80	11.88 ±8.80
H_1	169.61 ±70.68	54.28 ±18.61	93.79** ±18.16	33.04** ±6.19	109.71* ±44.01	52.90** ±8.63	0.05* ±0.02	0.07** ±0.02	0.08 ±0.06	0.02 ±0.00	44943.74** ±10442.86	23899.99** ±4392.69	27.43* ±7.59	40.26** ±8.56
H_2	124.13 ±61.49	37.47 ±16.20	61.35** ±15.80	24.47** ±5.38	86.05* ±38.29	51.58** ±7.51	0.04 ±0.02	0.05* ±0.02	0.07 ±0.05	0.01 ±0.00	32111.97* ±9085.28	16415.47** ±3821.64	19.56* ±6.60	26.20** ±7.45
h^2	0.00 ±0.24	-0.57 ±10.87	18.88 ±10.60	9.10 ±3.61	15.78 ±25.68	38.07** ±5.04	0.01 ±0.01	0.01 ±0.01	0.02 ±0.03	0.00 ±0.00	45112.67* ±6092.98	32299.32** ±2562.15	20.16 ±4.43	25.62** ±4.99
E	3.88 ±10.25	1.36 ± 2.70	3.12 ±2.63	0.65 ±0.90	0.69 ±6.38	0.50 ±1.25	0.00 ±0.00	0.00 ±0.00	0.00 ±0.01	0.00 ±0.00	1354.18 ±1514.21	247.15 ± 636.94	0.39 ±1.10	0.98 ±1.25
$(H_1/D)^{1/2}$	1.17	1.85	1.9	1.81	3.6	3.09	3.6	3.84	8.38	2.97	3.65	1.72	3.35	3.56
$(H_2/4H_1)$	0.18	0.17	0.16	0.19	0.22	0.24	0.21	0.21	0.21	0.23	0.18	0.17	0.18	0.16
$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$	1.11	0.79	3.35	2.42	0.86	1.29	1.29	2.25	1.06	1.75	2.31	2.84	2.64	3.21

Appendix 1: Pages A1-A12.

INSTRUCTIONS FOR OBJECTIVE DESCRIPTION OF VARIETY
Pumpkin, Squash, Gourd of *Cucurbita pepo* L.

1. Subject & Purpose of these Guidelines

These guidelines for testing apply to all varieties of *Cucurbita pepo* L. Their purpose is to tabulate many characteristics in order to establish the distinguishing phenotypic features of various cultivars of this species.

2. Material Required

a. The applicant, upon receiving a PVP application number and seed-depository letter from the PVP Examiner, will deposit 3000 (three thousand) seeds at the institution indicated on the depository form.
b. The seed sample should meet normal commercial requirements for germination, which should be stated by the applicant.
c. The sample must not have undergone any treatment unless the competent authorities allow or request such treatment. If the seed sample has been treated, full details of the treatment must be given.

3. Conduct of Testing

a. The minimum duration of the test of the variety shall be two independent growing cycles and the test may be done at one or more localities.
b. The test should be conducted under conditions ensuring satisfactory growth of the plants and normal expression of the characteristics of the variety under examination.
c. The size of the plots must be large enough to allow the plants to realize their potential. The plots also must be large enough to allow removal of plants or parts of plants for measurement or counting, if necessary, without jeopardizing later observations, such as those to be made at the end of the growing cycle. Each characteristic for testing should be based on **a total of at least 24 plants (12 per growing cycle)**. Separate plots for observations and for measurements can be used but only if they have been subjected to similar growing and environmental conditions.
d. Testing for special purposes (disease resistance, vitamin content, etc.) may be established.

4. Methods and Observations

a. All observations determined by measurement or counting should be made on at least 12 plants or parts taken from each of 12 plants.
b. For the assessment of uniformity, a population standard of 3% should be applied. Where the test is conducted on 24 plants, the maximum number of off-types allowed would be 2.

5. Grouping of Varieties

a. The collection to be grown should be divided into groups to facilitate the assessment of distinctness. Any characteristic suitable for grouping purposes must be one which is (i) expressed by the economically important part of the plant (the fruit), (ii) recognized by all concerned, (iii) known to vary only slightly within a variety, (iv) known to vary only slightly under various environmental conditions, and (v) known to be reflective of genetic relationships. **Fruit shape** is the only characteristic of *Cucurbita pepo* meeting all of these requirements and has been used to establish edible-fruited variety groups (Figure 1) (see H.S. Paris, 1986, A proposed subspecific classification for *Cucurbita pepo*, Phytologia 61: 133–138).
b. The applicant has the full responsibility, upon submitting the variety for testing, to indicate the appropriate group to which the variety belongs (see description below and Figure 1). The applicant is free to suggest appropriate control varieties from the same group.

The following list of varieties is not intended to be used as the only allowable comparison varieties.

-**Acorn**: turbinate, top-shaped with ridges and furrows. Examples: Table Queen, Table Ace, Table Gold, Taybelle, Sweet Dumpling.

-**Cocozelle**: long to very long cylindrical, tends to bulge at stylar end or at both stylar and peduncle end. Length-to-width ratio at least 3.5:1, often much more. Examples: Italiano Largo, Striato d'Italia, Arlika, Opal, Verte d'Italie, Costata Romanesca, Portofino, Lungo Fiorentino.

-**Crookneck**: elongate with narrow, often curved neck. Examples: Dixie, Pavo, Horn of Plenty, Gentry, Yellow Summer Crookneck.

-**Pumpkin**: round or nearly round; oblate, globular, spherical, oval. Examples: One Ball, Eight Ball, Ronde de Nice, Small Sugar, Connecticut Field, Howden, Winter Luxury, Tours.

-**Scallop**: (syn.: Patty Pan, Patisson, Custard, Button, etc.), flattened with lobes. Examples: Peter Pan, Sunburst, Starship, Sunny Delight, White Bush Scallop, Flying Saucer.

-**Straightneck**: elongate with constriction of short thick neck. Examples: Cougar, Lemon Drop, Enterprise, Early Prolific Straightneck, Saffron.

-**Vegetable marrow**: short, tapered cylindrical or dumpy. Length-to-width ratio ranging from 1.5:1 to 3.0:1. Examples: Anita, Clarita, Beirut, Magda, Grey Zucchini OP, Hurakan, Vegetable Spaghetti.

-**Zucchini**: (syn.: Courgette). Uniformly cylindrical, length-to-width ratio usually approximating 4:1. Examples: Black Beauty, Black Zucchini, Fordhook Zucchini, Aristocrat, Gold Rush, Senator, Spineless Beauty, Raven, Golden Rod.

-**Gourd (non- or marginally edible)**: Various shapes, small size, ornamental, not for culinary use. Examples: Miniature Ball, Autumn Wings, Bicolor Pear, Orange, Orange Warted

c. The applicant will conduct the test using **appropriate varieties from the same group** as controls. These varieties should include any from the same group that, based on descriptive accounts, might be closely similar to the variety tested.

Exhibit C

U.S. DEPARTMENT OF AGRICULTURE
AGRICULTURAL MARKETING SERVICE
SCIENCE AND TECHNOLOGY
PLANT VARIETY PROTECTION OFFICE
BELTSVILLE, MD 20705

OBJECTIVE DESCRIPTION OF VARIETY
Pumpkin/Squash/Gourd (Cucurbita pepo)

NAME OF APPLICANT (S)	TEMPORARY OR EXPERIMENTAL DESIGNATION	VARIETY NAME

ADDRESS (Street and No. or RD No., City, State, Zip Code and Country)	FOR OFFICIAL USE ONLY PVPO NUMBER

PLEASE READ ALL INSTRUCTIONS CAREFULLY:

In the spaces on the left, enter the appropriate numbers that describe the characteristics of the application variety. On the right, enter the appropriate numbers that describe the characteristics of the most similar comparison variety. Right justify whole numbers by adding leading zeros if necessary. The variety that you choose for comparison should be the most similar one in terms of overall morphology, background and maturity. Please follow the guidelines on page 1 for conducting the trials. The comparison variety should be grown in field trials with the application variety for two independent growing cycles, at one or more localities, in the region and season of best adaptability. In general, measurements of quantitative traits should be taken on at least 24 randomly selected plants or plant parts to obtain averages and statistics that describe a typical field of the variety. (Form technical content last updated March 2007.)

General Descriptors:	Comparison Variety Name _____
___ **01. Fruit Shape/ Variety Group (Figure 1; also see instruction 5b above):** 1 = Acorn 2 = Cocozelle 3 = Crookneck 4 = Pumpkin 5 = Scallop 6 = Straightneck 7 = Vegetable marrow 8 = Zucchini 9 = None of the above, specify shape: _____ (e.g. pyriform, bottle, hourglass, fusiform, etc.) 10 = Gourd, specify shape: _____ (e.g. spherical, oblate, egg, pear, spoon, crown-of-thorns, star, winged, etc.)	___ 01. Fruit Shape/ Variety Group
___ **02. Expected primary usage:** 1 = Culinary 2 = Ornamental 3 = Both	___ 02. Expected primary usage
___ **03. What parts of the plant provide expected primary usage (above):** 1= Mature fruit 2 = Immature fruit 3 = Flowers 4 = Vegetation 5 = Seeds	___ 03. Part of plant for #02 above
04. Cotyledons measured between full expansion of first and second true leaves:	04. Cotyledons:
__ . __ __ 04a. Length to width ratio (example: 0.00)	__ . __ __ 04a. Length to Width ratio
____ 04b. Apex 1 = Notched 2 = Not notched	___ 04b. Apex
____ 04c. Veining 1 = Obscure 2 = Obvious	____ 04c. Veining
Application Variety	Comparison Variety

Application Variety	Comparison variety
Main Stem:	Main Stem:
05. Main stem green color, when plants have 20 true leaves on the main stem:	05. Main Stem Color:
___ 05a. Main color: 1 = Light (Cocozelle, Black Beauty, Ma'yan, Vegetable Spaghetti) 2 = Dark near base only (Early Prolific Straightneck) 3 = Dark spots at nodes (Sihi Lavan) 4 = Dark for nearly the entire length (Fordhook Zucchini, Jack O'Lantern, Howden)	___ 05a. Main color
___ 05b. White marks at nodes: 1 = Absent 2 = Present	___ 05b. White marks at nodes
___ 05c. Yellow marks (associated with precocious yellow gene complex) at nodes: 1 = Absent 2 = Present	___ 05c. Yellow marks at nodes
_____ **06. Growth habit when plants have 20 true leaves on the main stem:** Bush 1 = True-bush (Fordhook Zucchini, Cocozelle, Ronde de Nice, Benning's Green Tint) 2 = Semi-bush (Taybelle, Table Ace, Jackpot) Vine 3 = Moderate vine (Small Sugar, Spookie, Magic Lantern, Table Queen) 4 = Rampant vine (Howden, Connecticut Field)	___ 06. Growth habit
____ **07. Tendrils when plants have 20 true leaves on the main stem:** 1 = Absent or rudimentary 2 = Present and elongated	___ 07. Tendrils
08. Main stem internode dimensions when observed after the 20th internode has developed:	08. Internode dimensions
____ 08a. Length 1 = Internode length constant from 5th to 15th internode 2 = Internode length increases from 5th to 15th internode	___ 08a. Length
____ 08b. Width 3 = Internode width constant from 5th to 15th internode 4 = Internode width decreases from 5th to 15th internode	___ 08b. Width
Petioles:	Petioles:
09. Petioles derived from main stem when observed after the 20th node has developed:	09. Petiole measurements:
__ . __ __ 09a. Length to medial width ratio of 10th petiole (example: 0.00)	__ . __ __ 09a. L:W ratio of 10th petiole
__ . __ __ 09b. Length to medial width ratio of 15th petiole (example: 0.00)	__ . __ __ 09b. L:W ratio of 15th petiole
____ **10. Petiole spininess (prickles) when observed after the 20th internode has developed:** 0 = Smooth (Spineless Beauty) 1 = Slightly spiny (Goldy, Fordhook Zucchini) 2 = Moderately spiny (Cocozelle) 3 = Noticeably spiny (Early Prolific Straightneck) 4 = Very spiny (Clarita) 5 = Extremely spiny	___ 10. Petiole spininess
____ **11. Petiole angle of 6th through 15th petioles on main stem (between ground and petiole) after the 20th internode has developed, measured when the main stem is at a 90-degree angle with the ground:** 1 = Horizontal (Caserta, less than 10 degrees) 2 = Nearly horizontal (Goldy, Fordhook Zucchini, 10 to 30 degrees) 3 = Intermediate (30 to 45 degrees) 4 = Vertical or nearly vertical (45 degrees or greater)	___ 11. Petiole Angle
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Laminae:	Laminae:
____ **12. Lobing of 10th and 15th laminae on main stem (Figure 2):** 0 = Not lobed 1 = Shallowly lobed 2 = Medium lobed 3 = Deeply lobed 4 = Very deeply lobed	___ 12. Lobing
13. Dimensions of leaf laminae after the 20th internode has developed (length measured from the point of petiole attachment to the apex of the lamina; maximal width measured at 90-degree angle to the length of the lamina):	13. Leaf laminae dimensions:
__ . __ __ 13a. Length to maximal width ratio of 10th true leaf (example: 0.00)	__ . __ __ 13a. L:W ratio of 10th true leaf
__ . __ __ 13b. Length to maximal width ratio of 15th true leaf (example: 0.00)	__ . __ __ 13b. L:W ratio of 15th true leaf
____ **14. Silver blotching or mottling (genetic, not leaf-silvering disorder) of adaxial surface of laminae after the 20th internode has developed:** 1 = Silver blotching completely absent over time (Costata Romanesca, Early Prolific Straightneck) 2 = Silver blotching present early in development, then disappearing 3 = Silver blotching over a small amount of the surface 4 = Silver blotching over a moderate amount of the surface 5 = Silver blotching over much of the surface (Caserta)	___ 14. Silver blotching
Flowers:	Flowers:
___ **15. Number of flowers per node:** 1 = Averaging clearly less than one 2 = One (almost always) (Fordhook Zucchini, Cocozelle) 3 = Often more than one 4 = Consistently more than one (Yellow Summer Crookneck)	___ 15. Number of flowers per node
16. Staminate flower on day of anthesis on main stem between nodes 11 and 20 (Figure 3):	16. Staminate flower measurements:
__ __ __ mm 16a. Length from base of calyx to tip of corolla	__ __ __ mm 16a. Length of petal
__ __ __ mm 16b. Exterior width at top of calyx cup	__ __ __ mm 16b. Width of petal
__ __ __ mm 16c. Pedicel length	__ __ __ mm 16c. Pedicel length
__ __ __ mm 16d. Length of anther column	__ __ __ mm 16d. Length of anther column
___ **17. Dominant color of corolla of staminate flower, on day of anthesis:** 1 = Orange-yellow 2 = Light yellow 3 = Nearly white	___ 17. Dominant staminate flower color
___ **18. Ring at base of interior of staminate corolla:** 1 = Absent 2 = Yellow 3 = Green and yellow 4 = Light green 5 = Dark green	___ 18. Ring at base of staminate corolla
___ **19. Ring at base of interior of pistillate corolla:** 1 = Absent 2 = Yellow 3 = Green and yellow 4 = Light green 5 = Dark green	___ 19. Ring at base of pistillate corolla
20. Pistillate flower on day of anthesis:	20. Pistillate flower measurements:
__ __ __ mm 20a. Length from base of calyx to tip of corolla	__ __ __ mm 20a. Length of petal
__ __ __ mm 20b. Pedicel length	__ __ __ mm 20b. Pedicel length
___ **21. Ovary color on day prior to anthesis:** 1 = Green (Black Beauty, Fordhook Zucchini, Cocozelle, Clarita) 2 = Green turning yellow (Yellow Summer Crookneck) 3 = Yellow (Goldy, Gold Rush, Multipik) 4 = Bicolor green and yellow (Zephyr, Flying Saucer)	___ 21. Ovary color
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Immature Fruit:	Immature Fruit:
22. Immature fruit size (3–5 days past anthesis) (Figure 4):	22. Immature fruit size
__ . __ __ 22a. Length (through the axis) to medial width ratio (example: 0.00)	__ . __ __ 22a. L:W ratio (to medial width)
__ . __ __ 22b. Length (through the axis) to maximal width ratio (example: 0.00)	__ . __ __ 22b. L:W ratio (to maximal width)
23. Immature fruit color (3–5 days past anthesis):	23. Immature fruit color
___ 23a. Main color: 1 = Intense green (Fordhook Zucchini, Black Beauty, Jack O'Lantern, Senator, Spineless Beauty, Raven) 2 = Light green (Arlika, Clarita, Small Sugar, Ronde de Nice) 3 = Intense yellow (Goldy, Gold Rush, Golden Rod) 4 = Light yellow (Early Prolific Straightneck, Yellow Summer Crookneck, Multipik, Dixie, Gentry) 5 = Intense bicolor (Sunburst, Nova) 6 = Light bicolor 7 = Striped green (Cocozelle, Costata Romanesca, Caserta) 8 = Striped yellow 9 = Striped bicolor, or quadricolor (Zephyr, Flying Saucer)	___ 23a. Main color
___ 23b. If striped, the darker stripes are: 1 = Broad and contiguous (Cocozelle, Costata Romanesca) 2 = Narrow and not contiguous (Caserta, Verte d'Italie)	___ 23b. Description of darker stripes
____ **24. Immature fruit flecks:** 1 = Small (Nero di Milano, Raven, Magic Lantern) 2 = Medium (Fordhook Zucchini, Nano Verde di Milano) 3 = Large (Ortolano di Faenza, Striato Pugliese, Costata Romanesca, Grey Zucchini OP, Clarita, Spineless Beauty, Howden, Ronde de Nice)	___ 24. Immature fruit flecks
____ **25. Immature fruit warting:** 1 = Absent (Cocozelle, Fordhook Zucchini, Ronde de Nice, Gentry) 2 = Present (Early Prolific Straightneck, Yellow Summer Crookneck, Early Summer Crookneck)	___ 25. Immature fruit warting
Mature Fruit:	Mature Fruit:
____ **26. Mature fruit surface topography (fill in the blank with the most appropriate choice) (Figure 5):** Ribbing present (swelling above vascular tracts): 1 = Prominent and along entire length (Costata Romanesca) 2 = Slight, more prominent near peduncle (Fordhook Zucchini) 3 = Slight, near peduncle (Grey Zucchini OP, Small Green Algerian) Furrowing (angularly depressed above vascular tracts) and/or ridging (angularly raised between vascular tracts) 4 = Prominent, along nearly entire length (Taybelle, Mammoth Table Queen) 5 = Moderate (Sweet Dumpling) Scalloping (roundly lobed between vascular tracts): 6 = Prominent, at equatorial region (Benning's Green Tint) 7 = Not so prominent, at equatorial region (Scallopini) 8 = Prominent, at peduncular region (Sunny Delight) 9 = Not so prominent, at peduncular region 10 = Prominent, at stylar region (Sunburst) 11= Not so prominent, at stylar region Lobing (broadly and roundly protruding between the vascular tracts and shallowly depressed along the vascular tracts, along nearly the entire length of the fruit) 12 = Prominent (Jack-Be-Little) 13 = Not so prominent Grooving (very narrow, shallow depressions along vascular tracts and midway in-between) 14 = Distinct (Howden) 15 = Not so distinct (Winter Luxury) Wrinkling (irregular surface) 16 = Distinct 17 = Indistinct 18 = Completely smooth	___ 26. Mature fruit topography
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Mature Fruit (continued):	Mature Fruit (continued):
27. Mature fruit dimensions (at least 40 days past anthesis) (Figure 4):	27. Mature fruit dimensions:
__ . __ __ 27a. Length (through the axis) to medial width ratio (Example: 0.00)	__ . __ __ 27a L:W ratio (to medial width)
__ . __ __ 27b. Length (through the axis) to maximal width ratio (Example: 0.00)	__ . __ __ 27b. L:W ratio (to maximal width)
___ **28. Mature fruit warting:** 1 = Absent (Cocozelle, Fordhook Zucchini, Ronde de Nice) 2 = Sparse, small (Gentry) 3 = Sparse, large (White Bush Scallop) 4 = Many, small 5 = Many, large (Orange Warted, Yellow Summer Crookneck)	___ 28. Mature fruit warting
___ **29. Mature fruit rind:** 1 = Lignified (when cutting mature fruit, little cracks form) 2 = Not lignified (when cutting mature fruit, they slice smoothly and easily)	___ 29. Mature fruit rind lignified
___ **30. Mature fruit stylar scar:** 1 = Protruding 2 = Flat 3 = Depressed	___ 30. Mature fruit stylar scar
___ **31. Mature fruit stylar end:** 1 = Depressed (Howden) 2 = Nearly Flat (Fordhook Zucchini, True French) 3 = Convex (Yellow Summer Crookneck)	___ 31. Mature fruit stylar end
___ **32. Mature fruit peduncle end:** 1 = Depressed 2 = Nearly flat 3 = Convex	___ 32. Mature fruit peduncle end
33. Mature fruit peduncle (Figure 6):	33. Mature fruit peduncle dimensions:
__ . __ __ 33a. Length (through the axis) to medial width ratio (Example: 0.00)	__ . __ __ 33a. L:W ratio (to medial width)
__ . __ __ 33b. Length (through the axis) to maximal width (near fruit attachment) ratio (Example: 0.00)	__ . __ __ 33b. L:W ratio (to maximal width)
___ **34. Mature fruit surface:** 1 = Netted (Winter Luxury) 2 = Cracked (Golden Zucchini) 3 = Neither	___ 34. Mature fruit surface
35. Mature fruit exterior color: ___ 35a. Main color: 1 = Light green 2 = Dark green (Table Queen) 3 = Black green (Fordhook Zucchini, Taybelle) 4 = Grey green 5 = Grey 6 = Light orange 7 = Pale orange 8 = Medium orange (Winter Luxury, Grey Zucchini OP) 9 = Intense orange (Jack O'Lantern, Howden) 10 = Yellow orange 11 = Light yellow orange 12 = Light yellow (Vegetable Spaghetti) 13 = Intense yellow (Early Prolific Straightneck) 14 = Nearly white (White Bush Scallop) Complex colors (give combination of choice above with color covering most of the fruit surface first)	___ 35a Main fruit exterior color
___, ___ 35b. Striped (Cocozelle 1, 8; Delicata 11, 2)	___, ___ 35b. Striped pattern
___, ___ 35c. Bicolor (Sunburst 10, 1)	___, ___ 35c. Bicolor pattern
___, ___, ___, ___ 35d. Quadricolor (Carnival 2, 4, 6, 11)	___, ___, ___, ___ 35d. Quadricolor pattern
___ **36. Mature fruit mesocarp (flesh) color:** 1 = Intense Orange (Winter Luxury) 2 = Light Orange (Connecticut Field, Fordhook Zucchini) 3 = Intense Yellow (Mongogo) 4 = Light Yellow (Early Prolific Straightneck) 5 = White (White Bush Scallop) 6 = White tinged green	___ 36. Mature fruit flesh color
___ **37. Mature fruit endocarp (placenta) color:** 1 = Orange 2 = Yellow 3 = White	___ 37. Mature fruit placenta color
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Seed:	Seed:
38. Seed cavity:	38. Seed cavity measurements:
__ . __ __ 38a. Length (through the axis) to medial width ratio (Example: 0.00)	__ . __ __ 38a. L:W ratio (to medial width)
__ . __ __ 38b. Length (through the axis) to maximal width ratio (Example: 0.00)	__ . __ __ 38b. L:W ratio (to maximal width)
___ **39. Seed hull (from mature fruit harvested on candidate variety):** 1 = Absent 2 = Present but rudimentary 3 = Present with normal appearance	___ 39. Seed hull
40. Seed dimensions (average for 12 mature seeds from open-pollinated fruit harvested on candidate variety):	40. Seed measurements
__ . __ __ 40a. Length to width ratio (Example: 0.00)	__ . __ __ 40a. L:W ratio
__ . __ __ 40b. Length to thickness ratio (Example: 0.00)	__ . __ __ 40b. L:Thickness ratio
__ . __ __ 40c. Width to thickness ratio (Example: 0.00)	__ . __ __ 40c. W:Thickness ratio
____ **41. Resistance to biotic or abiotic stresses:** 1 = None 2 = Yes, as qualified In Exhibit B or D (specify disease resistance/tolerance): _____ _____ _____ _____ _____ _____	___ 41. Resistance to biotic or abiotic stresses _____ _____ _____ _____ _____ _____
____ **42. Unique features that are not listed in the current 'Exhibit C' and/or are strongly environmentally dependent or occur sporadically (i.e.: peduncle characteristics, immature or mature fruit length or contents, width, or weight, stylar scar size, pollen color, seed-coat characteristics, branching, etc.):** 1 = None 2 = Yes, as described herein: _____ _____ _____ _____ _____ _____	___ 42. Unique features not listed elsewhere in the application _____ _____ _____ _____ _____

43. On additional pages, attach photographs of mature fruits of both the application variety and the comparison variety, showing external and internal coloring, with a ruler in the photograph to indicate scale.

Additional photographs of the plant, flowers, immature fruits, or other plant parts could also be helpful in providing a full description of the variety to readers. Please provide such photographs if you believe they would be helpful.

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Figure 1. Fruit shapes

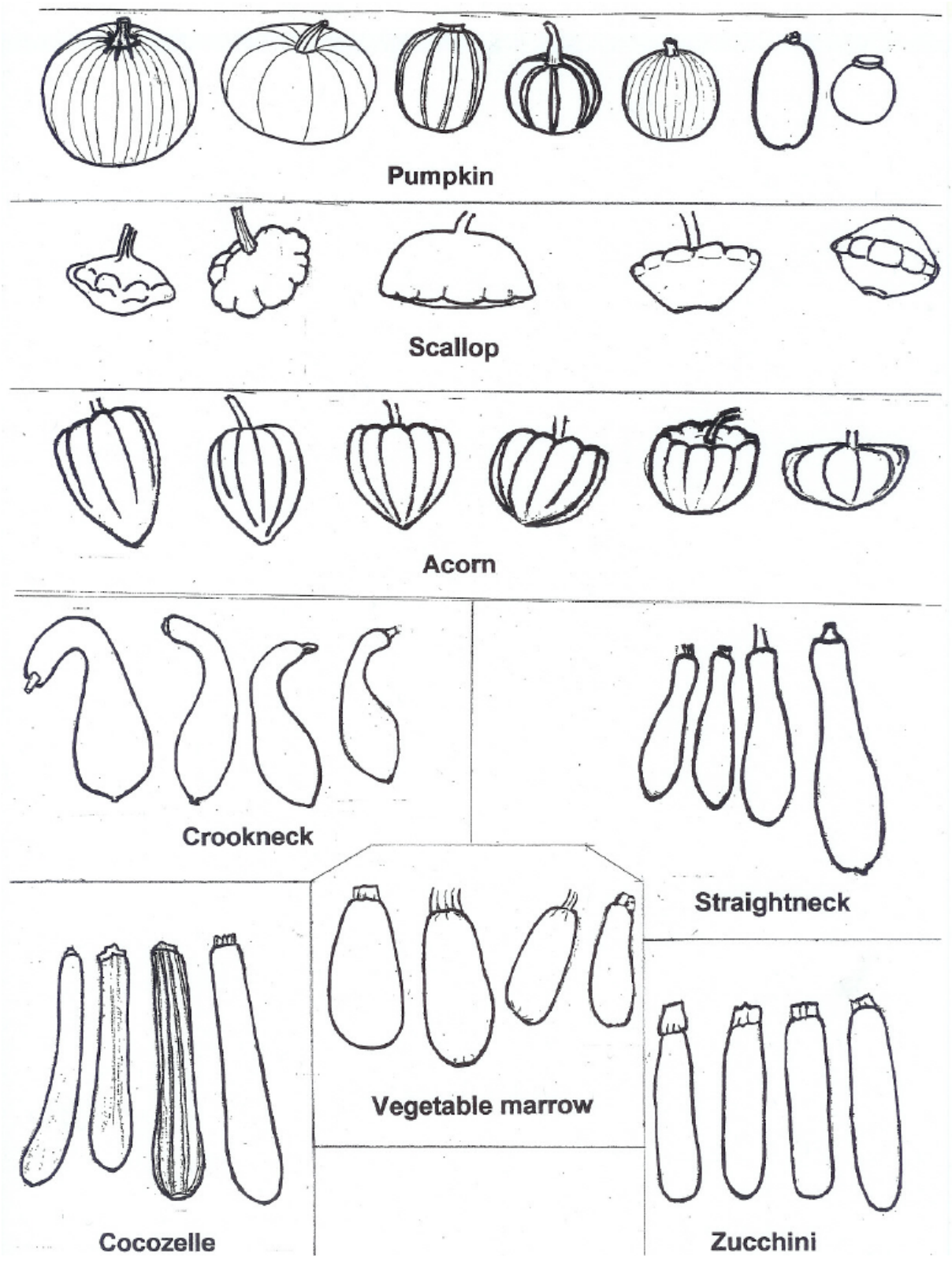


Figure 2. Leaf lobing

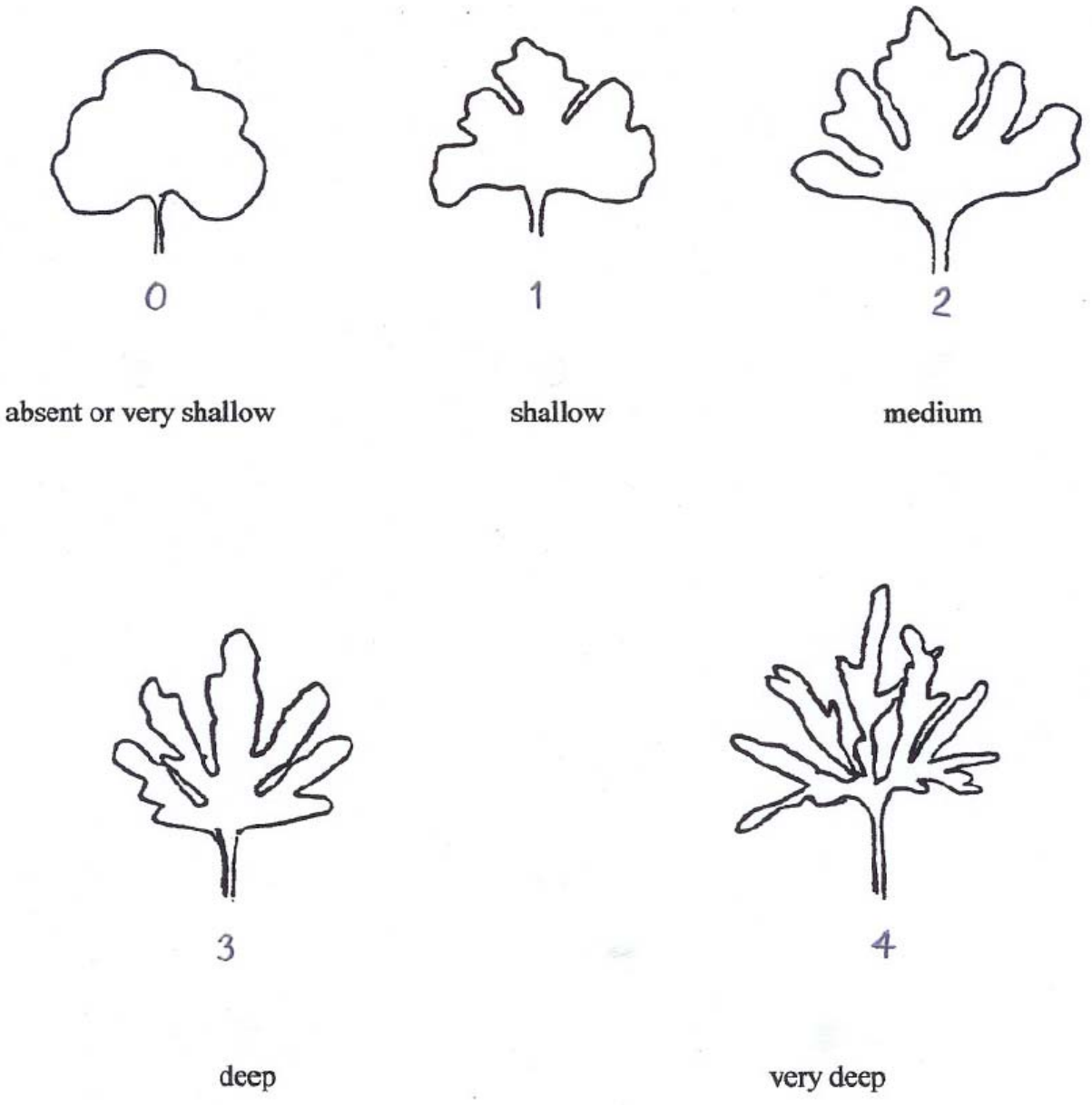


Figure 3. Flower measurements

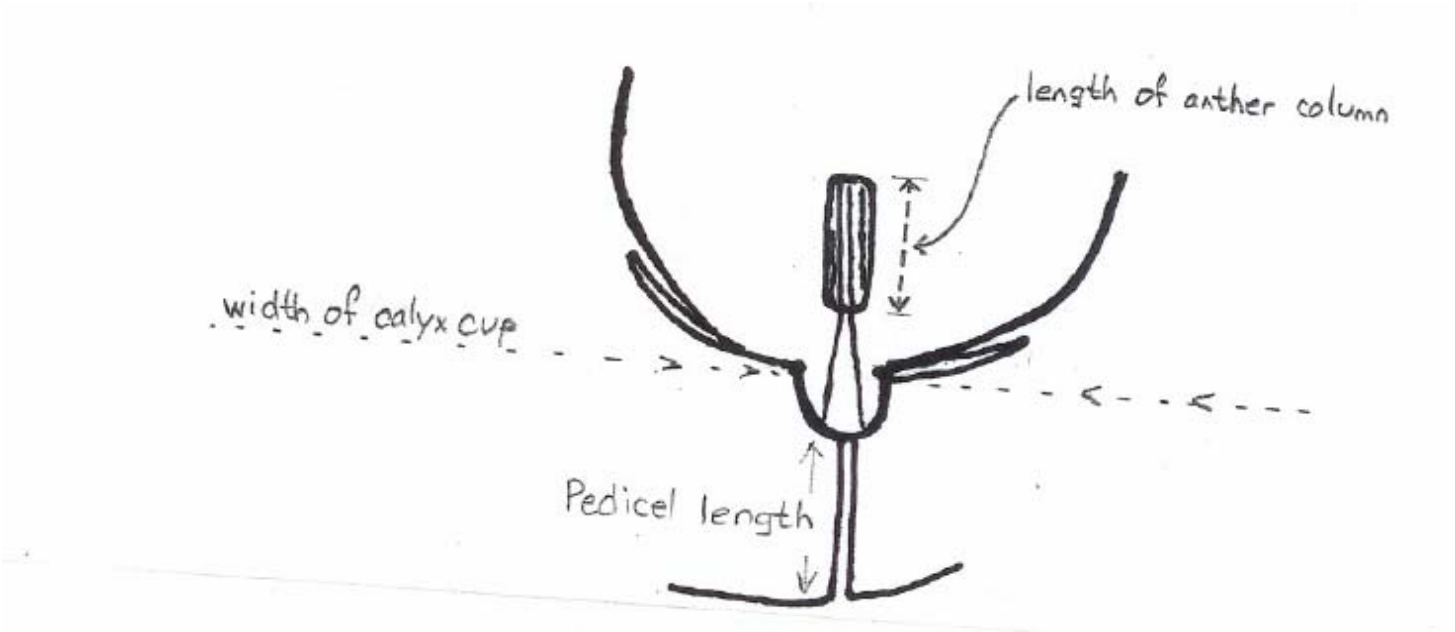


Figure 4. Fruit measurements

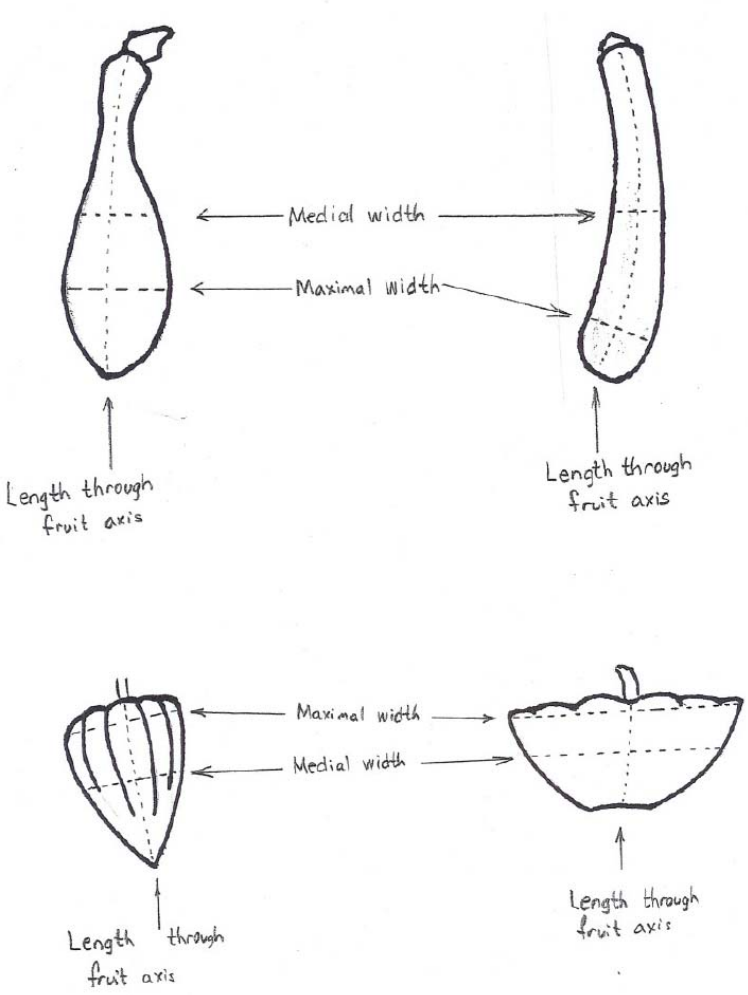


Figure 5. Fruit cross-sections

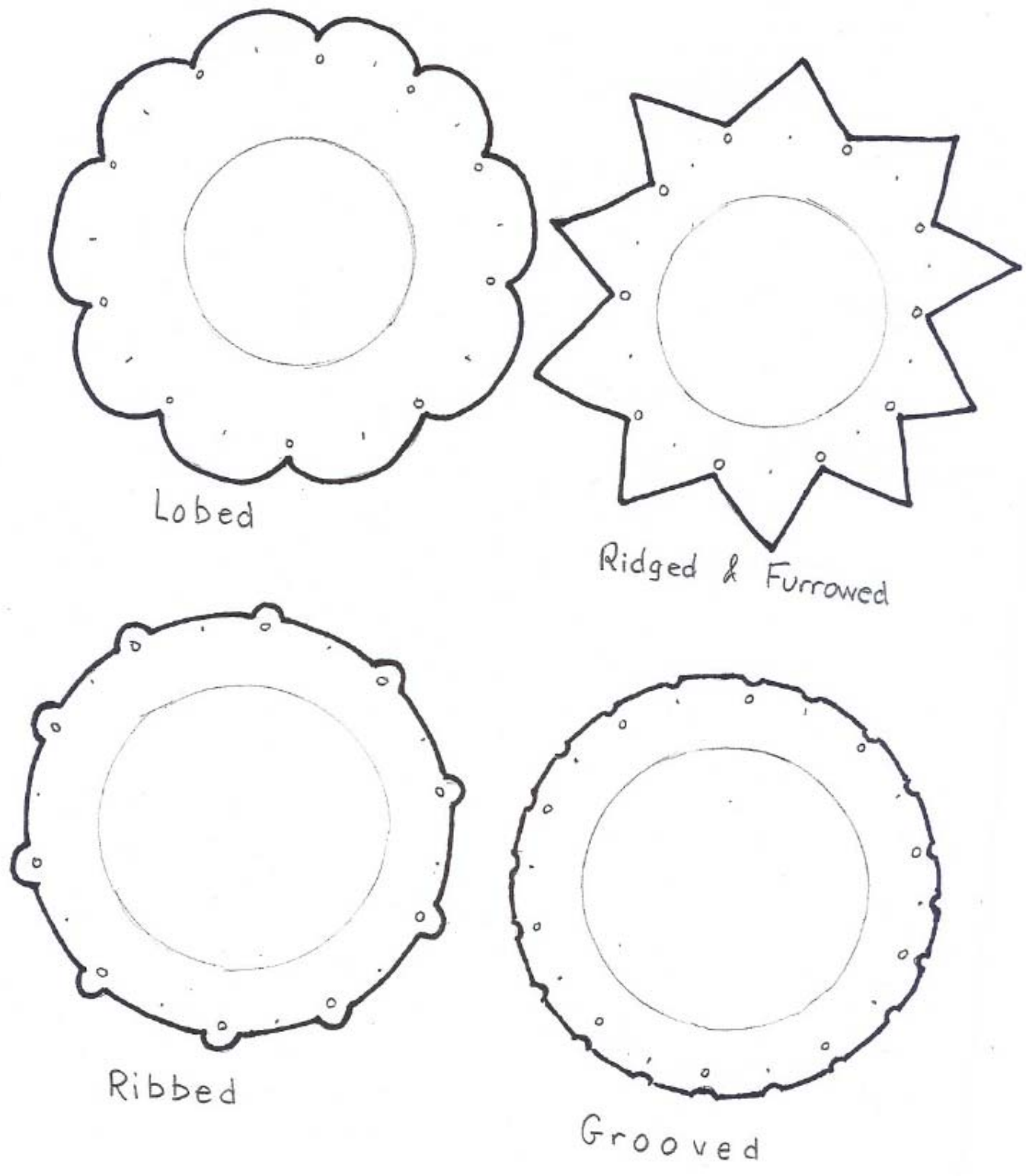
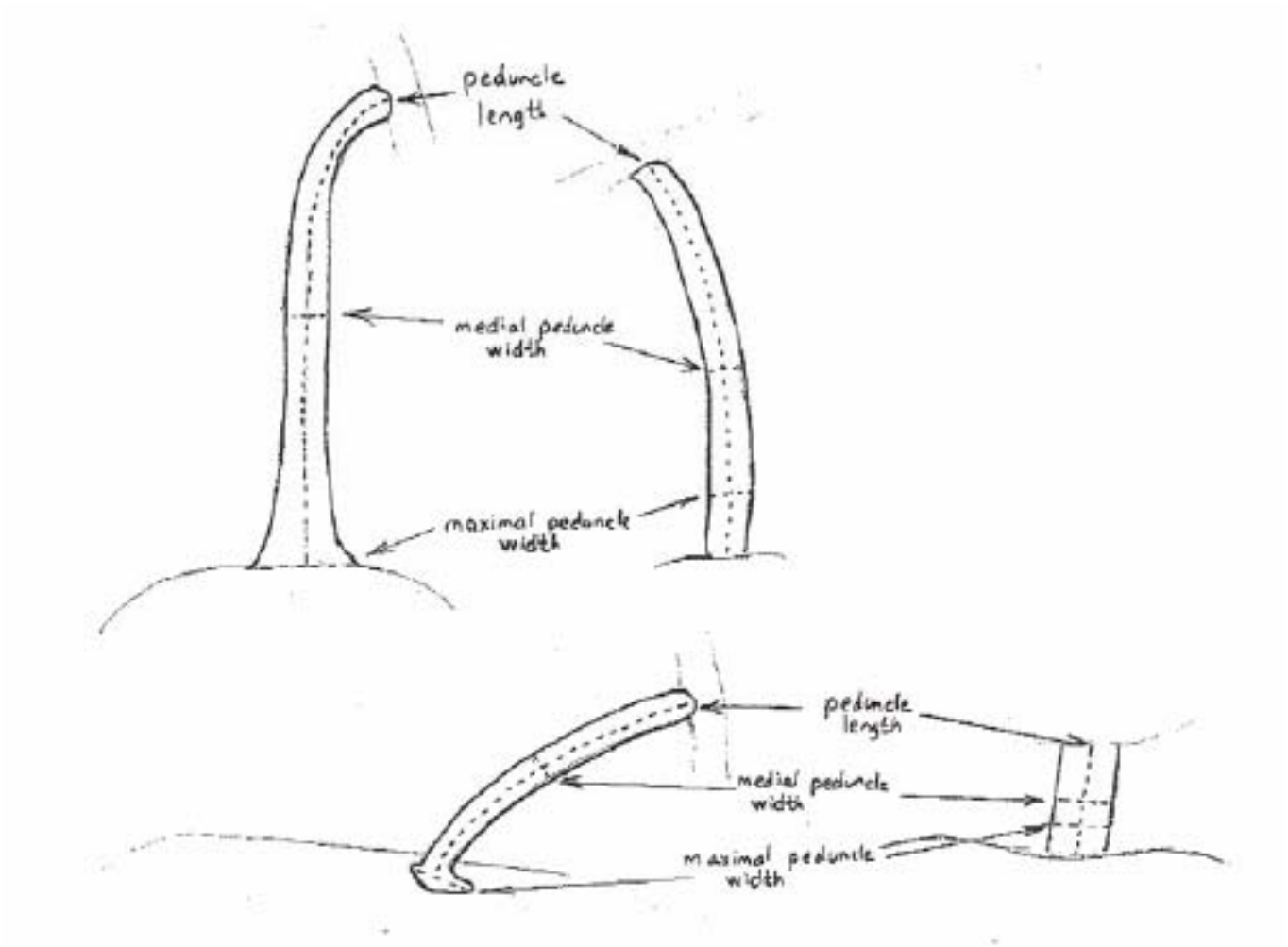


Figure 6. Peduncle measurements



Appendix 2: B1-B11.

INSTRUCTIONS FOR OBJECTIVE DESCRIPTION OF VARIETY
Pumpkin, Squash, Gourd of all species EXCEPT *Cucurbita pepo* L.

1. Subject & Purpose of these Guidelines

These Guidelines for testing apply to all varieties of pumpkins, squash, and gourds except for those belonging to the species *Cucurbita pepo* L. Their purpose is to tabulate many characteristics in order to establish the distinguishing phenotypic features of various cultivars of this species.

2. Material Required

a. The applicant, upon receiving a PVP application number and seed-depository letter from the PVP Examiner, will deposit 3000 (three thousand) seeds at the institution indicated on the depository form.
b. The seed sample should meet normal commercial requirements for germination, which should be stated by the applicant.
c. The sample must not have undergone any treatment unless the competent authorities allow or request such treatment. If the seed sample has been treated, full details of the treatment must be given.

3. Conduct of Testing

a. The minimum duration of the test of the variety shall be two independent growing cycles and the test may be done at one or more localities.
b. The test should be conducted under conditions ensuring satisfactory growth of the plants and normal expression of the characteristics of the variety under examination.
c. The size of the plots must be large enough to allow the plants to realize their potential. The plots also must be large enough to allow removal of plants or parts of plants for measurement or counting, if necessary, without jeopardizing later observations, such as those to be made at the end of the growing cycle. Each characteristic for testing should be based on **a total of at least 24 plants (12 per growing cycle)**. Separate plots for observations and for measurements can be used but only if they have been subjected to similar growing and environmental conditions.
d. Testing for special purposes (disease resistance, vitamin content, etc.) may be established.

4. Methods and Observations

a. All observations determined by measurement or counting should be made on at least 12 plants or parts taken from each of 12 plants.
b. For the assessment of uniformity, a population standard of 3% should be applied. Where the test is conducted on 24 plants, the maximum number of off-types allowed would be 2.

5. Grouping of Varieties

The applicant should correctly classify the variety to species together with citation of the botanical authority (for example: *Cucurbita moschata* Duchesne). The applicant should suggest, upon submitting the variety for testing, the market type to which the variety belongs and suggest control varieties of the same species and type.

U.S. DEPARTMENT OF AGRICULTURE
AGRICULTURAL MARKETING SERVICE
SCIENCE AND TECHNOLOGY
PLANT VARIETY PROTECTION OFFICE
BELTSVILLE, MD 20705

Exhibit C

OBJECTIVE DESCRIPTION OF VARIETY
Pumpkin/Squash/Gourd (*Cucurbita spp.* ; non pepo's)

NAME OF APPLICANT (S)	TEMPORARY OR EXPERIMENTAL DESIGNATION	VARIETY NAME

ADDRESS (Street and No. or RD No., City, State, Zip Code and Country)	FOR OFFICIAL USE ONLY PVPO NUMBER

PLEASE READ ALL INSTRUCTIONS CAREFULLY:

In the spaces on the left, enter the appropriate numbers that describe the characteristics of the application variety. On the right, enter the appropriate numbers that describe the characteristics of the most similar comparison variety. Right justify whole numbers by adding leading zeros if necessary. The variety that you choose for comparison should be the most similar one in terms of species, overall morphology, background and maturity. Please follow the guidelines on page 1 for conducting the trials. The comparison variety should be grown in field trials with the application variety for two independent growing cycles, at one or more localities, in the region and season of best adaptability. In general, measurements of quantitative traits should be taken on at least 24 randomly selected plants or plant parts to obtain averages and statistics that describe a typical field of the variety. (Form technical content last updated March 2007.)

Application Variety	Comparison Variety
General Descriptors:	Comparison Variety Name _____
01. Species: _____ **(Scientific name, including botanical authority, is mandatory for acceptance of the application).**	01. Species: _____
___ **02. Expected primary usage:** 1 = Culinary 2 = Ornamental 3 = Both 4 = Other (please describe) _____	___ 02. Expected primary usage _____
___ **03. What parts of the plant provide expected primary usage (above):** 1 = Mature fruit 2 = Immature fruit 3 = Flowers 4 = Vegetation 5 = Seeds	___ 03. Part of plant for #02 above
04. Cotyledons measured between full expansion of first and second true leaves:	04. Cotyledons:
__ . __ __ 04a. Length to width ratio (example: 0.00)	__ . __ __ 04a. Length to Width ratio
____ 04b. Apex 1 = Notched 2 = Not notched	___ 04b. Apex
____ 04c. Veining 1 = Obscure 2 = Obvious	____ 04c. Veining

Application Variety	Comparison variety
Main Stem:	Main Stem:
05. Main stem green color, when plants have 20 true leaves on the main stem:	05. Main Stem Color:
___ 05a. Main color: 1 = Light 2 = Dark near base only 3 = Dark spots at nodes 4 = Dark for nearly the entire length	___ 05a. Main color
___ 05b. White marks at nodes: 1 = Absent 2 = Present	___ 05b. White marks at nodes
___ 05c. Yellow marks (associated with precocious yellow gene complex) at nodes: 1 = Absent 2 = Present	___ 05c. Yellow marks at nodes
_____ **06. Growth habit when plants have 20 true leaves on the main stem:** Bush 1 = True-bush (Gold Nugget, Redondo del Tronco) 2 = Semi-bush (Bush Pink Banana) Vine 3 = Moderate vine (Butternut) 4 = Rampant vine (Atlantic Giant, Long Island Cheese)	___ 06. Growth habit
____ **07. Tendrils when plants have 20 true leaves on the main stem:** 1 = Absent or rudimentary 2 = Present and elongated	___ 07. Tendrils
08. Main stem internode dimensions when observed after the 20th internode has developed:	08. Internode dimensions
____ 08a. Length 1 = Internode length constant from 5th to 15th internode 2 = Internode length increases from 5th to 15th internode	___ 08a. Length
____ 08b. Width 3 = Internode width constant from 5th to 15th internode 4 = Internode width decreases from 5th to 15th internode	___ 08b. Width
Petioles:	Petioles:
09. Petioles derived from main stem when observed after the 20th node has developed:	09. Petiole measurements:
__ . __ __ 09a. Length to medial width ratio of 10th petiole (example: 0.00)	__ . __ __ 09a. L:W ratio of 10th petiole
__ . __ __ 09b. Length to medial width ratio of 15th petiole (example: 0.00)	__ . __ __ 09b. L:W ratio of 15th petiole
Laminae:	Laminae:
____ **10. Lobing of 10th and 15th laminae on main stem (Figure 1):** 0 = Not lobed 1 = Shallowly lobed 2 = Medium lobed 3 = Deeply lobed 4 = Very deeply lobed	___ 10. Lobing
11. Dimensions of leaf laminae after the 20th internode has developed (length measured from the point of petiole attachment to the apex of the lamina; maximal width measured at 90-degree angle to the length of the lamina):	11. Leaf laminae dimensions:
__ . __ __ 11a. Length to maximal width ratio of 10th true leaf (example: 0.00)	__ . __ __ 11a. L:W ratio of 10th true leaf
__ . __ __ 11b. Length to maximal width ratio of 15th true leaf (example: 0.00)	__ . __ __ 11b. L:W ratio of 15th true leaf
____ **12. Silver blotching or mottling (genetic, not leaf-silvering disorder) of adaxial surface of laminae after the 20th internode has developed:** 1 = Silver blotching completely absent over time (Waltham Butternut, Gold Nugget) 2 = Silver blotching present early in development, then disappearing 3 = Silver blotching over a small amount of the surface 4 = Silver blotching over a moderate amount of the surface 5 = Silver blotching over much of the surface	___ 12. Silver blotching
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Flowers:	Flowers:
___ **13. Number of flowers per node:** 1 = Averaging clearly less than one 2 = One (almost always) 3 = Often more than one 4 = Consistently more than one	___ 13. Number of flowers per node
14. Staminate flower on day of anthesis on main stem between nodes 11 and 20 (Figure 2):	14. Staminate flower measurements:
__ __ __ mm 14a. Length from base of calyx to tip of corolla	__ __ __ mm 14a. Length of petal
__ __ __ mm 14b. Exterior width at top of calyx cup	__ __ __ mm 14b. Width of petal
__ __ __ mm 14c. Pedicel length	__ __ __ mm 14c. Pedicel length
__ __ __ mm 14d. Length of anther column	__ __ __ mm 14d. Length of anther column
___ **15. Dominant color of corolla of staminate flower, on day of anthesis:** 1 = Orange-yellow 2 = Intense yellow 3 = Light yellow 4 = Nearly white 5 = Other (please describe) _____	___ 15. Dominant staminate flower color _____
___ **16. Ring at base of interior of staminate corolla:** 1 = Absent 2 = Yellow 3 = Green and yellow 4 = Light green 5 = Dark green	___ 16. Ring at base of staminate corolla
___ **17. Ring at base of interior of pistillate corolla:** 1 = Absent 2 = Yellow 3 = Green and yellow 4 = Light green 5 = Dark green	___ 17. Ring at base of pistillate corolla
18. Pistillate flower on day of anthesis:	18. Pistillate flower measurements:
__ __ __ mm 18a. Length from base of calyx to tip of corolla	__ __ __ mm 18a. Length of petal
__ __ __ mm 18b. Pedicel length	__ __ __ mm 18b. Pedicel length
___ **19. Ovary color on day prior to anthesis:** 1 = Green 2 = Green turning yellow OR Bi-color green and yellow (Gold Nugget) 3 = Yellow (PI 165558, Prizewinner)	___ 19. Ovary color
Immature Fruit:	Immature Fruit:
___ **20. Fruit shape:** 1 = Spherical 2 = Globe OR Oblate (round, but wider than long) (Long Island Cheese, Musquee de Provence) 3 = Oval OR Oblong (round, but longer than wide) (Upper Ground Sweet Potato) 4 = Bell (Waltham Butternut) 5 = Considerably longer than wide (length to maximal width > 2.0:1) (Lunga di Napoli) 6 = Pyriform (Virginia Mammoth, Golden Cushaw) 7 = Hourglass (Hercules, Toonas Makino) 8 = Turban (Turks Turban, Bonnet Rouge) 9 = Turbinate (top-shaped) (White Rind Sugar) 10 = Fusiform (Hubbard) 11 = Drum-shaped (Buttercup) 12 = Other (please, describe) _____ _____ _____	___ 20. Fruit Shape
21. Immature fruit size (3–5 days past anthesis) (Figure 3):	21. Immature fruit size
__ . __ __ 21a. Length (through the axis) to medial width ratio (example: 0.00)	__ . __ __ 21a. L:W ratio (to medial width)
__ . __ __ 21b. Length (through the axis) to maximal width ratio (example: 0.00)	__ . __ __ 21b. L:W ratio (to maximal width)
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Immature Fruit (continued):	Immature Fruit (continued):
22. Immature fruit color (3–5 days past anthesis):	22. Immature fruit color
___ 22a. Main color: 1 = Intense green 2 = Light green (Waltham Butternut) 3 = Yellow (Prizewinner) 4 = Bicolor 5 = Striped green 6 = Other (please describe) _____ _____	___ 22a. Main color
___ 22b. If striped, the darker stripes are: 1 = Broad and contiguous (Guatemala Blue) 2 = Narrow and not contiguous	___ 22b. Description of darker stripes
____ **23. Immature fruit flecks:** 1 = Small 2 = Médium 3 = Large (Waltham Butternut)	___ 23. Immature fruit flecks
____ **24. Immature fruit warting:** 1 = Absent (Waltham Butternut, Redondo del Tronco) 2 = Present	___ 24. Immature fruit warting
Mature Fruit:	Mature Fruit:
____ **25. Mature fruit surface topography (fill in the blank with the most appropriate choice) (Figure 4):** Ribbing present (swelling above vascular tracts): 1 = Prominent and along entire length (*Luffa acutangula* Rocksberry) 2 = Slight, more prominent near peduncle 3 = Slight, near peduncle Furrowing (angularly depressed above vascular tracts) and/or ridging (angularly raised between vascular tracts) 4 = Prominent, along nearly entire length (Yokohama, White Rind Sugar, Long Island Cheese, Musquee de Provence, Rouge Vif d'Etampes, Atlantc Giant) 5 = Moderate (Upper Ground Sweet Potato, Lumina, Queensland Blue, Gold Nugget) Scalloping (roundly lobed between vascular tracts): 6 = Prominent, at equatorial region 7 = Not so prominent, at equatorial region 8 = Prominent, at peduncular region 9 = Not so prominent, at peduncular region 10 = Prominent, at stylar region 11= Not so prominent, at stylar region Lobing (broadly and roundly protruding between the vascular tracts and shallowly depressed along the vascular tracts, along nearly the entire length of the fruit) 12 = Prominent (Yokohama, White Rind Sugar, Long Island Cheese, Musquee de Provence, Rouge Vif d'Etampes, Atlantc Giant) 13 = Not so prominent (Upper Ground Sweet Potato, Lumina, Crown Prince, Gold Nugget) Grooving (very narrow, shallow depressions along vascular tracts and midway in-between) 14 = Distinct 15 = Not so distinct Wrinkling (irregular surface) 16 = Distinct 17 = Indistinct 18 = Completely smooth	___ 25. Mature fruit topography
26. Mature fruit dimensions (at least 40 days past anthesis) (Figure 3):	26. Mature fruit dimensions:
__ . __ __ 26a. Length (through the axis) to medial width ratio (Example: 0.00)	__ . __ __ 26a L:W ratio (to medial width)
__ . __ __ 26b. Length (through the axis) to maximal width ratio (Example: 0.00)	__ . __ __ 26b. L:W ratio (to maximal width)
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Mature Fruit (continued):	Mature Fruit (continued):
___ **27. Mature fruit warting:** 1 = Absent (Waltham Butternut, Gold Nugget) 2 = Sparse, small (Galeux des Antilles) 3 = Sparse, large (Toonas Makino) 4 = Many, small (Essex Hybrid) 5 = Many, large (Marina di Chioggia)	___ 27. Mature fruit warting
___ **28. Mature fruit rind:** 1 = Lignified (when cutting mature fruit, little cracks form) (Gold Nugget) 2 = Not lignified (when cutting mature fruit, they slice smoothly and easily) (Waltham Butternut)	___ 28. Mature fruit rind lignified
___ **29. Mature fruit stylar scar:** 1 = Protruding 2 = Flat 3 = Depressed	___ 29. Mature fruit stylar scar
___ **30. Mature fruit stylar end:** 1 = Depressed (Prizewinner) 2 = Nearly Flat 3 = Convex (Bush Pink Banana, Gill's Blue Hubbard, Delicious)	___ 30. Mature fruit stylar end
___ **31. Mature fruit turban:** 1 = Absent (Waltham Butternut) 2 = Present 3 = Small (Buttercup) 4 = Large (Turk's Turban) Colors: _____	___ 31. Mature fruit turban
___ **32. Mature fruit peduncle end:** 1 = Depressed 2 = Nearly flat 3 = Convex	___ 32. Mature fruit peduncle end
33. Mature fruit peduncle (Figure 5): __ . __ __ 33a. Length (through the axis) to medial width ratio (Example: 0.00) __ . __ __ 33b. Length (through the axis) to maximal width (near fruit attachment) ratio (Example: 0.00)	33. Mature fruit peduncle dimensions: __ . __ __ 33a. L:W ratio (to medial width) __ . __ __ 33b. L:W ratio (to maximal width)
___ **34. Mature fruit surface pattern (choose all that apply):** 1 = Netted (Golden Cushaw) 2 = Corky (Galeuse d'Eysines) 3 = Cracked (Japanese Pie) 4 = Rough (Valencia) 5 = None of above (please describe) _____	___ 34. Mature fruit surface pattern
35. Mature fruit exterior color: 35a. Main color (please describe) : _____ _____ _____ Color Chart Name _____ Color Chart Value _____ 35b. Complex colors (give combination of color, with color covering most of the fruit surface first) _____ _____ _____ Color Chart Name _____ Color Chart Value _____	Mature fruit exterior color: 35a. Main color _____ _____ _____ Color Chart Name _____ Color Chart Value _____ 35b. Complex colors: _____ _____ _____ _____ Color Chart Name _____ Color Chart Value _____
___ **36. Mature fruit mesocarp (flesh) color:** 1 = Intense Orange 2 = Light Orange 3 = Intense Yellow 4 = Light Yellow 5 = Brown 6 = Green 7 = White tinged green 8 = White 9 = Other (describe) _____ _____	___ 36. Mature fruit flesh color
___ **37. Mature fruit endocarp (placenta) color:** 1 = Orange 2 = Yellow 3 = Brown 4 = Green 5 = White 6 = Other (please describe) _____ _____	___ 37. Mature fruit placenta color
Application Variety	Comparison Variety

Application Variety	Comparison Variety
Seed:	Seed:
38. Seed cavity:	38. Seed cavity measurements:
__ . __ __ 38a. Length (through the axis) to medial width ratio (Example: 0.00)	__ . __ __ 38a. L:W ratio (to medial width)
__ . __ __ 38b. Length (through the axis) to maximal width ratio (Example: 0.00)	__ . __ __ 38b. L:W ratio (to maximal width)
___ **39. Seed hull (from mature fruit harvested on candidate variety):** 1 = Absent 2 = Present but rudimentary 3 = Present with normal appearance	___ 39. Seed hull
40. Seed-coat color (from mature fruit harvested on candidate variety): **Please, describe:** _____ _____ _____	40. Seed coat color: _____ _____ _____
41. Seed dimensions (average for 12 mature seeds from open-pollinated fruit harvested on candidate variety):	41. Seed measurements
__ . __ __ 41a. Length to width ratio (Example: 0.00)	__ . __ __ 41a. L:W ratio
__ . __ __ 41b. Length to thickness ratio (Example: 0.00)	__ . __ __ 41b. L:Thickness ratio
__ . __ __ 41c. Width to thickness ratio (Example: 0.00)	__ . __ __ 41c. W:Thickness ratio
____ **42. Resistance to biotic or abiotic stresses:** 1 = None 2 = Yes, as qualified In Exhibit B or D (specify disease resistance/tolerance): _____ _____ _____ _____ _____ _____	___ 42. Resistance to biotic or abiotic stresses _____ _____ _____ _____ _____ _____
____ **43. Unique features that are not listed in the current 'Exhibit C' and/or are strongly environmentally dependent or occur sporadically (i.e.: peduncle characteristics, immature or mature fruit length or contents, width, or weight, stylar scar size, pollen color, seed-coat characteristics, branching, etc.):** 1 = None 2 = Yes, as described herein: _____ _____ _____ _____ _____ _____	___ 43. Unique features not listed elsewhere in the application _____ _____ _____ _____ _____

44. On additional pages, attach photographs of mature fruits of both the application variety and the comparison variety, showing external and internal coloring, with a ruler in the photograph to indicate scale.

Additional photographs of the plant, flowers, immature fruits, or other plant parts could also be helpful in providing a full description of the variety to readers. Please provide such photographs if you believe they would be helpful.

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Robinson, R.W. and D.S. Decker-Walters. 1997. Cucurbits. CAB International, Wallingford, Oxon, UK.

Figure 1. Leaf lobing

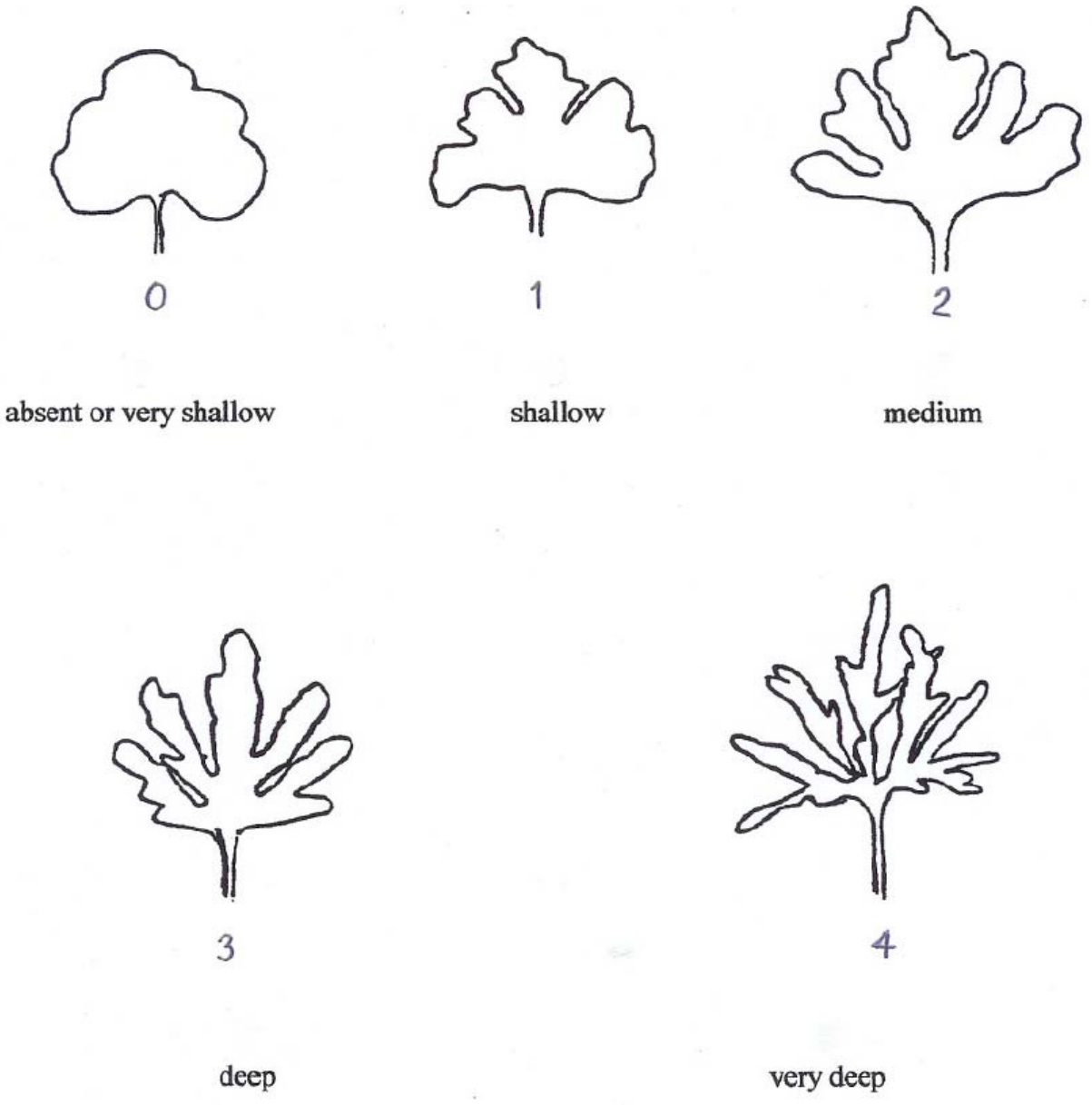


Figure 2. Flower measurements

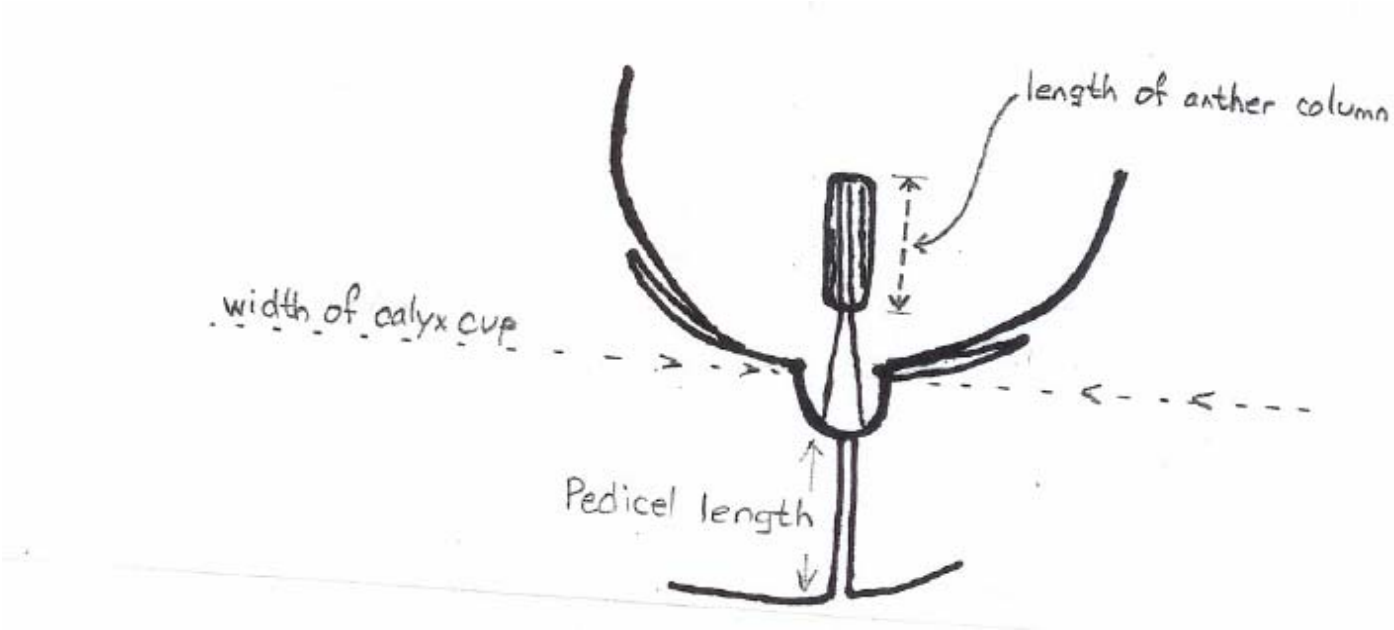


Figure 3. Fruit measurements

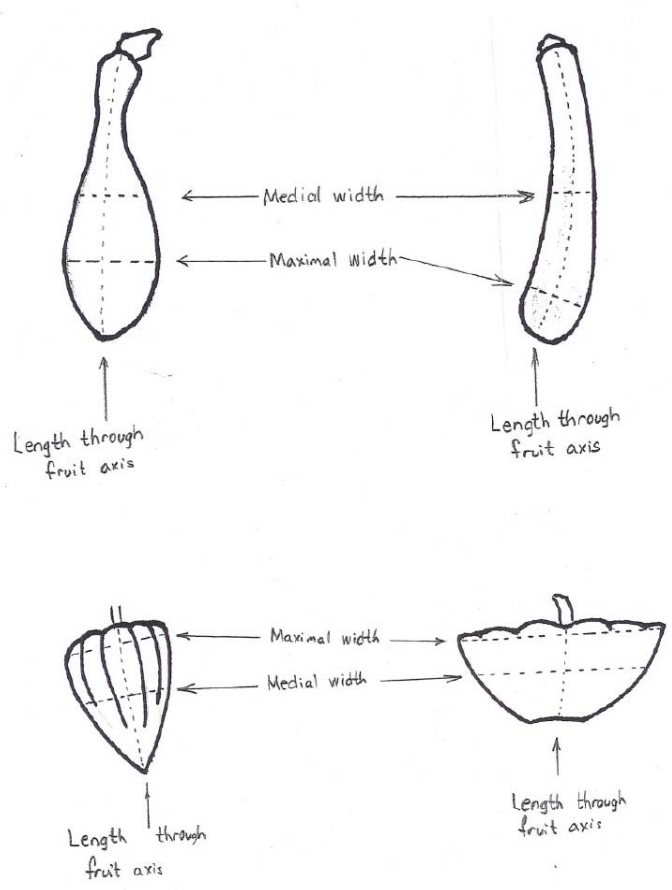


Figure 4. Fruit cross-sections

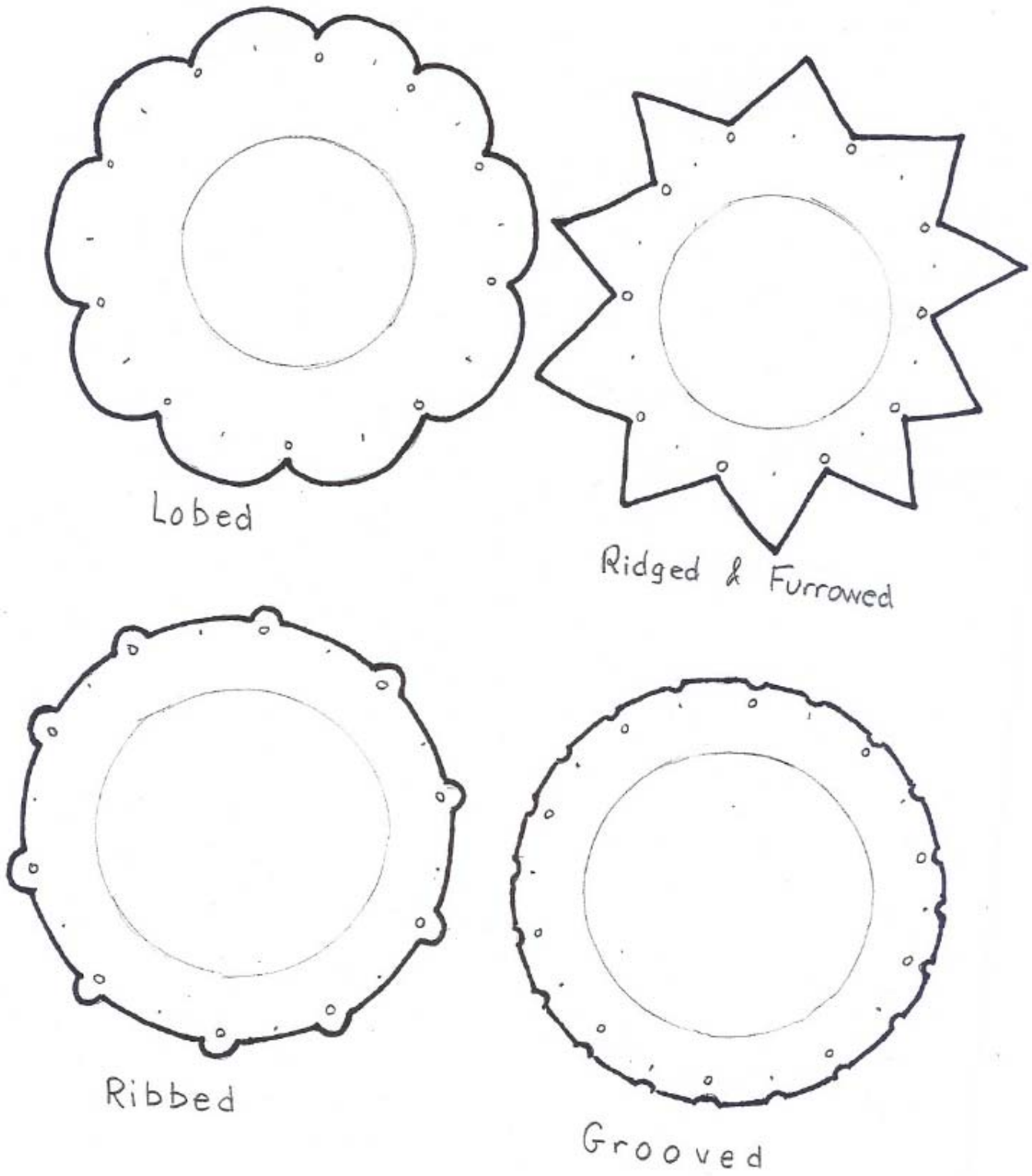
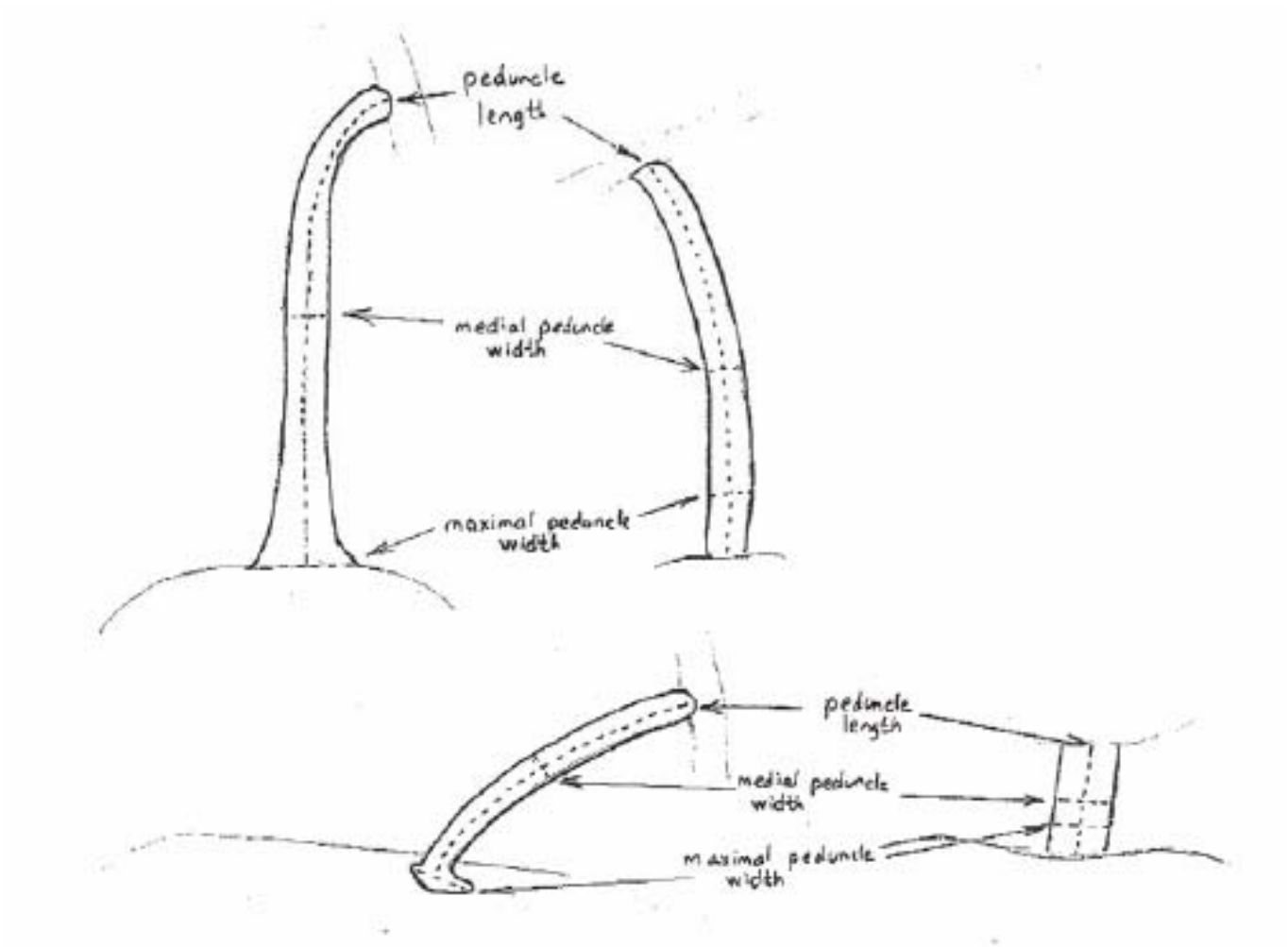


Figure 5. Peduncle measurements



Gene List for Watermelon, 2007

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Introduction

Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) is a major cucurbit crop that accounts for 6.8% of the world area devoted to vegetable crops (FAO, 2002). Watermelon is grown for its fleshy, juicy, and sweet fruit. Mostly eaten fresh, they provide a delicious and refreshing dessert especially in hot weather. The watermelon has high lycopene content in the red-fleshed cultivars: 60% more than tomato. Lycopene has been classified as a useful in the human diet for prevention of heart attacks and certain types of cancer (Perkins-Veazie et al., 2001).

Watermelon is native to central Africa where it was domesticated as a source of water, a staple food crop, and an animal feed. It was cultivated in Africa and the Middle East for more than 4000 years, then introduced to China around 900 AD, and finally brought to the New World in the 1500s. There are 1.3 million ha of watermelon grown in the world, with China and the Middle Eastern countries the major consumers. China is the largest watermelon producer, with 68.9% of the total production. The other major watermelon producing countries are Turkey, Iran, Egypt, United States, Mexico and Korea (FAO, 2002). In the United States, watermelon is used fresh as a dessert, or in salads. U.S. production is concentrated in Florida, California, Texas, and Georgia (USDA, 2002), increasing from 1.2 M tons in 1980 to 3.9 M tons in 2002, with a farm value of $329 million (USDA, 2002).

Watermelon is a useful crop species for genetic research because of its small genome size, and the many available gene mutants. Genome size of watermelon is 424 million base pairs (Arumuganathan and Earle 1991). DNA sequence analysis revealed high conservation useful for comparative genomic analysis with other plant species, as well as within the Cucurbitaceae (Pasha 1998). Like some of the other cultivated cucurbits, watermelon has much genetic variability in seed and fruit traits. Genetic investigations have been made for some of those, including seed color, seed size, fruit shape, rind color, rind pattern, and flesh color.

This is the latest version of the gene list for watermelon. The watermelon genes were originally organized and summarized by Poole (1944). The list and updates of genes for watermelon have been expanded and published by Robinson et al. (1976), the Cucurbit Gene List Committee (1979, 1982, and 1987), Henderson (1991 and 1992), Rhodes and Zhang (1995), and Rhodes and Dane (1999). This current gene list provides an update of the known genes of watermelon, with 163 total mutants grouped into seed and seedling mutants, vine mutants, flower mutants, fruit mutants, resistance mutants, protein (isozyme) mutants, DNA (RFLP and RAPD) markers, and cloned genes.

Researchers are encouraged to send reports of new genes, as well as seed samples of lines containing the gene mutant to the watermelon gene curator (Todd C. Wehner), or to the assistant curator (Stephen R. King). 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 (Cucurbit Gene List Committee, 1982; Robinson et al., 1976) before choosing a gene name and symbol. Please choose a gene name and symbol with the fewest characters that describes the recessive mutant, and avoid use of duplicate 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. The watermelon gene curators of the Cucurbit Genetics Cooperative are collecting seeds of the type lines for use by interested researchers, and would like to receive seed samples of any of the lines listed.

This gene list has been modified from previous lists in that we have 1) expanded the description of the phenotypes of several of the gene mutants, 2) added descriptions for phenotypes of interacting gene loci, 3) continued to identify type lines that carry each form of each gene, 4) identified the gene mutant lines that are in the curator collections, 5) added genes that have not previously been described: *gy* (Jiang and Lin, 2007), *ins, Scr* and *Yb* (Gusmini and Wehner, 2006), *ms-3* (Bang et al., 2006), *pl (Yang, 2006), prv* (Guner et al., 2008a), *and zym-CH* (Xu et al, 2004), and 6) corrected some of the errors in gene descriptions or references from previous lists.

Watermelon Gene Lists

- Poole, 1944: 15 genes total
- Robinson et al., 1976: 10 genes added, 25 genes total
- Robinson et al., 1979: 3 genes added, 28 genes total
- Robinson et al., 1982: 2 genes added, 30 genes total
- Henderson, 1987: 3 genes added, 33 genes total
- Henderson, 1991: 3 genes added, 36 genes total (plus 52 molecular markers)
- Rhodes and Zhang, 1995: 3 genes added, 39 genes total (plus 109 molecular markers)
- Rhodes and Dane, 1999: 5 genes added, 44 genes total (plus 111 molecular markers)
- Guner and Wehner, 2003: 8 genes added, 52 genes total (plus 111 molecular markers)
- Wehner, 2007: 8 genes added, 60 genes total (plus 111 molecular markers)

Gene Mutants

Seed and seedling genes

Three major genes control seed coat color: *r, w* (Poole et al., 1941), and *t* (McKay, 1936), for red, white, and tan seed coat, respectively. The genes interact to produce six phenotypes: black (*RR TT WW*); clump (*RR TT ww*); tan (*RR tt WW*); white with tan tip (*RR tt ww*); red (*rr tt WW*); and white with pink tip (*rr tt ww*) (Kanda, 1951). A fourth gene, *d* was suggested by Poole et al. (1941) as a modifier, producing a black, dotted seed coat when dominant for *r, t, and*

w, but having no effect on other seed coat color genotypes. These four genes do not account for the green seed coat color found in some wild accessions.

The genes (*s*) and (*l*) for short and long seed length (sometimes called small and large seed size) control seed size, with *s* epistatic to *l* (Poole et al., 1941). The genotype *LL SS* gives medium size, *ll SS* gives long, and *LL ss* or *ll ss* gives short seeds. The *Ti* gene for tiny seed was reported by Tanaka et al. (1995). Tiny seed from 'Sweet Princess' was dominant over medium-size seed and controlled by a single dominant gene. The small seed gene behaved in a manner different from Poole's medium-size seed cultivar, where short was recessive to medium-size seeds. Tanaka et al. (1995) suggested that the *Ti* gene was different from the *s* and *l* genes. Unfortunately, the origin of short- and long-seed genes was not described in Poole's paper. Tomato seed is shorter and narrower than the short seeded genotype, *ll ss*, with a width x length of 2.6 x 4.2 mm. The trait is controlled by the *ts* (Zhang, 1996; Zhang et al., 1994a) gene, with genotype *LL ss tsts*. The interaction of the four genes for seed size (*l, s, Ti* and *ts*) needs to be investigated further. However, the original type-lines for the *s* and *l* genes are not available.

Cracked seed coat *cr* (El-Hafez et al., 1981) is inherited as a single gene that is recessive to smooth seed coat. There is no seed available of the type line, 'Leeby', but there are other lines available having a seed cracking trait that may be allelic, such as PI 593350. Egusi seed trait is controlled by the *eg* gene (Gusmini et al., 2004), and has fleshy pericarp covering the seeds. However, after washing and drying, the seeds are difficult to distinguish from the smooth (noncracked) seeds of the normal type. Pale leaf (*pl*) is a spontaneous chlorophyll mutant with light green foliage that can be observed as early as the cotyledon stage (Yang, 2006).

Vine genes

Several genes control leaf or foliage traits of watermelon. Nonlobed leaf (*nl*) has sinuate leaves rather than the lobed leaf type of the typical watermelon (Mohr, 1953). According to nomenclature rules, the trait should be named directly for the mutant trait (sinuate leaves, *sn*), rather than for the absence of the normal trait (nonlobed, *nl*).

Seedling leaf variegation *slv* (Provvidenti, 1994) causes a variegation resembling virus infection on seedlings. It is linked or pleiotropic with *Ctr* for cool temperature resistance. The yellow leaf (*Yl*) gene results in yellow leaves, and is incompletely dominant to green leaves (Warid and Abd-El-Hafez, 1976). Delayed green leaf *dg* (Rhodes, 1986) causes pale green cotyledons and leaves for the first few nodes, with later leaves developing the normal green color. Inhibitor of delayed green leaf (*i-dg*) makes leaves normal green even when they have the *dgdg* genotype (Rhodes, 1986). The juvenile albino *ja* (Zhang et al.,1996b) gene causes reduced chlorophyll in seedling tissues, as well as leaf margins and fruit rind when plants are grown under short day conditions. The dominant gene *Sp* (Poole, 1944) causes round yellow spots to form on cotyledons, leaves and fruit, resulting in the fruit pattern called moon and stars. For more information on *Sp*, see the fruit gene section below.

So far, four dwarf genes of watermelon have been identified that affect stem length and plant habit: *dw-1* (Mohr, 1956; Mohr and Sandhu, 1975) and *dw-1s* (Dyutin and Afanas'eva, 1987) are allelic, and *dw-1, dw-2* (Liu and Loy, 1972), and *dw-3* (Huang et al., 1998) are non-allelic. Dwarf-1 plants have short internodes due to fewer and shorter cells than the normal plant type. Plants with *dw-1s* have vine length intermediate between normal and dwarf, and the hypocotyls were somewhat longer than normal vine and considerably longer than dwarf. The *dw-1s* is recessive to normal plant type. Plants with *dw-2* have short internodes due to fewer cells than the normal type, and plants with *dw-3* have leaves with fewer lobes than the normal leaf.

The golden yellow mutant is controlled by the single recessive gene *go*, where the stem and older leaves are golden yellow (Barham, 1956). The type line for *go* is 'Royal Golden'. One benefit of the *go* gene is that the fruit become golden yellow as they mature, so it might be useful as a maturity indicator for fruit harvest. The gene *tl* (formerly called branchless, *bl*) results in tendrilless branches after the 5th or 6th node (Lin et al., 1992; Rhodes et al., 1999; Zhang et al., 1996a). Also, plants have half the number of branches of the normal plant type, vegetative meristems gradually become floral, tendrils and vegetative buds are replaced by flowers (with a large percentage being perfect), and growth becomes determinate.

Flower genes

The andromonoecious gene *a* (Rosa, 1928) controls monoecious (*AA*) vs. andromonoecious (*aa*) sex expression in watermelon. Andromonoecious plants have both staminate and perfect flowers, and appears to be the wild type. Light green flower color is controlled by the single recessive gene, *gf* (Kwon and Dane, 1999). A gynoecious mutant was discovered in 1996, and is controlled by a single recessive gene, *gy* (Jiang and Lin, 2007). The gynoecious type may be useful for hybrid production, or for cultivars having concentrated fruit set.

Five genes for male sterility have been reported. Glabrous male sterile (*gms*) is unique, with sterility associated with glabrous foliage (Ray and Sherman, 1988; Watts, 1962, 1967). A second male sterile *ms-1* (Zhang and Wang, 1990) produces plants with small, shrunken anthers and aborted pollen. A third male sterile mutant appeared simultaneously with dwarfism, and the dwarf gene was different from the three known dwarf genes. It was named male sterile dwarf (*ms-dw*) by Huang et al. (1998). All male sterile genes reduce female fertility as well. These mutants have been used in hybrid production, but have not been as successful as hoped, since they often have low seed yield. A new, spontaneous male sterile mutant (*ms-2*) with high normal seed set has been identified, and will be more useful for hybrid production (Dyutin and Sokolov, 1990). Recently, a male sterile mutant having unique foliage characteristics (*ms-3*) was reported by Bang et al. (2006).

Fruit genes

Considerable attention has been given to genes affecting fruit type in watermelon. Fruit shape is controlled by a single, incompletely dominant gene, resulting in fruit that are elongate (*OO*), oval (*Oo*), or spherical (*oo*) (Poole and Grimball, 1945; Weetman, 1937). A single gene controls furrowed fruit surface *f* (Poole, 1944) that is recessive to smooth (*F*). The type line for furrowed was not given by Poole, but cultivars such as Stone Mountain and Black Diamond have furrowed fruit surface, in contrast to cultivars such as Mickylee with smooth fruit surface.

Explosive rind (*e*) causes the fruit rind to burst or split when cut (Porter, 1937), and has been used to make fruit easily crushed by harvest crews for pollenizer cultivars such as SP-1 that have small fruit not intended for harvest. Tough rind (*E*) is an important fruit trait to give cultivars shipping ability. Rind toughness appears to be independent of rind thickness. The interaction of rind toughness and thickness needs to be studied. A single recessive gene *su* (Chambliss et al., 1968) eliminates bitterness in fruit of *C. lanatus*, and is allelic to the dominant gene (*Su*) for bitter flavor in the fruit of the colocynth (*Citrullus colocynthis*).

Watermelon flesh color is controlled by several genes to produce scarlet red, coral red, orange, salmon yellow, canary yellow, or white. Genes conditioning flesh colors are *B* (Shimotsuma, 1963), *C* (Poole, 1944), *i-C* (Henderson et al., 1998), *Wf* (Shimotsuma, 1963), *y* (Porter, 1937) and *y-o* (Henderson, 1989; Henderson et al., 1998). Canary yellow (*C*) is dominant to other colored flesh (*c*). Coral red flesh (*Y*) is dominant to salmon yellow (*y*). Orange flesh (*y-o*) is a

member of multiple allelic system at that locus, where *Y* (coral red flesh) is dominant to both *y-o* (orange flesh) and *y* (salmon yellow), and *y-o* (orange flesh) is dominant to *y* (salmon yellow). In a separate study, two loci with epistatic interaction controlled white, yellow, and red flesh. Yellow flesh (*B*) is dominant to red flesh. The gene *Wf* is epistatic to *B*, so genotypes *WfWf BB* or *WfWf bb* were white fleshed, *wfwf BB* was yellow fleshed, and *wfwf bb* was red fleshed. Canary yellow flesh is dominant to coral red, and *i-C* inhibitory to *C*, resulting in red flesh. In the absence of *i-C*, *C* is epistatic to *Y*.

A single dominant gene, *Scr*, produces the scarlet red flesh color of 'Dixielee' and 'Red-N-Sweet' instead of the lighter, coral red (*scr*) flesh color of 'Angeleno Black Seeded' (Gusmini and Wehner, 2006). Additional studies are needed to determine the interaction of *Scr* with *Y*, *y-o* and *y*, and the interaction of *C* with *Y*, *y-o* and *y*.

Although flesh color is shown to be controlled by single genes, the fruit in a segregating generation from a cross between two different inbreds is often confusing. Often there are different flesh colors in different areas of the same fruit. One possible hypothesis to explain the presence of the abnormal types is that the expression of the pigment is caused by several different genes, one for each area of the fruit. Thus, the mixed colorations would have been caused by recombination of these genes. It may be useful to have a separate rating of the color of different parts of the flesh to determine whether there are genes controlling the color of each part: the endocarp between the carpel walls and the mesocarp (white rind); the flesh within the carpels, originating from the stylar column; and the carpel walls.

Fruit rind pattern genes

The gene *Sp* produces spotted fruit, making interesting effects as found on cultivars such as 'Moon and Stars' (Poole, 1944). The type line for the *Sp* gene is 'Moon and Stars'. There are several cultivars having the term 'Moon and Stars' in their name, apparently having different genetic background plus the *Sp* gene, so that should be taken into account when doing genetic studies. The *Sp* trait is difficult to recognize on the fruit when the fruit are solid light green in color, but is easy to observe on solid medium green, solid dark green, gray, or striped fruit (Gusmini and Wehner, 2006). Golden yellow was inherited as a single recessive gene *go* (Barham, 1956) derived from 'Royal Golden' watermelon. The immature fruit had a dark green rind which becomes more golden yellow as the fruit matures. The stem and older leaves also become golden yellow, and the flesh color changes from pink to red.

An unusual stripe pattern is found on 'Navajo Sweet' called intermittent stripes, with gene symbol *ins* (Gusmini and Wehner, 2006). The recessive genotype produces narrow dark stripes at the peduncle end of the fruit that become irregular in the middle and nearly absent at the blossom end of the fruit. Stripes on normal fruit, such as 'Crimson Sweet' are fairly uniform from peduncle to blossom end. The yellow belly, or ground spot, on 'Black Diamond Yellow Belly' is controlled by a single dominant gene, *Yb*. The recessive genotype, 'Black Diamond' has a ground spot that is white (Gusmini and Wehner, 2006).

Weetman (1937) proposed that three alleles at a single locus determined rind pattern. The allelic series was renamed to *G*, *gs*, and *g* by Poole (1944), since *g* was used to name the recessive trait 'green', rather than *D* for the dominant trait 'dark green'. The *g-s* gene produces a striped rind, but the stripe width (narrow, medium, and wide stripe patterns) has not been explained as yet. Porter (1937) found that dark green was completely dominant to light green (yellowish white, in his description) in two crosses involving two different dark green cultivars ('Angeleno' and 'California Klondike'). He reported incomplete dominance of dark green in the cross 'California Klondike' x 'Thurmond Gray', the latter cultivar being described as yellowish green. Thus, gray rind pattern should be described further as either

yellowish green ('Thurmond Gray') or yellowish white ('Snowball').

The watermelon gene *p* for pencilled rind pattern has been reported in the gene lists since 1976 (Robinson et al. 1976). The name "penciled" first appeared in 1944 to describe inconspicuous lines on self-colored rind of 'Japan 6' (Poole, 1944), but the spelling was changed later to "pencilled" in the gene lists. The cross 'Japan 6' x 'China 23' was used by Weetman to study the inheritance of solid light green vs. striped rind, and lined (later renamed pencilled) vs. netted rind (Weetman, 1937). 'Japan 6' had solid light green rind with inconspicuous stripes, usually associated with the furrow. 'China 23' had dark green stripes on a light green background and a network running through the dark stripes (netted type). Weetman confirmed his hypothesis of two independent genes regulating the presence of stripes and the pencilled vs. netted pattern, recovering four phenotypic classes in a 9:3:3:1 ratio (striped, netted : striped, pencilled : non-striped, netted : non-striped, pencilled) in the F2 generation and in a 1:1:1:1 ratio in the backcross to the double recessive non-striped, pencilled 'Japan 6'. However, Weetman did not name the two genes.

Seeds of the two type lines used by Weetman ('Japan 6' and 'China 23') are not available, nor are Porter's data and germplasm, thus making it difficult to confirm the inheritance of the *p* gene or to identify current inbreds allelic to pencilled and netted rind patterns. In 1944, Poole used the experiment of Weetman to name the single recessive gene *p* for the lined (pencilled, or very narrow stripe) type. The inheritance of the *p* gene was measured by Weetman against the netted type in 'China 23' and not a "self-colored" (or solid green) type as reported by Poole. Previously, Porter reported that studies of rind striping were underway and specifically cited a pencilled pattern in the F1 of the cross 'California Klondike' x 'Golden Honey' (Porter, 1937). Probably, the *P* allele produces the netted type, as originally described by Weetman.

The *m* gene for mottled rind was first described by Weetman in 'Long Iowa Belle' and 'Round Iowa Belle' (Weetman, 1937). Weetman described the rind as "medium-dark green with a distinctive greenish-white mottling", the 'Iowa Belle' (IB) type. In the cross 'Iowa Belle' X 'China 23', Weetman observed that the IB type was inherited as a single recessive gene. However, in the cross 'Iowa Belle' X 'Japan 6', he recovered the two parental types (IB and non-IB, respectively) along with an intermediate type (sub-IB), described as inconspicuous mottling. In the backcross to 'Iowa Belle' (the recessive parent for the mottled rind), though, the traits segregated with a perfect fit to the expected 1:1 ratio. He explained the presence of the intermediate type as determined by interfering genes from 'Japan 6'. There was no other mention of the IB-type until Poole (1944) attributed its inheritance to the *m* gene from 'Iowa Belle', based on the article by Weetman. 'Iowa Belle' is not currently available and the IB mottling has not been identified in other mutants since the 1937 study by Weetman.

The homozygous genotypes produced by the genes known to regulate rind color and pattern in watermelon should have the following phenotypes (type-line shown in parentheses): *GG MM PP* or *GG MM pp* = solid dark green ('Angeleno'), *GG mm* = mottled dark green ('Iowa Belle', not available), *gg MM* = solid light green ('?'), *gg MM pp* = pencilled ('Japan 6', not available), *gg PP* = yellowish green or gray ('Thurmond Gray'), and *gsgs PP* = medium-stripe netted ('Crimson Sweet'). It would be useful to study *g, m, p,* and other genes controlling rind pattern, to determine the interactions and develop inbred lines having interesting patterns for the genestock collection.

Resistance genes

Resistance to race 1 and 3 of anthracnose (*Colletotrichum lagenarium*, formerly *Glomerella cingulata* var. *orbiculare*) is controlled by a single dominant gene *Ar-1*

(Layton, 1937). Resistance to race 2 of anthracnose is also controlled by a single dominant gene *Ar-2-1* (Winstead et al., 1959). The resistant allele *Ar-2-1* is from W695 citron as well as PI 189225, PI 271775, PI 271779, and PI 299379; the susceptible allele *ar-2-1* is from 'Allsweet', 'Charleston Gray', and 'Florida Giant'; resistance in *Citrullus colocynthis* is due to other dominant factors, with resistance from R309 and susceptibility from 'New Hampshire Midget' (Love and Rhodes, 1988, 1991; Sowell et al., 1980; Suvanprakorn and Norton, 1980; Winstead et al., 1959).

Resistance to race 1 of *Fusarium oxysporum* f. sp. *niveum* is controlled by a single dominant gene *Fo-1* (Henderson et al., 1970; Netzer and Weintall, 1980). Gummy stem blight, caused by *Didymella bryoniae* (Auersw.) Rehm is inherited by a recessive gene *db* (Norton, 1979). Watermelons were resistant to older races of *Sphaerotheca fuliginea* present in the U.S. in the 1970s, but a single recessive gene *pm* (Robinson et al., 1975) for high susceptibility to powdery mildew was found in the plant introduction, PI 269677. Races 1W and 2W of powdery mildew are now present in the U.S., and induce a susceptible reaction in most cultivars. PI 269677 is highly susceptible to the new races.

Resistance to *Papaya ringspot virus-watermelon strain* was reported in accessions PI 244017, PI 244019 and PI 485583. It was controlled by a single recessive gene, *prv* (Guner et al., 2008). A moderate level of resistance to *Zucchini yellow mosaic virus* was found in four landraces of *Citrullus lanatus*, but was specific to the Florida strain of the virus. Resistance was conferred by a single recessive gene *zym-FL* (Provvidenti 1991). A high level of resistance to *Zucchini yellow mosaic virus*-Florida strain was found in PI 595203 that was controlled by a single recessive gene, *zym-FL-2* by (Guner and Wehner 2008). It was not the same as *zym-FL* because the virus caused a different reaction on PI 482322, PI 482299, PI 482261, and PI 482308. The four accessions were resistant in the study by Provvidenti, but susceptible in the study by Guner and Wehner. Resistance to the China strain of *Zucchini yellow mosaic virus* was reported in PI 595203, controlled by a single recessive gene *zym-CH* (Xu et al. 2004). The gene may be allelic to *zym-FL-2*, but it is difficult to test a segregating F2 progeny for resistance to two different viruses found in different parts of the world.

Xu et al. (2004) reported that PI 595203, which is resistant to ZYMV, was moderately resistant to *Watermelon mosaic virus* (WMV, formerly *Watermelon mosaic virus 2)*. Strange et al. (2002) reported that PI 595203 also was resistant to *Papaya ringspot virus*-watermelon strain. The high tolerance to WMV was controlled by at least three recessive genes. Broad-sense heritability was high (0.84 to 0.85, depending on the cross), and narrow-sense heritability was low to high (0.14 to 0.58, depending on the cross).

Genes for insect resistance have been reported in watermelon. Fruit fly (*Dacus cucurbitae*) resistance was controlled by a single dominant gene *Fwr* (Khandelwal and Nath, 1978), and red pumpkin beetle (*Aulacophora faveicollis*) resistance was controlled by a single dominant gene *Af* (Vashishta and Choudhury, 1972). Stress resistance has been found in watermelon. Seedlings grown at temperatures below 20°C often develop a foliar mottle and stunting. A persistent low temperature is conducive to more prominent foliar symptoms, malformation, and growth retardation. The single dominant gene *Ctr* was provided cool temperature resistance (Provvidenti, 1992, 2003).

The morphological and resistance genes of watermelon, including gene symbol, synonym, description, references, availability (y), and photograph.(z)

Symbol	Synonym	Gene description and type lines	References	Supplemental references	Availability	Photograph (click for larger image)
a	-	*andromonoecious*; recessive to monoecious; *a* from 'Angeleno' (black seeded); *A* from cultivars 'Conqueror' and 'Klondike'.	Rosa, 1928	Porter, 1937; Poole, 1944	C	*a*
Af	-	*Aulacophora faveicollis* resistance; resistance to the red pumpkin beetle; dominant to susceptibility; Af from Sl.72 and Sl.98 inbreds; af from 'Sugar Baby'.	Vashishta and Choudhury, 1972	-	?	*Af*
Ar-1	*B, Gc*	*Anthracnose resistance to races 1* and *3* of *Glomerella cingulata* var. *orbiculare (Colletotrichum lagenarium)*; *Ar-1* from 'Africa 8'*, 'Africa 9'*, and 'Africa 13'* and 'Charleston Gray'**; *ar-1* from 'Iowa Belle 476', 'Iowa Belle 487'* and N.C.9-2, N.C.11, and 'New Hampshire Midget'**.	Layton, 1937*	Hall et al., 1960; Robinson et al., 1976; Winstead et al., 1959**	C	
Ar-2-1	-	*Anthracnose resistance to race 2* of *Colletotrichum lagenarium*; *Ar-2-1* from W695 citron* and PI 189225, PI 271775, PI 271779, and PI 299379**; *ar-2-1* from 'Allsweet', 'Charleston Gray', and 'Florida Giant'; resistance in *Citrullus colocynthis* is due to other dominant factors; resistance from R309***; susceptibility from 'New Hampshire Midget'.	Winstead et al., 1959*	Love and Rhodes, 1988***, 1991; Sowell et al., 1980**; Suvanprakorn and Norton, 1980	P	
B	*Y*	*Yellow flesh; Wf* is epistatic to *B* (*Y* renamed *B* by Henderson*); flesh color segregated into 12 white, 3 yellow and 1 red in the F2; *WfWf BB* or *WfWf bb* white fleshed; *wfwf BB* yellow fleshed; *wfwf bb* red fleshed; *B* from breeding line V.No.3 and *b* from V.No.1.	Shimotsuma, 1963	Henderson, 1992*	?	
C	-	*Canary yellow flesh*; dominant to pink; *i-C* inhibitory to *C*, resulting in red flesh; in the absence of *i-C*, *C* is epistatic to *Y; CC* from 'Honey Cream'* and NC-517, *cc* from 'Dove'*; *CC YY I-C I-C* from 'Yellow Baby' F1** and 'Yellow Doll' F1**; *cc yoyo I-C I-C* from 'Tendersweet Orange Flesh'**; *cc yy I-C I-C* from 'Golden Honey'**; *cc YY i-C i-C* from 'Sweet Princess'**.	Poole, 1944*	Henderson et al., 1998**	C	

cr	-	*cracked seed coat;* recessive to *Cr* (non-cracked) seed coat; *cr* from 'Leeby' and *Cr* from 'Kaho' and 'Congo'.	El-Hafez et al., 1981	-	?	
Ctr	-	*Cool temperature resistance; Ctr* from line PP261-1 (a single plant selection of PI 482261 from Zimbabwe); *ctr* from 'New Hampshire Midget'; resistant to leaf mosaic injury when grown at air temperature below 20°C.	Provvidenti, 1992	Provvidenti, 2003	P	*Ctr*
d	-	*dotted seed coat*; black dotted seeds when dominant for color genes *r, t,* and *w; d* is a specific modifier of black seed coat color wherein *RR TT WW DD* is solid black and *RR TT WW dd* is dotted black seed coat; *d* from 'Klondike' and 'Hope Giant'; *D* from 'Winter Queen'.	Poole et al., 1941	Poole, 1944; Kanda, 1951	C	
db	-	resistance to *gummy stem blight* caused by *Didymella bryoniae*; *db* from PI 189225; *Db* from 'Charleston Gray'.	Norton, 1979	-	P	
dg	-	*delayed green*; cotyledons and young leaves are initially pale green but later develop chlorophyll; first reported to be hypostatic to *I-dg*; more recent evidence indicates a simple recessive; *dg* from breeding line 'Pale 90'; *Dg* from 'Allsweet'.	Rhodes, 1986	-	?	
dw-1	-	*dwarf-1*; short internodes, due to fewer and shorter cells than normal forms; allelic to *dw-1s; dw-1* from 'Bush Desert King' (also, 'Bush Charleston Gray', 'Bush Jubilee', 'Sugar Bush'); *Dw-1* from 'Sugar Baby' and 'Vine Desert King'.	Mohr, 1956	Liu and Loy, 1972	C	*dw-1*
dw-1-s	-	*short vine*; allelic to *dw-1*; vine length intermediate between normal and dwarf; hypocotyl somewhat longer than normal vine and considerably longer than dwarf; *dw-1-s* recessive to normal; *dw-1-s* from 'Somali Local' (All-Union Research Institute of Plant Growing No.4641).	Dyutin and Afanas'eva, 1987	-	?	*dw-1-s*
dw-2	-	*dwarf-2*; short internodes, due to fewer cells; *dw-2* from inbred line *WB-2*; *Dw-2* from 'Sugar Baby'	Liu and Loy, 1972	Mohr and Sandhu, 1975	?	*dw-2*

		and 'Vine Desert King'.				
dw-3	-	*dwarf-3*; dwarf with fewer leaf lobes (intermediate between normal leaf and non-lobed leaf); *dw-3* from 'Dwarf Male-Sterile Watermelon *(DMSW)*'; *Dw-3* from 'Changhui', 'Fuyandagua', and 'America B'.	Hexun et al., 1998	-	?	*dw-3*
e	*t*	*explosive rind*; thin, tender rind, bursting when cut; *e* from 'California Klondike'; *E* from 'Thurmond Gray'.	Porter, 1937	Poole, 1944	?	
eg	-	*egusi seed*; immature seeds with fleshy pericarp, becoming normal at maturity; *eg* from PI 490383 selection NCG-529 and PI 560006; *Eg* from 'Calhoun Gray' and 'Charleston Gray'.	Gusmini et al., 2003	-	C	
f	-	*furrowed fruit surface*; recessive to smooth; type inbreds not given; *f* like 'Stone Mountain' or 'Black Diamond'; *F* like 'Mickylee'.	Poole, 1944	-	M	
Fo-1	-	*Fusarium wilt resistance for race 1*; dominant gene for resistance to race 1 of *Fusarium oxysporum* f. sp. *niveum*; *Fo-1* from 'Calhoun Gray' and 'Summit'; *fo-1* from 'New Hampshire Midget'.	Henderson et al., 1970	Netzer and Weintall, 1980	C	
Fwr	-	*Fruit fly resistance caused by Dacus cucurbitae*; dominant to susceptibility; *Fwr* from breeding lines J 18-1 and J 56-1; *fwr* from 'New Hampshire Midget', 'Bykovski', 'Red Nectar' and breeding line 'J 20-1'.	Khandelwal and Nath, 1978	-	?	*Fwr*
g	*d*	*light green fruit rind pattern*; light green fruit recessive to dark green *(G)* and striped green *(g-s)*; *g* from 'Thurmond Gray' and *G* from 'California Klondike'.	Weetman, 1937	Poole, 1944; Porter, 1937	?	*g*
g-s	*ds*	*striped green fruit rind pattern;* recessive to dark green but dominant to light green skin; *g-s* from 'Golden Honey'; *G* from 'California Klondike'.	Weetman, 1937	Poole, 1944	C	
gf	-	*light green flower color; gf* from 'KW-695' and 'Dalgona'; *Gf* from Korean watermelon accession 'SS-4'.	Kwon and Dane, 1999	-	?	*gf*
gms	*msg*	*glabrous male sterile*; foliage lacking trichomes; male sterile	Watts, 1962, 1967	Robinson et al., 1976*; Ray and	?	*gms*

		caused by chromosome desynapsis (named glabrous male sterile by Robinson*); *gms* from 'Sugar Baby' irradiated with gamma rays.		Sherman, 1988		
go	*c*	*golden yellow color of older leaves and mature fruit;* (named golden by Robinson*); *go* from 'Royal Golden'; *Go* from 'NC 34-9-1' and 'NC 34-2-1'.	Barham, 1956	Robinson et al., 1976*	C	
gy	-	*gynoecious flowering habit;* recessive mutant has all pistillate flowers on the vine; Gy from elite cultivars.	Jiang and Lin, 2007	-	-	*gy*
i-C	*i*	*inhibitor of canary yellow*, resulting in red flesh (renamed by Rhodes and Dane*); *CC YY I-C I-C* from 'Yellow Baby' F1 and 'Yellow Doll' F1; *cc yoyo I-C I-C* from 'Tendersweet Orange Flesh'; *cc yy I-C I-C* from 'Golden Honey'; *cc YY i-C i-C* from 'Sweet Princess'.	Henderson et al., 1998	Rhodes and Dane, 1999*	C	
i-dg	-	*inhibitor of delayed green*; Epistatic to *dg; I-dg I-dg dgdg* plants are pale green; and *i-dg i-dg dgdg* plants are normal; *dg* from breeding line Pale 90; *Dg* from 'Allsweet'; *i-dg* gene was lost when advanced inbreds were made.	Rhodes, 1986	Jiang, X.T. and D.P. Lin, 2007	L	
ins	-	*intermittent stripes*; narrow dark stripes at the peduncle end of the fruit becoming irregular in the middle and nearly absent at the blossom end of the fruit; *ins* from 'Navajo Sweet'; *Ins* from 'Crimson Sweet'.	Gusmini and Wehner, 2006	-	C	
ja	-	*juvenile albino*; chlorophyll in seedlings, leaf margins, and fruit rind reduced when grown under short days; *ja* from 'Dixielee mutant' and 'G17AB' F2; *Ja* from 'Sweet Princess' and '20J57'.	Zhang et al., 1996b	-	?	
l	-	*long (or large) seeds*; interacts with *s*; long recessive to medium or short; *LL SS* for medium, *ll SS* for long, and *LL ss* or *ll ss* for short seed; *ll SS* from 'Peerless'; *LL SS* from 'Klondike'; *LL ss* from 'Baby Delight'.	Poole et al., 1941	-	?	
m	-	*mottled skin*; greenish white mottling of fruit skin; randomly-distributed, irregularly-shaped light green spots on a mostly	Weetman, 1937	Poole, 1944	?	

		solid dark-green rind pattern; *m* from 'Long Iowa Belle' (seeds not available) and 'Round Iowa Belle' (seeds not available); *M* from 'Japan 4' (seeds not available) and 'China 23' (seeds not available).				
ms-1	*ms*	*male sterile*; plants with small, shrunken anthers and aborted pollen; *ms-1* from 'Nongmei 100'; *Ms* from most cultivars, e.g. 'Allsweet'.	Zhang and Wang, 1990	Zhang et al., 1994b	?	
ms-2	-	*male sterile* with high seed productivity; *ms-2* from 'Kamyzyakskii'; *Ms-2* from cultivars like 'Allsweet'.	Dyutin, and Sokolov, 1990	-	?	
ms-3	-	*male sterile* with unique foliar characteristics; *ms-3* from ????; *Ms-3* from cultivars like 'Allsweet'.	Bang et al., 2006	-	?	
ms-dw	-	*male sterile, dwarf; ms-dw* from 'Dwarf Male-Sterile Watermelon (DMSW)'; *Ms-dw* from 'Changhui', 'Fuyandagua', and 'America B'.	Huang et al., 1998	-	?	*ms-dw*
nl	-	*nonlobed leaves*; leaves lack the typical lobing; sinuate leaves (named nonlobed by Robinson*); leaves lack the typical lobing of most cultivars, slightly lobed with the sinus obscure; incomplete dominance; *Nl* is not sinuate, but pinnatifid (deeply pinnately lobed, with prominent sinuses) like most cultivars; *nl* from spontaneous mutant of 'Black Diamond', and probably 'Sunshade; *Nl* from 'Black Diamond', and most cultivars such as 'Allsweet' and 'Calhoun Gray'.	Mohr, 1953	Robinson et al., 1976*	C	
O	-	*Elongate fruit*; incompletely dominant to spherical, so that *Oo* is oval; *O* from 'Long Iowa Belle'; *o* from 'Round Iowa Belle', 'China 23', 'Japan 4', and 'Japan 6'.	Weetman, 1937	Poole and Grimball, 1945	P	
p	-	*pencilled lines on skin;* inconspicuous stripes; greenish-white mottling* (called pencilled by Robinson**); inconspicuous, very narrow, pencil-width stripes	Weetman, 1937*	Robinson et al., 1976**	?	

		running the length of the fruit (originally spelled penciled by Poole); recessive to netted fruit; *p* from 'Japan 6' (seeds not available) and *P* from 'China 23' (seeds not available).				
pl	-	*pale leaf*; seedlings are pale green in color; *pl* from breeding line HY477; *Pl* from 'Allsweet'.	Yang, 2006	-	?	
pm	-	*powdery mildew susceptibility;* susceptibility to *Sphaerotheca fuliginea* is recessive; *pm* from PI 269677; *Pm* from 'Sugar Baby' and most cultivars.	Robinson et al., 1975	-	P	
prv	-	*Papaya ringspot virus-watermelon strain resistance*; resistance to PRV-W is recessive; *prv* from PI 244017, PI 244019, and PI 485583; *Prv* from 'Allsweet', 'Calhoun Gray', and 'New Hampshire Midget'.	Guner et al., 2008a	-	P	
r	-	*red seed coat*; genes *r*, *t* and *w* interact to produce seeds of different colors; dotted black from 'Klondike' *(RR TT WW*); clump from 'Sun Moon and Stars' (*RR TT ww*); tan from 'Baby Delight' (*RR tt WW*); white with tan tip from 'Pride of Muscatine' (*RR tt ww*); red from citron (*rr tt WW*); white with pink tip from 'Peerless' (*rr tt ww*).	Poole et al., 1941	-	?	
s	-	*short (or small) seeds*; epistatic to *l*; long recessive to medium or short; *LL SS* for medium, *ll SS* for long, and *LL ss* or *ll ss* for short seed; *ll SS* from 'Peerless'; *LL SS* from 'Klondike'; *LL ss* from 'Baby Delight'.	Poole et al., 1941	-	?	
Scr	-	*Scarlet red flesh color*; dark red color of the fruit flesh (darker red than the *YY* red color of 'Angeleno Black Seeded'); *Scr* from 'Dixielee' and 'Red-N-Sweet'; *scr* from 'Angeleno Black Seeded'.	Gusmini and Wehner, 2006	-	C	
slv	-	*seedling leaf variegation*; conferred by a single recessive gene in PI 482261; linked or pleiotropic with a dominant allele for resistance to cool temperature injury (20°C for greenhouse-	Provvidenti, 1994	-	P	*slv*

		grown plants); *slv* from PI 482261 (resistant to ZYMV-FL); *Slv* from 'New Hampshire Midget'.				
Sp	-	*Spotted cotyledons, leaves and fruit*; dominant to uniform foliage and fruit color; *Sp* from 'Sun, Moon and Stars'* and 'Moon and Stars'**; *sp* from 'Allsweet'.	Poole, 1944*	Rhodes, 1986**	C	
su	*Bi, suBi*	*suppressor of bitterness*; (*su* named by Robinson*); non-bitter fruit; *su* from 'Hawkesbury'; *Su* from bitter-fruited mutant of 'Hawkesbury'; bitterness in *C. colocynthis* is due to *Su Su genotype*.	Chambliss et al., 1968	Robinson et al., 1976*	?	*su*
t	*bt*	*tan seed coat*; genes *r*, *t* and *w* interact to produce seeds of different colors; dotted black from 'Klondike' *(RR TT WW)*; clump from 'Sun Moon and Stars' (*RR TT ww*); tan from 'Baby Delight' (*RR tt WW*); white with tan tip from 'Pride of Muscatine' *(RR tt ww)*; red from citron (*rr tt WW*); white with pink tip from 'Peerless' (*rr tt ww*).	McKay, 1936	Poole et al., 1941	?	
Ti	-	*Tiny seed*; dominant over medium seed (*ti*); *Ti* from 'Sweet Princess'; *ti* from 'Fujihikari'.	Tanaka et al., 1995	-	?	
tl	*bl*	*tendrilless* (formerly called *branchless**), after 4th or 5th node, vegetative axillary buds are transformed into flower buds and leaf shape is altered; *tl* from 'Early Branchless'; *Tl* from breeding lines 'G17AB', 'ASS-1', 'YF91-1-2', and S173 breeding line.	Rhodes, Zhang, Baird and Knapp, 1999; Zhang, Rhodes, Baird and Skorupska, 1996a	Lin, Tong, Wang, Zhang and Rhodes, 1992*	?	*tl*
ts	*tss*	*tomato seed*; seeds smaller than short (*LLss* or *llss*), almost the size of a tomato seed; *ts* from tomato seed Sugar Baby mutant; *Ts* from 'Gn-1'.	Zhang et al., 1994a	Zhang, 1996	C	
w	-	*white seed coat*; genes *r*, *t* and *w* interact to produce seeds of different colors; dotted black from 'Klondike' (*RR TT WW*); clump from 'Sun Moon and Stars' (*RR TT ww*); tan from 'Baby Delight' (*RR tt WW*); white with	Poole et al., 1941	-	?	

		tan tip from 'Pride of Muscatine' (*RR tt ww*); red from citron (*rr tt WW*); white with pink tip from 'Peerless' (*rr tt ww*).				
Wf	*W*	*White flesh*; (named white flesh by Robinson*); *Wf* is epistatic to *B* (*Y* renamed *B* by Henderson**); *WfWf BB* or *WfWf bb* white fleshed; *wfwf BB* yellow fleshed; *wfwf bb* red fleshed; *B* from breeding line V.No.3 and *b* from V.No.1; flesh color segregated into 12 white, 3 yellow and 1 red in the F2.	Shimotsuma, 1963	Robinson et al., 1976*; Henderson, 1992**	?	
y	*rd*	*yellow flesh*; recessive to coral (light) red flesh (*Y*); *y* from 'Golden Honey'; *Y* from 'Angeleno' (black seeded).	Porter, 1937	Poole, 1944; Henderson, 1989; Henderson et al., 1998	C	
y-o	-	*orange flesh*; allelic to *y; Y* (red flesh) is dominant to *y-o* (orange flesh) and *y* (salmon yellow flesh); *y-o* (orange flesh) is dominant to *y* (yellow flesh); cc *y-oy-o I-C I-C* from 'Tendersweet Orange Flesh'; *cc yy I-C I-C* from 'Golden Honey'; *cc YY i-C i-C* from 'Sweet Princess'.	Henderson, 1989; Henderson et al., 1998	Poole, 1944; Porter, 1937	C	
Yb	-	*yellow belly*; yellow colored ground spot on the fruit; *Yb* from 'Black Diamond Yellow Belly'; *yb* from 'Black Diamond'.	Gusmini and Wehner, 2006	-	C	
Yl	*Y*	*Yellow leaf*; incompletely dominant to green leaf (*yl*); (*Y* renamed *Yl* by Henderson*). *Yl* from 'Yellow Skin'.	Warid and Abd-El-Hafez, 1976	Henderson, 1991*	?	*Yl*
zym-CH	-	*Resistance to zucchini yellow mosaic virus* (*ZYMV-CH*); resistance is specific to the China strain; *zym-CH* from PI 595203, *Zym-FL* from elite cultivars.	Xu et al., 2004	-	P	
zym-FL	*zym*	*Resistance to zucchini yellow mosaic virus* (*ZYMV-FL*); resistance is specific to the Florida strain; *zym-FL* from PI 482322, PI 482299, PI 482261, and PI 482308 (Provvidenti, 1991); higher resistance in PI 595203 (Egun), PI 386026, PI 386025 (Boyhan et al.), and in PI 386019, PI 490377, PI 596662, PI 485580, PI 560016, PI 494528,	Provvidenti, 1991	Boyhan et al., 1992; Guner et al., 2008b	P	

		PI 386016, PI 482276, PI 595201 (Guner et al.); *Zym-FL* from elite cultivars.				

z Asterisks on cultigens and associated references indicate the source of information for each.
y C = Mutant available from Cucurbit Genetics Cooperative watermelon gene curator; M = molecular marker or isozyme; P = mutants are available as standard cultivars or accessions from the plant introduction collection; ? = availability not known; L = mutant has been lost.

The isozymes and molecular markers for watermelon, including gene symbol, synonym, description, references and availability.(y)

Symbol	Synonym	Gene description and type lines	References	Supple-mental references	Availability
Aco-1	-	*Aconitase-1*.	Navot et al., 1990	-	M
Aco-2	-	*Aconitase-2.*	Navot et al., 1990	-	M
Adh-1	-	*Alcohol dehydrogenase-1*; one of five codominant alleles, each regulating one band	Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Adh-1-1	-	*Alcohol dehydrogenase-1-1*; one of five codominant alleles, each regulating one band; found in *C; lanatus* var. *citroides* and *C. colocynthis*.	Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Adh-1-2	-	*Alcohol dehydrogenase-1-2*; one of five codominant alleles, each regulating one band; found in *C. lanatus* var. *citroides* and *C. colocynthis.*	Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Adh-1-3	-	*Alcohol dehydrogenase-1-3*; one of five codominant alleles, each regulating one band; found in *Praecitrullus fistulosus*.	Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Adh-1-4	-	*Alcohol dehydrogenase-1-4*; one of five codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Aps-1	-	*Acid phosphase*-1.	Navot et al., 1990; Navot and Zamir 1986, 1987; Zamir et al., 1984	-	M
Aps-2-1	-	*Acid phosphatase*-2-1; one of two codominant alleles, each regulating one band; found in *C. lanatus* and *C. colocynthis.*	Navot et al., 1990; Navot and Zamir 1986, 1987	-	M
Aps-2-2	-	*Acid phosphatase*-2-2; one of two codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir 1986, 1987	-	M
Dia-1	-	*Diaphorase-1*	Navot et al., 1990	-	M
Est-1	-	*Esterase-1*; one of six codominant alleles, each regulating one band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M

Est-1-1	-	*Esterase-1-1*; one of six codominant alleles, each regulating one band; found in *C. lanatus* var. *citroides* and *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-1-2	-	*Esterase-1-2*; one of six codominant alleles, each regulating one band; found in *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-1-3	-	*Esterase-1-3*; one of six codominant alleles, each regulating one band; found in *Praecitrullus fistulosus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-1-4	-	*Esterase-1-4*; one of six codominant alleles, each regulating one band; found in *C. ecirrhosus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-1-5	-	*Esterase-1-5*; one of six codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-2	-	*Esterase-2*; one of five codominant alleles, each regulating one band; found in *C. lanatus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-2-1	-	*Esterase-2-1*; one of five codominant alleles, each regulating one band; found in *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-2-2	-	*Esterase-2-2*; one of five codominant alleles, each regulating one band; found in *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-2-3	-	*Esterase-2-3*; one of five codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Est-2-4	-	*Esterase-2-4*; one of five codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Fdp-1	-	*Fructose 1,6 diphosphatase-1*.	Navot et al., 1990; Navot and Zamir, 1986	-	M
For-1	-	*Fructose 1,6 diphosphatase-1*.	Navot et al., 1990	-	M
Gdh-1	-	*Glutamate dehydrogenase-1*; isozyme located in cytosol.	Navot and Zamir, 1986	-	M
Gdh-2	-	*Glutamate dehydrogenase-2*; isozyme located in plastids.	Navot et al., 1990; Navot and Zamir, 1986	-	M
Got-1	-	*Glutamate oxaloacetate transaminase-1*; one of four codominant alleles, each regulating one band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-1-1	-	*Glutamate oxaloacetate transaminase-1*; one of four codominant alleles, each regulating one band; found in *C. colocynthis* and *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-1-2	-	*Glutamate oxaloacetate transaminase-1-2*; one of four codominant alleles, each regulating one band; found in *C. lanatus* var. *citroides.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got 1-3	-	*Glutamate oxaloacetate transaminase-13*; one of four codominant alleles, each regulating one band; found in	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M

		Acanthosicyos naudinianus.			
Got-2	-	*Glutamate oxaloacetate transaminase-2*; one of five codominant alleles, each regulating one band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-2-1	-	Glutamate oxaloacetate transaminase-21; one of five codominant alleles, each regulating one band; found in C. colocynthis.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-2-2	-	*Glutamate oxaloacetate transaminase-22*; one of five codominant alleles, each regulating one band; found in *C. ecirrhosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-2-3	-	*Glutamate oxaloacetate transaminase-2-3*; one of five codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-2-4	-	*Glutamate oxaloacetate transaminase-24*; One of five codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Got-3	-	*Glutamate oxaloacetate transaminase-3.*	Zamir et al., 1984	-	M
Got-4	-	*Glutamate oxaloacetate transaminase-4.*	Navot et al., 1990; Zamir et al., 1984	-	M
hsp-70	-	*heat shock protein 70*; one gene presequence 72-kDa hsp70 is modulated differently in glyoxomes and plastids.	Wimmer et al., 1997	-	M
Idh-1	-	*Isocitrate dehydrogenase-1*	Zamir et al., 1984	-	M
Lap-1	-	*Leucine aminopeptidase-1.*	Navot et al., 1990; Navot and Zamir, 1986	-	M
Mdh-1	-	*Malic dehydrogenase-1*; one of two codominant alleles, each regulating one band; found in *C. lanatus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Mdh-1-1	-	*Malic dehydrogenase-1-1*; one of two codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Mdh-2	-	*Malic dehydrogenase-2*; one of three codominant alleles, each regulating one band; found in *C. lanatus.*	Navot and Zamir, 1987	-	M
Mdh-2-1	-	*Malic dehydrogenase-2-1*; one of three codominant alleles, each regulating one band; found in *C. colocynthis.*	Navot and Zamir, 1987	-	M
Mdh-2-2	-	*Malic dehydrogenase-2-2*; one of three codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot and Zamir, 1987	-	M
Me-1	-	*Malic enzyme-1*; one of three codominant alleles, each regulating one band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Me-1-1	-	*Malic enzyme-1-1*; one of three codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Me-12	-	*Malic enzyme-12*; one of three codominant alleles, each regulating one	Navot et al., 1990; Navot and Zamir, 1986, 1987;	-	M

		band; found in *C. colocynthis.*	Zamir et al., 1984		
Me-2	-	*Malic enzyme-2.*	Zamir et al., 1984	-	M
Pgd-1	*6 Pgdh-1*	*6-Phosphogluconate dehydrogenase-1*; one of three codominant alleles, each regulating one plastid band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgd-1-1	*6 Pgdh-1-1*	*6-Phosphogluconate dehydrogenase-1-1*; one of three codominant alleles, each regulating one plastid band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgd-1-2	*6 Pgdh-1-2*	*6-Phosphogluconate dehydrogenase-1-2*; one of three codominant alleles, each regulating one plastid band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgd-2	*6 Pgdh-2*	*6-Phosphogluconate dehydrogenase-2*; one of five codominant alleles, each regulating one cytosolic band; found in *C. lanatus*.	Navot and Zamir, 1986; Zamir et al., 1984	-	M
Pgd-2-1	*6 Pgdh-2-1*	*6-Phosphogluconate dehydrogenase-21*; one of five codominant alleles, each regulating one cytosolic band; found in *C. ecirrhosus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgd-2-2	*6 Pgdh-2-2*	*6-Phosphogluconate dehydrogenase-2-2*; one of five codominant alleles, each regulating one cytosolic band; found in *Praecitrullus fistulosus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgd-2-3	*6 Pgdh-2-3*	*6-Phosphogluconate dehydrogenase-2-3*; one of five codominant alleles, each regulating one cytosolic band; found in *C. colocynthis*.	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgd-2-4	*6 Pgdh-2-4*	*6-Phosphogluconate dehydrogenase-2-4*; one of five codominant alleles, each regulating one cytosolic band; found in *Acanthosicyos naudinianus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgi-1	-	*Phosphoglucoisomerase-1*; one of three codominant alleles, each regulating one plastid band; found in *C. lanatus*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Pgi-1-1	-	*Phosphoglucoisomerase-11*; one of three codominant alleles, each regulating one plastid band; found in *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Pgi-1-2	-	*Phosphoglucoisomerase-1-2*; one of three codominant alleles, each regulating one plastid band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Pgi-2	-	*Phosphoglucoisomerase-2*; one of six codominant alleles, each regulating one cytosolic band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgi-2-1	-	*Phosphoglucoisomerase-2*-1; one of six codominant alleles, each regulating one cytosolic band; found in *C. lanatus* and *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgi-2-2	-	*Phosphoglucoisomerase-2-2*; one of six codominant alleles, each regulating one	Navot et al., 1990; Navot and Zamir, 1986, 1987;	-	M

		cytosolic band; found in *C. ecirrhosus.*	Zamir et al., 1984		
Pgi-2-3	-	*Phosphoglucoisomerase-2-3*; one of six codominant alleles, each regulating one cytosolic band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgi-2-4	-	*Phosphoglucoisomerase-2-4*; one of six codominant alleles, each regulating one cytosolic band; found in *C. lanatus* var. *citroides*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgi-2-5	-	*Phosphoglucoisomerase-2-5*; one of six codominant alleles, each regulating one cytosolic band; found in *Acanthosicyos naudinianus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgm-1	-	*Phosphoglucomutase-1*; one of four codominant alleles, each regulating one plastid band; found in *C. lanatus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgm-1-1	-	*Phosphoglucomutase-1-1*; one of four codominant alleles, each regulating one plastid band; found in *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgm-1-2	-	*Phosphoglucomutase-1-2*; one of four codominant alleles, each regulating one plastid band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgm-1-3	-	*Phosphoglucomutase-1-3*; one of four codominant alleles, each regulating one plastid band; found in *Praecitrullus fistulosus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Pgm-2	-	*Phosphoglucomutase-2;* one of four codominant alleles, each regulating one cytosolic band; found in *C. lanatus*.	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgm-2-1	-	*Phosphoglucomutase-2-1*; one of four codominant alleles, each regulating one cytosolic band; found in *Acanthosicyos naudinianus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgm-2-2	-	*Phosphoglucomutase-2-2*; one of four codominant alleles, each regulating one cytosolic band; found in *C. lanatus*.	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Pgm-2-3	M	*Phosphoglucomutase-2-3*; one of four codominant alleles, each regulating one cytosolic band; found in *Praecitrullus fistulosus.*	Navot and Zamir, 1987; Zamir et al., 1984	-	M
Prx-1	-	*Peroxidase-1*; one of seven codominant alleles, each regulating one band; found in *C. lanatus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-11	-	*Peroxidase-11*; one of seven codominant alleles, each regulating one band; found in *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-12	-	*Peroxidase-12*; one of seven codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-13	-	*Peroxidase-13*; one of seven codominant alleles, each regulating one band; found in *C. lanatus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M

Prx-14	-	*Peroxidase-14*; one of seven codominant alleles, each regulating one band; found in *C. ecirrhosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-15	-	*Peroxidase-15*; one of seven codominant alleles, each regulating one band; found in *C. lanatus* and *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-16	-	Peroxidase-16; one of seven codominant alleles, each regulating one band; found in Acanthosicyos naudinianus.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Prx-2	-	*Peroxidase-2.*	Navot and Zamir, 1987	-	M
Prx-3	-	*Peroxidase-3.*	Navot and Zamir, 1987	-	M
Sat	-	*Serine acetyltransferase*; catalyzes the formation of O-acetylserine from serine and acetyl-CoA.	Saito et al., 1997	-	M
Skdh-1	-	*Shikimic acid dehydrogenase-1.*	Zamir et al., 1984	-	M
Skdh-2	-	*Shikimic acid dehydrogenase-2*; one of six codominant alleles, each regulating one band.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Skdh-21	-	*Shikimic acid dehydrogenase-21*; one of six codominant alleles, each regulating one band; found in *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Skdh-22	-	*Shikimic acid dehydrogenase-22*; one of six codominant alleles, each regulating one band; found in *C. colocynthis.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Skdh-23	-	*Shikimic acid dehydrogenase-23*; one of six codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Skdh-24	-	*Shikimic acid dehydrogenase-24*; one of six codominant alleles, each regulating one band; found in *C. ecirrhosus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Skdh-25	-	*Shikimic acid dehydrogenase-25*; one of six codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Sod-1	-	*Superoxide dismutase-1*; one of three codominant alleles, each regulating one band; found in *C. lanatus.*	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Sod-11	-	*Superoxide dismutase-11*; one of three codominant alleles, each regulating one band; found in *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Sod-12	-	*Superoxide dismutase-12*; one of three codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987; Zamir et al., 1984	-	M
Sod-2	-	*Superoxide dismutase-2*; one of two codominant alleles, each regulating one band; found in *C. lanatus.*	Navot and Zamir, 1987	-	M
Sod-21	-	*Superoxide dismutase-21*; one of two codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus*.	Navot and Zamir, 1987	-	M

Sod-3	-	*Superoxide dismutase-3*; one of two codominant alleles, each regulating one band; found in *C. lanatus.*	Navot and Zamir, 1987	-	M
Sod-31	-	*Superoxide dismutase-31*; one of two codominant alleles, each regulating one band; found in *Praecitrullus fistulosus.*	Navot and Zamir, 1987	-	M
Spr-1	-	*Seed protein-1.*	Navot and Zamir, 1986	-	M
Spr-2	-	*Seed protein-2.*	Navot and Zamir, 1986	-	M
Spr-3	-	*Seed protein-3.*	Navot and Zamir, 1986	-	M
Spr-4	*Spr-4*	*Seed protein-4.*	Navot et al., 1990; Navot and Zamir, 1986	-	M
Spr-5	*Spr-5*	*Seed protein-5.*	Navot et al., 1990; Navot and Zamir, 1986	-	M
Tpi-1	-	*Triosephosphatase isomerase-1*. one of four codominant alleles, each regulating one band; found in *C. lanatus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Tpi-11	-	*Triosephosphatase isomerase-11*; one of four codominant alleles, each regulating one band; found in *C. colocynthis*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Tpi-12	-	Triosephosphatase isomerase-12; one of four codominant alleles, each regulating one band; found in Praecitrullus fistulosus.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Tpi-13	-	*Triosephosphatase isomerase-13*; one of four codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus*.	Navot et al., 1990; Navot and Zamir, 1986, 1987	-	M
Tpi-2	-	*Triosephosphatase isomerase-2*; one of three codominant alleles, each regulating one band; found in *C. lanatus*.	Navot and Zamir, 1987	-	M
Tpi-21	-	*Triosephosphatase isomerase-21*; one of three codominant alleles, each regulating one band; found in *Acanthosicyos naudinianus.*	Navot and Zamir, 1987	-	M
Ure-1	-	*Ureaase-1.*	Navot and Zamir, 1987	-	M

y C = Mutant available from Cucurbit Genetics Cooperative watermelon gene curator; M = molecular marker or isozyme; P = mutants are available as standard cultivars or accessions from the plant introduction collection; ? = availability not known; L = mutant has been lost.

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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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Nuez Viñales, Fernando. Instituto de Conservación, COMAV; Univ. Politécnica; Camino de Vera s/n; 46022 Valencia, Spain. **email:***fnuez@btc.upv.es*. Genetics and plant breeding

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Owens, Ken. Magnum Seeds, Inc.; 5825 Sievers Road; Dixon CA 95620, USA. **email:***kobreeding@hotmail.com*. Cucumber breeding

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Paris, Harry. Dept. Vegetable Crops; A.R.O. Newe Ya'ar Research Ctr.; P.O. Box 1021; Ramat Yishay 30-095 , Israel. **email:***hsparis@volcani.agri.gov.il*. Breeding and genetics of squash and pumpkin

Peiro Abril, José Luis. Apartado de Correos no. 2; E 04720 Aguadulce , Spain. **email:***peiroab@larural.es,jlp@ramiroarnedo.com*. Melon, cantaloupe, watermelon, squash, cucumber breeding, gentics, in vitro

Perl-Treves, Rafael. Faculty of Life Sciences; Bar-Ilan University; Ramat-Gan 52900 , Israel. **email:***perl@brosh.cc.biu.ac.il*.

Picard, Florence. Vilmorin; Route du Manoir; 49 250 La Minitre , France. **email:***Florence.picard@vilmoria.com*.

Pitrat, Michel. INRA; Domaine St. Maurice; BP 94; 84143 Montfavet cedex , France. **email:***Michel.Pitrat@avignon.inra.fr*. Melon, disease resistance, mutants, genetic map

Polewczak, Lisa. Syngenta Seeds; 10290 Greenway Road; Naples FL 34114, USA. **email:***l.polewczak@gmail.com*. Squash, cantaloupe, watermelon breeding & genetics

Poostchi, Iraj. 97 St. Marks Road; Henley-on-Thames; The United Kingdom RG9 1LP, United Kingdom. **email:**. Breeding cantaloupes, melons and watermelons

Portyankin, Aleksey. Research Institute of Greenhouse Veg. Prod.; 2-Khutorskaya 11/1; Stroenie 1; 127287 Moscow, Russia. **email:***port75_alex@mail.ru*.

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Ray, Dennis. Dept. Plant Sci.; Univ. of Arizona; P.O. Box 210036; Tucson AZ 85721-0036, USA. **email:***dtray@**email**.arizona.edu*. Genetics and cytogenetics of *Cucumis melo* and *Citrullus* spp.

Reitsma, Kathy. North Central Regional Plant Introduction Sta.; Iowa State University; Ames IA 50011-1170, USA. **email:***kathleen.reitsma@ars.usda.gov,kreitsma@iastate.edu*. curator of cucurbit germplasm

Reuling, Gerhard T.M.. Nunhems Netherlands B.V.; P.O. Box 4005; 6080 AA Haelen, Netherlands. **email:***g.reuling@nunhems.com*. Breeding long cucumber

Robinson, R. W.. Emeritus Prof. , Dept. Hort. Sci.; NY Agri. Expt. Station; Cornell University; Geneva NY 14456-0462, USA. **email:***rwr1@nysaes.cornell.edu*. Breeding and genetics of cucurbits

Rodenburg, Marinus. East-West Seed Indonesia; Desabenteng, Campaka; P.O. Box 1 Purwakarta , Indonesia. **email:***rien@ewsi.co.id*.

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Seedworks India PVT. LTD. No 167; CQAL LAYOUT; Sahakar Nagar; Bangalore, Karnataka 560092, India. **email:***snjayasimha@seedworksindia.com*. Breeding aspects of watermelon, cucumber, ridge gourd, bottle gourd, bittergourd

Shetty, Nischit V. Seminis Vegetable Seeds; 432 TyTy Omega Road; Tifton GA 31794, USA. **email:***nischit.shetty@seminis.com*. Cucumber breeding

Shimamoto, Ikuhiro. 146-11 Daigo; Kashihara, NARA 634-0072, Japan. **email:***shimamoto@suika-net.co.jp*.

Simon, Phillip W. USDA-ARS-Vegetable Crops; Dept. of Horticulture, Univ. of Wis.; 1575 Linden Dr.; Madison WI 53706-1590, USA. **email:***psimon@wisc.edu*. Breeding and genetics

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Swanepoel, Cobus. Pannar; P.O. Box 19; Greytown KZN 3250, South Africa. **email:***cobus.swanepoel@pannar.co.za*.

Tatlioglu, Turan. Martar Tohumculuk A.S.; Han Mahallesi; 5 Eylül Caddesi No. 7; Susurluk (Balikesir) 10600, Turkey. **email:***turantatlioglu@yahoo.com*. Hybrid breeding, sex inheritanc, sex genes

Taurick, Gary. Harris Moran Seed Co.; 5820 Research Way; Immokalee FL 34142, USA. **email:***g.taurick@harrismoran.com*. Development of commercial hybrids of pickle, slicer and Beit Alpha cucumbers

Theurer, Christoph. GlaxoSmithKline Consumer Healthcare GmbH & Co. KG; Consumer Healthcare Gmbh&Co.KG; Benzstrasse 25; D-71083 Herrenberg , Germany.
email:*Christoph.Theurer@gsk.com*.

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Vadra Halli, Satish. #1/2, Krishna Road; Basavanagudi; Bangalore 560004 Karnataka, India.
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Vardi, Eyal. Origene Seeds Ltd.; Givat Brenner 60948 , Israel.
email:*eyal@origeneseeds.com*.

Wehner, Todd. Dept. Horticultural Science; Box 7609; North Carolina State Univ.; Raleigh NC 95616, USA.
email:*todd_wehner@ncsu.edu*. Pickling/slicing cucumber, watermelon, luffa gourd, selection, disease resistance, yield, genetics and breeding

Weng, Yiqun. USDA Vegetable Crops Research Unit; University of Wisconsin, 1575 Linden Dr., Madison WI 53706 USA. email: yiqun.weng@ars.usda.gov

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*. Pumpkin and squash breeding and genetics; disease and insect resistance; cucurbit evolution and domestication

Whitwood, Tim. 738 Castle St; Geneva NY 00681-9030, USA.
email:*timw@ruppseeds.com*.

Williams, Tom V. 2329 Pinewood Circle; Naples, FL 34105, USA.
email:*tvwilli@earthlink.net; tvwili@aol.com*. Watermelon consultant

Winkler, Johanna. Saatzucht Gleisdorf GmbH; Am Tieberhof 33; A-8200 Gleisdorf, Austria.
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Wu, Mingzhu. Hort. Instit.; Xinjiang Acad. Agric. Sci; Nachang Road No. 38; Urumqi Xinjiang 830000 , P.R. of China.
email:*mzwu@x263.net*.

Yorty, Paul. Qualiveg Seed Production; 3033 E., 3400 N.; Twin Falls ID 83301, USA. **email:**. Cucurbit breeding

Zhang, Xingping. Syngenta Seeds; 21435 Co. Rd. 98; Woodland CA 95695, USA.
email:*xingping.zhang@syngenta.com*. Watermelon and melon genetics & breeding

Zhang, Shengping. Institute of Vegetables & Flowers; Chinese Academy of Agric. Sci.; No 12 Zhongguancun Nandajie; Beijing 100081 , P.R. of China.
email:*zhangshp2007@hotmail.com*. Cucumber genetics & breeding

Zhou, Ihichen. Xinjiang XiYu Seeds Co., LTD.; No. 32 Eastern Ningbian Road; Changji Xingiang 831100, P.R. of China.
email:*xiyuseedsxj@hotmail.com*. Breeding watermelon, melon, squash and other cucurbits

2007 CGC Membership by Country

Argentina
Fernando Lopez-Anido
INTA EEA La Consulta

Australia
Mark Herrington

Austria
Tamas Lelley
Martin Pachner
Johanna Winkler

Brazil
Romulo Fujito Kobori
Wison Roberto Maluf

China, Peoples Republic of
HaiQing Bao
Jin Feng Chen
Li Haizhen
Qing Ma
Wenge Liu
Mingzhu Wu
Shengping Zhang
Ihichen Zhou

Czech Republic
Bohuslav Holman
Aleš Lebeda

Egypt
M. Hossam Aboul-Nasr

France
Sylvie Baudracco-Arnas,
Francois Bertrand
Nathalie Boissot
Frank De Langen
Frederic Ignart
Robert Legnani
Mansour Majde
Julien Mazet
Florence Picard
Michel Pitrat

Germany
Christoph Theurer

India
Laxman Aurangabadkar
Tusar Behera
Srinivas Ranganath
Seedworks India PVT. LTD
Satish Vadra Halli

Indonesia
Marinus Rodenburg
Fatkhu Rokhman

Israel
Harel Belotserkovsky
Yosi Burger
Emanuel Cohen
Haim Davidi
Zvi Karchi
Nurit Katzir
Merav Kenigswald
Harry Paris
Rafael Perl-Treves
Eyal Vardi

Italy
Erik de Groot
Nadia Ficcadenti
Gianni Gatto
Elen Jones-Evans

Japan
Toshi Furuki
Toshitsugu Hagihara
Kimio Ito
Kenji Kato
Yuichi Matsumoto
Ikuhiro Shimamoto

Korea, Republic of
Myeong-Cheoul Cho
Young-Hyun Om

Malta
Everaldo Attard

Mexico
Sergio Garza-Ortega

Netherlands, The
Eric Bal
Wouter De Ruiter
Kees Hertogh
Rene Hofstede
Jan Hoogland
Marcel Kelfkens
Jaap Mazereeuw
Gerhard T.M. Reuling

New Zealand
Doug Grant

Philippines, The
Renita Beronilla

Poland
Katarzyna Niemirowicz-Szczytt

Russia
Aleksey Portyankin

South Africa
Cobus Swanepoel

Spain
Jesus Abad Martin
María Angeles Buil Benedi
Wim Deleu
Maarten Den Hertog
Maria L. Gómez-Guillamón
Peter Kraakman
Fernando Nuez Viñales
Gloria Palomares
José Luis Peiro Abril

Sweden
Louis Carl Lehmann

Thailand
Sumitra Asavasena
Vinich Chuanchai
Simon Jan de Hoop
Usa Duangsong
Supat Mekiyanon

Turkey
Turan Tatlioglu

United Kingdom
Halina Dawson
Iraj Poostchi

2007 CGC USA Membership by State

Alabama
Dane, F

Arkansas
Morelock, T

Arizona
Ray, D

California
Gabor, B
Himmel, P
Johnson, B
Juarez, B
Knerr, LD
Lanini, B
McCreight, JD
Ouyang, W
Owens, K
Poulos, JM
Randhawa, L
Randhawa, P
Tolla, G
Zhang, X

Connecticut
Connolly, B.

Florida
Dombrowski, C.
Guner, N
Gusmini, G
Maynard, DN
Polewczak, L.
Taurick, G
Williams, TV
Kabelka, E.

Georgia
Boyhan, GE
Groff, D
Shetty, NV

Iowa
Block, C
Merrick, LC
Reitsma, K

Idaho
Yorty, P

Illinois
Frobish, M

Indian
Martyn, R

Maryland
Everts, K.
Kirkbride, Jr., JH
National Agricultural Library
Ng, TJ

Maine
Johnston, R

Michigan
Grumet, R

North Carolina
Kumar, R.
Wehner, T

New Hampshire
Loy, JB

New York
Andres, TC
Goldman, AP
Jahn, M
Jahn, M
Munger, HM
Robinson, RW
Whitwood, T
Whitwood, T.

Ohio
Bell, D

Oklahoma
Davis, AR

Oregon
Myers, J.R.
Myers, JR
Reiten, J

Pennsylvania
Stephenson, AG

Puerto Rico
Wessel-Beaver, L

Rhode Island
Brown, R

South Carolina
Harris, K.R.
Kousik C. (S.)
Ling, K-S

Texas
Crosby, K
King, SR
Lester, G
Neill, A

Wisconsin
Havey, MJ
Lower, RL
Simon, PW
Weng, Y.

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.