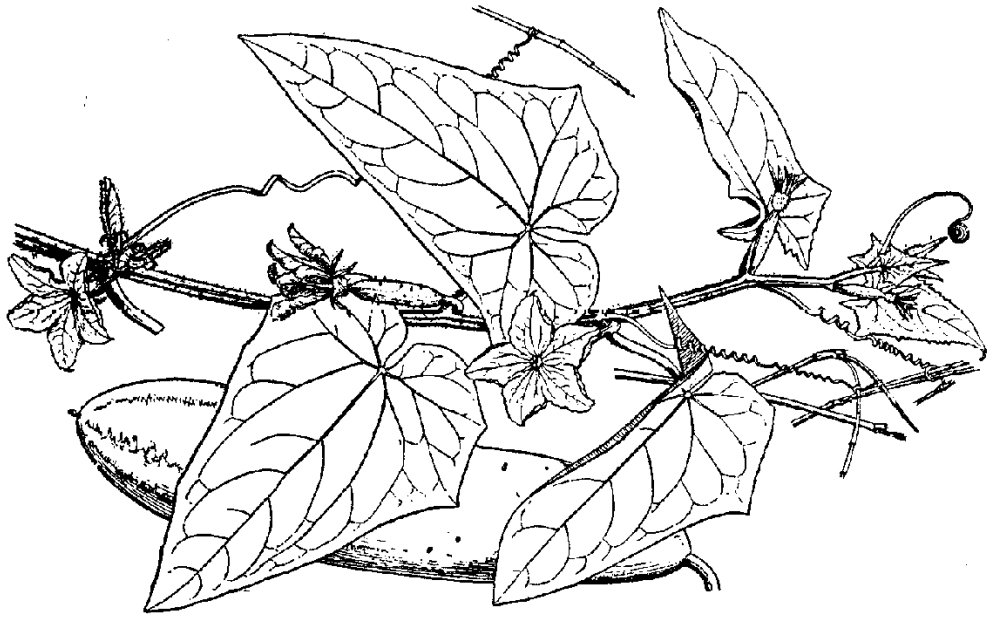
Cucurbit Genetics Cooperative

2002



25

Cucurbit *Genetics* Cooperative

August 2002

ISSN 1064-5594

2118 Plant Sciences Building
College Park, Maryland
20742-4452 USA

Tel: (301) 405-4345
Fax: (301) 314-9308
Internet: *tn5@umail.umd.edu*

http://ars-genome.cornell.edu/cgc/

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://ars-genome.cornell.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.

ISSN 1064-5594

NEWS & COMMENT

RESEARCH REPORTS

Cucumber (*Cucumis sativus)*

Melon (*Cucumis melo*)

Watermelon (*Citrullus lanatus*)

Cucurbita spp.

Cucurbit Genetics Cooperative News!!

Timothy J Ng, CGC Chair
University of Maryland, USA

Apologies are in order for the delay of CGC 25 (2002). We had anticipated that the 25th anniversary issue of the CGC Report would have been issued at the regular time in the regular manner. Unfortunately, a combination of events including the 11 September 2001 attacks (the University of Maryland is in the Washington DC area), a tornado that severely damaged the University of Maryland campus shortly thereafter, the unanticipated loss of our webspace on the U.S. Plant Genome server, and unexpected delays all served to lengthen the time between the issuance of CGC 24 and CGC 25. As a means of apology, all CGC members who were paid up through 2001 or who joined in 2002/2003 will have their membership extended an additional year free of charge.

For your information, CGC 24 (2001) was mailed approximately a week before the 11 September attack on the US. Unfortunately, as mentioned earlier the University of Maryland is located in the Washington DC area and some of our mail goes through the Washington DC Brentwood post office. This was the post office that was shut down due to several workers dying from the anthrax attack, and mail was held there for a considerable period of time while the building underwent a thorough decontamination. If you did not receive your copy of CGC 24, please notify Tim Ng and he will send a replacement copy.

CGC 26 (2003) is currently on schedule for mailing in August. At that time, it will probably be accompanied by a mail/email ballot for members to vote on a change in our by-laws. The primary reason for this is that the responsibilities of the CGC Chair has increased considerably over the past 25 year, to the point where the CGC Coordinating Committee feels that the duties should be more equitably divided among three CGC members, one for administrative efforts such as CGC membership renewals and correspondence, one for development and maintenance of the CGC website, and one for final editing and publication of the CGC Report. Since this represents a change in the structure of CGC, it requires a majority vote from the CGC membership prior to implementation.

Comments…….

From the CGC Coordinating Committee: CGC Report No. 26 will be published in August 2003. Contributors to the CGC Report should check the website (*http://www.umresearch.umd.edu/cgc*) for deadlines, and for instructions on preparing and submitting manuscripts. As always, we are eager to hear from CGC members regarding our current activities and future direction of CGC.

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

It is hoped that scientists will consult these lists as well as the rules of gene nomenclature for the Cucurbitaceae before selecting a gene name and symbol. Thus, inadvertent duplication of gene names and symbols will be prevented. The rules of gene nomenclature (published in each CGC Report) 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.

From the CGC Gene Curators: CGC has appointed curators for the four major cultivated crops: cucumber, melon, watermelon and Cucurbita spp. Curators are responsible for collecting, maintaining, and distributing upon request stocks of know marker genes. CGC members are requested to forward samples of currently held gene stocks to the respective Curator.

Meanwhile, we are pleased to announce two winners of the CGC logo contest. Amanda Neill of the Botanical Research Institute of Texas designed the watermelon/DNA design which is reproduced on the front cover of CGC 25, and Tarek Kapiel of Cairo University in Egypt designed the new CGC/DNA logo which is now on the homepage of the CGC website. Both Amanda and Tarek will receive two-year memberships in CGC for their efforts. Our thanks to all who participated in the CC logo contest!

IInd International Symposium on Cucurbits – Tsukuba, Japan
Kajim Abak, chief of the ISHS Cucurbit Working Group
Shigeo Nishimura, Convener

The IInd International Symposium on cucurbits was held from September 28 until October 1, 2001 at Tsukuba Science city in Japan under the sponsorship of the International Society of Horticultural Science (ISHS) and the Japanese Society of Horticultural Science. The one hundred sixty eight participants came from 25 different countries. Recent results of research on all aspects of science and technology on cucurbits were presented and actively discussed in 36 oral and 59 poster presentations. The program was divided into 5 sessions, namely: Biotechnology, Genetics and Breeding, Environmental Physiology, Disease Resistance and Post-Harvest.

Many interesting studies were reported. In the Biotechnology session, for instance, technologies for an efficient haploid and doubled haploid production in melon were presented as well as information on DNA markers and genetic maps of melon and watermelon, and on fruit development and maturation mechanisms.

During the Genetics and Breeding session among other subjects the India origin of the no-netted melons in Asia, as well as the small seeded melons such as the variety Makuwa, widely produced in east Asia, was disclosed. In the Environmental Physiology session interesting information was presented on the modeling of greenhouse cucumber production based on studies about the partitioning of photo-assimilates within a plant. Also results of research were reported on a marked change of the cytokinine composition by grafting of cucumber and on the possible involvement of auxin-inducible genes in the hydrotropic response of the clinorotated roots.

Classification of pathogenesis in 21 strains of *Pseudoperonospora cubensis* in cucurbits collected from European countries was presented in the Disease Resistance session, and in the Post Harvest session, amongst other items guidelines for quality maintenance of melon in USA were given as well as information on extension of the shelf life of melon fruit by the ethylene inhibitor 1-methylcyclopropene and on nondestructive evaluation methods of fruit qualities using laser.

In all sessions there was a marked increase of presentations on molecular studies in cucurbits as is the case in other fields.

The highlight of the Symposium was the open forum entitled “Cucurbits of Silk Road” which was specially planned by the Organizing Committee because the cucurbits symposium was held in Asia for the first time. In the forum, five Asian researchers gave interesting introductions to the participants of the symposium and the citizens of Tsukuba city on many varieties of Asian cucurbits and their research topics from Turkmenistan, India, China, Korea and Japan. In the general discussion, the importance of the maintenance of genetic diversity in these regions was stressed by many participants. It was concluded that efforts to this effect should be made.

Participants were offered a professional tour to visit cucurbit farmers around Tsukuba city. A typical Japanese cucumber farmer we visited produced cucumbers all year round using plastic houses. We also had the opportunity to inspect an automatic packing station managed by a farmer’s union in the region. If cucumber farmers used this facility, he only had to harvest his cucumbers and bring them to this station. We also visited a melon farmer, who quite uniquely owns an open market with regional restaurant by himself and sells the produce including melons to tourists coming around. Finally we had a farewell party at a farmer’s open market in a heartwarming environment. We are sure that everyone had a pleasant time in this professional tour.
It was decided to meet each other again after 4 years in IIIrd International Symposium on cucurbits either in Australia or in China. (Editors note: the IIIrd International Symposium on Cucurbits is now scheduled for 2005 in Australia. Meanwhile, the Proceedings for the IInd International Symposium on Cucurbits is available from ISHS as Acta Horticulturae 588; see *http://www.actahort.org/books/588/* for more details.

Watermelon Research and Development Working Group
22nd Annual Meeting – 2002
Benny D. Bruton, Chairman
USDA/ARS, Lane, Oklahoma

The Annual Meeting of the Watermelon Research & Development Working Group (WRDWG) was on Sunday, February 3, 2002 in Kissimmee, Florida. The meeting was held at the Hyatt Orlando in conjunction with The Southern Association of Agricultural Scientists (S.A.A.S.) and the Southern Region American Society for Horticultural Sciences (SR: ASHS). We had an excellent program this year with an attendance of approximately 75 people. As per the request of the members, we met for a full day this year.

The program began with a welcome from Benny Bruton, Chair, who provided an update on the WRDWG webpage at *http://www.lane-ag.org/h2omelon/watermelon.htm*. He asked members to update htheir email addresses and phone numbers, and encouraged non-members to fill out the forms at the website and submit them for processing into the WRDWG database for Scientists and Areas of Expertise. He also encouraged all members and interested parties to submit information on hot topics such as new diseases or new releases.

Seed company releases were provided by Don Dobbs (Willhite Seed), Glen Ruttencutter (S8unSeeds), Brenda Lanini (Harris Moran), Fred McChuistion (Seminis), Tom Williams (Syngenta) and Pete Suddarth (Abbot & Cobb).

For the 2001 statewide watermelon trials, the following presentations were made:

Rich Hassell, Clemson University Coastal Research Station, South Carolina, "*Watermelon Cultivar Evaluations in Oklahoma*"

Warren Roberts, Oklahoma State University, Lane, Oilahoma. "*Watermelon cultivar Evaluations in Oklahoma"*

Don Maynard, University of Florida, Bradenton, FL, "*Review of the Florida Statewide Watermelon Trials*"

Frank Dainello, Texas A&M University, College Station, "*Review of the Texas Statewide Watermelon Trials*"

Dan S. Egel, Southwest Purdue Ag Center, Vincennes, "*Review of the Indiana Statewide Watermelon Trials*"

George Boyhan, University of Georgia, Statesboro, Georgia. "*Statewide Watermelon Trials for Georgia, 2001*"

J.R. Schultheis, North Carolina State University, Horticultural Science Dept., "*2001 Watermelon Cultivar Trial Results, North Carolina*"

Bob and Maggie Kent of Kent Honeybees, Inc. (Edinburg TX) then gave a talk on bees and pollination entitled "You Grow It – We Buzz It."

Following the lunch break, two miscellaneous reports were presented:

Robert L. Jarrett, USDA/ARS, Plant Genetic Resources Unit, Griffin, GA. "*Watermelon Germplasm: Past, present and future*"

Diana Musto, Research Associate, National Watermelon Promotion Board, Orlando, FL. "*Review of 2001 Research Projects*"

These presentations were followed by research reports:

Levi, A. U.S. Vegetable Laboratory, USDA-ARS, 2875 Savannah Highway, Charleston, SC 29414-5334; "Progress in Constructing Linkage Map for Watermelon*"*

Davis, A., Fish, W., and Perkins-Veazie, P. US Department of Agriculture-Agricultural Research Service, Lane, OK; "*Spectrophotometric Method of Lycopene Quantitation in Watermelon*"

Perkins-Veazie, P., Collins, J.K., Edward, A. and Clevidance, B. U.S. Department of Agriculture-Agricultural Research Service, Lane, OK; "*Uptake of watermelon Lycopene by Humans and Other New Lycopene News*"

Leskovar, D.I.,[1] *Bang, H.J.,[1] Kolenda, K.,[1] Franco, J.A., [2] and Perkins-Veazie, P.[3] [1] Texas Agricultural Experiment Station, Dept. Horticultural Sciences, Texas A&M University, Uvalde, TX 78801;[2] Departmento de Produccion Agraria, Universidad Politecnica de Cartagena, Cartagena, Spain; [3] USDA ARS, SCARL, Lane, OK 74555; "*Limited Irrigation Influences Yield, Fruit Quality and Lycopene Content of Watermelon*"

Thies, J.A.* and Levi, A. U.S. Vegetable Laboratory, USDA-ARS, 2875 Savannah Highway, Charleston, SC 29414-5334; "*Response of Selected Citrullus Plant Introductions to the Peanut Root-knot Nematode* (*Meloidogyne Arenaria Race 1*)"

Gerald Holmes, G[1] and Schultheis, J.R.[2] North Carolina State University, (1) Dept. Plant Pathology, (2) Horticultural Science Dept. "*Relative Susceptibility of Watermelon Cultigens to Ozone in North Carolina, 2000-2001*"

Guner, N., Wehner, T.C., an Pesic-Van Esbroeck, Z. North Carolina State University, Raleigh, NC "*Screening for PRSV-W Resistance in Watermelon*"

Gusmini, G. and Wehner, T.C. North Carolina State University, Raleigh, NC "*Screening for GSB Resistance in Watermelon*"

Neppl, G.P. and Wehner, T.C. North Carolina State University, Raleigh, NC "*Effect of Plot Size on Yield Variation in Watermelon*"

Egel, D.S., Ramasubramaniam, H., and Barber, S. SW Purdue Ag Program, Vincennes, IN 47591; "*Mature Watermelon Vine Decline Update*"

Roberts, W. Oklahoma State University, Lane, Oklahoma "*Cultivar Evaluations: Consistency among Investigators"*

Bruton, B.D. USDA-ARS, Lane, Oklahoma. "*Squash Bug: Vector of Serratia marcescens, Causal Agent of Cucurbit Yellow Vine Disease*"

These reports were followed by a discussion of seed sources for fusarium wilt differentials, then refreshments complements of the National Watermelon Promotion Board (Kissimmee FL).

Report to the Watermelon Research Group
Submitted to WRDWG on 3 February 2002
R.L. Jarrett, USDA/ARS. Griffin, GA

Personnel: Personnel currently assigned to the maintenance of the *Citrullus* collection include the curator (RLJ) and Field Services personnel in Griffin and Byron GA.

Inventory and Regeneration: The current inventory of the *Citrullus* collection can be viewed at *www.ars-grin.gov/npgs/searchgrin.html*. Copies of pe-GRIN can be obtained by contacting the curator (770/228-7303) or the database operator (770/229-3297). This portable database is available free of charge and can be searched using your office PC.

The *Citrullus* collection inventory remains at about 1,600 accessions. The Griffin location is making headway in dealing with the backlog of materials awaiting regeneration. In 2001, 150 *Citrullus* Plant Introductions (PIs) were regenerated with controlled pollination in Byron. Average seed yield per cage averaged 2,000 to 5,000, sufficient for local seed stock replenishment and long-term backup.

At the present time, approximately 95% of the *Citrullus* PIs are available for distribution. We hope to increase this number to 99% in 2002. Sixty-six duplicate accessions among the heirloom cultivars maintained at Fort Collins were eliminated in 2001**.**

Germplasm Acquisition: No *Citrullus* germplasm was acquired via plant exploration in 2001. To the curator's knowledge, no *Citrullus* exploration proposals were submitted for funding in 2001.

Germplasm Characterization: All *Citrullus* germplasm grown for regeneration in 2001 was characterized using the morphological descriptors as listed on the ARS-GRIN web site. We would like to expand on the value of the descriptor data by adding characteristics (or character states) that the user community finds useful. Please forward any suggestions or comments regarding descriptors to the curator.

***Citrullus* Core Collection:** We continue to encourage the use of the core collection as a starting point in future germplasm evaluation studies. Accessions belonging to the core collection are flagged as such on GRIN.

Plans for 2001: In 2002, we intend to continue with our previously established regeneration/characterization plan. Space permitting, we will begin regenerating accessions of heirloom cultivars currently maintained only at NSSI.

Contacts:
Curator: R.L. Jarret – *bjarret@gaes.griffin.peachnet.edu*
Database Operator: M. Spinks – *s9ms@ars-grin.gov*
Research Leader: G. Pederson – *gpederson@ars-grin.gov*

Cucurbit Crop Germplasm Committee
James D. McCreight
Chair, Cucurbit Crop Germplasm Committee
Jimccreight@pw.ars.usda.gov

Germplasm Evaluation Proposals – FY 2004

Each year the U.S. National Plant Germplasm System (NPGS funds a limited number of proposals for evaluation of crop germplasm. Proposals are reviewed by the appropriate Crop Germplasm Committee (CGC) and forwarded to the USDA, ARS National Program Staff for the final funding decision. Proposals will only be approved for germplasm evaluation *per se*, not for the selection, enhancement, or improvement. All proposals are evaluated on the national need for evaluation data, the likelihood of success, and the likelihood that the data will be entered into GRIN and shared with the user community. Cucurbit evaluation proposals for funding in FY 2004 are due to the Cucurbit CGC by **August 1, 2003.** Contact the CCGC Chair for details including proposal guidelines and timeline for submission and review.

Plant Exploration and Exchange Proposals – 2004

Each year the U.S. Department of Agriculture, Agricultural Research Service (USDA, ARS) solicits proposals for plant explorations and exchanges to acquire germplasm for inclusion in the U.S. National Plant Germplasm System (NPGS). Plant exploration proposals are for foreign and domestic (U.S.A.) germplasm exploration. Plant exchange proposals fund foreign trips to arrange germplasm exchanges with foreign genebanks. Any qualified U.S. scientist may submit a proposal.

According the USDA, ARS, Plant Exchange Office (PEO), National Germplasm Resources Laboratory statistics, an average of 10 explorations were funded each year during the last 10 years (1993-2002). NPGS funded three explorations for cucurbits while the number of explorations for other crops during this time ranged from zero to 13.

A proposal may be for a specific exploration or exchange, or it may be combined with another exploration or exchange, respectively, designed primarily to collect or exchange other species. Combined explorations or exchanges, where feasible, help to reduce costs and increase efficiency of money available for explorations and exchanges. Combined explorations and exchanges enable scientists to remain at home and concentrate on their field research while someone carries out the often arduous task of collecting and documenting.

All plant exploration and exchange proposals must be supported by the appropriate Crop Germplasm Committee (CGC). The Cucurbit CGC reviews proposals for collection of cucurbits and forwards them to the PEO for final review and decision by the Plant Germplasm Operations Committee and approval by the USDA, ARS National Program Staff.

The guidelines for plant exploration and exchange proposals are designed to guide prospective explorers and exchangers through the necessary background study required to obtain the information necessary for sound planning and effective implementation of explorations and exchanges.

Those contemplating an exploration or exchange are advised to contact the Chair, Cucurbit CGC (above) regarding Cucurbit CGC exploration priorities and review.`

Upcoming Meetings

Organization/Meeting	Date(s)	Location	Contact
Cucurbit Genetics Cooperative (In conjunction with the ASHS 2003 Centennial Conference)	3 Oct 2003 1:30 to 2:30 p.m.	Rhode Island Convention Center Room 550B Providence, Rhode Island	Timothy J. Ng *tn5@umail.umd.edu* *http://www.umresearch.umd.edu/cgc*
Pickling Cucumber Improvement Committee (PCIC) (in conjunction with the 2003 Pickle Packers International Annual Meeting and Trade Show)	22 Oct 2003	Sheraton Hotel & Convention Ctr New Orleans, Louisiana, USA	James Adkins *Adkins@udel.edu*
Watermelon Research & Development Working Group (in conjunction with the 2003 Southern Association of Agricultural Scientists Meeting)	13-18 Feb 2004	Tulsa, Oklahoma, USA	Benny Bruton *bbruton-usda@lane-ag.org* *http://www.lane-ag.org/H2omelon/watermelon.htm*
8th Eucarpia Cucurbitaceae 2004	July 2004	Czech Republic	Ales Lebeda *lebeda@prfholnt.upol.cz* *http://www.cucurbitaceae.upol.cz/*
2nd International Oil Pumpkin Conference (in connection with 8th EUCARPIA Cucurbitaceae 2004)	July 2004	Czech Republic	Penelope Lichtenecker (*pslicht@nextra.at*) Harry Paris (*hsparis@volcani.agri.gov.il*) Tamas Lelley (*lelley@ifa-tulln.ac.at*) Thomas Andres (*tom@andres.com*)
3rd ISHS International Symposium on Cucurbits	2005	Australia	Gordon Rogers *Gordon@ahr.com.au*
Cucurbitacee 2006	2006	North Carolina, USA	Gerald Holmes (*Gerald_Holmes@ncsu.edu*) Jonathan Schultheis (*Jonathan_Schultheis@ncsu.edu*) Todd Wehner (*Todd_Wehner@ncsu.edu*) *http://cuke.hort.ncsu.edu/cucurbit/meetings/ccrbitceae06mtg.html*

Cucumber Recombinant Inbred Lines

Jack E. Staub, Linda K. Crubaugh and Gennaro Fazio
USDA-ARS Vegetable Crops Research Unit, University of Wisconsin-Madison, Department of Horticulture, 1575 Linden Dr. Madison WI 53706

Release Announcement. A set of recombinant inbred (RIL) cucumber lines (*Cucumis sativus* L.) is being released by U. S. Department of Agriculture, Agricultural Research Service as genetic stock and for breeding purposes. These RIL were developed in conjunction with mapping experiments that sought to identify molecular markers linked to economically important traits (i.e., yield components) controlled by quantitative trait loci (QTL) in F_3 families derived from a GY-7 x H-19 mating (1 and 2). These F_3 families were self-pollinated to produce RIL that were assessed in two years in field tests at the University of Wisconsin Experiment Station, Hancock, WI (HES). A RIL-based map was constructed using 14 single sequence repeats (SSR), 24 sequence characterized amplified regions (SCAR), 27 amplified fragment length polymorphisms (AFLP), 62 random amplified polymorphic DNA (RAPD), 1 single nucleotide polymorphism (SNP), and 3 economically important morphological [*F* (gynoecy), *de* (determinate habit), *ll* (little leaf)] markers (3). This map consists of seven linkage groups spanning 706 cM with mean marker interval of 5.6 cM.. The RIL described herein can be used in conjunction this map to identify additional qualitative (e.g., disease resistance) and quantitative (e.g., fruit yield and quantity components) traits and for use in the development of inbred backcross lines for extensive genetic analyses (e.g., fine mapping).

Description of inbred lines used to create RIL. The monoecious, indeterminate, little leaf (40 cm^2) line H-19 (University of Arkansas-Fayetteville, 1993) was crossed with the gynoecious, determinate cucumber experimental line GY7 (tested as experimental line G421; University of Wisconsin-Madison, 1997) possessing standard-sized leaves (80 cm^2). H-19 plants normally have 5 to 15 primary lateral branches depending on the environment, and possess a sequential fruiting habit (i.e., several fruit enlarge on a branch). In contrast, GY7 has relatively few branches (1 to 3), and exhibits strong crown set and sequential fruit inhibition.

Development of RIL. An F_1 plant resulting from an GY7 x H-19 mating was self-pollinated to produce 250 F_2 progeny which were then self-pollinated by single seed descent to obtain 168 F_2S_6 recombinant inbred lines (RILs). The sex expression of plants exhibiting the gynoecious character during the formation of RILs was modified by treatment with silver thiosulfate to allow for self-pollination.

Evaluation and description of RIL. Recombinant inbred lines, parents and F_1 were evaluated in one locations (HES) in 1999 and 2000. RILs were arranged in randomized complete block design with three replications per location. Each replication had 12 plants and consisted of single rows with plants spaced 13 cm apart in rows to include edge borders positioned on 1.5 m centers corresponding to a plant density of ~51,000 plants/ha. Data were collected on plant habit, days to anthesis, sex expression, leaf type, number of lateral branches originating from the mainstem, and fruit number and fruit length/diameter ratio. Considerable variation in the traits examined among RIL was observed in plant habit (determinate and indeterminate), earliness (45 to 57 days to anthesis), sex type (gynoecious and monoecious), lateral branches (1 to 9), fruit number (1 to 7 fruit per plant), and L:D (2.8 to 3.1). Multiple branching lines were identified that produced commercially acceptable fruit (Figure 1). Complete descriptions of RILs are detailed by Fazio (3).

Availability

Breeder's seed, produced under screen isolation, will be provided to U.S. hydrid-seed producers and cucumber breeders by J.E. Staub, ARS/USDA, Dept. of Horticulture, Univ. of Wisconsin, Madison, WI 53706. The development of mapping information from these RIL was partially supported by grant No. IS-2708-96 from the U.S.-Israel Binational Agricultural Research and Development (BARD) Fund.

Figure 1. Gynoecious multiple lateral determinate cucumber germplasm.

Literature Cited

1. Serquen, F. C., J. Bacher, and J. E. Staub. 1997a. Genetic analysis of yield components in cucumber (*Cucumis sativus* L.) at low plant density. J. Amer. Soc. Hort. Sci. 122:522-528:1997.
2. Serquen, F. C., J. Bacher, and J. E. Staub. 1997b. Mapping and QTL analysis of a narrow cross in cucumber (*Cucumis sativus* L.) using random amplified polymorphic DNA markers. Mol. Breeding 3:257-268.
3. Fazio, G. 2001. Comparative study of marker-assisted and phenotypic selection and genetic analysis of yield components in cucumber. Ph.D. Diss., University of Wisconsin, Madison. (Diss. Abstr. 3033308.)

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

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

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

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

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

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

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

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

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

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

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

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

Literature Cited

1. Staub, J. E. and R. S. Kupper. 1985. Results of the use of *Cucumis sativus* var. *hardwickii* germplasm following backcrossing with *Cucumis sativus* var. *sativus*. HortScience 20:436-438
2. Staub, J. E., C. E. Peterson, L. K. Crubaugh and M. J. Palmer. 1992. Cucumber population WI 6383 and derived inbreds WI 5098 and WI 5551. HortScience 27:1340-1341.
3. Staub, J. E. and L. Crubaugh. 1995. Selection of multiple lateral determinate cucumber genotypes. Cucurbit Genetics Cooperative Rpt. 18:5-6.
4. Staub, J. E., J. Bacher and L. Crubaugh. 1995. Problems associated with the selection of determinate cucumber (*Cucumis sativus* L.) plant types in a multiple lateral background. Cucurbit Genetics Cooperative Rpt. 18:7-9.
5. Staub, J. E., F. Serquen, and M. Gupta. 1996. Genetic markers, map construction and their application in plant breeding. HortScience 31:729-741

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

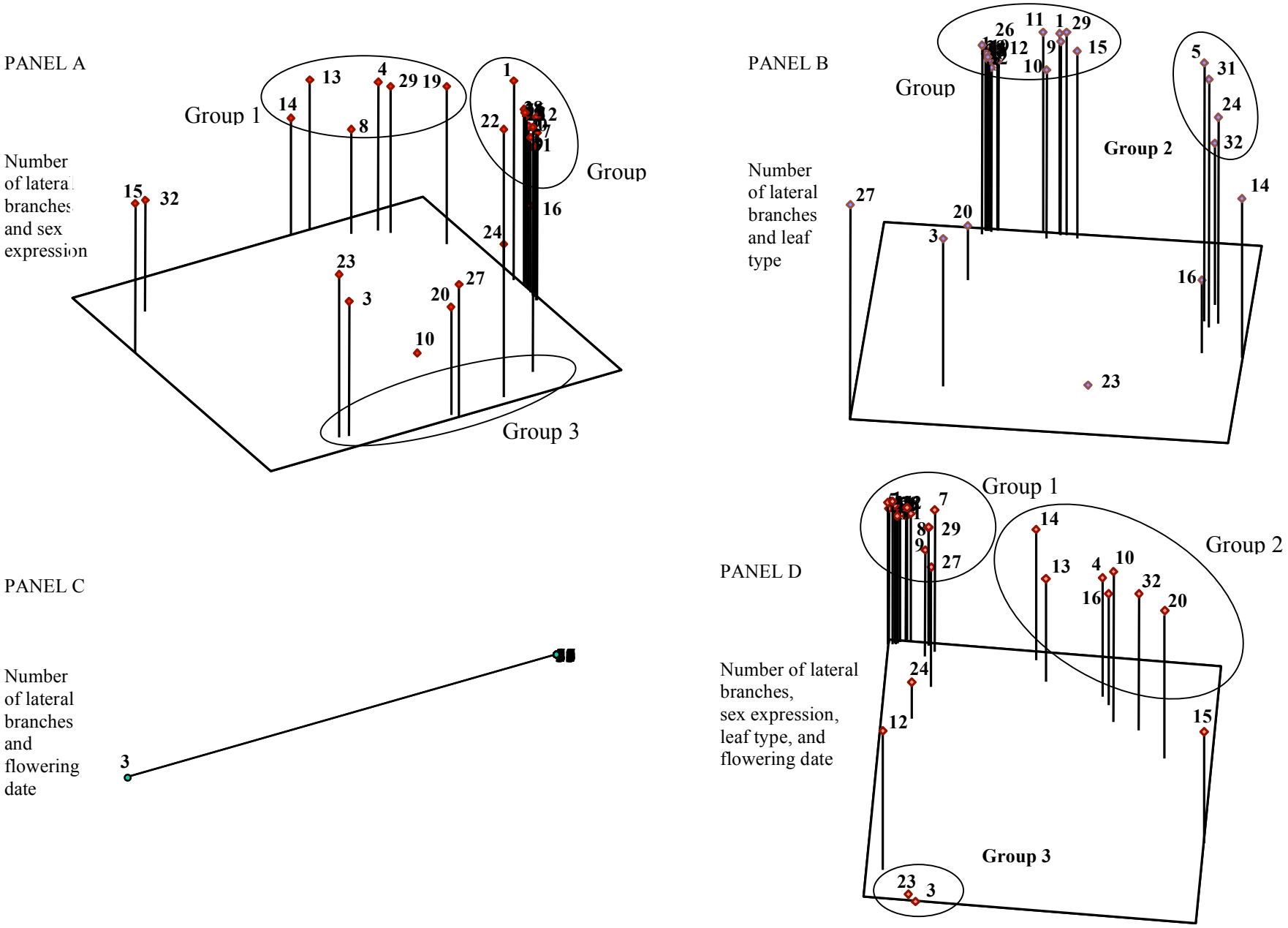


Table 1. Mean and standard deviation of traits of parental lines and progeny in cucumber.

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

Species and Races Composition of Powdery Mildew on Cucurbits in Bulgaria

Nikolay Velkov and Stoika Masheva
Institute of Horticulture and Canned Foods, Plovdiv 4003, 32 Brezovsko shosse Str., Bulgaria

Introduction. Powdery mildew is one of the main fungal diseases infecting cucurbits (*Cucurbitaceae*) in Bulgaria, both in the field and greenhouse. Several pathogens can cause powdery mildew in cucurbits: *Sphaerotheca fuliginea* (Schlecht.: Fr.)Poll, *Erysiphe cichoracearum* DC *ex* Merat and *Leveillula taurica* (Lev.)Arn. (16). The most widespread species causing powdery mildew on cucurbits are *S. fuliginea* and *E. cichoracearum* (5, 10, 13). *L. taurica* has been reported on greenhouse cucumber (6, 20).

Races of *S. fuliginea* are not known in cucumber (*Cucumis sativus*), *Cucurbita spp*. and watermelon (*Citrullus lanatus*). In 1926, race 1 of *S. fuliginea* on melon (*Cucumis melo*) was differentiated for the first time in the USA (15). Race 2 was reported in 1938 (8). The third race of *S. fuliginea* appeared in the USA in 1978 (18) and in Israel in 1988 (4). Races 1 and 2 of *S. fuliginea* were later identified in Spain and Greece (1, 21). In France, Pitrat et al. (14) reported the existence of 7 races of *S. fuliginea* and 2 races of *E. cichoracearum*.

In Bulgaria, Tafradzhiiski (17) reported that *S. fuliginea* was widespread on field-grown cucurbits. Elenkov et al. (7) described *Leveillula cucurbitacearum* (Golov.) as a causal agent of powdery mildew on cucumber in the glasshouse. Lozanov and Angelov (11) reported that race 1 and 2 of *S. fuliginea* infest melon in the region of Gorna Oryahovitsa. However, until this report, no systematic work has been undertaken to establish the causal agent(s) of powdery mildew that are active in both field and greenhouse conditions in Bulgaria.

The aim of this study was to establish species and races composition of causal agents of powdery mildew on greenhouse cucumber in Bulgaria, and to determine which species is predominant in field grown cucurbits in the south-central parts of Bulgaria.

Materials and Methods: In order to establish the species and race composition of powdery mildew on cucumber in the greenhouse in Bulgaria (2000-2001), germplasm was observed in 18 glasshouses in different parts of the country. During the autumn in the fields of the south-central parts of Bulgaria, 88 isolates of powdery mildew were collected from various cucurbits in 45 locations.

The identification of powdery mildew species was based on morphology of conidia (shape and size, presence or absence of fibrosin bodies, side germination of conidia) or by features of cleistothecia (size of peridial cell, number of asci and ascospore) (13).

Some melon differential lines were used in order to identify physiological races of *S. fuliginea* (Table 1). Plants of melon lines were grown in glasshouse isolators in 5 liter pots containing composted soil. Artificial inoculation was conducted by water suspension inoculation of conidia on cotyledons (60 spores concentration) as determined under 6.3x0.20 microscope magnification. Six plants from each melon line were evaluated four weeks after inoculation.

Results and Discussion: By microscopic examination of morphological features of conidiospores of powdery mildew collected from cucumber plants in 18 glasshouses in Bulgaria, *S. fuliginea* was determined to be the significant species causing infection. After inoculation and visual assessment of differential melon lines, it was established that for glasshouse cucumber in Bulgaria, the causal agent of powdery mildew is race 1 of *S. fuliginea*. Other authors reported similar greenhouse results in Greece (21), where race 1 of *S. fuliginae* was the most frequently encountered pathogen on cucumber. In France (3), however, 39% of the isolates from greenhouse cucumber were identified as *E. cichoracearum*. In Germany, Ulbrich et al. (19) also reported severe damage by *E. cichoracearum* on cucumber. In our investigation, infection by *E. cichoracearum* or *L. taurica* was not found in the 18 glasshouses sampled. Possibly this phenomenon is

associated with climatic conditions that are unfavorable for the development of these two pathogens.

During the autumn in the south-central parts of Bulgaria, 74% of the cucurbit hosts were infected by *S. fuliginea*, 3% were infected by *E. cichoracearum,* and 23% were determined to be a mixed infection by the above-mentioned pathogens. In contrast, in Hungary (13) *S. fuliginea* and *E. cichoracearum* were observed to infest cucurbits in equal frequencies. In the Czech and the Slovak Republics (9, 10) *E. cichoracearum* prevailed, and in France (2) *E. cichoracearum* was identified in 9% to 39% of the isolates collected.

In our study, powdery mildew isolates were collected from cucumber, squash and melon (Table 2). Of the samples collected, 79% to 89% were infected by *S. fuliginea*. On pumpkin, the infection by *S. fuliginea* was 54% lower, but the mixed infection by the two pathogens was observed to be 38%. The fact that only *S. fuliginea* was observed to infect *Lagenaria vulgaris* may be due to the small number of samples taken. A mix of both pathogens was detected in all samples of watermelon.

These results confirm the conclusion by Tafradzhiiski (17) that, in Bulgaria, *S. fuliginea* is widespread. In contrast, however, it was found that *E. cichoracearum* was encountered on 3% of samples and 23% in mixed infection. However, Tafradzhiiski observed *E. cichoracearum* on only one host. Although infection by *E. cichoracearum* was observed in field experiments, 3-4 weeks after initial observations, *S. fuliginea* and *E. cichoracearum* were both detected, with the former pathogen was in highest frequency.

In conclusion, it was found that the causal agent of powdery mildew on glasshouse grown cucumber in Bulgaria is race 1 of *S. fuliginea*. Furthermore, during the autumn in the fields of the south-central parts of Bulgaria, *S. fuliginea* was the predominant pathogen for inciting powdery mildew on cucurbits.

Acknowledgements. The authors thank Dr. M. Pitrat, INRA, Station de Génétique et d' Amélioration des Fruits et Légumes, Montfavet, France for supplying seeds of melon differential lines.

Literature Cited

1. Alvarez, J.M., M. L. Gomes-Cuillamon, N. A. Tores, I. Canovas and E. Floris. 2000. Virulence differences between two Spanish isolates of *Sphaerotheca fuliginea* race 2 on melon. In: N. Katzirs & H. S. Paris, eds., Proc. Cucurbitaceae 2000: 67-69. Acta Hort. 510. ISHS 2000.
2. Bardin, M., J. Carlier and P. C. Nicot. 1999. Genetic differentiation in the French population of *Erysiphe cichoracearum* a causal agent of powdery mildew of cucurbits. Plant Pathology 48: 531-540.
3. Bertrand, F., M. Pitrat, A. Glandard and J. M. Lemaire. 1992. Diversite et variabilite des champgnous responsables de l´oïdium des cucurbitacées. Phytoma. 438: 46-49.
4. Cohen, R., N. Katzir, S. Schreiber and R. Geenberg. 1996. Occurrence of *Sphaerotheca fuliginea* race 3 on cucurbits in Israel. Plant Disease v.80 (3): 344.
5. Crüger V.G.1977. Hürth Fischenich Wissenswertes über den gurkenmehltau. Gemüse. 3: 72-74.
6. El-Ammari S.S. and M. Wajid Khan.1983. *Leveillula taurica* Powdery Mildew on Greenhouse Cucumbers in Libia. Plant Disease / May 1983: 553-555.
7. Elenkov, E., I. Tafradzhiiski and G. Neshev.1975. A new pathogen of powdery mildew of cucumber in Bulgaria. Plant Protection. 5: 36-38.
8. Jagger I.C., T. W. Whitaker and D.R. Porter.1938 Inheritance in *Cucumis melo* of resistance to powdery mildew (*Erysiphe cichoracearum*). Phytopathology, 28: 671.
9. Křistkova, E. and A. Lebeda.2001. Aggressiveness of powdery mildew isolates on *Cucurbita maxima*. CGC Rpt. 24:73-76.
10. Lebeda, A. 1983. The genera and species spectrum of cucumber powdery mildew in Czechoslovakia. Phytopathology. 108: 71-79.
11. Lozanov, P. and D. Angelov. 1983. Studies on the racial composition of powdery mildew (*Sphaerotheca fuliginea* Poll.) in melons. Reports of second national symposium of plant immunity, Plovdiv-1983, v. III. p. 35-41.
12. Mohamed Y.F., M. Bardin, P. C. Nicot and M. Pitrat. 1995. Causal agent of powdery mildew of cucurbits in Sudan. Plant Disease. 79(6): 634-636.
13. Nagy, G. 1970. Die identifizierung des mehltaus der kürbisgewächse auf grund der konidienmerkmale. Acta Phytopathologica Academicae Scentiarum Hungaricae. (2-4): 231-248.
14. Pitrat, M., C. Dogimont and M. Bardin. 1998. Resistance to fungal diseases of foliage in melon. In: J. D. McCreight (ed.) Cucurbitaceae '98. pp. 167-173 ASHS. Alexandria. VA.
15. Prior E.D., and T.W. Whitaker. 1942. The reaction of cantaloupe strains to powdery mildew. Phytopathology. 32: 995-1004.
16. Sitterly, W.R. 1978. Powdery mildews of cucurbits. In: D. M. Spencer, ed., The Powdery mildews. pp. 359-371. Academic, New York.
17. Tafradzhiiski, I. 1964. Study on cucurbit powdery mildew. Ph.D. Thesis, (in Bulgarian).
18. Thomas, C. E. 1978. A new biological race of powdery mildew of cantaloupes. Plant Dis. Reptr. 62: 223.
19. Ulbrich A.and S.E. Smolka. 1994, Erste Funde von kleistothezien der beiden Echten Mehtan arten *Sphaerotheca fuliginea* und *Erysiphe cichoracearum* an Gewaechshausgurken (*Cucumis sativus*) in Deutschland. Nachrichtenblatt des Dentschen Pflanzenschutzdienstes. V.46 (7): 154-159.
20. Vakalounakis, D. J., E. Klironomou and A. Papadakis. 1994. Species spectrum, host range and distribution of powdery mildew on Cucurbitaceae in Crete. Plant Pathology. 43: 813-818.
21. Vakalunakis D.J. and E. Klironomou. 1995. Race and mating type identification of powdery mildew on cucurbits in Greece. Plant Pathology. 44: 1033-1038.

Table 1. Reaction of melon differential lines to races of *Sphaerotheca fuliginea*. (Mohamed Y. F. et al. 1995, Pitrat M. et al. 1998).

Melon lines	Race 0	Race 1	Race 2	Race 2	Race 3
			Europe	USA	
Hale's Best Jumbo	nt[1]	S	S	S	S
Iran H	S	S	S	S	nt
Védrantais	R	S	S	S	S
PMR 45	R	R	S	S	S
PMR 5	R	R	R	R	S
Edisto 47	R	R	R	S	R
Seminole	R	R	R	R	R

[1]S – susceptible; R – resistant; nt - not tested.

Table 2. Isolates of powdery mildew from different hosts of *Cucurbitaceae* collected in the fields during 2000-2001 in south-central part of Bulgaria.

Pathogen species[1]		Sf		Sf + Ec		Ec	
Host species	Total[2]	Number[3]	% [4]	Number	%	Number	%
Cucumber -*Cucumis sativus*	29	23	79	4	14	2	7
Melon - *Cucumis melo*	9	8	89	1	11	0	0
Squash - *Cucurbita maxima*	29	25	86	4	14	0	0
Pumpkin- *C. pepo var.giromontia*	13	7	54	5	38	1	8
Lagenaria vulgaris	2	2	100	0	0	0	0
Watermelon - *Citrullus lanatus*	6	0	0	6	100	0	0

[1]Sf - *Sphaerotheca fuliginea*; Ec - *Erysiphe cichoracearum*
[2]Total number of collected isolates on different hosts.
[3] Number of collected isolates on different hosts.
[4]Percentage ratio of casual agents of powdery mildew on different hosts.

Application of Induced Resistance in Cucumber Disease Control

Qing Ma[1], and Hongwen Cui[2]
[1]College of Plant Protection, and [2]College of Horticulture, Northwest Sci-tech University of Agriculture and Forestry, Yangling, Shaanxi 712100, China

Induced resistance in plants increases the ability of susceptible plants to withstand pathogens in a non-genetic way. Induced systemic resistance can be an effective control strategy since it often leads to control of multiple pathogens. The resistant reaction usually is not race-specific, and in some cases may result in simultaneous resistance to fungi, bacteria and viruses.

The phenomenon of induced resistance was first reported by Bernad (1909). Chester (1933) later reported the systemic resistance in plants. However, the term systemic acquired resistance (SAR) was officially proposed by Ross (1961), who reported the resistance in tobacco plants following local infection with tobacco mosaic virus.

Resistance-inducing factors include both biotic and abiotic ones. In cucumber, a primary inoculation with the fungus *Colletotrichum lagenarium* induced SAR against a dozen diseases caused by fungal and bacterial as well as viral pathogens. Resistance can persist for a few days to many weeks. Inoculation of the first leaf, followed 2-3 weeks later by a second booster inoculation, protected plants up to flowering in cucumber.

Kloepper and Schroth (1978) reported that certain root-colonizing bacteria could promote radish growth in greenhouse and field trials and named the bacteria plant growth-promoting rhizobacteria (PGPR). Recently, it was reported that certain PGPR strains protected plants through mechanisms associated with SAR against pathogens that cause foliar disease symptoms. Field experiments in cucumber demonstrated that plants grown from seed treated with PGPR sustained a significantly lower incidence of bacterial wilt disease. PGPR strains have been selected that, when applied as seed treatments, induce systemic resistance of cucumber against anthracnose. Some strains protect plants against damage from several pathogens[7,14].

The induction of resistance in parts remote from the site of primary inoculation is postulated to result from the translocation of systemic signal produced at the site of primary infection. This signal primes the plant against further pathogen attacks, probably triggering a complexity of defense responses.

Induced resistance may several kinds of mechanisms. It may involve a higher rate of papillae formation in previously uninfected leaves in cucumber[6], the production of pathogenesis-related proteins, an oxidative burst, etc.[5,15].

Induced resistance depends on the initial stimulus. There are different signal transduction pathways. These pathways rely on endogenous regulators such as salicylic acid (SA), ethylene and jasmonic acid to induce defense reactions. In defense against pathogens, SA is a key component of the signal transduction pathway that activates resistance against many plant pathogens, including fungi, bacteria, and viruses[8]. Components of the early signal transduction pathway include nitric oxide (NO), which activates G proteins and opens Ca^{2+} channels. Aconitase is a possible target of NO and may regulate the iron availability required for the production of the toxic hydroxyl radical that could be involved in HR cell death.

Biochemical studies showed that many new proteins accumulate after induction of SAR, including small acidic and basic proteins. In cucumber, galacturonic acid, gallic acid, oxalic acid, protocatechuic acid, phloroglucinol, salicylic acid, trimelletic acid etc., can act as elicitors to induce systemic resistance to *Colletotrichum lagenarium*. Salicylic acid as an elicitor can induce resistance to *Cladosporium cucumerinum*, where chitinase accumulates only in treated leaves.

Conventional induced resistance requires prior inoculation of plants with a necrosis-inducing pathogen, which makes practical use in agriculture unlikely. Several research groups are currently testing chemical compounds as foliar sprays to induce resistance.

For inorganic compounds, spray treatment of the lower leaves of cucumber plants with phosphate salts induced local and systemic resistance against

Colletotrichum lagenarium and *Sphaerotheca fuliginea*[10,11]. Calcium sequestration at the site of application by phosphates is thought to generate an endogenous SAR signal. In cucumber, powdered SiO_2 preparations induce SAR accompanied by enhanced activities of chitinase, β -1,3-glucanase, peroxidase, and polyphenoloxidase[12]. Si applied to the soil protects cucumber against *Pythium* spp., with the induction of biochemical changes related to defense[2]

For natural organic compounds, salicylic acid can induce systemic resistance to *Colletotrichum lagenarium* in cucumber. Plant extracts of *Reynoutria sachalinensis* induced peroxidases, β -1,3-glucanase and phenolic compounds to powdery mildew infection.[3]. Chitosan can induce resistance to *Pythium aphanidermatum* in cucumber[4]. Experiments showed that the oligomers of chitosan from fungus can protect cucumber leaves against *Sphaerotheca fuliginea*. Inoculation with bacterium *Pseudomonas syringae* pv. *syringae* (Pss61) resulted in systemic protection in cucumber, inducing PR-genes and SAR against several pathogens[13].

In synthetic compounds, 2,6-dichloroiso-nicotinic acid results in systemic protection in cucumber against various foliar diseases besides *Sphaerotheca fuliginea*, and against damping-off and seedling rot of cucumber caused by *Rhizoctonia solani*.[9]. Benzo-thiadiazole (BTH), a chemical activator of plant disease resistance, has no known direct antifungal effect and is thought to play a role similar to that of salicylic acid in the signal transduction pathway leading to systemic acquired resistance. BTH, when applied to cucumber, induced systemic resistance to *Pythium* damping-off, *Colletotrichum lagenarium* and induced accumulation of chitinase to *Cladosporium cucumerinum*[1]. BABA (DL-3-amino-butyric acid) induced resistance in cucumber against *Sphaerotheca fuliginea.* DF-391, a novel non-fungicidal synthetic pyridine derivative, is active against cucumber anthracnose .

The nature of the systemic induced resistance response of cucumber against pathogens will soon be determined by using cytological, biochemical and molecular techniques. As more and more SAR genes are transferred into plant genomes, many trangenic resistant plants will be developed. In the near future, more such genes will be cloned and applied to agriculture.

Literature Cited

1. Benhamou, N. and R.R. Belanger, 1998. Induction of systemic resistance to *Pythium* damping-off in cucumber plants by benzothiadiazole: Ultra-structure and cytochemistry of the host response. Plant Journal 14: 13-21.
2. Cherif M., A.Asselin, and R.R. Belanger. 1993.Defense responses induced by soluble silicon in cucumber roots infected by *Pythium spp*. Phytopathology 82:236-242.
3. Daayf, F., A. Schmidtt, and R.R. Belanger. 1995. The effects of plant extracts of *Reynoutria sachalinensis* on powdery mildew development and leaf physiology of long English cucumber. Plant Disease 79, 577-580.
4. El Ghaouth, A., L. Arul, J. Grenier, N. Benhamou, A. Asselin, and R. Belanger. 1994. Effect of chitosan on cucumber plants: suppression of *Pythium aphanidermatum* and induction of defense reactions. Phytopathology 84, 313-320.
5. Kastner, B., R. Tenhaken, and H. Kauss. 1998. Chitinase in cucumber hypocotyls is induced by germinating fungal spores and by fungal elicitor in synergism with inducers of acquired resistance. Plant Journal 13: 447-454.
6. Kovats, K., A. Bindeer, and H.R. Hohhl. 1991. Cytology of induced systemic resistance of cucumber to *Colletorichum lagenarium*. Planta 183: 484-90.
7. Liu, L., J.W. Kloepper, S. Tuzun. 1995. Induction of resistance in cucumber by plant growth-promoting rhizobacteria: duration of protection and effect of host resistance on protection and root colonization. Phytopathology 85: 1064-1068.
8. Metraux, J.P., H. Siger, J. Ryals, et al. 1990. Increase in salicylic acid at the onset of systemic acquired resistance in cucumber. Science 250, 1004-1006.
9. Metraux, J.P., P. Ahl-Goy, T. Staub, et al. 1991. Induced systemic resistance in cucumber in response to 2,6-dichloro-isonicotinic acid and pathogens. In: Advances in Molecular genetics of Plant-Microbe Interactions, ed. H Hennecke, DPS Verma, pp. 432-439. Amsterdam: Kluwer.

10. Reuveni, M., V. Agapov, and R. Reuveni. 1996. Controlling powdery mildew caused *Sphaerotheca fuliginea* in cucumber by foliar sprays of phosphate and potassium salts. Crop Protection 15: 49-53.
11. Reuveni, M., V. Agapov, and R. Reuveni. 1995. Suppression of cucumber powdery mildew (*Sphaerotheca fuliginea*) by foliar spray of phosphate and potassium salts. Plant Pathology 44: 31-39.
12. Schneider, M. and WR. Ullrich 1994.Differential induction of resistance and enhanced enzyme activities in cucumber and tobacco caused by treatment with various abiotic and biotic inducers. Physiol. Mol. Plant Pathol. 45:291-304.
13. Smith, J.A., R. Hammerschmidt, and D.W. Fulbright. 1991. Rapid induction of systemic resistance in cucumber by *Pseudomonas syringae* pv. *syringae*. Physiol. Mol. Plant Pathol. 38: 223-235.
14. Wei, G., J.W. Kloepper, and S. Tuzun. 1995. Induced systemic resistance to cucumber diseases and increased plant growth by plant growth-promoting rhizobacteria under field conditions. Phytopathology 86: 221-224.
15. van Loon, L. C. (1997). Induced resistance in plants and the role of pathogenesis-related proteins. European Journal Plant Pathol 103, 753-6

Agrobacterium-Mediated Transformation in Cucumber (*Cucumis sativus* L.)

A. Vasudevan[1], A. Ganapathi[1], N. Selvaraj[2], M. Muruganantham[1] and G. Vengadesan[1]
[1]Department of Biotechnology, Bharathidasan University, Thiruchirappalli - 620 024, Tamil Nadu, India, and [2]Department of Botany, Periyar E.V.R College, Thiruchirappalli - 620 023,Tamil Nadu, India. Email: ganap@bdu.ernet.in

Introduction. Cucumber (*Cucumis sativus* L.) is an important horticultural crop. Its fruits are used for slicing and pickling and juice extraction worldwide. In India, both the fruits and seeds have long been used in the manufacture of traditional medicines that act as skin conditioners, diuretics and body coolants. Thus, cucumber is a potential candidate for an edible vaccine (6). In India, studies on cucumber tissue culture in general and transformation in particular are very limited (1). In the present study, a reliable transformation and regeneration protocol is reported for cv. Green Long, which is widely cultivated in India.

Materials and Methods. The monoecious cucumber cultivar Green Long (obtained from Ramachandra Bhageluram Maurya Co., India) was used for this study. The seeds were surface-sterilized and kept on sterile moist cotton for 24h. After 24h, the seed coats were separated and removed without disturbing the cotyledons. The cotyledons were carefully dissected eliminating the embryonic axis. The distal end of the cotyledon explants was cut and these explants were vertically inoculated in such a way that the distal end was touching the experimental medium used. MS medium containing 3% sucrose (Himedia Laboratories Co., Mumbai, India), 0.8% agar (Himedia Laboratories Co., Mumbai, India) with BA (1mg/l) was used for shoot regeneration. The pH of the medium was adjusted to 5.8 before autoclaving at 121^{o}C for 20min. The cultures were kept at 25±2^{o}C at a 16h photoperiod with the light intensity of 30 µmol m^{-2} s^{-1} under diffuse cool white fluorescent lamps.

The *Agrobacterium timefaciens* strain EHA 105 was used for this study (2). It is a super virulent leucinopine type, with a binary plasmid (pGA492GI, provided by Rafael Perl-Treves, Bar Ilan University, Israel) with *npt* II (kan resistant), and bar (phosphonothricin resistant) genes driven by the CaMV 35S promoter.

The proximal end of the cotyledon explants was pricked to make wounds using a sterile needle to induce *Agro* infection. The explants (80-100per treatment) were dipped in bacterial suspension containing acetosyringone (20 µl/l) for 10 min, followed by washing in sterile distilled water two to three times, and finally blotted with sterile Whatman No. 1 filter paper. The explants were co-cultivated in MS basal medium devoid of any PGR, pH 5.4, and kept at 27^{o}C in the dark for 48h. The explants were then transferred to shoot regeneration medium containing MS salts, 1 mg/l BA, 3% sucrose, 0.8% agar, 25 mg/l kanamycin and 300 mg/l cefotaxime, and grown for 15 days. Thereafter, the regenerated shoots were separated from explants and cultured *in vitro* on PGR free MS medium containing 100 mg/l kanamycin and 300 mg/l cefotaxime to select transgenic cucumber shoots.

GUS assay: The regenerated plants were assayed for the expression of gusAint gene following the histochemical procedure described by Jefferson et al. (3).

PCR analysis: PCR analysis of transformed cucumber shoots was carried out as per the method of Nishibayashi et al. (5) using *npt* II primer with 800 bp.

Results and Discussion: The factors responsible for enhancing transformation frequency in cucumber have been studied earlier (7). With the help of this study, an effort was focused on evaluating the *Agrobacterium*-mediated gene transfer in cucumber cv. Green Long, the most popular cultivar in India.

Multiple shoots were induced from the proximal end of cotyledon explants infected by *Agrobacterium* on shoot induction medium supplemented with 25mg/l kanamycin and 300mg/l cefotaxime. After 15 days of initial culture, explants with multiple shoots were

transferred onto MS medium containing 100 mg/l kanamycin and 300 mg/l cefotaxime to select transgenic cucumber shoots. The adventitious shoots from explants infected by *Agrobacterium* maintained their green colour and grew normally. The GUS assay was performed to confirm the transformation event. The GUS expression was lower in transformed shoots co-cultivated without acetosyringone than with co-cultivation with acetosyringon, whereas in the acetosyringone treatment, the transformed shoots showed strong GUS activity (Fig 1). Our results are agreement with Nishibayashi et al. (4), who reported that acetosyringone was an essential for effective cucumber transformation. The kanamycin resistant shoots were selected randomly and examined by PCR for the presence of the integrated *npt* II gene. The DNA of transformed shoots integrated with *npt* II primer and produced a band of the expected size of 800bp. The DNA of non-transformed (negative control) shoots did not exhibit the band of 800 bp. The amplified DNA from the binary vector pGA492GI (positive control) produced a band of 800 bp (Fig 2). In the present investigation, about 21% of infected explants produced shoots, out of which only 12% of the shoots were fully transformed. In conclusion, the present protocol could be applied to improve Green Long by introducing the gene of interest via *Agrobacterium*.

Literature Cited

1. Ganapathi, A. and R. Perl-Treves. 2000. *Agrobacterium*-mediated transformation in *Cucumis sativus* L. via direct organogenesis. Acta Horticulturae. 510: 405-407.

2. Hood, E.E., S.B. Gelvin, L.S. Melchers, and A. Hoekema. 1993. New *Agrobacterium* vectors for plant transformation. Transgenic Res. 2: 208-218.

3. Jefferson, R. A. and T.A. Kavanagh. 1987. GUS fusions: β- Glucuronidase as a sensitive and versatile gene fusion marker in higher plants. EMBO J. 6: 3901-3907.

4. Nishibayashi, S., H. Kaneko, and T. Hayakawa. 1996. Transformation of cucumber (*Cucumis sativus* L.) plants using *Agrobacterium tumefaciens* and regeneration from hypocotyl explants. Plant Cell Rep. 15: 809-814.

5. Sambrook, J., E.F. Fritsch, and T. Maniatis. 1989. Molecular cloning, a laboratory manual. 2nd edition. Cold Spring Harbor Laboratory Press. 1402-1404.

6. Sharma A K., A. Mohanty J. Singh, and A.K. Tyagi. 1999. Transgenic plants for the production of edible vaccines and antibodies for immunotherapy. Curr. Sci. 77: 524-529.

7. Vasudevan, A., A. Ganapathi., N. Selvaraj, and G. Vengadesan. 2001. Factors influencing GUS expression in cucumber (*Cucumis sativus* L.). Ind. J. Biotechnol. (In press).

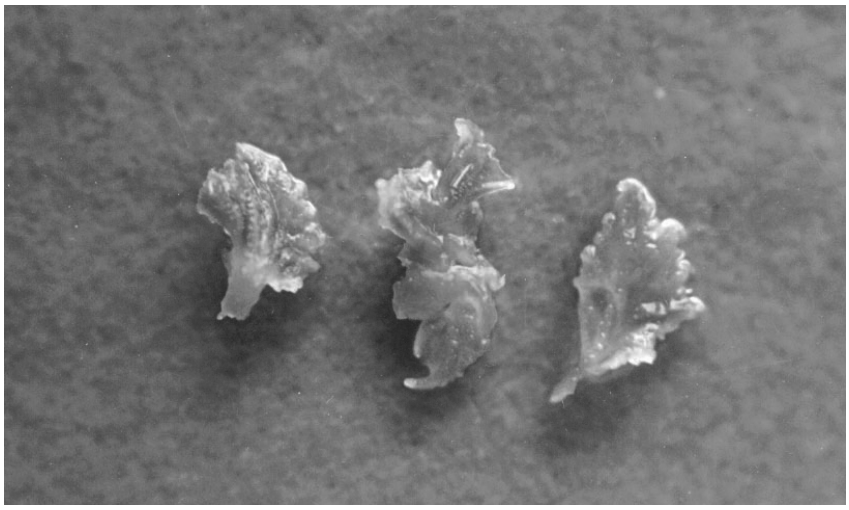


Figure 1. Transgenic shoots (2-3 weeks) showing GUS positive.

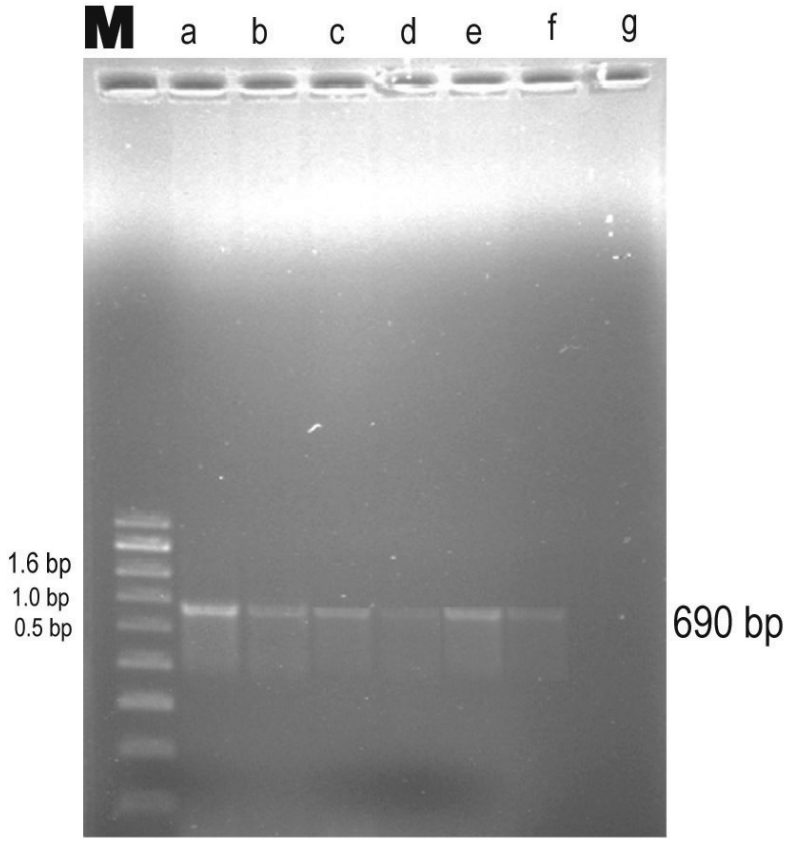


Figure 2. PCR amplification of the *npt* II gene from genomic DNA isolated from transgenic plants of EHA 105/pGA492GI (lane a, b, c, d, e,) and positive vector control (lane f). Lane g is the negative control (untransformed plant using two specific primer sequences of the *npt* II coding region).

Inheritance of Resistance to Fusarium Wilt in Local Germplasm of *Cucumis melo* subsp. *melo* conv. *adzhur*

Longo, O., A. Ambrico, D. Schiavone and F. Ciccarese
Department of Biology and Plant Pathology - University of Bari, Italy, Via G. Amendola 165/A, 70126 Bari, Italy, E-mail: fciccare@agr.uniba.it

Introduction. In Southern Italy and especially in Apulia, 'Carosello' [*Cucumis melo* L. subsp. *melo* conv. *adzhur* (Pang.) Grebensc] is extensively grown. This cucurbit is a relic of melon cultivars, and immature fruits are eaten raw or in salads as an alternative to cucumber (3). In numerous 'Carosello' plantings, especially in the greenhouse, a serious disease caused by *Fusarium oxysporum* f. sp. *melonis* was observed. Further studies on the physiological specialization of isolates derived from diseased plants showed that pathogen populations do not exhibit pathogenic variability and belong to race 0 of *F. oxysporum* f. sp. *melonis* (2).

'Carosello' has been cultivated for a long time in Apulia, and many local ecotypes have been selected by individual growers. Previous investigations on the reaction of local 'Carosello' germplasm collected directly from growers to race 0 of *F. oxysporum* f. sp. *melonis* supplied interesting and promising results. In particular, one 'Carosello' ecotype (BA1-7) showed resistance to Fusarium wilt (1). In this paper the inheritance of Fusarium wilt resistance in the BA1-7 ecotype of 'Carosello' is reported.

Materials and Methods. A single resistant plant of the original 'Carosello' ecotype (BA1-7) was self-fertilized and progeny were submitted to a new artificial inoculation cycle. In order to characterize the resistance in the BA1-7 ecotype, a plan of crosses and self-fertilizations were set-up. The cv. Bianco leccese of 'Carosello' was used as the susceptible parent. The progenies of F_1, F_2 and backcrosses to the resistant parent (BC-R) and with susceptible parent (BC-S) were submitted to artificial inoculation with the F_7 isolate belonging to race 0 of *F. oxysporum* f. sp. *melonis*. The artificial inoculations were made by dipping roots of seedlings in the pathogen fungal suspension (4 x 10^6 Colony Forming Units) for 2-3 minutes.

Disease severity was assessed according to an empirical scale from 0 to 4 in which 0 = healthy plants and 4 = dead plants or plants with severe symptoms. About 100 plants were screened for each parental line and about 180 plants of F_1, F_2, BC-R and BC-S generations were screened. Gene segregation was evaluated by the chi-square test (χ^2).

Results and Discussion. The high resistance to race 0 of *F. oxysporum* f. sp. *melonis* observed in the original BA1-7 ecotype of 'Carosello' was confirmed in the selfed progeny in this test (Figure 1). The segregation ratios strongly fit a single, dominant gene model conferring resistance in BA1-7 (Table 1). In preliminary observations (4), the BA1-7 ecotype of 'Carosello' showed valuable agronomic characteristics and therefore could be used where Fusarium wilt is a major problem. Further tests with other races of *F. oxysporum* f. sp. *melonis* and allelism tests with other resistance sources are needed to determine if this resistance gene is the same as previously reported (5) or a new gene.

Literature Cited

1. Ciccarese F., Ambrico A., Schiavone D. e Longo O., 1999. Ricerca di fonti di resistenza a *Fusarium oxysporum* f. sp. *melonis* in germoplasma locale di *Cucumis melo*. *Italus Hortus, 6*, (*4*), 37.
2. Ciccarese F., Longo O. e Ambrico A.; 2000. Attacchi di tracheofusariosi su Carosello in Puglia e indagini sulla composizione razziale di *Fusarium oxysporum* f. sp. *melonis*. *Inf. fitopat*. *7-8*, 59-61.
3. Hammer K., Hanelt P., Perrino, P., 1986. Carosello and the taxonomy of *Cucumis melo* L. especially for its vegetable races. *Kulturpflanze, 34*, 249-259.
4. Longo O., 2001. Individuazione e caratterizzazione di fonti di resistenza verso

Fusarium oxysporum f. sp. *melonis* in germoplasma locale di *Cucumis melo*. Thesis of PhD in "Plant Pathology", Department of Biology and Plant Pathology - University of Bari, Italy, pp. 73.

5. Risser G., Banihashemi Z., Davis D. W., 1976. A proposed nomenclature of *Fusarium oxysporum* f. sp. *melonis* races and resistance genes in *Cucumis melo*. *Phytopathology*, *66*, 1105-1106.

Table 1 - Observed segregation for Fusarium wilt resistance of the BA1-7 ecotype of 'Carosello' (*Cucumis melo* L. subsp. *melo* conv. *adzhur*) and Chi-square (χ^2) goodness of fit test.

Pedigree	Number of plants R:S[a]		Expected[b] ratio	χ^2	P
	R[a]	S			
BA1-7	98	0	98:0	-	-
Bianco leccese	0	96	0:96	-	-
F_1	185	0	185:0	-	-
F_2	125	44	127:42	0.031	> 0.90
BC-R	169	0	169:0	-	-
BC-S	98	96	97:97	0.021	> 0.90

[a]R =resistant and S = susceptible
[b]single, dominant gene model for inheritance of resistance

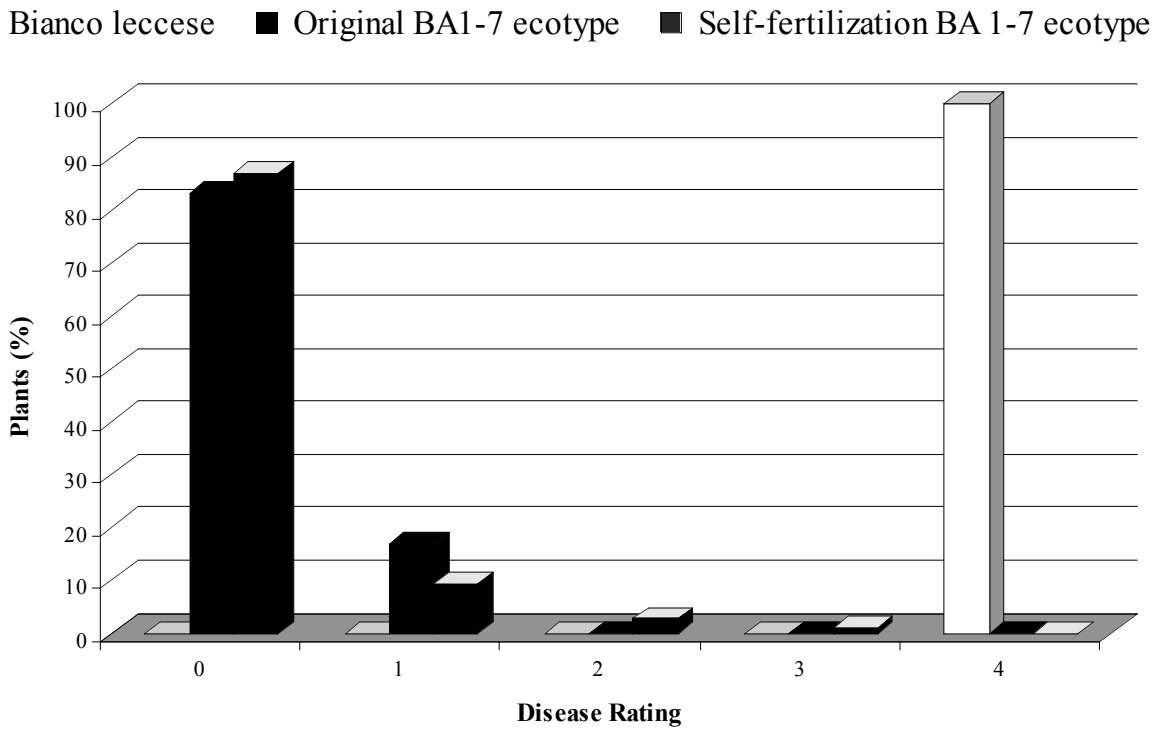


Figure 1 - Reactions to *Fusarium oxysporum* f. sp. *melonis* race 0 of cv Bianco leccese, and the original and selfed BA1-7 ecotype of 'Carosello'. Disease rating scale: 0 = healthy, no symptoms to 4 = plant death, very severe symptoms.

Powdery Mildew Race 1 in Imperial Valley, California

James D. McCreight
United States Department of Agriculture, Agricultural Research Service, U.S. Agricultural Research Station, 1636 E. Alisal St., Salinas, California 93905 U.S.A.

Melon production in Imperial Valley, California was hit by powdery mildew in 1925 (3). 'PMR 50', which was developed from a cross of California Accession #525 x 'Hale's Best' was released in 1932. 'PMR 45' was released in 1936 after four more generations of selection for horticultural type (4). Resistance to powdery mildew in these cultivars was practically complete; inconspicuous spots of mildew were rarely found on them until mid-season 1938 when a few fields of 'PMR 45' developed powdery mildew, which spread until nearly all fields of it were infected (5). Resistance to this new race (race 2) began with a cross of PI 79376 x 'Hale's Best' and was combined with race 1 resistance from 'PMR 45' to yield three race 2-resistant selections: 'PMR 5', 'PMR 6' and 'PMR 7' in 1942 and 1943, respectively (8). Race 2 has been generally considered to be present in Imperial Valley since that time.

Two species of fungi are known to incite powdery mildew on melon (7). The early reports of powdery mildew in Imperial Valley referred to the pathogen as *Erisyphe cichoracearum* DC *ex* Merat. Later, *Sphaerotheca fuliginea* (Schlecht. ex Fr.) Poll.), was found to be widespread (see Pitrat et al., 1998 for a listing of reports).

Nine races of powdery mildew incited by *S. fuliginea* have been documented (2, 7) in melon. The objective of this research was to determine at one site the present race of powdery mildew in Imperial Valley, an important late spring-early summer melon production area of the U.S.A.

Materials and Methods

Ten powdery mildew race differentials (7) were direct-seeded on 20 March 2002 and watered via subsurface drip irrigation on 21 March at the University of California Desert Research and Education Center (DREC). Seeds were planted in hills spaced ca. 75 cm apart within rows (beds) on 2 m centers. There were two hills per plot, and entries were randomized in two replications. 'Top Mark', susceptible to all races except race 0, was planted in two adjacent border beds along one side and at each end of the test plot.

Powdery mildew infection was evaluated on 18 June (rep 1) and 19 June (rep 2). Infection of true leaves as evidenced by mycelial growth and sporulation was rated with the unaided eye on a 1 to 9 scale. Infection of cotyledons and true leaves as evidenced by mycelial growth and sporulation was rated on a 1 to 9 scale as follows: 1, no evidence of disease; 2, trace of hyphae; 3, hyphae restricted; 4, few colonies present, sporulation; 5, scattered colonies, sporulation; 6, numerous colonies, sporulation; 7, ≈50% of adaxial surface covered with hyphae and spores, few colonies on abaxial surface, abundant sporulation; 8, >50% of adaxial surface covered with hyphae and spores, scattered colonies on abaxial surface, abundant sporulation; and 9, >75% of adaxial surface covered with hyphae and spores, numerous or coalesced colonies on abaxial surface. Means were assigned to one of two categories: Resistant (R) ≤ 3.0; and Susceptible (S) > 3.0.

Results and Discussion

Powdery mildew species identification of a sample from Iran H was confirmed to be *Podosphaera xanthii* from examination of conidia for the presence of fibrosin bodies and production of forked germ tubes (1, 6).

Mildew was more severe on Iran H than on 'Vedrantáis' and 'Top Mark' (Table 1); no mildew was evident on the other differentials. The results clearly indicated presence of race 1 at this site in Imperial Valley: Iran H, 'Vedrantáis' and 'Top Mark' were susceptible, and 'PMR 45' and the other six powdery mildew race differentials were resistant (7).

DREC is not in an isolated area of Imperial Valley. Numerous commercial melon fields occurred within a kilometer of the test; one field was within 50 m. Although powdery mildew race 1 was present in the Imperial Valley in this study, race 2 or other powdery mildew races may also occur in this production area. Additional sampling sites and dates will be needed to make this determination.

Literature Cited

1. Ballantyne, B. 1975. Powdery mildew on cucurbitaceae, identity, distribution, host range and sources of resistance. Proc. Linnean Soc. of New South Wales 99:100-120.

2. Hosoya, K., M. Kuzuya, T. Murakami, K. Kato, K. Narisawa, and H. Ezura. 2000. Impact of resistant melon cultivars on *Sphaerotheca fuliginea*. Plant Breeding 119:286-288.

3. Jagger, I. 1926. Powdery mildew of muskmelon in the Imperial Valley of California in l925. Phytopathology 16:1009-1010.

4. Jagger, I. C. and G. W. Scott. 1937. Development of powdery mildew resistant cantaloup No. 45. USDA Circ. 441:6.

5. Jagger, I. C., T. W. Whitaker, and D. R. Porter. 1938. A new biologic form of powdery mildew on muskmelons in the Imperial Valley of California. Plant Disease Reporter 22:275-276.

6. Kable, F. P. and J. B. Ballantyne. 1963. Observation on the cucurbit powdery mildew in the Ithaca district. Plant Disease Reporter 47:482.

7. Pitrat, M., C. Dogimont, and M. Bardin. 1998. Resistance to fungal diseases of foliage in melon, p. 167-173. In: J. D. McCreight. (ed.). Cucurbitaceae '98: Evaluation and enhancement of cucurbit germplasm., ASHS Press, Alexandria, Va.

8. Pryor, D. E., T. W. Whitaker, and G. N. Davis. 1946. The development of powdery mildew resistant cantaloupes. Proceedings of the American Society for Horticultural Science 47:347-356.

Table 1. Reactions of 10 melon powdery mildew race differentials to natural infection in a field test at Holtville, California.

Differentials	Disease Rating	Disease Reaction
Iran H	9.0	S
Top Mark	5.0	S
Vedrantáis	4.5	S
PMR 45	1.0	R
PMR 5	1.0	R
WMR 29	1.0	R[z]
PI 414723	1.0	R
MR-1	1.0	R
PI 124111	1.0	R
PI 124112	1.0	R

[z]one replication

Adenine Sulphate and L-Glutamine Enhance Multiple Shoot Induction from Cotyledon Explants of Melon (*Cucumis melo* L. cv. Swarna)

M. Muruganantham[1], A. Ganapathi[1], N. Selvaraj[2], R. Prem Anand[1], A.Vasudevan[1], and G.Vengadesan[1]

[1]Department of Biotechnology, School of Life Sciences, Bharathidasan University, Tiruchirappalli 620 024, Tamil Nadu, and [2]Department of Botany, Periyar E.V.R college, Thiruchirappalli - 620 023. Tamil Nadu, India. Email: ganabiotech@rediffmail.com

Introduction. *Cucumis melo* L.is a popular commercial as well as household vegetable in India. Among various uses, it is mainly known for fresh salad and pickling. However, this economically important crop is susceptible to a number of devastating insects and diseases (7) including papaya ringspot virus and cucumber green mottle mosaic virus, which seriously limit productivity. Hence, this crop deserves improvement in terms of disease resistance, abiotic stress and higher yield. Melon is known to be recalcitrant to regeneration (1,2). The development of tissue culture protocols is one of the solutions to address these problems. The present study was conducted to produce multiple shoots in a local cultivar of melon by using important additives, adenine sulphate (AdS) and glutamine, in the culture medium.

Materials and Methods. The Indian melon cultivar Swarna (Indo-American Hybrid Seeds (India) Pvt. Ltd., Bangalore, India) was used in the present study. Seeds were surface sterilized by the usual sterilization procedure (3). The seed coats were aseptically removed and the two cotyledons were separated from the embryonic axis. Mature cotyledons were used as explants. The cotyledonary pieces with intact proximal ends (0.5 cm) were inoculated in Murashige and Skoog (MS) medium (4) containing 0.8% bacto agar, 3% sucrose and combinations of the growth regulators BA, Kinetin (Kn), and the additives AdS and L-glutamine. Every treatment was tested at five different concentrations (mg/l): BA – 0.5, 1.0, 1.5, 2.0, 2.5. Kn - 0.5, 1.0, 1.5, 2.0, 2.5. AdS – 5, 10, 15, 20, 25. L-Glutamine - 5, 10, 15, 20, 25.

To facilitate shoot elongation, the regenerated shoots were grown in MS medium fortified with gibberellic acid (GA_3) (0.5mg/l). The cultures were maintained at 25 ± 2º C under white fluorescent light (Philips India Pvt. Ltd.) with a photon flux of (30µ mol m^{-2} s^{-2}) at a 16h photoperiod.

Results and Discussion. *Effect of cytokinins*. Multiple adventitious shoot buds were induced from the proximal end of the cotyledons in MS medium containing BA (2.0mg/l) or Kn (1.5mg/l) after 10-12 days of inoculation. A maximum number of shoots (12.2/explants) was obtained after 3-4 weeks of culture supplemented with only BA (2.0 mg/l) (Table 1). Lower numbers of shoots were produced in medium containing Kn (1.5mg/l). Similar results were observed by others in melon (3,5) and in cucumber (6). The shoots were subcultured in medium with the same composition.

Effect of BA with additives. Multiple adventitious shoot buds (Fig. 1) were initiated from the proximal end of the explants after 2-3 weeks of inoculation in MS medium containing BA in combination with AdS and glutamine. A maximum number of 30.6 shoots/explant was produced with BA (2.0mg/l), AdS (15mg/l) and glutamine (15mg/l) in two subcultures (Table 1). The present study revealed that a combination of additives (AdS and glutamine) with optimal concentration of BA (2.0mg/l) promoted the highest shoot bud induction as well as adventitious shoot production (Fig 2). The regenerated shoots were elongated in MS medium with (0.5mg/l) GA_3 (Fig 3). This protocol is rapid, less time consuming and highly reproducible, and could be applied in genetic manipulation of this cultivar by transformation methodologies.

Multiple shoot development from cotyledon explant of *Cucumis melo* L.

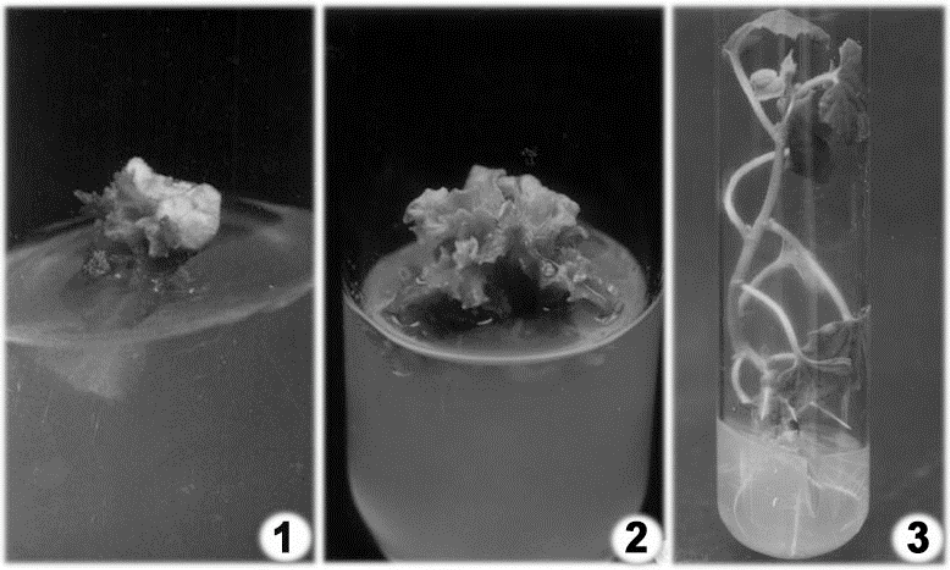


Fig 1: Shoot bud initiation
Fig 2: Shoot proliferation
Fig 3: Shoot elongation

Table 1. Effect of plant growth regulators and additives on multiple shoot induction from mature cotyledon explants of melon (*C. melo* cv. Swarna) cultured on MS medium.

Treatment (mg/l)		Number of shoots/explants	Shoot length (cm)
BA	2.0	12.2 b	6.2 b
Kn	1.5	2.0 h	n.d.
BA + AdS	2.0 + 15	9.2 c	5.0 c
BA + L-Glutamine	2.0 + 15	8.0 d	4.3 d
BA + AdS + L-Glutamine	2.0 + 15 + 15	30.6 a	7.9 a
Kn + AdS	1.5 + 15	6.3 e	4.0 de
Kn + L-Glutamine	1.5 + 15	5.0 f	2.3 f
Kn + AdS + L-Glutamine	1.5 + 15 + 15	4.0 g	2.0 g

Means with the same letter in a column are not significantly different according to Duncan's Multiple Range Test at the 5% level.
n.d.- not determined.

Literature cited

1. Gaba, V. Feldmerser, E. Galon A. et al., 1995. Genetic transformation of a recalcitrant melon (Cucumis melo L.) variety. In: Lester, G. Dunlap, J, ed. Proc. Of Cucurbitaceae 94. City: Edinburg, TX, Gateway printing; 188-190.

2. Gaba, V. Elman, E. Perl Treves, R. et al. A theoretical investigation of the genetic variability in the ability of Agrobacterium to transform *Cucumis melo* L. In: Gomez-Guillamon, M. L. Soria, C.Cuartero, J. *et al*., eds. Cucurbits towards 2000. Proc. 6th Eucarpia meeting on Cucurbit Genetics and Breeding, Malaga, Spain, 1996: 172-178. ISBN 605-5163 6.

3. Gaba, V. Schlarman, E. Elman, O. Sagee, A. A. Watad, and C. Gray, D.J. 1999. *In vitro* studies on the Anatomy and Morphology of bud regeneration in melon cotyledon 35: 1-7.

4. Murashige, T. Skoog, F. 1962. A revised medium for rapid grown and bioassays with tobacco tissue cultures. Physiol. Plant 15: 473-497.

5. Singh, M. N. Misra, A. K. and Bhatnagar, S.P. 1996. In vitro production of plants from cotyledon explants of *Cucumis melo* L. and their successful transfer to field. Phytomorphology, 46: 395-402.

6. Vasudevan, A. Selvaraj, N. Sureshkumar, P. and Ganapathi, A. 2001. Multiple shoot induction from shoot tip explants of Cucumber (*Cucumis sativus* L.) CGC 24: 8-12.

7. Whitaker, T.W., and Davis, G.N. 1962. Cucurbits. Leonard Hill, London

Characteristics of Planting and Cultivar Selection in Oklahoma Watermelon Production

W. Lu, M. Biernacki, J. Duthie, W. Roberts, M. Taylor, and J.V. Edelson
Wes Watkins Agricultural Research and Extension Center, OSU, Lane, OK, USA
Email: wenhua@lane-ag.org

Production of watermelon [*Citrullus lanatus* (Thunburg) Matsumura and Nakai] in Oklahoma encompasses a range of climatic conditions (Oklahoma Agricultural Statistics Service, 2001) and soil types. A statewide survey of watermelon production was carried out in 1998 and 1999 to provide baseline data for characteristics of fields, planting, cultivar, harvest, and management practices. We have previously reported characteristics of fields and variation in these characteristics among geographic regions from this survey (Lu et al., 2002). This report provides results of characteristics of planting and cultivar selection and variation in these characteristics among geographic districts.

Methods. There are four administrative districts in the Cooperative Extension Service (Oklahoma Cooperative Extension Service, 2002). We surveyed 40 fields representing 340 ha in 1998 and 62 fields representing 920 ha in 1999 in three out of the four districts where most watermelon production occurred (Lu et al., 2002). We pooled data from both years in analyses and provided the sample size (N) whenever there were missing data.

Results. Approximately 37% of fields by number and 48% by area were planted on raised beds. A bed averaged 0.14±0.05 m high with a range of 0.07-0.61 m and 0.90±0.18 m wide with a range of 0.37-1.83 m (N=35). Raised beds were found on 80% of large fields by number and 75% by area, on 40% of medium fields by number and 42% by area, and on 32% of small fields by number and 26% by area. Statewide, the greatest proportion of fields with raised beds was observed in the southwest district: 22% by number and 38% by area.

Growers used double row planting in 21% of fields by either number or area (N=100). Distance between double rows averaged 0.91 m. Distance between single rows was 3.89±0.15 m (ranging 1.2-7.5 m). Distance between plants within a row averaged 1.07±0.05 m (ranging 0.15-3.0 m). For fields planted with double rows of watermelon, 52% were on raised beds by number and area. Fields with double rows on raised beds increased to 65% by area in the southwest district, whereas by area only 1% in the northeast district and 34% in the southeast district.

About 33% of fields by number representing 45% of total production area were direct-seeded. About 50% of transplanted fields by area were in large ($\geq$40 ha), 40% in medium (10 to 39 ha), and 10% in small ($\leq$10 ha) fields. All large fields received transplants. Direct seeding comprised 50, 61, and 78% of fields by number, but only 25, 70, and 74% by area in the southwest, northeast, and southeast districts, respectively. The southwest district had the largest production area with transplants (75%).

Planting method (direct seeding vs. transplanting) did not appear to be correlated with planting date. The earliest direct seeding was 20 April 1998 and 25 March 1999 and the latest 21 May 1998 and 5 June 1999. The earliest transplanting was 13 April 1998 and 4 April 1999 and the latest 20 May 1998 and 8 June 1999. Growers mostly planted before mid May (Table 1). However, planting date differed regionally as the southwest district had 52.6% of fields by number and 56.6% by area planted early before 25 April, while the northeast and southeast districts had only 22% by number, and 29 and 19% by area planted as early (Table 1). The southwest district had also the lowest percentages of number of fields and production area (both less than 10%) planted late after 20 May. The northeast and southeast districts had at least 23% of fields by either number or area planted as late (Table 1). Among transplanted fields, about 47% by number and 55% by area received transplants early before 25 April, 39% by number and 40% by area between 25 April and 20 May received transplants, and the remaining fields received transplants late after 20 May.

Large fields had higher proportions of early planting than small and medium fields. By number and area respectively, 26 and 30% of small, 40 and 38% of medium, and 60% of large fields were planted early before 25 April; 49 and 42% of small, 45 and 47% of medium, and 40% of large fields were planted between 25 April and 20 May; and 25 and 28% of small, 15% of medium, and 0% of large fields were planted late after 20 May.

Growers used 36 cultivars during the two year survey. 'Allsweet' and 'Black Diamond' were the most frequently used among 19 diploid inbred (open-pollinated) cultivars (14 and 13% by number, 13 and 8% by area, respectively). 'Sangria' and 'Royal Sweet' were the most frequently used among 12 diploid hybrid cultivars (12 and 7% by number, 7 and 9% by area, respectively). Triploid hybrid (seedless) cultivars planted included 'Abbott Cobb 5244', 'Tri-X 313', 'Sugar Time', 'Summer Sweet', and 'Fandango'. Triploid hybrids were in 13% of fields by number but 36% by area; diploid hybrids were in 47% of fields by number and 34% by area; and open-pollinated cultivars were in the remaining 40% of fields by number and 30% by area (Table 2). Triploid cultivars were observed only in the southwest district (Table 2). Among large fields, 80% by number and 87% by area were planted with triploid cultivars. Among medium fields 18% by number and 21% by area were planted with triploid cultivars. Among small fields 4% by either number or area were planted with triploid cultivars. Fields with raised bed receive triploids 77% by number and 75% by area. Fields of double row configuration received the 3 cultivar genotypes in about equal area. Fields received any of the 3 genotypes mostly before mid May.

Growers often used more than one watermelon cultivar in a field. Triploid cultivars required use of a diploid pollenizer. In addition, a mix of more than one cultivar genotype was common. Altogether, multiple cultivars were planted in 73% of fields by number and 80% by area (N=66). Among fields with multiple cultivars, 50% by either number or area were planted with 2 cultivars, 29% by number and 39% by area planted with 3 cultivars, and the remaining 21% by number and 11% by area with 4 to 7 cultivars. Fields had 16, 17, and 32% by number, 8, 12, and 52% by area in the southwest, northeast, and southeast districts planted with multiple cultivars, respectively.

Among 36 transplanted fields, 36% by number and 66% by area received triploids; 58% by number and 31% by area received diploid hybrids. The remaining small proportion received open-pollinated cultivars. Among 66 direct-seeded fields, none received triploids; 59% by number and 62% by area received diploid hybrids; and 41% by number and 38% by area received open-pollinated cultivars.

Conclusions. Most fields were direct-seeded before mid May in single rows without raised beds with multiple cultivars in Oklahoma. Fields with raised beds or transplants were primarily planted to triploid cultivars. Raised bedding, double row planting, and planting date did not correlate with cultivar. Growers in the southeast district most often planted multiple cultivars. Growers in the southwest district most often used raised beds, planted early, used transplants, and grew triploid cultivars.

Literature Cited

1. Lu, W., M. Biernacki, J. Duthie, W. Roberts, M. Taylor, and J. Edelson. 2002. Characteristics of watermelon (*Citrullus lanatus*) fields and production in Oklahoma. In Proceedings of Cucurbits 2002 Conference, in press.

2. Oklahoma Agricultural Statistics Service. 2001. Oklahoma agricultural statistics 2000. Oklahoma Department of Agriculture, Oklahoma City, OK.

3. Oklahoma Cooperative Extension Service. 2002. Administrative districts and area specialists. In 2002 Personnel Directory, pp 24-25. Oklahoma State Univ.

Table 1. Total number and total hectare of watermelon fields under different planting dates during an extensive statewide survey in 1998 and 1999 in Oklahoma, where dates were early before 25 April, medium from 25 April to 20 May, and late after 20 May

Date	Total number of fields				Total area of fields (ha)			
District	Early	Medium	Late	Total	Early	Medium	Late	Total
NE	4	9	5	18	36.42	59.09	29.14	124.65
SE	10	24	12	46	73.66	207.15	104.41	385.21
SW	20	15	3	38	424.53	290.57	34.40	749.50
Statewide	34	48	20	102	534.61	556.81	167.95	1259.37

Table 2. Total number and total hectare of watermelon fields with different cultivar genotypes during an extensive statewide survey in 1998 and 1999 in Oklahoma

	Total number of fields				Total area of fields (ha)			
Genotype	Open	Diploid	Triploid	Total	Open	Diploid	Triploid	Total
District	pollinated	hybrid	hybrid		pollinated	hybrid	hybrid	
NE	7	11		18	58.28	66.37		124.65
SE	19	27		46	149.68	235.54		385.21
SW	15	10	13	38	162.69	129.91	456.91	749.50
Statewide	41	48	13	102	370.64	431.81	456.91	1259.37

Watermelon Production of Gansu Province in China

Cheng Weidong[1], Cui Hongwen[2] and Su Wei[3]

[1]Gansu Academy of Agricultural Science, Lanzhou, Gansu Province, P.R. China, 7310070, [2]Lanzhou, Gansu Province, Northwest Sci-Tech University of Agriculture and Forestry, Yangling Shaanxi, P.R. China, 712100, and [3]Research Institute of Agricultural Science, Zhangye City, Gansu Province, P.R. China, 734000

Gansu Province is located in the middle part of China (E longitudes 92°13' to 108°46' and N latitudes 32°31' to 42°57'). It is one of the most famous areas in China for production of watermelon and melon with excellent quality, due to the special climate.

Climate Characteristics of Gansu Province. Gansu abounds with sunlight. More than 75% of the region has at least 2500h per year sunshine (the highest has 3400h per year), much more than other areas with the same latitudes. The amount of solar radiation is 445.0-663.6 KJ/㎝² per year in Gansu, with sunlight days 74%. The annual precipitation is little, ranging from 40-538. mm in the production area. (Lanzhou in the middle part) the annual precipitation is less than 300 mm and mainly concentrated in late July to September. The annual evaporation from land surface is 1400-4000 mm. The daily range of temperature in the season of watermelon growth is about 12-16C. The climate from east to west in Gansu transitions into a continent dry climate from a semi - humid climate. Due to the special climate Gansu has become a very important seed production base of watermelon and melon with large fruit and good quality in China.

Meanwhile, drought is also a limitary factor to the product of watermelon and melon in Gansu. Because of little rainfall irrigation culture is an important method for agriculture production but is restricted by a shortage of water resources. Production is also impacted often by cotton aphid infestations, virosis, sun-scald resulted from high temperatures, drought, solar radiation, and sometimes by frost in the early spring and by sandstorms.

Watermelon cultivars suitable for Gansu Province. Virtually all types of watermelon and melon are suitable for the Gansu region, due to the various climates present. These include introduced varieties belong to the Russian ecological type, the East Asian ecological type, and ecological type of North China.

For historical reasons, the germplasm of the local types is mainly from Russian and North China ecological sources, with large fruit and drought resistance but without resistance to excessive moisture.

Cultivation Characteristics and Key Technologies of Watermelon Culture.

Direct sowing in Open Field. The main production technique is direct sowing in the open field for most areas. Seedling transplanting and tunnel production are only used in the suburbs, although this practice is becoming bigger and bigger year by year because of higher economic returns. With the use of film coverings beginning in the 1980's, the traditional direct sowing on an open field has been improved into shallow sowing under film, shallow sowing covered by thinner soil (1.0 cm thickness instead of 2.5 cm), then breaking the film immediately emergence to aid the seedlings.

Growth during the Summer. Usually watermelon production stops during the summer in Gansu, and the harvest production begins in early fall. So plants should he protected from virosis and sun-scald when high temperatures arise.

Sand culture and irrigation culture. Sand culture in the middle region and high ridges (> 20 cm) in the western region is usually employed in Gansu. The sand culture culture, similar to the film culture, depends only on natural rainfall and 2-3 irrigations. The high ridge culture must be irrigated 3-5 times during the vegetative growth period, and every 7-15 days during the reproductive period, with 600-800 m^3/km^2 water per time.

Seed production. Because of plentiful sunlight and heat units, Gansu produces not only good watermelon but also seeds that are full and high yielding. The seeds produced in Gansu province are 20% heavier than those produced in eastern provinces. With F_1 hybrid production of watermelon beginning in 1980s, seed production has developed quickly in Gansu. The seed output increases greatly by means of applying high plant densities (39,000 - 46,500 plants/km^2) and single vine pruning, which yields very high returns to the farmers and enterprises. Furthermore, Gansu has become into one of the most important seed production regions for watermelon, with more and more seed enterprises coming up from domestic and abroad.

Major problems in watermelon production.

Variety. Besides the Gansu market, most of the fresh fruit would be exported to other markets in China. "Hongyou No.2", an old variety, is tolerant to transportation and storage, but the fruit quality is not good enough. In recent years "Xinong No. 8" has been produced on a large scale; it is tolerant to storage with good quality, but its tolerance to transporting is not as good as that of "Hongyou No.2". The demand for large-sized fruit is declining because family size is decreasing in cities and towns. So, there is new emphasis on developing new varieties with tolerance to transportation and storage, good quality, resistance diseases, and small fruit, which must have a good market for the next few years.

Using–seed Watermelon production. Using–seed watermelon production in Gansu is very special in China, but there is a scarcity of market information and the market requirement are not stable. So, the further investigation and research concerning the market is necessary for production in future.

Seed production of watermelon. In order to encourage more seed enterprises to come to Gansu to develop seed industry, it is very important to improve management, to have a good investing environment, to establish an ideal reputation, and to coordinate various relations.

Analysis of Sugar Content of Watermelon (*Citrullus lanatus* (Thunb.) Mansf.)

Cheng Weidong[1], Cui Hongwen[2] and Zhang Bingkui[2]
[1]Gansu Academy of Agricultural Science, Lanzhou, Gansu Province, P.R. China, 7310070, and
[2]Lanzhou, Gansu Province, Northwest Sci-Tech Universtity of Agriculture and Forestry, Yangling Shaanxi, P.R. China, 712100

Sugar content is one of the most important economic parameters for watermelon (*Citrullus lanatus* (Thunb.) Mansf.). This paper provides the research results on the sugar content of different parts of the fruit and different cultivars of watermelon.

Materials and Methods. Seven cultivars (lines) were used in this experiment (Line 129, Line 130, Line 84, Line 85, Line 87, Line 124, and Line 125). Line 129 and Line 130 were tetraploid lines, and the other lines were diploid. All the seeds of these cultivars came from the Gansu Academy of Agricultural Science.

Ten fruits of each cultivar were prepared for the measurement of sugar content. The samples were taken from five sites in the fruit (center part, stem end part, omphalic part, sunlight-side part and ground-side part), and the samples of the four sites other than the center part were taken 1 cm below the skin of the fruit. The sugar content was measured by a Sacharometer WYT produced in Quanzhou, Fujian, and all data of sugar content for each site of each fruit for each cultivar were recorded.

Results. The sugar content of the watermelon varied greatly and was different in different parts of the fruit (Table 1). The average sugar content of the center part was 8.86%, and had the highest sugar content compared to other parts of the fruit. The sugar content of the stem part, omphalic part, sunlight-side part and ground-side part were 7.48%, 7.44%, 7.20%, and 6.99%, respectively. The sugar content of the ground-side part was significantly lower than the sunlight-side part. The sugar content of the stem end part and ground-side part was significantly higher than the sunlight-side part and ground-side part. The percentage of sugar content of the stem part was close to the omphalic part, similar to the results reported by Wang Jian et al. (2001). Wang Jian reported that the sugar content of omphalic part was higher than stem part. Generally, for the diploid cultivars the sugar content of the center part $\geq$ stem part $\geq$ omphalic part $\geq$ sunlight-side part $\geq$ ground-side part. It was very interesting to note that the sugar content of all parts of the fruits of tetraploid cultivars were similar to each other except the center part of the fruit, and that the difference of the sugar content among the stem part, omphalic part, sunlight-side part and ground-side part was not significant (Table 1).

There was a large difference in sugar content between tetraploid cultivars and diploid cultivars, and among the diploid cultivars. Line 129 has the highest sugar content and the Line 84 has the lowest sugar content, with sugar contents of 8.70% and 5.95%, respectively. The difference of the sugar content between the highest cultivar and the lowest cultivar was 2.75%.

It is important to note that the two tetraploid

cultivars had a higher sugar content than any of the diploid cultivars. The sugar content of the tetraploid cultivars was between 8.48% and 8.70%, and the diploid cultivars was between 5.95% and 7.87%.

Discussion and Conclusion. The tetraploid cultivars may have had had higher sugar content than the diploid cultivars because they had fewer seeds. The development of seeds requires much more nutrient materials than the development of the vegetative organs. So, under the same cultivated conditions the diploid cultivars use more of their nutrient materials for seed development, finally leading to the decreased sugar content, whereas the tetraploid cultivars had a lower requirement of nutrient materials for their seed development. This result is consistent with that reported by Tan Suying et al. (2000).

This research showed that the sugar content of the tetraploid cultivars was distributed more uniformly inside of the fruit than the diploid cultivars, and this phenomenon may be due the distribution of the seeds inside the fruit. The tetraploid cultivars not only had fewer seeds, but these seeds were distributed more uniformly, so that the sugar content changed little and accumulated uniformly in the fruits.

For the diploid cultivars, the sugar content of the stem end part and omphalic part was significantly higher than the sunlight-side part and ground-side. This may be the result of the arrangement of seeds inside of the fruit. Generally, watermelon seeds are situated on both sides of the fruit, and these parts have a lower sugar content.

Literature Cited

1. Wang Jian, et al. 2001. China Watermelon and Melon. Chinese Agriculture Press, Beijing.
2. Tan Suying, et al. 2000. Seedless Watermelon Culturing and Breeding, Chinese Agriculture Press, Beijing.

Table 1 The Sugar Content of Different Parts of Fruit of Watermelon

Cultivars (lines)	Sugar content %					
	Center part	Stem end part	Omphalic part	Sunlight-side part	Ground-side part	Average (X)
129(4X)	9.61A	8.23B	8.72B	8.52B	8.42B	8.70A
130(4x)	!0.02A	8.31B	7.92B	7.91B	8.22B	8.48B
124(2X)	8.43A	7.90BC	8.00AB	7.56C	7.41C	7.87C
125(2X)	8.66A	8.01B	7.68B	6.91C	6.75C	7.60D
87(2 X)	8.36A	7.28B	6.72D	7.89B	7.66BC	7.58D
85(2X)	9.51A	6.98B	6.66B	6.15C	5.58D	6.98E
84(2X)	7.41A	5.27C	5.23C	6.08B	5.78B	5.95F
AverageX	8.86A	7.48B	7.44B	7.20C	6.99D	

The different letters in the Table indicate significant differences for each parameter separately at $P \leq 0.01$
(Duncan's Multiple range Test).
Numbers in the Table are average of ten replications.

Sweetness in Diploid and Triploid Watermelon Fruit

Donald N. Maynard, Amy M. Dunlap, and Brian J. Sidoti
Gulf Coast Research and Education Center, University of Florida, 5007 60th St. E., Bradenton, FL 34203

Internal watermelon fruit quality is a composite of flesh color and texture, freedom from defects (such as hollowheart), optimum maturity, sweetness, seed size and frequency in diploids, and freedom from seeds in triploids (Maynard, 2001).

According to Maynard (2001), "sweetness, one of the prime quality factors in watermelon fruit is related to total soluble solids (TSS), as measured by °Brix with a refractometer." The U.S. Standards for Grades of Watermelons (USDA, 1978) indicates watermelons may be labeled as having good internal quality with 8% TSS as determined in a random sample by an approved refractometer. Likewise, fruit may be labeled as having very good internal quality with TSS of 10% or greater. Having personally sampled thousands of watermelon fruit, it is my contention that fruit with 8% TSS are in fact not very good and those with 10% TSS are barely enjoyable. Most people would thoroughly enjoy fruit with 11%-12% TSS".

TSS is a measure of the concentration of the reducing sugars fructose and glucose and the nonreducing sugar sucrose. The relative concentration of these sugars is influenced by cultivar and stage of maturity. Glucose and fructose concentrations generally increase up to 24 days after pollination (DAP) and decline thereafter. Sucrose is first detectable at 20 DAP and increases thereafter. The relative concentration of these sugars is important since they vary in perceived sweetness with sucrose having a value at 1.0, glucose 0.60-0.75, and fructose 1.40-1.75. Accordingly, cultivars or maturity that result in high fructose concentrations is a desirable feature (Elmstrom and Davis, 1981).

TSS are determined routinely by watermelon breeders and cultivar evaluators as one estimator of fruit quality along with a myriad of other characteristics.

Methods. Diploid and triploid watermelon cultivars and advanced experimental hybrids were evaluated each spring season from 1991 through 2001 at the University of Florida's Gulf Coast Research and Education Center at Bradenton. The number of entries in each class was determined by commercial seed producer submissions. TSS were determined on two fruit in each plot at each harvest. Accordingly, determinations were made on 12 fruit with three replications and two harvests or on 16 fruit with four replications and two harvests for each entry. A hand-held refractometer (Atago ATC-1, 32-10 Honcho, Itabashi-ku, Tokyo 173-001, Japan) was used from 1991 to 1998 and a digital refractometer (Atago PR-101) was used from 1999 to 2001 for TSS determinations. Fruit were sampled by cutting from stem to blossom end, removing a section of tissue from the center (heart) of the fruit, and squeezing a few drops of juice on the refractometer prism surface. TSS data were subjected to analysis of variance and Duncan's multiple range test was used for mean separation (SAS, 2001).

Results. TSS for diploid and triploid watermelon cultivars that were evaluated at least four seasons are shown in Table 1. The range in diploid TSS was from 11.4% for 'Festival' to 12.6% for 'Sultan'. For triploid cultivars, TSS varied from 11.7% for 'Jack of Hearts' to 13.4% for 'Tri-X-Carousel'. TSS of 11 triploid cultivars exceeded the highest diploid fruit TSS. Only two triploid cultivars ('Summer Sweet 5032' and 'Jack of Hearts') had TSS that were lower than the second highest TSS that was found in diploid 'Royal Majesty' fruit.

The average TSS of diploid and triploid watermelon fruit by year from 1991 through 2001 averaged over all cultivars and determinations in that year is shown in Table 2. Average TSS in triploid fruit was higher than that in diploid fruit in 9 of 11 years and there was no difference in the other 2 years. TSS in diploid fruit varied from 11.1% in 1991

(Maynard, 1991) to 12.9% in 2000 (Maynard and Dunlap, 2000) while triploid fruit TSS ranged from 12.0 in 1991 and 1997 (Maynard, 1997) to 13.8% in 2000. The 1991 (486 mm) and 1997 (423 mm) spring seasons were characterized by much higher than normal rainfall during the growing season, whereas rainfall was sparse during the spring 2000 (114 mm) season. Accordingly, the highest TSS in watermelon fruit occur in seasons of low rainfall, usually accompanied by high light and low disease incidence; conditions that also favor high TSS. The 11-year average TSS was higher in triploid fruit, 12.7%, than in diploid fruit, 11.8%.

What factors may account for or contribute to higher TSS in triploid watermelon fruit than in diploid fruit? Some possibilities are: 1) energy used to produce seeds in diploid fruit is diverted to sugar production in triploid fruit, 2) triploid plants are generally larger than diploid plants and therefore have greater photosynthetic potential, 3) triploid fruit are generally smaller than diploid fruit so that equivalent sugar content is concentrated in triploid fruit. There may be other explanations as well.

Literature Cited

1. Elmstrom, G. W. and P. L. Davis. 1981. Sugars in developing and mature fruits of several watermelon cultivars. J. Amer. Soc. Hort. Sci. 106:330-333.

2. Maynard, D. N. 1991. Seedless watermelon variety evaluation, Spring 1991. GCREC (University of Florida) Res. Rept. BRA1991-21.

3. Maynard, D. N. 1997. Triploid watermelon cultigen evaluation, Spring 1997. GCREC (University of Florida) Res. Rept. BRA1997-15.

4. Maynard, D. N. 2001. An introduction to the watermelon p. 9-20. In: D.N. Maynard (ed.) Watermelons. Characteristics, production and marketing. ASHS Press, Alexandria, Va.

5. Maynard, D. N. and A. M. Dunlap. 2000. Triploid watermelon cultigen evaluation, Spring 2000. GCREC (University of Florida) Res. Rept. BRA2000-4.

6. SAS. 2001. SAS Institute Inc., Cary, N.C.

7. U.S. Dept. Agr. 1978. U.S. standards for grades of watermelons. AMS, USDA, Washington, D.C.

Table 1. Total soluble solids of diploid and triploid watermelon cultivars included in at least four trials. Gulf Coast Research and Education Center, University of Florida.

Diploid				**Triploid**		
	Years	**Soluble**			**Years**	**Soluble**
Cultivar	**(no.)**	**Solids (%)**		**Cultivar**	**(no.)**	**Solids (%)**
Sultan	6	12.6 a[z]		Tri-X-Carousel	4	13.4 a
Royal Majesty	5	12.1 ab		Tri-X-Palomar	4	13.3 ab
Sangria	11	12.0 bc		Revolution	4	13.2 ab
Royal Sweet	9	12.0 bc		Millennium	8	13.2 a-c
Regency	7	11.9 b-d		Constitution	4	13.1 a-c
Royal Star	9	11.8 b-d		Freedom	5	13.1 a-c
Piñata	4	11.7 b-d		Gem Dandy	4	13.0 a-d
Legacy	4	11.7 b-d		Summer Sweet 5544	4	12.9 c-d
Fiesta	11	11.6 b-d		Tri-X-Shadow	5	12.9 b-d
Starbrite	8	11.6 b-d		Millionaire	11	12.7 c-e
Mardi Gras	6	11.6 b-d		Tiffany	5	12.7 c-e
Barron	4	11.5 cd		Genesis	9	12.6 d-f
Festival	4	11.4 d		Tri-X-313	14	12.6 d-f
				Summer Sweet 5244	9	12.6 d-f
				Revelation	4	12.5 d-f
				Scarlet Trio	7	12.5 d-f
				Sunrise	5	12.5 ef
				Summer Sweet 2532	4	12.4 ef
				Nova	6	12.3 fg
				King of Hearts	8	12.3 fg
				Queen of Hearts	8	12.3 fg
				Crimson Trio	10	12.2 fg
				Summer Sweet 5032	4	11.9 h
				Jack of Hearts	4	11.7 h

[z]Mean separation in columns by Duncan's multiple range test, 5% level.

Table 2. Total soluble solids of diploid and triploid watermelons by year. Gulf Coast Research and Education Center, University of Florida.

	Diploid			Triploid	
		Average			Average
	Entries	Soluble Solids		Entries	Soluble Solids
Year	(no.)	(%)		(no.)	(%)
1991	16	11.1 b[z]		27	12.0 a
1992	20	11.9 b		20	13.3 a
1993	25	11.9 b		39	12.8 a
1994	17	12.1 a		25	12.3 a
1995	20	12.2 a		28	12.4 a
1996	29	11.3 b		38	12.7 a
1997	36	11.3 b		32	12.0 a
1998	36	11.3 b		21	12.6 a
1999	32	11.7 b		28	13.1 a
2000	34	12.9 b		50	13.8 a
2001	27	12.0 b		37	13.0 a
11-year average		11.8 b		11-year average	12.7 a

[z]Mean separation in rows by Duncan's multiple range test, 5% level.

Disease Assessment Scales for Seedling Screening and Detached Leaf Assay for Gummy Stem Blight in Watermelon

Gabriele Gusmini[1], and Todd C. Wehner[1] and Gerald J. Holmes[2]
[1]Department of Horticultural Science, and [2]Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695-7609

Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) is a major vegetable crop in the U.S. Gummy stem blight, caused by *Didymella bryoniae* (Auersw.) Rehm [=*Mycosphaerella citrullina* (C.O.Sm.) Gross. and *Mycosphaerella melonis* (Pass) Chiu & Walker] and its anamorph *Phoma cucurbitacearum* (Fr.:Fr.) Sacc. [=*Ascochyta cucumis* Fautrey & Roum] (4), is one of the most important diseases of this crop. Resistance to gummy stem blight in watermelon was ranked by U.S. researchers as the third most important trait for germplasm evaluation, following fruit blotch and Fusarium wilt (2).

Gummy stem blight on watermelon plants is evident as crown blight, stem cankers, and extensive defoliation (7). Pycnidia and, less frequently, perithecia are produced in the diseased tissues and appear as black fruiting bodies which can be collected for single spore isolation (17, 21).

Adequate control of gummy stem blight is difficult, even when using fungicide applications and good horticultural practices, and there are several reports of acquired resistance of *D. bryoniae* to fungicides (3, 5, 6, 8, 18). Therefore, genetic resistance is a very attractive alternative (9-11).

The first two steps in every breeding program for plant resistance to pathogens are: 1) screening of the available germplasm, and 2) continuous testing for resistance of the segregating generations F1 and subsequent during the development of new varieties. The two most widely used methods for screening for resistance to pathogens are seedling screening [i.e. in watermelon (1), muskmelon (20), squash (19), and cucumbers (15)], and detached leaves assay [i.e. in watermelon (12), cucumber (14), tobacco (16), and tomato and pepper (13)].

In this report we present two disease assessment scales for gummy stem blight, one for screening watermelon seedlings, and one for a detached leaf assay.

The purpose of developing this disease assessment scale was to make an easy and efficient system for screening large numbers of accessions from the watermelon germplasm collection. The two disease assessment scales were used for seedling and detached-leaf assays which were run in addition to the field assay. The assays will be useful for inheritance studies where large numbers of plants per generation and crosses (population) must be rated. The ordinal scale was adopted for the seedling assay instead of the interval Horsfall-Barratt scale, because it permitted us to record lesions either on leaves or on stems. Leaf ratings are important because plant yield and survival is affected by leaf area, which is reduced by severe disease epidemics. Stem ratings are important because large, localized lesions can kill the plant, especially those lesions located near the base (crown) of the plant.

The detached leaf assay used an interval scale in order to make it easy and reliable for people (greenhouse technicians, nursery technicians, students, etc.) to use without much training.

Disease assessment scale for seedling screening assay

0 = no symptoms
1 = yellowing on leaves (suspect of disease only)
2 = moderate symptoms (<20% necrosis) on leaves only
3 = slight symptoms (21-45% necrosis) on leaves only
4 = severe symptoms (>45% necrosis) on leaves only
5 = some leaves dead, no symptoms on stem
6 = moderate symptoms (<20% necrosis) on leaves, with necrosis also on petioles and stem (<3 mm long)

7 = slight symptoms (21-45% necrosis) on leaves, with necrosis also on petioles and stem (3-5 mm long)
8 = severe symptoms (>45% necrosis) on leaves, with necrosis also on petioles and stem (>5 mm long)
9 = plant dead

Disease assessment scale for detached leaf assay
The disease assessment scale proposed for the detached leaf assay is an interval type scale which considers the percent of necrotic leaf-blade, including veins. Yellowing and other color changes are not considered reliable indicators of disease, because the leaves in Petri plates sometimes dehydrate and turn chlorotic in the absence of the pathogen. The scale is a discontinuous 0 to 9 scale, to connect it mnemonically to the seedling screening scale and to the lower limit of the percent interval.

0 = necrosis on 0% of leaf-blade; no symptoms
2 = necrosis on 20-30% of leaf-blade
4 = necrosis on 40-50% of leaf-blade
6 = necrosis on 60-70% of leaf-blade
8 = necrosis on 80-90% of leaf-blade
9 = necrosis on 100% of leaf-blade; leaf dead

Photographs
Photographs representing these disease assessment scales are available at the website http://cuke.hort.ncsu.edu/cucurbit/wmelon/gsbrating/gsbindex.html

Literature Cited

1. Dias, R. d. C. S., M. A. d. Queiroz, M. Menezes, and M. A. De Queiroz. 1996. Identification of sources of resistance to *Didymella bryoniae*. Horticultura Brasileira 14(1):15-17.

2. Jarret, B., B. Rhodes, T. Williams, and G. W. Elmstrom. 1996. Cucurbit germplasm committee report: watermelon. 30 pp.

3. Kato, T., K. Suzuky, J. Takahashy, and K. Kamoshita. 1984. Negatively correlated cross-resistance between benzimidazole fungicides and methyl N-(3,5-dichlorophenyl) carbamate. J. Pestic. Sci. (9):489-495.

4. Keinath, A. P., M. W. Farnham, and T. A. Zitter. 1995. Morphological, pathological, and genetic differentiation of Didymella bryoniae and Phoma spp. isolated from cucurbits. Phytopathology 85(3):364-369.

5. Keinath, A. P., and T. A. Zitter. 1998. Resistance to benomyl and thiophanate-methyl in *Didymella bryoniae* from South Carolina and New York. Plant Disease 82:479-484.

6. Malathrakis, N. E., and K. J. Vakalounakis. 1983. Resistance to benzimidazole fungicides in the gummy stem blight pathogen *Didymella bryoniae* on cucurbits. Plant Pathol. 32:395-399.

7. Maynard, D. N., and D. L. Hopkins. 1999. Watermelon fruit disorders. HortTechnology 9(2):155-161.

8. Miller, M. E., T. Isakeit, J. X. Zhang, and B. D. Bruton, Gummy stem blight and black rot of melons, in Melon production system in South Texas. Annual Research report., M.E. Miller, Editor. 1997, Texas A&M University: Weslaco.

9. Norton, J. D., G. E. Boyhan, D. A. Smith, and B. R. Abrahams. 1993. 'AU-golden producer' watermelon. HortScience 28(6):681-682.

10. Norton, J. D., G. E. Boyhan, D. A. Smith, and B. R. Abrahams. 1995. 'AU-Sweet' Scarlet' watermelon. HortScience 30:393-394.

11. Norton, J. D., R. D. Cosper, D. A. Smith, and K. S. Rymal. 1986. AU-Jubilant and AU-Producer Watermelons. HortScience 21:1460-1461.

12. Rhodes, B., X. Zhang, R. A. Dean, J. Frick, and J. Zhang. 1992. Use of detached leaf assay for race 1 and race 2 anthrachnose resistance in a diallel cross with *Citrullus*. CGC Report (15):84-86.

13. Sharon, E., Y. Okon, Y. Bashan, and Y. Henis. 1982. Detached leaf enrichment: a method for testing small numbers of *Pseudomonas syringae* pv. *tomato* and *Xanthomonas campestris* var. *vesicatoria* in seed and symptomless leaves of tomato and pepper. J. Applied Bacteriol. 53:371-377.

14. St. Amand, P. C., and T. C. Wehner. 1995. Greenhouse, detached-leaf, and field testing methods to determine cucumber resistance to gummy stem blight. J. American Soc. Hort. Sci. 120(4):673-680.

15. St. Amand, P. C., and T. C. Wehner. 2001. Heritability and genetic variance estimates for leaf and stem resistance to gummy stem blight in two cucumber populations. J Am Soc Hortic Sci 126(1):90-94.

16. Tedford, E. C., T. L. Miller, and M. T. Nielsen. 1990. A detached-leaves technique for detecting *Phytophthora parasitica* var. *nicotianae* in tobacco. Plant Disease 74:313-316.

17. van Steekelenburg, N. A. M. 1983. Epidemiological aspects of *Didymella bryoniae*, the cause of stem and fruit rot of cucumber [*Cucumis sativus*].

18. van Steekelenburg, N. A. M. 1987. Resistance to benzimidazole and dicarboximide fungicides in *Botrytis cinerea* and *Didymella bryoniae* in cucumbers in The Netherlands. Med. Fac. Landbouww. Rijksuniv. Gent. 52:875-880.

19. Zhang, Y. P., K. Anagnostou, M. Kyle, and T. A. Zitter. 1995. Seedling screens for resistance to gummy stem blight in squash. Cucurbit Genetics Cooperative Report 18:59-61.

20. Zhang, Y. P., M. Kyle, K. Anagnostou, and T. A. Zitter. 1997. Screening melon (*Cucumis melo*) for resistance to gummy stem blight in the greenhouse and field. HortScience 32(1):117-121.

21. Zitter, T. A., D. L. Hopkins, and C. Thomas, Compendium of cucurbit diseases. 1996, APS Press: St. Paul. p. 27-28.

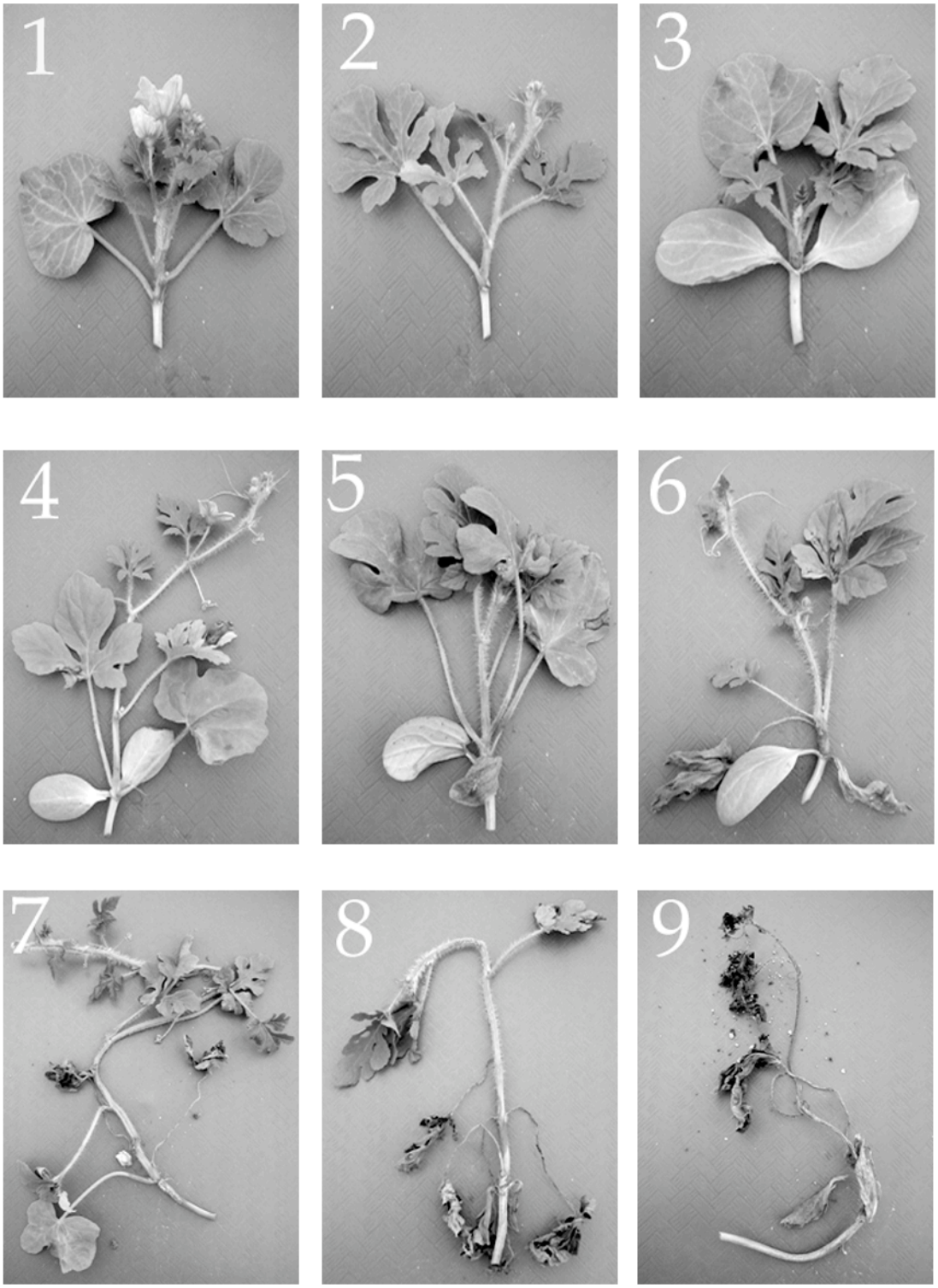


Figure 1. Photographs of the gummy stem blight disease rating assay for watermelon seedlings.

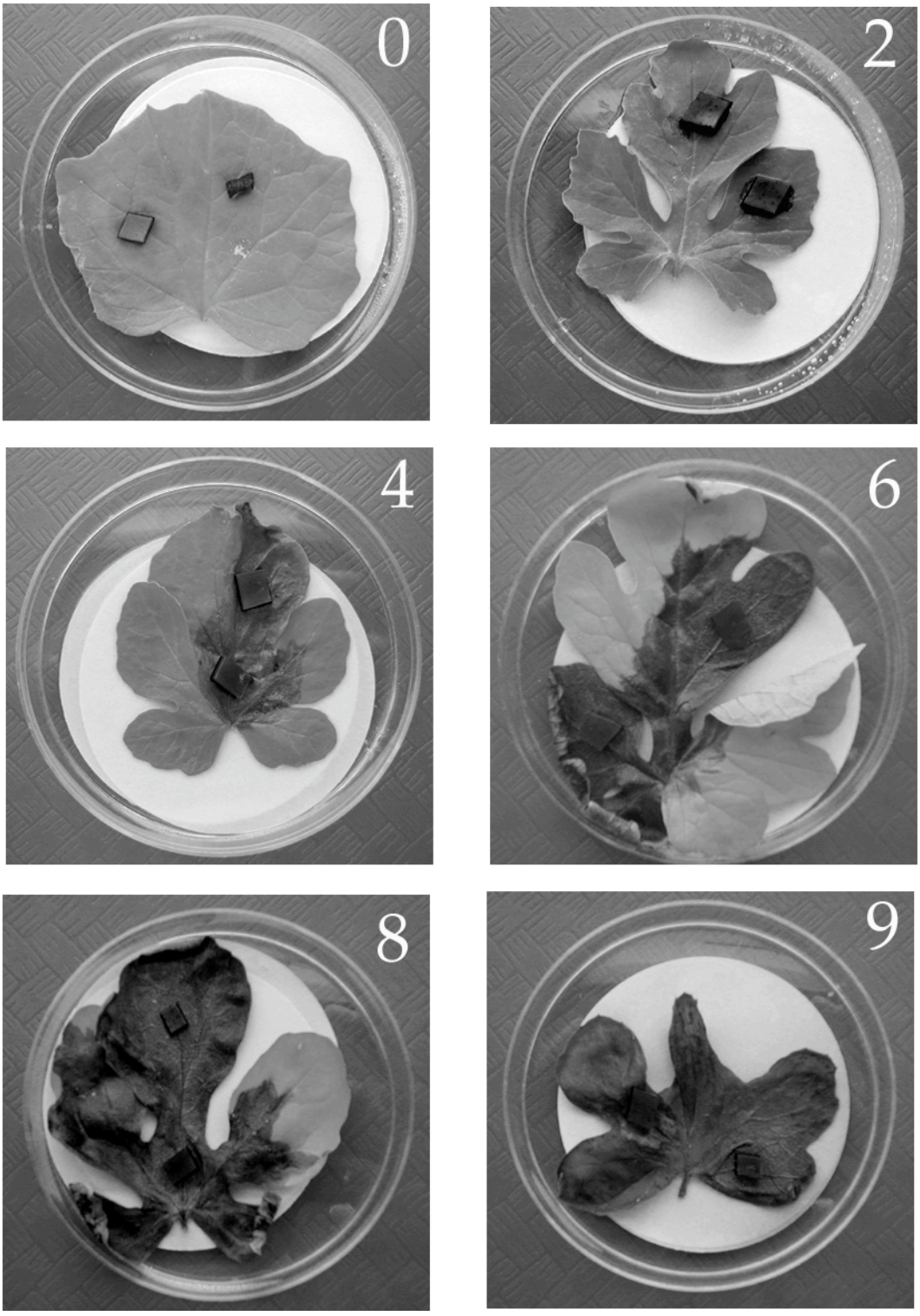


Figure 2. Photographs of the gummy stem blight disease rating assay for watermelon detached leaves.

A Postscript to Duchesne's Cucurbit Legacy

Harry S. Paris
Department of Vegetable Crops, Agricultural Research Organization, Newe Ya'ar Research Center, P. O. Box 1021, Ramat Yishay 30-095, Israel

A. N. Duchesne (1747-1827) conducted the first in-depth taxonomic study of the genus *Cucurbita*, documenting variation in *C. pepo* and designating *C. maxima and C. moschata*. The most complete written account of his work was published as a small book in 1786 (1). Copies of this book are available for study in several libraries in Paris and London (3). Duchesne documented the results of his work with realistic, life-like watercolor drawings, 20 of which have now been published (4). The collection consisting of the original 364 plates is housed in the Bibliothèque Centrale du Muséum National d'Histoire Naturelle, Paris, catalogued as manuscript no. 5007. For years they were unaccompanied by any written material.

Duchesne's "mémoire," which presumably contained the details of the plant materials and methodology of his 6-year study with *Cucurbita* and had been read before the French Academy of Sciences in 1779, has not been found. However, the curator of manuscripts of the Central Library of the Museum recently located there several misplaced documents related to Duchesne's work on *Cucurbita*, which she has placed with the drawings and brought to my attention.

There are 6 such documents. The first and most important is a letter by Duchesne to the staff of the Museum (addressed to "Citoyens Professeurs") which accompanied his bequeathing of the drawings to that institution. The letter bears the date 12 frimaire an 8 de la republique, that is, 3 December 1799. The drawings, made from 1769 through 1774, had originally been bequeathed to the Bibliothèque Royale, which, after the French Revolution, became the Bibliothèque Nationale. I had thought (4) that these drawings might have already been moved for safe keeping to the Museum during the tumultuous days of the Revolution. From Duchesne's letter to the staff of the Museum, we learn that his reasons were more mundane. Born to a father who was in charge of maintenance of the royal buildings, Duchesne was in financial straits after the Revolution (5). He had hoped to extract a payment for the drawings from the Bibliothèque Nationale in order to support his family, but this was not forthcoming. As he considered his drawings not to have the artistic quality of those made by other naturalists and kept at the Bibliothèque Nationale, and as he considered his drawings to be on the subject of natural history, he decided that their proper place would be Muséum National d'Histoire Naturelle. No mention is made of the drawings having been accompanied by the mémoire or any other written material, hence the mémoire appears to have been separated from the drawings by then.

The second document is a reprint of Duchesne's article on *Cucurbita* in Tessier and Thouin's encyclopedia of agriculture, published in 1793 (2). The third is a 3-page document, perhaps incomplete, and does not appear to me to be in Duchesne's handwriting and contains the spelling "gourges" instead of "courges". The subject matter concerns a part of the collection, the number series 1 through 24, all of which were ornamental gourd cultigens.

The fourth document refers to Duchesne's articles in Lamarck's and Tessier and Thouin's encyclopedias and hence was composed no earlier than 1793. This document is a 14-page series of notes made from the drawings of the mature fruits. Although much like those published by Duchesne (1), these notes include direct references to fruits of numbers 94 through 98, which are *C. moschata* and *C. maxima*, numbers to which Duchesne did not refer to directly in his publications. No notations were included for the lettered drawings, that is, those of plants, plant parts, flowers, and young fruits.

The fifth document is a single page entitled "Tableau des Courges" and compares tables of

classification presented in Duchense's works until 1793. The comparisons are not always, correct, however, as a table with Latin species epithets is presented as from Duchesne's mémoire of 1779 but could not be from then (3) but is actually that published in his book of 1786 (1).

The sixth document consists of four pages and is entitled "Travail des Pépons cultivés et peints par Ant. Nic. Duchesne". This is a complete list of all of the drawings, numbered (mature fruits) and lettered (young fruits, flowers, plants and plant parts), contained in the collection. Among the listings is a plate, bearing the letter X, of six drawings made by Lucette Duchesne in 1796. No. 48 is not listed and, as I noted elsewhere (4), there is no drawing no. 48 in the collection even though this number had descendants through cross-pollination.

I thank Mme. Pascale Heurtel, Conservatrice des Manuscrits, Bibliothèque Centrale du Muséum National d'Histoire Naturelle, Paris, France, for notifying me of the finding these documents and for her dedicated assistance.

Acknowledgements. Contribution No. 111/2002 from the Institute of Field & Garden Crops, Agricultural Research Organization, Bet Dagan, Israel.

Literature Cited

1. Duchesne, A.N. 1786. Essai sur l'histoire naturelles des courges. Panckoucke, Paris, 46 pp.

2. Duchesne, A.N. 1793. Courge, *Cucurbita*, in A.H. Tessier and A. Thouin (eds.), Encyclopédie Méthodique, Agriculture 3: 605-614. Panckoucke, Paris.

3. Paris, H.S. 2000. First two publications by Duchesne of *Cucurbita moschata* (*Cucurbitaceae*). Taxon 49: 305-319.

4. Paris, H.S. 2000. Paintings (1769-1774) by A. N. Duchesne and the history of *Cucurbita pepo*. Ann. Bot. 85: 815-830.

5. Sylvestre, A.F. de. 1827. Notice biographique sur M. Ant.-Nicolas Duchesne. Huzard, Paris, 26 pp.

No Segregation Distortion in Intersubspecific Crosses in *Cucurbita pepo*

Harry S. Paris
Department of Vegetable Crops, Agricultural Research Organization, Newe Ya'ar Research Center, P. O. Box 1021, Ramat Yishay 30-095, Israel

A number of loci affecting fruit and stem coloration have been identified in *Cucurbita pepo* L. (2). Two cases of segregation distortion were reported recently. One involved a cross between a gourd of *C. pepo* subsp. *texana* (Scheele) Filov and a zucchini-type cultigen (*C. pepo* subsp. *pepo*) (6). The other was reported for the *D* gene in reciprocal backcross progenies involving a bush inbred of 'Vegetable Spaghetti' (*C. pepo* subsp. *pepo* Vegetable Marrow Group, *d/d*), as the recurrent parent, and 'Early Prolific Straightneck' (*C. pepo* subsp. *texana* Straightneck Group, D^s/D^s), as the donor parent (3). In this case, adherence to the expected 1:1 backcross ratio was observed when the F_1 was the female parent and 'Vegetable Spaghetti' was the male. However, in the reciprocal cross, that is when the F_1 was used as the male and 'Vegetable Spaghetti' as the female, a highly significant deviation from the expected 1:1 ratio was observed. For both cases of segregation distortion, it was thought that distortion might occur through microgametophyte competition rooted in the distance of the parents (belonging to different subspecies) and/or fruit shape (belonging to different cultivar-groups), and might reflect a more widespread phenomenon in *C. pepo*.

To further test this idea, reciprocal crosses were made between 'Table Queen' (*C. pepo* subsp. *texana* Acorn Group) with 'Verte non-coureuse d'Italie' (*C. pepo* subsp. *pepo* Cocozelle Group). The former cultivar has vine growth habit (*bu/bu*), dark stems (*D/D*), and non-striped (*l-1/l-1*), light-colored (*Qi/Qi*) young fruits and the latter cultivar has bush growth habit (*Bu/Bu*), light stems (*d/d*), and striped ($l\text{-}1^{St}/l\text{-}1^{St}$), intense-colored (*qi/qi*) young fruits (1,2,4,5). The F_1s, as expected, had bush growth habit, dark stems, and striped, light-colored young fruits (*Bu/bu D/d* $l\text{-}1^{St}$*/l-1 Qi/qi*). Four F_1 plants, derived from using 'Table Queen' as the female parent, were reciprocally crossed with four plants of that cultivar, plant-for-plant. Similarly, five F_1 plants, derived from using 'Verte non-coureuse d'Italie' as the female parent, were reciprocally crossed with five plants of that cultivar, plant-for-plant. Thirty-two seeds of each of the progenies of each backcross (18 progenies in all), were planted in 128-cell styrofoam trays on 5 March 2001 and transplanted to the field 21 days later. Each plant was scored for growth habit, stem color, fruit striping, and young fruit color when the first well-formed fruit was from 3 to 5 days past anthesis.

Almost every one of the results for individual plants segregated in accordance with the expected 1:1 ratio in the backcross (Table 1). There were two exceptions, one involving *Qi* with 'Table Queen' as the donor and the other involving $l\text{-}1^{St}$ with 'Verte non-coureuse d'Italie' as the donor. In both cases, the excess was for the dominant allele of the donor. The totals for 1165, 1165R, 1166, and 1166R conformed well to the expected 1:1 backcross ratios for all four segregating loci. The *Bu* and *l-1* loci, and the *D* and *qi* loci, appear to be inherited independently (Table 2).

Segregation for the four loci was entirely in accordance with expected 1:1 backcross ratios. Segregation distortion was not observed in either set of reciprocal backcrosses. Wide crossing within *C. pepo*, that is, across subspecies and/or cultivar-groups, cannot alone be responsible for the segregation distortions heretofore observed.

Acknowledgements. Contribution No. 112/2002 from the Institute of Field & Garden Crops, Agricultural Research Organization, Bet Dagan, Israel.

Table 1. Segregation for stem color, growth habit, fruit striping, and young fruit color in backcrosses involving 'Table Queen' (TQE, *C. pepo* subsp. *Texana* Acoprn Group, genotype *bu.bu D/D l-l-1 Qi/Qi*) and 'Verte non-coureuse d'Italie' (VNI, *C. pepo* subsp. *Pepo* cocozelle Group, genotype *bu/Bu d/d l-1St-/l-1St qi/qi*).

	Number of plants				**Number of plants**			
Line*	**D/d**	**d/d**	X^2	***P***	**Qi/qi**	**qi/qi**	X^2	***P***
1165	19	11	2.133	0.15	13	17	0.533	0.46
1165a	15	17	0.125	0.72	19	13	1.125	0.28
1165b	17	15	0.125	0.72	19	13	1.125	0.04
1165c	13	18	0.806	0.37	21	10	6.903	0.08
Total	64	61	0.036	0.85	72	53	2.888	
1165R	19	10	2.793	0.09	17	12	0.431	0.50
1165Ra	15	15	0.000	1.00	16	14	0.133	0.71
1165Rb	14	18	0.500	0.47	16	16	0.000	1.00
1165Rc	14	15	0.034	0.85	14	15	0.034	0.85
Total	62	5	0.133	0.71	63	57	0.300	0.58
Line*	**Bu/Bu**	**bu/bu**	X^2	***P***	**l-1St/l-1**	**l-1/l-1**	X^2	***P***
1166	16	15	0.032	0.85	13	18	0.806	0.37
1166a	17	14	0.290	0.58	19	12	1.581	0.21
1166b	19	12	1.581	0.21	14	17	0.290	0.58
1166c	17	14	0.290	0.58	13	18	0.806	0.37
1166d	16	16	0.000	1.00	18	14	0.500	0.47
Total	85	71	1.256	0.26	77	79	0.026	0.86
1166R	17	14	0.290	0.58	14	17	0.290	0.58
1166Ra	13	17	0.533	0.46	13	17	0.533	0.46
1166Rb	18	13	0.806	0.37	15	16	0.032	0.85
1166Re	14	18	0.500	0.47	16	16	0.000	1.00
1166Rd	13	14	0.037	0.85	19	8	4.481	0.03
Total	75	76	0.007	0.93	77	74	0.060	0.80

*The 1165 lines employed TQE as donor parent and VNI as recurrent parent. The 1166 lines employed VNI as donor parent as TQE as recurrent parent. Lines designated R were derived using the F_1 as female and recurrent parent as male; lines not designated R were derived using the F_1 as male and recurrent parent as female.

Table 2. Breakdown into four genotypes in the mutual, reciprocal backcrosses of Table Queenm (TQE,*C. pepo* subsp. *Texana* Acorn Group, genotype *bu/bu D/D l-1 Qi/Qi*) and Verte non-coureuse d'Italie (VNI, *C. pepo* subsp. *Pepo* Cocozelle Grop, genotype *Bu/Bu d/d l-1St/l-1St qi/qi*).

Female Parent	Male Parent	Number of plants					X^2	*P*
		Total	D/d Qi/qi	D/d Qi/qi	d/d Qi/qi	d/d qi/qi		
VNI	F_1	125	34	30	38	23	3.928	0.26
F_1	VNI	120	35	27	28	30	1.267	0.73
Total	Total	245	69	57	66	53	2.755	0.44

Female Parent	Male Parent	Number of plants					X^2	*P*
		Total	Bu/bu l-1St/l-1	Bu/bu l-1/l-1	bu/bu l-1St/l-1	bu/bu l-1/l-1		
TQE	F_1	156	38	47	39	32	2.923	0.42
F_1	TQE	151	38	47	39	37	0.065	0.99
Total	Total	307	76	84	78	69	1.495	0.68

Literature Cited

1. Denna, D.W. and H.M. Munger. 1963. Morphology of the bush and vine habits and the allelism of the bush genes in *Cucurbita maxima* and *C. pepo* squash. Proc. Amer. Soc. Hort. Sci. 82: 370-377.

2. Paris, H.S. 2000. *Quiescent intense* (*qi*): a gene that affects young but not mature fruit color intensity in *Cucurbita pepo*. J. Hered. 91: 333-339.

3. Paris, H.S. 2000. Segregation distortion in *Cucurbita pepo*, in: N. Katzir and H.S. Paris, eds., Proceedings of Cucurbitaceae 2000, the 7th Eucarpia Meeting on Cucurbit Genetics and Breeding. Acta Hort. 510: 199-202.

4. Paris, H.S. and Y. Burger. 1989. Complementary genes for fruit striping in summer squash. J. Hered. 80: 490-493.

5. Paris, H.S. and H. Nerson. 1986. Genes for intense pigmentation of squash. J. Hered. 77: 403-409.

6. Wilson, H.D. and J.S. Payne. 1994. Crop/weed microgametophyte competition in *Cucurbita pepo*. Amer. J. Bot. 81: 1531-1537.

Inheritance of Gray Leaf Color in a Material Derived from a *Cucurbita maxima* Duch. x *C. moschata* Duch. Hybrid

F. López-Anido, E. Cointry, I. Firpo, S.M. García, and S. Gattuso
Fac. de Cs. Agrarias, Universidad Nacional de Rosario, CC 14, Zavalla S2125 ZAA, Argentina

Introduction. In southern Latin America *C. maxima* has been largely bred for immature fruit consumption given rise to the so-called "zapallito" varieties. This culinary use is very popular and has pre-Columbian cultural roots. It is believed that this species was domesticated from *C. andreana* Naud. (2). Commercial cultivars and landraces of zapallito present no mottled leaves, soft mature flesh and generally short internodes, giving a typical compact plant. *C. moschata* cultivars have been used for mature fruit harvest, they present vine habit, good quality mature flesh and mottled leaves.

In *Cucurbita* species interspecific crosses have played an important role in the breeding work (5), especially the crosses between C. *maxima* and C. *moschata.* They have proven to be useful in transferring good attributes from one to another and even used as commercial hybrids (6). Recently, in a C. *maxima* x C. *moschata* hybrid progeny a novel gray leaf color type was identified and its inheritance examined. The information is of importante for the potential inclusion of this leaf color variant in breeding programs.

Material and Methods. In 1995 in the Rosario National University zapallito breeding program crosses between *C. maxima* cv. Any and *C. moschata* cv. Butternut-Local were conducted in an attempt to obtain materials that could be harvested either in an immature or mature state. In 1996 the hybrid population was field evaluated in order to start a selfing scheme. A large variation was observed among plants: some resembled the *C. moschata* parent in the vine growth and mottled leaves, others presented the typical compact plant habit of zapallito. A distinctive uniformly gray leaf plant was observed (Figure 1), selfed and identified as 'I-3'. During 1997 and 1998 S_1 and S_2 progenies were advanced showing uniform gray leaves. In 1999 and 2000 crosses were made with 'A-10-2-2', a uniform green leaf zapallito inbred line, obtaining F_1, F_2, BC1 and BC2 generations. The segregation study was conducted at the Experimental Field of the Rosario National University in an early sowing date (1 December 2001) and, when seeds were available, repeated in a late sowing date (13 February 2002). In each case the plants presenting normal green and gray leaf color were counted four weeks after the sowing date.

Since a similar uniformly silvery-leaf form was observed in *C. pepo* (4) and its nature due to air spaces under the epidermal layer (3), an optical microscopic examination was also conducted upon normal green and gray leaf sections. Both fresh and fixed (formaldehyde, ethanol, acetic acid, water, 2:10:1:3.5) leaves were used. Transverse sections of the leaves measuring 10 μm were prepared with a hand microtome and stained with Safranin and Fast Green (1). Sections were mounted in synthetic balsam.

Results and Discussion. Results of the segregation study are presented in Table 1. Leaf color fits a monogenic inheritance, the gray form being recessive to normal green. We propose the symbol *grl* (*grey leaf*) to designate the gene controlling this trait.

The microscopic observation failed to relate the distinctive gray leaf color to any apparent differences in air spaces among palisade cells nor between palisade cells and epidermal layer. Its nature should be further investigated.

Acknowledgements. This research was supported by PICT 08-07333 and PIP 1083/98 grants.

Figure 1. Expanded normal green (left) and gray (right) leaves.

Table 1. Goodness of fit X^2 test for normal green and gray leaf plant segregation evaluated in an early (E) and late (L) sowing date.

Generation	Sowing Date	No. of plants		Expected Ratio	X^2	P
		Green	Gray			
A-10-2-2	E	30	-	1:0		
	L	16	-	1:0		
I-3-14-5	E	-	49	0:1		
	L	-	42	0:1		
F_1 (A-10-2-2 x I-3-14-5)	E	26	-	1:0		
	L	16	-	1:0		
F_1 (I-3-14-5 x A-10-2-2)	E	31	-	1:0		
F_2 (A-10-2-2 x I-3-14-5)	E	113	35	3:1	0.14	0.5-0.75
	L	36	15	3:1	0.53	0.25-0.50
F_2 (I-3-14-5 x A-10-2-2)	E	27	8	3:1	0.08	0.75-0.90
BC (A-10-2-2 x I-3-14-5) x A-10-2-2	E	37	-	1:0		
	L	47	-	1:0		
BC (A-10-2-2 x I-3-14-5) x I-3-14-5	E	45	40	1:1	0.29	0.50-0.75
	L	27	25	1:1	0.08	0.75-0.90

Literature cited

1. Dizeo de Strittmatter, C. 1979. Modificación de una coloración de Safranina Fast-green. Bol. Soc. Arg. Bot. 18: 121-122.

2. Millan, R. 1945. Variaciones del zapallito amargo *Cucurbita andreana* y el orígen de *Cucurbita maxima*. Rev. Arg. Agron 12:86-93.

3. Scarchuk, J. and J.M. Lent. 1965. The structure of mottled-leaf summer squash. J. Hered. 56:167-168.

4. Shifriss, O. 1982. On the silvery-leaf trait in *Cucurbita pepo* L. Cucurbit Genet. Coop. Rpt. 5:48-49.

5. Whitaker, T. W. and G.W. Bohn. 1950. The taxonomy, genetics, production and uses of the cultivated species of *Cucurbita*. Econ. Bot. 4:52-81.

6. Whitaker, T. W. and R.W. Robinson. 1986. Squash breeding. *In*: Breeding Vegetables Crops. M.J. Bassett Ed. pp 209-242. AVI Publishing Co.

Resistance to Silverleaf Disorder is Controlled by a Single Recessive Gene in *Cucurbita moschata* Duchense

Moisés González-Román and Linda Wessel-Beaver
Dept. of Agronomy and Soils, University of Puerto Rico, P.O. Box 9030, Mayaguez, Puerto Rico 00691-9030

Silverleaf disorder is induced by its namesake, the silverleaf whitefly *Bemisia argentifolii* Bellows and Perring. The disorder is characterized by an opaque, grey leaf color on the adaxial surface of leaves. In severe cases the entire leaf may be silvered, as well as the petioles, flowers and fruit. Silverleaf affects most genotypes of the domesticated species of *Cucurbita* (6). In Puerto Rico, foliage of all local tropical pumpkin (*C. moschata*) cultivars, including 'Soler', becomes silvered even in the presence of low whitefly populations. However, fruits of tropical pumpkin are usually not silvered. Thus, the economic impact of silvering is not as great as in *C. pepo* L. and *C. maxima* Duchense. However, if intense silvering occurs at an early stage, tropical pumpkin plants will often be slow to develop and generally unproductive.

Various sources of resistance to silvering have been identified in *C. moschata*. These include 'Butternut' and lines derived from Butternut including 'Waltham', and an apparently unrelated source, PI 162889, a Paraguayan land race (6, 7). Cultivars of *C. pepo* have also been reported to show varying levels of resistance to silvering (2, 4, 5). Carle et al. (1) concluded that two to four recessive genes might be involved in silverleaf resistance in *C. pepo*. The objective of our study was to determine the inheritance of resistance to the silverleaf disorder in *C. moschata*.

Materials and Methods: Five F_2 and two backcross (BC) populations were created from crosses between five silverleaf resistant and three silverleaf susceptible lines. Resistant genotypes included 1.) a line derived from selfing PI 162889, 2.) 'Waltham', and lines derived mainly from butternut types: 3.) BN111, 4.) E9706-4-5 and 5.) E9706-3-2. Susceptible genotypes included (1) a line derived from 'Soler', and 2.) TP411 and 3.) TP312, both from the University of Florida. All susceptible lines are tropical pumpkin types. The parental, F1, F2 and BC populations were direct seeded in Isabela, Puerto Rico on 24 April 2001. A drip irrigation system was used. Observations were taken at 5, 6 and 7 weeks after planting following Paris et al. (3). Observations at 6 and 7 weeks generally agreed with those at 5 weeks. Data from week 5 was used in the chi-square analysis. Only individuals with a rating of "0" were classified as non-silvered (resistant).

Results and Discussion: Several previous attempts to study the inheritance of silverleaf in *C. moschata* gave ambiguous results that were partly attributed to variable or low whitefly populations (8 and unpublished data). Carle et al.(1) also attributed variation in expression of silverleaf in *C. pepo* to the level of whitefly infestation. Low or variable populations of whitefly result in distortion of segregation ratios because plants are misclassified as resistant. In this study, whitefly populations were high and uniform. Indicator plants of 'Soler' were planted throughout the field and were uniformly silvered (resistant lines were uniformaly resistant). No counts were taken, but throughout the field leaves with many (sometimes 100 or more) adult whiteflies, as well as nymphs, could be observed. All progeny of F_1 resistant x susceptible populations were susceptible to silverleaf. The intensity of silvering was less in F_1 progeny than in the susceptible parents, suggesting incomplete dominance (data not shown). However, since classification of intensity of silvering is somewhat subjective, we grouped all levels of silvering (1 to 5) in one phenotypic class and only considered a complete dominance model. Both the F_2 and BC data fit this model, with the F_2 segregating 3 silvered to 1 non-silvered and the BC segregating 1:1 (Table 1), suggesting that a single dominant gene controls whitefly-induced silverleaf. We

propose the symbol *Sl* (*Silverleaf*) for the gene that expresses this trait (and *sl* for silverleaf resistance). When selecting for resistance it is essential to have an adequate whitefly population to prevent selection of non-resistant escapes.

Acknowledments. The authors wish to thank Mr. Obed Román Hernández for his technical assistance. This research was supported by the Puerto Rico Agricultural Experiment Station.

Literature cited

1. Carle, R. B., S. Webb y A. Chandler. 1998. Genetic analysis of resistance to whitefly silvering in *Cucurbita pepo* L. In: J.D. McCreight (ed.). Cucurbitaceae '98: Evaluation and enhancement of cucurbit germplasm. Amer. Soc. Hort. Sci., Alexandria, Va.

2. McAuslane, H. J., S. E. Webb y G. W. Elmstrom. 1996. Resistance in germplasm of *Cucurbita pepo* to silverleaf, a disorder associated with *Bemisia argentifolii* (Homoptera: Aleyrodidae). Florida Entomol. 79(2):206-221.

3. Paris, H. S., H. Nerson y Y. Burger. 1987. Leaf silvering of *Cucurbita*. Can. J. Plant Sci. 67:593-598.

4. Paris, H. S., P. J. Stoffella y C. A. Powell. 1993. Sweetpotato whitefly, drought stress, and leaf silvering of squash. HortScience 28(2):157-158.

5. Paris, H. S., P. J. Stoffella y C. A. Powell. 1993. Differential susceptibility to leaf silvering in *Cucurbita pepo*. HortScience 28(6):657-658.

6. Wessel-Beaver, L. 1997. Screening for silverleaf resistance in *Cucurbita* accessions. Cucurbit Genetics Coop. Report. 20:54-56.

7. Wessel-Beaver, L. 1998. Sources of whitefly-induced silvering resistance in *Cucurbita*. En: J.D. McCreight (ed.). Cucurbitaceae '98: Evaluation and enhancement of cucurbit germplasm. Amer. Soc. Hort. Sci., Alexandria, Va.

8. Wessel-Beaver, L. 2000. Inheritance of silverleaf resistance in *Cucurbita moschata*. En: N. Katzir y H. S. Paris (eds.). Proc. Cucurbitaceae 2000. Acta Hort. 510, ISHS 2000.

Control of Sex Expression in Summer Squash (*Cucurbita pepo* L.)

Cheng Yongan, Zhang Bingkui, Zhang Enhui, Zhao Zunlian

Northwest Sci-Tech University of Agriculture and Forestry, Yangling Shaanxi, P.R.China, 712100

Abstract. The sex expression of pumpkin [*Cucurbita pepo* L.] was found to be controlled by foliar sprays with ethephon, GA and $AgNO_3$. Ethephon (2-chloroethyl phosphoric acid) at a concentration of 50 mg/l cause increase of femaleness and inhibition of male flower, while gibberellin at a concentration of 1000 mg/l and $AgNO_3$ at a 200/300 mg/l caused increase of maleness and inhibition of female flowers. The foliar spray stage was at the cotyledon-stage. Different varieties responded similarly in sex expression with ethephon, gibberellin and $AgNO_3$. Ethephon at a concentration of 100 mg/L caused plant injury or death. Gibberellin at a concentration of 1000 mg/l caused excessive growth.

Introduction. The sex expression of summer squash is determined by genetics as well as environment (e.g. photoperiod, temperature etc.). Because of low temperatures and short photoperiods in early spring, the summer squash cultivated in spring usually have more female flowers and fewer male flowers. This affects the regular pollination and fruit setting. In autumn, because of high temperatures and long photoperiods, summer squash usually exhibit more male flowers and fewer female flowers. This will cause decreases of its fruit yield. Many kinds of plant-growth regulator have been used in production of *Cucurbita* crops (Halevy 1963, Galun et al 1965, Iwahor et al 1970). Usually, the utilization of ethephon, GA_3, $AgNO_3$ are very common (Robinson et al 1960, Splittstoesser 1970, George 1971)[1]. Employment of any one of chemicals, or manipulating temperature and/or illumination will cause a change of sex expression in summer squash. However, manipulating temperature and/or illumination is more difficult than applying chemicals. The aim of this research is to determine the effect of certain chemicals on the sex expression of summer squash.

Materials and Methods. The cultivars employed in this experiment were "9805"and "021m". Chemically, pure ethephon, GA_3 and $AgNO_3$ were used for chemical treatments.

Concentrations of GA_3 were 50,100,1000 mg/l, concentrations of $AgNO_3$ was 2000,300 mg/l respectively. Experiments were carried out in a greenhouse at the Vegetable and Flower Institute. Solutions were applied by hand using a small sprayer. The plants employed for this test were sprayed at the cotyledon stage and 4-leaf stage. In each stage, plants were sprayed 3 times with a time interval of 3 days. The control was a distilled water spray. Ten normal plants were selected for each treatment. The treatments were arranged randomly with 3 repetitions. Between-row and between-plant is 70 cm and 50 cm respectively. The cultivating practice is same as that used for commercial production. After plant size reached 20 nodes or more, the number of female and male flowers was counted. The data in all tables is the average of all plants treated, and these data were subjected to variance analysis.

Results and Analysis. *Effect of ethephon on sex expression of C. pepo*. Table 1 shows that the effect of 50mg/L ethephon on sex expression is significant. In comparison with the control, the number of female flower was increased by 69%. The treatment with 100mg/l affects the normal growth and development of the plants. The plants were small, weak and had too many branches; some plants died. These results indicated that the effect of treatment with 100mg/l is not significant on sex expression in *C. pepo,* and is is similar to that of previous reports [1].

Table 1. The effect of ethephon on sex expression of pumpkin [*Cucurbita pepo* L.]

Treatment	Node position of the first female flower	Significant level		Average No. of female flower/plant	Significant level		Average No. of male flower/plant	Significant level	
		5%	1%		5%	1%		5%	1%
CK	7.7	ab	AB	7.1	B	A	12.7	a	A
Ethephon (50mg/L)	5.5	b	B	12.1	A	A	3.7	c	C
Ethephon (100mg/L)	8.3	a	A	6.2	B	A	6.0	b	B

Table 2. The effect of GA_3 and $AgNO_3$ on sex expression of *Cucurbita pepo L.*

Treatment	Node position of the first female flower	Significant level		Average No. of female flower/plant	Significant level	
		5%	1%		5%	1%
GA_3 (100 mg/L)	1.0	a	A	18.7	a	A
$AgNO_3$ (300 mg/L)	1.0	a	A	17.4	a	AB
$AgNO_3$ (200 mg/L)	1.0	a	A	17.3	a	AB
GA_3 (100 mg/L)	1.0	a	A	15.4	b	BC
GA_3 (50 mg/L)	1.0	a	A	15.3	b	BC
CK	1.3	b	b	12.7	c	C

Table 3. The effect of different treating stage on male expression of[*Cucurbita pepo* L.]

Treating stage	The first node position of male flower			Average No. of male flower		
	CK	G 50	Ag 200	CK	G 50	Ag 200
Cotyledon stage	1.3	1.0a	1.0a	12.7	15.3a	17.3a
4-Leaf stage	1.3	1.2a	1.2a	12.7	13.7b	15.1b

Effect GA_3 and $AgNO_3$ on sex expression in C. pepo. Table 2 shows that the effect of GA_3 and $AgNO_3$ on male flower inducement is significant at the 0.01 level. The node position of the first male flower was decreased and the number of male flowers was increased. Different concentrations of GA_3 had different effects on male flower inducement. The number of male flowers with 100 mg/l GA_3 was 18.7, and the number of male flowers with 50 mg/; GA $_3$ was 15.3 or 15.4. The effect of 100 mg/l and 200 mg.l on male flower inducement was similar.

Effect of treatment stage with GA_3 and AgNO on sex expression in C. pepo. By treating with 50mg/l GA_3 and 200 mg/l $AgNO_3$, node position on the first male flower was similar in two treatment stages, but the number of male flowers was different. The number of male flowers treated in cotyledon stage was more than that treated in 4-leaf stage (Table 3). According to previous research[3,4] about floral differentiation in cucumber, at 5 or 6-leaf stage the sex expression of floral bud under 10th node cannot be changed through the chemical regulator. Chemical regulator may change only sex expression of floral buds up to the 10^{th} node. This experiment indicatd that the effect of treating in 4-leaf stage could be seen after the 20^{th} node. This showed that *C. pepo*. was similar to cucumber in floral differentiation. This research also showed that different treatment stages did not affect the node position of the first male flower.

Conclusion and discussion. Previous research results [1,2,3,4,9] showed that the ethephon is effective in controlling expression of female flowers. GA_3 and $AgNO_3$ are effective in controlling expression of male flowers. This test indicated that the ethephon, GA_3 and $AgNO_3$ also have similar effect on the sex expression of *C. pepo*.L. With respect to chemical treatment, starting from the cotyledon stage and spraying twice is recommended. The 50mg/l ethephon treatment was the best concentration in this test.

The GA_3 and $AgNO_3$ have similar effects on sex expression, but their effect on field production is somewhat different. Li Shuxuan [4] believed that, in the range from 50-2000mg/l, the effect of GA_3 was in direct proportion with concentration.
This study found that 1000mg/l GA_3 affected the normal growth and development of *C. pepo* L. The plants that were treated with 200/300 mg/l $AgNO_3$ grew normally. These results agree with previous research [2,3] which reported that the treatment effect of $AgNO_3$ was better than that of GA_3. Therefore, $AgNO_3$ should be selected to use first for male flower inducement.

Literature Cited

1. Li Shuxuan at al. Sex expression and chemical control in cucumber and pepo. Journal of Plant Physiology, 1979.15(1): 83-91.
2. Qu Chengqiang. The utilization of AgNo3 on cucumber. Agricultural Sci-Tech of Gansu .1984, (3): 27-28.
3. Ma Dehua et al. Cucumber Cultivating Techniques. Agricultural Press, Beijing, 1999.
4. Li Shuxuan. Effect of ethephon and GA_3 on sex expression in pepo. Journal of Plant Physiology, 1981, 7(3): 265-271.
5. Wang Yumei. Effect of ethephon on sex differentiation and early Yield. Agricultural Sci-Tech of Inner Mongolia, 1984, (4): 40-41.
6. Wang Qiaomei et al. Effect of chemical regulator and polyamine on sex differentiation in cucumber. Journal of Horticulture, 1997,21(1): 48-52.
7. Wang Qiaomei et al. Study on sex expression in art pumpkin. Chinese Vegetable, 1995, (4): 50-53
8. Ying Zhenshi et al. Effect of ethane, ethephon and CCC on sex differentiation in pepo. Journal of Horticulture, 1987,14(1): 42-47.
9. Ying Zhenshi et al. Relationship among sex expression, endogenous ethene and activity of oxidizing enzyme in cucumber and pepo. Journal of Horticulture, 1990, 17(1): 51-57

Study on Affinity of Sexual Hybridization between *Cucurbita maxima* D. and *Cucurbita moschata* D.

Cheng Yongan, Zhang Bingkui, Zhang Enhui, Zhao Zunlian

Northwest Sci-Tech University of Agriculture and Forestry, Yangling Shaanxi, P.R. China, 71210

Abstract. The 3 inbred lines of *Cucurbita maxima* D. (P1, P6, P7) and 4 inbred lines of *Cucurbita moschata* D. (P2, P3, P4, P5) were used to study crossing affinity. The results showed that there was incompatibility between P6, P7 and P2, P3, P4, P5. There is incompatibility between P1 and P4, P5. P1 and P2, P3 were cross-compatible..

Introduction. The Xi-yang squashes are a fine type among cultivated species of *Cucurbita maxima* D. Because of their good quality and special flavour, the Xi-yang squashes are well liked by Chinese consumers in recent years. Because the Xi-yang squashes originated from a high elevation area of the southern part of Peru and northern Part of Bolivia and Argentina,[1], they are sensitive to diseases of viruses and powdery mildew under high temperatures. So, the production of this kind of vegetable was limited. *C. moschata* originated from the central and southern part of America. Because of long periods of cultivation in China there are a lot of local varieties with tolerance to high temperature and drought, resistance to diseases, and good adaptability in China. But the quality of China squash is poor. In recent years, improving the resistance and adaptability of summer squash by using China squash has been the common aspiration of many Chinese experts. The results of previous studies showed there are some crossing barriers between *C. maxima* and *C. moschata*[2,3,4] . At the same time, different cultivars perform differently[2,5]. The objective of this research was to provide a scientific basis for improving summer squash by using of *C. moschata.*

Materials and Methods. The materials employed in this experiment were: P1 (12-97-55), a selfed-line of a Japanese cultivar of *C. maxima* , P2 (12-97-55), a selfed-line of *C. moschata;* P3 98 1 7 4 , a selfed-line of an Israel cultivar of *C. moschata* P4 (99-7-3), a selfed-line of a Thailand cultivar of *C. moschata* P5 (97-5-7-2), a selfed-line of an America cultivar of *C. moschata;* P6 (97-12-3-1), a selfed-line of a Taiwan cultivar of *C. maxima* and P7 (97-10-4-3), a selfed-line of a Taiwan cultivar of *C. maxima.* The Vegetable and Flower Institute of the Horticultural College of Northwest Sci-Tech University of Agriculture and Forestry provided all of the tested materials. From spring of 1997 to summer of 2001, all experiments were carried out in the experimental field of the Vegetable and Flower Institute. In every combination, 10 normal mother plants were used and 3 repetitions were designed. The second flower of each plant was pollinated. The dates in Table 1 are the average of 3 repetitions. The seed setting situation was observed after 70 days after pollination. The number of surviving plants and other characters were observed in F_1 and F_2 generations.

Results and Analysis. The results of this experiment are presented in Table 1. The crossing affinity between *C. maxima* and *C. moschata* differed with different self-lines. The dates in Table 1 demonstrated that there was no crossing barrier between P1 and P2, P3 and there is incompatibility between P1 and P4, P5. These results illustrate that different lines of *C. moschata* have different affiniies to *C. maxima*. In breeding practice, improving the Xi-yang squashes by using the high affinity selfed line of *C. moschata* may be possible.

Discussion. The number of normal seed per fruit best defined the compatibility between *C. maxima* and *C. moschata* crosses. In this experiment there were no significant differences in fruit set among the different combinations. These results are different from those of Li Bingdong [5] The number of seeds per fruit was almost the same as its mother plant, only the percentage of regular seeds is different. For incompatible crosses, there were only a few regular seed (or even no regular seeds) in a fruit. These results are same as the results of Lin Depei [1] and Li Bingdong [5] et al. For compatible crosses, the number of regular seeds per fruit is almost same as that of its parents and the fertility of F_1 and F_2 generation is normal. Parental characteristics were exhibited in progeny.

Table 1. Interspecies hybridization between *Cucurbita maxima* D. and *C. moschata* D

C. maxima×*C. moschata*	No. of flowers crossed	Percentage of fruit(%)	No. of regular seed/fruit	Survive percentage of F_1 plants
P1 (12-97-55)♂	30	79	356 a	99.0 a
P1 (12-97-55)×P2 (12-97-56)	30	81	347 a	98.0 a
P1 (12-97-55)×P3 (98-1-7-4)	30	77	293 a	96.7 a
P1 (12-97-55)×P4 (99-7-3)	30	73	4 b	25.0 b
P1 (12-97-55)×P5 (97-5-7-2)	30	76	2 b	0 b
P6 (97-12-3-1)♂	30	82	223 a	99 .0a
P6 (97-12-3-1)×P2 (12-97-56)	30	79	0 b	0 b
P6 (97-12-3-1)×P3 (98-1-7-4)	30	76	0 b	0 b
P6 (97-12-3-1)×P4 (99-7-3)	30	82	0 b	0 b
P6 (97-12-3-1)×P5 (97-5-7-2)	30	80	0 b	0 b
P7 (97-12-3-1)♂	30	75	207 a	99.0 a
P7 (97-10-4-3)×P2 (12-97-56)	30	70	0 b	0 b
P7 (97-10-4-3)×P3 (98-1-7-4)	30	73	0 b	0 b
P7 (97-10-4-3)×P4 (99-7-3)	30	71	0 b	0 b
P7 (97-10-4-3)×P5 (97-5-7-2)	30	76	0 b	0 b

Note: Pollination in PM 6-8h every day, picking fruit after pollination - 50 days, collecting seed after picking fruit - days [6,7]. Duncan's test, the same small letter indicated no significance at P=0.05 level.

Literature Cited

1. Lin Depei. 2001. Origin and systematic botany of squash plant. Chinese watermelon and muskmelon,2001(1):36-38
2. Lin Depei. 2000. Inheritance gene and interspecies cross of squash plant. Chinese watermelon and muskmelon, 2000(3):41-44
3. Cheng Yongan et al. Preliminary Study on innovation of squash germplasm. Acta Agriculturae Boreali-occidentalis sinica, 2001,10(1):100-102
4. Chinese Vegetable and Flower Institute. 1987. Cultivation of Vegetable Crops in China. Agricultural Press, Beijing .
5. Squash branch of CSHS. 2001. Paper Collection of symposium. Beijing.
6. Li Bingdong et al. 1996. Biology researches and breeding progress of gourd crops (*Cucurbita* L.). Chinese Vegetable, 1996(6): 48-50.
7. Zhao Fukuan et al. 2000. The genotype and relationship between fruit ripeness and seed germinating within fruit in *Cucurbita moschata*. Beijing Horticulture, 2000(3): 13-14.

Germplasm Innovation by Interspecific Crosses in Pumpkin

Cheng Yongan, Zhang Bingkui, Zhang Enhui, and Zhao Zunlian
Northwest Sci-Tech University of Agriculture and Forestry, Yangling Shaanxi, P.R.China 712100

Abstract. Wide cross compatibility was used to cross four species in *Cucurbita*, and the expression of their botanical traits in the F_1 was studied in 1998-2000. The results showed that the F_1 hybrids among them could be achieved by repeat pollination at the bud and flowering stage. The F_1 plants exhibited heterosis in vegetative growth, disease resistance, and showed a wide variety in botanical traits. There were metaxenia effects on taste of flesh and the color of pumpkin.

Introduction. There is extensive pumpkin cultivation in China, but research about pumpkins is sparse and germplasm for breeding is very limited. Interspecific crosses are an effective way to create new germplasm. The aim of this research was to produce additional pumpkin germplasm for breeding work.

Materials and Method. In this experiment *Cucurbita moschata*, *C. pepo, C. maxima* and *C. argyrosperma* were used for interspecific crosses through artificial pollination. *C. moschata* cultivars used for maternal parent were Huang Niutui, Bate, Dongsheng, America Huangyou, Japanese squash etc. To overcome crossing barriers for interspecific hybridization, the repeat pollination, bud pollination, and mixed pollen pollination methods were used, and the resulting fruit and seed set were determined. The number of surviving plants and the change in characters were investigated in F_1 and BC_1 generations. After the F_1 generation, segregating progenies were selected according to our breeding objectives.

Results and Analysis. Results of this experiment are given in Table 1.

C. moschata x C. pepo. Crossing barriers existed between these two species. The percentage of seed setting is 1%-2%, and the embryo was not developed normally.

C. moschata x *C. maxima,* The percentage of seed set was about 40%-50% and the percentage was different with different cultivars. The highest number of normal seeds per fruit is 197 and the lowest was 13. Almost all seeds were not well filled-out. Seed coat was similar to that of the paternal parent.

C. moschata x C. argyrosperma. The percentage of seed set was about 10%. The highest number of seeds per fruit was 90 normal seeds (using a Russian cultivar). The color of the seed coat was different with different cultivars.

C. moschata x C. moschata. There was no crossing barrier. The size and number of seeds per fruit was different with different cultivars. The percentage of seed set was above 90%.

C. argyrosperma x C. pepo. Percentage of seed setting is about 10%. The seed coat is similar to that of the paternal parent. The color of a few seeds varied.

C. argyrosperma x C. maxima. There was no crossing barrier between them. The percentage of seed set was about 60-70%. The seed plumpness was poor and about 30%-40% of seeds were not perfect. Seed coat varied.

C. argyrosperma x C. moschata D. The percentage of seed set is about 10-25%. Usually there were 60-70 seeds in a fruit.

Discussion. By means of repeat pollination, bud pollination, and mixed pollen pollination, it was possible to obtain interspecific F_1 seed in *Cucurbita*. Heterosis was evident in the progeny, and new germplasm can be obtained through these interspecific crosses. In the test of interspecies cross, different cultivars within a species performed differently. This result is similar to those reported by Lin Depei[3].

Table 1. Result of interspecies hybridization in pumpkin

Combination	No. of flowers crossed	No. of fruit set	No. of normal seeds	No. of survival plants in F_1	Fertility of F_1 backcross
C. moschata x C. pepo	75	11	17	5%	A few seeds
C. moschata x C. maxima	25	4	407	70%	A few seeds
C. moschata x C. argyosperma	25	7	175	Almost 0	A few seeds
C. moschata x C. moschata	100	63	1782	96%	—
C argyosperma x C. pepo	75	9	164	15%	Fertility
C. argyosperma x C. maxima	5	2	231	30%	Fertility
C. argyosperma x C. moschata	25	6	383	56%	—

Lin Depei [3] and an FAO report (1983) reported that *C. moschata* was on a central position in the interspecies relationship of annual pumpkin. Whitaker believed that crossing between pumpkin and true squash is incompatible. Our experiments found that *C. moschata* x *C. maxima* and *C. argyrosperma* x *C. maxima* were cross compatible, similar to the results of Li Bingdong [4]. Thus, it would appear that *C. maxima* may be used as a bridge for interspecies crosses.

Literature Cited

1. Chinese Vegetable and Flower Institute. Cultivation of Vegetable Crops in China. Agricultural Press, Beijing 1987.
2. Lin Depei. Origin and systematic botany of squash plant. Chinese watermelon and muskmelon, 2001(1):36-38.
3. Lin Depei. Inheritance gene and interspecies cross of squash plant. Chinese watermelon and muskmelon, 2000(3):41-44.
4. Li Bingdong et al. Biology researches and breeding progress of gourd crops (*Cucurbita* L.). Chinese Vegetable, 1996 (6): 48-50.
5. Zhao Fukuan et al. The genotype and relationship between fruit ripeness and seed germinating within fruit in *Cucurbita moschata* D. Beijing Horticulture, 2000(3): 13-14.
6. Zhu Peixian et al. Effect of pollinating techniques of F1 seed yields in summer squash. Chinese Vegetable, 1996 (1):31-32.

Aggressiveness Variation in Czech Isolates of *Erysiphe cichoracearum* Pathotype AB1B2CCm

Eva Křístková[1] and Vladimír Vinter[2]

[1]Research Institute of Crop Production Praha, Division of Genetics and Plant Breeding, Department of Gene Bank, Workplace Olomouc, Šlechtitelů 11, 783 71 Olomouc–Holice, and [2]Palacký University, Faculty of Science, Department of Botany, Šlechtitelů 11, 783 71 Olomouc-Holice, Czech Republic

Introduction. *Erysiphe cichoracearum* /*Ec*/ is the predominating powdery mildew species on cucurbits in the Czech Republic (5). Its occurrence and spreading on cucurbits can be influenced not only by virulence, but also by aggressiveness of isolates within natural pathogen populations. Both forms of pathogenicity have an impact on plant cultivation and protection and should be considered in resistance breeding. The purpose of this study was to describe the aggressiveness variation within a group of *Ec* isolates of a known pathotype.

Material and Methods. A total of 27 *Ec* isolates were collected from field cultures of cucurbits (*Cucurbita pepo*, *C. maxima*, *Cucumis sativus*) at different regions of the Czech Republic in 1997-1998. They were maintained *in vitro* on the cotyledons of *Cucumis sativus* cv. Marketer according to Bertrand (2).

The determination of pathotypes followed the methods proposed by Bertrand (2). The set of differential plant genotypes was composed by *Cucumis sativus* cv. Marketer (A), *Cucumis melo* genotypes Védrantais (B1) and PMR 45 (B2), *Cucurbita pepo* cv. Diamant F1 (C), *Cucurbita maxima* cv. Goliáš (Cm) and *Citrullus lanatus* cv. Sugar Baby (D). Seeds of *C. pepo* and *C. lanatus* were provided by Dr. F. Bertrand (France), seed material of *C. melo* genotypes was supplied by Dr. M. Pitrat (France), *C. sativus* and *C. maxima* originated from the Czech germplasm collection (RICP, Gene Bank workplace in Olomouc).

Response of differential genotypes to the *Ec* isolates was evaluated *in vitro* as described by Bertrand (2). Leaf discs 1.5 mm in diameter were cut out from well developed leaves of plants 6-9 weeks old and placed on agar medium in Petri dishes. Each genotype was represented by five discs in at least two replications. Leaf discs were inoculated by dusting with powdery mildew conidia from *C. sativus* cotyledons. Incubation of isolates was performed in a growth chamber with day/night temperatures of 17 ºC/15 ºC and a 12-h photoperiod with a light intensity of 100.9 $\mu mol\ m^{-1}s^{-1}$.

Intensity of mycelium growth and sporulation on each disc was assessed visually 4, 7, 10 and 14 days after inoculation on a scale of 0 (no mycelium growth) to 4 (more than 75% of disc surface covered by mycelium) according to Lebeda (8). On a given genotype, isolates with an average intensity of sporulation 0-1 at the time of last evaluation were classified as avirulent and those with scores 2-4 were considered virulent as proposed by Bardin et al. (1). The pathotype formula of isolate indicates compatible response of differential genotypes.

Within a group of 27 *Ec* isolates pathotypes AC, ACm, ACCm, ACCmD, AB1C, AB1CD, AB2C, AB1B2, AB1B2CCm, AB1B2CCmD, B1B2C and B1B2CCmD were distinguished. As the pathotype AB1B2CCm was represented by 30% of isolates tested, the aggressiveness study was aimed at this group.

The aggressiveness of isolates was derived from their infection development. The average value of infection degree (ID) on each differential genotype was expressed as a % of disc surface covered by mycelium at time of each evaluation. The value of total infection degree (TID-%) was counted from all subsequent evaluations as a percentage of maximum potential score. Data were treated statistically by one-way analyses of variance and LSD multiple range analyses in a programme Statgraphics (3).

Results and Discussion. *Ec* isolates of pathotype AB1B2CCm were collected in five distinct districts of the Czech Republic (Table 1), representing different eco-geographic conditions as summarized

Table 1. Origin and aggressiveness of *Erysiphe cichoracearum* isolates (pathotype AB1B2CCm) on differential genotypes

Isolate number	Host plant	District	TID (%) on differential genotypes A	B1	B2	C	Cm	D	mean TID(I)
6/98	*C. pepo*	Třebíč	31.2	14.6[H]	16.7	52.1	31.2	16.7	29.16 a*
29/97	*C. pepo*	Olomouc	27.5	31.2	33.4	15.0[H]	46.3	0.0	30.42 a
11/97	*C. maxima*	Kolín	41.6	27.1	33.3	36.3	37.5	8.3	35.16 a
70/98	*C. maxima*	Olomouc	27.1	25.0	25.0	79.2	27.1	6.2	36.68 a
44/97	*C. pepo*	Olomouc	93.8	68.8	29.2	11.3[H]	36.3	3.8	47.88 ab
38/97	*C. pepo*	Blansko	65.0	54.2	31.2	38.8	68.8	10.0	51.60 ab
23/97	*C. maxima*	Prostějov	81.3	60.4	50.0	81.3	46.3	0.0	63.86 b
20/97	*C. sativus*	Olomouc	73.8	nd	nd	58.8	67.5	0.0	66.70 b
mean TID (G)			55.16c*	31.26b	40.19bc	46.60bc	44.96bc	5.63a	

differential genotypes:
A *C. sativus* cv. Marketer
B1 *C. melo* Védrantais
B2 *C. melo* PMR 45
C *C. pepo* cv. Diamant F1
Cm *C. maxima* cv. Goliáš
D *C. lanatus* cv. Sugar Baby

mean TID (I) do not include TID (%) on genotype D
* - homogeneous groups (LSD 95%)
nd - aggressiveness (TID) not determined
[H] - heterogeneous response

on the web site http://www.chmi.cz/meteo/ok/. The district of Třebíč, situated on the Bohemian-Moravian Highlands with the average air temperature during vegetative period of 12.6 ºC, is considered to be the coldest one. The average temperature increases in districts of Blansko, Prostějov and Olomouc. The average air temperature during the vegetative period of 15.2 ºC in Olomouc is similar to the situation in Kolín, which is situated in Labe river aluvium in the warm region of Bohemia.

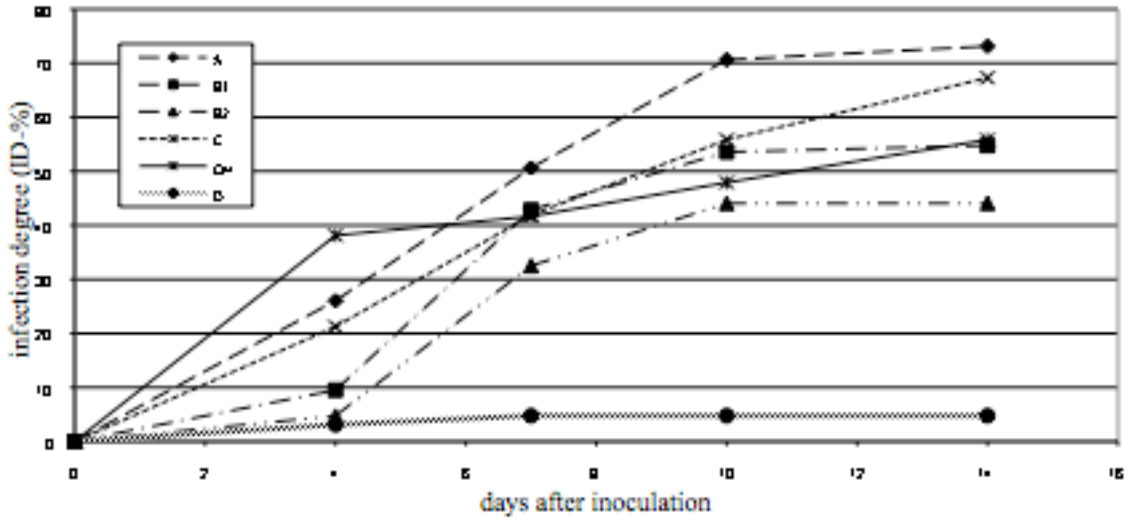
The mean values of total infection degree TID(I) of each *Ec* isolate counted from TID´s on differential genotypes A, B1, B2, C and Cm are considerably variable. The aggressiveness of isolates is not in relation to the original climatic conditions. According to the mean TID(I), isolates from opposite climatic conditions (districts of Třebíč and Kolín) were ranged to the same homogeneous group and on contrary, individual isolates from district of Olomouc expressed different levels of total infection degree (Table 1). Similar phenomenon was reported for some other powdery mildews, e.g. by Suliman et al (11) for *Leveillula taurica* isolates on pepper.

Isolates under study were collected on three different host plant species - cucumber, squash and pumpkin. The number of isolates from each species corresponds to the recent epidemiological observations in the Czech Republic (5). While *C. pepo* and *C. maxima* are common hosts of Erysiphales, the powdery mildew infection occurs on cucumbers only under conditions of high infection pressure. The *Ec* isolate 20/97 was collected on *C. sativus* in a proximity of greenhouse with heavily infected cucurbits.

The mean TID(I) value for *Ec* isolates from *C. pepo* was 39.77, for isolates from *C. maxima* 45.23 and for one isolate from *C. sativus* 66.70. These data have only an informative value. For the explanation of potential role of original host plant species on isolate aggressiveness further studies should include a larger host plant species spectrum.

The aggressiveness of *Ec* isolates on differential genotypes expressed by values TID(G) varied significantly (Table 1). Isolates of the same virulence (pathotype AB1B2CCm) were the most aggressive on the genotype A (*C. sativus*) with the mean value

Figure 1.Infection development of *E. cichoracearum* isolates pathotype AB1B2CCm on pathotype differential genotypes



of TID(G) = 55.16. Interactions with genotypes C (*C. pepo*), Cm (*C. maxima*) and B2 (*C. melo* PMR 45) resulted in medium level of total infection degree. The mean value of TID(G) on *C. melo* Vědrantais (genotype B1) was 31.26 only. A sporadic mycelium growth on *C. lanatus* (genotype D) leaf discs was recorded for five isolates, exhibiting low and/or medium level of their general aggressiveness capacity (TID/I/). These results correspond with data given by Sittterly (10) that within Cucurbitaceae cucumbers, squashes and pumpkins are generally highly susceptible to the powdery mildew infection and watermelons are the most resistant ones. The response of melons (*C. melo*) in genotype depending. The values TID(G) are in positive relation to the frequency of cultivation of each species in the Czech Republic. While cucumbers, squashes and pumpkins are commonly cultivated crops, growing melons and watermelons is very limited.

The infection development of *Ec* isolates on differential genotypes is given by the Figure 1. The infection development on Cm genotype (*C. maxima*) was very fast during first four days after inoculation, during the next ten days the infection progress was comparatively slower and finally the infection degree reached a medium value when compared to the infection development on other genotypes. The trend of infection development on genotypes B1, B2 (*C. melo*), C (*C. pepo*) and A (*C. sativus*) was similar with differences in absolute values of disease infection on each genotype. Within this group the genotype A was the most susceptible one at time of each evaluation and at the final evaluation the infection degree reached the maximum value (Figure 1). No substantial changes in mycelium development on genotypes A, B1, B2 and D between third and fourth evaluations were recorded, but infection degree on genotypes C and Cm increased at that period at ca 10%. Such phenomenon can be influenced by host leaf tissue capacity in providing substrate for pathogen continuous development.

In spite of the above mentioned general characterization of isolates, the infection development of individual isolates on each genotype varied considerably. A heterogeneous response of genotypes B1 and C to three isolates was noticed (Table 1). Isolates 23/97, 38/97 and 44/97 were partly virulent also to the *C. melo* line MR-1 which is considered as resistant to the powdery mildew (7). Their infection degrees on this genotype evaluated on leaf discs *in vitro* reached the values of 16.7, 25.0 and 8.3 at time of the last evaluation (14 days after inoculation) (7). Virulence of *Ec* isolates on *C. lanatus* (genotype D) was already reported by Křístková and Lebeda (6). Virulent isolates originated from the same district (Třebíč) as isolate 6/98 with the highest value of TID on this genotype.

Differences in aggressiveness within individual isolates were not associated with original host plant species and/or region of their collecting. Both temperature and host plant species influence *Ec* conidia size under natural conditions (4). Similarly the relation between temperature and aggressiveness of isolates was described for a group of obligate biotrophs – downy mildews, e.g. by Pietrek and Zinkernagel (9). The effects of original climatic conditions and temperature during *in vitro* cultivation on isolate aggressiveness should be studied in more details.

Ec isolates under study were the most aggressive on cucumber under *in-vitro* conditions, but recently the powdery mildew infection is very rare under field conditions of the Czech Republic. This phenomenon can be explained by occurrence of cucumber downy mildew (*Pseudoperonospora cubensis*) and by competition mechanisms between both groups of pathogens (obligate biotrophs) resulting in elimination of powdery mildew. This situation can contribute to future changes in pathogenicity of *Ec* populations and their geographic distribution.

Acknowledgements. The authors thank Prof. A. Lebeda (Palacký University in Olomouc, Czech Republic) for his support to this work. This research was developed within the framework of the „National Programme of Conservation and Utilization of Genetic Resources of Cultivated Plants“ (Czech Ministry of Agriculture, Praha).

Literature Cited

1. Bardin, M., P. C. Nicot, P. Normand, and J. M. Lemaire. 1997. Virulence variation and DNA polymorphism in *Sphaerotheca fuliginea,* causal agent of powdery mildew of cucurbits. Europ. J. Plant Pathol. **103,** 545-554.
2. Bertrand, F. 1991. Les oïdiums des Cucurbitacées. Thèse Université Paris-Sud-Orsay. Spécialité "Phytopathologie", 225 pp.
3. Koschin, F. (Ed.). 1992. Statgraphics, user´s guide. Grada, Prague, Czech Republic, 349 pp.
4. Křístková, E. 1999. Biology and epidemiology of Erysiphales on *Cucurbita* spp. Doctor thesis, Palacký University in Olomouc, Czech Republic, 224 pp.
5. Křístková, E. and A. Lebeda. 1999. Powdery mildew of cucurbits in the Czech Republic – species, pathotype and race spectra. In. The First International Powdery Mildew Conference, Programme and Abstracts, August 29 – September 2, 1999, Avignon, France, pp. 14-15.
6. Křístková E. and A. Lebeda. 2000. *Citrullus lanatus* – a Potential Host of Powdery Mildew in the Czech Republic. Cucurbit Genetics Cooperative Report, 23:46-48.
7. Křístková E., A. Lebeda and B. Sedláková, 2001. Virulence variation in Czech isolates of cucurbit powdery mildew on *Cucumis melo* genotypes MR-1 and PI 124112 (submitted for press).
8. Lebeda, A. 1986. Cucumber powdery mildew (*Erysiphe cichoracearum, Sphaerotheca fuliginea*). In. Lebeda, A. (Ed.) Methods of testing vegetable crops for resistance to plant pathogens, Sempra, Research Institute of Vegetable Growing and Breeding Olomouc, Czechoslovak Scientific – Technical Society, Olomouc, Czech Republic, pp. 87-91 (in Czech).
9. Pietrek, G. and V. Zinkernagel, 1999. *Pseudoperonospora valerianellae*, the downy mildew of Lamb´s lettuce (*Valerianella locusta*). In. Lebeda, A. and E. Křístková (Eds.) Eucarpia Leafy Vegetables ´99. Palacký University Olomouc, Czech Republic, pp. 205-209.
10. Sitterly, W.R. 1978. Powdery mildews of cucurbits. In. Spencer, D.M. (Ed.) The powdery mildews. Academic Press New York, San Francisco, pp.359-379.
11. Suliman, M.E., M. Bardin, A.M. Daubéze, Z.F. Mohamed and P.C. Nicot. 1999. Aggressiveness of *Leveillula taurica* on pepper. In. The First International Powdery Mildew Conference, Programme and Abstracts, August 29 – September 2, 1999, Avignon, France, pp. 57-58.

Resistance of Cucurbits to the Powdery Mildew, *Sphaerotheca fuliginea* (Schlecht.) Poll.

Qing Ma[1], Hongwen Cui[2], Lei Qiang[1] and Hui Sun[1]
[1]College of Plant Protection, and [2]College of Horticulture, Northwest Sci-tech University of Agriculture and Forestry, Yangling, Shaanxi 712100, China

Introduction. Powdery mildew, caused by *Spharotheca fuliginea* (Schlecht.) Poll., is one of the major diseases affecting field and glasshouse cucurbit production around the world. It mainly attacks cucumber (*Cucumis sativus* L.), summer squash (*Cucurbita pepo* L.), and pumpkin (*Cucurbita moschat*a Duch.), while on watermelon (*Citrullus lanatus* (Thunb) Mansfeld) and balsam pear (*Momordica charantia* L.) it cause less damage. Since the fungus is an obligatory parasite, selecting and planting resistant cultivars is the most fundamental way to control the disease. Although some research has been done on the resistance mechanisms in cucumber[3], the resistance expression differences in various cucurbits and their mechanisms are still unclear. Here the histopathological resistant mechanisms to the fungus are compared and studied in cucumber, summer squash, pumpkin, watermelon, and balsam pear.

Materials and Methods. *Host plants and pathogen inoculation*. The seeds of cucumber (cv. Changcun Thorn), pumpkin, watermelon, and balsam pear were sown in flowerpots of 15 cm in diameter, which were placed in a greenhouse with temperature of 20-25C. The plants were inoculated with *Spharotheca fuliginea* (Schlecht.) Poll. at the four-true-leaf stage. An isolate of the fungus, obtained from naturally infected field-grown cucumber plants, was maintained on a growth chamber-grown susceptible cucumber (cv. Changchun Thorn) whose leaves were shaken 24h before application to dislodge old, nonviable spores. Spores from a detached leaf were tapped onto the surface of the second true leaf.

Sampling and tissue processing for light microscopy. Leaf samples were taken at 12, 24, 48, 72, and 96h after inoculation, made transparent with saturated trichloroacetaldehyde monohydrate, and stained with lactophenol-cotton blue solution. Observations were made by means of Olympus light microscope.

Results and discussion. The infection process of *Spharotheca fuliginea* (Schlecht.) Poll. on leaves of the cucumber can be divided into the followings steps. First, the conidia germinated to produce germ tubes with their distal ends expanding into appressoria, in the middle of which the infecting pegs are formed and penetrate through the host epidermal cell walls and papillae to produce haustoria, absorbing the nutrients of plants. After the formation of primary haustorium, conidium produced another germ tube, which also can form haustoria and developed into hyphae, and then the primary germ tubes continued to grow and branch. The papillae were also deposited between the host cell wall and plasmalemma. The conidium could produce 2 to 6 germ tubes, and generally 3 to 4, all of which can form haustoria and mycelia. Finally, the conidia produced.

The conidia could germinate normally and produce germ tubes on leaves of all cucurbit materials examined, without any significant differences on the germination rate and the frequency of appressorium formation among various genera. Sometimes, however, thin appressoria produced, especially on the watermelon and balsam pear. There were little thin appressoria on the cucumber (cv. Changchun Thorn) and pumpkin, except when inoculated in high density. The thin appressoria rarely could successfully penetrate through epidermal cell to form haustoria and mycelia.

Observed at 24h after inoculation, papillae could be formed in all the cultivars of cucurbits investigated, but no distinct regularity among various genera, suggesting that it is not related with resistance. When the fungus penetrates the host epidermal cells, the papillae were formed under host cell walls. The spherical or semi-spherical papillae were observed on all of the cucurbit materials. The frequency of papilla formation was not associated with resistance, but the frequencies of haustorium formation under papillae on the cucumber cv. Changchun Thorn and

pumpkin were much higher than those on watermelon and balsam pear. The formation of haustoria marks successful penetration, thus the penetration rate differs among different cucurbit materials and hausturium formation rate also differs in the later period of infection.

Resistance was not related with the number of germ tubes at a single infection site, but related with the branch capacity of mycelia. The branches of mycelia in cucumber cultivar Changchun Thorn and pumpkin are greater than those in watermelon and balsam pear, forming larger clone. 96h after inoculation, the lengths of clones on cucumber 'Changchun Thorn', pumpkin, watermelon and balsam pear were 899.67, 813, 371.3 and 236.7μm, respectively, showing the resistance in those cucurbits was increasing in the above order.

The times when the host cell starts to necrotize vary among the different cucurbits. More epidermal cell necrosis occurs at 24h after inoculation in watermelon and at 48h in balsam pear, and a little necrosis occur in cucumber 'Changchun Thorn' and pumpkin in later periods of inoculation.

This study examined the interaction of cucurbits with *Spharotheca fuliginea* (Schlecht.) Poll. by whole leaf transparency, revealing out the histopathological characteristics of cucurbit resistance to powdery mildew and providing some evidence for resistant breeding.

The development process of cucurbit powdery mildew differs somewhat with that of wheat powdery mildew, in which the conidium first produces a primary germ tube, then the primary germ tube stops development, and the conidium produces a secondary germ tube, which develops into mycelium and produces haustorium to penetrate the wheat. Thus the conidium of wheat powdery mildew generally produces mycelium from a single germ tube to form a clone, whereas the cucurbit powdery mildew produces many germ tubes, and all of which can produce haustoria and develop into mycelia.

The function of papillae in resistance to powdery mildews has been studied extensively in other crops[1]. The production of papillae is believed to be the widespread response of host plants to the fungal penetration. It is found in the resistance research on wheat powdery mildew that the frequency of papillae is not related with the resistance level, but related with haustorium formation under papillae. The functions of papillae in resistance might be related with the time, components, and hardness of papilla occurrance[2]. More cytochemical research is needed.

Hypersensitive response is thought to be the most essential resistance reaction in host plants. The hypersensitive response occurs later in balsam pear. Thus whether there exists any other resistance mechanisms in balsam pear needs to be further studied.

Literature cited

1. Koga, H., Bushnell, W.R., and Zeyen R J. 1990. Specificity of cell type and timing of events associated with papilla formation and hypersensitive reaction in leaves of *Hordeum vulgare* attacked by *Erysiphe graminis* f. sp. *hordei*. Can. J. Bot. 68: 2344-2352
2. Ma, Q. and Cui H. 1996. The relationship between papilla formation and resistance of cucumber to *Sphaerotheca fuliginea* (Schlecht.) Poll. Cucurbit Genetics Cooperative Report 19: 30-31
3. Ma, Q., Cui, H., Zang, G., Shi, Y., and Qiu, G. 1996. Histopathology on the cucumber resistant to *Sphaerotheca fuliginea* (Schlecht.) Poll. Acta Agri. Bor.-occid. Sinica. 5(3): 1-4

Developing Bitter Gourd (*Momordica charantia* L.) Populations with a Very High Proportion of Pistillate Flowers

D. Ram, Sanjeet Kumar, M.K. Banerjee, Billu Singh and Sanjay Singh
Indian Institute of Vegetable Research, 1 Gandhinagar (Naria), Post Box # 5002, Varanasi-221 005, India. Email: pdveg@up.nic.in

The occurrence of gynoecism in bitter gourd (*Momordica charantia* L.) is very rare, although a population with high proportion of pistillate flowers has been developed and utilized for hybrid development (1). We identified gynoecious plants of bitter gourd with absolute expression of gynoecism and recently presented the first report on its preliminary characterization (2). This report describes the development of five populations with very high proportions of pistillate flowers from these gynoecious plants.

During the summer season (February sown) of 2000, three gynoecious plants, *viz*., Gy23 Gy63 and Gy263B were obtained in three germplasm populations. In the July 2000, planting, segregation in the F_1 generation for gynoecious and monoecious plants was observed due to the existence of heterozygous gene(s) for gynoecism in the utilized male plants. It was concluded that the gynoecism trait in identified plants was heritable and under the control of certain major recessive gene(s) (2). In a F_1 cross, developed using Gy63 (gynoecious plant obtained in VRBT-63 population) and VRBT-63 (monoecious plant), one monoecious plant (with 87.7% pistillate flowers) was obtained and selfed. The pollen of this monoecious plant was utilized for sib mating to one gynoecious plant (100% pistillate flowers) obtained in the same cross. During the rainy season of 2001, selfed F_2 and full sib (F_2 sib) progenies were raised. Four F_2 and one F_2 sib plants were selected for further advancement. Observations on the number of staminate and pistillate flowers were recorded throughout the F_2 crop (Table 1). Among the four F_2 plants, three plants were gynoecious (100% pistillate flowers) and one plant was monoecious (94.4% pistillate flower) and from the full sib F_2 family one selected plant was gynoecious (Table 1). The pollen from the monoecious plant was used to pollinate the four gynoecious plants creating full sib F3 seeds. The monoecious plant was also selfed creating selfed F3 seed. During summer season of 2002, all the families (one F_3 and four F_3 sibs) were raised and observations with respect to proportion of staminate and pistillate flowers were recorded on five randomly selected plants from each population (Table 1).

Results pertaining to the proportion of pistillate flowers in F_2 and F_3 generations revealed that like five F_2 plants, plants of all the five F_3 populations had very high proportion (> 90%) of pistillate flowers, which ranged from 91.0% in line 333/2 to 99.3% in line 323/4 (Table 1). All F_3 populations were also characterized by the recovery of at least one absolute gynoecious plant (100% pistillate flowers). During the same season, PIBG-1 an improved variety and Pusa Hybrid-1 a promising hybrid, had 11.3% and 13.4% pistillate flowers, respectively. Further, unlike most of the bitter gourd populations, all plants of these five populations were characterized by the emergence of pistillate flowers at lower nodes. The maximum of 70% pistillate flowers has been reported in a bitter gourd line, which was utilized to develop hybrids (1). Hence five F_3 populations developed during this study are not only promising for yielding increased number of fruits, but also for their utilization in the hybrid seed production after further advancement of 2-3 generations through selection of gynoecious plants and sib-pollinating with plants having a very high proportion of pistillate flowers.

Table 1. Proportion of pistillate flowers in five F_2 plants of the cross Gy63 x VRBT-63 and five F_3 populations derived from the respective F_2.

Generation (# of plants)	Lines	Proportion of pistillate flowers (%)				
		333/1	333/2	333/3	333/4	323/4
F_2/F_2 sibs (1)		94.4	100	100	100	100
F_3/F_3 sibs (5)		94.27	91.01	93.0	91.72	99.3
		(86.13-100)	(98.5-100)	(82.03-100)	(95-100)	(98.86-100)

Although we have been able to maintain the absolute gynoecious plants through sib-pollination, the detailed genetic study of gynoecism is in progress in order to determine the most appropriate and predictive method(s) of its maintenance through crossing. Thus, it would be imperative to identify suitable molecular markers associated with the sex habit, so that gynoecious plants can be identified at a very early stage and more efficiently utilized in hybrid seed production. Nevertheless, considering the paramount importance of gynoecious lines in cost effective hybrid seed production, it would also be imperative to develop micro-propagation protocol(s) for its large-scale multiplication and examine its feasibility in hybrid seed production of bitter gourd.

Literature Cited

1. W.B., Zhou, S.B. Luo, J.N. Luo, et al. 1998. An early maturing and high yielding bitter gourd F_1 hybrid Culii No -1. Plant Breeding Abstracts 68: 1002.
2. D. Ram, S. Kumar, M.K. Banerjee, and G. Kalloo. 2002. Occurrence, identification and preliminary characterization of gynoecism in bitter gourd (*Momordica charantia*). Indian J. Agric. Sci. (in press).

A Micropropagation Protocol for *Ecballium elaterium* (L.) A. Rich.

E. Attard[1] and H. Attard[2]
[1]Institute of Agriculture, University of Malta, Msida, MSD 06, Malta, and [2]College of Agriculture, Luqa Road, Qormi, QRM08, Malta

Introduction: Squirting cucumber, *Ecballium elaterium* (L.) A. Rich. (Cucurbitaceae), is a wild medicinal plant found abundantly in the Mediterranean region. It has been utilized as a rootstock for many cucurbitaceous crops, mainly attributed to its resistance to abiotic as well as biotic stress (2). Important pharmacological uses (1, 9) are attributed to the bitter principles, cucurbitacins (5), which make the crop inedible. Micropropagation was aimed at determining the regeneration potential of this resistant rootstock.

Materials and Methods: *E. elaterium* seeds were obtained from immature fruit collected in the Southern region of Malta. The fruit were washed with tap water for 15 min., surface sterilized with 70 % ethanol for 30 sec, soaked in 10 % hypochlorite solution for 20 min and rinsed in three changes of sterile distilled water. Seeds were carefully removed under aseptic conditions, and placed on Murashige and Skoog (MS) basal medium (7). Two weeks from germination, node explants were taken for tissue culture.

The sectioned node explants were inoculated on MS medium containing different plant growth regulators (PGRs) or additives (Table 1), and every 4 weeks the surviving explants were either subcultured on the same medium or transferred to a different medium, in cases of impaired growth. The conditions for growth were 25 ± 1 °C and 3250 ± 250 lx. Bud multiplication, shoot elongation, root production and callus induction and proliferation were observed. The plantlets were transferred to Jiffy® pots (Sigma, U.S.A.) and closed in a Phytatray® (Sigma, U.S.A.) to maintain a high percentage of humidity. With the emergence of roots from the pot, the plantlets were transferred to larger pots until flowering.

The results were analyzed statistically by the one-way analysis of variance (ANOVA) followed by the Bonferroni post-hoc test for equality of means. Only $p \leq 0.05$ were considered statistically significant.

Results and Discussion: *Effects of PGRs on explants*. The effects of the different PGRs or additives on the nodal explants are shown in table 1. The best responses for shoot multiplication were with NAA/BAP combination (Figure 1), followed by Ki ($p<0.05$, $v=10$). BAP responded synergistically with auxins unlike Ki. Nodal explants produced more than 5 shoots within 1 month especially with the NAA/BAP combination. In *Gomphrena* species, the index was three or more shoots per nodal segment after 1 month (8). A low auxin (0.1 mg/l NAA) and a high cytokinin (5 – 10 mg/l BAP) combination were optimum. For *E. elaterium*, decreasing the auxin concentration decreased the bud multiplication effect. As regards shoot elongation, the best and significant response was observed with Ki, BAP and GA_3. In their absence no elongation took place indicating that the plant in culture does not store or produce any endogenous cytokinins. Also cucurbitacins have anti-gibberellic activity (6) hence intrinsic gibberellins that may be possibly present are inhibited by these secondary metabolites. When NAA was completely omitted from the media, shoot elongation was noted in all treated shoot explants. Callus production was seen with all PGRs or additives except for IAA and charcoal. The 2,4-D/Ki combination showed significant effects on callus production with no effects on the other parameters. This goes in accordance with the observations made by Esaka (3) on *Cucurbita pepo* explants. Rooting was a parameter that posed several problems in the regeneration of *Ecballium elaterium* plantlets. In fact, the whole plantlet was not regenerated in tissue culture. Although IAA induced rooting, the low response might be due to the fact that IAA produces a response in the concentration range between 1 and 30 mg/l (4). Nevertheless, if the auxin had a higher activity, callus induction and proliferation might have

Fig. 1. Emergence of multiple shoots from nodal explants treated with the NAA/BAP combination

Fig. 2. Flowering and fruiting of the micropropagated *E. elaterium* plantlets.

Table 1. The overall effects of different media[z] on the different parameters studied.

	Percentage for each Stimulus (%)			
	Multiplication	**Elongation**	**Callus**	**Rooting**
IA/Ki	8.80	16.70[x]	5.76	8.73
NA A/BAP	26.39[x]	7.31	13.89	0.90
KI	23.09[x]	19.27[x]	3.60	6.55
2,4-D/Ki	0.00	0.00	14.39[x]	0.00
IBA	0.00	0.00	14.39[x]	26.19[x]
NA A/BAP (1/2)[y]	14.66	8.56	14.39[x]	0.00
MS	0.00	0.00	14.39[x]	26.19[x]
IAA	0.00	0.00	0.00	3.49
BAP	0.00	19.27[x]	14.39[x]	26.19[x]
Charcoal	16.50[x]	9.63	0.00	0.00
GA_3	10.56	19.27[x]	2.88	5.24

[z] The media contained MS medium and 1 mg/L of each PGR or additive listed: indole acetic acid (IAA), kinetin (Ki), naphthalene acetic acid (NAA), benzylamino purine (BAP), 2,4-dichlorophenoxyacetic acid (2,4-D) indole butyric acid (IBA) and gibberellic acids (GA_3).

[y] NA a?BAP (1/2) contains 0.5 mg/L of BNAA and 1 m g/L of BAP.

[x] p,0.05 (v=10).

The experiment was repeated three time with 15 replicates.

Table 2. Time (days) for rooting and repotting for the four treatments.

	IAA		**GA_3**	
	+R.H.[z]	**-R.H.**	**+R.H.**	**-R.H.**
Rooting in Jiffy® pots	10	23	46	63
Repotting	25	37	58	72

[z] Rooting hormone powder (1% NAA and thiram, Secto,UK).
The experiment was repeated three times with 10 replicates.

set in and hence posing a problem to the rooting process.

Transfer of explants. Based on the above findings, the shoot explant grown on GA_3 and IAA media were selected for pot trials, with the use of a rooting hormone (1 % NAA and thiram, Secto, UK). The best treatment was IAA cultures treated with rooting hormone (Table 2). For the IAA with rooting hormone treatment, flowering took place at approximately day 62 from transfer to Jiffy® pot. This was eventually followed by fruiting (Figure 2).

In conclusion, an ideal protocol would involve the germination of seeds on MS medium followed by the inoculation of node explants on NAA/BAP for three consecutive subcultures at 4-week intervals, elongation on GA_3 medium for another 4 week and an auxin (IAA) shock for 1 week, in tissue culture. Subsequently shoots should be treated with rooting hormone (NAA), transferred to Jiffy pots and after 3 to 4 weeks the plantlets should be repotted and acclimatized for another 4 to 5 weeks. Our results give a clear protocol for the regeneration of the squirting cucumber for possible use as a resistant rootstock for the edible cucurbitaceous crops.

Literature Cited

1. Attard, E., A. Scicluna-Spiteri, M. Grixti and A. Cuschieri. 1996. The cytotoxic activity of Cucurbitacin E and Busulphan on ovarian and stomach cancer cells *in vitro*: A comparative study. Xjenza 1:29–34.
2. Bar-Nun, N., and A.M. Mayer. 1990. Cucurbitacins protect cucumber tissue against infection by *Botrytis cinerea.* Phytochem., 29:787–791.
3. Esaka, M. 1993. *Cucurbita pepo* (Pumpkin): *In vitro* production of ascorbate oxidase. In: Bajaj, Y.P.S., ed. Biotechnology in Agriculture and Forestry: Medicinal and Aromatic Plants IV. Volume 21, Berlin: Springer-Verlag. pp. 115 – 131.
4. Finnie, J.F. and J. Van Staden. 1994. *Gloriosa superba* L. (Flame Lily). Micropropagation and *in vitro* production of colchicines. In: Bajaj, Y.P.S., ed. Biotechnology in Agriculture and Forestry: Medicinal and Aromatic Plants VI. Volume 26, Berlin: Springer-Verlag. pp. 146–166.
5. Lavie, D. and E. Glotter. 1971. The Cucurbitanes; a Group of Tetracyclic Triterpenes; Progress in the Chemistry of Organic Natural Products XXIX; New York; U.S.A. - English Translation, pp. 352-354.
6. Morgan, E.D. and I.D. Wilson. 1999. Insect Hormones and Insect Chemical Ecology. In: Barton, D.; Nakanishi, K., ed. Comprehensive Natural Products Chemistry, Volume 8, UK: Elsevier, pp. 320 – 321.
7. Murashige, T. and F. Skoog. 1962. A revised medium for rapid growth and bioassays with tobacco tissue cultures. Physiol. Plant. 15:473–497.
8. Vieira, C.C.J., H. Mercier, E.P. Chu and R.C.L. Figueiredo-Ribeiro. 1994. *Gomphrena* species (globe amaranth): *In vitro* culture and production of secondary metabolites. In: Bajaj, Y.P.S., ed. Biotechnology in Agriculture and Forestry: Medicinal and Aromatic Plants VII. Volume 28, Berlin: Springer-Verlag. pp. 257–270.
9. Yesilada, E., S. Tanaka, E. Sezik and M. Tabata. 1988. Isolation of an anti-inflammatory principle from the juice of *Ecballium elaterium*. J. Nat. Prod. 51:504–508

Rapid Detection of Cucurbitacins in Tissues and *in vitro* Cultures of *Ecballium elaterium* (L.) A. Rich.

E. Attard
Institute of Agriculture, University of Malta, Msida MSD 06, Malta.
E-mail: everaldo.attard@um.edu.mt

Introduction: Cucurbitacins are highly oxygenated compounds abundantly found in Cucurbitaceous genera such as Citrullus, *Cucumis*, *Cucurbita* and *Luffa* (11). A relatively common cucurbitacin found in Cucurbitaceous species is cucurbitacin E (CuE). Although cucurbitacins exhibit positive effects both pharmacologically (1-3, 6, 14, 17) and in protecting the plants from certain diseases (5), they have a high degree of bitterness even at concentrations lower than 10 ppb (10). With the emergence of new cultivars, the expression of the genes that favor the production of cucurbitacins can be enhanced leading to the production of an inedible cultivar. To determine the efficacy of a method that detects these cucurbitacins in plant tissues we have selected an "indicator plant" that stores an abundance of these compounds. Locally, the squirting cucumber (*Ecballium elaterium*) is also being used as a rootstock in general practice to graft cucurbitaceous crops, owing to the disease resistance of the squirting cucumber to several pests and diseases. The reference cucurbitacin, in this study, was CuE.

Materials and Methods: *Ecballium elaterium* tissue culture material was obtained from a callus stabilized on Murashige and Skoog (13) medium (MS, pH 5.7) containing 5 mg/l naphthalene acetic acid (NAA) and 1 mg/l benzylamino purine (BAP) and from shoot explants grown on 0.1 mg/l NAA and 1 mg/l BAP. Local *Ecballium elaterium* fruit were collected from Marsascala, washed, sliced and the juice strained off. The fresh callus material and fruit juice were dried in an oven at 40 °C for 24 hours. For the cucurbitacin determination, the dried material was ground in a mortar until pulverized completely, homogenized with absolute ETOH (5 ml), reduced to a volume of 2 ml on a water bath and then filtered through a 0.22 µm filter (Schleicher & Shuell, Germany). For CuE, the dried material was extracted by $CHCl_3$ (5 ml) and then mixed with an equal volume of petrol (12). The filtrate was dissolved in absolute ETOH (5 ml), reduce likewise to 2 ml and then filtered through a 0.22 µm membrane pore size.

Standard CuE used to produce the standard curve was provided and authenticated by Prof. D. Lavie (Rehovot, Israel). The solvents used were all HPLC grade obtained from Sigma Co. Ltd. (U.S.A.). The water used for HPLC was passed through a 0.22 µm filter (Schleicher & Shuell, Germany) and degassed.

Chromatographic conditions. HPLC was performed using a Kontron Instruments HPLC system (Herts, U.K.) consisting of two HPLC pumps (Kontron 422), an Autosampler 465 and a Diode Array detector 440. The detection was recorded on a computer via the on line Microsoft Windows program for Kontron Instruments - KromaSystem 2000 Version 1.60. The column was a Bio-Sil C18 HL 90-5S column (Bio-Rad, CA, U.S.A., 250 x 4.6 mm i.d., 5 µm particle diameter, 90 Å pore size). Since the elution was of the gradient type, a mobile phase of acetonitrile:water starting at a ratio of 2:8 and ending with a ratio of 45:55 at 35 minutes. The flow rate was 2.0 ml/min and CuE was detected by UV absorption at 229 nm. Each sample was run in duplicates for 3 independent experiments.

Spectrophotometric conditions. All samples (100 µl, in duplicate), together with various concentrations of CuE standard (0.017 to 1.113 mg/ml), were mixed with 100 µl of a 2 % phosphomolybdic acid (PMA) solution (BDH, U.K.) in absolute ETOH (15) at room temperature, using a 96-well plate (NUNC, Denmark). The absorbance was measured at 492 nm after 5 minutes on a MTP reader (STATFAX 2100, U.S.A.). The results were expressed as percentage weight calculated on dry callus weight. Standard curves were plotted for both analytical methods. For the HPLC, dilutions of standard CuE were prepared in the range of 0.02 and 0.32 mg/ml, while for the spectrophotometric method dilutions ranged from 0.017 to 1.113 mg/ml were used. CuE was quantified

by HPLC by considering the peak area, while for the spectrophotometric method it was quantified by determining the optical density, and both extrapolated on the standard curve. All quantitative determinations were subjected to regression analysis and ANOVA (one-way analysis of variance) using the BMDP/DYNAMIC v. 7.0 (Cork, Ireland) statistical package to determine the significance of the results.

Results and Discussion: The retention time of CuE, when analyzed by HPLC, was 34.01 ± 0.12 min. Figure 1 shows that CuE is distinctively collected from the fruit extract as opposed to the other cucurbitacins and their glycosides. However, the analysis is time-consuming and therefore not suitable for processing large numbers of samples, as previously indicated (8). In the present study, the retention time for CuE goes in accordance with the value obtained (33.92 min) for the same compound extracted from *Cucurbita* species by Halaweish and Tallamy (9). The initial qualitative analysis led to the development of a more rapid but still sensitive technique.

According to Balbaa et al. (4), a triphenyl tetrazolium test gave consistent results in assaying cucurbitacins. Despite this, although there was a positive reaction between the tetrazolium salt and CuE , our results were inconsistent (unpublished). Another method (16) reported for measuring cucurbitacin content in *Hemsleya dolichocarpa* used the dimethylaminobenzaldehyde reagent for a spectrophotometric reaction, as described in the Chinese Pharmacopoeia (7). However, we obtained false positive results by this method in the determination of the cucurbitacin content. In the same research work, phosphomolybdic acid was mentioned as a spraying reagent for a thin-layer chromatography densitometric method, at wavelengths of 510 nm and 600 nm. An ethanol solution was also indicated by Stahl and Jork (15) for triterpene identification as a spraying reagent in TLC analysis.

A spectrophotometric reagent was prepared from a 2 % solution of PMA in absolute ETOH and used in the 96-well plate assay. The reaction between standard CuE and PMA after about 5 minutes was scanned over the 200 to 500 nm range to determine qualitatively the absorbance at different wavelengths (Fig. 2). Eventually 492 nm, one of the preset wavelengths in the ELISA readers, was selected as the test wavelength. The reaction was performed over a period of 10 minutes, measuring the absorbance at 492 nm every minute. The best reaction time was 5 min. The 96-well plate format was selected, as samples can be prepared at µl volumes and tested within a short time period. Two calibration curves were set-up for CuE standard for the HPLC and spectrophotometric assays (Fig. 3). These showed highly significant correlation coefficients (R^2=0.9942 and 0.9994, for PMA and HPLC, respectively, v=4). Fresh fruit and callus samples were extracted with ETOH and then subjected to both methods. The approximate time for the two investigations was 7 min and 11.25 h for the PMA and HPLC, respectively. The values obtained were calculated in mg/ml according to the respective standard curves and then plotted against each other to test for their correlation. In fact, there was a good fit (R^2=0.9869, v=7), between the two assays. Since the PMA assay is suitable for cucurbitacins, additional extraction steps were required to isolate CuE (12) and determine it using the 96-well plate assay.

Surprisingly, for tissue cultures treated with NAA/BAP, the sole cucurbitacin emerging in the crude ethanol extract was CuE (98.41 %). This was compared to the extracted CuE (98.24 %), with a yield of 100 % as detected by HPLC. This new assay has proven to be an alternative procedure to the HPLC procedure, achieving results in a shorter time but still with great consistency. The use of this assay for other plant extracts containing cucurbitacin E should be investigated further.

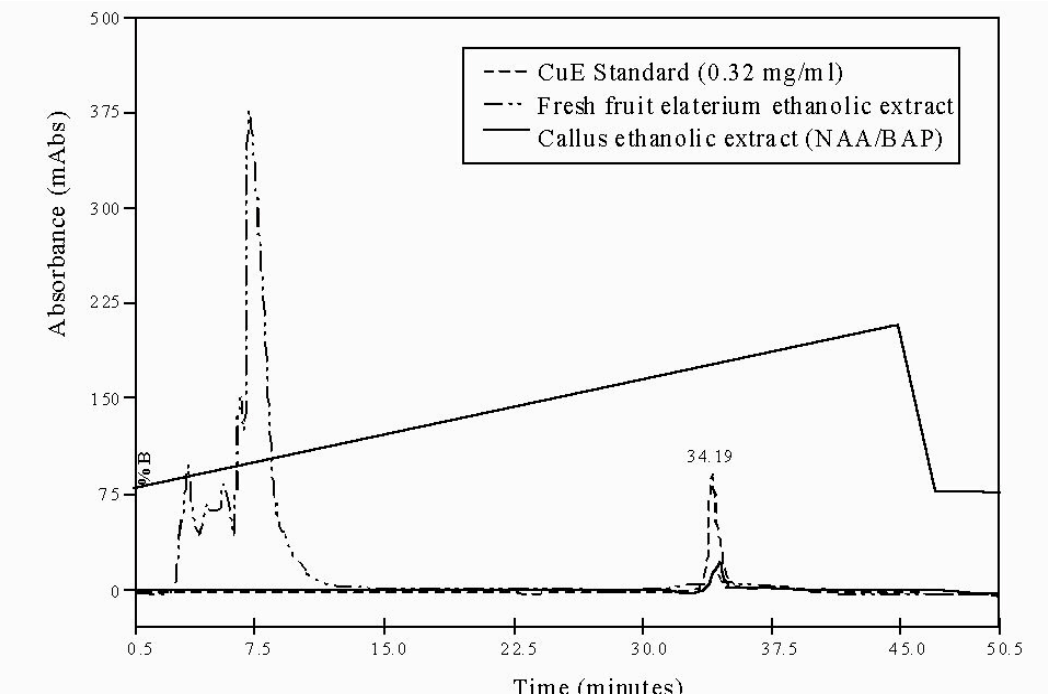


Figure 1: HPLC chromatograms of an authentic sample of Cucurbitacin E (0.32 mg/ml), a fresh fruit elaterium dried ethanolic extract and a callus ethanolic extract (NAA/BAP).

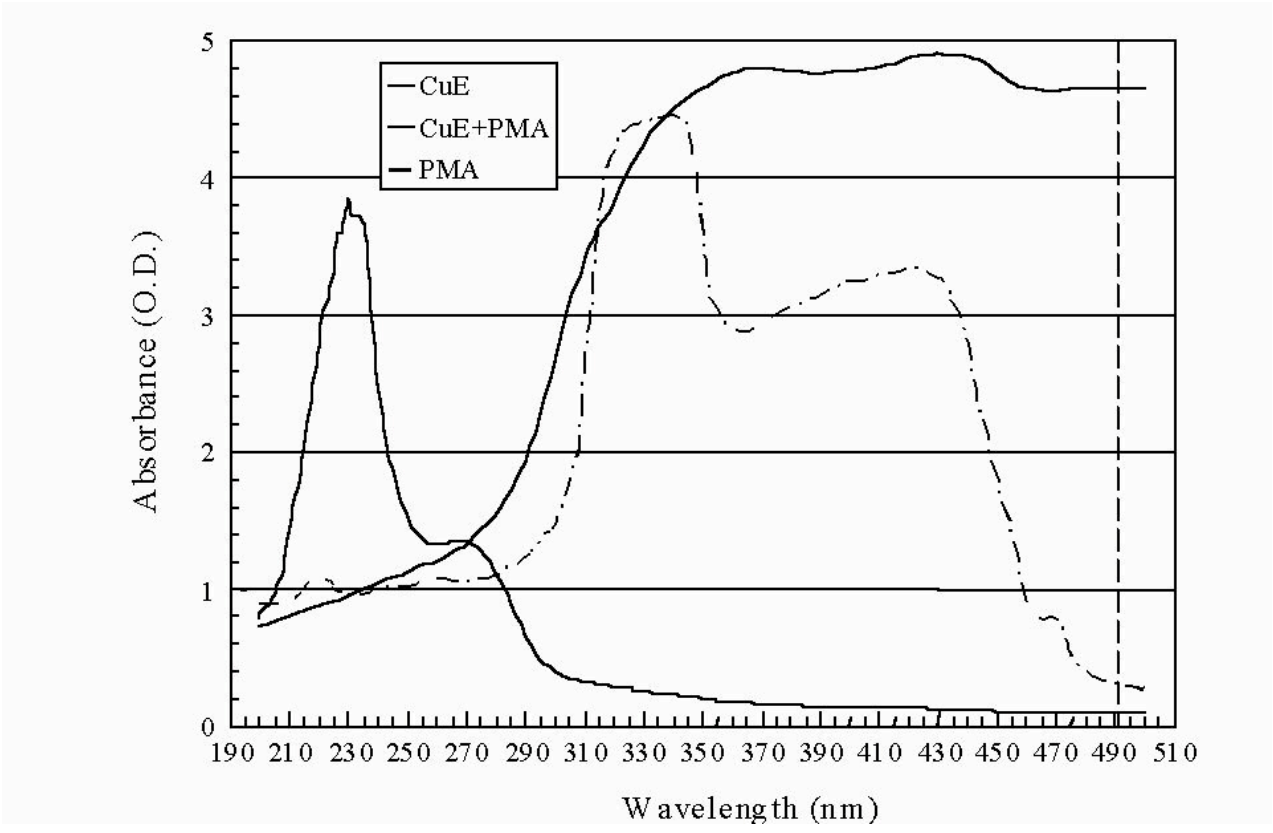


Figure 2: The U.V. profile for Cucurbitacin E, PMA and their reaction after 5 minutes at a waveleingh scan from 200 - 500 nm on a GBC-UV/VIS spectrophotometer.

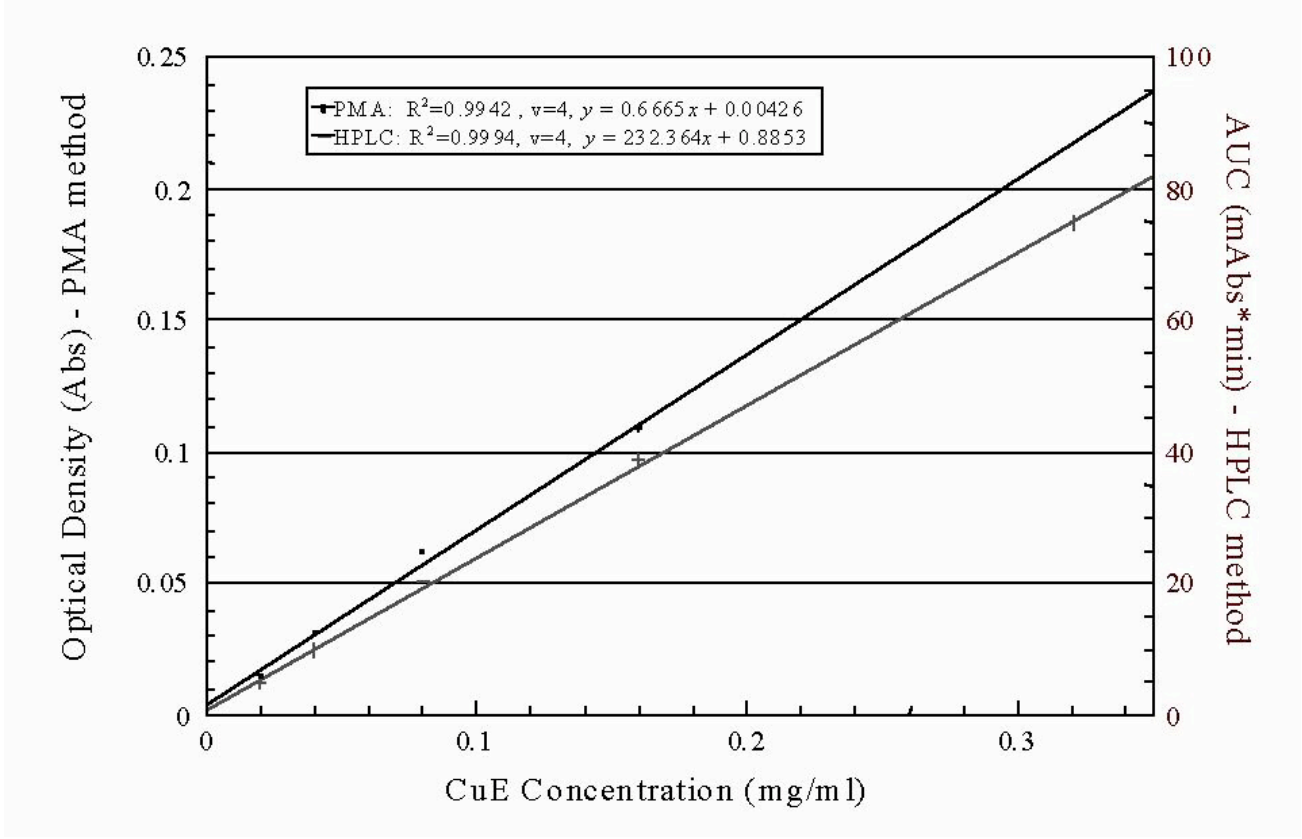


Figure 3: The standard curves for Cucurbitacin E with the CuE/PMA reaction and HPLC treatments.

Literature Cited

1. Arisawa, M., J. M. Pezzuto, A. D. Kinghorn, G. A. Cordell, and N. R. Farnsworth. 1984. Plant anticancer agents. XXX: Cucurbitacins from *Ipomopsis aggregata* (Polemoniaceae). J. Pharm. Sci. 73:411-413.
2. Attard, E., A. Scicluna-Spiteri, M. Brincat, and A. Cuschieri. 1999. The effects of Cucurbitacin E on the proliferation of prostate and breast cancer cell lines, and peripheral T-lymphocytes. Maltese Fourth Med. School Conf. R034:145.
3. Attard, E., A. Scicluna-Spiteri, M. Grixti, and A. Cuschieri. 1996. The cytotoxic Activity of Cucurbitacin E and Busulphan on ovarian and stomach cancer cells *in vitro*: A comparative study. Xjenza 1:29-34.
4. Balbaa, S.I, A.Y. Zaki, and S.M. El-Zalabani. 1978. Qualitative study of the cucurbitacin content in *Ecballium elaterium* (A. Rich) growing In Egypt. Egypt. J. Pharm. Sci. 19:253-259.
5. Bar-Nun, N., and A.M. Mayer. 1990. Cucurbitacins protect cucumber tissue against infection by *Botrytis cinerea.* Phytochem., 29:787–791.
6. Basaran, A., N. Basaran, and K.H. Baser. 1993 . Chromosome aberrations induced by Aflatoxin B_1 in rat bone marrow cells in vivo and their suppression by *Ecballium elaterium.* Fitoterapia LXIV:310-313.
7. Chinese Pharmacopoeia, 1977. Part 1, People's Health Press, Beijing, China, pp. 531 – 534.
8. Gorski, P. M., A. Jaworski, S. Shannon, and R.W. Robinson. 1985. Rapid TLC and HPLC test for cucurbitacins. Cucurbit Genetics Cooperative Report 8:69-70.
9. Halaweish, F.T., and D.W. Tallamy. 1993. Quantitative determination of cucurbitacins by high performance liquid chromatography and high performance thin layer chromatography. J. Liq. Chrom. 16:497-511.
10. Kirschman J.C. and R.L. Suber. 1989. Recent food poisonings from cucurbitacin in traditionally bred squash. Fd. Chem. Toxic., 27:555–556.
11. Lavie, D., and E. Glotter. 1971. The Cucurbitanes; a Group of Tetracyclic Triterpenes; Progress in the Chemistry of Organic Natural Products XXIX; New York; U.S.A. - English Translation; pp. 352-354.
12. Lavie, D., and S. Szinai. 1958. The constituents of *Ecballium elaterium* L. II. α-Elaterin. J. Am. Chem. Soc. 80:707-710.
13. Murashige, T., and F. Skoog. 1962. A revised medium for rapid growth and bioassays with tobacco tissue cultures. Physiol. Plant 15:473-497.
14. Musza, L.L., P. Spreight, S. McElhiney, C.J. Barrow, A.M. Gillum, R. Cooper, and L.M. Killar. 1994. Cucurbitacins, cell adhesion inhibitors from *Conobea scoparioides*. J. Nat. Prod. 57: 1498-1502.
15. Stahl, E., and H. Jork. 1969. Thin Layer Chromatography. 2nd Edition. Springer-Verlag, Germany, p. 887.
16. Yang, P., S., Liu, Z. Cao, W. Chang, and C.T. Che. 1991. Cucurbitacin contents in *Hemsleya dolichocarpa.* Am. J. Chin. Med XIXX:51-56.
17. Yesilada, E, S.Tanaka, E. Sezik, and M. Tabata. 1988. Isolation of an anti-inflammatory principle from the juice of *Ecballium elaterium*. J. Nat. Prod. 51:504-508.

2002 Gene List for Melon

Michel Pitrat
INRA, Station de Génétique et d'Amélioration des Fruits et Légumes, BP 94, 84143 Montfavet cedex (France)

Gene lists of melon have been published previously, the last one in 1998 (109, 17, 18, 93, 95, 96). They included different types of genes: disease and pest resistance genes, isozymes, leaf, stem, flower, fruit and seed characters.. The 2002 list includes a total number of 162 loci, QTLs for Cucumber Mosaic Virus resistance, ethylene production during fruit maturation and ovary and fruit shape, and one cytoplasmic mutant (*cyt-Yt*) (Table 1).

Genes have also been cloned in melon (mRNA or complete gene with eventually intron…). Only genes with complete sequences are listed in Table 2. Most of them are related to fruit maturation. About 50 partial clones, for instance Resistance Gene Homologues, are also available in databases.

Genetic maps using different types of molecular markers have been published (4, 12, 25, 26, 86, 92, 122). Linkages between isozymes (114) and between phenotypic mutants (94) have also been reported. These maps have been constructed using different melon genotypes as parents and some markers cannot be transferred easily from one map to another or are not polymorphic between all the parents (Table 3). There is not yet a reference saturated map of melon. Moreover very few phenotypic traits have been mapped.

Allelism tests have often not been performed, inflating the number of described genes. This is particularly clear for *Powdery mildew resistance* but also for many other traits. This could be because accessions previously described with this trait are not (or no more) available. It is strongly recommended to send seed samples along with reports of new genes to the melon gene curators. They should consult the lists and the rules of gene nomenclature for the *Cucurbitaceae* (110, 17) before proposing a gene name and symbol.

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

Gene symbol		Character	LG[z]	References
Prefered	Synonym			
a	***M***	***andromonoecious*. Mostly staminate, fewer perfect flowers; on *A*_ plants, pistillate flowers have no stamens; epistatic to *g*.**	**4, II**	**103, 111, 121**
ab	-	*abrachiate*. Lacking lateral branches. Interacts with *a* and *g* (*e.g. ab ab a a G*_ plants produce only staminate flowers).		39
Ac	**-**	***Alternaria cucumerina* resistance (in MR-1).**		**116**
Aco-1	***Ac***	***Aconitase-1*. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224769.**	**A**	**114**
Acp-1	*APS-11, Ap-1*[1]	*Acid phosphatase-1*. Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has two bands.		36

Acp-2	***Acp-1***	***Acid phosphatase-2*. Isozyme variant with two alleles, each regulating one band, in PI 194057, PI 224786. Relationship with *Acp-1* is unknown.**		**114**
Acp-4	**-**	***Acid phosphatase-4*. Isozyme variant with two alleles, each regulating one band, in PI 183256, PI 224786. Relationship with *Acp-1* unknown, different from *Acp-2*.**		**114**
Af	-	*Aulacophora foveicollis* resistance. Resistance to the red pumpkin beetle.		119
Ag	**-**	***Aphis gossypii* tolerance. Freedom of leaf curling following aphid infestation (in PI 414723).**		**11**
Ak-4	**-**	***Adenylate kinase*. Isozyme variant with two alleles, each regulating one band, in PI 169334.**		**114**
Ala	-	*Acute leaf apex*. Dominant over obtuse apex, linked with *Lobed* leaf. (*Ala* in Maine Rock, *ala* in PV Green).		43
alb	**-**	***albino*. White cotyledons, lethal mutant (in Trystorp).**		**5**
Al-1	Al_1	*Abscission layer-1*. One of two dominant genes for abscission layer formation. See *Al-2*. (*Al-1 Al-2* in C68, *al-1 al-2* in Pearl).		115
Al-2	A_{l2}	*Abscission layer-2*. One of two dominant genes for abscission layer formation. See *Al-1*.		115
Al-3		***Abscission layer-3*. One dominant gene for abscission layer formation (in PI 161375). Relationship with *Al-1* or *Al-2* is unknown.**	**VIII**	**91**
Al-4		***Abscission layer-4*. One dominant gene for abscission layer formation (in PI 161375). Relationship with *Al-1* or *Al-2* is unknown.**	**IX**	**91**
bd	-	*Brittle dwarf*. Rosette growth with thick leaf. Male fertile, female sterile (in TAM-Perlita45).		20
Bi	**-**	***Bitter*. Bitter seedling (common in honeydew or in Charentais type while most American cantaloupes are *bi*).**		**69**
Bif-1	*Bif*	*Bitter fruit-1*. Bitterness of tender fruit in wild melon. Relations with *Bi* are unknown.		88
Bif-2	-	*Bitter fruit-2*. One of two complementary independent genes for bitter taste in young fruit: *Bif-2_ Bif-3_* are bitter. (Relationships with *Bi* and *Bif-1* are unknown).		73
Bif-3	-	*Bitter fruit-3*. One of two complementary independent genes for bitter taste in young fruit: *Bif-2_ Bif-3_* are bitter. (Relationships with *Bi* and *Bif-1* are unknown).		73
cab-1	**-**	***cucurbit aphid borne* yellows virus resistance-*1*. One of two complementary independent genes for resistance to this polerovirus: *cab-1 cab-1 cab-2 cab-2* plants are resistant. (in PI 124112).**		**29**

cab-2	**-**	***cucurbit aphid borne* yellows virus resistance-*2*. One of two complementary independent genes for resistance to this polerovirus: *cab-1 cab-1 cab-2 cab-2* plants are resistant. (in PI 124112).**		**29**
cb	*cb*$_1$	*cucumber beetle* resistance. Interacts with *Bi*, the nonbitter *bi bi cb cb* being the more resistant (in C922-174-B).		84
cf	**-**	***cochleare folium*. Spoon-shaped leaf with upward curling of the leaf margins (spontaneous mutant in Galia).**		**68**
cl	-	*curled leaf*. Elongated leaves that curl upward and inward. Usually male and female sterile.		20
Cys	-	*Cucurbit Yellow Stunting* Disorder virus resistance. One dominant gene for resistance to this crinivirus in TGR-1551.		70
dc-1	-	*Dacus cucurbitae-1* resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See *dc-2*.		112
dc-2	-	*Dacus cucurbitae-2* resistance. One of two complementary recessive genes for resistance to the melon fruitfly. See *dc-1*.		112
dl	**-**	***dissected leaf* (in URSS 4). Highly indented leaves.**	**10**	**31**
***dl*^{v}**	***cl***	***dissected leaf Velich*. First described as *cut leaf* in Cantaloup de Bellegarde. Allelic to *dl*.**	**10**	**120**
dl-2	-	*dissected leaf-2*. First described as «hojas hendidas».		35
dlet	*dl*	*delayed lethal*. Reduced growth, necrotic lesions on leaves and premature death.		129
Ec	**-**	***Empty cavity*. Carpels are separated at fruit maturity leaving a cavity. *Ec* in PI 414723, *ec* in Védrantais.**	**III**	**90**
ech	**-**	***exaggerated curvature of the hook*. Triple response of seedlings germinating in darkness in presence of ethylene. *ech* in PI 161375, *Ech* in Védrantais.**	**I**	**91**
f	**-**	***flava*. Chlorophyl deficient mutant. Growth rate reduced (in K 2005).**	**8**	**100**
fas	**-**	***fasciated* stem (in Vilmorin 104).**		**40**
Fdp-1	**-**	***Fructose diphosphate-1*. Isozyme variant with two alleles, each regulating one band, in PI 218071, PI 224688.**		**114**
Fdp-2	**-**	***Fructose diphosphate-2*. Isozyme variant with two alleles, each regulating one band, in PI 204691, PI 183256.**		**114**
fe	**-**	***fe* (iron) inefficient mutant. Chlorotic leaves with green veins. Turns green when adding iron in the nutrient solution.**		**83**
Fn	**-**	***Flaccida necrosis*. Semi-dominant gene for wilting and necrosis with F pathotype of Zucchini Yellow Mosaic Virus (*Fn* in Doublon, *fn* in Védrantais).**	**2, V**	**108**

Fom-1	***Fom*$_1$**	***Fusarium oxysporum melonis* resistance. Resistance to races 0 and 2 and susceptibility to races 1 and 1,2 of Fusarium wilt (*Fom-1* in Doublon, *fom-1* in Charentais T).**	**5, IX**	**107**
Fom-2	***Fom*$_{1,2}$**	***Fusarium oxysporum melonis* resistance. Resistance to races 0 and 1 and susceptibility to races 2 and 1,2 of Fusarium wilt. (*Fom-2* in CM 17187, *fom-2* in CharentaisT).**	**6, XI**	**107**
Fom-3	**-**	***Fusarium oxysporum melonis* resistance. Same phenotype as *Fom-1* but segregates independently from *Fom-1*. (*Fom-3* in Perlita FR, *fom-3* in CharentaisT).**		**130**
G	**-**	***gynomonoecious*. Mostly pistillate, fewer perfect flowers. Epistatic to *a a A_ G_* monoecious; *A_ g g* gynoecious; *a a G_* andromonoecious; *a a g g* hermaphrodite.**		**103**
gf	**-**	***green flesh* color. Recessive to salmon. (*gf* in honeydew, *Gf* in Smiths' Perfect cantaloupe).**	**IX**	**51**
gl	**-**	***glabrous*. Trichomes lacking (in Arizona glA).**	**3**	**38**
gp	-	*green petals*. Corolla leaf like in color and venation.		79
Gpi	**-**	***Glucosephosphate isomerase*. Isozyme variant with two alleles, each regulating one band, in PI 179680.**		**114**
Gs	-	*Gelatinous sheath* around the seeds. Dominant to absence of gelatinous sheath.		41
gyc	**-**	***greenish yellow corolla*.**		**128**
gy	***n, M***	**gynoecious. Interacts with *a* and *g* to produce stable gynoecious plants (*A_ g g gy gy*) (in WI 998).**		**60, 62**
h	**-**	***halo* cotyledons. Yellow halo on the cotyledons, later turning green.**	**4, II**	**82**
Idh	**-**	***Isocitrate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 224688.**	**A**	**114**
Imy	-	*Interveinal mottling and yellowing* resistance. Resistance to a complex of viruses in PI 378062.		49
jf	-	*juicy flesh*. Segregates discretely in a monogenic ratio in segregating generations.		13
L	-	*Lobed* leaf. Dominant on non lobed, linked with *Acute leaf apex*. (*L* in Maine Rock, *l* in P.V. Green).		43
lmi	**-**	***long mainstem internode*. Affects internode length of the main stem but not of the lateral ones (in 48764).**	**8**	**74**
Liy	**-**	***Lettuce infectious yellows* virus resistance. One dominant gene for resistance to this crinivirus in PI 313970.**		**75**

Lt	**-**	***Liriomyza trifolii* (leafminer) resistance (in Nantais Oblong).**		**28**
M-Pc-5	-	*Modifier of Pc-5*. Gene *Pc-5* for downy mildew resistance (see *Pc-5*) is dominant in presence of *M-Pc-5*, recessive in the absence of *M-Pc-5*.		2
Mc	**-**	***Mycosphaerella citrullina* resistance. High degree of resistance to gummy stem blight (in PI 140471).**		**104**
Mc-2	Mc^i	*Mycosphaerella citrullina* resistance-2. Moderate degree of resistance to gummy stem blight (in C-1 and C-8.)		104
Mc-3	-	*Mycosphaerella citrullina* resistance-3. High level of resistance to gummy stem blight in PI 157082, independent from *Mc*.		131
Mc-4	-	*Mycosphaerella citrullina* resistance-4. High level of resistance to gummy stem blight in PI 511890. Relationships with *Mc* and *Mc-3* unknown.		131
Mca	-	*Macrocalyx*. Large, leaf like structure of the sepals in staminate and hermaphrodite flowers (*Mca* in makuwa, *mca* in Annamalai).		42
Mdh-2	**-**	***Malate dehydrogenase-2*. Isozyme variant with two alleles, each regulating one band, in PI 224688, PI 224769.**	**B**	**114**
Mdh-4	**-**	***Malate dehydrogenase-4*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923.**	**B**	**114**
Mdh-5	**-**	***Malate dehydrogenase-5*. Isozyme variant with two alleles, each regulating one band, in PI 179923, PI 180283.**	**B**	**114**
Mdh-6	**-**	***Malate dehydrogenase-6*. Isozyme variant with two alleles, each regulating one band, in P 179923, PI 180283.**	**B**	**114**
Me	-	*Mealy* flesh texture. Dominant to crisp flesh. (*Me* in *C. callosus*, *me* in makuwa).		41
Me-2	**-**	***Mealy* flesh texture-2 (in PI 414723).**		**90**
Mpi-1	**-**	***Mannosephosphate isomerase-1*. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.**	**A**	**114**
Mpi-2	**-**	***Mannosephosphate isomerase-2*. Isozyme variant with two alleles, each regulating one band, in PI 183257, PI 204691.**	**A**	**114**
ms-1	ms^1	***male sterile-1*. Indehiscent anthers with empty pollen walls in tetrad stage.**	**3**	**8**
ms-2	ms^2	***male sterile-2*. Anthers indehiscent, containing mostly empty pollen walls, growth rate reduced.**	**6, XI**	**10**
ms-3	***ms-L***	***male sterile-3*. Waxy and translucent indehiscent anthers, containing two types of empty pollen sacs.**	**12**	**77**
ms-4	**-**	***male sterile-4*. Small indehiscent anthers. First male flowers abort at bud stage (in Bulgaria 7).**	**9**	**71**

ms-5	**-**	***male sterile-5*. Small indehiscent anthers. Empty pollen (in Jivaro, Fox).**	**13**	**67**
Mt	-	*Mottled* rind pattern. Dominant to uniform color. Epistatic with *Y* (not expressed in *Y_*) and *st* (*Mt_ st st* and *Mt_ St_* mottled; *mt mt st st* striped, *mt mt St_* uniform). (*Mt* in Annamalai, *mt* in makuwa).		41
Mt-2	**-**	***Mottled* rind pattern (in PI 161375). Relationship with *Mt* unknown.**	**II**	**90**
Mu	-	*Musky* flavour (olfactory). Dominant on mild flavor (*Mu* in *C. melo callosus*, *mu* in makuwa or Annamalai).		41
Mvd	-	*Melon vine decline* resistance. Semi-dominant gene for partial resistance to *Acremonium cucurbitacearum* and *Monosporascus cannonballus* (in Pat 81 *agrestis* melon).		52
My	-	*Melon yellows* virus resistance. Semi-dominant gene, in Nagata Kin Makuwa, for partial resistance to this crinivirus.		37, 81
n	**-**	***nectarless*. Nectaries lacking in all flowers (in 40099).**		**6**
Nm	**-**	***Necrosis* with *Morocco* strains of Watermelon Mosaic Virus, a potyvirus (*Nm* in Védrantais, *nm* in Ouzbèque).**		**105**
nsv	**-**	**Melon *necrotic spot virus* resistance. One recessive gene for resistance tothis carmovirus in Gulfstream, Planters Jumbo.**	**7, XII**	**19**
O	**-**	***Oval* fruit shape. Dominant to round; associated with *a*.**		**121**
Org-1	-	*Organogenic* response for *in vitro* shoot regeneration. Partially dominant. Interacts with an additive model with *Org-2*.		80
Org-2	-	*Organogenic* response for *in vitro* shoot regeneration. Partially dominant. Interacts with an additive model with *Org-1*.		80
p	**-**	***pentamerous*. Five carpels and stamens; recessive to trimerous (in Casaba).**	**XII**	**111**
Pa	**-**	***Pale* green foliage. *Pa Pa* plants are white (lethal); *Pa pa* are yellow (in 30567).**	**3**	**76**
Pc-1	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See *Pc-2*.**		**16, 117**
Pc-2	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary incompletely dominant genes for downy mildew resistance (in PI 124111). See *Pc-1*.**		**16, 117**
Pc-3	**-**	***Pseudoperonospora cubensis* resistance. Partial resistance to downy mildew (in PI 414723).**		**33**
Pc-4	**-**	***Pseudoperonospora cubensis* resistance. One of two complementary genes for downy mildew resistance in PI 124112. Interacts with *Pc-1* or *Pc-2*.**		**63**

Pc-5	-	*Pseudoperonospora cubensis* resistance. One gene in Line 5-4-2-1 which interacts with *M-Pc-5* in the susceptible line K15-6 (*Pc-5* is dominant in presence of *M-Pc-5*, recessive in the absence of *M-Pc-5*).		2
Pep-gl	**-**	***Peptidase with glycyl-leucine*. Isozyme variant with two alleles, each regulating one band, in PI 218070.**	**B**	**114**
Pep-la	**-**	***Peptidase with leucyl-alanine*. Isozyme variant with two alleles, each regulating one band, in PI 183256.**		**114**
Pep-pap	**-**	***Peptidase with phenylalanyl-proline*. Isozyme variant with two alleles, each regulating one band, in PI 183256.**		**114**
Pgd-1	*6-PGDH-2*[1] *Pgd-2*[1]	*Phosphoglucodehydrogenase-1*. Isozyme variant with two alleles, each regulating one band.The heterozygote has one intermediate band.		36
6-Pgd-2	**-**	***6-Phosphogluconate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 161375, Védrantais. Relationship with *Pgd-1* is unknown.**	**IX**	**4**
Pgd-3	***Pgd***	***6-Phosphogluconate dehydrogenase*. Isozyme variant with two alleles, each regulating one band, in PI 218070. Relationship with *Pgd-1* and *6-Pgd-2* is unknown.**	**A**	**114**
Pgi-1	*PGI-1*[1]	*Phosphoglucoisomerase-1*. Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		36
Pgi-2	*PGI-2*[1]	*Phosphoglucoisomerase-2*. Isozyme variant with two alleles, each regulating two bands. The heterozygote has three bands.		36
Pgm-1	*PGM-2*[1] *Pgm-2*[1]	*Phosphoglucomutase-1*. Isozyme variant with two alleles, each regulating two bands. The heterozygotes has three bands.		36
Pgm-2	***Pgm***	***Phosphoglucomutase*. Isozyme variant with two alleles, each regulating one band, in PI 218070, PI 179923. Relationship with *Pgm-1* is unknown.**	**A**	**114**
pH	**-**	***pH*(acidity) of the mature fruit flesh.Low pH value in PI 14723 dominant to high pH value in Dulce**	**VIII**	**25**
pin	**-**	***pine-seed* shape (in PI 161375).**	**III**	**92**
Pm-1	***Pm*[1] *Pm-A ?***	***Powdery mildew* resistance-1. Resistance to race 1 of *Sphaerotheca fuliginea* (in PMR 45).**		**55**
Pm-2	***Pm*[2] *Pm-C ?***	***Powdery mildew* resistance-2. Interacts with *Pm-1*. Resistance to race 2 of *Sphaerotheca fuliginea* (in PMR 5 with *Pm-1*).**		**9**
Pm-3	***Pm*[3]**	***Powdery mildew* resistance-3. Resistance to race 1 of *Sphaerotheca fuliginea* (in PI 124111).**	**7**	**47, 48**
Pm-4	***Pm*[4]**	***Powdery mildew* resistance-4. Resistance to *Sphaerotheca fuliginea* (in PI 124112).**		**47, 48**
Pm-5	***Pm*[5]**	***Powdery mildew* resistance-5. Resistance to *Sphaerotheca fuliginea* (in PI 124112).**		**47, 48**

Pm-6	**-**	***Powdery mildew* resistance-6. Resistance to *Sphaerotheca fuliginea* race 2 (in PI 124111).**		**61**
Pm-7	**-**	***Powdery mildew* resistance-7. Resistance to *Sphaerotheca fuliginea* race 1 (in PI 414723).**		**1**
Pm-E	**-**	***Powdery mildew* resistance-E. Interacts with *Pm-C* in PMR5 for *Erysiphe cichoracearum* resistance.**		**34**
Pm-F	**-**	***Powdery mildew* resistance-F. Interacts with *Pm-G* in PI 124112 for *Erysiphe cichoracearum* resistance.**		**34**
Pm-G	**-**	***Powdery mildew* resistance-G. Interacts with *Pm-F* in PI 124112 for *Erysiphe cichoracearum* resistance.**		**34**
Pm-H	**-**	***Powdery mildew* resistance-H. Resistance to *Erysiphe cichoracearum* and susceptibility to *Sphaerotheca fuliginea* (in Nantais oblong).**		**34**
Pm-w	***Pm-B ?***	***Powdery mildew* resistance in WMR 29. Resistance to *Sphaerotheca fuliginea race 2.***	**2, V**	**94**
Pm-x	**-**	***Powdery mildew* resistance in PI 414723. Resistance to *Sphaerotheca fuliginea.***	**4, II**	**94**
Pm-y	**-**	***Powdery mildew* resistance in VA 435. Resistance to *Sphaerotheca fuliginea***	**7, XII**	**94**
***Prv*^{1}**	***Wmv***	***Papaya Ringspot virus* resistance. Resistance to W strain of this potyvirus (formerly Watermelon Mosaic Virus 1) (in B 66-5, WMR 29, derived from PI 180280). Dominant to *Prv*^{2}.**	**5, IX**	**98, 123**
***Prv*^{2}**	**-**	***Papaya Ringspot virus* resistance. Allele at the same locus as *Prv*^{1} but different reaction with some strains of the virus (in 72-025 derived from PI 180283). Recessive to *Prv*^{1}.**	**5, IX**	**57, 98**
Prv-2	**-**	***Papaya Ringspot virus* resistance-2 (in PI 124112). Relationship with *Prv* is unknown.**		**78**
Px-1	*PRX-11*	*Peroxidase-1*. Isozyme variant with two codominant alleles, each regulating a cluster of four adjacent bands. The heterozygote has five bands.		36
Px-2	*Px*$_{2A}$ *Prx2*	*Peroxidase-2*. Isozyme variant with two codominant alleles, each regulating a cluster of three adjacent bands. The heterozygote has 4 bands.		14, 22
r	**-**	***red* stem. Red pigment under epidermis of stems, especially at nodes; tan seed color (in PI 157083).**	**3**	**7, 76**
ri	-	*ridge*. Ridged fruit surface, recessive to ridgeless. (*ri* in C68, *Ri* in Pearl).		115
s	-	*sutures*. Presence of vein tracts on the fruit (« sutures »); recessive to ribless.		3
s-2	**-**	***sutures-2* on the fruit rind (in PI 161375). Relationship with *s* is unknown.**	**XI**	**90**
Sfl	*S*	*Subtended floral leaf*. The floral leaf bearing the hermaphrodite flowers is sessile, small and encloses the flower. (*Sfl* in makuwa, *sfl* in Annamalai).		42

si-1	***b***	***short internode-1*. Extremely compact plant habit (bush type) (in UC Topmark bush).**	**1**	**27**
si-2	**-**	***short internode-2*. Short internodes from 'birdnest' melon (in Persia 202).**		**87**
si-3	**-**	***short internode-3*. Short internodes in Maindwarf.**		**64**
Skdh-1	-	*Shikimate dehydrogenase-1*. Isozyme variant with two codominant alleles, each regulating one band. The heterozygote has three bands.		14, 44
slb	*sb*	*short lateral branching*. Reduction of the elongation of the lateral branches, in LB.		85
So	-	*Sour* taste. Dominant to sweet.		65
So-2	**-**	***Sour* taste-2 (in PI 414723). Relationship with *So* is unknown.**		**90**
sp	-	*spherical* fruit shape. Recessive to obtuse; dominance incomplete.		3, 72
spk	**-**	***speckled* fruit epidermis (*spk* in PI 161375 or PI 414723, *Spk* in Védrantais).**	**VII**	**92**
st	-	*striped* epicarp. Recessive to non-striped.		46
st-2	***st***	***striped epicarp-2*. Present in Dulce, recessive to non-striped in PI 414723. Relationship with *st* is unknown.**	**XI**	**25**
v	**-**	***virescent*. Pale cream cotyledons and hypocotyls; yellow green foliage (mainly young leaves).**	**11**	**50**
v-2	**-**	***virescent-2*.**		**32**
v-3	**-**	***virescent-3*. White cotyledons which turn green, light green young leaves which are normal when they are older.**		**101**
Vat	**-**	***Virus aphid transmission* resistance. Resistance to the transmission of several viruses by *Aphis gossypii* (in PI 161375).**	**2, V**	**97**
w	**-**	***white* color of mature fruit. Recessive to dark green fruit skin. (*w* in honeydew, *W* in Smiths' Perfect cantaloupe).**		**51**
wf	**-**	***white flesh*. Recessive to salmon. *Wf* epistatic to *Gf_*.**		**15, 53**
Wi	-	White color of *immature* fruit. Dominant to green.		65
Wmr	**-**	***Watermelon Mosaic virus 2* (potyvirus) resistance (in PI 414723).**	**II**	**45**
Wt	**-**	***White testa*. Dominant to yellow or tan seed coat color.**		**46**
Wt-2	**-**	***White testa-2* (in PI 414723). Relationship with *Wt* unknown.**	**IV**	**90**
Y	**-**	***Yellow* epicarp. Dominant to white fruit skin.**		**46**
yg	**-**	***yellow green* leaves. Reduced chlorophyll content.**	**6, XI**	**124**

***yg*^{W}**	***lg***	***yellow green Weslaco*. First described as *light green* in a cross Dulce x TAM-Uvalde. Allelic to *yg*.**		**21**
yv	**-**	***yellow virescence*. Pale cotyledons; yellow green young leaves and tendrils; bright and yellow petals and yellow stigma; etiolated; older leaves becoming green.**	**1**	**127**
yv-2	***yv-X***	***yellow virescence-2*. Young leaves yellow green, old leaves normal green.**	**5, IX**	**102**
Zym	***Zym-1***	***Zucchini Yellow Mosaic* virus resistance. Resistance to pathotype 0 of this potyvirus (in PI 414723).**	**4, II**	**99**
Zym-2	**-**	***Zucchini Yellow Mosaic* potyvirus resistance. One of three complementary genes (see *Zym* and *Zym-3*) for resistance to this potyvirus (in PI 414723).**		**24**
Zym-3	**-**	***Zucchini Yellow Mosaic* potyvirus resistance. One of three complementary genes (see *Zym* and *Zym-2*) for resistance to this potyvirus (in PI 414723).**		**24**
		Quantitative Trait Loci (QTLs)		
cmv	-	*cucumber mosaic virus* resistance. Three recessive genes have been described in the cross Freemans's cucumber x Noy Amid. Seven QTLs are involved in resistance to three different strains of this cucumovirus in the cross Védrantais x PI 161375.		30, 58
eth		*ethylene* production in fruit (climacteric crisis). Four QTLs described in the cross Védrantais x PI 161375.		91
fl	-	*fruit length*. Four QTL described in the cross Védrantais x PI 161375 and 4 QTLs in the cross Védrantais x PI 414723, one is common to both crosses.		89
fs	-	*fruit shape* (ratio fruit length/fruit width). Six QTL described in the cross Védrantais x PI 161375 and 2 QTLs in the cross Védrantais x PI 414723, which are common to both crosses.		89
fw	-	*fruit width*. Five QTL described in the cross Védrantais x PI 161375 and 1 QTLs in the cross Védrantais x PI 414723.		89
ovl	-	*ovary length*. Six QTL described in the cross Védrantais x PI 161375.		89
ovs	-	*ovary shape* (ratio ovary length/ovary width). Six QTL described in the cross Védrantais x PI 161375.		89
ovw	-	*ovary width*. Eight QTL described in the cross Védrantais x PI 161375.		89
		Cytoplasmic Factors		
cyt-Yt	-	*cytoplasmic yellow tip*. Chlorophyll deficient mutant with yellow young leaves, turning green when becoming older. Maternally inherited		106

[z] Linkage group to which this gene belongs: Letters correspond to (114), arabic numbers to (94) and roman numbers to (92). See Table 3.

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

Gene symbol	Gene accession	(Putative) Function	Submitted by	LG[z]	Ref.
Cm-AAT	AB075227	Alcohol acetyltransferase GeAAT	Ishimaru M.		
Cm-AAT2	AF468022	Putative alcohol acyltransferase (AT2)	El Yahyaoui F. *et al*		
Cm-ACO1	X95551	1-aminocyclopropane-1-carboxylate (ACC) oxidase 1	Lasserre E. *et al*	V	66
Cm-ACO2	X95552	1-aminocyclopropane-1-carboxylate (ACC) oxidase 2	Lasserre E. *et al*	VIII	66
Cm-ACO3	X95553	1-aminocyclopropane-1-carboxylate (ACC) oxidase 3	Lasserre E. *et al*		66
Cm-ACS1	AB025906	1-aminocyclopropane-1-carboxylate (ACC) synthase 1	Yamamoto M. *et al*	XI	126
Cm-ACS1	AB032935	1-aminocyclopropane-1-carboxylate (ACC) synthase	Shiomi S. *et al*	XI	
Cm-ACS2	D86242	1-aminocyclopropane-1-carboxylate (ACC) synthase 2	Ishiki Y. *et al*		54
Cm-ACS2	AB032936	1-aminocyclopropane-1-carboxylate (ACC) synthase 2	Shiomi S. *et al*		
Cm-AGPP-mlf2	AF030383 AF030384	ADP-glucose pyrophosphorylase large subunit (mlf2)	Park S.-W. *et al*		
Cm-AGPP-msf1	AF030382	ADP-glucose pyrophosphorylase small subunit (msf1)	Park S.-W. *et al*		
Cm-AmT1	AY066012	Aminotransferase 1	Taler D. *et al*		
Cm-AmT2	AF461048	Aminotransferase 2	Taler D. *et al*		
Cm-AO1	AF233593	Ascorbate oxidase AO1	Sanmartin M. *et al*		
Cm-AO3	Y10226	Ascorbate oxidase AO3	Pateraki I. *et al*		
Cm-AO4	AF233594	Ascorbate oxidase AO4	Sanmartin M. *et al*		
Cm-AOS	AF081954	Allene oxide synthase (AOS)	Tijet N. *et al*		
Cm-ASR1	AF426403 AF426404	Abscisic acid response protein (Asr1)	Hong S.-H. *et al*		

Cm-CCM	D32206	Cucumisin (serine protease)	Yamagata H. *et al*		125
Cm-CHI1	AF241266	Chitinase 1	Zou X. *et al*		
Cm-CHI2	AF241267 AF241538	Chitinase 2	Zou X. *et al*		
Cm-E8	AB071820	Regulator of ethylene synthesis, similar to *Le-E8*	Fujimori A. *et al*		
Cm-EIL1	AB063191	Transcription factor Ethylene Insensitive 1 for At-EIN3-like protein	Sato T. *et al*		
Cm-EIL2	AB063192	Transcription factor Ethylene Insensitive 2 for At-EIN3-like protein	Sato T. *et al*		
Cm-ERS1	AF037368	Putative ethylene receptor ERS1	Sato Nara K. *et al*	I	113
Cm-ERS1	AB049128	Ethylene receptor ERS1	Furukawa H.		
Cm-ETR1	AF054806	Putative ethylene receptor (ETR1)	Sato Nara K. *et al*		113
Cm-ETR1	AB052228	Ethylene receptor (ETR1)	Furukawa H.		
Cm-GAS1	AY077642	Galactinol synthase (GAS1)	Volk G.M. *et al*		
Cm-GAS2	AY077641	Galactinol synthase (GAS2)	Volk G.M. *et al*		
Cm-GLD	AF252339	L-galactono-1,4-lactone dehydrogenase	Pateraki I. and Kanellis A.K.		
Cm-HMG-CoA	AB021862	3-hydroxy-3-methylglutaryl coenzyme A reductase	Kato-Emori S. *et al*		59
Cm-HPL	AF081955	Fatty acid 9-hydroperoxide lyase (HPL)	Tijet N. *et al*		118
Cm-ITS1	AF006802	Internal Transcribed Spacer 1	Jobst J. *et al*		56
Cm-ITS2	AF013333	Internal Transcribed Spacer 2	Jobst J. *et al*		56
Cm-Lec17	AF520577	17 kDa phloem lectin (Lec17)	Dinant S. *et al*		
Cm-Lec17-1	AF517156	17 kDa phloem lectin Lec17-1	Dinant S. *et al*		
Cm-Lec17-3	AF517157	17 kDa phloem lectin Lec17-3 mRNA	Dinant S. *et al*		
Cm-Lec26	AF517154	26 kDa phloem lectin (Lec26)	Dinant S. *et al*		
Cm-MPP	AF297643	Mitochondrial processing peptidase beta subunit	He C. *et al*		

Cm-PG1	AF062465	Polygalacturonase precursor (MPG1)	Hadfield K.A. *et al*
Cm-PG2	AF062466	Polygalacturonase precursor (MPG2)	Hadfield K.A. *et al*
Cm-PG3	AF062467	Polygalacturonase precursor (MPG3)	Hadfield K.A. *et al*
Cm-ProETR1	E51774	Promoter of melon ethylene receptor	Ezura H. *et al* Patent JP 2001037484-A 14 13-FEB-2001
Cm-PSY1	Z37543	Phytoene synthase	Karvouni Z. *et al*
Cm-TCTP	AF230211	Translationally controlled tumor protein-related protein	Gomez-Lim M.A. *et al*

[z] Linkage group to which this gene belongs according to 92.

Table 3. Genes and QTLs localization and correspondance between linkage groups using common markers such as phenotypic traits or molecular markers (mainly SSR according to 23).

94[z]	4[z]	122[z]	114[z]	12[z]	86[z]	92[z]	25[z]	Genes	QTLs
1	-	-	-	-	-	-	-	*si-1, yv*	
2	2+ K	-	-	6	4	V	-	*Cm-ACO1, Fn, Pm-w, Vat*	*fl5.1, fw5.2*
3	-	-	-	-	-	-		*gl, ms-1, Pa, r*	
4	D	-	-	3	8	II	IV	*a, h, mt-2, Pm-x, Zym*	*cmv2.1, cmv2.2, eth2.1, fl2.1, fs2.1, fs2.2, fw2.1, ovl2.1, ovl2.2, ovs2.1, ovs2.2, ovw2.1*
5	5	-	-	11	7	IX	II	*Al-4, Fom-1, gf, 6-Pgd2, Prv, yv-2*	*cmv9.1, fw9.1, ovl9.1, ovs9.1*
-	-	-	A	-	-	-	-	*Aco-1, Idh, Mpi-1, Mpi-2, Pgd-3, Pgm-2*	
6	6	III	-	1	5	XI	III	*Cm-ACS1, Fom-2, ms-2, s-2, yg*	*eth11.1, fs11.1*
7	7	-	-	3	11	XII	-	*nsv, p, Pm-Y*	*cmv12.1, cmv12.2, fs12.1, fw12.1, ovs12.1, ovw12.1*
8	-	-	-	-	-	-	-	*f, lmi*	
9	-	-	-	-	-	-	-	*dl*	
10	-	-	-	-	-	-	-	*ms-3*	
11	-	-	-	-	-	-	-	*ms-4*	
12	-	-	-	-	-	-	-	*ms-5*	
13	-	-	-	-	-	-	-	*V*	
-	C	-	-	10	10	IV	-	*Wt-2*	*fl4.1, fw4.1, ovl4.1*
-	E	-	-	3+8+ 13 (+17?)	1	VIII	I	*Al-3, Cm-ACO2, pH*	*cmv8.1, fl8.1, fl8.2, fs8.1, fs8.2, ovl8.1, ovs8.1, ovs8.2, ovw8.1*
-	F	-	-	-	3	VII	VI	*Spk*	*fw7.1, ovl7.1, ovs7.1*

-	G	-	-	3+12	6	I	VIII	*ech, Cm-ERS1*	*eth1.1, fl1.1, fs1.1, ovs1.1*
-	J	-	-	-	2	III	V	*Cm-ACS5, Ec, pin*	*cmv3.1, cmv3.2, eth3.1*
-	-	-	B	-	-	-	-	*Mdh-2, Mdh-4, Mdh-5, Mdh-6, Pep-gl*	
-	A	-	-	4+7	9	X	-		*ovw10.1*
-	B	-	-	9	12	VI	-		*fl6.1*

N.B. If *6-Pgd-2* (4) and *Pgd-3* (114) correspond to the same locus, which is probable but not yet demonstrated, lines 5 and 6 of this table can be merged.
[z] Bibliographical references

Literature cited

1. Anagnostou, K., M. Jahn and R. Perl-Treves. 2000. Inheritance and linkage analysis of resistance to zucchini yellow mosaic virus, watermelon mosaic virus, papaya ringspot virus and powdery mildew in melon. Euphytica 116:265-270.
2. Angelov, D. and L. Krasteva. 2000. Dominant inheritance of downy mildew resistance in melons. *in* Proceedings of Cucurbitaceae 2000 (Ed. Katzir, N. and H.S. Paris), 19-23/03/2000, Ma'ale Ha Hamisha (ISR). 273-275.
3. Bains, M.S. and U.S. Kang. 1963. Inheritance of some flower and fruit characters in muskmelon. Indian J Genet Pl Breed 23:101-106.
4. Baudracco-Arnas, S. and M. Pitrat. 1996. A genetic map of melon (*Cucumis melo* L.) with RFLP, RAPD, isozyme, disease resistance and morphological markers. Theor Appl Genet 93:57-64.
5. Besombes, D., N. Giovinazzo, C. Olivier, C. Dogimont and M. Pitrat. 1999. Description and inheritance of an *albino* mutant in melon. Cucurbit Genet Coop Rep 22:14-15.
6. Bohn, G.W. 1961. Inheritance and origin of nectarless muskmelon. J Hered 52:233-237.
7. Bohn, G.W. 1968. A red stem pigment in muskmelon. Veg Improv Newslet 10:107.
8. Bohn, G.W. and T.W. Whitaker. 1949. A gene for male sterility in the muskmelon (*Cucumis melo* L.). Proc Amer Soc Hortic Sci 53:309-314.
9. Bohn, G.W. and T.W. Whitaker. 1964. Genetics of resistance to powdery mildew race 2 in muskmelon. Phytopathology 54:587-591.
10. Bohn, G.W. and J.A. Principe. 1964. A second male-sterility gene in the muskmelon. J Hered 55:211-215.
11. Bohn, G.W., A.N. Kishaba, J.A. Principe and H.H. Toba. 1973. Tolerance to melon aphid in *Cucumis melo* L. J Amer Soc Hort Sci 98:37-40.
12. Brotman, Y., L. Silberstein, I. Kovalski, J. Klingler, G. Thompson, N. Katzir and R. Perl-Treves. 2000. Linkage groups of *Cucumis melo*, including resistance gene homologues and known genes. *in* Proceedings of Cucurbitaceae 2000 (Ed. Katzir, N. and H.S. Paris), 19-23/03/2000, Ma'ale Ha Hamisha (ISR). 441-448.
13. Chadha, M.L., K.S. Nandpuri and S. Singh. 1972. Inheritance of some fruit characters in muskmelon. Indian J Horticult 29:58-62.
14. Chen, F.C., C.H. Hsiao, Y.M. Chang and H.W. Li. 1990. Isozyme variation in *Cucumis melo* L. I. Peroxidase and shikimate dehydrogenase variation in four melon varieties and its application for F1 hybrid identification. J Agric Res China 39:182-189.
15. Clayberg, C.D. 1992. Interaction and linkage tests of flesh color genes in *Cucumis melo* L. Cucurbit Genet Coop Rep 15:53.
16. Cohen, Y., S. Cohen, H. Eyal and C.E. Thomas. 1985. Inheritance of resistance to downy mildew in *Cucumis melo* PI 124111. Cucurbit Genet Coop Rep 8:36-38.
17. Committee, C.G.L. 1982. Update of cucurbit gene list and nomenclature rules. Cucurbit Genet Coop Rep 5:62-66.
18. Committee, C.G.L. 1986. Gene list for muskmelon (*Cucumis melo* L.). Cucurbit Genet Coop Rep 9:111-120.
19. Coudriet, D.L., A.N. Kishaba and G.W. Bohn. 1981. Inheritance of resistance to muskmelon necrotic spot virus in a melon aphid resistant breeding lines of muskmelon. J Amer Soc Hort Sci 106:789-791.
20. Cox, E.L. 1985. Three new seedling marker mutants in *Cucumis melo*. HortScience 20:657 (Abstr.).
21. Cox, E.L. and K.E. Harding. 1986. Linkage relationships of the light green mutant in cantaloupe. HortScience 21:940 (Abstr.).
22. Dane, F. 1983. Cucurbit. *in* Isozymes in plant genetics and breeding, part B (Ed. Tanksley, S.D. and T.J. Orton), Elsevier Science Publication, Amsterdam (NL). 369-390.

23. Danin-Poleg, Y., N. Reis, G. Tzuri and N. Katzir. 2001. Development and characterization of microsatellite markers in *Cucumis*. Theor Appl Genet 102:61-72.
24. Danin-Poleg, Y., H.S. Paris, S. Cohen, H.D. Rabinowitch and Z. Karchi. 1997. Oligogenic inheritance of resistance to zucchini yellow mosaic virus in melons. Euphytica 93:331-337.
25. Danin-Poleg, Y., Y. Tadmor, G. Tzuri, N. Reis, J. Hirschberg and N. Katzir. 2002. Construction of a genetic map of melon with molecular markers and horticultural traits, and localization of genes associated with ZYMV resistance. Euphytica 125:373-384.
26. Danin-Poleg, Y., N. Reis, S. Baudracco-Arnas, M. Pitrat, J.E. Staub, M. Oliver, P. Arús, C.M. de Vicente and N. Katzir. 2000. Simple Sequence Repeats in *Cucumis* mapping and map merging. Genome 43:963-974.
27. Denna, D.W. 1962. A study of the genetic, morphological and physiological basis for the bush and vine habit of several cucurbits. *Thesis* Cornell University, Ithaka (N.Y., U.S.A.). pp.
28.Dogimont, C., D. Bordat, C. Pages, N. Boissot and M. Pitrat. 1999. One dominant gene conferring the resistance to the leafminer *Liriomyza trifolii* (Burgess) Diptera: Agromyzidae in melon (*Cucumis melo* L.). Euphytica 105:63-67.
29. Dogimont, C., A. Bussemakers, J. Martin, S. Slama, H. Lecoq and M. Pitrat. 1997. Two complementary recessive genes conferring resistance to Cucurbit Aphid Borne Yellows Luteovirus in an Indian melon line (*Cucumis melo* L.). Euphytica 96:391-395.
30. Dogimont, C., L. Lecomte, C. Périn, A. Thabuis, H. Lecoq and M. Pitrat. 2000. Identification of QTLs contributing to resistance to different strains of cucumber mosaic cucumovirus in melon. *in* Cucurbitaceae 2000, VIIth EUCARPIA Meeting on Cucurbit Genetics and Breeding (Ed. Katzir, N. and H. Paris), 19-23/03/2000, Ma'ale Hahamisha (ISR). 391-398.
31. Dyutin, K.E. 1967. (A spontaneous melon mutant with dissected leaves) (in Russian). Genetica 9:179-180.
32. Dyutin, K.E. 1979. (Inheritance of yellow-green coloration of the young leaves in melon) (in Russian). Tsitologia i genetika 13:407-408.
33. Epinat, C. and M. Pitrat. 1989. Inheritance of resistance of three lines of muskmelon (*Cucumis melo*) to downy mildew (*Pseudoperonospora cubensis*). *in* 'Cucurbitaceae 89' (Ed. Thomas, C.E.), 29/11-02/12/1998, Charleston (USA). 133-135.
34. Epinat, C., M. Pitrat and F. Bertrand. 1993. Genetic analysis of resistance of five melon lines to powdery mildews. Euphytica 65:135-144.
35. Esquinas Alcazar, J.T. 1975. 'Hojas hendidas', a nuevo mutante en *Cucumis melo* L. Inst Nac Investig Agrar Ser: Prod Veget 5:93-103.
36. Esquinas Alcazar, J.T. 1981. Allozyme variation and relationships among Spanish land races of *Cucumis melo* L. Kulturpflanze 29:337-352.
37. Esteva, J. and F. Nuez. 1992. Tolerance to a whitefly-transmitted virus causing muskmelon yellows disease in Spain. Theor Appl Genet 84:693-697.
38. Foster, R.E. 1963. Glabrous, a new seedling marker in muskmelon. J Hered 54:113-114.
39. Foster, R.E. and W.T. Bond. 1967. Abrachiate, an androecious mutant muskmelon. J Hered 58:13-14.
40. Gabillard, D. and M. Pitrat. 1988. A fasciated mutant in *Cucumis melo*. Cucurbit Genet Coop Rep 11:37-38.
41. Ganesan, J. 1988. Genetic studies on certain characters of economic importance in muskmelon (*Cucumis melo* L.). *Thesis* Annamalai University (India), 254 pp.
42. Ganesan, J. and C.N. Sambandam. 1979. Inheritance of certain qualitative characters in muskmelon (*Cucumis melo* L.). Annamalai Univ Agric Res Annals 9:41-44.
43. Ganesan, J. and C.N. Sambandam. 1985. Inheritance of leaf shape in muskmelon (*Cucumis melo* L.) I. A qualitative approach. Annamalai Univ Agric Res Annals 12:53-58.
44. Gang, T. and J. Lee. 1998. Isozyme analysis and its application for purity test of F1 hybrid seeds in melons. J Korean Soc Horticult Sci 39:266-272.
45. Gilbert, R.Z., M.M. Kyle, H.M. Munger and S.M. Gray. 1994. Inheritance of resistance to watermelon mosaic virus in *Cucumis melo* L. HortScience 29:107-110.
46. Hagiwara, T. and K. Kamimura. 1936. Cross-breeding experiments in *Cucumis melo*. Tokyo Horticul School Pub
47. Harwood, R.R. and D. Markarian. 1968. The inheritance for resistance to powdery mildew in the cantaloupe variety Seminole. J Hered 59:126-130.
48. Harwood, R.R. and D. Markarian. 1968. A genetic survey of resistance to powdery mildew in muskmelon. J Hered 59:213-217.
49. Hassan, A.A., M.M. Merghany, K.A. Abdel-Ati, A.M. Abdel-Salam and Y.M. Ahmed. 1998. Inheritance of resistance to interveinal mottling and yellowing disease in cucurbits. Egypt J Horticult 25:209-224.
50. Hoffman, J.C. and P.E. Nugent. 1973. Inheritance of a virescent mutant of muskmelon. J Hered 64:311-312.

51. Hughes, M.B. 1948. The inheritance of two characters of *Cucumis melo* and their interrelationship. Proc Amer Soc Hortic Sci 52:399-402.
52. Iglesias, A., B. Picó and F. Nuez. 2000. A temporal genetic analysis of disease resistance genes: resistance to melon vine decline derived from *Cucumis melo* var. *agrestis*. Plant Breeding 119:329-334.
53. Iman, M.K., M.A. Abo-Bakr and H.Y. Hanna. 1972. Inheritance of some economic characters in crosses between sweet melon and snake cucumber. I. Inheritance of qualitative characters. Assiut J Agricult Sci 3:363-380.
54. Ishiki, Y., A. Oda, Y. Yaegashi, Y. Orihara, T. Arai, T. Hirabayashi, H. Nakagawa and T. Sato. 2000. Cloning of an auxin-responsive 1-aminocyclopropane-1-carboxylate synthase gene (CMe-ACS2) from melon and the expression of ACS genes in etiolated melon seedlings and melon fruits. Pl Science 159:173-181.
55. Jagger, I.C., T.W. Whitaker and D.R. Porter. 1938. Inheritance in *Cucumis melo* of resistance to powdery mildew (*Erysiphe cichoracearum*). Phytopathology 28:761.
56. Jobst, J., K. King and V. Hemleben. 1998. Molecular evolution of the internal transcribed spacers (ITS1 and ITS2) and phylogenetic relationships among species of the family Cucurbitaceae. Mol Phytogenet Evol 9:204-219.
57. Kaan, J.F. 1973. Recherches sur la résistance du melon aux maladies, notamment à la mosaïque de la pastèque et au *Pseudoperonospora*, appliquées au type variétal "Cantaloup Charentais". *in* EUCARPIA meeting on melon (Ed. Risser, G.), June 19-22, 1973, Avignon (FRA). 41-49.
58. Karchi, Z., S. Cohen and A. Govers. 1975. Inheritance of resistance to Cucumber Mosaic Virus in melons. Phytopathology 65:479-481.
59. Kato-Emori, S., K. Higashi, K. Hosoya, T. Kobayashi and H. Ezura. 2001. Cloning and characterization of the gene encoding 3-hydroxy-3-methylglutaryl coenzyme A reductase in melon (*Cucumis melo* L. *reticulatus*). Mol Genet Genom 265:135-142.
60. Kenigsbuch, D. and Y. Cohen. 1987. Inheritance of gynoecious sex type in muskmelon. Cucurbit Genet Coop Rep 10:47-48.
61. Kenigsbuch, D. and Y. Cohen. 1989. Independent inheritance of resistance to race 1 and race 2 of *Sphaerotheca fuliginea* in muskmelon. Plant Disease 73:206-208.
62. Kenigsbuch, D. and Y. Cohen. 1990. The inheritance of gynoecy in muskmelon. Genome 33:317-327.
63. Kenigsbuch, D. and Y. Cohen. 1992. Inheritance of resistance to downy mildew in *Cucumis melo* PI 124112 and commonality of resistance genes with PI 124111F. Plant Disease 76:615-617.
64. Knavel, D.E. 1990. Inheritance of a short internode mutant of 'Mainstream' muskmelon. HortScience 25:1274-1275.
65. Kubicki, B. 1962. Inheritance of some characters in muskmelons (*Cucumis melo*). Genet Polonica 3:265-274.
66. Lasserre, E., T. Bouquin, J.A. Hernandez, J. Bull, J.C. Pech and C. Balagué. 1996. Structure and expression of three genes encoding ACC oxidase homologs from melon (*Cucumis melo* L.). Mol Gen Genet 251:81-90.
67. Lecouviour, M., M. Pitrat and G. Risser. 1990. A fifth gene for male sterility in *Cucumis melo*. Cucurbit Genet Coop Rep 13:34-35.
68. Lecouviour, M., M. Pitrat, C. Olivier and M. Ricard. 1995. *Cochleare folium*, a mutant with spoon shaped leaf in melon. Cucurbit Genet Coop Rep 18:37.
69. Lee, C.W. and J. Janick. 1978. Inheritance of seedling bitterness in *Cucumis melo*. HortScience 13:193-194.
70. López-Sesé, A.I. and M.L. Gómez-Guillamón. 2000. Resistance to Cucurbit Yellowing Stunting Disorder Virus (CYSDV) in *Cucumis melo* L. HortScience 35:110-113.
71. Lozanov, P. 1983. Selekcija na mazkosterilni roditelski komponenti za ulesnjavana na proizvodstvoto na hibridni semena ot papesi. Dokl. na parva naucna konferencija po genetika i selekapa, Razgrad.
72. Lumsden, D. 1914. Mendelism in melons. New Hampshire Agric Exper Sta Bull 172:58pp.
73. Ma, D., L. Sun, Y.H. Liu, Y. Zhang and H. Liu. 1997. A genetic model of bitter taste in young fruits of melon. Cucurbit Genet Coop Rep 20:27-29.
74. McCreight, J.D. 1983. A long internode mutant in muskmelon . Cucurbit Genet Coop Rep 6:45.
75. McCreight, J.D . 2000. Inheritance of resistance to Lettuce Infectious Yellows virus in melon. HortScience 35:1118-1120.
76. McCreight, J.D. and G.W. Bohn. 1979. Descriptions, genetics and independent assortment of red stem and pale in muskmelon (*Cucumis melo* L.). J Amer Soc Hort Sci 104:721-723.
77. McCreight, J.D. and G.W. Elmstrom. 1984. A third male-sterile gene in muskmelon. HortScience 19:268-270.
78. McCreight, J.D. and P. Fashing-Burdette. 1996. Resistance of PI 124112 and 'Eldorado-300' melons (*Cucumis melo* L.) to papaya ringspot virus watermelon strain. *in* Cucurbits toward 2000. VIth EUCARPIA meeting on Cucurbit Genetics and Breeding (Ed. Gómez-Guillamón, M.L., C. Soria, J. Cuartero, J.A. Torès and R. Fernandez-Munoz), 28-30/05/1996, Málaga (ESP). 298-301.
79. Mockaitis, J.M. and A. Kivilaan. 1965. A green corolla mutant in *Cucumis melo* L. Naturwissenschaften 52:434.

80. Molina, R.V. and F. Nuez. 1996. The inheritance of organogenic response in melon. Plant Cell Tissue Organ Cult 46:251-256.
81. Nuez, F., B. Picó, A. Iglesias, J. Esteva and M. Juarez. 1999. Genetics of melon yellows virus resistance derived from *Cucumis melo* spp. *agrestis*. Eur J Plant Pathol 105:453-464.
82. Nugent, P.E. and J.C. Hoffman. 1974. Inheritance of the halo cotyledon mutant in muskmelon. J Hered 65:315-316.
83. Nugent, P.E. and H.S. Bhella. 1988. A new chlorotic mutant of muskmelon. HortScience 23:379-381.
84. Nugent, P.E., F.P.J. Cuthbert and J.C. Hoffman. 1984. Two genes for cucumber beetle resistance in muskmelon. J Amer Soc Hort Sci 109:756-759.
85. Ohara, T., A. Kojima, T. Wako and D. Ishiuchi. 2001. Inheritance of suppressed-branching in melon and its association with some other morphological characters. J Japan Soc Hort Sci 70:341-345.
86. Oliver, J.L., J. Garcia-Mas, M. Cardús, N. Pueyo, A.I. López-Sesé, M. Arroyo, H. Gómez-Paniagua, P. Arús and C.M. de Vicente. 2001 Construction of a reference linkage map of melon. Genome 44:836-845.
87. Paris, H.S., H. Nerson and Z. Karchi. 1984. Genetics of internode length in melons. J Hered 75:403-406.
88. Parthasarathy, V.A. and C.N. Sambandam. 1981. Inheritance in Indian melons. Indian J Genet Pl Breed 41:114-117.
89. Périn, C., L.S. Hagen, N. Giovinazzo, D. Besombes, C. Dogimont and M. Pitrat. 2002. Genetic control of fruit shape acts prior to anthesis in melon (*Cucumis melo* L.). Mol Genet Genom 266:933-941.
90. Périn, C., C. Dogimont, N. Giovinazzo, D. Besombes, L. Guitton, L. Hagen and M. Pitrat. 1999. Genetic control and linkages of some fruit characters in melon. Cucurbit Genet Coop Rep 22:16-18.
91. Périn, C., M.C. Gomez-Jimenez, L. Hagen, C. Dogimont, J.C. Pech, A. Latché, M. Pitrat and J.M. Lelièvre. 2002. Molecular and genetic characterisation of a non-climacteric phenotype in melon reveals two loci conferring altered ethylene response in fruit. Plant Physiol 129:300-309.
92. Périn, C., L.S. Hagen, V. de Conto, N. Katzir, Y. Danin-Poleg, V. Portnoy, S. Baudracco-Arnas, J. Chadoeuf, C. Dogimont and M. Pitrat. 2002. A reference map of *Cucumis melo* based on two recombinant inbred line populations. Theor Appl Genet 104:1017-1034.
93. Pitrat, M. 1990. Gene list for *Cucumis melo* L. Cucurbit Genet Coop Rep 13:58-68.
94. Pitrat, M. 1991. Linkage groups in *Cucumis melo* L. J Hered 82:406-411.
95. Pitrat, M. 1994. Gene list for *Cucumis melo* L. Cucurbit Genet Coop Rep 17:135-147.
96. Pitrat, M. 1998. 1998 Gene list for melon. Cucurbit Genet Coop Rep 21:69-81.
97. Pitrat, M. and H. Lecoq. 1980. Inheritance of resistance to cucumber mosaic virus transmission by *Aphis gossypii* in *Cucumis melo*. Phytopathology 70:958-961.
98. Pitrat, M. and H. Lecoq. 1983. Two alleles for Watermelon Mosaic Virus 1 resistance in melon. Cucurbit Genet Coop Rep 6:52-53.
99. Pitrat, M. and H. Lecoq. 1984. Inheritance of Zucchini Yellow Mosaic Virus resistance in *Cucumis melo* L. Euphytica 33:57-61.
100. Pitrat, M., C. Ferrière and M. Ricard. 1986. *Flava*, a chlorophyll deficient mutant in muskmelon. Cucurbit Genet Coop Rep 9:67.
101. Pitrat, M., C. Olivier and M. Ricard. 1995. A virescent mutant in melon. Cucurbit Genet Coop Rep 18:37.
102. Pitrat, M., G. Risser, C. Ferrière, C. Olivier and M. Ricard. 1991. Two virescent mutants in melon (*Cucumis melo*). Cucurbit Genet Coop Rep 14:45.
103. Poole, C.F. and P.C. Grimball. 1939. Inheritance of new sex forms in *Cucumis melo* L. J Hered 30:21-25.
104. Prasad, K. and J.D. Norton. 1967. Inheritance of resistance to *Mycosphaerella citrullina* in muskmelon. Proc Amer Soc Hortic Sci 91:396-400.
105. Quiot-Douine, L., H. Lecoq, J.B. Quiot, M. Pitrat and G. Labonne. 1988. Evidence for a biological and serological variability in a potyvirus infecting cucurbit: the papaya ringspot virus (PRSV). *in* EUCARPIA meeting 'Cucurbitaceae 88' (Ed. Risser, G. and M. Pitrat), 31/05-02/06/1998, Avignon (FRA). 35-42.
106. Ray, D.T. and J.D. McCreight. 1996. Yellow-tip: a cytoplasmically inherited trait in melon (*Cucumis melo* L. J Hered 87:245-247.
107. Risser, G. 1973. Étude de l'hérédité de la résistance du melon (*Cucumis melo*) aux races 1 et 2 de *Fusarium oxysporum* f.sp. *melonis*. Ann Amélior Plantes 23:259-263.
108. Risser, G., M. Pitrat, H. Lecoq and J.C. Rode. 1981. Sensibilité variétale du melon au virus du rabougrissement jaune du melon et à sa transmission par *Aphis gossypii* Glov. Hérédité de la réaction de flétrissement. agronomie 1:835-838.
109. Robinson, R.W. 1979. New genes for the Cucurbitaceae. Cucurbit Genet Coop Rep 2:49-53.
110. Robinson, R.W., H.M. Munger, T.W. Whitaker and G.W. Bohn. 1976. Genes of the cultivated Cucurbitaceae. HortScience 11:554-568.
111. Rosa, J.T. 1928. The inheritance of flower types in *Cucumis* and *Citrullus*. Hilgardia 3:233-250.

112. Sambandam, C.N. and S. Chelliah. 1972. *Cucumis callosus* (Rottl.) Logn., a valuable material for resistance breeding in muskmelons. *in* 3rd International Symposium Sub-tropical Horticulture (Ed. 63-68.
113. Sato-Nara, K., K.I. Yuhashi, K. Higashi, K. Hosoya, M. Kubota and H. Ezura. 1999. Stage- and tissue-specific expression of ethylene receptor homolog genes during fruit development in muskmelon. Plant Physiol 119:321-329.
114. Staub, J.E., V. Meglic and J.D. McCreight. 1998. Inheritance and linkage relationships of melon (*Cucumis melo* L.) isozymes. J Amer Soc Hort Sci 123:264-272.
115. Takada, K., K. Kanazawa and K. Takatuka. 1975. Studies on the breeding of melon for resistance to powdery mildew. II. Inheritance of resistance to powdery mildew and correlation of resistance to other characters. Bull Veg Ornamental Crops Res Stn A2:11-31.
116. Thomas, C.E., J.D. McCreight and E.L. Jourdain. 1990. Inheritance of resistance to *Alternaria cucumerina* in *Cucumis melo* line MR-1. Plant Disease 74:868-870.
117. Thomas, C.E., Y. Cohen, J.D. McCreight, E.L. Jourdain and S. Cohen. 1988. Inheritance of resistance to downy mildew in *Cucumis melo*. Plant Disease 72:33-35.
118. Tijet, N., C. Schneider, B.L. Muller and A.R. Brash. 2001. Biogenesis of volatile aldehydes from fatty acid hydroperoxides: molecular cloning of a hydroperoxide lyase (CYP74C) with specificity for both the 9- and 13-hydroperoxides of linoleic and linolenic acids. Arch. Biochem. Biophys. 386:281-289.
119. Vashistha, R.N. and B. Choudhury. 1974. Inheritance of resistance to red pumpkin beetle in muskmelon. Sabrao J 6:95-97.
120. Velich, I. and I. Fulop. 1970. A new muskmelon type of cut leaf character. Zoldsegtermesztes 4:107-112.
121. Wall, J.R. 1967. Correlated inheritance of sex expression and fruit shape in *Cucumis*. Euphytica 16:199-208.
122. Wang, Y.H., C.E. Thomas and R.A. Dean. 1997. A genetic map of melon (*Cucumis melo* L.) based on amplified fragment length polymorphism (AFLP) markers. Theor Appl Genet 95:791-797.
123. Webb, R.E. 1979. Inheritance of resistance to watermelon mosaic virus in *Cucumis melo* L. HortScience 14:265-266.
124. Whitaker, T.W. 1952. Genetic and chlorophyll studies of a yellow-green mutant in muskmelon. Plant Physiol 27:263-268.
125. Yamagata, H., T. Masuzawa, Y. Nagaoka, T. Ohnishi and T. Iwasaki. 1994. Cucumisin, a serine protease from melon fruits, shares structural homology with subtilisin and is generated from a large precursor. J Biol Chem 269:32725-32731.
126. Yamamoto, M., H. Asama, H. Nakagawa, T. Hirabayashi and T. Sato. 1999. Nucleotide sequence of a wound- and ripening-related 1-aminocyclopropane-1- carboxylate synthase gene (CMe-ACS1, Accession No. AB025906) in melon (*Cucumis melo* L. cv. AMS) (PGR99-128). Plant Physiol 121:311.
127. Zink, F.W. 1977. Linkage of virescent foliage and plant growth habit in muskmelon. J Amer Soc Hort Sci 102:613-615.
128. Zink, F.W. 1986. Inheritance of a greenish-yellow corolla mutant in muskmelon. J Hered 77:363.
129. Zink, F.W. 1990. Inheritance of a delayed lethal mutant in muskmelon. J Hered 81:210-211.
130. Zink, F.W. and W.D. Gubler. 1985. Inheritance of resistance in muskmelon to Fusarium wilt. J Amer Soc Hort Sci 110:600-604.
131. Zuniga, T.L., J.P. Jantz, T.A. Zitter and M.K. Jahn. 1999. Monogenic dominant resistance to gummy stem blight in two melon (*Cucumis melo*) accessions. Plant Disease 83:1105-1107.

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.

References

1. CGC Gene List Committee. 1982. Update of cucurbit gene list and nomenclature rules. CGC 5:62-66.
2. Rieger, R., A. Michaelis and M.M. Green. 1976. Glossary of Genetics and Cytogenetics (4th ed.). Springer-Verlag.
3. Robinson, R.W., H.M. Munger, T.W. Whitaker and G.W. Bohn. 1976. Genes of the Cucurbitaceae. HortScience 11:554-568.

Cucurbit Genetics Cooperative
2001-2002 Membership Directory

Aboul-Nasr, M. Hossam. Dept. Horticulture, Fac. Agriculture, Assiut University, Assiut, Egypt. Phone: 2088310952; Fax: 2088332875; Email: abou-lnasr@mailcity.com. Vegetable production and plant tissue culture.

Akkermans, Doretta. PT East West Seed Indonesia, P.O. Box 1, Campaka, Purwakarta 41181, W. Java, Indonesia. Phone: 0264-201871; Fax: 0264-201875; Email: doretta@ibm.net. Cucumber, watermelon and melon breeding.

Andres, Thomas C. The Cucurbit Network, 5440 Netherland Ave., #D24, Bronx, NY, 10471-2321. Phone: (718) 601-7329; Fax: (718) 601-7329; Email: tom@andres.com.. *Cucurbita* systematics.

Attard, Everaldo. 14, Calendula, Triq ir-Rebbiegha, Siggiewi (QRM 13), Malta. Phone: +356 32402323;Fax: +356 21346519; Email: everaldo.attard@um.edu.mt. Research on the economic importance of *Ecballium elaterium* (squirting cucumber).

Ayuso, Maria Cruz. Seminis Vegetable Seeds Iberica, Ctra Nac 301, Km 432a, 30319 Miranda-Cartagena Murcia, Spain. Phone: 34-968-550080; Fax: 34-968-550676; Email: mariacruz.ayuso@seminis.com.

Bao, HaiQing. Xinjiang Western China Seed Group, No. 25 Luzhou Road, Changji, Xinjiang 831100, P.R. China. Phone: (0994) 2345202; Fax: (0994) 2348415. Watermelon & melon breeding, hybrid seed production techniques, variety evaluation.

Barham, Warren S. Barham Seeds, Inc., 7401 Crawford Dr., Gilroy, CA, 95020- 5421. Phone: (408) 847-3056; Fax: (408) 847-6988; Email: wsbarham@garlic.com. Watermelon and melon breeding.

Baudracco-Arnas, Sylvie. ASL, Site Agroparc Bat. 1, 755, Chemin des Meinajaries, BP. 1202, 84911 Avignon Cedex 9, Cedex 9, France. Phone: 04.90 84 00 46; Fax: 04.90 84 00 47; Email: sba.asl@pol.fr. Melon molecular biologist.

Beaver, Linda. See *Wessell-Beaver, Linda*

Berenji, Janos. Inst. Field & Vegetable Crops, 21470 Backi Petrovac, Yugoslavia. Email: berenji@EUnet.yu.

Bi, Irie A. Zoro. Universitie Abobo-Adjame, UFR des Sciences de la Nature, 02 BP 801 Abidjan 02, Cote d'Ivoire, West Africa. Email: banhiakalou@yahoo.fr. Germplasm collection and classification for *Cucumis melo* var. *agrestis, Citrullus lanatus* ssp. *Lanatus, Citrullus* spp., *Cucumeropsis mannii,* and *Lagenaria siceraria.*

Blazey, Douglas A. Yates Vegetable Seeds, Research Farm, Burroway Road, Narromine, N.S.W. 2821, Australia. Phone: (068) 89-1144.

Boissot, Nathalie INRA, Domaine Duclos, Petit-Bourg BP 515, 97165 Pointe'Pitre cedex, Guadeloupe (F.W.I.). Phone: (0)590 25 59 45; Fax: (0)590 94 11 72; Email: boissot@antilles.inra.fr..

Bosma, Monique ENZA ZADEN, De Enkhuizer Zaadh. b.v., Postbox 7, 1600 AA Enkhuizen, The Netherlands. Phone: 02280-315844; Fax: 0228-315960; Email: Bosma@enzazaden.nl.

Boyhan, George E. University of Georgia, P.O. Box 8112, GSU, Statesboro, GA, 30460. Phone: (912) 681-5639; Fax: (912) 681-0376; Email: gboyhan@uga.cc.uga.edu. Melon and watermelon breeding.

Brown, Rebecca Dept. Hort., Oregon St. Univ., Ag Life Sci Bldg 4017, Corvallis, OR, 97331. Phone: (541) 737-5462; Email: brownr@bcc.orst.edu. Virus resistance, *Cucurbita* germplasm, squash breeding.

Bruton, Benny USDA, ARS, P.O. Box 159, Lane, OK, 74555. Phone: (580) 889-7395; Fax: (580) 889-5783; Email: bbruton-usda@lane-ag.org. Vine declines of cucurbits; postharvest fruit rots.

Burger, Yosi. New Ya'ar Research Center, P.O. Box 1021, Ramat Yishay 30095, Israel. Phone: 972-4-9539517; Fax: 972-4-9836936; Email: burgery@volcani.agri.gov.il.

Çaglar, Gülat. KSU, Ziraat Fakultesi, Bahce Bitkileri Bolumu, 46060, Kahramanmaras, Turkey.

Phone: 90-344-237666/384; Fax: 90-344-2230048; Email: gulat@ksu.edu.tr. Cucumber breeding.

Carey, Edward E. "Ted". Kansas State R&E Center at Olathe, 35125 W. 135th St., Olathe, KS, 66061. Phone: (816) 806-3734; Fax: (785) 532-6949; Email: tcarey@oznet.ksu.edu. Breeder with interest in cucurbits.

Carle, R. Bruce. Hollar Seeds, PO Box 0106, Rocky Ford, CO, 81067-0106. Phone: (719) 254-3539; Fax: (719) 254-3539; Email: bruce@hollarseeds.com. Watermelon and squash breeding.

Chen, Fure-Chyi. Dept. Plant Industry, Natl. Pingtung Univ. Sci. & Techn., Neipu, Pingtung 91207, Taiwan, Rep. China. Phone: 886-8-774-0267; Fax: 886-8-774- 0371; Email: furechen@mail.npust.edu.tw. Gene transfer, breeding, tissue culture and isozymes.

Chen, Jin Feng. Nanjing University, Nanjing 210095, China. Phone: 86-25-4396279; Fax: 86-25-4432420.

Ching, Alejandro "Alex". Alternative Crops Res Ctr, NW MO St U, 106 Valk, 800 Univ Dr, Maryville, MO, 64468. Phone: (660) 562-1126; Fax: (660) 562-1621; Email: alching@mail.nwmissouri.edu. Breeding & introduction of new cucurbits. Production & nutritional quality.

Cho, Myeong-Cheoul. National Horticultural Research Inst. RDA, #540-41, Tap-Dong, Suwon, 441-440, Republic of Korea. Phone: 82)031-290-6180; Fax: 82)031-290-6100; Email: chomc@rda.go.kr. Breeding disease resistant squash varieties.

Chuanchai, Vinich. Chiatai Seeds Co,, Ltd., 295-303 Songsawad Road, Samphantawong District, Bankok, Thailand 10100. Phone: (662) 233-8191; Fax: (662) 639-6063; Email: chiatai@ksc.th.com.

Chung, Paul. Seminis Vegetable Seeds, Inc., 37437 State Highway 16, Woodland, CA, 95695. Phone: (530) 666-6120; Fax: (530) 668-0219; Email: paul.chung@svseeds.com. Melon breeding.

Coffey, Robyn. Willhite Seed, Inc., P.O. Box 23, Poolville, TX, 76487. Phone: (817) 599-8656; Fax: (817) 599-5843; Email: robyn@willhiteseed.com.

Cohen, Roni. Newe Ya'ar Research Center, P.O. Box 1021, Ramat Yishay 30095, Israel. Phone: 972-4-953-9516; Fax: 972-4-983-6936. Email: robico@volcani.agri.gov.il. Plant pathology; root and foliar diseases of cucurbits.

Cohen, Yigal. Department of Life Sciences, Bar-Ilan University, Ramat-Gan 52 100, Israel. Phone: 9723-5318251; Fax: 9723-6771088. Melon.

Cook, Kevin L. Syngenta Seeds, Veg-NAFTA, 10290 Greenway Road, Naples, FL, 34114. Phone: (941) 775-4090; Fax: (941) 774-6852; Email: kevin.cook@syngenta.com. Breeding of summer squash.

Crosby, Kevin. Texas A&M Univeristy, 2415 East Hwy 83, Weslaco, TX, 78596. Phone: (956) 968-5585; Fax: (956) 969-5620; Email: k-crosby@tamu.edu. Microthecium stem canker on melon.

Cui, Hongwen. Dept. Horticulture, Northwestern Agric. Univ., Yangling, Shaanxi 712100, P.R. China. Cucumber breeding.

Dane, Fenny. Auburn University, 101 Funchess Hall, Auburn,m AL 36849. Phone: (344) 844-3046; Fax: (334) 844-3131; Email: fdane@acesag.auburn.edu. *Citrullus* genomics.

Davis, Angela. USDA, ARS, P.O. Box 159, Hwy. 3 West, Lane, OK, 74555. Phone: (580) 889-7395; Fax: (580) 889-5783; Email: adavis-usda@lane-ag.org. Germplasm improvement.

de Groot, Erik. Breeding, Sementi Nunhems S.R.L., Via Ghiarone, 2, 40019 S. Agata Bolognese, Italy.

De Hoop, Simon Jan. East-West Seed Co., 50/1 Moo 2, Sainoi-Bang Buathong Rd., A Sainoi Nonthaburi, 11150 Thailand. Phone: (66)-2- 597-1255; Fax: (66)-2-597-1229; Email: simond@eastwestseed.co.th. Cucurbit breeding.

De Langen, Frank. Mas St. Pierre, 13210 St Remy de Provence, France. Email: frank.delangen@clause.fr.

Decker-Walters, Deena. The Cucurbit Network, P.O. Box 560483, Miami, FL, 33256. Phone: (305) 669-9281; Fax: (305) 661-5984; Email: cucurbitnetwork@netscape.net. Communication via The Cucurbit Network; the whole family Cucurbitaceae.

Della Vecchia, Paulo T. Agroflora S/A, Caixa Postal 427, 12.900-000 Braganca, Paulista - SP, Brazil. Phone: (011) 7871-0855; Fax: (011) 7843-6572. Breeding & genetics, seed production and disease resistance of melon and squash.

Den Hertog, Maarten. Ryk Zwaan, Paraje el Algarroo 47, El Ejido, Almeria 04700, Spain. Phone: 34-9505-81-58; Fax: 34-9505-81920; Email: s.gribnau@rykzwaan.nl.

Denlinger, Phil. Mt. Olive Pickle Co., Inc., P.O. Box 609, Mount Olive, NC, 28365. Phone: (919) 658-2535; Fax: (919) 658-6090.

Di Nitto, Louis Victor. Sunseeds, 8850 59th Ave., N.E., Brooks, OR, 97305. Phone: (503) 393-3243; Fax: (503) 390-0982. email: louie.dinitto@sunseeds.com. Melon (*Cucumis melo*).

Dogan, Remzi. Kaplikaya Mah. Sukent Sites 1, K Blok, No: 7, Bursa, Turkey 16320. Phone: +90 224 3679879; Fax: +90 224 2236570; Email: remzi@may.com.tr. Hybrid breeding and resistance breeding of cucumbers, watermelons, cantaloupes, squashes.

Drowns, Glenn. Sand Hill Preservation Center, 1878 230th Street, Calamus, IA, 52729. Phone: (319) 246-2299; Email: gdrowns@cal-wheat.k12.ia.us.. Genetic preservation of all cucurbits. Taxonomy of *Cucurbita moschata* and *Cucurbita argyrosperma*.

Duangsong, Usa, Limagrain Veg. Seeds Asia, 119/9 Moo 1, Baan Khao, Muang, Kanchanaburi 71000, Thailand. Phone: 66-2-636-2521-1; Fax: 66-2-636-2524; Email: duangsong@marcopoloseed.com.

Eigsti, Orie J. 1602 Winsted, College Green, Goshen, IN, 46526. Phone: (219) 533-4632. Fusarium wilt resistance in tetraploid *Citrullus lanatus* lines, to eliminate crop rotation.

Elmstrom, Gary. c/o Sunseeds, 7087 E. Peltier Road, Acampo, CA, 95220. Phone: (209) 367-8369; Fax: (209) 367-1066; Email: gelmstrom@afes.com. Triploid watermelon breeding.

Ezura, Hiroshi. Plant Biotech Inst, Ibaraki Agric Ctr, Ago, Iwama, Nishi-ibaraki, 319-0292, Ibaraki, Japan. Phone: 0299-45-8330; Fax: 0299-45-8351; Email: ezura@nocs.tsukuba-noc.affrc.go.jp.

Fito, Laia. Plant Molec Marker & Pathol Dept, Semillas Fito S.A., c/Selva de Mar, lll, 08019 Barcelona, Spain. Phone: 34 93 3036360; Fax: 34 93 3036373; Email: eulalia@fito.es. Disease resistance and quality of melons (esp. Spanish) & cucumber; breeding schemes & genetic markers.

Gabert, August C. Sunseeds, USA. 8850 59th Ave. NE, Brooks, OR, 97305-9625. Phone: (503) 390-3243; Fax: (503) 390-0982. Email: augie.gaber@sunseeds.com. Cucumber breeding and genetics.

Gabor, Brad. Seminis Vegetable Seeds, 37437 State Hwy 16, Woodland, CA, 95695. Phone: (530) 669-6233; Fax: (530) 666-1620; Email: brad.gabor@seminis.com. Plant pathology.

Ganapathi, A. Dept. Biotechnology, Bharathidasan University, Tiruchirappalli - 620 024, India. Phone: 91-0431-660386; Fax: 91-0431-660245; Email: ganap@bdu.ernet.in.

Garza Ortega, Sergio. Univ Sonora, Dept Agric y Ganaderia, Iturbide #32 Jalisco/N. Heroes, Hermosillo, Sonora 83040, Mexico. Phone: 52-662-213-3013; Fax: 52-662-213-8006: Email: sgarza@rtn.uson.mx. Breeding of *Cucurbita* spp.; testing of new muskmelon lines.

Gatto, Gianni. Esasem Spa, Via San Biagio 25, 37052 Casaleone (VR), Italy. Phone: 0442/331633; Fax: 0442/330834.

Gautier, Jacques. Gautier Graines, BP 1, 13530 Eyragues, France. Phone: 33 (0) 4 90 420 270; Fax: 33 (0) 4 90 240 271; Email: gautier@gautiergraines.fr.

Goldman, Amy P. 164 Mountain view Road, Rhinebeck, NY 12572. Phone: (845) 266-4545; Fax: (845) 266-5232; Email: agoldthum@aol.com. Heirloom melons and watermelons; ornamental gourds. Garden writing.

Gómez-Guillamón, M. Luisa. Estacion Experimental La Mayora, 29750 Algarrobo- Costa, Malaga, Spain. Phone: 34-952-5526560; Fax: 34-952-5526772; Email: guillamon@mayora.csic.es.

Groff, David. 530 Mt. Olive Church Rd., Tifton, GA, 31794. Phone: (229) 382-9452; Email: dave_groff@yahoo.com. Breeding of squash, cucumber, melon and watermelon.

Grumet, Rebecca. Dept. Hort., Plant & Soils Building, Michigan State University, East Lansing, MI, 48824-1325. Phone: (517) 353-5568; Fax: (517) 353- 0890; Email: grumet@msu.edu. Disease resistance, gene flow, tissue culture and genetic engineering.

Gusmini, Gabriele. 5506 Crabtree Park Ct., Raleigh, NC 27612. Phone: (919) 786-0653; Fax: (919) 515-2505\; Email: ggusmin@unity.ncsu.edu. Watermelon breeding.

Hagihara, Toshitsugu. Hagihara Farm Co., Ltd., 984 Hokiji, Tawaramoto, Shiki Nara, 636-0222,

Japan. Phone: 07443-3-3233; Fax: 07443-3-4332; Email: cucurbit@mahoroba.ne.jp.

Haim, Davidi. Hazera Quality Seed Ltd., Mivhor Farm Doar, Sede Gat 79570, Israel.

Hassan, Ahmed Abdel-Moneim. Department of Vegetable Crops, Fac. Agriculture, Cairo University, Giza, Egypt. Phone: 724107 & 724966. Cucumber, melon, squash & watermelon germplasm evaluation and breeding for disease resistance, incl. viruses.

Havey, Michael J. USDA/ARS, Department of Horticulture, University of Wisconsin, Madison, WI, 53706. Phone: (608) 262-1830; Fax: (608) 262-4743; Email: mjhavey@facstaff.wisc.edu.

Hentschel, Richard. Pickle Packers Intl., Inc., P.O. Box 606, St. Charles, IL, 60174-0606. Phone: (630) 584-8950; Fax: (630) 584-0759; Email: staff@ppii.org. Trade Association for pickle vegetables, primarily cucumbers, peppers and cabbage.

Herman, Ran. Zeraim Gedera Ltd., P) Box 103, Gedera 70750, Israel. Phone: 972-52-927079; Fax: 902-8-8594376; Email: ran@zerim.co.il.

Herrington,Mark. Maroochy Research Station, P.O.Box 5083, SCMC, Nambour, QLD, Australia 4560. Phone: 61 07 54449637; Fax: 61 07 54412235; Email: mark.herrington@dpi.qld.gov.au. Winter squash, breeding, virus resistance.

Hertogh, Kees. Nickerson-Zwaan b.v., PO Box 28, 4920 AA Made, The Netherlands. Phone: 31-162-690811; Fax: 31-162 90970; Email: skees.hertogh@nickerson-zwaan.com.

Himmel, Phyllis. Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA, 95695. Phone: (530) 669-6182; Email: phyllis.himmel@svseeds.com. Viral diseases of cucurbits.

Hirabayashi, Tetsuo. Nihon Horticultural Production Inst., 207 Kamishiki, Matsudo-shi, Chiba-ken 270-2221, Japan. Phone: 0473-87-3827; Fax: 0473-86-1455. Varietal improvement of cucurbit crops, especially melon, cucumber and pumpkin.

Hollar, Larry A. Hollar & Co., Inc., P.O. Box 106, Rocky Ford, CO, 81067. Phone: (719) 254-7411; Fax: (719) 254-3539; Email: larry.hollar@hollarseeds.com. Cucurbit breeding and seed production.

Holle, Miguel. CALCE 2, #183 Urb. El Rancho, Miraflores - Lima 18, Peru. Phone: 51-14-383749; Fax: 51-14-351570; Email: m.holle@cgiar.org. Plant genetic resources.

Holman, Bohuslav. Bzinska Str. 1420, Bzenec, CZ-696 81, Czech Republic. Phone: 420-631-384470; Fax: 420-631-384972; Email: bholman@iol.cz. Cucumber breeding and seed production

Humaydan, Hasib. Ag Consulting International, 317 Red Maple Drive, Danville, CA, 94506. Phone: (925) 736-1241; Fax: (925) 736-1241; Email: humaydan@aol.com.

Hutton, Mark. University of Maine, PO Box 179, Monmouth, ME, 04259. Phone: (207) 933-2100; Email: mhutton@umext.maine.edu. Cucurbit breeding and producion.

Iamsangsri, Suphot. Limagrain Veg. Seeds Asia, 119/9 Moo 1, Baan Khao, Muang, Kanchanaburi 71000, Thailand. Phone: 66-2-636-2521-1; Fax: 66-2-636-2524.

Ignart, Frederic. Centre de Recherche TEZIER, Route de Beaumont, Domaine de Maninet, 26000 Valence, France. Phone: (33) 75575757; Fax: (33) 75552681; Email: frederic.ignart@tezier.com. Squash and melon breeding.

Ikegami, Takayuki. Sakata Seed Corp., 1743-2 Yoshioka, Kakegawa, Shizuoka, 436-0115, Japan. Phone: 81-0537-26-1111; Fax: 81-0537-26-1110. Cell biology.

Ito, Kimio. Vegetable Breeding Laboratory, Hokkaido Natl. Agric. Expt. Sta., Hitsujigaoka, Sapporo, Japan 062-8555. Phone: 011(851)9141; Fax: 011(859)2178; Email: kito@cryo.affrc.go.jp.

Jahn, Molly Kyle. Cornell Univ, Dept Plant Brdng, 312 Bradfield Hall, Ithaca, NY, 14853-1902. Phone: (607) 255-8147; Fax: (607) 255-6683; Email: mmk9@cornell.edu. Melon and squash breeding and genetics.

Jain, Jaagrati. B-149 M. P. Enclave, Pitampura, Delhi-110034, India. Email: jaagratijain@rediffmail.com. Melon genetics & tissue culture.

Johnston, Rob, Jr. Johnny's Selected Seeds, 184 Foss Hill Road, Albion, ME, 04910-9731. Phone: (207) 437-9294; Fax: (207) 437-2422; Email: rjohnston@johnnyseeds.com. Squash and pumpkins.

Kampmann, Hans Henrik. Breeding Station Danefeld, Odensevej 82, 5290 Marslev, Denmark. Phone: 65 95 17 00; Fax: 65 95 12 93.

Kanda, Minoru. Kanda Seed Co., Ltd., 262 Shinga, Kashihara, Nara, 634-0006, Japan. Phone: 0744-22-2603; Fax: 0744-22-9073; Email: NAG00014@NIFTY.COM.

Kapiel, Tarek. P.O.Box 550, MAADI. Cairo, Egypt. Email: kapiel@hotmail.com

Karchi, Zvi. 74 Hashkedim St., Kiryat-Tivon 36501, Israel. Phone: 04-9830107; Fax: 972-4-9836936. Cucurbit breeding, cucurbit physiology.

Kato, Kenji. Fac. Agriculture, Okayama Univ., 1-1-1 Tsushima Naka, Okayama, 700, Japan. Phone: 81-86-251-8323; Fax: 81-86-254-0714; Email: kenkato@cc.okayama-u.ac.jp. Use of molecular markers for QTL mapping and cultivar identification in melon.

Katzir, Nurit. Newe Ya'ar Research Center, ARO, P.O. Box 1021, Ramat Yishay, 30095, Israel. Phone: 972-4-9539554; Fax: 972-4-9836936; Email: katzirn@volcani.agri.gov.il.

Keita, Sugiyama. Kurume Branch, Natl Res Inst, Veg/OrnPlnts/Tea, Kurume, Fukuoka 839-8503, Japan. Phone: 81-942-43-8271; Fax: 81-942-43-7014. Watermelon.

Khan, Iqrar A. Dept. Crop Sciences, Cool. Agric., Sultan Qaboos Univ., PO Box-34, Al-Khod 123, Sultanate of Oman. Phone: (+968) 515-213; Fax: (+968) 513-418, Email: iqrar@squ.edu.om.

King, Joseph J. Seminis Vegetable Seeds, Inc., 37437 State Highway 16, Woodland, CA, 95695. Phone: (530) 666-6262; Fax: (530) 666-5759; Email: joe.king@seminis.com. Genetics and breeding of melon, cucumber and squash.

King, Stephen R. Texas A&M University, 1500 Research Pkwy, suite A120, college Station, TX 77845. Phone: (979) 845-2937; Fax: (979) 862-4522; Email: srking@tamu.edu. Watermelon breeding.

Kirkbride, Joseph H., Jr. USDA-ARS, Systematic Bot & Mycol Lab, Rm 304, Bldg 011A, BARC-West, Beltsville, MD, 20705-2350. Phone: (301) 504-9447; Fax: (301) 504-5810; Email: jkirkbri@asrr.arsusda.gov. Systematic taxonomy of the Cucurbitaceae.

Klapwijk, Ad. De Ruiter Zonen CV, Postbus 1050, 2660 BB Bergschenhoek, The Netherlands. Phone: 010-5292253; Fax: 010-5292410.

Knerr, Larry D. Shamrock Seed Company, 3 Harris Place, Salinas, CA, 93901- 4586. Phone: (831) 771-1500; Fax: (831) 771-1517; Email: lknerr@shamrockseed.com. Varietal development of honeydew and cantaloupe.

Konno, Yoshihiro. Asahi Ind., Biol. Engin. Lab., 222 Wataruse, Kamikawa-machi, Kodama-gun, Saitama 367-0394, Japan. Phone: 81-274-52-6339; Fax: 81-274-52-4534; Email: y.konno@asahi-kg.co.jp. Watermelon breeding.

Kraakman, Peter. DeRuiter Zohen, Torre Caribe 7D, Aguadulce (Almeria), Spain. Email: Peter.Kraakman@deruiterseeds.com.

Křístková, Eva. Res Inst Crop Prod, Praha-Ruzyne, Workplace Olomouc, Slechtitelu 11, 738 71 Olomouc, Czech Republic. Phone: 420-68-5228355; Fax: 420-68-5228355; Email: olgeba@ova.pvtnet.cz. Gene bank curating of cucurbitaceous vegetables; powdery mildew resistance in *Cucurbita*.

Kuginuki, Yasuhisa. National Institute Veg/Orn/Tea, Crop Research Station, Ano, Mie 514-2392, Japan. Phone: 0592-68-1331; Fax: 0592-68-1339. Breeding for resistance to disease.

Kuhlmann, Hubert. GlaxoSmithKline Consume Healthcare GmbH & Co. KG, Benzstrasse 25, D-71083 Herrenberg, Germany. Phone: (07032) 922-122; Fax: (07032) 922-202; Email: Hubert.Kuhlmann@gsk.com..

Kuti, Joseph O. 1112 Kathleen, Kingsville, TX 78363. Phone: Breeding and genetics; host-parasite interrelationships; postharvest physiology.

Kwack, Soo Nyeon. Dept Hort Breeding, Mokpo Natl Univ, Dorimri, Chonggyemyun, Muangun, Chonnam 534-729, Korea.

Lanini, Brenda. Harris Moran Seed Co., 9241 Mace Blvd., Davis, CA 95616. Phone: (530) 756-1382; Fax: (530) 756-1016; Email: b.lkanini@harrismoran.com.

Lebeda, Aleš. Palacky University, Dept. Botany, Slechtitelu 11, 783 71 Olumouc, Czech Republic. Phone: 420/68/5228825; Fax: 420/68/5241027; Email: lebeda@prfholnt.upol.cz. Cucurbitaceae, genetic resources, diseases, fungal variability, resistance breeding, tissue culture.

Lee, Do-Hyon. Novartis Seeds Co., Ltd., 8th fl. SungAm Bldg. #114, Nonhyun- dong, Kangnam-ku, Seoul, Korea 135-010. Phone: +82 2 3218 5400; Fax: 82 2 516 2286. Disease resistance.

Lee, Sang Yeb. Breeding Res. Inst., Dongbuhannong Chem., #481-3, Deng Bong-RT, YangSeong-Myun, An Seong, Kyung Ki, South Korea 456-930. Phone: 31-674-6911-5; Fax: 31-674-6916; Email: *syleehan@hanmail.net*.

Legg, Erik. Syngenta Seeds, 12 Chemin de l'Hobit BP 27, Saint-Sauveur 31790, France. Phone: 22-562-799957; Fax: 33-562-799996; Email: *erik.legg@syngenta.com*. Genetics; phylogeny, resistance, molecular markers.

Lehmann, Louis Carl. Louie's Pumpkin Patch, Brinkgatan 6, SE-268 32, Svalov, Sweden. Phone: 46-418-66 3602; Fax: 46-418-663602; Email: *pumpkin.patch@swipnet.se*. Cucurbita - testing of squash and pumpkin for use in Southern Sweden.

Lelley, Tamas. Inst Agrobiotech, Dept Plant Biotech, Konrad Lorenz Str. 20, Tulln, Lower Austria, Austria 3430. Phone: +43 2272 66280 204; Fax: +43 2272 66280 203; Email: *lelley@ifa-tull.ac.at*. *Cucurbita* spp.

Lester, Gene. USDA/ARS, Subtropical Agric Res Lab, 2413 E. Highway 83, Bldg. 200, Weslaco, TX, 78596. Phone: (956) 447-6322; Fax: (956) 447-6323; Email: *glester@welasco.ars.usda.gov* Stress, pre/postharvest physiology and human wellness nutrient content of melons.

Levi, Amnon. U.S. Vegetable Laboratory, 2875 Savannah Highway, Charleston, SC, 29414. Phone: (843) 556-0840; Fax: (834) 763-7013; Email: *alevi@awod.com*.

Lin, Depei. Xinjiang Xiyu Seed Co Ltd, No. 32 East Ningbian Rd., Changji 831100, China. Phone: 86-994-2388298; Fax: 86-994-2348415; Email: *xxyhl-cj@mail.xj.cninfo.net*. Watermelon, melon and *Cucurbita* breeding.

Liu, Wenge. Zhengzhou Fruit Research Inst, Chinese Academy of Agric Sci, Zhengzhou, Henan, P.R. China 450009. Phone: (0371) 6815703; Fax: (0371) 6815771; Email: *wlirong@public2.zz.ha.cn*. Watermelon breeding, male sterility, tetraploids, triploids.

Lopez Anido, Fernando. Universidad Nacional Rosario, CC 14, Zavalla S 2125 ZAA, Argentina. Phone: 54-3414970057; Fax: 54-3414970085; Email: *felopez@fcagr.unr.edu.ar*. Breeding of *Cucurbita pepo* L. (caserta type).

Love, Stephen Loyd. Aberdeen R&E Center, P.O. Box AA, Aberdeen, ID, 83210. Phone: (208) 397-4181; Fax: (208) 397-4311; Email: *slove@uidaho.edu*. Small scale private watermelon breeding with emphasis on adaptation to cold climates.

Lower, Richard L. Coll. Agriculture, Univ. Wisconsin, 1450 Linden Drive, Room 240, Madison, WI, 53706. Phone: (608) 262-2349; Fax: (608) 265-6434; Email: *richard.lower@ccmail.adp.wisc.edu*. Effects of plant type genes on yield, sex- expression, growth parameters, pest resistance & adaptability.

Loy, J. Brent. Dept. Plant Biology, Univ. New Hampshire, Durham, NH, 03824. Phone: (603) 862-3216; Fax: (603) 862-4757; Email: *jbloy@christa.unh.edu*. Squash, melon, pumpkin. Genetics, breeding, plasticulture, mulch, rowcovers.

Maluf, Wilson Roberto. Dept. de Agricultura/UFLA, Caixa Postal 37, 37200-000 Lavras-MG, Brazil. Phone: (035) 829-1326; Fax: (035) 829-1301; Email: *wrmaluf@ufla.br*. Cucumbers, melons, squashes.

Martin, Heidi. Queensland Horticultural Institute,. LMB 7, MS 437, Warrego Hwy., Queensland, Australia 4343. Phone: 61 7 54662222; Fax: 61 7 54623223; Email: *Heidi.Martin@dpi.qld.gov.au*. Plant pathology, with interest in melon diseases, especially watermelon fruit blotch.

Martyn, Ray D. Dept. Botany & Plant Pathology, Purdue Univ., 915 West State St., West Lafayette, IN, 47907-1155. Phone: (765) 494-4615; Fax: (765) 494-0363; Email: *Martyn@btny.purdue.edu*. Soilborne diseases of watermelon and melon, particularly the Fusarium wilts and vine declines.

Matsuura, Seiji. Kiyohara Breeding Sta., Tohoku Seed Co., 1625 Nishihara, Himuro, Utsunomiya, Japan. Phone: 0286-34-5428; Fax: 0286-35-6544.

Mayberry, Mella-Dee. Seminis Vegetable Seeds, 37437 State Hwy 16, Woodland, CA, 95695. Phone: (530) 669-6185; Fax: (530) 666-2308; Email: *Mella-Dee.Mayberry@seminis.com*.

Maynard, Donald N. University of Florida, 5007 60th Street East, Bradenton, FL, 34203. Phone: (941) 751-7636; Fax: (941) 751-7639; Email: *dnmara@mail.ifas.ufl.edu*. Tropical moschata improvement; watermelon variety evaluation and production practices.

McClurg, Charles A. University of Maryland, Dept. Natural Resource Sci., College Park, MD, 20742-

4452. Phone: (301) 405-4342; Fax: (301) 314-9308; Email: cm19@umail.umd.edu. Production and culture of cucurbit crops.

McCreight, J.D. USDA-ARS, 1636 E. Alisal St., Salinas, CA, 93905. Phone: (831) 755-2864; Fax: (831) 755-2814; Email: jmccreight@pw.ars.usda.gov. Melon breeding and genetics.

McGrath, Desmond John. Dept. Primary Ind., Hortic. Res. Sta., P.O. Box 538, Bowen, Queensland 4805, Australia. Phone: +61-7-4785 2255; Fax: +61-7-4785 2427; Email: mcgratdj@prose.dpi.qld.gov.au. Disease resistance in *Cucumis melo*, particularly gummy stem blight.

Meadows, Mike. Syngenta Seeds, Inc., 10290 Greenway Road, Naples, FL, 34114. Phone: (941) 775-4090; Fax: (941) 774-6852; Email: mike.meadows@syngenta.com. Vegetable diseases.

Merrick, Laura C. Dept. Agron., Iowa St. Univ, G207 Agronomy Hall, Ames, IA, 50011-1010. Phone: (515) 294-7636; Fax: (515) 294-3163; Email: lmerrick@iastate.edu. *Cucurbita* evolution; cucurbit germplasm evaluation and conservation; ethnobotany and evolution.

Miranda, Baldwin. Sakata Seed America, P.O, Box 1118, Lehigh Acres, FL. 33970. Phone: (941) 369-0032; Fax: (941) 369-7528; Email: bmiranda@sakata.com.

Mochizuki, Tatsuya. NARC – KyushuOkinawa Reg. 2421, Suya, Nishigoshi-machi, Kikuchi-gu, Kumamoto 861-1192, Japan. Phone: 81-96-242-7682; Fax: 81-96-242-7769; Email: tmochi@affrc.go.jp.

Morelock, Ted. Dept. Horticulture & Forestry, University of Arkansas, Fayetteville, AR, 72701. Phone: (501) 575-2603; Fax: (501) 575-8619; Email: morelock@comp.uark.edu. Cucumber breeding.

Munger, H.M. Cornell University, 252 Emerson Hall, Ithaca, NY, 14853. Phone: (607) 255-7820; Fax: (607) 255-6683; Email: hmm11@cornell.edu. Cucurbit breeding and disease resistance.

Myers, James R. Dept. Horticulture, Oregon State Univ., 4137 Ag Life Sciences Bldg., Corvallis, Oregon, 97331. Phone: (541) 737-3083; Email: myersja@bcc.orst.edu.

Nadel, Michael. 10851 Woodbine Street, Los Angeles, CA, 90034. Phone: (310) 838- 7675; Fax: (310) 202-7466; Email: dansonseed@mediaone.net. Breeding summer squash, cucumbers, melons and watermelons.

Nannes, Jeroen Seminis Vegetable Seeds, P.O. Box 93, 2675 ZH Honselersdijk, The Netherlands. Email: jnannes@svseeds.nl. Breeding slicing cucumber.

Navazio, John P. Chriseed, P.O. Box 98, Mount Vernon, WA, 98273-0098. Phone: (360) 336-9727; Fax: (360) 424-9520; Email: john_navazio@alfseed.com. Breeding for increased pigments in cucurbits, carrots and beets.

Neill, Amanda. The Botanical Research Inst. Of Texas, 509 Pecan St., Fort Worth, TX, 76102-4060. Email: aneill@brit.org. *Gurania* and *psiguria.*

Ng, Timothy J. Dept. Natural Resource Sci., University of Maryland, College Park, MD, 20742-4452. Phone: (301) 405-4345; Fax: (301) 314-9308; Email: tn5@umail.umd.edu. Melon breeding and genetics; postharvest physiology; seed germination.

Niemirowicz-Szczytt, Katarzyna. Warsaw Ag Univ, Dept Gen & Plt Brdng, ul. Nowoursynowska 166, 02-766 Warsaw, Poland. Phone: (48-22) 843 09 82; Fax: (48-22) 843 90 61; Email: niemirowicz@alpha.sggw.waw.pl. Cucumber, melon, winter and summer squash, watermelon - genetics, breeding, tissue culture, biotechnology.

Nuez, Fernando. Cat.de Genetica, ETS Ingen. Agron., Univ. Politecnica, Camino de Vera, 14, 46020 Valencia, Spain. Phone: 34 (6) 387-74-21; Fax: 34 (6) 387-74- 29; Email: fnuez@btc.upv.es. Genetics and plant breeding.

Oliver, Marc. Syngenta Seeds, SAS. 12, Chemin de l'Hobit, 31790 Saint-Sauveur, France. Phone: 33 (0) 562799838; Fax: 33 (0) 562799990; Email: marc.oliver@syngenta.com. Cucurbit genetic technology.

Om, Young-Hyun. Natl Horticultural Res Inst, 475 Imok-Dong, Suwon 440-310, Republic of Korea. Phone: 82-0331-290-6171; Fax: 82-0331-295-9548; Email: omyh@nhri.go.kr. Breeding of cucurbit vegetables.

Omara, Sadig Khidir. Dept. Horticulture, Fac. Agric. Sci., University of Gezira, Wad Medani, P.O. Box 20, Sudan.

Ouyang, Wei. Magnum Seeds, Inc. 5825 Sievers Rd., Dixon, CA, 95620. Phone: (707) 693-6815; Fax: (707) 693-6814; Email:

weiouyang1@yahoo.com. Squash, watermelon, and melon breeding.

Owens, Ken. Magnum Seeds, Inc. 5825 Sievers Road, Dixon, CA, 95620. Phone: (707) 693-6815; Fax: (707) 693-6814; Email: kobreeding@hotmail.com. Cucumber breeding.

Pachner, Martin. Hadikgasse 44/3, A-1140 Wien, Austria. Phone: 43/(0)2272/66280/256; Fax: 43/(0)2272/66280/203; Email: *pachner@ifa-tulln.ac.at*.

Palomares, Gloria. Dept Biotecnologia, Univ Politecnica, Camino de Vera, s/n., E-46022 Valencia, Spain. Phone: 34(6)387-7426; Fax: 34(6)387-7429; Email: gpaloma@btc.upv.es. Genetic improvement in horticultural plants.

Paris, Harry. Dept. Vegetable Crops, A.R.O., Newe Ya'ar Research Ctr, PO Box 1021, Ramat Yishay 30-095, Israel. Phone: 972-4-9894516; Fax: 972-4-9836936; Email: hsparis@volcani.agri.gov.il. Breeding and genetics of squash and pumpkin.

Piero Abril, Jose Luis. Apartado de Correos no. 2, E 04720 Aguadulce, Almeria, Spain. Phone: +34 950 34 22 35; Fax: +34 950 34 22 35; Email: pieroab@laral.es. Breeding melons, watermelons and cucumber.

Perl-Treves, Rafael. Dept. Life Science, Bar-Ilan University, Ramat-Gan, Israel 52900. Phone: 972-3-5318249; Fax: 972-3-5351824; Email: perl@brosh.cc.biu.ac.il.

Peter, K.V. Kerala Agriculture University, PO KAU Vellankkara, Trichur, India 680656. Phone: 011-91-487-370347; Fax: 011-91-487370019; Email: vckau@vsnl.com.

Peterson, Paul S. Plant Pest Diagnostic Center, 3294 Meadowview Road, Sacramento, CA, 95832-1448. Phone: (916) 262-1139; Fax: (916) 262-1190; Email: ppeterso@cdfa.ca.gov. Laboratory germination and seed quality assessment.

Pettit, Fred. Epcot Science, Walt Disney World Co., Lake Buena Vista, FL 32830-0040. Phone: (407) 560-7367; Fax: (407) 560-7227.

Picard, Florence. Vilmorin, Route du Manoir, 49 250 La Menitre, France. Email: vilmorin01@brettcomp.com.

Pitrat, Michel. INRA, Domaine St. Maurice, BP 94, 84143 Montfavet cedex, France. Phone: (33) 90 31 63 30; Fax: (33) 90 31 63 98; Email: Michel.Pitrat@avignon.inra.fr. Melon, disease resistance, mutants, genetic map.

Poostchi, Iraj. 97 St. Marks Road, Henley-on-Thames RG9 1LP, England. Phone: (01491) 574959; Fax: (10491) 574500. Breeding cantaloupes, melons and watermelons.

Poulos, Jean M. Seminis Vegetable Seeds, Via Canneto Di Rodi, Borgo Sabotino Latina, 04010 Italy. Phone: 39-773- 643722; Fax: 39-773-643729; Email: jpoulos@svseeds.nl.

Price, E. Glen. Sugar Creek Seed, Inc., P.O. Box 508, Hinton, OK, 73047. Phone: (405) 542-3920; Fax: (405) 542-3921; Email: sgrcrksd@hintonet.net. Seedless watermelon; polyploidy, genetics, breeding, cytogenetics.

Provvidenti, Rosario. Cornell Univ., Dept. Plant Pathology, NY State Agric. Experiment Sta., Geneva, NY, 14456-0462. Phone: (315) 787-2316; Fax: (315) 787- 2389; Email: rp13@cornell.edu. Breeding & genetics of resistance to viral diseases of cucumber, squash, melon, watermelon & other cucurbits.

Ramirez, Maria del Pilar. Ciudad de la Investigacion, Universidad de Costa Rica, San Jose, Costa Rica. Phone: 506-2073192; Fax: 506-20763190; Email: pramirez@cibcm.ucr.ac.cr. Viruses in cucurbits, production of resistant transgenic plants.

Randhawa, Lakhwinder. Sutter Seeds, 1469 Stewart Road, Yuba City, CA 95993. Phone: (530) 674-2512/2566; Fax: (530) 674-2721; Email: *sutteresearch@aol.com*. Watermelon, squash nd melon breeding, disease and virus resistance, germplasm, biotechnology.

Randhawa, Parm. CA Seed & Plant Labm, 7877 Pleasant Grove Rd., Elverta, CA 95626. Phone: (916) 655-1581; Fax: (916) 655-1582; Email: randhawa@calspl.com.

Ray, Dennis. Department of Plant Sciences, University of Arizona, Tucson, AZ, 85721. Phone: (520) 621-7612; Fax: (520) 621-7186; Email: dtray@u.arizona.edu. Genetics and cytogenetics of *Cucumis melo* and *Citrullus* spp.

Reiten, Joel. Territorial Seed Co., P.O. Box 157, Cottage Grove, OR, 97424. Phone: (541) 942-9547; Fax: (541) 942-9881; Email: tsc@ordata.com. Bacterial wilt resistance, as well as virus resistance obtained through traditional breeding methods.

Reuling, Gerhard T.M. Nunhems Zaden B.V., P.O. Box 4005, 6080 AA Haelen, The Netherlands. Phone: 31-475-599344; Fax: 31-475-591361; Email: g.reuling@nunhems.com. Cucumber breeding.

Rhodes, Bill B. Clemson Univ./Horticulture, Poole Agricultural Center, Clemson, SC, 29634-0375. Phone: (864) 656-0410; Fax: (864) 656-4960; Email: BRhodes@clemson.edu. Watermelon genetics, breeding, micropropagation, disease resistance, male sterility, triploids.

Robinson, R.W. Dept. Hort. Sci., New York State AES, Hedrick Hall, Geneva, NY, 14456-0462. Phone: (315) 787-2237; Fax: (315) 787-2397; Email: rwr1@cornell.edu. Breeding and genetics of cucurbits.

Robledo, Claude. Seminis - Recherch France, Mas de Rouzel - Chemin des Canaux, 30900 Nimes, France. Phone: 33-4-66-387974; Fax: 33—44-66-387981; Email: crobledo@seminis.com. Melon breeding.

Roig, Luis A. Departamental Biotechnology, ETS Ingen. Politec., Camino de Vera 14, 46022 - Valencia, Spain. Phone: 34(6) 3877424; Fax: 34(6) 3877429.

Rorem, Kent. Seminis Vegetable Seeds, P.O. Box 667, Arvin, CA, 93203. Phone: (805) 854-2390; Fax: (805) 854-4379. Melon and watermelon breeding and disease resistance.

Ruttencutter, Glen. Sunseeds, 7087 E. Peltier Road, Acampo, CA 95220. Phone: (209) 367-1064; Fax: (209) 367-1066; Email: glen.ruttencutter@sunseeds,com.

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

Sanghani, Amul. Unicorn Agrotech Ltd., 1-7-139/3, S.D. Road, Hyderabad, A.p., India 500 003. Phone: +91 40 7811554; Fax: +91 40 7842399; Email: uniagro@hd1.vsnl.net.in.

Schultheis, Jonathan R. Dept. Horticulture, 264 Kilgore Hall, North Carolina St. University, Raleigh, NC, 27695-7609. Phone: (919) 515-1225; Fax: (919) 515-2505; Email: jonathan_schultheis@ncsu.edu. Cultural management of cucurbits; plant spacing, establishment, nutrition, pollination & cultivar evaluation.

Shetty, Nischit V. Seminis Vegetable Seeds, 432 TyTy Omega Road, Tifton, GA, 31794. Phone: (229) 386-8701; Fax: (229)288-8805; email: nischit.shetty@seminis.com. Cucumber breeding.

Shifriss, Oved. 21 Walter Avenue, Highland Park, NJ, 08904-1709. Precocious pigmentation in *Cucurbita*.

Shindo, Eiichi. 282-4-1-102 Ushiku, Ichihara, Chiba, Japan 290-0225. Phone: 0470-82-2413, Email: e-shindo@mikadoagri.com. Watermelon, melon, pumpkin.

Simon, Philipp W. USDA/ARS-Veg Crops, Dept. Hort., Univ. Wisconsin, 1575 Linden Dr., Madison, WI, 53706. Phone: (608) 262-1248; Fax: (608) 262-4743; Email: psimon@facstaff.wisc.edu. Breeding and genetics.

Sipeyre, Bruno. Mas de Rouzel, Seminis Frace, Chemin des Canaux, 30900 Nimes, France. Phone: 04 66 38 79 78; Fax: 04 66 38.79 81. Email: bsipeyre@svseeds.nl. Plant breeding.

Staub, Jack E. USDA-ARS, Dept. Horticulture, Univ. Wisconsin, Madison, WI, 53706-1590. Phone: (608) 262-0028; Fax: (608) 262-4743; Email: jestaub@facstaff.wisc.edu. Cucumber breeding & genetics, physiology, biochemical genetic markers, evolution, environmental stress.

Stephenson, Andrew G. 208 Mueller Lab, Penn State University, University Park, PA, 16802. Phone: (814) 863-1553; Fax: (814) 865-9131; Email: as4@psu.edu.

Stravato, Vittorio Mario. via Carlo Levi n. 18, 04022 Fondi -Latina, Italy. Phone: 771-510729; Fax: 771-555036; Email: sumas@tiscalinet.it. Disease resistance in Cucurbitaceae species.

Summers, William L. Iowa State University, Dept. Horticulture, Rm. 251, Ames, IA, 50011-1100. Phone: (515) 294-1978; Fax: (515) 294-0730; Email: summers@iastate.edu. Genetic improvement of watermelon.

Sušić, Zoran. Inst. Srbija - Ctr Vegetable Crops, Karadjordjeva St. 71, 11420 Smederevska Palanka, F.R. Yugoslavia. Phone: 381-26-323-170; Fax: 381-26-323- 785; Email: cfvcsp@eunet.yu. Genetics and breeding of *Cucurbita* species; cucumber breeding.

Swanepoel, Cobus. Pannar, P.O. Box 19, Greytown KZN 3250, South Africa. Phone: 27-33-413-9643; Fax: 27-33-417-1208; Email: cobus.swanepoel@pannar.co.za.

Tatlioglu, Turan. Institut of Applied Genetics, Univ. Hannover, Herrenhauser Str. 2, 3000 Hannover, Germany. Phone: (+49)511762-5675; Fax: (+49)511762-3608; Email: turan.tatlioglu@mbox.genetik.uni-hannover.de. Hybrid breeding, male sterility (GMS, CMS) and sex inheritance.

Taurick, Gary. Harris Moran Seed Co., P.O. Box 392, Sun Prairie, WI, 53590. Phone: (608) 837-6574; Fax: (608) 837-3758; Email: g.taurick@harrismoran.com. Development of commercial hybrids of pickle, slicer and Beit Alpha cucumbers.

Teppner, Herwig. Inst. Botany, Karl-Franzens Univ., Holteigasse 6, A-8010 Graz, Austria. Phone: 316-380-5656; Fax: 316-380-9883; Email: herwig.teppner@kfunigraz.ac.at. Systematics, morphology, ecology, crops & medicinal plants (teaching) and small scale breeding.

Thomas, Claude E. USDA-ARS, U.S. Vegetable Laboratory, 2875 Savannah Highway, Charleston, SC, 29414. Phone: (803) 556-0840; Fax: (843) 763-7013; Email: cthomas@awod.com. Disease resistance in cucurbits.

Thompson, Gary A. Univ Arkansas LR, Dept Appl Sci, 575 ETAS Bldg, 2801 S. University Ave, Little Rock, AR, 72204-1099. Phone: (501) 371-7506; Fax: (501) 569-8020; Email: gathompson@ualr.edu. Biotechnology.

Tolla, Greg. Seminis Vegetable Seeds, 432 TyTy Omega Rd., Tifton, GA, 31794. Phone: (229) 386-8701; Fax: (229) 386-8805. Email: greg.tolla@seminis.com. Cucumber breeding and genetics.

Vakalounakis, Demetrios J. Plant Protection Inst., N.A.R.F., P.O. Box 1802, 711 10 Heraklio, Crete, Greece. Phone: 3081-240.986; Fax: 3081-245.858; Email: vakaloun@nefeli.imbb.forth.gr.

van Kooten, Henk C. Seminis Vegetable Seeds, Wageningse Afweg 31, 6702 PD Wageningen Utrecht 6702PD, The Netherlands. Phone: 31-317-468468; Fax: 31-317-468469; Email: henkvan.kooten@seminis.nl. Breeding pickling cucumber.

van Luijk, Maartje "Marleen". East West Seed Co., Jose Dela Cruz St Matimbubong, San Idelfonso Bulacan, The Philippines. Phone: 63 44 9011370; Fax: 63 44 9011250; Email: info.ph.@eastwestseed.com. Breeding of cucurbits adapted to tropical conditions.

Vardi, Eyal. Hazera Genetics, Mivhor M.P. Lachish Daron 79354, Israel. Phone: 972-8-68781328; Fax: 972-8-6814057; Email: vardi@hazera.com.

Vecchio, Franco. c/o Sementi Nunhems, via Ghiarone, 2, S. Agata Bolognese, BO, Italy 40019. Phone: #39-051-6817411; Fax: #39-051-6817400; Email: Franco.Vecchio@nunhems.com. Breeding zucchini.

Walters, Terrence. The Cucurbit Network, P.O.Box 560483, Miami, FL, 33156. Phone: (305) 669-9281; Fax: (305) 661-5984; Email: cucurbitnetwork@netscape.net. Communication via The Cucurbit Network; the whole family Cucurbitaceae.

Wang, Gang. 84 Orange Street, Woodbridge, NJ, 07095. Email: w2140@hotmail.com. Watermelon and melon breeding.

Watterson, Jon. Seminis Vegetable Seeds, Inc., 37437 Highway 16, Woodland, CA, 95616. Phone: (530) 669-6157; Fax: (530) 666-6791. Cucumber, melon, watermelon, squash, pumpkin, gourd germplasm and disease resistance.

Wehner, Todd C. Dept. Horticultural Science, Box 7609, North Carolina St. Univ., Raleigh, NC, 27695-7609. Phone: (919) 515-5363; Fax: (919) 515-2505; Email: todd_wehner@ncsu.edu. Pickling/slicing cucumber, watermelon, luffa gourd; selection, disease resistance, yield, genetics & chilling.

Wessel-Beaver, Linda. Agronomy & Soils Dept., Univ. Puerto Rico, PO Box 9030, Mayaguez, PR, 00681-9030. Phone: (787) 832-4040; Fax: (787) 265-0220; Email: l_beaver@rumac.upr.clu.edu. Pumpkin & squash breeding; disease resistance; insect resistance.

Williams, Tom V. Syngenta Seeds, 10290 Greenway Road, Naples, FL, 34114-3199. Phone: (941) 775-4090; Fax: (941) 774-6852; Email: tom.williams@syngenta.com. Watermelon breeding.

Winkler, Johanna. Saatzucht Gleisdorf GesmbH, Am Tieberhof 33, 8200 Gleisdorf, Austria. Phone:

43 3112 21050; Fax: 43 3112 21055; Email: winkler.szgleisdorf@utanet.at.

Wolff, David W. Sakata Seed America, Inc., P.O. Box 1118, Lehigh Acres, FL, 33970-1118. Phone: (941) 369-0032 x13; Fax: (941) 369-7528; Email: dwolff@sakata.com. Watermelon breeding and genetics; molecular markers.

Wu, Mingzhu. Hort Inst, Xinjiang Acad Agric Sci, Nanchang Road NO. 38, Urumqi, Xinjiang 830000, China. Phone: 86-0991-45331331; Fax: 86-0991-4533133; Email: mawu@x263.net.

Yamanaka, Hisako. Yamato-Noen Co., Ltd., 110, Byodobo-cho, Tenri-City, Nara, Japan 632-0077. Phone: 07436-2-1182; Fax: 07436-3-3445.

Yang, Dong-Hoon. Seminia Korea Res. Inst., #331-3, Jeonjoong, Kangwaemyun, Chongwon-kun, chungbuk, 363-950, Republic of Korea. Phone: +82-41-862-5441; Fax: +82-41-862-0799; email: dhyang@SeminisAsia.com. Breeding of watermelon, bottle gourd and melon varieties which have good fruit quality and disease resistance,

Yorty, Paul. Qualiveg Seed Production, 3033 E., 3400 N., Twin Falls, ID, 83301. Phone: (208) 733-0077; Fax: (208) 733-0077. Cucurbit breeding.

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

Zhang, Xingping. Syngenta Seeds, 21435 Rd 98, Woodland, CA, 95695. Phone: (530) 666-0986; Fax: (530) 666-5273; Email: xingping.zhang@syngenta.com. Watermelon and melon genetics & breeding.

Zitter, Thomas A. Cornell Univ., Dept. Plant Pathology, 334 Plant Science Building, Ithaca, NY, 14853-5908. Phone: (607) 255-7857; Fax: (607) 255-4471; Email: taz1@cornell.edu. Fungal and viral diseases; disease resistance.

CGC Members in the United States

Alabama
Fenny Dane

Arizona
Dennis Ray

Arkansas
Ted Morelock
Gary A. Thompson

California
Warren S. Barham
Paul Chung
Gary Elmstrom
Brad Gabor
Phyllis Himmel
Hasib Humaydan
Joseph J. King
Larry D. Knerr
Brenda Lanini
Mella-Dee Mayberry
J.D. McCreight
Michael Nadel
Wei Ouyang
Ken Owens
Paul S. Peterson
Parma Randhawa
Lakwinder Randhawa
Kent Rorem
Glen Ruttencutter
Jon Watterson
Xingping Zhang

Colorado
R. Bruce Carle
Larry A. Hollar

Florida
Kevin L. Cook
Deena Decker-Walters
Donald N. Maynard
Mike Meadows
Baldwin Miranda
Fred Pettit
Terrence Walters
Tom V. Williams
David W. Wolff

Georgia
George E. Boyhan
David Groff
Nischit V. Shetty
Greg Tolla

Idaho
Stephen Loyd Love
Paul Yorty

Illinois
Richard Hentschel

Indiana
Orie J. Eigsti
Ray D. Martyn

Iowa
Glenn Drowns
Laura C. Merrick
William L. Summers

Kansas
Edward E. "Ted" Carey

Maine
Mark Hutton
Rob Johnston

Maryland
Joseph Kirkbride
Charles A. McClurg
Timothy J. Ng

Michigan
Rebecca Grumet

Missouri
Alejandro "Alex" Ching

New Hampshire
J. Brent Loy

New Jersey
Oved Shifriss
Gang Wang

New York
Thomas C. Andres
Amy P. Goldman
Molly Kyle Jahn
H.M. Munger
Amanda Neill
Rosario Provvidenti
R.W. Robinson
Thomas A. Zitter

North Carolina
Phil Denlinger
Gabriele Gusmini
Jonathan R. Schultheis
Todd C. Wehner

Oklahoma
Benny Bruton
Angela Davis
E. Glen Price

Oregon
Rebecca Brown
Louis Victor Di Nitto
August C. Gabert
James R. Myers
Joel Reiten

Pennsylvania
Andrew G. Stephenson

Puerto Rico
Linda Wessel-Beaver

South Carolina
Amnon Levi
Bill B. Rhodes
Claude E. Thomas

Texas
Robyn Coffey
Kevin Crosby
Stephen R. King
Joseph O. Kuti
Gene Lester

Washington
John P. Navazio

Wisconsin
Michael J. Havey
Richard L. Lower
Philipp W. Simon
Jack E. Staub
Gary Taurick

International CGC Members

Argentina
Fernando Lopez Anido

Australia
Douglas A. Blazey
Desmond John McGrath
Mark Herrington
Heidi Martin

Austria
Tamas Lelley
Martin Pachner
Herwig Teppner
Johanna Winkler

Brazil
Paulo T. Della Vecchia
Wilson Roberto Maluf
Waldelice Oliveira de Paiva

China, Republic of
Jin Feng Chen
Depei Lin
Mingzhu Wu
HaiQing Bao
Hongwen Cui
Jiannong Zhang
Wenge Liu

Costa Rica
Maria del Pilar Ramirez

Czech Republic
Bohuslav Holman
Eva Křístková
Aleš Lebeda

Denmark
Hans Henrik Kampmann

Egypt
M. Hossam Aboul-Nasr
Ahmed Abdel-Moneim Hassan
Tarek Kapel

England
Iraj Poostchi

France
Sylvie Baudracco-Arnas
Frank De Langen
Frederic Ignart
Erik Legg
Florence Picard
Michel Pitrat
Claude Robledo
Bruno Sipeyre
Marc Oliver
Jacques Gautier

Germany
Hubert Kuhlmann
Turan Tatlioglu

Greece
Nicholas E. Fanourakis
Demetrios J. Vakalounakis

Guadeloupe (F.W.I.)
Nathalie Boissot

India
A. Ganapathi
Jaagrati Jain
Amul Sanghani
K.V. Peter

Indonesia
Doretta Akkermans

Israel
Yosi Burger
Ron Cohen
Yigal Cohen
Davidi Haim
Ran Herman
Zvi Karchi
Nurit Katzir
Harry Paris
Eyal Vardi
Rafael Perl-Treves

Italy
Jean M. Poulos
Erik de Groot
Gianni Gatto
Vittorio Mario Stravato
Franco Vecchio

Japan
Hiroshi Ezura
Toshitsugu Hagihara
Tetsuo Hirabayashi
Takayuki Ikegami
Minoru Kanda
Kenji Kato
Sugiyama Keita
Yoshihiro Konno
Yasuhisa Kuginuki
Seiji Matsuura
Tatsuya Mochizuki
Takeo Saito
Kimio Ito
Hisako Yamanaka
Eiichi Shindo

Korea, Republic of
Soo Nyeon Kwack
Young-Hyun Om
Do-Hyon Lee
Sang Yeb Lee
Dong-Hoon Yang
Myeong-Cheoul Cho

Malta
Everaldo Attard

Mexico
Sergio Garza Ortega

Netherlands, The
Monique Bosma
Kees Hertogh
Ad Klapwijk
Jeroen Nannes
Gerhard T.M. Reuling
Henk C. van Kooten

Oman, Sultanate of
Iqrar A. Khan

Peru
Miguel Holle

Philippines, The
Maartje "Marleen" van Luijk

Poland
Katarzyna Niemirowicz-Szczytt

South Africa
Cobus Swanepoel

Spain
Maria Cruz Ayuso
Laia Fito
M. Luisa Gómez-Guillamón
Peter Kraakman
Fernando Nuez
Gloria Palomares
José Luis Peiro Abril
Luis A. Roig
Maarten Den Hertog

Sudan
Sadig Khidir Omara

Sweden
Louis Carl Lehmann

Taiwan
Fure-Chyi Chen

Thailand
Simon Jan De Hoop
Usa Duangsong
Suphot Iamsangsri
Vinich Chuanchai

Turkey
Gülat Çaglar
Remzi Dogan

Yugoslavia
Janos Berenji
Zoran Sušić

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.