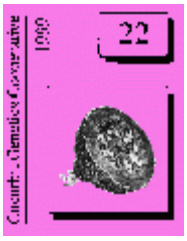
Cucurbit Genetics Cooperative



Report No. 22

July 1999

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Cucurbit Genetics Cooperative Report 22:v-ix (article 0) 1999

Cucurbitaceae 2000

VIIth EUCARPIA Meeting on Cucurbit Genetics and Breeding

Cucurbitaceae 2000, the VIIth Eucarpia Meeting on Cucurbit Genetics and Breeding, will be held in Israel on March 19-23, 2000. The meeting will offer the opportunity to get together and discuss the latest developments in cucurbit genetics, breeding, germplasm enhancement, pathology and related fields. This promises to be an exciting scientific program, and a unique opportunity to visit Israel in the year 2000.

The meeting will convene at the Ma'ale Hachamisha Resort and Convention Center, situated in the beautiful Judean Hills on the road to Jerusalem. All sessions will take place at this venue, and the meeting will be conducted in English.

The *Organizing Committee* for Cucurbitaceae 2000 consists of Nurit Katzie (Chair), Ron Cohen, Menahem Edelstein and Zvi Karshi, all of Newe Ya'ar Research Center, ARO. The *Advisory Board* includes Shlomo Cohen (Volcani Center, ARO), Yigal Cohen (Bar-Ilan University), Guy Elyashiv (Zeraim Ltd,), Haim Nerson (Newe Ya'ar Research Center, ARO, Rivka Offenbach (R&D Arava), Harry S. Paris (Newe Ya'ar Research Center, ARO), Rafael Perl-Treves (Bar-Ilan University), Arthur Schaffer (Volcani Center, ARO) and Eyal Vardi (Hazera Ltd).

The Ma'ale Hachamisha Resort and Convention Center is a 30 minute drive from Ben Gurion International Airport and a 15 minute drive from Jerusalem. The hotel has spacious, air-conditioned guestrooms with private baths, radio, telephone and TV. A full range of indoor and outdoor recreation facilities are available. These include Spa and Health Club, offering an indoor heated pool and an outdoor swimming pool (in season), tennis courts, lawns and gardens, restaurants and coffee shops.

During the meeting we will visit the Arav, Israel's premier region for winter growing of cucurbits, the Deed Sea and the historical site of Massada. There will be a special program for accompanying persons, and also several options for post-conference tours.

Israel is situated on the crossroads of thee continents and offers a variety of scenic, historical and cultural attractions. Jerusalem, Bethlehem, Nazareth, the Dead Se and many other exciting sites are all within less than a day's drive from the Ma'ale Hachamisha Kibbutz. We welcome you to experience the historical, biblical and modern aspects of this exceptional land and its people.

COMMENTS

From the CGC Coordinating Committee: The Call for Papers for the 2000 Report (CGC Report No. 23) will be mailed in October 1999 Papers should be submitted to the respective Coordinating Committee members by 313 January 2000, although the late submissions may be considered if received prior to our processing deadline. The Report will be published by July 2000. 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 known marker genes. CGC members are requested to forward samples of currently held gene stocks to the respective Curator.

NEWS

The second announcement, including the "Call for Papers," will be sent in September, 1999 to those who responded to the first announcement. The format for scientific manuscripts will follow that of the CGC Style Guide. For more information, contact the Secretariat/Organizers at:

- *EUCARPIA CUCURBITACEAE 2000*
- *C/O International Travel & Congress Ltd.*
- *P.O. Box 29313, Tel Aviv 61292, Israel*
- *Tel: +972-3-7951444*
- *Fax: +972-3-5107716*
- *Email: 100264.2432@compuserve.com*

Also, the latest information about Cucurbitaceae 2000 can always be found at the CGC website: http://probe.nalusda.gov/otherdocs/cgc

CGC Business Meetings

Timothy J. Ng, Chair

The 1998 cucurbit Genetics Cooperative Business Meeting was held on 15 July in charlotte, North Carolina, and was reported on in CGC Report No. 21 (1998). The 1999 CGC Business Meeting was held on 28 July 1999 in Minneapolis, Minnesota, with Dennis Ray (CGC Coordinating Committee Member for watermelon) presiding. A full report of this meeting will appear in CGC Report No. 23 (2000).

Watermelon Research and Development Working Group

Joint Report

Cucurbitaceae /98, Pacific Grove, California (1 December, 1998) and 19th Annual Meeting, memphis, Tennessee (31 January 1999)

Benny D. Brown, Chair.

The Watermelon Research and Development Working Group (WRDWG) met on tuesday, December 1, 1998 in Pacific Grove, California. The meeting was held at the Asilomar Conference Center in Conjunction with the Cucurbitaceae '98. More than 50 people were present and many more turned away because of seating capacity. Seven research reports were presented, generating a lot of discussion. The 19th Annual Meeting of the WRDWG was on sunday, January 31, 1999 in Memphis, Tennessee. The meeting was held at the Peabody Hotel in conjunction with The Southern Association of Agricultural Scientists (S.A.A.S.), the Southern Region American Society for Horticultural Sciences (SR:ASHS), the Southern Region American Society for Horticultural Sciences (SR:ASHS) and the Southern Division: American Phytopathology Society (SD:APS). We had an excellent attendance with more than 50 people present at the meeting. Six research reports, a status report on watermelon germplasm, and a short film on research projects supported by the National Watermelon Promotion Board, were presented to the group stimulating much interest and discussion among the participants. The WRDWG has continued to grow in attendance and influence since its inception. The group has grown from three people in 1982 to more than 50 people in 1999. Dr. Gary Elmstrom was Chairman of the group from about 1982 through 1992. Dr. Ray Martyn was

Chairman of the group from 1992 until 1997. We are now a very dynamic group with the common goal of expanding knowledge for the watermelon industry. Consequently, we re indebted to both Dr. Elmstrom and Dr. Martyn for their leadership.

I. Research Updates. One of the more difficult chores that the Chairman has to do is take notes of the research presentations and make sense out of it later. These are brief summaries of the presentations. At the end of each summary, it will be noted which meeting (i.e., C'98, SAAS) the information was presented. You are encouraged to contact the individual scientist if you need additional information.

Dr. George Boyhan [*gboyhan@arches.uga.edu*] University of Georgia, discussed the Web Page being developed for WRDWG. Dr. Boyhan has done a lot of work to get the Web Page up and running. We are indebted to him for that. Thanks a lot.

Mr. Ron Kiothera [*rkother@clemson.edu*] and Dr. Anthony Keinath [*tknth@clemson.edu*], department of Plant Pathology and Physiology, Clemson University, are studying the *Phoma* spp. - *Didymella bryoniae* complex. There are three distinct groups of fungi that can cause confusion for those working on the gummy stem blight pathogen (*Didymella bryonae*). they have developed PCR primers (three) to differentiate between *Phome cucurbitacearum* (*didymella bryonae*) , *Phome* I, and *Phoma* II. *Phome* II (which has a sexual stage) can be very confusing in culture. There are dramatic differences in the ability of these fungi to cause disease on watermelon. The CR can also be used for testing seed for presence of the respective fungi. (C'98 and SAAS)

Dr. Warren Roberts[*wroberts@lane-ag.org*] Department of Horticulture, Oklahoma State University, is working toward standardization of variety evaluations and data accumulation. the objective is to form a groundwork for a coalition of workers that would allow for increased uniformity and increased information exchange throughout the watermelon industry. Details need to be worked out as to the specific format, data, and evaluations that will be required. (SAAS)

Mr. Sam Pair [*spair-usda@lane-ag.org*], USDA-ARS, Lane, Oklahoma, gave an overview of the research on Yellow Vine of watermelon. the disease is associated with a phloem-limited bacterium that is likely vectored by a leaf-hopper insect according to his research. The main characteristic symptom is a honey-brown discoloration of the phloem. the disease was first observed in Texas and Oklahoma watermelons in 1991. However in 1998, the disease was confirmed by PCR in Tennessee on watermelon and pumpkin. consequently, the watermelon crop in the southeastern US may also be at risk. (C'98 and SAAS)

Dr.John Damicone [*jpd3898@okstate.edu*].Department of Entomology and Plant Pathology, Oklahoma State University, is working on control of foliar disease of watermelons with an emphasis on anthracnose. His research has shown that Topsin plus Dithane gave good control as well as Bravo alone. In 1998, *Xanthomonas campestris* pv *cucurbitaceae* was responsible for severe defoliation of pumpkin.the disease caused up to 30% defoliation in watermelon in 1997. This is a disease new to Oklahoma and not much is known about the epidemiology. (SAAS)

Dr. Todd Wehner [*todd_wehner@ncsu.edu*], Department of Horticulture, North Carolina State University, is testing more than 1200 watermelon PIs for resistance to papaya ring spot virus type W (PRSV-W). PRSV-W was formerly called watermelon mosaic virus 1 (WMV-1). Inoculation methods were developed for the purpose of screening the germplasm, Tests were run to determine the optimum seedling stage for inoculation ranging from the cotyledon to the four true leaf stage. Results indicted that the rub method on the first true leaf was the most satisfactory method to establish symptoms. The most virulent isolate was selected for further evaluations. Testing should be completed by spring of 1999. Dr. Wehner has a list of diploid inbreds (or OPs) that he is collecting seed and pedigree information on. If you can assist, please contact Todd at his email address for the list and any information that you may have. (C'98 and SAAS)

Dr. Joe Norton, Department of Horticulture, Auburn University, gave an overview of his watermelon breeding program over the years which included such releases as AU-Jubilant, AU Sweet Scarlet, and others. He noted that they honey bee population in georgia and many other areas of the United States is critically low. At the present rate, honey bees may become an endangered species which ultimately is impacting cucurbit production. (C'98 and SAAS)

Dr. Tom Zitter [*tax1@cornell.edu*],Department of Plant Pathology, Cornell University, discussed pathogenicity and virulence of *Didymella bryoniae.* Other nonpathogenic or weakly virulent *Phoma* species are sometimes isolated from infected tissue, complicating identification of the pathogen. PCR primers can be used to differentiate between *Phoma cucurbitacearum* (*Didymella bryoniae*) and other *Phoma* spp. Twenty *D. bryoniae* isolates, collected from cucurbits, all caused similar disease reaction on inoculated cucurbits, indicating similarity among *Didymella* isolates in level of virulence. (C'98)

Dr. Bruce Carle [*rbcwm@gnv.ifas.ufl,edu*], University of Florida, discussed the situation with race 2 of *Fusarium oxysporum* f. sp. *niveum* in watermelon. At present, there is no known commercial cultivar with adequate resistance to this race. Using PI 296341, various crosses have been made to incorporate Fusarium race 2 resistance into horticulturally acceptable material. Good progress is being made in several lines. His virus resistance work in watermelon is also progressing nicely. (C'98)

Dr. Benny Bruton [*bbruton-usda@lane-ag.org*] USDA-ARS, Lane, Oklahoma, discussed the situation with watermelon germplasm at Griffin, Georgia. A preliminary report was sent out in June,. If you did not get a copy, we will have it on our WRDWG Web Site, which is in the process of being moved to the Lane Research Station in Lane, Oklahoma. The new Web Site should be up and running by September, 1999. The URL will be: *http://www.lane-ag.org/H2oMelon/watermelon.htm.*

Another topic that was discussed is a seed source for the watermelon differentials for determining race of *Fusarium oxysporum* f. sp. *niveum.* Dr. Todd Wehner agreed to get the differential germplasm. test it for purity, and increase it for distribution. Germplasm, can be hard to find and impossible to know the genetic purity. I hope that, in the future, we can find someone to produce the differentials and offer them for sale.

II. News From the National Watermelon Promotion Board (NWPB). Mr. William Watson, [*H20melon@watermelon.org*], NWPB Executive Director, was not able to attend due to prior commitments. William did provide the group with a film of research projects that have been supported by NWPB as well as research proposals that have been funded for 1999. The NWPB Board of Directors voted to add two more projects begun last year.

1) A new project at the Lane Research Station, Lane, OK, will investigate the content and health properties of lycopene, a powerful antioxidant in watermelon. USDA-ARS investigator Dr. penelope Perkins-Veaz9e will lead a team of researchers from USDA, Oklahoma State University, and Texas A&M, who will determine yield, stability, and quality of lycopene from marketable fruit and from watermelons considered culls.

2) In another new project, a team of researchers from Oklahoma State University will set up a system to better collect and disseminate production-related research to watermelon industry members. Researchers see a need to regularly communicate and relay information to the watermelon industry about cultivar and pesticide evaluations, fertility rates, and cultural practices. The group hopes to develop a national information exchange group to establish a mechanism for distributing research results and information to all facets of the watermelon industry.

3) The Board of Directors voted to expand the work of Purdue University plant pathologist Richard Latin, who has developed a weather-based prediction system designed to reduce fungicide use without increasing the risk of serious disease outbreaks. The system is called MELCASE (Melon Disease Forecaster). Growers have relied upon MELCAST to provide temperature and moisture readings that enable them to spray at the most opportune time, thereby improving disease control while reducing fungicide costs.

4) The Board also voted to continue University of Florida research by plant pathologist Dr. Don Hopkins who is investigating how to marshal a plant's natural defense system to control disease through chemicals known as plant defense activators. These activators have no direct toxic effect on pathogenic fungi or bacteria and are not classified as fungicides. Early finding indicate these activators are effective in preventing the spread of bacterial fruit blotch in the greenhouse and would be effective in reducing the amount of fruit blotch in the field.

The NWPB has budgeted $50,000 annually through 2001 to support research that addresses the following five research priority areas: (1) postharvest physiology ./quality, (2) resistance, epidemiology, and control, (3) standardization of variety evaluations and data accumulation, (4) removal and disposal of plastic mulch, and (5) disease forecast systems.

III. New Business. It was decided at the SAAS Meeting that we should invite all interested people (national and international) to become involved with our group. Once we get the Web site working we want to enter their personal data into the system. We will have a search engine so that a person can find an expert in watermelon culture, fertility, plastic mulch, postharvest problems, foliar diseases, or soilborne diseases, etc. This information should provide a very nice service to research and extension personnel to find needed information. We do not intend to try to duplicate information that is covered on other Web Pages. Hopefully, we will have the system up and running before long.

IV. Next Meeting. the 20th Annual Watermelon Research and Development Working Group meeting will be from 1"00 to 5:00 p.m. on Sunday, 30 January 2000, in Lexington, Kentucky.

V. Special thanks. The WRDWG would like to extend a special thanks to Dr. Tom Williams of Novartis Seeds, Inc. for sponsoring refreshments at this year;s annual meeting. We appreciate your support! We would also like to thank the past

refreshment sponsors Sunseeds (1998), Barham Seeds (1997), American SunMelon (1996), Willhite Seeds (1995), Asgrow Seed Company (1994), and American SunMelon (1993).

For more WRDWG information, please contact Dr., benny D. Bruton [*bbruton-usda@lane-ag.org*], US Department of Agriculture, Agricultural Research service, Lane, Oklahoma 74555. (Ph.: 580/889-7395; Fax:580/889-5783.

Cucurbit Crop Germplasm Committee (CCGC) Update

J.D. McCreight (Chair)

The cucurbit Crop Germplasm Committee met in Asilomar, California in conjunction with Cucurbitaceae '98 on December 3, 1998.

Kathy Reitsma, Curator of cucurbits, North Central Regional Plant Introduction Station, Ames, Iowa provided an update on germplasm activities. She stated that the budget remains tight, and that they are barely keeping up with the workload. A backlog of cucurbit characterization data at Ames awaits entry into GRIN, due in part to the lack of a computer specialist to oversee data entry. Data in the Prime-based GRIN system are not available in the Oracle-based system. Mark Bohning [*dvmumb@ars_grin.gov*] commented that PCGRIN is difficult to use, and that perhaps the GRIN Database Management Unit could improve the data downloading process.

Henry Munger suggested inclusion of a database field in GRIN for useful traits. Laura Merrick stated that descriptors were already in GRIN. Dr. Munger wanted accessions of value to be marked for high priority for maintenance. Ms. Reitsma stated that accessions are regenerated if seed is in short supply, or if the accession has been requested. She requested that germplasm users return remnants of accessions that have low numbers of seeds.

Laura Merrick, Iowa State University, commented that the classification of *Cucumis* accessions be made easier for users to find and name them. Ms. Reistma suggested that John Wiersma (USDA-REE-ARS-BA-PSI-SB&M LAB, Bioscience RM 330, 10300 Baltimore Blvd, Beltsville, MD 20705-0000), be contacted for improvements. Deena Decker-Walters and Molly Jahn requested that botanical variety and subspecies be included in GRIN. Kathy Reitsma and Bob Jarret are reclassifying accessions to proper species.

Charles Block, Plant Pathologist, RPIS, Ames, reported the occurrence on *Cucumis melo* accessions of a bacterial leaf disease that was similar to watermelon fruit blotch incited by *Acidovorax acenae* spp. *cirulli.*

Bob Jarret, Curator for *Citrullus, Cucurbita* and other cucurbits, reported on the germplasm activities at the Southern RPIS, Griffin, Georgia. He stated that a low percentage of accessions are available, and that many stocks are unavailable. The USDA, ARS station at Byron is now being used for caged seed increases. ARS facilities at Parlier, California, and Miami, Florida, have also been used for seed increases. Dr. Jarret stated that limited funds for germplasm characterization and increase warrant the use of a designated core collection. Claude thomas, USDA, ARS, Charleston, South Carolina, made a motion that the CCGC write the USDA-ARS National Program Staff about the poor funding for cucurbit increases at Griffin. This was seco0ndd and unanimously passed.

Richard Robinson, New York Experiment Station, Geneva, provided an update on the Northeastern RPIS, Geneva, new York. Larry Robertson was hired to replace Jim McGerson who resigned in 1998. The Geneva collection contains 975 PI accessions of ca. 16 species of cucurbits, plus 132 accessions yet to be numbered. Dr. Robinson expressed concern about the small number (9) of *Cucurbita* accessions increased in 1998 relative to the number of accessions with low germination (5 accessions 60%), or no recent germination test (480). Nine 12 x 48 ft. cages had been purchased for field increases of cucurbits using honeybees in lieu of hand-pollination.

Michel Pitrat, INRA, Montfavet, stated that France has 100 USDA accessions in its melon collection of 800 total accessions, and that seeds are increased by seed companies for the collection each year.

Two proposals for FY 1999 were submitted after the deadline for cucurbit germplasm evaluation. A proposal from Professor Poostchi, to translate and publish in book form descriptions of cucurbits of Iran was discussed. Seeds of the described accessions would be submitted to the US-NPGS.

The Wehner-McCreight expedition to Zimbabwe is being planned for April 1999 for collection of *Cucumis* and *Citrullus*.

Todd Wehner suggested that all crop evaluation priority lists be revised to account for the work that has been completed in the past few years.

New Books of Interest to CGC Members

Cucurbitaceae '98: Evaluation and Enhancement of Cucurbit Germplasm

J.D. McCreight (ed.)

1998	Paperback (8.5" x 11'	ASHS (*http://www.ashs.org/*)
ISBN 0-9615027-9-7	List: $35 + shipping (CGC and/or ASHS members $45 + shipping (non-members)	

The proceedings from Cucurbitaceae '98, which was held in December 1998 at the Asilomar Conference Center in Pacific Grove, California. The volume contains more than 60 papers presented at the meeting in the areas of germplasm resources, genetics, breeding, pathology, entomology and production. Advance your knowledge on the collection, preservation, characterization evaluation, and enhancement of cucurbit germplasm. To order by credit card, contact ASHS Press at 703/836-2418; fax the ASHS Press Print-and-Fax Order Form (obtainable from *http://www.ashs.org/*) to 703/836-6838 or email *ashpres@ashs.org.*

20th Century Bioscience: Professor O.J. Eigsti and the Seedless Watermelon

John H. Woodburn

"The life story of O.J. Eigsti and the seedless watermelon is interwoven with the evolution of genetics, horticulture, and education throughout the twentieth century." This biography describes the highs and lows of being a farmer, scientist, and teacher throughout much of the century. From his first entry level position at the Carnegie Institution of Washington at cold Spring Harbor, to full professorships at the University of oklahoma, Northwestern and Chicago State, this informative and entertaining biography follows the life and career of Prof. O.J.Eigsti from farm boy to highly successful botanist and educator, searching for the secret to a commercially successful seedless watermelon. The book can be ordered directly from Pentland Press, Inc., 5122 Bur Oak Circle, Raleigh, NC 27612 USA. (Ph.: 800/948-2786; fax: 919/781-9042.) Please inquire concerning shipping charges.

Upcoming Meetings of Interest to Cucurbit Researchers

MEETING	DATE	LOCATION	CONTACT
Pickle Packers Fall Business Conference	27-29 October 1999	Opryland Hotel, Nashville, Tennessee	Pickle Packers Intl. (630) 58-8950
			Benny D. Bruton

Watermelon Research and Development Group	30 January 2000	Lexington, Kentucky	(580) 889-7395
			bbruton-usda@lane-ag.org
Cucurbitaceae 2000 ***(EUCARPIA VII)***	19-23 March 2000	Ma'ale Hachamisha Resort & Convention Center, Israel	Nurit Katzir
			972-4-9539554
			geneweya@netvision.net.il
Cucurbit Genetics Cooperative	28 July 2000	Minneapolis, Minnesota	Timothy J. Ng
			(301) 405-4345
	?? July 2000	Orlando, Florida	*tn@umail.umd.edu*

Cucurbit Genetics Cooperative Report 22:1-2 (article 1) 1999

The Relationship Between ACC Synthase (*CS-ACS2*) and Monoecious Sex Phenotype in Cucumber (*Cucumis sativus L.*)

H. Mizusawa and S. Matsuura

Tohoku Seed Co., 1625 Himuro, Nishihara, Utsunomiya 321-3232, Japan

S. Kamachi and S. Sakai

Institute of Biological Sciences, University of Tsukuba, Ibaraki, 305-8527, Japan

In Japan, monoecious cucumber is very popular, and there are commercial varieties that possess various degrees of monoecious sex expression (i.e. ratio of pistillate to staminate flowers) is a quantitative trait and cross breeding for line development of stable monoecious sex types is difficult. Therefore, a selectable marker is needed to enhance breeding of monoecious sex phenotypes. Recently, it was suggested that ACC synthase (*CS-ACSIG*) is closely linked to or is the F-locus (gynoecious gene) (1), and that ACC synthase (*CS-ACS2*) is also associated with sex phenotypes in cucumber (2). In this report, we examined the relationship between*CS-ACS2* and the monoecious sex phenotype using an F_2 population derived from a cross between monoecious cucumber lines high and low expression of staminate flowers.

Materials and Methods. An F_2 population (130 individuals) was derived from a cross between 'Kyuuraku No.2' and 'Morioka No. 1'. The parents and F_1 as well as F_2 progeny were also used for experimentation. All plant materials were planted in a greenhouse in Utsunomiya, Japan, in the summer of 1995. Details of cultivation are given described in the Proceedings of Cucurbitaceae '98 (3). The number of female flowers appearing from the first to 17th node of the main stem were recorded for each plant.

Total DNA was isolated from the shoot apex of the lateral stem by CTAB method (4). total DNA of both parents were independently digested with nine restriction enzymes (Bam H1, Dra 1, Eco R1, Eco RV, Hind III, Sac I, Sal I and Xho 1). Thereafter, 3 µg DNA from each individual was electrophoresed through 0.8% agarose gel, and then transferred nylon membrane (Amersham). The cDNA clone of *CS-ACS2* was used as a probe for Southern blot analysis after being labeled with an ECL gene detection kit (Amersham). Membranes were hybridized overnight at 42 C in a hybridization buffer that was in the ECL kit. They were washed twice in a primary wash buffer that contained 0.5 x SSC, 0.4% SDS nd 6M urea at 42 C for 20 min, and then twice in a secondary wash buffer that contained 1.0 c SSC at room temperature for 10 min. The membranes were exposed to Fuji medical X-ray film for 1h after being soaked with a detection solution. Mean separations of the number of female flowers for each *CS-ACS2* genotype in F_2 population were performed using LSD tests.

Results and Discussion. An RFLP was detected between 'Kyuuraku No. 2' and 'Morioka No. 1' when their total DNAs were digested with Sac I enzyme as shown in Figure 1. The segregation of *CS-ACS2* in F_2 population (total DNAs were isolated from only 79 individuals) fitted a 1:2:1 ratio as shown in the Table 1. This results suggested that there is at least one additional copy of *CS-ACS2* in cucumber. The number of female flowers of 'Kyuuraku No. 2', 'Morioka No. 1', the F_1 hybrid and in each *CS-ACS2* F_2 genotype of are shown in Table 1. Significant differences were detected between the 'Kyuuraku No. 2' *AA* genotype and 'Morioka No. 1' *aa CS-ACS2* genotype. These results suggest that *CS-ACS2* may be associated with the monoecious sex phenotype and that *CS-ACS2* may be one of several genes that may control the expression of this trait. Since the expression monoecious sex phenotype is a quantitative, we think that *CS-ACS2* may be a good candidate for use as a selectable marker for capture of monoecious sex phenotypes with variable expression. However, its action in multiple stress environments (e.g., heat, light & water stress) has not been studied. Such experiments would provide information on the modifying effect of other genes on *CS-ACS2*.

Figure 1. Southern blot hybridization of 'Kyuuraku No. 2', 'Morioka No. 1' and theF_2 population. Total DNAs were digested with Sac I and electrophoresed on a 0.8% agarose gel. The blot was probed with *CS-ACS2*. K and M indicate 'Kyuuraku No. 2' and 'Moroioka No. 1' respectively. Arrows indicate RFLP bands where the marker is **?** -Hind III.

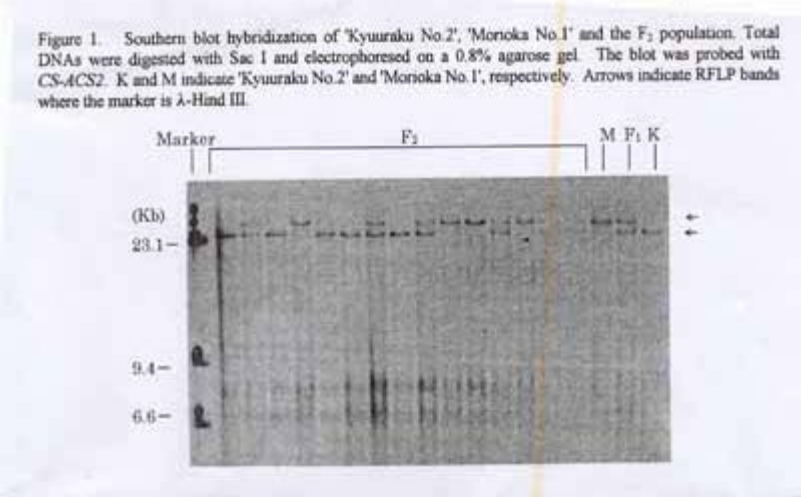

Table 1. Number of female flowers of 'Kyuuraku No. 2' (A), 'Morioka No. 1' (a), F_1 hybrid and in each CS-ACS2 genotype in F_2.

				Genotype of CS-ACS2 in F_2		
Character	**'Kyuuraku No. 2'**	**'Morioka No.1'**	**F_1 (K x M)[y]**	**AA**	**Aa**	**aa**
No. of female flowers	2.9 ±0.4	11.4 ± 0.5	3.8 ± 0.5	3.7 a[x]	5.9ab	7.5b
No. of plants	8	8	8	19	39	21

[z] Seventeen nodes examined per plant.

[y] K (AR) and M (aa) show 'Kyuuaraku No. 2' and 'Morioka No. 1', respectively.

[x] Means followed by the same letter do not differ at 5% significance level by Fisher's LSD-method.

Literature Cited

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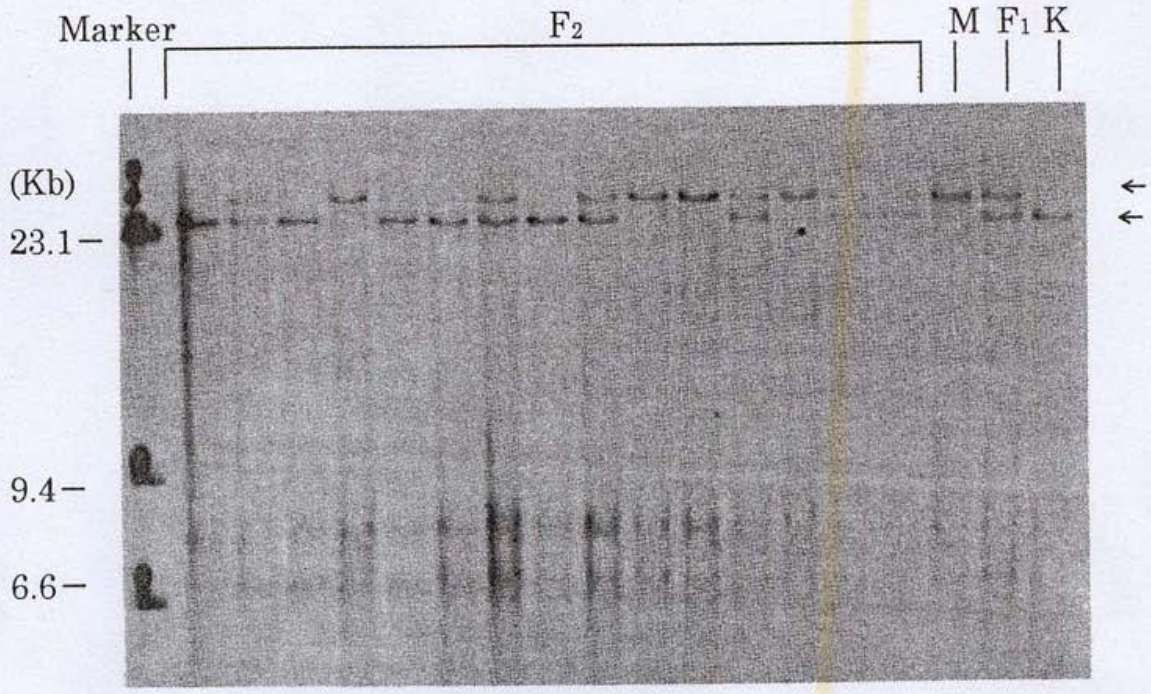
Figure 1. Southern blot hybridization of 'Kyuuraku No.2', 'Morioka No.1' and the F_2 population. Total DNAs were digested with Sac I and electrophoresed on a 0.8% agarose gel. The blot was probed with *CS-ACS2*. K and M indicate 'Kyuuraku No.2' and 'Morioka No.1', respectively. Arrows indicate RFLP bands where the marker is λ-Hind III.



Cucurbit Genetics Cooperative Report 22:1-2 (article 2) 1999

Genetic Path Analysis of Early Yield in Cucumber

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Early high yield in cucumber would be an important way for solving the problem of the absence of fresh vegetables in spring cultivation in china. Thus, breeders have paid more and more attention to the development of high yielding early lines and hybrids. It is essential to characterize the physiological mechanisms of early yield in order to increase the effectiveness of direct and indirect selection. Here is one of a series of studies on this aspect (1).

Materials and Methods. An experiment was conducted at the Horticulture Station of the Northwestern Agricultural University. Twenty-four cultigens were planted in a randomized block design with three replications. Ten plants of each cultigen were randomly chosen to evaluate for early yield (Y) and 14 relevant traits in the early stage of plant development. Traits were selected as follows: (1) node position of the first pistillate flower (x_1);(2) days from sowing to the first pistillate flowering plant in the population (x_2); (3) days from sowing to pistillate flowering of 50% of the plants (x_3);(4) days from sowing to first male flowering plant in the population (x_4); (5) days from sowing to staminate flowering in 50% of the plants (x_5);(6) leaf area per plant (x_6); (7) fruit length (x_7); (8) leaf number (x_8); (9) pistillate flower density (main vine) (x_{10}); (11) number of staminate flowers (main vine((x_{11}); (12) number of harvested fruits per plant (x_{12}); (13) average fruit weight (x_{13}); and (14) downy mildew index (x_{14}).

The early yield was considered as the primary trait while the other traits were considered secondary traits. On the basis of genetic correlation analysis, the path coefficients of each trait to early yield were obtained by partitioning the genetic correlation coefficient according to the formulas below:

$P_1+r_{12}P_2$	.....	$+r_{1m}P_m = r_{1y}$
$R_{21}P_1+ P_2+$	.....	$+r2_mP_m = r2_y$
$R_{m1}P_1+r_{m2}P_2+$	.....	$+P_m = P_{my}$

Path coefficient descriptors were designated as:

- P_i is the path coefficient of trait x_1 to early yield;
- r_{ij} is the genetic correlation coefficient between x_1 and x_j , and
- r_{iy} is the genetic correlation coefficient between x_i and yield.

The path coefficients obtained were tested, and if one or more were not significant, the trait with the smallest t or F value was eliminated and then coefficients were calculated again. This process continued until all path coefficients were significant (2).

Results. The results (Table 1) show the path coefficient obtained from progressive elimination of genetic correlation coefficients. Some coefficients were small. The first coefficient to be eliminated was pistillate flower density (x9) and then traits x10, x2, x1, x5, x6, x11 were eliminated sequestially thereafter. Only seven traits were retained after examination. The results of path analysis are shown in Table 2. The three traits with the largest direct action to early yield were average fruit weight (x13), number of harvested fruit per plant (x12_ and average fruit length (x7). Their actions were positive. Positive selection can be carried out for early maturity. Downy mildew index (x 14) had the least direct action in the path analysis, and primarily exerted an indirect influence on early yield via fruit length (x7). The days from sowing to pistillate flowering of 50% of the plants (x3) had a negative direct effect on early yield, and had a slightly larger negative indirect effect via the way of number of harvested fruit (x12). Days from sowing to first male flowering plant (x4) had a positive effect via fruit length (x7) and fruit weight (x13). Thus, it is suggested that selection be applied to earlier pistillate flowering and later male flowering plant when breeding for maturity. Although leaf number (x8) had a positive correlation with early yield, it had a certain negative direct action on early yield. On the other hand, it positively influenced early yield indirectly via fruit length (x7) and fruit weight (x13). These plant growth variables reflected the antagonism and unity between vegetative and reproductive plant development.

Discussion. Path analysis can be used to identify direct and indirect action of traits, and thus can be helpful during breeding. Because path analysis results are often not tested we suggest that the utility of path coefficients be thoroughly evaluated in order to document their utility before adapt ion to breeding programs. In addition, it should he mentioned that the traits eliminated during the path coefficient analysis have no direct action on the objective trait. Thus, we cannot rule out the possibility that traits are "pre-eliminated" during such analyses have no indirect action through the expression of other traits. If we take a multi-stage path analysis approach (i.e., analysis based on the action mechanism and the physiological principal), we may learn more about the status and correlation among the traits examined. The total determination (R) was R = 1.011. This made it impossible to estimate the standard error of path coefficient and the environment (Pe). This phenomenon

has been elucidated by classical variance and covariance analysis. A better method should be sought to solve this problem.

Table 1. Genetic correlation coefficient of 14 traits to early yield.

Traits	**X1**	**X2**	**X3**	**X4**	**X5**
(Genetic correlation coefficient)	-0.0329	-0.0265	-0.2187	0.336	-0.0414
Traits	**X6**	**X7**	**X8**	**X9**	**X10**
(Geneticcorrelation coefficient)	0.1215	0.4577	-0.1404	0.0126	0.0085
Traits	**X1**	**X12**	**X13**	**X14**	
(Genetic correlation coefficient)	0.1464	0.5778	0.4368	0.0205	

Table 2. Direct and indirect action of seven traits to early yield.

Traits	**Corella Corr. coef.**	**Direct Dir. act.**	**Indirect action of related traits**						
	(Riy)[z]	**(Pi)[y]**	**X3 -> Y**	**X4 -> Y**	**X7 -> Y**	**X8 -> Y**	**X12 -> Y**	**X13 -> Y**	**X1 -> Y**
X3	-0.218	-0.253		0.075	0.183	-0.066	-0.310	0.170	-0.018
X4	0.367	0.225	-0.084		0.175	-0.066	-0.075	0.241	-0.048
X7	0.741	0.393	-0.118	0.100		-0.095	0.067	0.434	-0.041
X8	0.460	-0.128	-0.130	0.117	0.292		-0.010	0.350	-0.031
X12	0.658	0.453	0.173	-0.042	0.058	0.003		0.027	0.008
X13	0.758	0.463	-0.093	0.007	0.369	-0.097	0.027		-0.028
X14	-0.237	0.086	0.052	-0.127	-0.187	0.046	0.042	-0.150	

[z] Correlation coefficient.

[y] Direct action of trait.

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Cucurbit Genetics Cooperative Report 22:5-7 (article 3) 1999

Transfer of Cucumber (*cucumis sativus* L.) Plantlets Regenerated from *in vitro* Culture

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When plantelets grow in an environment of constant temperature, high humidity, low light intensity and sterile surroundings, they exhibit a decrease in leaf photosynthesis rate, slow growth, thin leaf epidermis, reduced ability for stomatal opening and closure, poor water-controlling functions, and incomplete physiological and morphological function of the root system. Since their adaptability to adapt to an outside environment is poor, they require a transitional stage before transplanting (plantlets) to the open field. to date, there are many successful reports of plantlets being regenerated from cucumber *in vitro* culture, and there are also reports regarding the transfer of plantlets to pots (2,3,4). However, there is little detailed information about survival rte of plantlets after transfer to pots. Cai Rongqi (1) developed a transfer method named "T_2 medium rerooting" where plantlets derived using fertilized ovules are transferred during in vitro culture. The plantlet survival rate using this technique was 93.3%. The aim o four work was to test the effect of different transfer substrates, temperature treatment after planning, and plantlet size on survival rate after plantlet transfer to pots this would allow for a determination of optimal conditions during transfer.

Methods. rooted plantlets were regenerated during many subcultures of shoot tips or axillary buds from the cucumber breeding line 'Chang-176'. These were used as experimental materials. Films sealed on the top of vessels were removed and unsealed vessels were placed in a growth chamber maintained at 25$\pm$ 1C. with a 16-hour photoperiod provided by cool-white fluorescent light at 1500 lux. Uniform plantlets were "hardened-off" for 3 days before transfer to plastic pots. subsequently, rooted plantlets were taken from vessels, agar was washed off of their roots with tap water, and plantlets wee then transferred to plastic pots (diameter - 10 cm) containing different substrates. Plastic pots were put onto the enamel plate, and water was added to ensure constant humidity.

Three experiments (Exp. 1-3) were designed. In Exp. 1., four different substrates [vermiculite (A); fine sand:vermiculite = 2:1(B), fine sand:vermiculite:culture soil containing a mixture of 7:3 manure to soil] were compared to evaluate the effect of a transfer substrate on survival rate of plantlets after transfer.

Expt. 2 was designed to identify an optimal temperature after plantlets were transferred. Vermiculite was used as the transfer substrate. There were four constant temperature treatments, varying at 5 C intervals among 15-30 C, and one variable temperature treatment where plantlets were subjected to 15 C for 3 days and then 20 C for 7 days. Duration for each treatment was 10 days. Plantlets were acclimatized for 3 days under room temperature prior to transplanting.

In Exp. 3, plantlets were classified as small, medium and large. Plantlets of different sizes were transferred to plastic pots containing vermiculite. The experiment was conducted at 15 C for 3 days and then at 20 C for 7 days.

All experiments above were conducted in a growth chamber with strict temperature control. The transfer survival rte was recorded after 13 days when new leaves were produced by the plantlets. The "U-test" was used for percentage's determination.

Results. For Experiment 1, the number of rooted plantlets that survived in the plastic pots containing different substrates are presented in Table 1. Among the four transfer substrates, vermiculite was optimal (96.7% survival rte) and differed significantly from the other three substrates tested. Cultured soil was unfavorable for transfer survival of rooted plantlets.

Vermiculite had the best air permeability followed by fine sand containing vermiculite. Culture soil is rich in microbial and manure, but rooted plantlets did not grow well in this media. It was observed that rot at the junction between the root and the stem was the main reason for the low survival.

For Experiment 2, data of the effect of various temperature treatments on survival rate after transfer indicated that differential survival rates occurred among plantlets (Table 2.). Comparative analysis of data from temperature intervals between the 15-30 C, nd constant temperature treatments, indicated survival rate decreased with increasing temperature and that significant differences existed between the various temperature treatments. When given the changeable temperature treatment of 15 C for 3 days and then at 20 C for 7 days, plant survival was as high as 100%. This treatment was superior to all other values. Compared with treatments at 25 C and 30 C under constant temperature, the variable temperature treatment increased plant survival by a factor of 2.4 times and 10 times, respectively. These results can be explained by the fact that with increasing temperature transpiration increased, and water loss and nutrition waste likely increased. Plantlets for such treatments were unadaptable to the open field environment. Lower and changeable temperature treatments gradually improved the adaptability of plantlets to survive in an open field environment.

Since the results of the second experiment indicated that lower and changeable temperature could significantly improve survival rate after transfer, we used this temperature treatment in the Experiment 3. The results of the transfer of plantlets of different sizes are presented in Table 3. Results indicated that large plantlets having more than 5 leaves and 6.1 cm in height) survive remarkably well when transferred to the plastic pots (highest survival rate), while small plantlets had difficulties surviving.

Transplantation of plantlets into the open field results in different survival rates depending on treatment. Plants in plastic pots that had treatment survived treatment were put outside the room for 3 days to acclimatize to the outer environment. Plantlets were taken out of the plastic pots, and part of the root-bound substrate was removed. These plantlets were then transplanted into the open field. the survival rte after transplanting was as high as 92.9%. There was no difference in leaf morphology, growth habit, flower and fruit characteristics among those plantlets.

Conclusions. In conclusion, the data indicate that: (1) The highest survival rate could be obtained when rooted plantlet were transferred to the plastic pots containing vermiculite; (2) lower and changeable temperature (at 15 C for 3 days and then at 20 for 7 days) provided the highest survival rate after transfer to plastic pots (as high as 100%); and (3) the survival rate of large plantlets with more than 5 leaves and 6.1 cm in height was higher than smaller plantlets. Plantlets that survived the initial transfer were successfully transplanted into the open field (survival rates up to 92.9%). These plants flowered and set fruit.

In order to ensure a well-developed root system it is important to select a suitable transfer substrate. Our results showed that vermiculite is best transfer substrate among four substrates used. The use of lower and variable temperatures increased survival rate. this rate was slightly higher than the T_2 medium rerooting method put forward by Cai Rongqi (1998). The former procedure, however, does not include root pruning, which in our case saved 507 days rerooting time and simplified the transfer process. Therefore, we believe our method is simpler, more convenient, and more practical than that proposed by Cai Rongqi.

Table 1. Effect of different transfer substrates on survival rate of the transfer of cucumber plants to pots.

Transfer substrate	No. of plantlets transferred	No. of plantlets surviving	Rate of survival (%)
A	30	29	96.7 a
B	30	14	46.7 b
C	32	14	43.8 b
D	28	4	14.3 c

[z] The different letter indicated that the results of treatment are significantly different by U-C test at p = 0.01.

Table 2. Effect of temperature treatments on survival rate of the transfer of cucumber plants to the pots.

Temperature treatment (°C)	No. of plantlets transferred	No. of plantlets surviving	Rate of survived (%)	Note[x]

15	30	25	83.3 b	Constant
15 - 20	28	28	100.0 a	Changeable
20	28	18	64.3 c	Constant
35	33	14	42.4 d	Constant
30	28	3	10.7 e	Constant

Table 3. Effect of plantlet size on survival rate of cucumber plants transfer to pots.

Size of plantlet [y]	**No. of plantlets transferred**	**No. of plantlets surviving**	**Rate of survival (%)**
Small	16	6	40
Medium	16	12	75
Large	14	14	100

Plantlets were classified as 1) small (less than 3 leaves and lower than 3.5 cm in height); 2) medium (3 to 4 leaves and 3.5 to 5.0 cm in height), and 3) large (more than 5 leaves nd higher than 5.1 cm in height).

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Cucurbit Genetics Cooperative Report 22:8-10 (article 4) 1999

QTL Conditioning Yield and Fruit Quality Traits in Cucumber (*Cucumis sativus* L.)

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Introduction. Recent molecular appraisals of quantitative trait loci (QTL) have documented the importance of genotype (G) x environment (E) interactions in several crop species (Paterson et al., 1991 ; Stuber et al, 1992). Some of the observed differences in QTL expression have been attributed either to the statistical method used in evaluation of GxE (Dudley, 1993) or to experimental sampling biases (Beavis et al., 1994). Such GxE interactions for quantitatively inherited traits can occur in cucumber (*Cucumis sativus* var. *sativus* L.) (Wehner et al., 1989).

A genotype that has been used by cucumber breeders for the purpose of increasing yield in cucumber is *C. sativus* var. *hardwickii* (R) Alef. (hereafter referred to as *C.s.* var. *hardwickii*), a feral relative of *C.s.* var. *sativus* (Horst and Lower, 1978). This genotype possesses a multiple lateral-branching and sequential-fruiting habit not present in *C.s.* var. *sativus* lines.

Both RFLPs (Kennard et al., 1995) and RAPDs (Serquen et al., 1997) have been used to identify QTL for yield and quality in cucumber. However, the effects of growing environment on the action of QTL conditioning cucumber fruit yield and quality has not been assessed using molecular marker technologies. Therefore, we designed an experiment to identify QTL affecting yield and fruit quality traits in progeny derived from a cross between *C.s.* var. *sativus* and *C.s.* var., *hardwickii.*

Methods. An F_2 mapping population was constructed by crossing the gynoecious *C.s.* vr. *hardwickii* accession PI 183967 (P_2). Parental matings produced seed from which a single F_1 plant was selfed to obtain an F_2 bulk population, and F_2 plants were subsequently self-pollinated to produce 200 F_2S_1 families. In addition, 60 F_3 plants (different from those used to derive the F_2S_1 families) were backcrossed to both parents to generate $BC_1(P_1)$ and $BC_1(P_2)$ families for a North Carolina Design III evaluation.

The F_2S_1 families were evaluated for fruit yield and quality components in 1991 and 1992. Experimental units (plots) consisted of 2.1 m rows positioned on 1.5 m row centers. Individual plots were over-seeded and thinned to9 or 18 plants to obtain the desired planting density of 29.000 or 58,000 plants ha^{-1}, respectively. Backcross families were evaluated in 1992, using a randomized complete block design with four replications. Plots consisted of .5 m single-row plots set on 1.5 m row centers. Plots were over-seeded and thinned 13 plants per plot (~44,000 plants ha^{-1}).

Data were collected on days to anthesis, fruit number and weight, and fruit length and diameter (L/D). Best linear unbiased predictions (BLUPs) for F_2S_1 and BC family means per environments were calculated using PROC MIXED (SAS Institute, 1992).

Variance components and standard errors (S.E.) associated with F_2S_1 families (o ^{2}g), F_2S_1 family x year interaction (o ^{2}gy) or family x density (o ^{2}gd), and residual variances (o ^{2}), and their standard errors (S.E.) were calculated using PROC MIXED (SAS Institute, 1992). QTL were identified using an interval approach described by Lander and Botstein (1989) using the computer program, MAPMAKER-QTL (Lincoln and Lander, 1990).

Bulked leaf tissue from each F_2S_1 (utilized for genotyping F_2 individuals) and BC family was collected, extracted, and Southern blot hybridizations were performed according to Kennard et al. (1994). DNA was digested with *Dra*1, *Eco*RI, *Eco*RV, or *Hin*dIII (BRL, Gaithersburg, MD or Promega, Madison, WI). Digested DNA was electrophoresed, gels were stained in ethidium bromide, and DNA was transferred to Zetaprobe membranes (Biorad, Waverly, MA) according to (Sambrook et al., 1989). Previously identified cloned DNA fragments showing polymorphisms between the two parents were radio-labeled by random hexamer priming.

Results. Earliness, and fruit yield and quality components of cucumber were investigated by examining cross-progeny (BC and F_2S_1) derived from a wide mating [gynoecious *cucumis sativus* L. var. *sativus* line GY 14 x monoecious *C. sativus* var *.hardwickii* (R) Alef. PI 183967] (Table 1). A molecular marker map constructed from F_2 individuals was used to identify quantitative trait loci (QTL) for each trait examined, and to assess the consistency of QTL over years (1991 and 1992) and planting density (29,000 and 58,000 plants ha -1), QTL affecting earliness (days to anthesis and number of barren nodes), fruit yield (fruit number and weight at two harvest times) and shape [length (L), diameter (D), and L:D ratio] were identified. The traits examined were less affected by planting density than by year. While earliness and yield traits were largely under non-additive control, components of fruit shape exhibited additive genetic variance resulting in high values for narrow sense heritability estimates. While the number and map location of some QTL was relatively consistent over environments (years and planting density), differences in their number and location were found in F_2S_1 and BC families. Some of these differences could be attributed to disparities in population size, dominance and the amount of genotypic information available (F_2S_1 BC). Fruit L and D, and to a lesser extent L:D ratio, are developmentally dependent, and thus map placement of QTL was affected by the physiological stage of fruit development. QTL evaluation of the F_2S_1 generation revealed that earliness is determined by relatively few genes, and that the genetic control of early yield resides in the same chromosome regions as does days to anthesis. Positive genetic correlations were identified when plants of similar physiological age were compared at different harvest times in each of the environments (years) and genetic backgrounds (F_2S_1 , BC_1P_1 and BC_1P_2 families) examined. Thus, these factors which should be considered when assessing *C. sativus* var. *hardwickii*-derived germplasm and QTL profiles in cucumber.

Table 1. Multi-QTL models for cucumber traits evaluated at each of three environments (29,000 and 58,000 plants ha^{-1} in 1991 and 58,000 plants, ha^{-2}in 1992), final LOD ratio (LOD), and proportion of variance explained (R^2) by the model.

Linkage Group	**1991 F_2S_1**					**1991 F_2S_1**				**1992 F_2S_1**			
	29,000 ha^{-1}					**58,000 ha^{-1}**				**58,000 ha^{-1}**			
	Marker [x]	l	a	d		Marker	l	a	d	Marker	l	a	d
Anthesis (days)													
B	*F*	24	1.9	-0.6		*F*	24	1.9	-0.1	No data			
E	CsC029	65	3.9	-3.6		CsC029	65	3.6	-3.4				
F						Per	11	1.4	0.4				
	LOD = 10.0,	R^2 = 0.41				LOD = 10.0	R^2 = 0.46						
Fruit number at harvest (10,000 ha^{-1})													
A	CsP357	32	3.1	-1.9									
B	CsP287	67	2.8	9.4	CsP193	0	-2.4	9.6	*F*	24	24	-7.7	1.9
E	CsC613	45	-5.9	11.2	CsC613	50	-5.4	11.0					
E										CsC029	66	-8.3	2.7
	LOD = 7.9,	R^2 = 0.33			LOD = 5,	R^2 = 24				LOD = 15.1		R^2 = 0.56	
Fruit weight at harvest (Mg Ha^{-1})													
B	*F*	21	-2.3	4.4	*F*	20	-3.4	4.3		*F*	21	-4.8	0.6
B										CsP024	60	-3.2	-2.6

E	CsP215	44	-7.3	6.1								
E					Pep_pap62	-6.2	2.9					
E									CsC029	68	-5.6	-0.8
F	CsC443	7	-2.9	0.2								
F					CsP130	3	-3.3	0.2				
	LOD = 9.7	R^2 = 0.38			LOD= 10.4	R^2 = 0.42				LOD=22.5	R^2 = 0.69	
	Fruit L:D ratio (cm cm^{-1}) at late harvest											
A									*dm*	70	0.06	0.05
B	CsP024	52	-0.09	0.01	CsP024	59	-0.10	0.03				
C	CsP056	42	-0.16	0.00	CsP056	42	-0.16	-0.03	CsP056	38	-0.14	-0.01
D					CsE060	8	-07	-0.01				
E					CsP211	37	-0.11	0.01				
E									CsP475s30		-0.9	-0.01
G					CsP280	8	-0.07	0.00	CsP280	11	-0.9	-0.03
H	CsC166	23	-0.06	-0.08								

[x] Nearest (marker) to the putative QTL, map location (l) in cM, estimates of average effect of substitution of a GY14 allele by a Pl 183967 allele (a), and dominance deviation (d).

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Cucurbit Genetics Cooperative Report 22:11-13 (article 5) 1999

Physiological Effects of NaCl Stress on Cucumber Germination and Seedling Growth

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With the world wide development of salinizing soil, more attention has been paid to increasing a plant's ability to undergo osmotic change (resistance) and withstand salinizing stress. Under such stress conditions, growth and development of the plant are hindered, and some physiological metabolic processes are affected (1,2). There is little information on effects of salt stress on cucumber growth and metabolism. Therefore, seed vigor, seedling growth, and other physiological and biochemical indices were studied under different concentrations of salt to: (1) characterize the salt injury and salt tolerant mechanisms, and (2) provide a theoretical basis for salt tolerance breeding and cultivation in cucumber.

Methods. The cucumber cultivar 3511 was selected and stressed during germination and the cotyledon and second-leaf stage. At these growth stages plants were treated with 5 NaCl concentrations (0. 100, 200, 300 and 500 mmol/L) in a random block design with 4 replications.

Exp.1 Treatment in germination stage. After soaking in distilled water for 8 hours, 100 seeds (per block) were germinated under different liquid salt concentrations at 28 C. New salt liquid for each concentration was added every 24 hours. The number of germinated seeds whose sprout length was half of seed length were counted after 24 hours. This procedure was carried out once every 12 hours. The sprouts were weighed after 8 days, and then the germination rate, germination viability and seed vigor index were calculated for each treatment.

Exp. 2. Treatment in cotyledon stage. Ten dry seeds were sown in every seedling bowl with vermiculite (diameter 7.5 cm) nd each experimental unit was irrigated with a nutrient solution containing different salt concentrations depending on the treatment. All treatments were held at 28 C in the dark. The seedlings were cultured in a growth chamber at 28 C (d)/18 C (n) [d = 16 hr]. Salt liquid irrigation occurred two times from sowing to the cotyledon stage. Sprouting seed, tissue water, and amount of seedling growth were calculated at the end of experimentation for each treatment.

Exp. 3 Treatment in the second-leaf stage. Five seeds were sown in the culture medium. Different kinds of irrigation were used. Water was applied before sprouting, and the nutrient solution (0.09 lg urea+0.045g KH_2PO_{4+} 0.5 $MgSO_{4+}$ 1.215g Ca $(No_3)_2$/L) was used from sprouting to second-leaf stage. Then the seedlings were treated two times with an NaCl salt solution. Amount of growth and several physiological and biochemical indices were evaluated on the 8th day after treatment. The following data were taken: (1) chlorophyll content was measured using a spectrophotometer (3); (2) MDA content was measured by the method of Lin Guifang; (3) proline content measured by inhydrin colormetry (3); (4) soluble protein content was determined by the method of Coomassie brilliant blue G-250, and (5) cell membrane permeability was determined by electrical conductivity (3).

Results. Exp. 1. The effect NaCl stress on seed germination. Germination rate, germination viability and seed vigor index decreased with increasing NaCl concentrations (Table 1). No significant differences in germination rates were detected among of 0, 100, and 200 mmol/L treatments. Germination rates at these concentrations were significantly higher than seeds held at 300 and 500 mmol/L, and germination at these concentrations was significantly higher than those under 200, 300, 500 mmol/L. The seed vigor index under 0 mmol/L was significantly higher than those held at 200, 300, and 500 mmol/L.

Exp.2. The effect of NaCl stress on sprouting and seedling growth in cotyledon stage: effect on the speed of sprouting. The speed of sprouting and the germination rate decreased with increasing salt concentration (Table 2). The sprouting rate of seed held at the concentration from 0 to 200 mmol/L reached 96.3% five days after sowing, and the sprouting rate of seed held at 300 and 500 mmol/L ranged between 77.5% and 5.0% eight days after sowing.

The effect on seedling growth. Seedling height, stem diameter, leaf area, ratio of root and crown, root length and fresh

weight of seedling decreased with increasing NaCl concentration, and decreased by 1.9-42.9%,1.5-12.4%, 15.4-79.5%, 32.7-64.9%, 9.4-60.4$ and 8.1-89.5% respectively, when compared to contrasting treatments (Table 2).

The effect of water content in tissue. Water content in seedlings increased slightly under lower 100 mmol/L salt concentration, decreased when seedlings were held from 100 to 300 mmol/L, and decreased slightly when seedlings were held in from 300 to 500 mmol/L salt concentrations.

Exp. 3. The effect of NaCl stress on seedling growth and some physiological and biochemical index in the second leaf stage: effect on seedling growth. The seedling growth index has a tendency to decrease with increasing NaCl concentration (Table 3). Seedling height, stem diameter, leaf area, ratio of root and crown, and fresh weight of seedling were decreased by 6.6-14.1%, 3.9-14.3%, 7.2-15.8%, 26.3-60.5% and 28.8-50.6%, respectively, when compared with contrasting treatments. The seedlings died when salt concentration reached 500 mmol/L.

The effect of NaCl stress on some physiological and biochemical index of cucumber seedling. The chlorophyll, proline, MDA and injury rate of cell membrane has a tendency to increase with the increasing NaCl salt concentration, while soluble protein content had a tendency to decrease (Table 4). The injury rate of the cell membrane reflected the widest difference of effects when all salt concentration were considered. Proline content also showed wide differences among treatments. The difference in MDA contents and soluble protein content under different treatments was not significant. It is concluded that cell membrane injury rate and proline content were the most sensitive variables to salt stress of those variables considered.

Table 1. The effect of NaCl stress on seed germinating in cucumber.

NaCl (mmol/L)	Germination rate (%)	Germination viability (%)	Vigor index
0(ck)	99.0 aA	99.0 aA	2.98 aA
100	98.0 aA	98.0 aA	1.23 bB
200	90.3 aA	79.0 bB	0.31 cC
300	18.0 bB	73.0 cC	0.14 cC
500	0.0 cC	0.0 cC	0.00 cC

Table 2. The effect of NaCl stress on sprouting and seedling growth at the cotyledon stage in cucumber.

NaCl (mmol/L)	Sprouting rate (%)			Cotyledon stage					
	3d	5d	8d	Seedling height (cm)	Stem diameter (mm)	Leaf area (cm^2)	Rate of root and crown	Root length (cm)	Fresh weight of seedling (g)
0(ck)	91.5	98.75	98.75	3.17	2.02	5.47	0.171	6.61	0.694
100	76.25	98.75	98.75	3.11	1.99	4.63	0.115	5.99	0.638
200	23.75	96.25	96.25	2.75	1.97	3.54	0.085	4.47	0.520
300	1.25	66.25	77.50	1.87	1.85	2.35	0.064	3.58	0.343
500	0.00	1.25	5.00	1.81	1.77	1.12	0.060.	2.62	0.073

Table 3. The effect of NaCl stress on cucumber seedling growth at the second-leaf stage.

NaCl (mmol/L	Seedling height (cm)	Stem diameter (mm)	Leaf area (cm^2)	Rate of root and crown	Fresh weight of seedling (g)
0(ck)	6.23	2.59	19.93	0.19	12.03
100	5.82	2.49	18.50	0.14	8.56
200	5.53	2.36	17.04	0.10	6.77

300	5.46	2.22	16.78	0.08	5.94
500	0.00	0.00	0.00	0.00	0.00

Table 4. The effect of NaCl stress on some physiology and biochemical indices in cucumber seedlings.

NaCl (mmol/L)	Injury rate of cell membrane (%)	Proline (%)	MDA (-mol/l.g{Fw*}	Chlorophyll (%)	Soluble protein (mg/g []w)
O(ck)	0.0 dD	$4.55x10^{-3}$ cC	$7.6x10^{-3}$ aA	0.304 bB	3.24 aA
100	7.0 cD	$5.68x10^{-3}$ bcBC	$7.8x10^{-3}$ aA	0.361 aA	2.94 aA
200	13.8 bB	$7.21x10^{-3}$ bB	$8.1x10^{-3}$ aA	0.395 aA	2.75 aA
300	22.5 aA	$9.20x10^{-3}$ aA	$10.5x10^{-3}$ aA	0.403 aA	2.33 aA

*Fw = Fresh weight.

Figure 1. The effects of NaCl stress on water contents of cucumber seedlings.

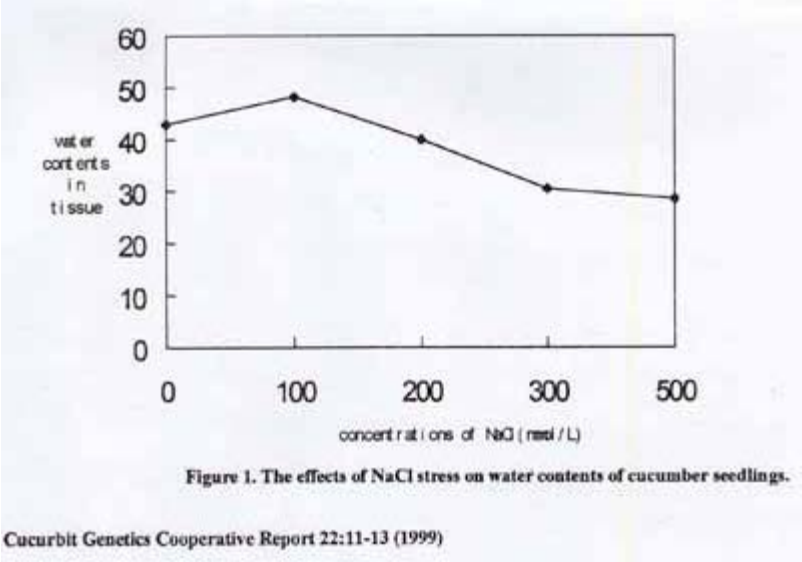

Figure 1. The effects of NaCl stress on water contents of cucumber seedlings.

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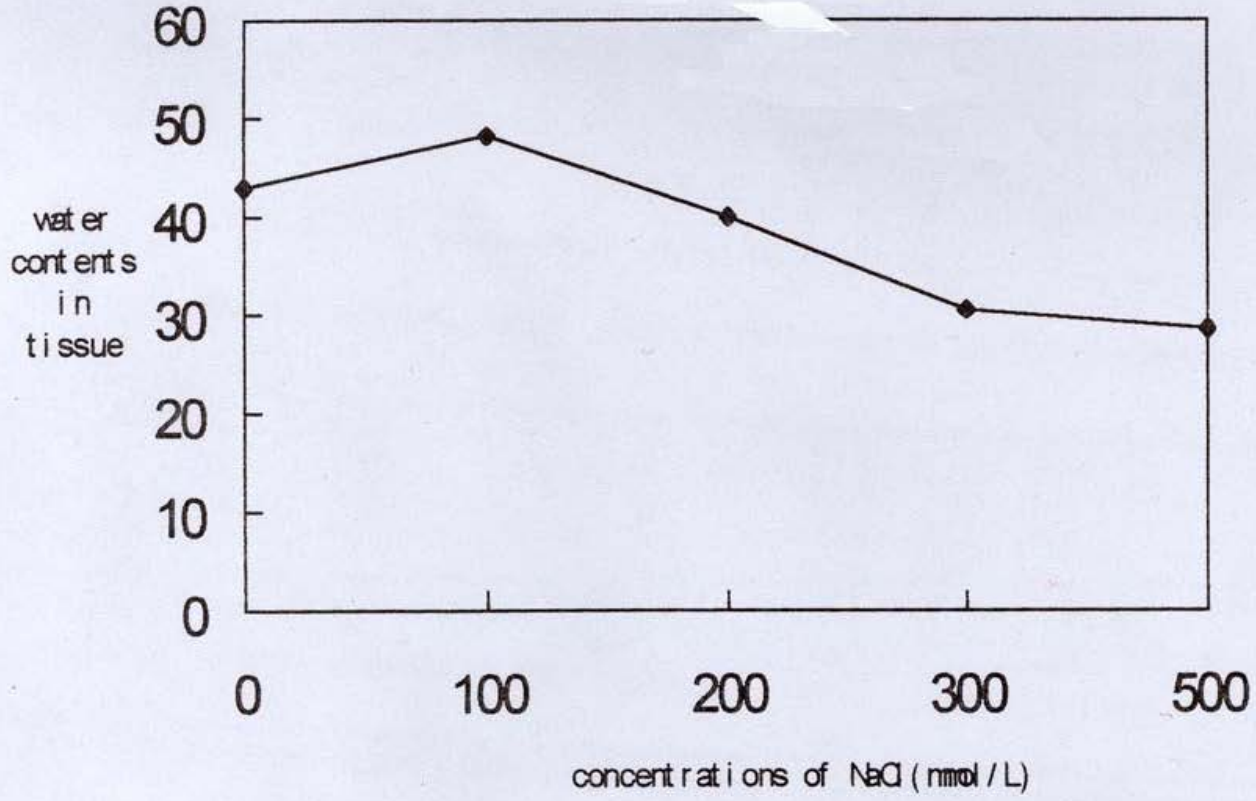

Figure 1. The effects of NaCl stress on water contents of cucumber seedlings.

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Description and Inheritance of an Albino Mutant in Melon

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A spontaneous albino mutant of *Cucumis melo* L. has been observed ion 'Trystrorp', an accession from Sweden. Cotyledons are white and plants died one to two weeks after germination. Germination of the seeds was very high in different generations indicating no lethal effect on the embryos. Because homozygous plants cannot be used as female or male parents, only heterozygous plants can be used for inheritance studies.

The F_1 between 'Trystorp' and 'Vedrantais' was backcrossed three successive times to 'Vedrantais' (a normal charentais type line). These plants were selfed after each backcross (BC_XS_1) in order to verify if they were heterozygous for albino or normal. All the heterozygotes were normal indicating that albinism is completely recessive. Selfed backcrosses segregating for albinism fit a 1:1 ratio (Table 1) in the different generations. the number of progenies fit a 3:1 ratio in the BC_1 and BC_2 , but in the BC_3 and BC_4 there was an excess of albinos (Table 2). The segregation observed on the total number of plants in the different progenies fits a 3:1 ratio. Therefore, the albino trait can be explained by the action of one recessive gene. No other albino mutants has been described to our knowledge. We propose this mutant be named *albino* with the symbol *alb*.

Table 1. Number of plants whose selfed progeny segregated for *albino* in successive backcrosses of the F_1('Trystorp' x Vedrantais') to 'Vedrantais'.

	Number observed			**X^2**	
	Segregating	**Non-segregating**	**Ratio tested**	**Value**	**Probability**
BC_1	9	5	1 : 1	1.143	29%
BC_2	8	12	1 : 1	0.800	37%
BC_3	10	7	1 : 1	0.529	47%
BC_4	7	12	1 : 1	1.316	25%
Total	**17**	**19**	**1 : 1**	**0.111**	**74%**

Table 2. Segregation for *albino* observed in selfed BC progenies.

Population	**Number observed**			**X^2**	
	Normal	**Mutant**	**Ratio tested**	**Value**	**Probability**
BC_1S_1					
95-2033	11	1	3 : 1	1.778	18%
95-2034	41	15	3 : 1	0.095	76%

95-2019	48	11	3 : 1	1.271	26%
95-2023	32	8	3 : 1	0.533	47%
Total BC_1S_1	**132**	**35**	**3 : 1**	**1.455**	**23%**
BC_2S_1					
96-1008	47	14	3 : 1	0.137	71%
96-1010	30	11	3 : 1	0.073	79%
96-1012	14	4	3 : 1	0.074	79%
96-1020	25	6	3 : 1	0.527	47%
Total BC_2S_1	**116**	**35**	**3 : 1**	**0.267**	**61%**
BC_3S_1					
97-1039	40	27	3 : 1	8.363	0.4%
97-1040	60	28	3 : 1	2.182	14%
Total BC_3S_1	**100**	**55**	**3 : 1**	**9.086**	**0.3%**
BC_4S_1					
98-1060	41	19	3 : 1	1.422	23%
98-1062	65	31	3 : 1	2.722	10%
Total BC_4S_1	**106**	**50**	**3 : 1**	**4.137**	**4%**
Total	**454**	**175**	**3 : 1**	**2.671**	**10%**

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Genetic Control and Linkages of Some Fruit Characters in Melon

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Introduction. *Cucumis melo* L. is a very polymorphic species, especially for fruit characters like ripening, shape, and flesh color. This variability has been used by botanists to subdivide melon into different major groups. Fruit characters are under genetic control, and the Mendel ian inheritance of some fruit characters like pentamerous locule number and sex expression were demonstrated a long time ago (13). More recently, several fruit-character genes were studied and characterized in the different horticultural groups (12). Improvement of fruit-1uality is an important melon breeding objective. Defining the genetic control of these characters will assist breeders, and their subsequent molecular mapping will contribute to the development of marker-assisted selection (MAS) (14).

In this paper, we describe the genetic control and linkage tests for genes involved in 9 major fruit characters in two different recombinant inbred line (RI) populations.

Methods. Parental lines were 'Vedrantais', an old French inbred line developed by Vilmorin, PI 161375, a Korean line, and PI 414723, an Indian line. The later two are multi-resistant lines used in several breeding programs. the populations studied were 120 F_6/F_7 RI derived from the cross 'Vedrantais x PI 161375 and 63 F_6/F_7 RI from the cross 'Vedrantais x PI 414723. the parents, F_1 and RI were cultivated under a plastic tunnel in a completely randomized block design with three replications in Avignon (Southern France) during the Summer of 1996 for the PI 414723 population and the Summer of 1997 for the PI 161375 population. four or more fruits of each line were evaluated for fruit characters. The segregation and independence of characters was evaluated using X^2 tests.

Results. Nine fruit characters show discrete segregation, eight are under monogenic control and one is under complementary, digenic control (Table 1). The digenic, complementary control of fruit abscission suggests the duplication of an ancestral gene. In a previous study, digenic complementary control of abscission layer formation was found in a cross between 'Pearl' and C68 (15). Genetic control of most of these characters have already been studied but no allelism tests have been done. We have given temporary names to most of the genes found in this study, according to previous work. To our knowledge, empty cavity hasn't been described in *Cucumis melo*. Carpels of the fruit were separated from each other at ripening leaving a cavity. A similar phenotype has been described in cucumber and named *Es-1* and *Es-2* (9).

None of the genes segregating in the RI Vedrantais x PI 161375 are linked (Table 2). Epistatic tests are necessary to establish the independence between *Al-3, Al-4* and the other genes. In the 'Vedrantais' x PI 414723 population, we found a possible linkage between *wf-2* and *s-3,* with a calculated genetic distance (2) of 28 cM Kosambi (7), and also between *Me-2* and *Ec* (23 cM, Table 3). However, the probabilities for these two linkages were very near the threshold limit (p), and the small population used (63 RI) could result in a spurious linkage. Mapping with molecular markers will confirm or disprove these results.

Interestingly, we can explain some very important phenotypic differences between the 3 parents with a few key loci, six for PI 161375 and four for PI 414723. If one disregards the important traits for shape and flavor, the major distinctions between melon horticultural group may be the results of a few key loci that play significant roles in the morphological differences between each group (3).

The major genes described here are now being incorporated into the molecular linkage map of melon we are developing. Moreover, we are planning to map quantitative trait loci (QTL) for fruit characters in our two populations. We hope to better understand the general control and gene interactions determining fruit characters in melon. the common parent of the two

populations will allow merging of the two maps to create an integrated map of melon (11). This will offer the melon community a useful tool for breeding. Other fruit-quality and/or morphology genes which segregate in other crosses will be included using a combination of bulked segregant analysis (10) and map merging. Our main objective is to map the major genes and QTLs defining fruit quality on an integrated reference map of melon.

Table 1. Genetic control of nine fruit characters in two recombinant inbred (RI) populations. The dominant character is listed first (**e.g.*.: orange/green, orange is dominant to green).

Character	Oberved frequencies	Theoregical segregation	X^2 value	X^2 Probability	Gene symbol	Reference
RI 'Vedrantais' x PI 161375						
Flesh color	55:49	1:1	0.35	55%	*gf-2*	(6)
orange/green						
Fruit abscission	80:23	3:1	0.59	44%	*Al-3, Al-4*	(15)
Abscission/non-abscission					.	
Spots on the rind	52:47	1:1	0.25	61%	*Mt-2*	(4)
Absebce/presence						
Placena number	45:62	1:1	2.14	14%	*p*	(13)
3/5						
Sutures on the rind	50:56	1:1	0.34	56%	*s-2*	(1)
Absence/presence						
RI 'Vedrantais x PI 414723						
Mealy flesh	22:24	1:1	0.087	77%	*me-2*	(4)
crisp/mealy						
Sour taste	22:24	1:1	0.087	77%	*So-2*	(8)
Sour/sweet						
Empty cavity	29:27	1:1	0.071	79%	*Ec*	This work
Empty/full						
Seed color	35:24	1:1	2.05	15%	*Wt-2*	(5)
Yellow/white						
Sutures on the rind	28:28	1:1	0	100%	*s-3*	(1)
Absence/presence						

Table 2. X^2 values for independence of several fruit trait genes in the RI population 'Vedrantais' x PI 161375. Probability associated with the X^2 value is shown in parentheses.

	sp-2	***p***	***s-2***
gf-2	1.58 (66%)	1.38 (71%)	3.56 (31%)
sp-2		4.62 (20%)	1.43 (70%)
p			3.79 (28%)

Table 3. X^2 values for independence of several fruit trait genes in the RI population 'Vedrantais' x PI 414723. Probably associated with the X^2 value is shown in parentheses.

	So-2	*Ec*	*wt-2*	*s-3*
me-2	2.76 (43%)	7.22 (6.5%) d=21.9 cM	1.82 (61%)	0.26 (97%)
So-2		0.42 (93%)	2.18 (53%)	0.43 (93%)
Ec			2.47 (48%)	0.93 (82%)
wt-2				8.66 (3.4% d=25.7 cM

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Identification of the Gene for Resistance to Fusarium Wilt Races 0 and 2 in *Cucumis melo* 'Dulce'

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Four races of *Fusarium oxysporum* f.sp. *melonis* (0,1,2, and 1,2) cause wilt in melons. three independent dominant genes were reported to confer resistance to Fusarium wilt. Resistance is race specific. Two genes have been identified as conferring resistance to races 0 and 2, *Fom-1* in 'Doublon' and 'Hemed' (Risser 1969, Zink et al. 1983, Katan and Katan 1992, Paris et al. 1993) and *Fom-3* in 'Perlita-FR' (Zink and Gubler 1985).

'Dulce' is another cultivar that is resistant to races 0 and 2 but susceptible to race 1. PI414723-S_5 (a ZYMV-resistant selection from PI414723, Danin-Poleg et al. 1997) is susceptible to races 0, 1 and 2.

The objectives of this study were to identify the gene(s) conferring the resistance in 'Dulce' and to map the gene(s) for resistance. For gene identification, 'Dulce' was crossed with 'Hemed' and 'Doublon' (Table 1). The parents and their F_1 and F_2 progenies were inoculated with *Fusarium oxysporum* f.sp.*melonis* races 0 and 2 separately. The melon cultivar 'En Dor' was used as a susceptible control (Katan and Katan 1992). Identification of the Fusarium race was confirmed using the differentials 'Doublon' and 'Hemed'.

For mapping of the resistance, F_2/F_3 families of the mapping population (PI414723-S_5'Dulce') were inoculated with fusarium,. From 20 to 42 plants of each of the 104 families were infected with race 0 or race 2 in three separate trials.

All 'Dulce', 'Hemed and 'Doublon' plants were, as expected, resistant to Fusarium races 0 and 2 (Table 1). All 'PI414723' and 'En Dor' plants were susceptible. All F_1 and F_2 plants resulting from crossing of 'Dulce' with 'Hemed' and 'Dulce' with 'Doublon' were resistant to both race 0 and race 2. No susceptible individuals were found among the 644 and 686 F_2 plants of the crosses with the two resistant accessions (Table 1). Therefore, the results indicated that the Fusarium resistance in 'Dulce' is conferred by the same gene as in 'Doublon' and 'Hemed', *Fom-1.*

The segregation of the resistance in the F_2/F_3 families of the mapping population was 24:51:29 (all resistant:segregants resistant and susceptible : all susceptible, respectively) in accordance with the expected 1:2:1 ratio (X^2 = 0.52 p=0.77). Resistance was analyzed together with 73 markers and located to linkage group 5. This is in agreement with the previous assignment of *Fom-1* to that linkage group (Baudracco-Arnas and Pitrat 1996).

Deviation from the expected segregation ratio was observed in seven of the 51 heterozygous F_2/F_3 families. In those families 40-53% of the plants were susceptible rather than 25% as expected. We observed the same phenomenon in other germplasm during the last few years. Deviation was previously reported by Baudracco-Arnas and Pitrat (1996). These findings and the non-uniform response of some genotypes to Fusarium wilt may differ among genetic backgrounds.

Table 1. Reaction to inoculation with Fusarium wilt races 0 and 2 in crosses between 'Dulce' and 'Doublon' nd 'Dulce; and 'Hemed'.

Parents and crosses	**Number of plants**			
	Race 0		**Race 2**	
	Resistant	**Susceptible**	**Resistant**	**Susceptible**
Dulce	35	35	35	0

Hemed	49	49	42	0
Doublon	42	42	42	0
PI414723-S_5	0	0	0	35
En Dor	0	0	0	35
F1 Dulce x Hemed	301	49	42	0
F2 Dulce x Hemed	343	301	343	0
F2 Dulce x Doublon		343	343	0

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Tibish, a Melon Type from Sudan

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Melon (*Cucumis melo* L.) is a polymorphic species that has been classified into several intra-specific groups. Naudin (1859) laid the foundation for such intra-specific grouping. His attempt for grouping melon types has remained valid up to the present time, with some amendments made later (4, 7, 8). Grebenschikov (1953) proposed another system for sub-classifying melons. He divided melons into two specific species: *cucumis melo* and *C. agrestis.* He subdivided them further into different sub-taxa, using the names species and sub-species for *C. agrestis* and specioid and sub-specioid for *C. melo*, which he subdivided into several convarieties. Hammer et al. (1986) followed almost the same system of Grebenschikov with some amendments, mainly by grouping *C. agrestis* and *C. melo* into one species and considering two sub-species (*agrestis* and *melo*). Both Naudin's and Grebenschikov's classifications have similarities and differences when compared together (Table 1). For instance the group *flexuosus* is very typical and is found in all classifications. All these classifications are based mai8nly on fruit characters and uses, and also to some other plant characters.

In Sudan five types of melons are known. They are different in their morphological features as well as the ways in which they are used, and hence they belong to different intra-specific groups of melon. Each of these types has a specific local name. They include the following:

1. **Adjour**, which is the snake cucumber (*C. melo flexuosus*). Its immature fruits are used raw in salad, and for pickling, but sometimes are cooked.
2. **Shamam**, which is the sweet melon (*C, melo cantalupensis*). Its full ripe sweet fruits are used in dessert.
3. **Tibish**, the immature fruits of this type are also eaten raw in salad, which is more popular with hot pepper and lime juice.
4. **Humaid**, this is a typical wild melon growing in Sudan. It belongs to the group *C. melo agrestis.*

The tibish type, which is a probable first step in the domestication of melon (6), seems to be different from the other groups of this species. From the observations made when collecting and characterizing several local collections of tibish in sudan, this type did not fit in either of the known intraspecific groups proposed by different authors. It has been classified as a cultivated type of *C. melo agrestis,* but the plant characters, with its medium to large dark green foliage, and medium sized fruits, are different from those characters of melons from the *agrestis* group as described elsewhere.

Tibish plants usually have dark green foliage of almost entire leaves which are more or less elongate. The leaf size is usually medium to large, with midrib length of the leaf lamina 8 cm or greater. The sex type of tibish plants is usually andromonoecious. Fruits normally are oval or oblate in shape, without ribs and with a smooth surface with dark green stripes, which appear on a background of green or light green color when fruits are immature. In some cases markings are lacking, as in the fruits of the seinat type, which could be considered as a sub-type of tibish. Upon full maturity and ripeness the predominant fruit skin color becomes yellowish-green to yellow with dark green stripes. Fruit size ranges between small and medium,, with a fruit length commonly between 8-15 cm, and width between 4-9 cm, but exceptional sizes can be found with fruit length more than 20 cm and width more than 10 cm. Flesh is usually whitish, more or less firm, and not sweet. External and internal aroma are lacking. to our knowledge tibish and seinat types of melons are grown only in sudan and not in neighboring countries.

Different types of melons are used as vegetables, i.e., fruits harvested before maturity and eaten raw, pickled or cooked, these types mainly include:

- ***flexuosus*** which was first described as *Cucumis flexuosus* L. It is grown in the Northern half of Africa, Western and

Central Asia until India.

- ***adzhur*** (Pang.) Grebenschikov, which was first described as *cucumis chate* Hasselq. fruits of this type are less elongated than *flexuosus* fruits. It is grown in the Mediterranean countries, as in Italy (where it is known as carosello) and Turkey.
- ***conomon*** which is grown in Eastern Asia. According to the proposal of Jeffrey (1980), Hammer et al. (1986) classified it within *C. melo agrestis* because of the hairiness character of the ovary. Nevertheless it is a cultivated type and not a wild *agrestis* one.
- ***momordica,*** a type quite specific to India.

Tibish is another type of vegetable melon which is different from all previously described intra-specific groups. Being so, we propose that tibish could be another intra-specific group of melon.

Table 1. Intra-specific classification of melon after Naudin (1859) and Grebenschikov (1953) and various modifications.

Naudin (1859)	**Whitaker & Davis (1962)**	**Munger & Robinson (1991)**	**Robinson & Decker-Walters (1997)**	**Grebenschikov (1953)**			**Hammer et al. (1986)**	
Species and tribe	Species and variety	Species and group	Species and group	Species and sub-species	Specioid and sub-specioid	Covariety	Species and sub-species	Covariety
Cucumis melo	*Cucumis melo*	*Cucmis melo*	*Cucumis melo*	*Cucumis agrestis*	*Cucumis melo*		*Cucumis melo*	
agrestis		agrestis	agrestis	agrestis figari			agrestis	conomon
cantalupensis reticulatus saccharinus	cantapulensis reticulatus	cantalupensis	cantalupensis		melo	cantalupa	melo	melo
inodorus	inodorus	inodorus	inodorus			zard		zard
						caasaba		casaba
								ambiguus
						adana		adana
						chandalak		chandalak
						ameri		ameri
flexuosus	flexuosus	flexuosus	flexuosus		flexuosus	flexuosus		flexuosus
						adzhur		adzhur
acidulsus	conomon	conomon	conomon		conomon	conomon		
						chinensis		
dudaim	dudaim	dudaim	dudaim		dudaim			dudaim
chito	chito	chito						
erythraesus								
		momordica	momordica					

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Changes in Lipid Peroxidation and antioxidant Status in Ripening Melon (*Cucumis melo* L.) Fruit

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Introduction. Mature melons become soft and dehydrated, even when storied in cool humid conditions. the short time inwhich fruits must be harvested, sold and consumed is a serious constraint to profitability. Studies on the timing and nature of ripening-associated events, which may lead to the production of new cultivars with improved storage ability or the development of better post-harvest handling techniques, are of critical importance to the industry.

Lipid peroxidation, a prominent feature of plant senescence and aging (Kumar and Knowles, 1993),may impair membrane structure and function (Thompson et al, 1997). Lipid peroxidation is a consequence of metabolic processes in plant cells which produce reactive oxygen species (ROS) such as superox9ide, hydrogen peroxide, and singlet oxygen. For every source of lipid peroxidation in the plant cell, there are corresponding defense mechanisms. Among the most important non-enzymatic defense mechanisms are the water-soluble reductants glutathione (GSH) and ascorbate (ASC), and the lipid-soluble vitamin e (Tocopherol). Vitamin E protects against oxygen radicals that initiate lipid peroxidation and serves as a scavenger of chain-propagating free radicals such as lipid peroxyl radicals (Winston, 1990). ASC and GSH are proposed to be direct free-radical scavengers in the cytoplasm and may act synergistically with vitamin E in the inhibition of oxidative damage to cell membranes.

Melon fruit show a progressive increase in membrane permeability, as measured by electrolyte leakage, as the fruit matures (Lester, 1988). this leakage proceeds most rapidly in the interior of the fruit, which ripens sooner. In a comparison between short-and long-storage life nonnetted melons electrolyte leakage increased with ripening and was always higher in the short-storage cultivar, whereas the long-storage life cultivar had little increase in membrane permeability as the fruit ripened (Lascan and Baccou, 1996). The loss of membrane integrity was associated with a breakdown of phospholipids. Membrane integrity thus seems to be an integral component of melon fruit ripening. The current study was aimed at evaluating lipid peroxidation and status of the antioxidants vitamin E, GSH and ASC during melon fruit development and senescence.

Methods. *Plant material* 'Perlita' melon were grown singly in pots in a greenhouse using a trellis system. Hermaphroditic flowers were pollinated and tagged at anthesis, with one to two fruits per plant were allowed to develop. Unripe fruit were harvested at 20, 30, and 40 days post0anthesis (PA) . Ripe fruit were harvested at the full-slip (FS) stage, which occurred from 42 to 49 days PA, and were either sampled that day or stored at 20 C and ambient humidity for 5 or 10 days. Thus, samples were taken at six different developmental stages, and four to six fruits were sampled at each stage.

For analyses, the epidermis was removed from the fruit and tissue was extracted from the endo-mesocarp (E/M), middle-mesocarp (M/M), and hypodermal-mesocarp (H/H) regions of the fruit. H/M was tissue up to 5 mm below the epidermis, E/M was taken from the mesocarp within 5 mm of the seed cavity, and M/M tissue was central to the exterior and interior of the fruit. Tissue sample were collected and frozen in liquid N_2, ground to a fine powder with dry ice, and stored at -80 C.

Chemical analyses. As a measure of lipid peroxidation, malondiadehyde (MDA) content was assayed by HPLC using the procedure of Iturbe-Ormaetxe et al. (1988). Vitamin E was assayed via a reverse-phase HPLC using the procedure of Spychalla and Desborough (1990). Reduced ascorbate determination was based on the reduction of Fe^{3+} to Fe^{2+} by ASC in acidic solution. The Fe^{2+} then forms a complex with bipyridyl, giving a pink color that was measured with a spectrophotometer (Law et al., 1983. Reduced glutathione was measured by a HPLC after derivation with 5,5'-ditho-bis-(2-nitrobenzoix acid) (Ranieri et al., 1993)

Results. As melons reach their climacteric peak, an abscission layer forms between the fruit and the vine a stage often referred to as full-slip (FS). The GS stage was reached at an average of 45 days PA in this study. At 20 days PA, melon flesh was quite firm and uniformly green. At 30 days PA, the E/M tissue had begun to show signs of the characteristic orange

color. M/M tissue was orange at 40 days PA, but firmness was not significantly different from 20 and 30 days PA. At FS, fruit firmness was approximately half of the unripe values (Data not shown). Fruit firmness continued to decline at FS+5 and FS+10 days, at which point fruits were soft and watery and the hypodermis had begun to exhibit necrotic spots.

MDA, a breakdown product of lipid hydroperoxides, was used as an indicator of lipid peroxidation. MDA content was similar for all three tissues types at a given stage of development (Fig. 1). MDA content increased throughout development, most dramatically in the period from FS+5 days to FS+1- days.

Three toicopherol (vitamin E) isomers (a , ß / ? and d) were detected in the chromatograms of melon tissues. Reverse-phase HPLC cannot separate the ß and ? isoforms, so this peak was designated as ß / ?. Total tocopherol concentration increased during development to maximal levels at FS or FS+5 days depending on tissue type (Fig. 2). Tocopherol levels were always several-fold higher in the H/M tissue as compared to E/M and M/M tissue. ASC concentrations increased slightly fro 20 to 40 days PA, the increased up to 3-fold in the period from 40 days PA to FS, and declined thereafter (Fig. 3). GSH concentrations were similar at 20 and 30 days PA, increased in the period from 30 days PA to FS, and then decreased to their lowest level at FS+10 days (Fig. 4).

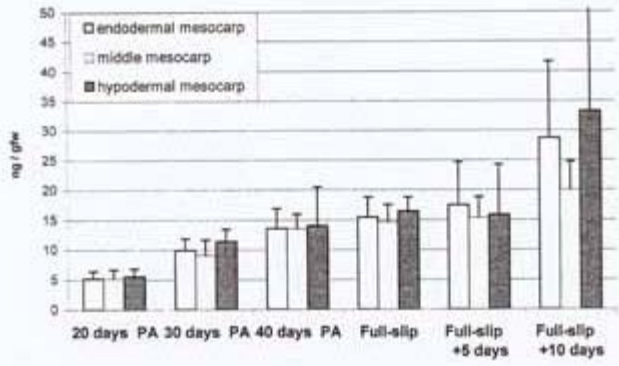

Fig. 1. Malondialdehyde levels in developing melon fruit. Each value is the mean ± SE of 4-6 fruit.

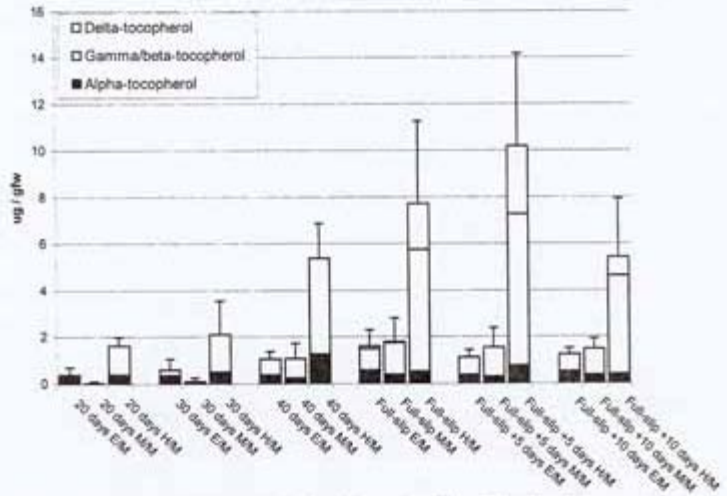

Fig. 2. Vitamin E (tocopherol) levels in developing melon fruit. Each value is the mean ± SE of 4-6 fruit.

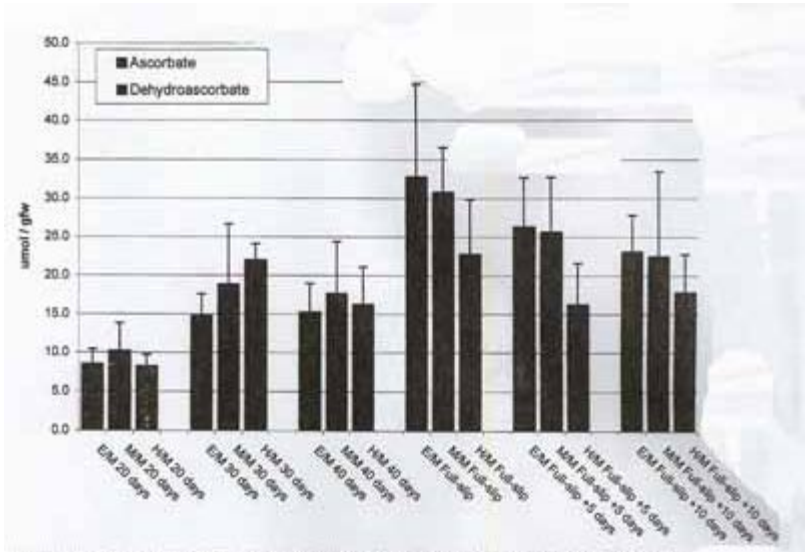

Figure 3. Ascorbate levels in developing melon fruits. Each value is the mean ± SE of 4-6 fruit.

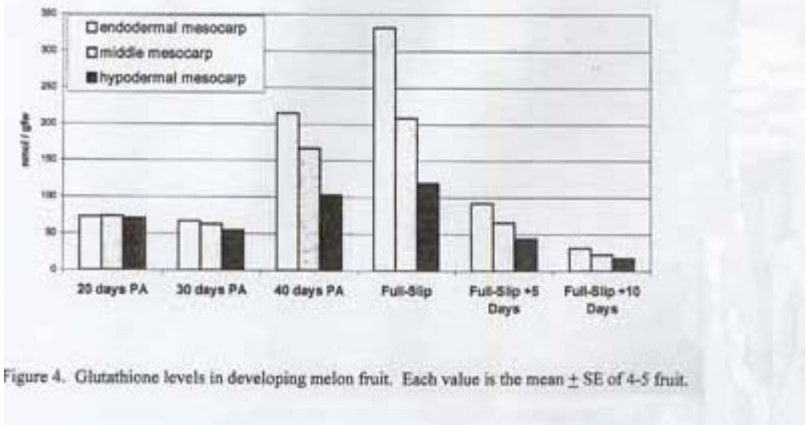

Figure 4. Glutathione levels in developing melon fruit. Each value is the mean ± SE of 4-5 fruit.

Discussion. ROS levels tend to increase when plants are exposed to stress (Shewfelt and Purvis, 1995). The peroxidation of lipids is the most frequently cited effect of this increase within the plant cell (Winston, 1990). The increasing levels of MDA in ripening melon fruits provides additional evidence of peroxidation and breakdown of lipids. This is consistent with previous studies showing increasing electrolyte leakage as melon fruits mature (Lester,1988).

The balance from an anti-oxidant state to a pro-oxidant state in the cell can be triggered by an increase in ROS formation, a decrease in a defense mechanism, or a combination of the two. The concentration of all three antioxidant levels coincided with a period from 40 days PA to FS+5 days, when MDA levels were relatively stable, suggesting that the tissue was successfully coping with the oxidative stress. However, in the senescing tissue from FS+5 days to FS+10 days, MDA levels again increased, indicating new lipid peroxidation. While ASC and vitamin E levels were roughly steady during this period, GSH declined dramatically. This may indicate a shift to a more pro-oxidant state leading to lipid peroxidation.

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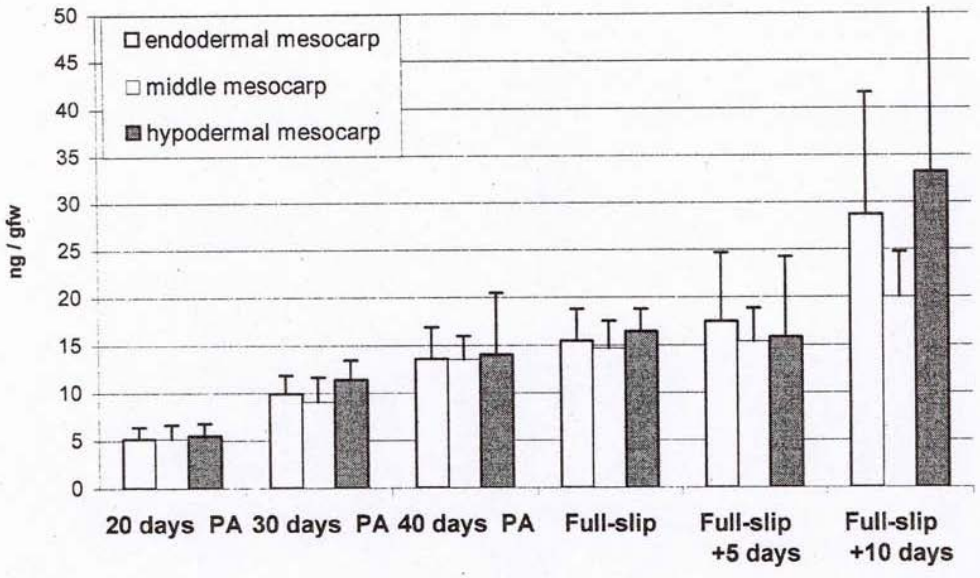

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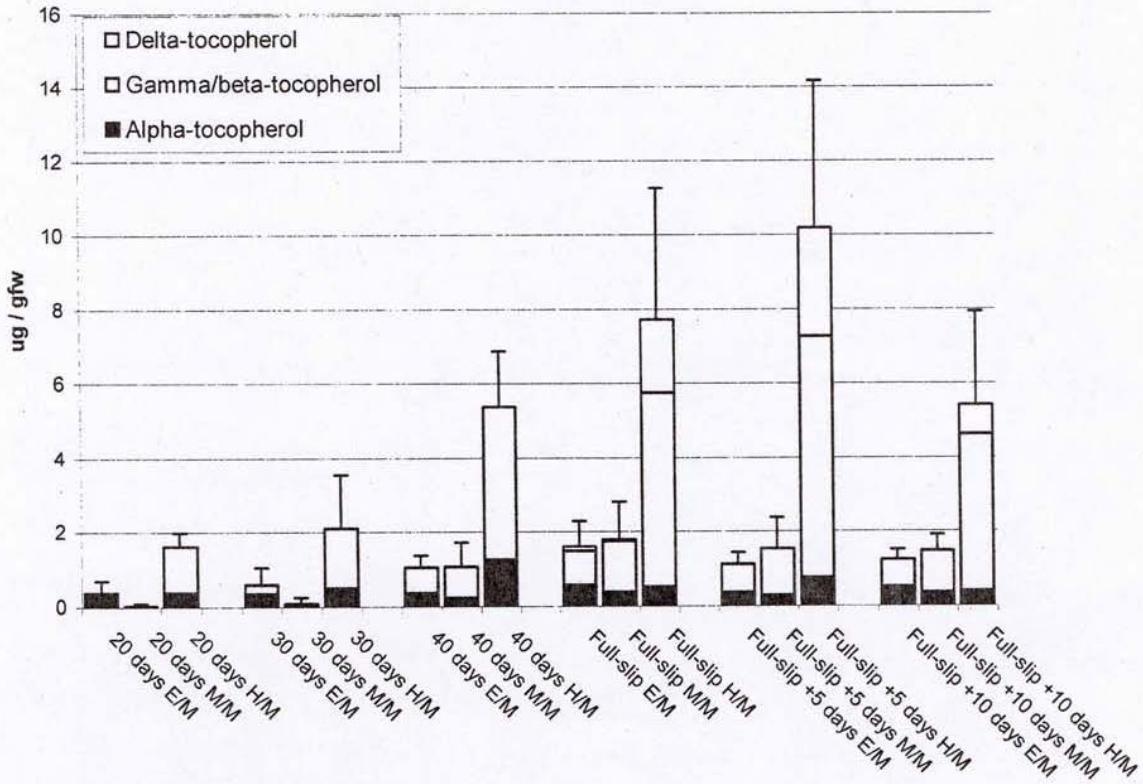

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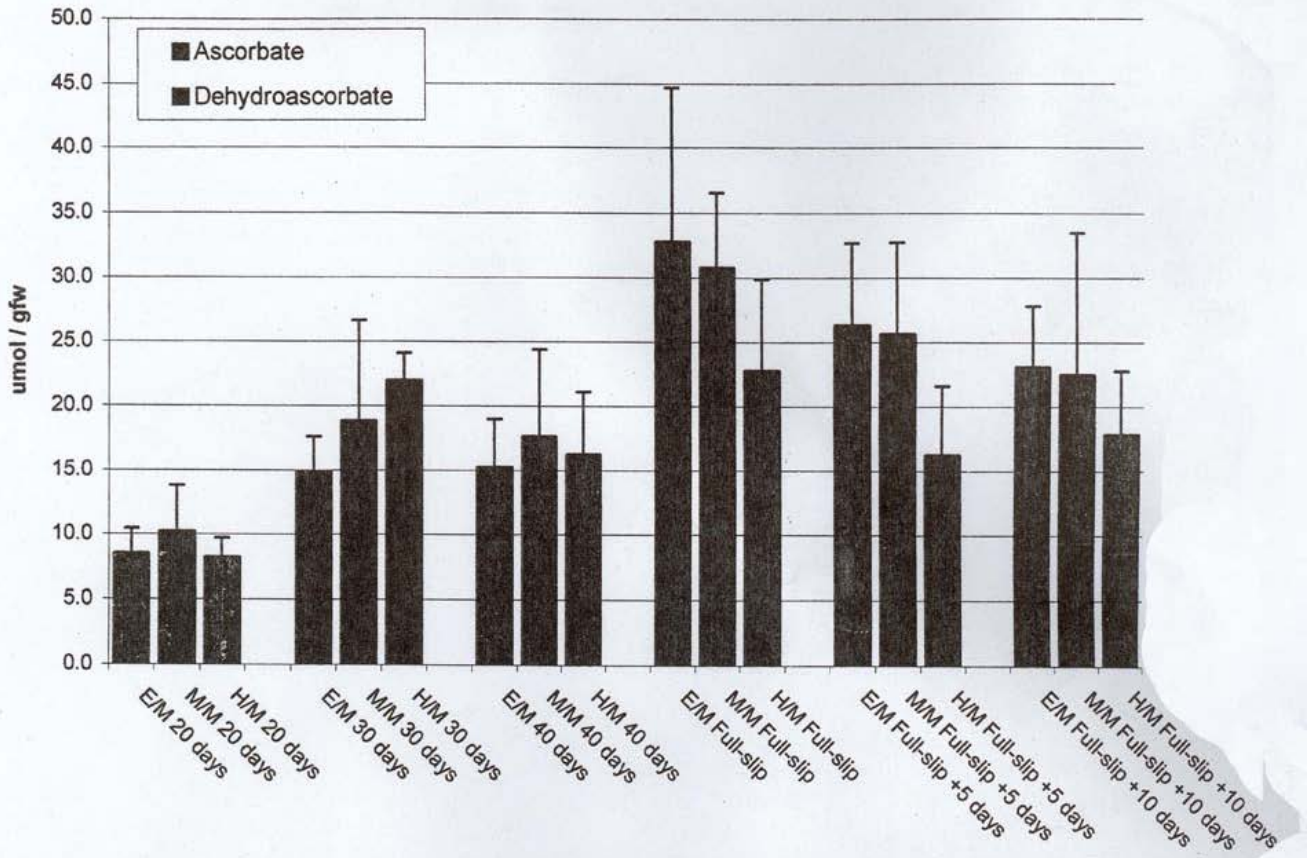

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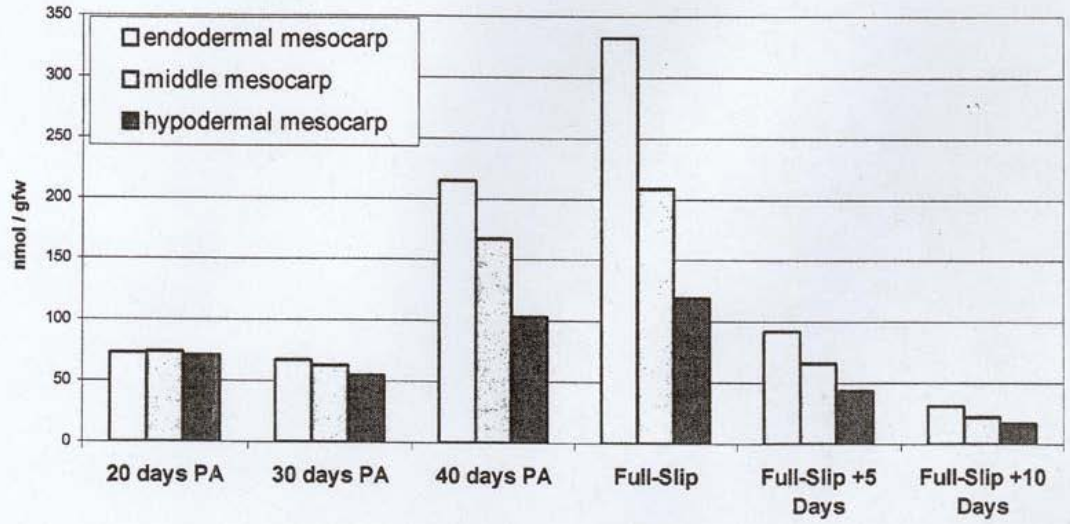

Figure 4. Glutathione levels in developing melon fruit. Each value is the mean ± SE of 4-5 fruit.

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A Tendrilless Mutant in Watermelon: Phenotype and Inheritance

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Introduction. Lin et al (1) described the mutant *branchless* with half the number of branches at the first five nodes. They reported this phenotype to be due to a single recessive gene *bl.*

We observed that the mutant did not produce tendrils in the field or greenhouse (2) and decided to characterize it more fully. A pruning experiment was conducted to test the hypothesis that the mutant loses the ability to differentiate a vegetative bud after the 4thor 5th node. To test whether the root system affects the mutant phenotype, we conducted a grafting experiment. We again examined the inheritance of the mutant when crossed with a normal and a dwarf phenotype.

Methods. Three treatments of five plants each were used in the *Pruning Experiment*: (1) the shoot tip was removed at the 10th node, as were the axillary buds for the first five nodes, 2) the shoot tip only was removed at the 10th node, and (3) no pruning was done.

Grafting Experiment: five wild-type scion were grafted on mutant rootstock and five mutant scions were grafted on wild-type rootstocks.

Inheritance Studies: The mutant (T) crossed with wild types A and B and a dwarf type C, and the F_1, F_2 and BC populations were scored for the trait.

Results. Photos 1 to 9 are arranged from left to right on the page.

Photo 1 (wild type) exhibits the normal arrangement of floral bud and tendril at a node. Photo 2 (mutant) shows a profusion of floral buds and no tendrils. Photo 3 exhibits two female flowers with abnormally long peduncles. Photo 4 compares the terminal shoot tip of a normal plant, with developing tendrils, normal leaflets and floral buds (left) and the terminal shoot tip of a mutant plant with no tendrils, abnormal leaflets and a cluster of floral buds (right). Photo 5 shows the chronological transformation of leaves on a mutant plant from an almost normal oak-like leaf appearance to a triangular shape with edges curling inward. The emerging leaves gradually lose their lobing and become triangular toward the end of the shoot. The *tendrilless* mutant, previously described as *branch less* (1) has more pleitropic effects. Branches are not produced after the 5th or 6th node. the vegetative meristems gradually become floral meristems. Tendrils and vegetative buds are replaced by flowers, with a significant number of perfect flowers, and growth becomes determinate.

Photo 6 of mutant plants, from left to right, shows that: (1) removal of the shoot tip at node 10 and the axillary buds for the first five nodes eliminates the ability of the mutant to produce any branches; (2) removal of the shoot tip at node 10

encourages branches at the first five nodes; and (3) no pruning at all results in a plant with two branches. Photo 7 of wild-type plants shows that : (1) removal of the shoot tip at node 10 and the axillary buds for the first five nodes results in lateral branches above the first 4-5 nodes; (2) removal of the shoot at the 10th node only results in the emergence of four lateral branches and (3) the unpruned wild-type has two branches.

Rootstock did not affect the mutant *tendrilless* (*T*) phenotype (Photos 8 and 9). Photo 8 shows the foliar development of the grafted branch of the mutant phenotype along with the lateral branches of the normal stock plant. In Photo 9, a similar pattern is seen.

The results of the inheritance studies are given in Tables 1 and 2. In Table 1, the cross between the two lines with normal phenotypes and the mutant resulted in F_1 plants with normal phenotype and F_2 plants that are segregated 3:1 for the *tendrilless* trait. In Table 2, a cross between the same *tendrilless* parent and a dwarf parent resulted in normal F_1 plants. The backcross progeny from the *tendrilless* parent fit a 1:1 normal:*tendriilless* segregation, but the backcross progeny from the dwarf parent did not fit a 1:1 normal:dwarf segregation. In the F_2 progeny, the *tendrilless* segregated 3:1 normal:*tendrilless*. The inheritance of the dwarf character in line C has not been determined, but the expression of the *tendriolless* phenotype does increase the number of individuals scored as dwarf phenotypes.

Conclusions. The *tendrilless* pleitropic mutant behaves like a simple recessive trait that eliminates vegetative buds above the 4th or 5th node We propose the notation *tendrilless* and the symbol tl for this recessive gene instead of the descriptor "branch less".

Table 1. Segregation in F_2 from two crosses of normal (A,B) x tendrilless (T) parent.

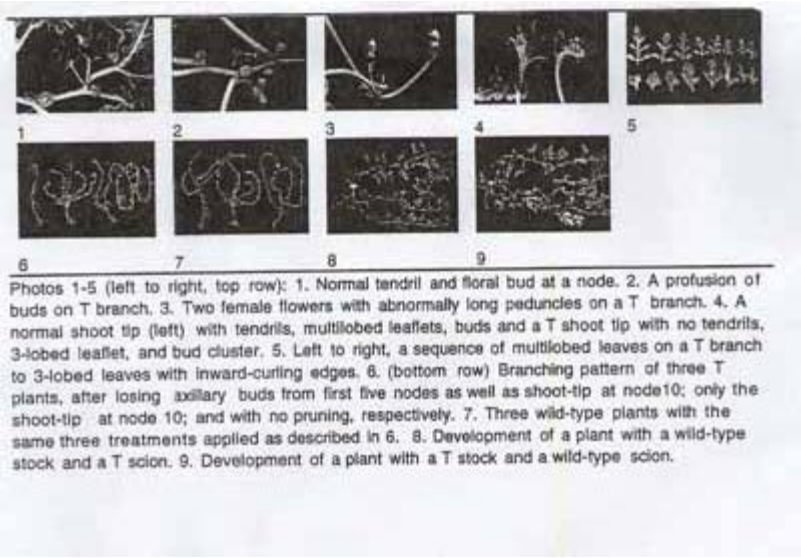
Parents, Progeny	TI- phenotype[1]	tl- ohenotype	Expected Ratio	X^2	P-Value
G17 AB (A)	28	0			
ASS-1 (B)	25	0			
B242 (T)	0	28			
(AxT) F_2	134	39	3:1	0.5568	0.50-0.25
(BxT) F_2	121	38	3:1	0.1027	0.75-0.50

[1] Phenotype is described in Results.

Table 2. Backcross and F_2 progeny from tendrilless (T) x normal parent (C).

Parents, Progeny	TI-Phenotype		tl-Phenotype		Ratio	X^2	P-value
	Vine	Dwarf	Vine	Dwarf			
B242 (T)			18				
YF91-1-2 (C)		16					
T x C	20						
(TxC) x T	25		23		1:1	0.0833	0.90-0.75
(TxC) x C	36	9			1:1	16.2000	<0.0001
(TxC)F_2 1993	150	37	51				
	187		66		3:1	0.1595	0.75-0.50
(TxC)F_2(1994)	410	57	99	62			
	467		161		3:1	0.1358	0.75-0.50

Photos 1-5 (left to right, top row): 1. Normal tendril and floral bud at a node. 2. A profusion of buds on T branch. 3. Two female flowers with abnormally long peduncles on a T branch. 4. A normal shoot tip (left) with tendrils, multilobed leaflets, buds and a T shoot tip with no tendrils, 3-lobed leaflet, and bud cluster. 5. Left to right, a sequence of multilobed leaves on a T-branch to 3-lobed leaves with inward-curling edges. 6. (bottom row) Branching pattern of three T plants, after losing axillary buds from first five nodes as well as shoot-tip at node 10; only the same three treatments applied as described in 6. 8. Development of a plant with a wild-type stock and a T scion. 9. Development of a plant with a T stock and a wild-type scion.



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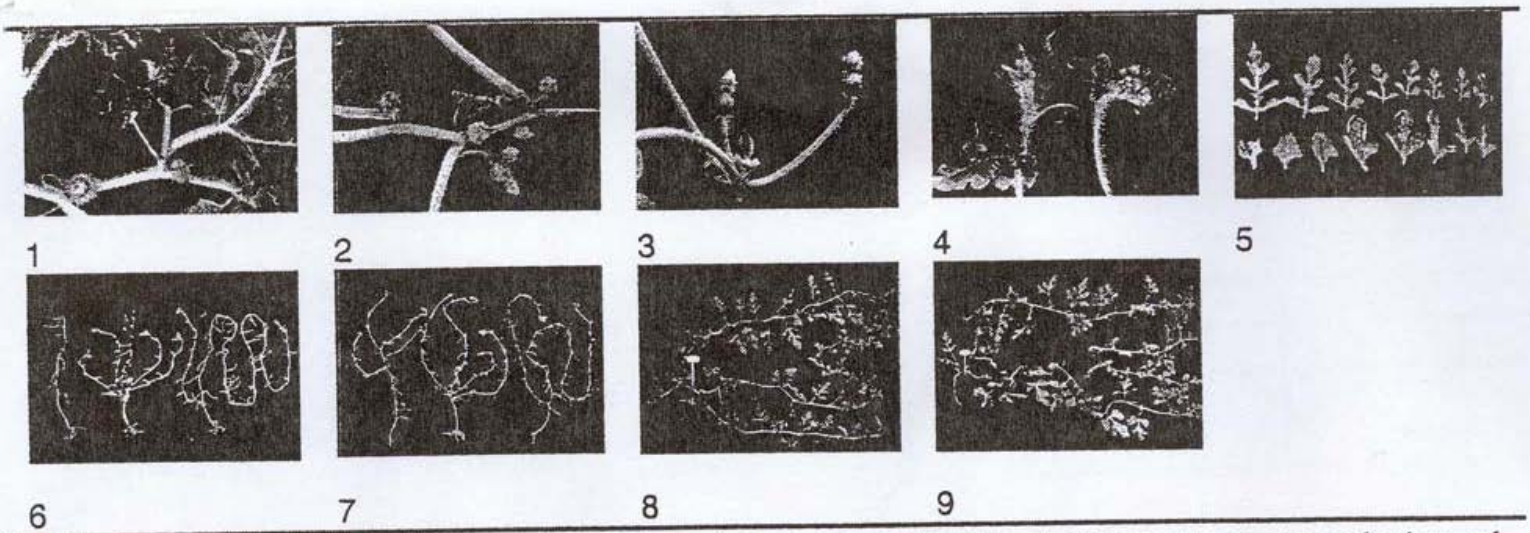

Photos 1-5 (left to right, top row): 1. Normal tendril and floral bud at a node. 2. A profusion of buds on T branch. 3. Two female flowers with abnormally long peduncles on a T branch. 4. A normal shoot tip (left) with tendrils, multilobed leaflets, buds and a T shoot tip with no tendrils, 3-lobed leaflet, and bud cluster. 5. Left to right, a sequence of multilobed leaves on a T branch to 3-lobed leaves with inward-curling edges. 6. (bottom row) Branching pattern of three T plants, after losing axillary buds from first five nodes as well as shoot-tip at node10; only the shoot-tip at node 10; and with no pruning, respectively. 7. Three wild-type plants with the same three treatments applied as described in 6. 8. Development of a plant with a wild-type stock and a T scion. 9. Development of a plant with a T stock and a wild-type scion.

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Inheritance of Light Green Flower Color (*gf*) in Watermelon (*Citrullus lanatus*)

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Introduction. Watermelon, *Citrullus lanatus* (Thunb,) is cultivated in many countries of the world. It is an important vegetable crop in Korea, where the acreage in 1998 was more than 35,000 ha. Although there have been many inheritance studies of watermelon mutants, watermelons have received relatively little genetic attention compared to other crops. Studies of the inheritance and linkages of various characteristics may give valuable information for the breeding of cultivated watermelon.

Many studies have been conducted to investigate the inheritance of morphological characteristics in watermelon (7). Yellow leaf, for example, was reported to be incompletely dominant to green leaf (6), while the andromonoecious character was found to be recessive to monoecious (2,4). Flower petal color is commonly yellow, but light green flowers were detected in watermelon accession kw695. This study was undertaken to determine the mode of inheritance of light green (petal) flower color.

Methods. The watermelon parent material used in this study, Kw-695 and Dalgona, was obtained from the Gene Bank of Rural Development Administration, while accession SS_4 was obtained from Seoul Seed Company in Korea. Controlled crosses were made in the greenhouse in 1998 between the different parents and F_1 hybrids to generate F_2 and backcross generations. To study the inheritance of light green-yellow flower color, parents F_1, F_2 and backcross generations were grown in 21 cm pots in a protected vinyl-house in 1999. Petal color determinations were made using a Chroma Meter (Minolta, CR-200) in the morning hours from 9-12 am. Each plant was examined 4-5 times over a five day period and classified as having yellow or light green flower color. Standard color ratings from Chroma Meter were classified with color index 'a' as: light green < - 10.0, yellow > -10.0.

Results. The results of the inheritance study are shown in Table 1. All F_1 hybrid plants resulting from the SS4 x Kw 695 and Dalgona x Kw 695 crosses produced yellow flowers. The resulting F_2 populations of these crosses segregated in a 3 yellow : 1 light green ratio. Backcross plants of F_1x SS 4 and F_1 x Dalgona produced yellow flowers. These same results were obtained both years and indicate that inheritance of the light green flower character in Kw 695 is governed by a single recessive gene. While the inheritance of fruit flesh and skin color (2,5), delayed green leaf color (3), yellow leaf color of older leaves and mature fruit and yellow leaf (1,6) have been published earlier, the inheritance of light green flower color was never reported. We propose the *gf* gene symbol for the light green flower trait.

Measurement of watermelon flower color with a Chroma Meter allowed for accurate identification and classification. Watermelon flower color is commonly controlled by three factors: L, a, and b (Table 2). On the average, light green flowers showed 'a' values < -12.0, while yellow flower color values were > -8.0. Light green flowers never showed 'a' < -10.0 Therefore, this study indicates that a Chroma Meter can be used for accurate flower color determinations for this trait in watermelon.

Kw-695 plants have large vines with large, light green leaves. The plants produce large oval fruit of bright yellow green color with irregular dark green stripes, bright yellow-orange, inedible flesh with very low sugar content (about 3.2^{-0} Brix), and light yellow seeds. We think that the trait could be useful as a marker to identify lines or commercial cultivars in watermelon breeding programs. Linkages between this trait and other genetic characters in watermelon will be investigated.

Table 1. Segregation of light green flower and yellow color in parent, F_1,F_2, backcross generations on watermelon.

Entry	No. of Tested Plant	Flower color		Expected ratio	X^2value	P
		Yellow	Light green			
1998 year						
Kw 695	**15**	0	15			
SS-4	14	14	0			
Dalgona	15	15	0			
F_1(SS-4)x Kw695)	10	10	0			
F_2	33	21	12	3.1	2.276	0.5-0.1
BCP1(SS4 x F_1)	22	22	0	1:0	0.059	0.9-0.5
BCP2(F_1 x KW-695)	17	9	8	1:1		
F_1(Dalgona x Kw 695)	12	12	0	1:0		
F_2	37	32	5	3:1	2.604	0.5-0.1
1999 year						
KW 695	14	0	14			
SS-4	13	13	0			
Dalgona	13	13	0			
F_1(SS-4 x Kw 695)	5	5	0	1:0		
F_2	81	81	25	3:1	1.458	0.5-0.1
BCP1(SS4 x F_1)	13	13	0	1:0		
BCP2(F_1 x Kw 695)	47	47	19	1:1	1.723	0.5-0.1
F_1(Dalgona x Kw 695)	5	5	0	1:0		
F_2						

	69	69	16	3:1	0.120	0.9-0.5
BCP1 (Dalgona x F_1)	12	12	0	1:0		
BCP2(F_1x Kw 695)	32	32	14	1:1	0.500	0.5-0.1

Table 2. Flower color determinations of parent, F_1, F_2 and backcross generations in watermelon.

		Color Index								
Entry	**Flower Color[y)]**	**L**	**a**	**b**	**Color space**					
KW 695	gf	66.65	-12.92	53.45						
SS-4	y	79.59	-7.85	62.97						
Dalgona	y	77.42	-7.17	58.12	White					
F_1(SS-4 x Kw695)	y	75.18	-7.24	59.78			**L**			
F_2	y	74.86	-6.59	65.82						
F_2	gf	65.95	-12.99	50.37					Yellow	
BCP1(SS4 x F_1)	y	75.23	-7.96	57.88				**-b**		
BCP2(F_1 x Kw 695)	y	75.25	-7.08	65.05	Green		**-a**		**+a**	Red
BCP2(F_1x Kw 695)	gf	66.84	-13.73	51.69						
F_1(Dalgona x Kw 695)	y	72.83	-6.95	61.17						
F_2	y	75.55	-6.94	62.28			**-b**		Gray	
F_2	gf	67.86	-12.35	49.26			Blue			
BCP1 (Dalgona x F_1)	y	76.42	-7.23	58.34						
BCP2(F_1 x Kw 695	y	75.21	-7.07	61.52	Black					
BCP2(F_1 x Kw 695	gf	65.82	-13.30	49.57						

y) : gf = light green flower, y = yellow flower (Normal)

Table 2. Flower color determinations of parent, F_1, F_2 and backcross generations in watermelon.

Entry	Flower Color y)	Color Index L	a	b
Kw 695	gf	66.65	-12.92	53.45
SS-4	y	79.59	- 7.85	62.97
Dalgona	y	77.42	- 7.17	58.12
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BCP2(F_1 x Kw 695)	gf	66.84	-13.73	51.69
F_1(Dalgona x Kw 695)	y	72.83	- 6.95	61.17
F_2	y	75.55	- 6.94	62.28
F_2	gf	67.86	-12.35	49.26
BCP1 (Dalgona x F_1)	y	76.42	- 7.23	58.34
BCP2(F_1 x Kw 695	y	75.21	- 7.07	61.52
BCP2(F_1 x Kw 695	gf	65.82	-13.30	49.57

y) : gf = light green flower, y = yellow flower(Normal)

Color space

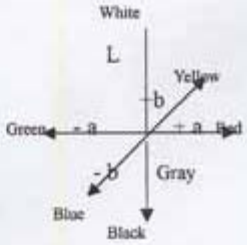

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Table 2. Flower color determinations of parent, F_1, F_2 and backcross generations in watermelon.

Entry	Flower Color y)	Color Index L	a	b
Kw 695	gf	66.65	-12.92	53.45
SS-4	y	79.59	- 7.85	62.97
Dalgona	y	77.42	- 7.17	58.12
F_1(SS-4 x Kw 695)	y	75.18	- 7.24	59.78
F_2	y	74.86	- 6.59	65.82
F_2	gf	65.95	-12.99	50.37
BCP1(SS4 x F_1)	y	75.23	- 7.96	57.88
BCP2(F_1x Kw 695)	y	75.25	- 7.08	65.05
BCP2(F_1 x Kw 695)	gf	66.84	-13.73	51.69
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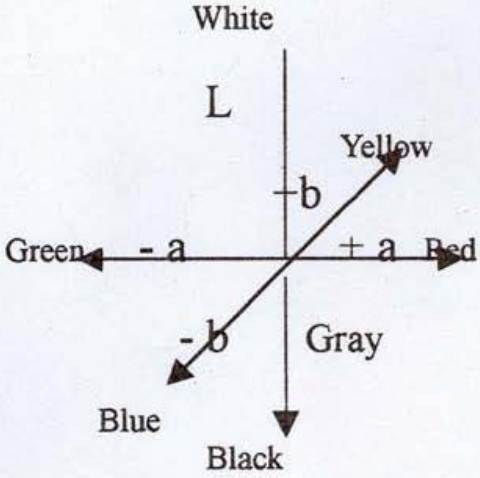
y) : gf = light green flower, y = yellow flower(Normal)

Color space



Cucurbit Genetics Cooperative Report 22:34-37 (article 13) 1999

Triploid and Tetraploid Watermelon (*Citrullus lanatus* (Thunb.) Matsum. and Nakai) Seed Size and Weight

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Introduction. Triploid watermelons are theoretically seedless and are the result of crosses between tetraploid female and a diploid male plants (1). Tetraploid plants are placed in crossing blocks with diploids, and if reproduction is by open-pollination, the resultant seed can be either tetraploid (4n) due to self-pollination, or triploid (3n) from pollination by a diploid. A sorting method was developed by Shimotsuma and Matsumoto (4) to distinguish 3n from 4n watermelon seed based on seed weight and thickness. They found that 3n seed were thinner and lighter than 4n seed, but both were thicker and heavier than diploid seed,

In the U.S. well into the 1990s, 3n watermelon seed was produced predominately by open-pollination, with the resultant mix of 3n and 4n seed separated by size before distribution. In addition, the resulting 3n and 4n plants could be distinguished in the field by the use of a genetic marker for fruit color (3, 5). The diploid parents have *dark green* (*D*) fruit, which is dominant to the *light green* (*d*) fruit of the tetraploid parents. Triploid plants resulting from this cross will have *striped green* (d^S) fruit .Tetraploid plants resulting from self-pollination will have *light green* fruit and can be culled from production fields, leaving the triploid plants with *striped green* fruit.

It was observed by the junior author, by use of the genetic marker system described above, that in some production fields up to 30% of the plants were tetraploid. While Shimotsuma and Matsumoto were able to separate 3n and 4n seed by thickness some 40 years ago, we questioned whether there had been inadvertent selection for thinner 4n seed since crossing blocks were direct-seeded, thus indirectly selecting for earliness in germination, emergence and development in tetraploid plants. In this study we took seed from a 4n x 2n cross to determine if we could separate the seed effectively by size as was done by Shimotsuma and Matsumoto (4).

Methods. Open-pollinated seed from a 4n x 2n cross were obtained from the late Mr. Herb Partridge (Munday Vegetable Growers Co-Op, Munday, TX). Seed were separated by thickness using a hand-held Manostat with accuracy to 0.1 mm. Each millimeter increment between 1.7 and 2.5 mm was considered a group. thirty-three seed from each group were selected, tested for germination, the germinated seed were transplanted to Speedling trays (Speedling, Inc.) in a greenhouse, and then transplanted to a field at The University of Arizona, Campus Agricultural Center (Tucson). Fewer plants were tested in the 1.4 to 1.6 mm and 2.6 to 3.1 mm ranges due to the small numbers of seed in these groups. In the field pollination was allowed to occur naturally, with the plants being visited by a variety of insects, but predominately by honeybees. For the plants that survived to maturity, fruit were scored for ploidy level using the genetic marker system describe above (*light green* 4n fruit and *striped green* 3n fruit). A t-test was used to determine whether there were significant (P#0.05) differences in seed thickness between 3n and 4n seed population.

The same seed lot was separated into seed weight groups. Each seed was weighted to the nearest 1.0 mg on a Mettler balance. Seed ranged from 21 to 110 mg, and 18 groups were formed, each consisting of 5 mg increments. Varying numbers of seed were germinated and transplanted as described for seed thickness. For most groups we were able to test 30 seed, but the smaller and larger weight groups had fewer seed available for testing. Ploidy level was determined on surviving plants by the genetic marker system described above, and differences determined utilizing a t-test.

Results. *Separation of seed by thickness* In the size groups 1.7 to 2.5 mm, germination ranged between 18 and 55%. In the

smaller and larger groups germination was 80 to 100%. Both 3n and 4n seed were observed in each size category. Separation of 3n and 4n seed by thickness was not possible by thickness; there were no significant differences between populations.

Separation by seed weight: Germination tended to increase with increased seed size (Table 2). Triploid and 4n seed were found in essentially all weight groups, and there were no significant differences observed between 3n and 4n seed by weight. The mean weights and standard deviations were essentially equal between 3n and 4n seed.

Efforts to separate 3n and 4n seed by size, as was done by Shimotsuma and Matsumoto (4), were unsuccessful in this study. This may be due to the commercial practice of direct-seeding tetraploid parent lines in crossing blocks, resulting in indirect selection for earliness in germination, emergence and fruit production. This inadvertent selection may have resulted in thinner 4n seed coats in these parent lines. In fact, thinner seed coats in 4n seed might be an advantage in that the resulting 3n seed would also have thinner seed coats. This might help with other cultural problems in triploid watermelons production, such as low germination level and slow germination rates (2).

Most seedless watermelon lines today are produced by controlled hand-pollinations, thus separation of 3n and 4n seed is not necessary. If lines are produced by open pollination it may be more beneficial to develop a genetic marker system for some seedling characteristic rather than a fruit characteristic that requires the expenditure of resources toward plants producing non-marketable fruit. If triploid plants are being transplanted into a production field, the development of a seedling selection system would allow for the elimination of unwanted plants before planting.

Table 1. Germination percentage and ploidy level of seed produced from a tetraploid x diploid cross and separated by thickness.

Size group (mm)	**No. of seed**	**Germination (5)**	**No. of seed scored as**	
			3n	**4n**
1.4 - 1.6	15	80	4	6
1.7	33	55	4	7
1.8	33	42	8	3
1.9	33	39	4	5
2.0	33	27	4	9
2.1	33	30	4	7
2.2	33	18	1	5
2.3	33	21	4	5
2.4	33	30	3	4
2.5	33	30	5	5
2.6 - 2.8	15	80	5	2
2.9 - 3.0	6	100	1	4
Total no.			47	62
Mean thickness mm $\pm$ s.d.			2.1 ± 0.4	2.1 ± 0.4^z

[z] t-value = 0.00, $P_{0.5} = 1.98$, $P > 0.90$

Table 2. Germination percentage and ploidy level of seed produced from a tetraploid x diploid cross and separated by weight.

	No. of seed	**Germination (%)**	**No. of seed scored as**	
			3n	**4n**
21-25	3	0	0	0

26-30	5	40	1	0
31-35	13	69	3	2
36-40	27	74	7	6
41-45	30	63	6	4
46-50	30	57	6	2
51-55	30	57	5	6
56-60	30	67	4	5
61-65	30	83	6	6
66-70	30	93	4	7
71-75	30	97	9	4
76-80	30	100	9	5
81-85	30	100	4	9
86-90	30	100	3	2
91-95	30	100	7	4
96-100	30	100	5	6
101-105	24	100	4	3
106-110	3	67	1	1
Total no.			84	72
Mean weight			67 $\pm$ 21.4	69.5 + 20.4[z]
(mg $\pm$ s.d.)				

[z] t-value = 0.50, $P_{0.5}$ = 1.96, P > 0.90

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Cucurbit Genetics Cooperative Report 22:38-40 (article 14) 1999

In vitro Generation of Tetraploid Watermelon with Two Dinitroanilines and Colchicine

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Introduction. Autotetraploid lines are the maternal parents of triploid watermelon hybrids. Chromosome doubling was first accomplished with the toxic alkaloid colchicine by applying colchicine in lanolin paste to the growing point. More satisfactory tissue culture treatments have since been developed (4). Dinitroanilines have been used to double chromosome numbers, and their effectiveness has previously been compare with other crops (1,3,5). The purpose of these trials was to compare *in vitro* chromosome doubling effectiveness using colchicine and the dinitroanilines, ethalfluralin (N-ethyl-N-2 methyl-2-propenyl)-2, 6-dinitro-4-(trifluomethyl) benzanine), and oryzalin (3,5-dinitro-N4, N4dipropylsulfanilamide).

Methods. Single buds isolated from clones of an F_3 seed were treated with colchicine (100, 500, 1000, 1500 µM) or dinitroanaline (5, 10, 50, 100 µM) in baby food jars with liquid MS medium plus 3% darkness on a platform shaker at 100 rpm for 3, 6, or 9 days. The treated buds were placed on MS medium plus 3% sucrose in 0.7% agar with 10 µM BA. The shoots were subcultured every 30-40 days.

Nuclear isolation procedures are described by Li et al. (2).Factoral experiments were conducted on the single buds in baby food jars with filter sterilized liquid MS medium in the dark. Ten single buds of approximately the same size were randomly assigned to each of the treatments . Thus, the experimental design was a completely random design, with no blocking. The treatment structure was a two-way factorial design. One factor was concentration and the other was exposure time. concentrations for dinitroanalines were 0, 1, 5, 10, and 50 µM, and exposure times were 3, 6, and 9 days. For colchicine, the concentrations were 0, 100, 500, 1000 and 1500 µM,and the exposure times were 3, 6, 9, and 30 days. Zero concentration also served as a control for the chemical agent.

Experimental unit and observational unit were the same: one single bud and the clone derived from it. response factor was ploidy level of each clone, which was classified as a tetraploid or non-tetraploid by DNA contents measured with flow cytometry.

For each oryzalin or ethalfluralin treatment,, in a 5x3 grid there were 15 different media with all possible combinations of concentrations and days. For colchicine, 20 different media were prepared. Some loss (variable, but usually less than 10%) resulted from contamination. Whole excised single buds from a single clone were placed on a liquid medium with one of the factorial combinations of concentrations and days.

The data from each of the factoral designs for tetraploid generations were analyzed for each chemical agent. Data recorded included the number of explants and their derived clones. statistical analysis was conducted using the GLM procedure of the statistical analysis system (SAS Institute Inc., Cary, NC, 1996). Percentage data were analyzed using the FREQ procedure,

and CAT-MOD procedure (SAS), and the data sets that contained a large number of zeros were transformed using the square root transformation[$(y + 0.5)^{1/2}$] before GLM or CATMOD analysis, or just processed by Fisher's Exact Test. An analysis of variance was also conducted on the data by CATMOD procedure, GLM procedure, and Fisher's Exact Test (SAS). Paired comparisons were made using the three methods listed to compare the relative efficiency of tetraploid induction among these three chemicals (SAS)P, and to determine interaction and the main effects of concentrations and days for each chemical agent, respectively. All calculations were performed on contingency of ploidy level on the two factors (concentration and days). Specific hypotheses involving effect of different chromosome-doubling agent, concentration, and different time period on ploidy were tested using subsets of the overall contingency data (SAS).

Results. All of the treated buds survived the chromosome doubling treatments, but some browning was observed on the edges of the tiny leaves. No higher treatment levels of the dinitroanalines were attempted.

In contrast to oryzalin, ethalfluralin at 10 µM induced 50% tetraploids in 9 days, statistically as many as either dinitroaniline at the higher concentration of 50 µM (Fig. 1 and 2). concentrations of ethalfluralin between 10-50 µM should be tested. Because the dinitroanilines cost the same, ethalfluralin may be preferred over oryzalin.

Using colchicine, 30 days exposure time was more effective than 3, 6, or 9 days in inducing tetraploids (Fig. 3). At 30 days exposure, 1000 µM concentration was more effective than 100 µM in tetraploid induction. Because colchicine induces tetraploidy more slowly than these two dinitroanilines and is also more toxic and more expensive, the dinitroanilines are attractive candidate alternatives to colchicine for chromosome doubling in watermelon.

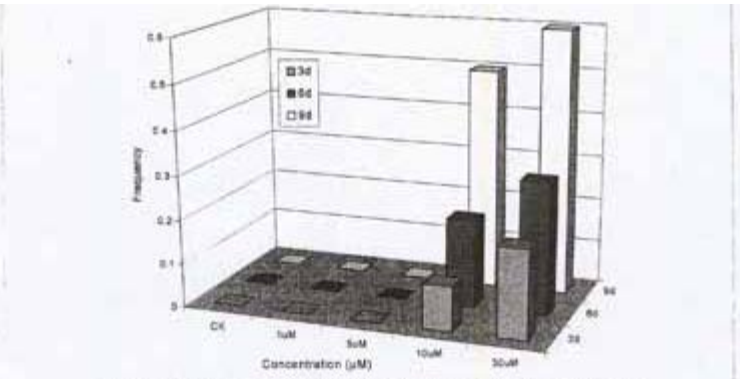

Fig. 1. Effect of ethalfluralin concentration [µM] and exposure time (days) on frequency of in vitro tetraploid induction in watermelon.

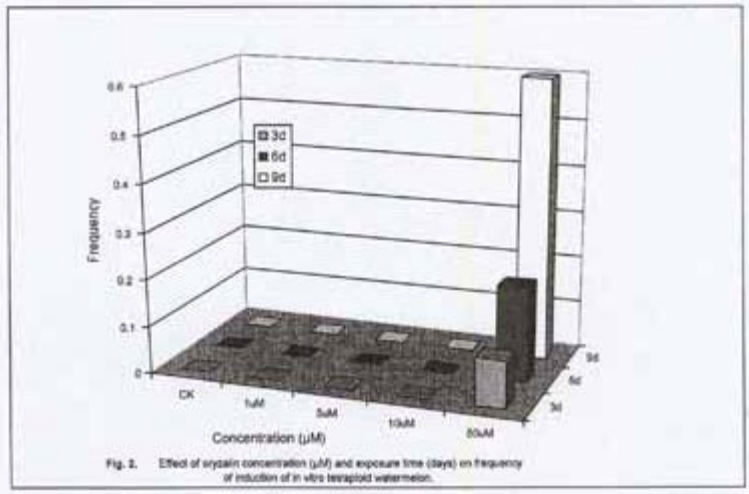

Fig. 2. Effect of oryzalin concentration (µM) and exposure time (days) on frequency of induction of in vitro tetraploid watermelon.

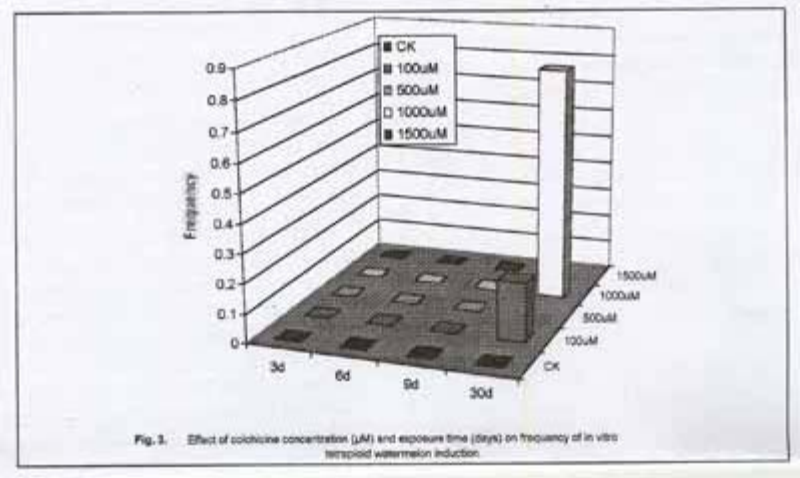

Fig. 3. Effect of colchicine concentration (μM) and exposure time (days) on frequency of in vitro tetraploid watermelon induction.

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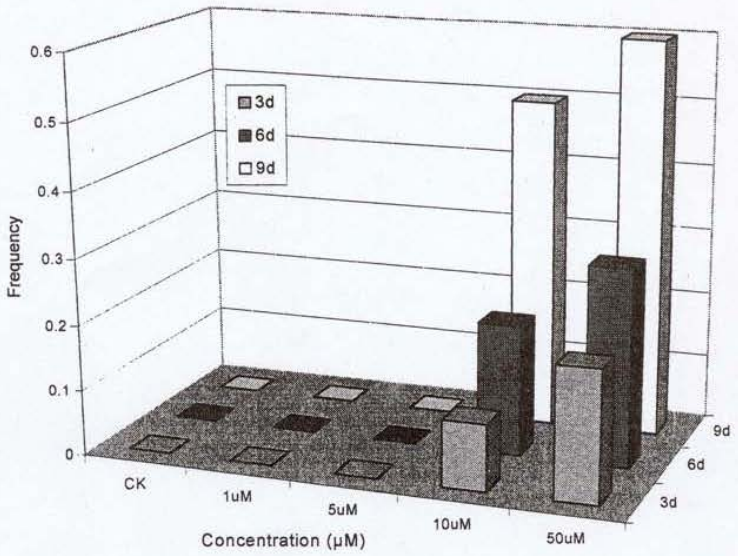

Fig. 1. Effect of ethalfluralin concentration (μM) and exposure time (days) on frequency of in vitro tetraploid induction in watermelon.

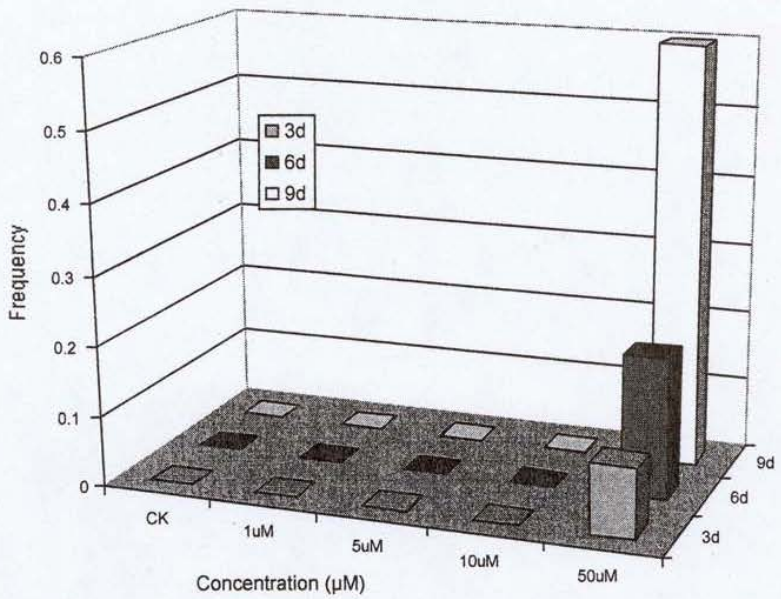

Fig. 2. Effect of oryzalin concentration (μM) and exposure time (days) on frequency of induction of in vitro tetraploid watermelon.

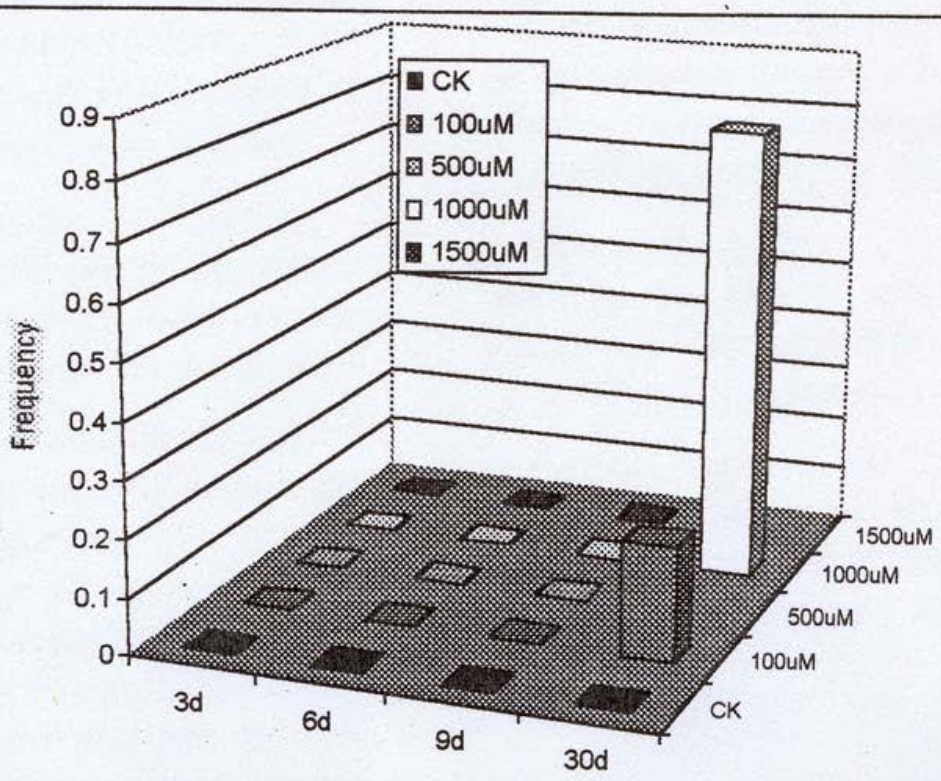

Fig. 3. Effect of colchicine concentration (μM) and exposure time (days) on frequency of in vitro tetraploid watermelon induction.

Cucurbit Genetics Cooperative Report 22:41-42 (article 15) 1999

An Improved Procedure for Isolation of High Quality DNA from Watermelon and Melon Leaves

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Our previous experiments in isolating DNA from watermelon leaves using the basic cetyltrimethylammonium bromide (CTAB) procedure (Saghi Maroof et al., 1984; Rogers and Bendich, 1985; Doyle and Doyle, 1987) resulted in: (1) poor DNA yields, (2) co-isolation of highly viscous polysacharides that interfered with DNA handling, (3) co-isolation of polyphenols and other secondary compounds that damaged the DNA by oxidation, and (4) partial or total DNA degradation due to the presence of endogenous nucleases. Thus, we modified the procedure by increasing the CTAB concentration (from 1 to 2.5%) and by adding 0.5% N-lauroyl sarkosine (Sarkosyl) to the DNA extraction buffer, This modification enhanced the breakage of cell and nuclear membranes, and resulted in increased release of DNA into the extraction buffer. It also enhanced the removal of polysaccharides and prevented interaction of polyphenols and endogenous nucleases with the DNA, resulting in high quality as well as high yields of DNA. the procedure presented here has been successfully used in our laboratory.

Procedure:

1. Collect young leaves and directly place them in a -80C freezer.
2. Grin 5 G leaves to a complete powder using 2 g sand (white quarts, -50 +70 mesh) and three rounds of liquid N.
3. Transfer the powder as fast as possible to a 50-ml polypropylene tube. Add 25-ml extraction buffer (60 C). Seal the tube hermetically and shake vigorously to ensure full contact of extraction buffer with tissue. Incubate for 30 min at 60 C. while incubating, shake the tube every 10 min.
4. Add 25 ml chloroform and shake the tube vigorously to ensure emulsification of organic and aqueous phases. Open the tube cap to release gas produced by the chloroform. Seal the cap.
5. Centrifuge for 5 min at 1,200 relative centrifuge force (RCF) (at 4C). Do not exceed 1,200 RCF, the combination of high detergent concentration, sand and chloroform may crack the tube at higher speeds.
6. Place the tubes on ice. Transfer the aqueous phase to a new 50 ml tube, and add 20 ml ice-cold isopropanol. Mix gently but thoroughly, and incubate for 20 min at -20 C.
7. Centrifuge for 15 min at 2,200-RCF (at 4 C).
8. Drain the tube gently and re-suspend the pellet with 2 ml TE (10:1) containing RNase A (100 µ g/ml). Transfer 1 ml to each of two micro-centrifuge tubes (1.6 ml tube) and incubate for 60 min at 37 C.
9. Centrifuge for 5 min at 12,000 rpm in a micro=centrifuge to remove polysaccharides and extraction buffer residues.
10. Transfer the supernatant to a new micro-centrifuge tube.
11. Add 500 µl chloroform, mix thoroughly, and centrifuge for 5 min at 12,000 rpm (in micro-centrifuge).
12. Transfer the upper aqueous phase to a new microcentrifuge tube.
13. Add 1/10 5M NaCl (100 µl to 1 ml) and 400 µl isopropanol. Incubate for 20 min at 20 C.
14. Centrifuge for 5 min at 12,000 rpm.
15. Wash pellet with 1 ml cold ethanol. Drain the tube on a paper towel for about 20 min. (At this stage be careful not to lose the DNA while flipping the tube). Re-suspend in 200-500 µl TE (10:1).
16. To clarify, the DNA solution from any residues, centrifuge for 5 min at 12,000 rpm, then transfer the supernatant to a new tube.

Extraction solution: 2.5% CTAB, 0.5% N-lauyrol sarkosine (Sarkosyl), 1.4 M NaCl 100 mM Tris (pH 8.5), 20 mM EDTA. Before extraction add: 1% soluble PVP (average molecular weight 40,000) and 1% insoluble PVP. Also, 5 µl of beta-mercaptoethanol to each 1 ml of extraction solution.

Conclusions. The high concentrations of CTAB and Sarkosyl in the extraction buffer significantly enhanced the quality and yield of DNA isolated from watermelon and melon leaves. Using this procedure we were ale to isolate DNA from a large

number of watermelon varieties and plant introductions (PIs), used for PCR-RAPD analysis (Figure 1). The present procedure may also be effective in the isolation of high quality DNA form other cucurbit species.

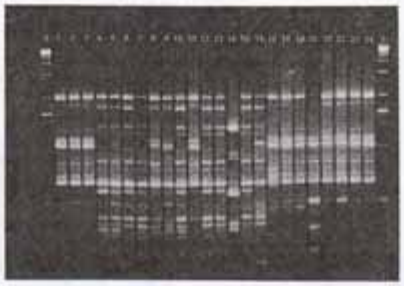

Figure 1. PCR-RAPD patterns (on agarose-gel) produced from DNA of watermelon varieties and plant introductions (PIs). The DNA used for the PCR-RAPD reactions was isolated using the procedure reported in this paper. Lanes are: 0) DNA markers showing molecular size, 1) Summit, 2) Sweet Princess, 3) Tiger Baby, 4) PI 189225, 5) PI 244018, 6) PI 244019, 7) PI 248774, 8) PI 255137, 9) PI 270562, 10) PI 270563, 11) PI 271779, 12) PI 299378, 13) PI 299379, 14) PI 346082, 15) PI 482252, 16) Griff. 14113, 17) PI 162667, 18) PI 165451, 19) PI 169289, 20) PI 169290, 21) PI 185635, 22) PI 185636, 23) PI 186975, 24) PI 189316, 25) PI 189317, 26) PI 192937, 27) PI 203551, 28) PI 248178.

Acknowledgment: We thank Susan Fox for technical assistance in DNA isolation and in preparing the figure for this manuscript.

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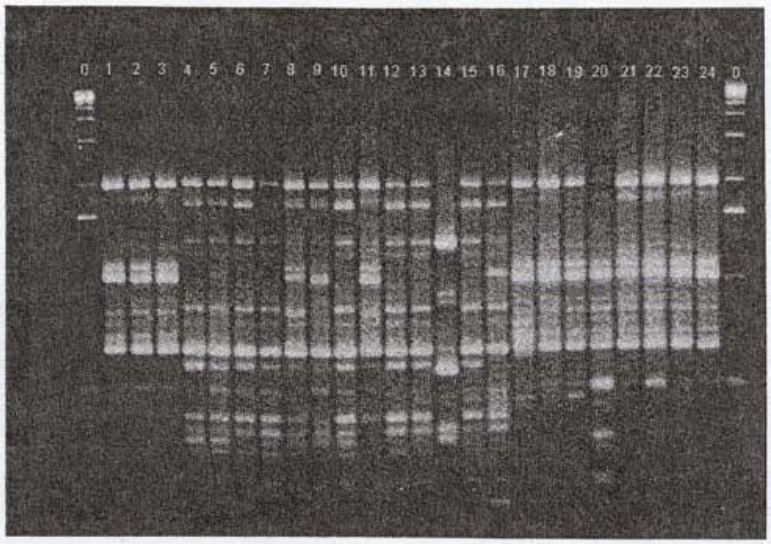

Figure 1. PCR-RAPD patterns (on agarose-gel) produced from DNA of watermelon varieties and plant introductions (PIs). The DNA used for the PCR-RAPD reactions was isolated using the procedure reported in this paper. Lanes are: 0) DNA markers showing molecular size, 1) Summit, 2) Sweet Princess, 3) Tiger Baby, 4) PI 189225, 5) PI 244018, 6) PI 244019, 7) PI 248774, 8) PI 255137, 9) PI 270562, 10) PI 270563, 11) PI 271779, 12) PI 299378, 13) PI 299379, 14) PI 346082, 15) PI 482252, 16) Griff. 14113, 17) PI 162667, 18) PI 165451, 19) PI 169289, 20) PI 169290, 21) PI 185635, 22) PI 185636, 23) PI 186975, 24) PI 189316, 25) PI 189317, 26) PI 192937, 27) PI 203551, 28) PI 248178.

Cucurbit Genetics Cooperative Report 22:43-46 (article 16) 1999

Preparation of Nuclei from *in vitro* Watermelon Shoot Tissue for Cell Flow Cytometry

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Introduction. To analyze the DNA of plant cell populations, it is necessary to prepare a homogenous sample of nuclei. Preparation of nuclei from *in vitro* samples of watermelon is desirable because the choice of genotype and ploidy level at this stage saves greenhouse labor and materials. Intuitively, cells and nuclei prepared from micropropagules should be more easily extracted and prepared in pure form than from older plants with more cell wall material and more vascular tissue. In an experiment to determine optimal tetraploid generation *in vitro* (see Li et al, this report), we also evaluated nuclear preparation techniques.

Methods. Treated buds (Li et al, 1999) were placed on MS medium plus 3% sucrose in 0.7% agar with 10 µlM BA. The shoots were subcultured every 30-40 days.

Nuclear isolation procedure came from authors 1, 2, 3, 4, 5, and 7 with modifications. *In vitro* leafy shoot samples, 0.01-2.00g from the fresh clonal cultures, were excused and weighed for cell flow cytometry. The samples were immediately immersed in PBS (20 mM phosphate buffer, 154mM sodium chloride, pH 7.2=7.4) in a polypropylene tube (100x7.5mm) for 1-36 hours at 4 C. For releasing intact nuclei, different time periods of chopping or blending were compared. In the chopping technique, single edge razor blade was used to manually chop the plant material in a plastic petri dish (100 x 15 mm) with 0.5 ml PBS solution on ice.

In the blending procedure, a blender (Tissue Tearor^{TM}, Model 985-370 type 2, variable speed 5,000-30,000rpm, Biospec Products, Inc.) was used on the plant material in a plastic petri dish (100x15mm) with 0.5 ml PBS solution on ice. For releasing intact nuclei, different time periods of chopping and blending were compared. Then the mixture was filtered through 2 layers of lens paper or 50 µm nylon mesh. The nuclei and cell debris were washed with 2 ml PBS, and the filtrate was stored at 4 C for 12-24 hr or used immediately. The filtrate was centrifuged at 180xg for 1 min to pellet intact cells and cell clumps at 4C. The supernatant was poured into another clean tube (100x7.5mm) and centrifuged again at 180xg for 10 min to pellet relatively purified nuclei. The nuclei pellet was resuspended in 200 µl solution [prepared in 15 ml PBS + 15 mg dithiothreitol (DTT) + 375 µl Triton X-100 (10%w/v + 60 µl PI (5 mg/ml) + 4 µl RNaseA (DNase-free, 10 mg/ml)]. The suspension was then blended and incubated at 37 C for 15 min. All manipulations were carried out on ice or at 4 C except for the RNA digestion. To confirm whether nuclei were released and their product, each each step was examined visually under an Olympus CH-2 phase-contrast or fluorescent microscope.

After incubation, the prepared samples were analyzed on an EPICS 751 flow cytomater (Coulter Corporation, Hialeah, FL) equipped with a data adquisition system. Excitation of PI was provided by the 488 nm line (100mW) of an arg9n laser (Model I-90, coherent) and the red fluorescence emitted by PI was collected through a 635 nm band pass filter. Chicken red blood

cells, with nuclear DNA content of 2.6 pg, were used as an internal standard. Samples of 20,000 nuclei were analyzed and the data were represented as histograms (Fig. 1). Only data collected from samples with G1/G0 peaks with coefficient of variations (cvs)≤ 5% were used in C-value estimates (3).

The mixture was filtered through 2-layer lens paper or 50 µm nylon mesh. the nuclei and cell debris were washed with 2 ml PBS, and the filtrate was stored at 4 C for 12-24 hr or used immediately. The filtrate was centrifuged at 180g for 1 min to pellet intact cell and cell clumps at 4 C. The supernatant was poured into a clean tube (100c7.5mm) and centrifuged again at 180g for 10 min to pellet relatively purified nuclei. The nuclei pellet was resuspended in 200 µl solution (prepared in 15ml PBS + 15mg dithiothreitol + 375 µl Triton X-100(10%w/v) + 60 µl PI (5 mg/ml)). The suspension was mixed and incubated at 37C for 15 min. The prepared samples were analyzed on an EPICS 751-flow cytometer (Coulter, FL) with a Cicero acquisition module and cyclops analysis software (Cytomation, CO) with the 488 nm line (100 mw) of an argon ion laser (Model I-90, coherent). The red fluorescence emitted by PI was collected through 635 nm band pass filter. Chicken red blood cells, with nuclear DNA content of 2.6 pg, were used as an internal standard. Samples of 20,000 nuclei were analyzed and the data represented as histograms.

Results. The amount of leaf sample and the method of preparing the nuclei were found to be critical. If the quantity was too small, the quantity of nuclei were not enough to proceed with the flow cytometric analyses. If the quantity was large, the extra nuclei were wasted. Intact nuclei are released much more efficiently by chopping than blending regardless of the time period (Table 1). A period of more than 3 hours but less than 24 hours was sufficient to release the nuclei into PBS without loss of their integrity.

Table 1. Effect of nuclear isolation techniques on yield of DNA from *in vitro* leafy shoots.

Method	Tissue (g)	Cell Disruption Time (min)	Yield, intact nuclei[z]
Fine Chopping	0.01	< 1 min	7
	0.03	< 1 min	18
	0.05	1-2 min	55[y]
	0.07	1-2 min	67[y]
<Apparent optimum>	**0.01**	**3-4 min**	**72[y]**
	0.50	4 min	66[y]
	1.0	5 min	70[y]
	0.50	4 min	66[y]
	1.0	5 min	70[y]
	2.0	>7 min	54[y]
Blend	0.05	30 sec. speed 1	0
	0.05	30 sec. speed 2	3
	0.05	30 sec. speed 3	7
	0.05	1 min, speed 1	4
	0.05	1 min, speed 2	3
	0.05	1 min, speed 3	15
	0.05	2 min, speed 1	20
	0.05	2 min, speed 2	17
	0.05	2 min speed 3	0
<Apparent optimum>	**0.05**	**3 min,speed 1**	**32**
	0.05	3 min, speed 2	12

	0.05	3 min, speed 3	0
	0.05	4 min, speed 1	28
	0.05	4 min, speed 2	9
	0.05	4 min, speed 3	0
	0.05	5 min, speed 1	22
	0.05	5 min, speed 2	3
	0.05	5 min, speed 3	0

[z]The yield was based on the average number of nuclei in 5 different ocular fields under a phase contrast microscope (5 x 40).

[y] Sharp peak appeared during flow cytometry.

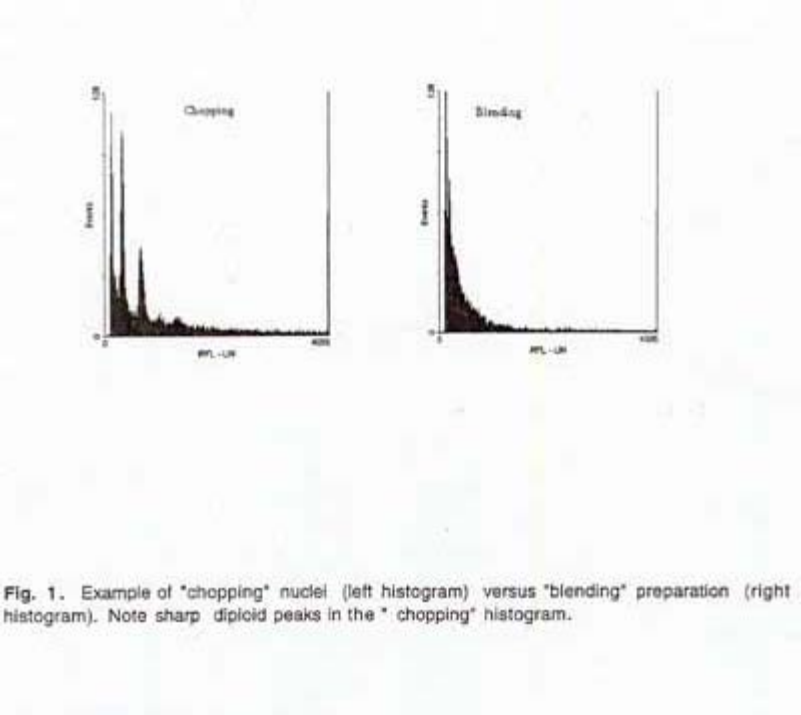

Fig. 1. Example of "chopping" nuclei (left histogram) versus "blending" preparation (right histogram). Note sharp diploid peaks in the " chopping" histogram.

Acknowledgements. The flow cytometer was made available through the College of Agriculture, Forestry and Life Sciences, and the South Carolina Experiment Station.

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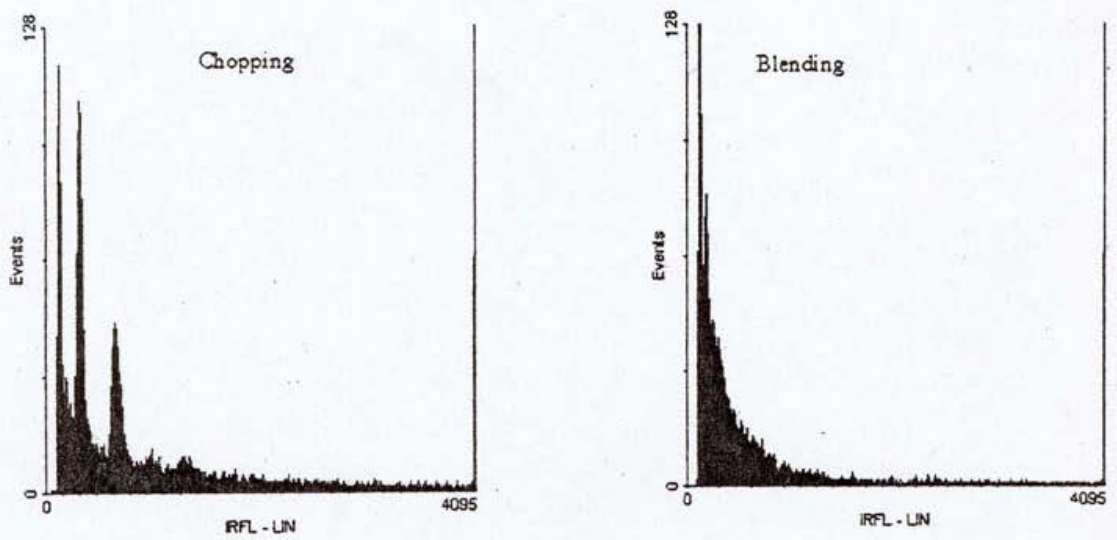

Fig. 1. Example of "chopping" nuclei (left histogram) versus "blending" preparation (right histogram). Note sharp diploid peaks in the " chopping" histogram.

Cucurbit Genetics Cooperative Report 22:47-49 (article 17) 1999

Crop Loss to Eight Diseases of Watermelon in North Carolina

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The Department of Plant Pathology at North Carolina State University set up a disease loss committee in 1978 for crops grown in North Carolina, in response to inquiries made by the National Agricultural Pesticide Impact Assessment Program. Crop coordinators, in consultation with colleagues having knowledge of the crops, were responsible for arriving at estimates of disease incidence (percentage of the crop production area affected by diseases including nematodes) and percentage reduction in crop value for North Carolina. Reports were generated from 1979 through 1988, when the program was discontinued. Data on watermelon (*Citrullus lanatus* (Thunb,) Matsum. & Nakai) are available, so we decided to analyze the most recent six years (1, 2, 3, 4, 5, 6) to identify the most important watermelon pathogens based on their incidence in North Carolina.

The data from the reports reviewed for the six years (1983 through 1988) were estimated from research plots, sample surveys and using the opinions of extension specialists and county agents. Each estimate was assigned to a confidence rating (1 to 3) indicting how the data was obtained and its reliability. a rating of 1 indicated 'confident' (actual disease measurements made through surveys or research tests). A rating of 2 indicated 'reliable' (estimates based on knowledge of the crop in relation to the general distribution and severity of the disease). a rating of 3 indicated 'indicative' (estimates were an educated guess).

Eight diseases were reported during the six years of the survey for watermelon. the estimated incidence of most pathogens remained constant over the five years (Table 1). Blossom end rot caused by *Choanephoba cucurbitarum* had the highest incidence of all pathogens for all six years, followed by damping off, gummy stem blight (*Didymella bryoniae* (Auersw.) Rehm), and root knot (nematodes of *Meloidogyne* spp.). The incidence of the above four diseases as well as rind necrosis was constant over the six years. However, the incidence of anthracnose (*Colletorichum orbicularae* Berk & Mont.) Arx) increased over years. Data for stem rot incidence was available only for 1988, with a disease incidence rating of 75. The data for all years were of rating class 3.

Based on the percentage loss of crop value, root-knot nematodes caused the greatest loss over the six years, accounting for nearly one third of all disease losses. The other important diseases causing crop losses were gummy stem blight and blossom end rot. Since the loss to root knot decreased in 1987 and 1988, and the loss to gummy stem blight remained constant, gummy stem blight was the most important disease in 1987 and 1988 (Table 2).

Root knot nematode cost the most in terms of dollars lost (including prevention costs), followed by gummy stem blight and blossom end rot. Dollars lost (including prevention costs) due to gummy stem blight increased over the six year period. Similar trends were also observed for blossom end rot, anthracnose and downy mildew (Table 3).

Table 1. Estimates incidence of eight diseases on all field-grown watermelons in North Carolina (1983 to 1988).

Rank	Disease	1983	1984	1985	1986	1987	1988	Mean
1	Blossom end rot	80	80	80	80	80	80	80
2	Damping off	70	70	70	70	70	70	70
3	Gummy stem blight	70	70	70	70	70	70	70
4	Root knot nematode	50	50	50	50	50	50	50
5	Anthracnose	10	10	25	25	25	25	20
6	Downy mildew	-	-	-	20	20	20	20

7	Rind necrosis	15	15	15	15	15	15	15
8	Leaf Spot	10	10	10	10	10	10	10
	Mean	44	44	46	43	43	43	42

Table 2. Estimated percentage loss in crop value caused by eight diseases on field-grown watermelons in North Carolina (1983 to1988).[z]

Rank	Disease	1983	1984	1985	1986	1987	1988	Mean
1	Blossom end rot	10.0	10.0	10.0	10.0	5.0	5.0	8.3
2	Damping off	7.0	7.0	7.0	7.0	7.0	7.0	7.0
3	Gummy stem blight	4.0	4.0	4.0	4.0	4.0	4.0	4.0
4	Root knot nematode	2.1	2.1	2.1	2.1	2.1	2.1	2.1
5	Anthracnose	1.0	1.0	2.5	2.5	2.5	2.5	2.0
6	Downy mildew	-	-	-	2.0	2.0	2.0	2.0
7	Rind necrosis	0.5	0.5	0.5	0.5	0.5	0.5	0.5
8	Leaf Spot	0.3	0.3	0.3	0.3	0.3	0.3	0.3
	Totals	24.9	24.9	26.4	28.4	23.4	23.4	26.2

[z] Estimated percentage loss of value calculated as the percentage dollar loss due to yield and quality reduction.

Table 3. Estimated cost (1000 dollars) of control (loss due to yield and quality reduction, and cost of prevention and control) of eight diseases on field-grown watermelons in North Carolina (1983 to 1988).[z]

Rank	Disease	1983	1984	1985	1986	1987	1988	Mean
1	Blossom end rot	265	773	616	89	594	867	4,006
2	Damping off	158	544	409	600	768	1,137	3,616
3	Gummy stem blight	75	284	224	337	431	639	1,990
4	Root knot nematode	34	118	158	221	283	418	1,232
5	Anthracnose	38	149	117	177	227	336	1,043
6	Downy mildew	-	-	-	179	229	338	746
7	Rind necrosis	25	83	46	53	67	98	372
8	Leaf Spot	5	21	17	25	32	48	149
	Totals	600	1,972	1,587	2,482	2,632	3,882	13,155

[z] Estimated cost calculated as the total dollar loss due to yield and quality reduction and cost of prevention and control by eight pathogens by years.

Table 4. Coefficients of determination (R^2) for estimated incidence, estimated percentage loss of crop value, estimated cost, and year of estimate for watermelons due to eight diseases in North Carolina 1983 to 1988).

Variable	Incidence[z]	Loss[Y]	Cost[X]
Year	0.988	0.945	0.922
Incidence		0.038	-0.023
Loss			0.956

[z] Estimated incidence calculated as the average incidence of eight pathogens by year.

[y] Estimated percentage loss of value calculated as the total dollar loss due to yield and quality reduction by eight pathogens by years.

[x] Estimated cost calculated as the total dollar loss due to yield and quality reduction and cost of prevention and control by eight pathogens by year.

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Cucurbit Genetics Cooperative Report 22:50-52 (article 18) 1999

Inheritance of Umbrella-like Leaf Shape in Materials Derived from *Cucurbita maxima* x *pepo* Hybrids

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Introduction. distant crosses in plants can be a tool for obtaining new forms for breeding and genetic investigations. Hybrids between squash (*Cucurbita maxima* Duch.) and pumpkin (*C. pepo* L.) were obtained in our Department over ten years ago (4). In the self-fertile BC_2 /F_2 progeny numerous variants have been selected (6). One of them was a new leaf shape, similar to the partially opened umbrella. this work presents the results of a genetic analysis of this trait.

Methods. Interspecific hybrids between *Cucurbita maxima* Duch., cv. Warzyna and *C. pepo* L., inbred line C2/3/9 (both components bred in our Department) were produced using the embryo rescue method, as described previously (4). They were self-incompatible and partially male-sterile, so, for obtaining the next generation, backcrosses with both parent were applied. Most of the BC_1 plants (obtained by means of embryo rescue) were used as maternal forms, because of their self-incompatibility and complete or partial male-sterility (5). Several male- and self- fertile plants were found in the BC_2 generation and it was possible to execute self-pollinations. In the BC_2/F_2 generation the selection of forms for further works has been started.

Results. *Recovery of variants with umbrella-like leaf shape.* In the BC_2/F_2 generation (derived from backcrosses with *C. maxima*) several plants were found with extensive chlorotic sectors on the leaves but still with very efficient photosynthesis. they were stabilized and in the subsequent third selected generation, three plants with normal green leaves but of unusual shape were segregated. Such a type of leaf shape has not hitherto been described in the literature, either for *Cucurbita* (2, 7) or *Cucumis* (3, 8). It was similar to a partially open umbrella (Fig. 1). Umbrella leaf has been described in cucumber, but is a completely different phenotype: "leaf margins turn down at low relative humidity making leaves look cupped" (1).

The plants with an umbrella-like leaf shape (*uml*) were self-pollinated and then sexually propagated and stabilized over three years. One of them segregated into plants with the regular leaf shape, plants with umbrella-like leaves of normal size and plants with umbrella-like, dwarf leaves (investigations on this phenotype are in progress), while the remaining plants turned out to be stable in the*uml* character.

Genetic analysis of umbrella-like leaf shape. The non-segregating progeny of the plant designated as P11.5.5 was used for genetic analysis (Table 1). All F_1 plants showed intermediate leaf shape (Fig. 2). Segregation observed in all progenies indicate monogenic inheritance, of an incompletely recessive character and not influenced by cytoplasmic factors (Table 1). So, this trait does not results from a new complementary interaction of genes of both distant parents, but rather is caused by mutation.

We propose to designate the gene controlling this trait as *uml.*

Table 1. Genetic analysis of umbrella-like leaf shape derived from hybrids *C. maxima* x *C. pepo.*

Cross	No. of plants	No. of plants with umbrella-like leaf shape		No. of plants with intermediate leaf shape		No. of plants with normal leaf shape		X^2
		observed	expected	observed	expected	observed	expected	
F_1(uml x W)	10	0	0	0	10	0	0	0.00
F (W x								

F_1 uml)	10	0	0	10	10	0	0	0.00
F_1 (uml x W) x uml	30	14	15	16	15	0	0	0.13
F_1(uml x W) x W	30	0	0	14	15	16	15	0.13
F_1(W x uml) x uml	30	14	15	16	15	0	0	0.13
F_1(W x uml) x W	30	0	0	16	15	14	15	0.13
F_1 (uml x W) self	90	25	22.5	42	45	23	22.5	0.49
F_1 (W x uml) self	90	19	22.5	50	45	21	22.5	1.20

W - *C. maxima* cv. Warzyna.
uml - forms with umbrella-like shape of leaves.

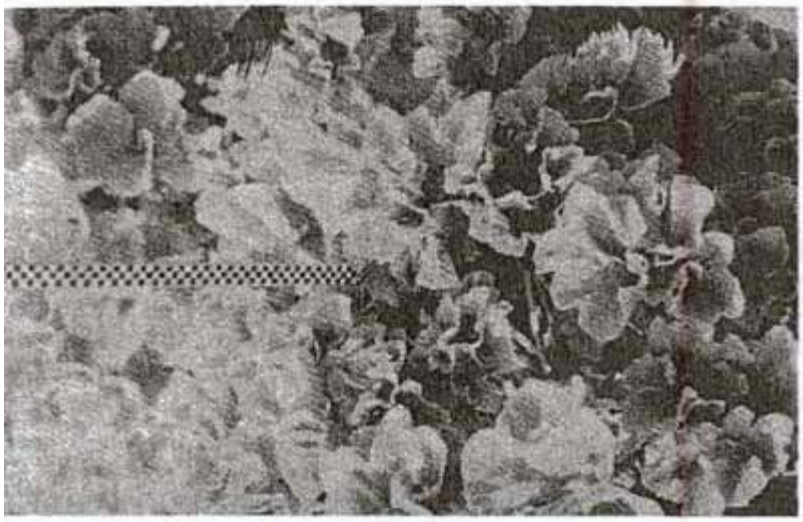
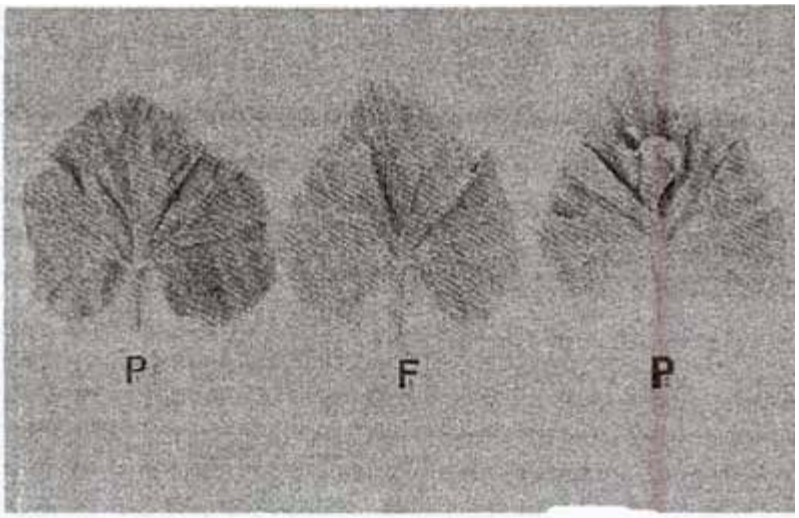


Fig.1. Plant with umbrella-like leaf shape growing in the field



eaves of plants: P_2 - *C. maxima* cv. Warzywna, F_1 - P_1 x P_2, F

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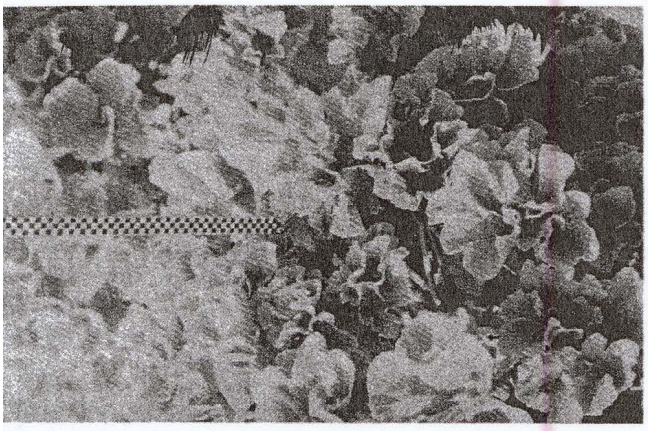
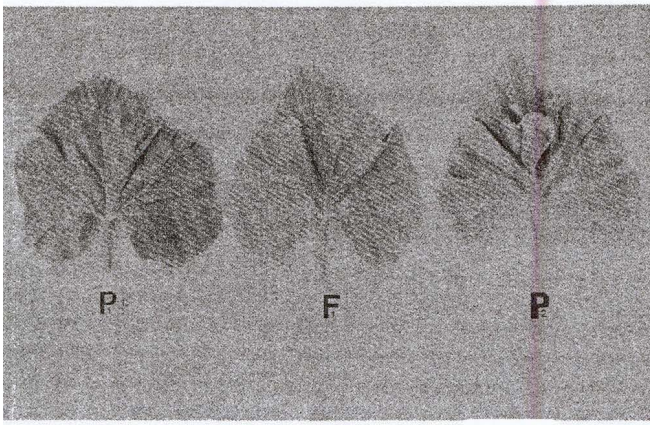


Fig.1. Plant with umbrella-like leaf shape growing in the field



eaves of plants: P_2 - *C. maxima* cv. Warzywna, F_1 - P_1 x P_2, P

Cucurbit Genetics Cooperative Report 22:53-54 (article 19) 1999

Disease Resistance of *cucurbita pepo* and *C. maxima* Genetic Resources

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Introduction. A collection of genetic resources of *Cucurbita pepo* and *Cucurbita maxima* was evaluated for resistance to the most important viral and fungal pathogens of cucurbitaceous vegetables in the Czech Republic.

Methods. The set of more than 400 accessions (PI), kindly provided by gene banks in ames and Geneva (USA), included local cultivars and landraces from around the world.

This collection has been evaluated for resistance to the cucumber mosaic cucumovirus (CMV) (3), watermelon mosaic potyvirus-2 (WMV-2) (2) and powdery mildew of cucurbits ({PM) (1). A group of selected accessions previously reported as highly resistant to CMV and WMV-2 were screened for resistance to the zucchini yellow mosaic potyvirus (ZYMV) (4).

The screening for resistance to the viruses was carried out under controlled conditions in a growth chamber or glasshouse after an artificial inoculation. Local Czech isolates of viruses were used. The resistance to powdery mildew was evaluated under field conditions of natural infection of *Erysiphe cichoracearum* and *Sphaerotheca fuliginea.* the infection degree was based on the visual evaluation of symptoms on host plants and in some cases, the presence of virus was controlled by DAS-ELISA.

Results. In spite of a relatively high susceptibility of both *Cucurbita* species to all above mentioned pathogens in general, a large variation of resistance within individual accessions was found. the genotypes with the highest level of resistance to CMV, WMV-2 and PM are listed in the Table 1.

The *C. maxima* species can be considered as more resistant to CMV, WMV-2, and PM as compared to the *C. pepo* response to these pathogens. No accession was found to be resistant to all pathogens under study (CMV, WMV-2 and PM) (1,2,3). The *C. pepo* accession PI 518687 could be used for WMV-2 and PM resistance breeding (1,3). The *C. maxima* accession PI 500483 expressed a promising level of resistance to CMV and WMV-2, similarly as four other *C. maxima* accessions ({O 295342, PI 368572, PI 458691 and PI 265557) (2,3). Unfortunately, all accessions under study were highly susceptible to ZYMV (4).

Table 1. *Cucurbita pepo* and *Cucurbita maxima* accessions ({POI number and/Origin/) with high level of resistance to the cucumber mosaic cucumovirus (CMV), watermelon mosaic potyvirus-2 (WMV-2) and powdery mildew of cucurbita (PM - *Erysiphe cichoracearum, Sphaerotheca fuliginea).*

CMV
C. pepo
PI 438699 / Mexico/
C. maxima
PI 176530 /Turkey/, PI 177891 /Turkey/, PI 265555 /Turkey/, PI295342 / Australia/, PI 368564 / Yugoslavia/. PI

368572 Yugoslavia/, PI 372458 /Yugoslavia/, PI 458685 /Argentina/, PI458691 Argentina/, PI 458693 /Argentina/, PI 482466 /Zimbabwe/, PI 490352 /Burkina/, PI 500483 /Zambia/.
WMV-2
C. pepo
PI 184745/Austria/, PI 265550 /Argentina/, PI 368570 /Yugoslavia, PI 379291 /Yugoslavia/, PI 458672 /Argentina/, PI 458662 /Argentina/, PI 458661 / Argentina/, PI 458709 /Argentina/, PI 500483 /Zambia/. PI 419081 /China/
PM
C. pepo
PI 176536 /Turkey/, PI 518687 /USA/, I 38700 /Mexico/, PI 442300 /Mexico/, PI 357937 /Yugoslavia/, PI 442296 /Mexico/, PI 507888 /Hungary/, PI 438823 /Mexico/, PI 442292/Mexico/
C. maxima
PI 458674 /Argentina/, PI 458673 / Argentina/, PI 458675 /Argentina /, /, PI 135370 /Afghanistan/, PI 137866 /Iran/, PI 165027/Turkey/PI 166046 /India/, PI 169404 /Turkey/

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Cucurbit Genetics Cooperative Report 22:55-56 (article 20) 1999

Selection of Squash (*Cucurbita pepo* L.) Lines Resistant to Zucchini Yellow Mosaic Virus (ZYMV) in Sudan

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Zucchini yellow mosaic virus causes a very serious disease of squash in Sudan, particularly in the central region. On many occasions it causes a total crop loss (2). A breeding program for its resistance was initiated at the University of Gezira in 1994. Twenty-one accessions were obtained from the North Central Plant Introduction Station (Ames, Iowa), and 15 breeding lines were obtained from Cornell University. Only two plants in two of the cornell breeding lines showed a high level (+8) of zucchini yellow mosaic resistance (ZYMR) (1). The first was in row 94-38 of the pedigree (91-757sib PJR + ZYMR pepo). The second was in row 94-37 of the pedigree (91-720-2self,Nigerian local. BC_2 cas. F_2 ZYMR.EPS). That level of resistance was retained in the F_1progenies when crossed with the popular susceptible cv, Eskandarany (Esk.) (95-13 and 95-14). Approximately 10% of the F_2 plants had a ZYMR level similar to that of the donor parents (1). The F_2 of 95-14 appeared to be the most promising for selection of highly resistant plants with a ZYMR level similar to that of the donor parent.

The F_2 and their derived F_3 populations were evaluated for ZYMR using a scale of 1 - 9 where 1 is susceptible and 9 is resistant. Mechanical inoculation with specific isolates (Su19 and E9) was used to test for ZYMR. Tissue immuno-blot assay was used to detect the presence of the virus. F_2 and F_3 populations were also evaluated for some horticultural characteristics such as plant vigor, stem color, leaf shape, leaf lobes, earliness and fruit characters at harvest.

Two plants in the F_2 population, namely 96-12-12 and 96-69-1 obtained by selfing of 95-14, showed a high level of resistance to ZYMV (=8). The F_3 derived from selfing of the two plants was artificially inoculated at INRA, Montfavet, France with the Sudanese isolate Su19 and a high intermediate level of resistance was observed (=6-7) in both progenies. Plant 96-12-12 was a very vigorous plant, intermediate in flowering and was very productive. The same F_3 was planted again in the field in Sudan in row 97-6 for the progeny of 96-12-12 and a high level of ZYMR was observed)=8) when artificially inoculated at INRA, Montfavet, France with French isolate E9, which is similar to isolate Su19 in aggressiveness. The same F_4 progeny was planted again in the field in Sudan in row 98-10 and a high uniform level of resistance was observed (=9). The fruit of plant 97-6-10 at harvest was cylindrical in shape, green in color and was one kilogram in weight at maturity (45 days after pollination).

Another selection in the F_5, 97-20-1, which was derived from the F_1 95-14, showed a high uniform level of resistance (=8) when artificially inoculated at INRA, Montfavet, France with the French isolate E9. A larger population of its F_6 (98-11 to 98-20) was tested in the field in sudan and a high uniform level of resistance was observed (=9). Plants of this line are vigorous, with lobed leaves, light green fruits and resistant to powdery mildew.

The F_2 population that was utilized for selection was a large segregating population (522 plants). A chi square test significantly deviated from the one gene model (1:2:1). The inheritance of resistance has been reported to be a single incomplete dominant gene that controls ZYMR (3,4) possibly affected by modifying genes (5).

This work succeeded in the fixation of two lines having a high level of ZYMR and desirable horticultural characteristics. One line (97-6-10self) is now at the F_4 and the other (97-20-1self) is now at the F_6.

Acknowledgement. The authors wish to thank H. Lecoq and M. Pitrat at INRA. Montfavet, France for their cooperation and encouragement.

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Cucurbit Genetics Cooperative Report 22:57-58 (article 21) 1999

Estimation of Genetic Parameters of Pumpkin under Low Income Conditions.

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The plant breeding approaches used by the informal seed sector has been little studied (1). However, in some crops such as pumpkin, this sector in cuba has maintained important genetic variability which has served to satisfy some farmer necessities after several years of low income conditions. In the framework of plant breeding, it is uncertain whether further genetic advances may be obtained through direct yield selection. Because yield is a complex trait influenced by many genes, some breeders use indirect selection of yield components in order to increase the principal aim of high yield.

At the same time, Cecarrelli (3) and Atlin and Frey (2) have reported how plant variability response under low income conditions may be different than the patterns obtained for crops growing favorably under artificial irrigation with chemical fertilizer and pesticide. Therefore, it seems to be advantageous to have an estimation of genetic parameters for selection with which to obtain better yield gains under low input conditions.

The present report intends to show the role of yield and its component selection on genetic response estimation under low income conditions.

Methods. Pumpkin seeds (*Cucurbita moschata* Duch.) from 10 fruits selected by farmers were each considered as a line (half sib families). These lines were sown two times: under low income conditions (5) during the sprig-summer (rainfall period) and the winter (dry period) seasons. Genetic response of fruit weight, number of fruits per plant and yield were determined according to Galvez (4) using 40% selection pressure.

Results. The estimation showed that the genetic response of yield and its components were superior in the winter season (Table 1), probably due to the environmental influence of weather conditions favorable to female flowering set. The response of number of fruits per plant was lower during the spring-summer season, High temperatures during this season may have resulted in flower and fruit abortion (Casanova, 1998, personal communication). The genetic response for this experimental series appeared to be negatively linked with yield, so a high genetic response occurred in the low-yield environment of the winter season while a low genetic response occurred in the high-yield summer season.

It is interesting to point out that yield has a superior or similar genetic response with regard to its components, suggesting that in half sib families some genetic advance could be made through direct selection 'the favorable genetic response estimated for yield, and the fact that pumpkin seed management by farmers had been able to intro9duce, exchange and select conditions for a seed flow between and within communities, allows the assumption of the farmers' capacity to make genetic advance in complex traits such as yield under low income conditions.

Table 1. Genetic response estimated for pumpkin under low income conditions.

	Yield (tons/ha)	**Number of fruit per plant**	**Fruit weight (kg)**
	Spring/Summer		
Genetic Response	0.62	0.252	0.7
Average	6.0845	2.6145	2.6121
	Winter		
Genetic Response	1.47	1.45	1.11
Average	3.1618	1.1967	2.2908

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Cucurbit Genetics Cooperative Report 22:59-60 (article 22) 1999

Health-Protection Composition of Pumpkin

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Pumpkin (*cucurbita moschata* Duch.) is well known as both vegetable and food. Recently studies have shown that pumpkin has an auxiliary effect on treating diabetes, hypertension and gastric ulcer (1,2). Fairchild et al. (1990) developed special food products made from pumpkin for diabetics and in clinical trials achieved good curative effects (3).

Pumpkin contains high levels of starch, sugar, protein, fat and vitamins, some of which perform important nutritional and health functions. 'Big Millstones', 'Ten Sisters', Pillow', 'Yellow Wolf' and 'Multicolored skin' are varieties of pumpkin widely planted in China. Their nutritive value are analyzed in this paper, providing reference data for developing advanced health food from pumpkin.

The results show that the five varieties all have high levels of amino acids, minerals, ß-carotene and vitamin C. The specific contents are shown in tables 1, 2 and 3. Big Millstones generally has more amino acids, ß-carotene and vitamin C than the other varieties. Aspartic acid, glutamate and arginine, which have health-protection functions, account for a large proportion of total amino acids. Arginine can hasten insulin generation. The auxiliary curative effect of pumpkin on treating diabetes may be related to this. In addition Cu, Cr, Zn and Mn are also related to the secretion of insulin. The high ration of K/Na has a diuresis effect (4), important to the prevention and treatment of diabetes.

Fruit of Big Millstones, so-called because of its similarity in appearance to millstones, weigh 6-9 kg. The orange colored pulp is fine textured and high in solids and nutritive content. Big Millstones pumpkin shows promise as raw material in the manufacture of natural health foods.

Table 1. Amino acid content of five varieties of pumpkins (g/100g).

Amino Acid	'Big Millstones	'Ten Sisters'	'Pillow'	'Yellow Wolf'	'Multicolored Skin'
Asp	0.397	0.185	0.226	0.068	0.196
Thr	0.016	0.014	0.012	0.010	0.014
Ser	0.034	0.030	0.021	0.021	0.037
Glu	0.173	0.086	0.012	0.138	0.170
Gly	0.020	0.016	0.014	0.020	0.016
Ala	0.034	0.022	0.022	0.020	0.036
Cys	0.007	0.005	0.066	0.005	0.005
Val	0.036	0.033	0.030	0.035	0.041
Met	0.007	0.006	0.006	0.007	0.007
Ile	0.019	0.018	0.015	0.027	0.029
Leu	0.036	0.031	0.027	0.042	0.040
Tyr	0.030	0.022	0.021	0.026	0.019

Phe	0.021	0.016	0.018	0.026	0.024
Lys	0.033	0.032	0.025	0.045	0.025
His	0.013	0.009	0.010	0.017	0.011
Arg	0.063	0.032	0.044	0.062	0.043
Pro	0.013	0.016	0.009	0.013	0.018
Try	0.021	0.021	0.010	0.014	0.016
Total	**0.992**	**0.589**	**0.644**	**0.608**	**0.769**

Table 2. Mineral content of five varieties of pumpkins.

Mineral	'Big Millstones	'Ten Sisters'	'Pillow'	'Yellow Wolf'	'Multicolored Skin'
K	257.0	123.0	213.0	109.0	192.0
Na	17.8	10.7	15.2	9.1	14.3
Zn	0.28	0.17	0.21	0.13	0.19
Cu	0.12	0.07	0.11	0.04	0.10
Cr	51.0	50.0	15.0	11.0	40.0
Mn	300.0	237.0	285.0	213.0	249.0

Table 3. ß-carotene and Vitamin C content of five varieties of pumpkin (mg/100g).

	'Big Millstones	'Ten Sisters'	'Pillow'	'Yellow Wolf'	'Multicolored Skin'
ß-carotene	1.970	1.250	0.740	0.340	0.284
Vitamin C	9.0	8.5	8.2	7.5	7.0

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Gene List for Watermelon

1999

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Lists of the genes of watermelon (*Citrullus lanatus* (Thunb.) Matsum. and Nakaio) have been published previously in HortScience, 1976 (40) and in the cucurbit Genetics Cooperative Report, 1979(3). 1982(4), 1985(5), 1991(8), 1992(9) and 1995(38). the current list provides an update of the known genes in watermelon. Table 1 of Expressed Sequence Tags (ESTs) was kindly provided from the GenBank data base by Jeong-Sheop Shin and Sunghan Ok (South Korea).

Gene symbol			
Preferred	**Alternate**	**Character**	**Reference**
a	-	*andromonoecious.* Recessive to monoecious.	32,34,42
Aco-1	-	*Aconitase-1*	26
Aco-2	-	*Aconitase-2*	26
Adh-1	-	*Alcohol dehydrogenase-1.* One of five codominant alleles, each regulating one band.	27, 28, 54
Adh-1^1	-	*Alcohol dehydrogenase-1*^{1} One of five codominant alleles, each regulating one band. found in *C. lanatus* var. *citroides* and *C. colocynthis.*	27, 28, 54
Adh-1^2	-	*Alcohol dehydrogenase-1*^{2}. One of five codominant alleles, each regulating one band. found in *C. lanatus* and *C. lanatus* var. *citroides.*	27,28, 54
Adh-1^3	-	*Alcohol dehydrogenase-1*^{3}. One of five codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	27, 28, 54
Adh-1^4	-	*Alcohol dehydrogenase-1*^{4} . One of five codominant alleles, each regulating one band. found in *Acanthosicyos naudinianus.*	27, 28, 54
Af	-	*Aulacophora faveicollis* resistance. Resistance to the red pumpkin beetle. Dominant to susceptiility.	47
Aps-1	*Acph-A*	*Acid phosphatase-1*	26, 27, 28, 54
Aps-2^1	-	*Acid phosphatase-2*^{1}. One of two codominant alleles, each regulating one band. Found in *C. lanatus* and *C. colocynthis.*	26, 27, 28
Aps-2^2	-	*Acid phosphatase-2*^{2}. One of two codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
Ar-1	*B, Gc*	*Anthracnose resistance to race 1* of *Glomerella cingulata* var. *orbiculare.*	7,17,51
		Anthraconose resistance to race 2 of *Colletotrichum lagenarium* derived	

Ar-2^{1}	-	from PI 299379 and PI 189225. Resistance in *Citrullus colocynthis* is due to other dominant factors.	20,21,45,46,52
b l	*tl*	*branch less.* Meristems for tendrils and branches are ultimately replaced by floral meristems.	18,39,58
C	-	*Canary yellow* flesh. Dominant to pink. *ii* inhibitory to *CC*, resulting in red flesh. In the absence of *ii*, CC isepistatic to *YY*.	31, 12
d	-	*dotted seed coat.* Black dotted seeds when dominant for r, t, and w.	14, 33, 34
db	-	*Resistance to gummy stem blight* caused by *Didymella bryoniae* from PI 189225. Recessive to susceptibility.	30
dg	-	*delayed green.* Cotyledons and young leaves are initially pale green but later develop chlorophyll. first reported to behypostatic to l-dg. More recent evidence (submitted for publication) indicate simple recessivenes.	37
Dia-1	-	*Diaphorase-1*	27
dw-1	-	*dwarf-1.* Short internodes, due to fewer, shorter cells than normal. allelic to dw-1^{S} .	19, 25
dw-1^{S}	-	*short vine.* Allelic to dw-1. Vine length interiediate between normal and dwarf. Hypocotyl somewhat longer thannormal vine and considerably longer than dwarf. dw-1^{S} recessive to normal.	8
dw-2	-	*dwarf-2.* Short internodes, due to fewer cells.	19, 24, 25
Fwr	-	*Fruit fly resistance* in watermelon. Dominant to susceptibility to *Dacus cucurbitae*.	15
g	*d*	*light green* skin. Light green fruit recessive to *dark green (D)* and *striped green* (*d*^{S})	29, 32, 47
g^{s}	d^{s}	*striped green* skion. Recessive to dark green but dominant to light green skin.	31, 51
Gdh-1	-	*Glutamate dehydrogenase-1.* Isozyme located in cytosol.	27
Gdh-2	-	*Glutamate dehydrogenase-2.* Isozyme located in plastids.	26, 27
gf	-	*green flower* color.	16
gms	*ms*$_{g}$	*glabrous male sterils.* Foliage lacking trichomes; male sterile - caused by chromosome desynapsis.	36, 49, 50
go	*c*	*golden.* Yellow color of older leaves and matue fruit.	1
Got-1	-	*Glutamate oxaloacetate transaminase-1* One of four codominant alleles, each regulating one band. Found in *C. lanatus.*	26,27,28, 54
Got-1^{1}	-	*Glutamate oxaloacetate transaminase-1*^{1}.One of four codominant alleles, each regulating one band. Found in *C. colocynthis* and *Praecitrullus fistulosus.*	26,27,28,54
Got-1^{2}	-	*Glutamate oxaloacetate transaminase-1*^{2}. One of four codominant alleles, each regulating one band. Found in *C. lanatus* var. *citrodes*.	26,27,28,54
Got-1^{3}	-	*Glutamate oxaloacetate transaminase-1*^{3}. One of four codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26,27,28,54
Got-2	-	*Glutamate oxaloacetate transaminase*-2. One of five codominant alleles, each regulating one band. Found in *C. lanatus.*	26,27,28,54
Got-2^{1}	-	*Glutamate oxaloacetate transaminase-1*^{1} One of five codominant alleles, each regulating one band. Found in *C. colocynthis.*	26,27,28,54
		Glutamate oxaloacetate transaminase-1^{2}. One of five codominant alleles,	

Got-2^2	-	each regulating one band,. Found in *C. ecirrhosus*.	26,27,28,54
e	*t*	*explosive rind.* Thin, tender rind, bursting when cut.	31,34
Est-1	-	*Esterase-1.* One of six codominant alleles, each regulating one band. Found in *C. lanatus.*	26,27,28
Est-1^1	-	*Esterase-1*^{1} . One of six codominant alleles, each regulating one band., Found in *C. lanatus* var. *citroides* and *C. colocynthis.*	26, 27, 28
Est-1^2	-	*Esterase-1*^{2} . One of six codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Est-1^3	-	*Esterase-1*^{3} . One of six codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	26, 27, 28
Est-1^4	-	*Esterase-1*^{4} One of six codominant alleles, each regulating one band. Found in *C. ecirrhosus.*	26 27, 28
Est-1^5	-	*Esterase-1*^{5} . One of six co-dominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
Est-2	-	*Esterase-2*. One of five codominant alleles, each regulating one band. Found in *C. lanatus.*	26, 27, 28
Est-2^1	-	*Esterase-2*^{1}. One of five codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Est-2^2	-	*Esterase-2*^{2}. One of five codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Est-2^3	-	*Esterase-2*^{3}. One of five codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	26, 27, 28
Est-2^4	-	*Esterase-2*^{4}. One of five codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
f	-	*furrowed* fruit surface. Recessive to smooth.	31
Fdp-1	-	*Fructose 1,6 diphosphatase-1.*	27, 28
Fo-1	-	Dominant gene for *resistance to race 1* of *Fusarium oxysporum* f. sp. *niveum.*	11, 29
For-1	-	*Fructose 1,6 diphosphatase-1*	26
Got-2^3	-	*Glutamate oxaloacetate transaminase-2*^{3}. One of five codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	26,27,28,54
Got-2^4	-	*Glutamate oxaloacetate transaminase-2*^{4}. One of five codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28, 54
Got-3	-	*Glutamate oxaloacetate transaminase-3.*	54
Got-4	-	*Glutamate oxaloacetate transaminase-4.*	26, 54
hsp70	-	*Heat shock protein 70.* One gene presequence 72-kDa hsp70 is modified differently in glyoxomes and plastids.	52
l-dg	-	*Inhibitor of delayed green.* Epistatic to *dg: dg dg l-dg* and *dg dg l-dg i-dg* plants are pale green; and *dg dg i-dg i-dg* plants are normal. This gene was not present in more advanced germplasm.	37
ldh-1	-	*lsocitrate dehydrogenase-1*	54
i-C	-	*inhibitor of canary yellow*, resulting in red flesh.	12

ja	-	*juvenile albino.* Chlorophyll reduced by short days in seedlings, leaf margins, rind.	58
l	-	*long* seed. Long recessive to medium length of seed; interacts with *s*.	33
Lap-1	-	*Leucine aminopeptidase-1*	26, 27
m	-	*mottled* skin. Greenish white mottling of fruit skin.	31, 51
ms	-	*male sterile*,	55, 56
ms^{dw}	-	*male sterile, dwarf*	13
Mdh-1	-	*Malic dehydrogenase-1.* One of two codominant alleles, each regulating one band. Found in *C. lanatus.*	28, 54
$Mdh\text{-}1^{1}$	-	*Malic dehydrogenase-1*^{1}. One of two codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	28, 54
Mdh-2	-	*Malic dehydrogenase-2.* One of three codominant alleles, each regulating one band. Found in *C. lanatus.*	28
$Mdh\text{-}2^{1}$	-	*Malic dehydrogenase-2*^{1}. One of three codominant alleles, each regulating one band. Found in *C. Colocynthis.*	28
$Mdh\text{-}2^{2}$	-	*Malic dehydrogenase-2*^{2}. One of three codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	28
$Me\text{-}1^{1}$	-	*Malic enzyme-1*^{1} .Oneof three codominant alleles, each regulating one band. Folund in *Praecitrullus fistulosus.*	26, 27, 28, 54
$Me\text{-}1^{2}$	-	*Malic enzyme-1*^{2} . One of three codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28, 54
Me-2	-	*Malic enzyme-2*	54
nl	-	*nonlobed leaves.* Leaves lack lobing; dominance incomplete.	23
O	-	*Elongate* fruit. Incompletely dominant to spherical.	31, 51
p	-	*pencilled* lines on skin. Inconspicuous; recessive to netted fruit.	31, 51
Pgd-1	*6 Pgdh-1*	*6-Phosphogluconate dehydrogenase-1.* One of three codominant alleles, each regulating one plastid band. Found in *C. lanatus.*	26, 27, 30, 54
$Pgd\text{-}1^{1}$	6 $Pgdh\text{-}1^{1}$	*6-Phosphogluconate dehydrogenase-1*^{1} . One of three codominant alleles, each regulating one plastid band. Found in *Praecitrullus fistulosus.*	26, 27, 28, 54
Pgd-2	*6 Pgdh-2*	*6-Phosphogluconate dehydrogenase-2.* One of five codominant alleles, each regulating one cutosolic band. Found in *C. lanatus.*	27, 54
$Pgd\text{-}2^{1}$	6 $Pgdh\text{-}2^{1}$	*6-Phosphogluconate dehydrogenase-2*^{1}. One of five codominant alleles, each regulating one cytosolic band. Found in *C. ecirrhjosus.*	28, 54
$Pgd\text{-}2^{2}$	6 $Pgdh\text{-}2^{2}$	*6-Phosphogluconate dehydrogenase-2*^{2} . One of five codominant alleles, each regulating one cytosolic band. Found in *Praecitrullus fistulosus.*	28, 54
$Pgd\text{-}2^{3}$	6 $Pgdh\text{-}2^{3}$	*6-Phosphogluconate dehudrogenase-2*^{3} . One of five codominant alleles, each regulating one cytosolic band. Found in *C. colocynthis.*	28, 54
$Pgd\text{-}2^{4}$	6 $Pgdh\text{-}2^{4}$	*6-Phosphogluconate dehudrogenase-2*^{4} . One of five codominant alleles, each regulating one cytosolic band. Found in *Acanthosicyos naudinianus.*	28, 54
Pgi-1	-	*Phosphoglucoisomerase-1.* One of three codominant lleles, each regulating one plastid band. Found in *C. lanatus.*	26, 27, 28
$Pgi\text{-}1^{1}$	-	*Phosphoglucoisomerase-1*^{1}. One of three codominant alleles, each regulating one plastid band. Found in*C. colocynthis.*	26, 27, 28.

Pgi-1^2	-	*Phosphoglucoisomerase-1*^{2}. One of three codominant alleles, each regulating one plastid band. Found in *Acanathiosicyos naudinianus.*	26, 27, 28
Pgi-2	-	*Phosphoglucoisomerase-2.* One of six codominant alleles, each regulating one cytosolic band. Found in *C. lanatus.*	26, 27, 28, 54
Pgi-2^1	-	*Phosphoglucoisomerase-2*^{1}. One of six codominant alleles, each regulating one cytosolic band. Found in *C. lanatus* and *C. colocynthis.*	26, 27, 28, 54
Pgi-2^2	-	*Phosphoglucoisomerase-2*^{2}. One of six codominant alleles, each regulating one cytosolic band. Found in *C. ecirrhosus.*	26, 27, 28. 54
Pgi-2^3	-	*Phosphoglucoisomerase-2*^{3} . One of six codominant alleles, each regulating one cytosolic band. Found in *Praecitrullus fistulosus.*	26, 27, 28, 54
Pgi-2^4	-	*Phosphoglucoisomerase-2*^{4}. One of six codominant alleles, each regulating one cytosolic band. Found in *C. lanatus* var. *citroides.*	26, 27, 28, 54
Pgi-2^5	-	*Phosphoglucoisomerase-2*^{5}. One of six codominant alleles, each regulating one cytosolic band. Found in *Acanthosicyos naudinianus.*	26, 27, 28, 54
Pgm-1	-	*Phosphoglucomutase-1.* One of four codominant alleles, each regulating one plastid band. Found in *C. lanatus.*	26, 27, 28, 54
Pgm-1^1	-	*Phosphogluycomutase-1*^{1}. One of four codominant alleles, each regulating one plastid band. Found in *C. colocynthis.*	26, 27, 28, 54
Pgm-1^2	-	*Phosphoglucomutase-1*^{2}. One of four codominant alleles, each regulating one plastid band. Found in *Acanthosicyos naudinianus.*	26, 27, 28, 54
Pgm-1^3	-	*Phosphoglucomutase-1*^{3}. One of four codominant alleles. each regulating one plastid band. Found in *Praecitrullus fistulosus.*	26, 27, 28, 54
Pgm-2	-	*Phosphoglucomutase-2.* One of four codominant alleles, each regulating one cytosolic band. Found in *C. lanatus.*	28, 54
Pgm-2^1	-	*Phosphoglucomutase-2*^{1}. One of four codominant alleles, each rgulating one cytosolic band. Found in *Acanthosicyos naudinianus.*	28, 54
Pgm-2^2	-	*Phosphoglucomutase-2*^{2}. One of four codominant alleles, each regulating one cytosolic band. Found in *C. lanatus.*	28, 54
Pgm-2^3	-	*Phosphoglucomutase-2*^{3}. One of four codominant alleles, each regulating one cytosolic band. Found in *Praecitrullus fistulosus.*	28, 54
pm	-	*powdery mildew susceptibility. Susceptibility to Sphaerotheca fulginea.*	41
Prx-1	-	*Peroxidase-1.* One of seven codominant alleles, each regulating one band. Found in *C. lanatus.*	26, 27, 28
Prx-1^1	-	*Peroxidase-1*^{1}. One of seven codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Prx-1^2	-	*Peroxidase-1*^{2}. One of seven codominant alleles, each regulating one band. Found in *Praecitrullous fistulosus.*	26, 27, 28
Prx-1^3	-	*Peroxidase-1*^{3}. One of seven codominant alleles, each regulating one band. Found in *C. lanatus.*	26, 27. 28
Prx-1^4	-	*Peroxidase-1*^{4}. One of seven codominant alleles, each regulating one band. Found in *C. ecirrhosus.*	26, 27, 28
Prx-1^5	-	*Peroxidase-1*^{5}. One of seven codominant alleles, each regulating one band. Found in *C. lanatus* and *C. colocynthis.*	26, 27, 28

Prx-1^{6}	-	*Peroxidase-1*^{6}. One of seven codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
Prx-2	-	*Peroxidase-2*	28
Prx-3	-	*Peroxidase-3*	28
r	-	*red* seed coat. Interacts with *w* and *t.*	33
s	-	*short* seeds. Epistatic to *l.*	33
Sat	-	*Serine acetyltransferase.* Catalyzes the formation of O-acetylserine from serine and acetyl-CoA.	43
Skdh-1	-	*Shikimic acid dehydrogenase-1*	54
Skdh-2	-	*Shikimic acid dehydrogenase-2.* One of six codominant alleles, each regulating one band.	26, 27, 28
Skdh-2^{1}!	-	*Shikimic acid dehydrogenase-2*^{1} . One of six codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Skdh-2^{2}	-	*Shikimic acid dehydrogenase-2*^{2}. One of six codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
Skdh-2^{3}	-	*Shikimic acid dehydrogenase-2*^{3}. One of six codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
Skdh-2^{4}	-	*Shikimic acid dehydrogenase-2*^{4} . One of six codominant alleles, each regulating one band. Found in *C. ecirrhosus.*	26, 27, 28
Skdh-2^{5}	-	*Shikimic acid dehydrogenase-2*^{5}. One of six codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	26, 27, 28
slv	-	*Seedling leaf variegation.* Conferred by a single recessive gene. Dominant allele at same locus in PI 482261.	35
Sod-1	-	*Superoxide dismutase-1.* One of three codominant alleles, each regulating one band. Found in *C. lanatus.*	26, 27, 28, 54
Sod-1^{1}	-	*Superoxide dismutase-1*^{1} . One of three codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28, 54
Sod-1^{2}	-	*Superoxide dismutase-1*^{2}. One of three codominant alleles, each regulating one band. Found in *Acanthosixyos naudinianus.*	26, 27, 28, 54
Sod-2	-	*Superoxide dismutase-2.* One of two codominant alleles, each regulating one band, Found in *C. lanatus.*	28
Sod-2^{1}	-	*Superoxide dismutase-2*^{1}. One of two codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	28
Sod-3	-	*Superoxide dismutase-3.* One of two codominant alleles, each regulating one band. Found in *C. lanatus.*	28
Sod-3^{1}	-	*Superoxide dismutase-3*^{1}. One of two codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	28
Sp	-	*Spotted* cotyledons, leaves and fruit.	37
Spr-1	-	*Seed protein-1*	27
Spr-2	-	*Seed protein-2*	27
Spr-3	-	*Seed protein-3*	27
Spr-4	*Sp-4*	*Seed protein-4*	26, 27

Spr-5	*Sp-5*	*Seed protein-5*	26, 27
su	*Bi*, su^{Bi}	*supressor of bitterness.* Non-bitter fruit. Bitterness in *C. colocynthis* is due to Su Su genotype.	2, 26
t	b^t	*tan* seed coat. Interacts with *r* and *w.*	22, 33
tl	*tl*	*tendrilless.* After 4^{th} or 5^{th} node, vegetative axiillary buds are transformed into flower buds and leaf shape is altered.	39, 57
Tpi-1	-	*Triosephosphatase isomerase-1.* One of four codominant alleles, each regulating one band. Found in *C. lanatus.*	26, 27, 28
$Tpi\text{-}1^1$	-	*Triosephosphatase isomerase-*1^1 . One of four codominant alleles, each regulating one band. Found in *C. colocynthis.*	26, 27, 28
$Tpi\text{-}1^2$	-	*Triosephosphatase isomerase-*1^2. One of four codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	26, 27, 28
$Tpi\text{-}1^3$	-	*Trsosephosphatase isomerase-*1^3. One of four codominant alleles, each rgulating one band. Found in *Acanthosicyos naudinianus.*	26, 27, 28
Tpi-2	-	*Triosephosphatase isomerase-2.* One of three codominant alleles, each regulating one band. Found in *C. lanatus.*	28
$Tpi\text{-}2^1$	-	*Trisephosphatase isomerase-*2^1. One of three codominant alleles, each regulating one band. Found in *Acanthosicyos naudinianus.*	28
$Tpi\text{-}2^2$	-	*Triosephosphatase isomerasei-*2^2. One of three codominant alleles, each regulating one band. Found in *Praecitrullus fistulosus.*	28
Ure-1	-	*Urease-1*	28
w	-	*white* seed coat. Interacts with *r* and *t.*	33
Wf	-	*White flesh. Wf* is epistatic tothe second gene b (or *C*?) which conditions *yellow (Canary yellow)* and red flesh. *WF_B_* and *WF_bb* are white fleshed, *wf wf B_* is yellow fleshed, and *wf wf b b* is red fleshed.	44
y	*f*	*yellow* flesh ('Golden Honey' type). Reessive to *Y (red* flesh).	10, 31, 34, 12
y^O	-	*orange* flesh (from 'Tendersweet Orange Flesh'). Allelic to *y.* (red *flesh*); y^O (*orange* flesh) and *y* (*yellow* flesh); y^O (*orange* flesh) is dominant to *y* (*yellow* flesh).	10, 12
Yl	-	*Yellow* leaf (from 'Yellow Skin'). Incompletely dominant to green leaf.	48

Table 1. Summaries of watermelon Expressed Sequence Tags (ESTs) with significant homology to known genes.

Putative Identity	Accession No.	Putative Identity	Accession No.
Primary metabolism		Photosystem I protein psaL	AI563046
3-ketoacyl-coA thiolase	AA660039	Photosystem I psaH protein	AI563128
3-methylcrotonyl-CoA carboxylase	AA660057	Photosystem I reaction center subunit III precursor	AA660032
ACC oxidase	AI563157	Photosystem II 10 kD polypeptide	AA660158

ACC synthrase	AI563272	Photosystem II oxygen-evolving complex protein 1	AA660158
Acetyl-CoA acyltransferase	AI563047	Photosystem II oxygen-evolving complex protein 2	AI563177
Acid phosphatase precursor	AA660161	Photosystem II oxygen-evolving complex protein 3	AI563234
Aconitate hydrase	AA660145	Photosystem II protein psbK	AI563267
Acyl-coA dehydrogenase and epoxide hydrolase	AA660045	Ribophorin I homologue	AI563050
Adenosylmethionine-8-amino-7-oxonoanoate aminotransferase	AA660037	Rubisco activase	AA660135
Amidophosphoribosyltransferase	AA660094	Rubisco small subunit	AA660026
AMP-binding protein	AA660131	Sedoheptulose-1, 7-biphosphatase chloroplast precursor	AA660026
Carbonic anhydrase	AA660102	Thioredoxin-f	AI563275
Chlorophyll A/B binding protein	AA660064	Transketolase	AI563214
CAB-21		UricaseII	AI563243
CP29	AI563142	**Amino acid synthesis and processing**	
CAB-36	AA660163	40S Ribosomal protein S2	AI563127
CAB-37	AA660116	40S Ribosomal protein S5	AA660095
CAB-151	AI563254	40S Ribosomal protein L3	AA660031
Cinnamoyl-CoA reductase	AI563265	50S Ribosomal protein L35	AI563242
Cytochrome b5	AA660129	60S Ribosomal protein L1B	AA660110

Cytochrome c oxidase subunit 1	AI563078	60S Ribosomal protein L23-1	AA660016
Cytochrome c!, heme protein	AI563065	60S Ribosomal protein L24	AI563148
Cytochrome P450 like_TBP	AI563252	60S Ribosomal protein L34	AA6600127
Deoxycytidylate deaminase	AI563080	60S Ribosomal protein L37A	AI563135
Electron transfer flavoprotein beta unit	AI563129	Alanine aminotransferase	AI563086
Ethylene-forming enzyme-like dioxgenase	AI563096	Alanyl-tRNA synthetase	AI563076
Ferredoxin	AI563096	Aminoacyl-t-RNA synthetase	AI563108
Formate dehydrogenase precursor	AA660126	Asparagine synthetase	AI563114
Fructose-bisphosphatase	AI563089	Chaperonin 10	AA660089
Fructose bisphosphate aldolase	AI563093	Chaperonin 10 beta subunit	AI563217
Fumarate hydratase	AI563262	ClpC protease	AI563160
Glucosyltransferase	AI563099	Cyclophilin	AA6600049
Glutamate dehydrogenase 2	AI563225	Cysteine synthase	AI563124
Glyceraldehyde-3-phosphate Dehydrogenase	AI563175	Elongation factor (EF-TuB)	AA660106
Ketol-acid reductoisomerase	AI563215	Glutamine synthetase root isozyme 4	AI563060
Lipase	AA660109	Glutamyl-tRNA synthetase	AI563051
Lipase (lysophospholipase)	AA660096	Glutathionine reductase cytosolic	AA660006
Maleate dehydrogenase	AA660028	Heat shock protein	AA660075
Malate oxidoreductase		Nucellin	

	AI563049		AI563122
Monodehydroascorbate reductase	AA660034	Peptide chain release factor 2	AI563239
NADH dehydrogenase	AA660051	Peptidyl-tRNA hydrolase	AI563056
NADH glutamate dehydrogenase	AA660052	P-Protein-like protein	AI563121
NADPH quinone oxidoreductase	AI563185	Protease (trypsin-like)	AI563071
N-carbamyl-L-amino acid Amidohydrolase	AA660138	Protease inhibitor (cysteine)	AI563159
Oxayl-CoA decarboxylase	AI563232	Protease inhibitor (Remti-V)	AI563140
Oxygen-evolving enhancer protein 2	AA660030	Protease inhibitor (serine)	AI563053
Oxygen-evolving enhancer protein 3	AA660156	Protease inhibitor Trichosanthes trypsin	AI563213
Phenylalanine ammonia lyase	AI563248	Protease inhibitor II	AI563224
Phospho-2-dehydro-3-Deoxyheptonate aldolase 1	AA660108	S-adenosyl methionine synthetase	AI563202
Phosphoglycerate kinase	AI563095	A-adenosylmethionine decarboxylase	AI563200
Photosystem I Accessory Protein E	AI563120	Spermidine synthase	AI563105
Photosystem I P700 apoprotein A1	AI563072	Threonine synthase	AI563068
		Translation initiation factor (eLF-4A.6)	AA660065

Putative Identity	**Accession No.**	**Putative Identity**	**Accession No.**
Translation initiation factor (elF-4E)	AA660115	Protein kinase YAKI	AA660097
Translation initiation factor SUi 1	AA660143	Protein phosphatase 2C	AA660004

		ppH1	
Tyrosyl-tRNA synthrase	AA660100	Protein phosphatase PP2A catalytic subunit (serine/threonine)	AA660155
Ubiquitin	AI563151	Ran binding protein 1	AA660005
Ubiquitin protein ligase E3	AI563218	Steroid binding protein	AI563210
Ubiquitin-conjugating enzyme E2	AI563249	**DNA, RNA related and gene expression**	
Secondary metabolism		Alfin-1	AI563088
Acetoacetyl-coenzyme A thiolase	AI563074	Ankyrin-like protein	AI563040
Chromoplast-specific carotenoid-associated protein	AI563106	Cys3His zinc-finger protein	AI563208
Cycloartenol Synthase	AI563211	DNA-binding protein	AA660085
Geranylgeranyl hydrogenase	AI563245	DNA-binding protein G2p	AI563197
Glutathionine s-transferase	AA660029	DNA-damage-repair/toleration protein	AA660003
Lipoxygenase	AA660152	Endonuclease P1	AA660099
Loxc homologue	AI563203	EREBP-4	AA660094
Membrane and transport		HD-ZIP protein	AI563062
ABC transporter	AI563287	Histone H1	AI563143
Acyl-binding/lipid transfer protein isoform I	AI563066	Histone H3.2	AA660088
Adenine nucleotide translocator	AI563236	Homeobox-leucine zipper protein hat22	AA660125
ATPase B subunit V-type	AA660024	Polyprimidin tract-binding protein 1	AI563235
ATPase beta subunit		Ribonucleoprotein	

	AI563144		AA660019
ATPase C subunit	AA66033	RNA helicase	AI563193
ATPase C subunit V-type 16KD protolipid chain	AA660091	RNA-binding protein RZ-1	AI563146
ATPase C gamma-subunit	AI563256	SCARECROW homolog	AA660090
ATPase metal-transporting P-type	AI5563274	Transcription factor	AI563116
ATPase P-type 4	AI563169	**Cell wall and metabolism**	
Coatomer, beta-prime subunit	AI563087	Beta-galactosidase precursor	AI563107
Cyclic nucleotide-regulated ion channel	AI563184	EDPG precursor	AA660101
Lipid-transfer protein	AA660082	Extensin-like protein	AI56152
Mitochondrial phosphate transporter	AI563176	Glycoprotein (hydroproline-rich)	AI563104
Monosaccharide transport protein	AA660083	Glycoprotein EP1	AI563103
Outer plastidial membrane protein	AA660042	Pectin methylesterase	AI563150
Oxoglutarate malate translocator	AI563181	Pectinsterase	AI563153
Probable membrane protein	AA660162	**Cell division**	
Protein translocase	AI563115	Chloroplast FtsH protease	AI563064
Pyrophosphate-energized vacuolar membrane proton pump	AA660118	UDP-glucose glucosyltransferase	AI563082
Scarlet protein	AA660060	**Defense**	
Tetracycline transporter-like protein	AA660060	Aquaporin	AI563055
Umecyanin	AA660011	Catalase	AI563227
Water-stress induced protein		DnaJ protein	

	AA660147		AI563180
Xylose permease	AA660154	DnaJ-1 protein	AA660002
Signal transduction		ERD15 protein	AI563233
ADP-ribosylation factor	AA660148	Ferritin	AI5563100
Calreticulin	AA660017	Fis1	AI563255
Ethylene receptor	AI563052	Hin1	AI563209
G-protein beta subunit	AA660061	Imidazole glycerol-phosphate dehydrase	AA660081
Phosphoenolpyruvate carboxykinase	AI563063	In2.1 protein	AI563162
Protein kinase (Arabidopsis/ putative receptor	AI563246	Jasmonate induced protein	AI563130
Protein kinase (novel serine/threonine)	AA660087	Manganese superoxide dismutase	AI563126
Protein kinase (receptor-like)	AA660112	Metallothionein-likeprotein	AI563198
Protein kinase (shaggy-like)	AA660105	Mlo protein	AI563090
Protein kinase AFC 2	AA660015	Oxidoreductase P2	AI563205
Protein kinase Xa21	AI563098	Polyphenol oxidase	AI563244
		Selenium-binding protein	AA660150
		Sti	AI563174
Putative Identity	**Accession No.**	**Putative Identity**	**Accession No.**
Treghalase	AI563125	IAA induced protein ARG2	AA660063
Others		KIAA 0005	AI563237
21kD protein precursor	AI563069	Lav-Z-pho C	AA660071
AP2 domain containing protein	AI563257	NAM	AI563260
Apoptosis protein MA-3		Peroxidase	

	AI563110		AI563266
AT103 protein	AI563042	Putative protein (different 4)	AI563228
CoL 2	AA660070	Putative small subunit	AA660111
CONSTANS	AI563221	Senescense-associated protein sen1	AI563212
Cuc 2	AA660001	Sip1 protein	AA660084
Diminuto	AI563189	Small glutamine-rich tetratricopeptide	AI563094
Dormancy-associated protein	AI563216	SRG1 protein	AI563058
Drosophila couch potato protein	AI563113	TIF9.10	AI563247
EST gb/N65759	AI5631133	T7N9.3	AA660079
Glycosylatable polypeptide	AI563268	TCTP protein	AI563270
GRPF1	AA660093	Unknown function protein	AI563043
Haemophilus influenzae permease	AA660093	Unknown protein (different 8)	AI563172
HvB12D homolog	AI563179	Unnamed protein (different 2)	AI563172
Hypothetical protein (different 26)	AI563261	Yease cat8 regulatory protein	AI563201

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Cucurbit Genetics Cooperative

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

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Cucurbit Genetics Cooperative

Stocks and Germplasm Desired or for Exchange

Rebecca Nelson Brown, Oregon State University, is looking for seeds of the *Cucurbita moschata* cultivar **Nigerian Local**. Her population of 'Nigerian Local' has become inbred and will no longer set seed. She hopes that crossing with another population of 'Nigerian Local' will reverse the inbreeding and restore self-fertility to her population. She is willing to trade seed from her population in return.

If you can assist, Rebecca can be contacted at:

- Rebecca Nelson Brown
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- 4017 Ag Life Science Bldg.
- Corvallis, Oregon 97331
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Cucurbit Genetics Cooperative

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34. **de Ruiter, A.C.** de Ruiter Zonen CV, Postbus 1050, 2660 BB Bergschenhoek, The Netherlands. Ph.: 010-5292204; FAX: 010-5216125. Breeding and seed production of cucumbers.
35. **Decker-Walters, Deena** The Cucurbit Network. 11901 Old Cutler Road, Miami, FL 33156-4242. Ph.: (305) 667-3800; FAX: (305) 661-5984. Email: *walters@servax,fiu.edu.* Communication via "The Cucurbit Network": the whole family Cucurbitaceae.
36. **Della Vecchia, Paulo T.** Agroflora S/A, Caixa Postal 427, 12.900-000 Braganca, Paulista - SP, Brazil. Ph.: (011) 7871-0855; FAX: (011) 7871-6572. Breeding& genetics, seed production and disease resistance of melon & squash.
37. **Denlinger, Phil** Mt. Olive Pickle Co., Inc., P.O. Box 609, Mount Olive, NC 28365. Ph.: (919) 658-2434; FAX: (919) 658-6090. Email: *cn1713@coastalnet.com.*
38. **Dhaliwal, Major Singh** Dept. of Vegetable Crops, L.S. & F. Punjab Agriculture University, Ludhiana-141001, Punjab, India
39. **DiNitto, Louis Victor** Sunseeds, 8850 59th Ave., N.E., Brooks, OR, 97305. Ph.: (503) 393-3243; FAX: (503) 390-0982. Melon (*Cucumis melo*).
40. **Dogimont, C.**,INRA, St. Maurice, BP 94, 84143 Montavet, France.
41. **Drowns, Glenn** Sand Hill Preservation Center, 1878 230th Street, Calamus, IA 52729. Ph.: (319) 246-2299. Genetic preservation of all cucurbits. Taxonomy of *Cucurbita moschata* and *Cucurbita argyrosperma.*
42. **Duangsong, Usa** Limagrain Veg. Seeds Asia, 119/9 Moo 1, Baan Khao, Muang, Kanchanaburi 71000, Thailand. Ph.: 66-2-636-2521-1; FAX: 66-2-636-2524. Email: *gongusa@loxinfo.co.th.*
43. **Eigsti, Orie J.**. 1602 Winsted, College Green, Goshen, ID 46526. Ph.: (219) 533-4632. Fusarium wilt resistance in tetraploid Citrullus lanatus lines, to eliminate crop rotation.
44. **El Jack, Ali Elamin** Dept. Horticulture, Fac. Agric. Sciences, University of Gezira, Wad-Medani, P.O. Box 20, Sudan.
45. **Elmstrom, Gary.** c/o Sunseeds, 7087 E.Peltier Road, Acampo, CA. Ph.: (209) 367-1064; FAX: (209) 367-1066. Email: *gelmstrom%sunseeds@mci-mail.com.* Triploid watermelon breeding.
46. **Everts, Kate** LESREC, Univ. Maryland, 27664 Nanticoke Road, Salisbury, MD 21801-1648. Ph.: (410) 742-8780; FAX: (410) 472-1922. Email: *ke35@umail.umd.edu*. Diseases of cucurbit vine crops.
47. **Ezura, Hiroshi** Plant Biotech Inst, Ibaraki Agric Ctr, Ago, Iwama, Nishi-iba 319-0292. Ibaraki, Japan. Ph.: 0299-45-8330; FAX: 0299-45-8351. Email: *ezura@nocs.tsukuba-noc.affrc.go.jp.*
48. **Ficcadenti, Nadia** Res Inst Veg Crops, Sect Ascoli Piceno, Via Salaria 1- Monsampolo del Tronto, Ascoli Piceno, 63030, Italy. Ph: + 39 735 701706; FAX: + 39 735 703684. Email: *orticolt@insinet.it.*
49. **Funakushi, Hisashi** Mikado Seed Growers Co., Ltd., 1203 Hoshikuki, Chuo-Ku, Chiba City 260, Japan. Ph.: 81-43-265-4847; FAX: 81-43-266-6444.
50. **Gaba, Victor** Dept. Virology, Inst. Plant Protection, A.R.O.,Volcani Center, P.O.B. 6, Bet Dagan 50250, Israel. Ph.:: 972-3-9683568/9; FAX: 972-3-9604180. E-mail:*vpgaba@volcani.bitnet*. Tissue Culture & Transformation.
51. **Gabert, August C.** Sunseeds, 8850 59th Avenue NE, Brooks, OR 97305-9625. Ph.: (503) 393-3243; FAX: (503) 390-0982. Email: *agabert%sunseeds@mci-mail.com.* Cucumber breeding and genetics.
52. **Garza, Ortega, Sergio** Univ Sonora, Dept Agric y Ganaderia, Iturbide #32 Jalisco/N. Heroes, Hermosillo, sonora 83040, Mexico. Ph: (62) 13-80-06; FAX: (62) 13-80-06. Email:*sgarza@rtn.uson.mx.* Breeding of *Cucurbita* spp.; testing of new muskmelon lines.
53. **Gatto, Gianni.** Esaem Spa, via San Biagio 25, 37052 Casaleone (VR), Italy. Ph.: 0442/331633; FAX: 0442/330834. Email: *GGatto@esaem.it*

54. **Gautier, Granes** Boite Postale No. 1, 13630, Eyragues, France. Ph.: 90.94.13.44; FAX: 90.92.83.96
55. **Gomez Paniagua, Humberto** Semillas Fito, S.A., Calle Selva de Mar, 111, 08019 Barcelona, Spain, Ph.: (34) 93 307 6212; FAX: (34) 93 3070264. Email: *humberto@abonados.cplus.es* Disease resistance and quality of melons (esp. Spanish) & cucumber; breeding schemes & genetic markers.
56. **Gomez-Guillamon, M. Luisa** Estacion Experimental "La Mayora":. 29750 Algarrobo-Costa, Malaga, Spain. Ph: (952) 51 10 00; FAX: (952) 51 12 52. E-mail: *guillamon@mayora.csid.es*
57. **Green, C.Ed** Seminis Vegetable Seeds, Inc. 37437 State Highway 16, Woodland CA, 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219.
58. **Groff, David.** Asgrow Seed Company, Rt. #1, Box 1907, Omega TyTy Road, Tifton, GA, 31794. Ph.: (912) 386-8701, FAX: (912) 386-8805. Breeding of squash, cuucumber, melon and watermelon.
59. **Grumet, Rebecca** Dept. Hort., Plant & Soils Building, Michigan State University, East Lansing, MI 48824-1325. Ph.: (517) 353-5568; FAX: (517) 353-0890. E-mail: *grumet@pilot.msu.edu.* Disease resistance, gene flow, tissue culture and genetic engineering.
60. **Gupta, Satish C.** Reitzel India Ltd., 220 Agil Campus, Whitefield Post, Bangalore 560066, India. Ph.: 91-080-8452415; FAX: 91-080-8453063.
61. **Hagihara, Toshitsugu** Hagihara Farm Co., Ltd., 984 Hokigi, Tawaramoto, Shiki, Nara, 636022, Japan. Ph.: 07443-3-3233; FAX: 07443-3-4332. Email: *cucurbit@mahoroba.ne.jp.*
62. **Haim, Davidi** Hazera Ltd., Mivhor Farm Doar, Sede Gat 79570, Israel.
63. **Han, Sang Joo** Seoul Seed Intl Co.Ltd., Chongill B/D, 736-17 Yeoksam-Dong, Seoul, Korea. Ph.: (2) 569-7147; FAX: 552-9439. Email: *seedexsj@hitel.kol.co.kr.* Disease resistance.
64. **Hassan, Ahmed Abdel-Moneim** Department of Vegetable Crops, Fac. Agriculture, Cairo University, Giza, Egypt. Ph.: 724107 & 724966. Cucumber, melon, squash & watermelon germplasm evaluation and breeding for disease resistance, incl. viruses.
65. **Havey, Michael J.** USDA/ARS, Department of Horticulture, University of Wisconsin, Madison, WI, 53706. Ph.: (608) 262-1830; FAX: (608) 262-4743, E-mail: *mjhavey@macc.wisc.edu.*
66. **Herman, Ran** "Zeraim" Seed Growers Company Ltd., Department of Breeding, Gedera 70 700, Israel. Ph.: 08-59 27 60; FAX: 08-594376.
67. **Hertogh, K.** Nickerson-Zwaan b.v., Postbus 19, 2990 AA Barendrecht, The Netherlands.
68. **Heuvelmans, Paul** Leen de Mos, groentezaden BV, Noordlandsewg 54, P.O. Box 54 2690 AB's-Gravenzande, The Netherlands. Ph.: + 31 174 41 20 31; FAX: + 31 174 41 73 57. Email: *paul.heuvelmans@leendemos.nl.* Plant breeding.
69. **Himmel, Phyllis** Asgrow-Seminis Vegetable Seeds, 500 Lucy Brown Lane, San Juan Bautista, CA 95045. FAX: (408) 623-2148. Email: *phyllis.himmel@svseeds.com*. Viral diseases of cucurbits.
70. **Hirabayashi, Tetsuo** Nihon Horticultural Production Institute, 207 Kamishki, Matsudo-shi, Chiba-ken, Japan. Ph.: 0473-87-3827; FAX: 0473-86-1455. Varietal improvement of cucurbit crops, especially melon, cucumber and pumpkin.
71. **Hollar, Larry A.** Hollar & Co., Inc., P. O. Box 106, Rocky Ford, CO 81067. Ph.:: (719) 254-7411; FAX: (719) 254-3539. e-mail: *lahollar@iguana.rural-net.net.* Cucurbit breeding and seed production.
72. **Holle, Miguel** CALCE 2, #183 Urb. El Rancho, Miraflores - Lima 18, Peru. Ph.: 51-14-383749; FAX: 51-14-351570. E-mail: *mholle@cipa.org.pe.* Plant genetic resources.
73. **Humaydan, Hasib** Ag Consulting International. 317 Red Maple Drive, Danville, CA 94506. Ph.: (510) 736-1241; FAX: (510) 736-1241.
74. **Hutton, Mark** Sakata Seed America, P/O. Box 1118, Lehigh Acres, FL, 33970-1118. Ph.: (941) 369-0021; FAX: (941) 369-7528. Email: *mhutton@sakata.com.* Squash breeding and cultivar development**.**
75. **Iamsangsri, Suphot** Limagrain Veg. Seeds Asia. 119/9 Moo 1, Baan Khao, Muang, Kanchanaburi 71000, Thailand. Ph: 66-2-636-2521-1; FAX: 66-2-636-2524.
76. **Ibrahim, Aly M.** USDA/ARS, 1636 E. Alisal St. Salinas, CA, 93905. Fax: (408) 753-2866. Cucumber, melon, watermelon.
77. **Ignart, Frederic** Centre de Recherche TEZIER, Route de Beaumont, Domaine de Maninet, Route de Beaumont, 26000 Valence, France. Ph.: (33) 75575757, FAX: (33) 75552681. Squash and melon breeding.
78. **Ikagami, Takayuki** Sakata Seed Corp., 1743-2 Yoshioka, Kakegawa, Shizuoka, 436-0115, Japan. Ph: 81-0537-26-1111; FAX: 81-0537-26-1110. Cell biology.
79. **Ito, Kimio** Vegetable Breeding Laboratory, Hokkaido Natl. Agric. Expt. S. Hitsujigaoka. Sapporo 062. Japan. Ph.: 011(851)9141; FAX: 011(859)2174. Email: *kito@cryo.affrc.go.jp.*
80. **Jahn, Molly Kyle** Cornell Univ, Dept. Plant Brdng & Biom, 312 Bradfield Hall, Ithica, NY 14853-1902. Ph.: (607) 255-8147; FAX: (607) 255-6683. Email: *mmk9@cornell.edu.* Melon and squash breeding and genetics.
81. **Jiang, Jiping** Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219. Developing disease screens for fungal diseases of cucurbits.

82. **Johnston, Rob Jr.** Johnny's Selected Seeds, Foss Hill Road, Albion, ME 04910-9731. Ph.:(207) 437-9294; FAX: (207) 437-2603. Email: *rob@johnnyseeds.com*. Squash and pumpkins.
83. **Kampmann, Hans Henrick** Breeding Station Danefield, Odensevej 82, 5290, Marslev, Denmark. Ph.: 65 95 17 00; FAX: 65 95 12 93.
84. **Karchi, Zvi** 74 Hashkedim St., Kiryat-Tivon 36501, Israel. Ph.:04-9830107; FAX: 972-4-9836936. Cucurbit breeding, cucurbit physiology.
85. **Kato, Kenji** Fac, Agriculture, Okayama Univ., 1-1-1- Tsushima Naka, Okayama, Japan 700. Ph.: 81-86-251-8323; FAX: 81-86-254-0714. E-mail: *kenkato@ccws2.cc.okayama-u.ac.jp* Use of molecular markers for QTL mapping and cultivar identification in melon.
86. **Katzir, Nurit** Newe Ya-ar Research Center, ARO, P.O. Box 1021, Ramat Yishay, 30095, Israel. Ph.: 972-4-9539554; FAX: 972-4-9836936. mail: *geneweya@netvision.net.il.*
87. **Keita, Sugiyama** Kurume Branch, Natl Res Inst, Veg/OrnPlnts/Tea,Kurume. Fukuoka 839-8503, Japan. Ph.: + 81-942-43-8271; FAX: + 81-942-43-7014. Email: *keita@nivot-km.affrc.go.jp.* Watermelon.
88. **Kerje, Torbjorn** IPGRI, c/o ICRAF, PO box 30677, Nairobi, Kenya. Ph.: 2544-2-521514; FAX: 254-2-521209. Email: *t.kerje@cgiar.org.* Genetic diversity of *Cucurbita* and *Cucumis,* particularly in Southern Africa.
89. **King, Joseph J.** Seminis Vegetable Seeds, Inc. 37437 State Hwy. 16, Woodland, CA 95695. Ph.: (916) 666-0931; FAX: (916) 668-5759. E-mail: *joe.king@svseeds.com.* Genetics and breeding of melon, cucumber and squash.
90. **King, Stephen R.** Seminis Vegetable Seeds, Inc. 37437 State Hwy. 16, Woodland, CA 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219. Email: *srking2570@aol.com.* Melon breeding.
91. **Kirkbride, Joseph H, Jr.** USDA-ARS. Systemic Bot & Mycol Lab, Rm 304, Bldg 011A, BARC- Beltsville, MD 20705. Ph.: (301) 504-9447; FAX: (301) 504-5810. E-mail:*jkirkbri@asrr.arsusda.gov.* Systematic taxonomy of the Cucurbitaceae.
92. **Klapwijk, Ad** de Ruiter Zonen CV. Postbus 1050 2660 BB Bergschenhoek, The Netherlands. Ph.: 010-5292253; FAX: 010-5292410.
93. **Knerr, Larry D.** Shamrock Seed Company. 3 Harris Place, Salinas, CA, 93901-4586. Ph.: (831) 771-1500; FAX: (831) 771-1517. E-mail: *ldkneerr@aol.com.* Varietal development of honeydew.
94. **Konno, Yoshihiro** Asahi Ind., Biol. Engin. Lab., 222 Wataruse, Kamikawa-machi, Saitama 36-03, Japan. Ph.: 0274-52-6339; FAX: 0274-52-4534. Watermelon breeding.
95. **Kouters, Jolanda** East-West Seed, Farm Lert Phan, 7 Moo 9, Tambon Maefaek Mai. Amphur Sansai, Chiangmai, 50290 Thailand. Ph.: (66) 53-848610; FAX: (66) 53-848611. Email: *research.th@eastwestseed.com*. Watermelon breeding.
96. **Kraakman, Peter** DeRuiter Zohen, Torre Caribe 7D, Aguadulce (Almeria), Spain. Email: *Peter.Kraakman@deruiterseeds.com.*.
97. **Kristkova, Eva** Res Inst Crop Prod, Praha-Ruzyne, Workplace Olomouc, Slechtitelu 11, 738 71 Olomouc, Czech Republic. Ph.: + 420-68-5228355; FAX: + 420-68-5228355. Email: *olgeba@ova.pvnet.cz.* Gene bank curating of cucurbitaceous vegetables; powdery mildew resistance in *Cucurbita.*
98. **Kuginuki, Yasuhisa** National Res. Institute Veg/Orn/Tea, Crop Research Station, Ano, Mie 514-23, Japan. Ph.: 0592-68-1331; FAX: 0592-68-1339. Breeding for resistance to disease.
99. **Kuhlmann, Hubert** Fink GmbH, Benzstrasse 25, D-71083 Herrenberg, Germany. Ph.: (07032) 922-122; Fax: (07032) 922-202.
100. **Kumar, Vasanth** Sunseeds India Private Ltd., No. 411, 80 Feet Road, R.T. Nag Bangalore - 560 032, India. Ph.: 91-80-333 8771; FAX: 91-80-333 1556. Email: *SUNINDIA / BLR / Vasanth%Sunseeds@mcimail.com.*
101. **Kuti, Joseph O.** Dept. Agron & Res Sci, Hort Crops Lab, Texas A&M University, Kingsville, TX, 78363. Ph.: (512) 593-3978; FAX: (512) 593-3788. E-mail: *j-kuti@tamuk.edu.* Breeding and genetics; host-parasite interrelationships; postharvest physiology.
102. **Kwack, Soo Nyeon** Dept Hort Breeding, Mokpo Natl Univ., Dorimri, Chonggyemyun, Muangun, Chonnam 534-729, Korea.
103. **Kwon, Cheol-Sang** Pusan Breeding Inst, Choong Ang Seed, 648-2 Kangdong-dong Ka Pusan, Korea 618-300. Ph.: + 82-51-972-8014; FAX: + 82-51-972-3206. Email: *k13483@chollian.net* Cucumber, watermelon,melon and squash breeding.
104. **Kwon, Young-Seok** Alpine Agriculture Expt. Sta. Heong-kye-Ri, doam-Myun, Pyeongchang-gun, Kangwon-Do, Repe. Korea 232-950. Watermelon germplasm evaluation and breeding for disease resistance.
105. **Lecouvior, Michel** Clause Semences,1, Avenue L. Clause, 91221 Bretigny-sur-Orge, CEDEX, France. FAX: (33) 04.90.92.21.55. Email: *Michel.lecouviour@Rhone-poulenc,com.*
106. **Lehmann, Louis Carl** Dept. Plant Breeding Reesearch. Swedish Univ. Agricultural Sci., S-268 31 Svaloev, Sweden.. Ph.: + + 46-418-667200; FAX: + + 46-418-667081. E-mail: *louis.lehmann@vf.slu.se. cucurbita* - testing of squash and pumpkin for use in Southern Sweden.

107. **Lelley, Tamas** Inst. Agrobiotech, Dept Plant biotech, Konrad Lorenz Str. 20, Tulln, Lower Austria, Austria 3430. Ph.: + 43 2272 66280 204; FAX: + 43 2272 66280 77. Email: *lelley@ifa-tull.ac.at.* cucurbita spp.
108. **Lester, Gene** USDA/ARS, Subtropical Agric Res Lab. 2301 S. International Blvd. Weslaco, TX 78596. Ph.: (210) 565-2647; FAX: (210) 565-6133. Email: *glester@pop.tamu.edu.* Stress and pre/postharvest physiology of melons.
109. **Lin, Depei** Sichuan Acdemic Agric. Science, Institute of Horticulture, Chengdu 610066, People's Rep. China. Ph.: (028) 4791732; FAX: (028) 4442025. Watermelon, melon and *Cucurbita* breeding.
110. **Lopez, Anido, Fernando** Catedra de Genetica, Fac. de Cs. Agrarias, UNR, CC 14, 2123 Zavilla, Argentina. Ph.: 54-41-970080; FAX: 54-41-970085. Email: *felopez@feagr.unr.edu.ar.* Breeding of *Cucurbita pepo* L. (caserta type).
111. **Love, Stephen Loyd.** Aberdeen R&E Center, P.O. Box AA, Aberdeen ID, 83210. Ph.: (208) 397-4181, Fax: (208) 397-4311. E-mail: *slove@uidaho.edu* Small scale private watermelon breeding with emphasis on adaptation to cold climates.
112. **Lower, Richard. L.** Coll. Agriculture, Univ. Wisconsin, 1450 Linden Drive, Room 240, Madison, WI 53706.Ph.: (608) 262-2349; FAX: (608) 265-6434. E-mail: *richard.lower@ccmmail.adp. wisc.edu.* Effects of plant type genes on yield, sex-expression, growth parameters, pest resistance & adaptability.
113. **Loy, J, Brent** G42 Spaulding, 38 College Rd., Dept. Plant Biology, UNH, Durham, NH 03824. Ph.: (603) 862-3216; FAX: (603) 862-4757. Email: *jbloy@christa.unh.edu.* Squash, melon, pumpkin. Genetics, breeding, plasticulture, mulch, rowcovers.
114. **Maggs, Gillian** National Herbarium (WIND). NBRI, Private Bag 13184, Windhoek, Namibia. Ph.: +264 61 3029111; FAX: + 264 61 3022177. Email: *gillianm@lianam.lia.net.*
115. **Maluf, Wilson Roberto** Dept. de Agricultra/UFLA, Caixa Postal 37, 37200-000, Lavras-MG, Brazil. Ph.: (035) 829-1326; FAX: (035) 829-1301. E-mail: *wmaluf@esal.ufla.br.* Cucumbers, melons, squashes.
116. **Markiewicz-Ladd, Krystina** Polonica International, P.O. Box 2305, Gilroy, CA 95021. Ph.: (408) 675-0103; FAX: (408) 842-1022 Email: *polonica@aol.com.* Melons - breeding, new germplasm, postharvest physiology, biotechnology, cultural practices, new diseases.
117. **Martyn, Ray D.** Dept. Botany & Plant Pathology, 1155 Lilly Hall, Purdue Univ West Lafayette, IN, 47907-1155. Ph.: (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.
118. **Matsuura, Seiji** Kiyohara Breeding Sta. Tohoku Seed Co. 1625, Nishihara, Himuro, Utsunomiya, Japan. Ph.: 0286-34-5428;. FAX: 0286-35-6544.
119. **Maynard, Donald N.** University of Florida, 5007 60th Street East, Bradenton, FL, 34203. Ph.: (941) 751-7636; FAX: (941) 751-7639. Email: *bra@giv.ifas.ufl.edu.* Tropical moschata improvement; watermelon variety evaluation and production practices.
120. **Mazereeuw, J.P.** SETO A.S., Cebecoy Caddesi. Akasya Apt. 45/1. 07100 Antalya, Turkey.
121. **McClurg. Charles A.** University of Maryland, Dept. Natural Resource Sci., College Park, MD 20742-4452. Ph.: (301) 405-4342; FAX: (301) 314-9308. E-mail: *cm19@umail.umd.edu* Production and culture of cucurbit crops.
122. **McCreight, J. D.** USDA-ARS, 1636 E. Alisal St., Salinas, CA 93905. Ph.:(831) 755-2864; FAX: (831) 755-2814. E-mail: *jmcreig@asrr.arsusda.gov.* Melon breeding and genetics.
123. **McGrath, Desmond John.** Dept. Primary Ind., Hortic. Res. Sta., P.O. Box 538, Bowen. 4805. Queensland, 4805, Australia. Ph.: + 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.
124. **Meadows, Mike** Novartis Seeds, Inc. 10290 Greensway Road, Naples, FL 34114. Ph.: (941) 775-4090; FAX: (941) 774-6852. Email: *Mike.Meadows@GWA.Sandoz.com.* Vegetable diseases.
125. **Melendez, Roberto Compean** Heriberto Valdez 647 PTE., C.P. 81200, Los Mochis, Senaloa, Mexico Ph.: (68) 18-37-22.
126. **Merrick, Laura C.** Dept. Agron., Iowa St. Univ., @101 Agronomy Hall, Ames, IA, 50011-1010. Ph.: (515)294-7636; FAX: (515) 294-3163. Email: *lmerrickistate.edu*. *Cucurbita* evolution; cucurbit germplasm evaluation and conservation; ethnobotany and evolution.
127. **Milerue, Sompong** Peto Thailand, P.O. Box 171, 99 Moo 2, Wiang-Y, Mae Gorn, A Muang Chiang Rai 57000, Thailand.
128. **Mochizuki, Tatsuya** Kurume Br, Natl Res Inst Veg/Orn/Tea, 1823 Mii-machi, Kurume Fukuoka 830, Japan. Ph.: 0942-43-8271; FAX: 0942-43-7014.
129. **Mohamed, El Tahir Ibrahim** PGR unit/Horticulture, Agr Res Corp, P.O. Box 126, Wad Medani, Sudan.
130. **Mohamed, Yousisf Fadlalla** Dept. Plant Pathology, Fac. Agric. Sci., Univ. Gezira, Wad Medani, P.O. Box 20, Sudan.
131. **Moraghan, Brian Joseph.** Asgrow Seed Co. P.O. Box 667, Arvin, CA 93203. Ph.:: (805) 854-2360; FAX: (805) 854-4379. Email: *brian.moraghan@svseeds.com.* Melon and watermelon breeding and disease resistance.
132. **Morelock, Ted** Horticulture & Forestry, University of Arkansa, Fayetteville, AR, 72701. Ph.: (501) 575-2603; FAX: (501) 575-8619. E-mail: *morelock@comp.uark.edu.* Cucumber breeding.

133. **Munger, H.M.** Cornell University, 252 Emerson Hall, Ithica NY 14853. Ph.: (607) 255-7820; FAX: (607) 255-6683. Email: *hmm11@cornell.edu* Cucurbit breeding and disease resistance.
134. **Nadel, Michael** 10851 Woodbine Street, Los Angeles, CA 90034. Ph: (310) 838-7675; FAX: (310) 202-7466. Email: *dansonseed@mediaone.net*. Breeding summer squash, cucumbers, melons and watermelons.
135. **Navazio, John P.** Chriseed, P.O. Box 1788, Mount Vernon, WA, 98273. Ph.: (360) 336-9727; FAX: (360) 424-9520. Breeding or increased pigments in cucurbits, carrots and beets.
136. **Nea, Larry** Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219. Cucumbers, melons, squash, watermelon.
137. **Ng, Timothy J.** Department Natural Resource Sci., University of Maryland, College Park, MD 20742-4452 .Ph.: (301) 405-4345; FAX: (301) 314-9308. E-mail: *tn5@umail.um.edu.* Melon breeding and genetics; postharvest physiology; seed germination.
138. **Niemirowicz-Szczytt, Katarzyna** Warsaw Ag. Univ. Dept. Gen & Plt Nrdmg, ul. Nowoursynowska 166, 02-766 Warsw, Poland. Ph.: 43 09 82; FAX: (48-22) 471562 Cucumber, melon, winter and summer squash, watermelon - genetics, breeding, tissue culture, biotechnology.
139. **Norton, Joseph D.** Dept. Horticulture, 101 Funchess Hall, Auburn Univ. Auburn, Al. 36849. Ph.: (205) 844-3031; FAX: (205) 844-3131. Breeding and genetics of melon and watermelon.
140. **Nuez, Fernando** Cat. de Genetica, ETS Ingen. Agron., Univ. Politenica, Camin 46020, Valencia, Spain. Ph.: 34(6) 387-74-29; FAX: 34 (6) 287-74-29. Email: *fnuez@btc.upv.es.* Genetics and plant breeding.
141. **Oliveira de Paiva, Waldelice** EMBRAPA/CNPAT - Caixa Postal 3761, Rua Dra. Sara Mesquita 2260511-110-Fortaleza-Ceara, Brazil Ph.: (085) 299.18.01; FAX: (085) 299.18.03. Email:*Walde@cnpat.embrapa.br* .Research with cucurbit species, especially *Cucumis,* and particularly *Cucumis melo.*
142. **Om, Young-Hyuan** Natl Horticultural Res Inst. 475 Imok-Dong, Suwon 440-310, Republic of Korea. Ph.: 82-0331-290-6171; FAX: 82-0331-295-9548. Email: *omyh@nhri.go.kr.* Breeding of cucurbit vegetables.
143. **Omara, Sadig Khdir** Dept. Horticulture, Fac. Agric. Sciences, University of Gezira, Wad Medani, P.O. Box 20, Sudan.
144. **Ouyang, Wei** Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA, 95695. Ph.:(916) 666-0931; FAX: (916) 668-0219. Squash & cucumber breeding.
145. **Owens, Ken**. Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA 95695. Ph.:(916) 666-0931; FAX: (916) 668-0219. Cucumber breeding.
146. **Palomares, Gloria**. Dept Biotechnologia, Univ Politecnia, Camino de Vera, s/n., E-46022 Valencia, Spain. Ph.: 34(6)387-421/7426; FAX: 34(6)387-429. E-mail: *gpaloma@btc.upv.es* Genetic improvement in horticultural plants.
147. **Paris, Harry** Division of Vegetable Crops, A.R.O., Newe Ya'ar Research Ctr., P.O. B Ramat Yishay 30-095, Israel . Ph.: 972-4-9894516; FAX: 972-4-836936. Email: *hsparis@netvision.net.il.* Breeding and genetics of squash and pumpkin.
148. **Pathak, Chandra** c/o Nath Sluis Ltd., Nath House, Nath Road, Aurangabad, 431005, India.
149. **Piero Abril, Jose Luis** Apartado de Correos no. 2, 04720 Aguadulce, Almeria, Spain. FAX: 34 50 34 34 01.
150. **Peri-Treves, Rafel** Dept. Life Science, Bar-Ilan University, Ramat-Gan, Israel 52900. E-mail: *peri@brosh.cc.biu.ac.il*
151. **Peter, K.V.** Natl. Ressearch Ctr for Spices, ICAR, Post Bag No. 1701, Mar Calicut - 673 012, Kerala, India.Ph.: 011-91-495-258457.
152. **Peterson, Paul S.** Plant Pest Diagnostic Center. 3294 Meadowview Road, Sacramento, CA, 95832-1448. Ph.: (916) 262-1139; FAX: (916) 262-1190. Email: *ppeterso@cdfa.ca.gov.* Laboratory germination and seed quality assesment.
153. **Picard, Florence** Vilmorin, La Menitre, 49250 Beaufort-en-Vallee, France.
154. **Pitrat, Michel** I.N.R.A., BP 94, 84143 Montfavet cedex, France. Ph.:(33) 90 31 63 00; FAX: (33) 90 31 63 9. E-mail: *Michel.Pitrat@avignon.infra.fr* Melon, disease resistance, mutants, genetic map.
155. **Pootstchi, Iraj** 97 St. Marks Road, Henley-on-Thames RG9 1LP, England. Ph.: (01491) 574959; FAX: (10491) 574500. Breeding cantaloupes, melons and watermelons.
156. **Poulos, Jean M.** Asgrow Italia, Veg. Seeds Srl. Pontinia Research Station, C.P. 110-04014 Pontina, Italy. Ph.: 39(0)773 848549; FAX: 39(0)773 848548.
157. **Price, E. Glen** Sugar Creek Seed, Inc. , P.O. Box 508, Hinton, OK 73047. Ph.: (405) 542-3920; FAX: (405) 542-3921. Seedless watermelon; polyploidy, genetics, breeding, cytogenetics.
158. **Provvidenti, Rosario** Cornell University, Dept. Plant Pathology, NY State Agric. Experiment Sta., Geneva, NY, 14456-0462. Ph.: (315) 787-2316; FAX: (315) 787-2389. E-mail *rp13@cornell.edu.* Breeding & genetics of resistance to viral diseases of cucumber, squash, melon, watermelon & other cucurbits.
159. **Punja, Zamir K.** Dept. BioSciences, Simon Fraser University, Burnaby, B.C. V5A 1S6, Canada. E-mail: *punja@sfu.ca.*
160. **Quisumbing, Alberto R. (Bert)** Delaware Valley Coll., Hort. Dept., 700 E. Butler Ave., Doylestown, PA 18901-2404. Ph.: (215) 489-2333; FAX: (215) 489-2404. Email: *quisumbb@devalcol.edu.* IPM in cucumbers, melons, and watermelons; host plant resistance to insects; marketing.

161. **Ramirez, Pilar** CIBCM, Universidad de Costa Rica, San Jose, Costa Rica. 506-253-5661 x3496; FAX: 506-224-6749. Email: *pramoirez@cari-ari.ucr,ac,cr.* Viruses in cucurbits, production of resistant transgenic plants.
162. **Ray, Dennis** Department of Plant Sciences, University of Arizona, Tucson, AZ 85721. Ph.: (520) 621-7612; FAX: (520) 621-7186. E-mail: *dtray@u.arizona.edu.* Genetics and cytogenetics of *Cucumis melo* and *Citrullus* spp.
163. **Reiten, Joel** Territorial Seed Co., P.O. Box 157, Cottage Grove, OR, 97424. Ph.: (541) 942-9547; FAX: (541) 942-9881. Email: *tsc@ordata.com.* Bacterial wilt resistance, as well as virus resistance obtained through traditional breeding methods.
164. **Reuling, G.** Nunhens Zaden B.V., P.O. Box 4005, 6080 Haelen, The Netherlands, Ph.: 0475-599222; FAX: 0475-599223 Email: *bre@nunhems.nl.* Cucumber breeding.
165. **Rhodes, Bill B.** Clemson Univ./Horticulture, Poole Agricultural Center, Clemson, SC, 29634-0375. Ph.: (864) 656-0410; FAX: (864) 656-4960. E-mail: *BRhodes@clemson.edu.* Watermelon genetics, breeding, micropropagation, disease resistance, male sterility, triploids.
166. **Rios, Labrada, Humberto** Instituto Nacional de Ciencias Agricolas (INCA). GP no 1 San Jose de las Lajas, Labana, Cuba cp 32700; FAX: 53 7 24 4209. Breeding pumpkin (*Cucurbita moschata*) for low input environments.
167. **Rizzo, Adriana A. do Nascimento** FCAV-UNESP Campus de Jaboticabal, Departmento de Horticultura, Rod. Carlos Tonnani, Km5, Jaboticabal-SP-Brazil Cep-1870-000. Email: *drarizzo@fcav.unesp.br.*
168. **Robinson, R. W.** Dept. Hort. Sci., New York State AES, Hedrick Hall, Geneva, NY 14456-0462 . Ph.: (315) 787-2237; FAX: (315) 787-2397. E-mail: *rwl@cornell.edu.* Breeding and genetics of cucurbits.
169. **Robledo, Claude** Seminis - Recherch France, Mas de Rouzel - chemen des Canaux 30900 Nimes, France. Ph.: 33(0) 4 66 38 79 80; FAX: 33(0)4.66 3.79.81. Melon breeding.
170. **Roig, Luis A.** Departamental Biotechnology, ETS.Ingen. Politec., Camino de 46022 - Valencia, Spain. Ph.: 34(6) 3877424; FAX: 34(6) 3877429.
171. **Saito, Takeo** Cucurbitaceae Breeding Lab. NIVOT, 1823, Mii, Kurume, fukuoka 839, Japan. Ph.: + 81-942-43-3271; FAX: + 81-942-43-7014. Email: *romario@nivoi-krm.affrc.go.jp.* Breeding melons resistant to diseases and insects; use of DNA markers for melon breeding.
172. **Sarfatti, Matti** Hazera Ltd. Research Dept., Mivhor, M.P., Lakhish Daram 79354, Israel.
173. **Schroeder, Robert Harold** Harris Moran Seed Co., 9241 Mace Blvd., Davis, CA. 95616. Ph.: (530) 756-1382; FAX: (530) 756-1016. Incorporating disease resistance into useful commercial cultivars.
174. **Schultheis, Jonathan R.** Dept. Hortioculture, 264 Kilgore Hall, North Carolina St. University, Raleigh, NC 27695-7609. Ph.: (919) 515-3131; FAX: (919) 515-7747. E-mail: *jonathan_schultheis@ncsu.edu.* Cultural management of cucurbits; plant spacing, establishment, nutrition, pollination & cultivar evaluation.
175. **Shetty, Nischit** Dept. Horticultural Science, Box 7609, North Carolina St Univ. Raleigh, NC, 27695-7609. Ph.: (919) 515-3178; FAX: (919) 515-2505. Email: *nischit_shetty@ncsu.edu.*
176. **Shiffris, Oved** Dept. Plant Sci., Cook College, Foran Hall./59 Dudley Road, new Brunswick, NJ 08903.Ph.: (732) 246-0028; FAX: (732) 932-9441. Gene expression during development in *Cucurbita.*
177. **Simon, Philipp W.** USDA/ARS-Veg Crops, Dept. Hort., Univ. Wisconsin, 1575 Linde Madison, WI 53706. ((608) 262-1248; FAX: (608) 262-4743. Email: *psimon@facstaff.wisc.edu.* Breeding and genetics.
178. **Sipeyre, Bruno** Mas de Rouzel, Chemin des Canaux, 30900 Nimes, France. Ph.: 66.84.21.32; FAX: 66.38.09.42.
179. **Skirvin, Robert M.** Univ. Illinois, Dept. Horticulture, 258 PABL, 1201 Gregory D Urbana, IL 61801. Ph.: (217) 333-1530; FAX: (217) 333-4777. E-mail:*skirvin@uxl.cso.uiuc.edu.* Micropropagation; somaclonal variation.
180. **Snyder, James W.** 1231 Kirkwood Drive, Vineland, NJ 08360. Ph.: (609) 794-3880; FAX: (609) 794-3881.
181. **Staub, Jack E.** USDA, ARS, Dept. Horticulture, Univ. Wisconsin, Madison, WI 53706-1590. Ph.: (608) 262-0028; FAX: (608) 262-4743. E-mail: *jestaub@facstaff.wisc.edu.* Cucumber breeding & genetics, physiology, biochemical genetic markers, evolution, environmental stress.
182. **Stephenson, Andrew G.** 208 Mueller Lab, Penn State University, University Park, PA, 16802. Ph.: (814) 863-1553; FAX: (814) 865-9131, E-mail: *as4@psu.psu.edu.*
183. **Stevens, M. Allen** Seminis Vegetable Seeds, Inc. 37437 State Highway 16, Woodland, CA, 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219. Direction of research..
184. **Stravato, Vittorio M.** c/o Peto Italiana S.R.1., Via Canneto di Rodi, 04010 Borgo Sabatino (LT), Italy. Ph.: 733-643336; FAX: 773-643722. Email: *Vstravato@svseeds.nl.*
185. **Summers, William L.** Iowa State University, Dept. Horticulture, Rm 251, Ames, IA 50011-1100. Ph.: (515)-294-1978; FAX: (515) 294-0730. E-Mail: *summers@iastate.edu.* Genetic improvement of watermelon.
186. **Susic, Zoran** Inst. "Srbija" - Ctr Vegetable Crops, Karadjordjeva 71, 11420 SAmederevska Palanka, F.R. Yougoslavia. Ph.: + 381-26-314 170; FAX: + 381-26-314 786. Email: *djelovac@eunet.yu*. Genetics and breeding of cucurbita species.
187. **Tatlioglu, Turan** Institut of Applied Genetics, Univ. Hannover, Herrenhauser Str. 3000 Hannover, Germany. Ph.: (+ 49)511762-5675; FAX: (+ 49)511762-3608. Email: *turan.tatlioglu@mbox.genetik.uni-hannover.de* Hybrid breeding,

male sterility(GMS, CMS) and sex inheritance.

188. **Taurick, Gary** Harris Moran Seed Co., P.O. Box 392, Sun Praire, WI, 53590. Ph.: (608) 837-6574; FAX: (608) 837-3758. Development of commercial hybrids of pickle, slicer and Beit Alpha cucumbers.
189. **Teppner, Herwig** Institute of Botany, Univ. Graz, Holteigasse 6, A-8010 Graz, Austria. Ph.: 316-380-5656; FAX: 216-380-9883. Systemastics, morphology, ecology, crops & medicinal plants (teaching) and small scale breeding.
190. **Thomas, Claude E.** USDA-ARS, U.S. Vegetable Labaratory, 2875 Savannah Highway, Charleston, SC 29414. Ph.: (803) 556-0840; FAX: (803) 763-7013. Email: *cthomas@awod.com.* Disease resistance in cucurbits.
191. **Thompson, Gary** Dept. Plant Sciences, University of Arizona, Tucson, AZ 85721. E-mail: *garyt@u.arizona.edu*
192. **Tolla, Greg** Asgrow SVS, 432 TyTy Omega Rd. Tifton, GA, 31794. Ph.: (912) 386-8701; FAX: (912) 386-8805. Cucumber breeding and genetics.
193. **Tsaftaris, A.S.** Dept. Genetics & Breeding of Plants, Aristotelian Univ. of T Thessaloniki, 54006, Greece.
194. **Vakalounakis, Demetrios J.** Plant Protection Inst. N.A.R.F., P.O. Box 1803, 711 10 Heraklion Crete, Greece. Ph.: 081-245858; FAX: +3081-245.858. Email: *vakaloun@nefeli.imbb.forth.gr.*
195. **van Eijk, Manuel** Linda Vista Farm, East West Seed Co., P.O. Box 9073, 3006 Baliuag, Phillippines, Ph.: 63-(0) 44 7641370; FAX: 63-(0)44 7641250. EmailL *research.ph@eastwestseed.com.* Breeding of bitter gourd, squash, cucumber, melon, watermelon, sponge gourd, and bottle gourd.
196. **van Kooten, Henk C. Seminis Veg Seeds -** Bruinsma , P.O. Box 93, 2675 ZH Honselersdijk. The Netherlands.Ph.: +31-174-61 50 15; FAX: + 31-174-61 50 20.
197. **Vardi, Eyal** Hazera Ltd., Mivhor Farm M.P. Lachish Daron 79354, Israel. Ph.: +972-7-6813228; FAX: + 972-7-6814057. Email: *vardi@hazera.com.*
198. **Walters, Terrence** The Cucurbit Network, 11901 Old Cutler Road, Miami, FL 33156-4242. Ph.: (305) 667-3800; FAX: (305) 661-5984. Email: *walters@servax.fiu.edu.* Communication via The Cucurbit Network, the whole family Cucurbitaceae.
199. **Wang, Gang** #84 Orange Street, Woodbridge, NJ 07095. Email: *w2140@hotmail.com.* Watermelon and melon breeding.
200. **Wang, Ming** Department of Horticulture, Northwestern Agricultural University, Yangling, Shaanxi 712100, P.R. China. Ph.: (0910)709-3426; FAX: (0910) 701-2559. Watermelon genetics and breeding.
201. **Warid, Warid A.** Cairo University Street, Apartment #4, Giza - 12211, Egypt. Breeding of cucurbits.
202. **Wasilwa, Lusike** Rutgers Blueberry/Cranberry Res Ctr, 125a Lake Oswego Rd., Chatsworth, NJ, 08019. Ph.: (609) 72601590; FAX: (609) 726-1593. Email: *wasilwa@aesop.rutgers.edu*. Disease screening, fungal genetics, evaluation of fungal diversity of *Colletotrichum* spp.
203. **Wehner, Todd C.** Dept. Horticultural Science, Box 7609, North Carolina St. Univ. Raleigh, NC 27695-7609. Ph.: (919) 515-5363; FAX: (919) 515-2505, E-mail: *todd_wehner@ncsu.edu* Pickling/slicing cucumber, watermelon, luffa gourd; selection, disease resistance, yield, genetics & chilling.
204. **Welbaum, Greg** VPI&SU, Dept. Horticulture, Sauners Hall, Blacksburg, VA. 24061-0327. Ph.: (540) 231-5801; FAX: (540) 231-3083. Email: *welbaum@vt.edu*. Seed physiology and stand establishment.
205. **Wessel-Beaver, Linda** Agronomy & Soils Dept., Univ. Puerto Rico, PO Box 9030. Ph.: (809) 832-4040, FAX: (809) 265-0220. E-mail: *l_beaver@rumac.upr.clu.edu.* Pumpkin & squash breeding; disease resistance; insect resistance.
206. **Wiebe, Wayne** Seminis Vegetable Seeds, Inc., 37437 State Highway 16, Woodland, CA 95695. Ph.: (916) 666-0931; FAX: (916) 668-0219. Cucurbit diseases and disease resistance.
207. **Williams, Tom V.** Novartis Seeds, 10290 Greenway Road, Naples, FL 34114-3199. Ph.: (941) 775-4090; FAX: (941) 774-6852. Watermelon breeding.
208. **Winkler, Johanna** Saatzucht Gleisdorf GesmbH, A-8200 Gleisdorf, Am Tieberhof 33, Austria. Ph.: + 43 (0) 3112 21050; FAX: + 43 (0) 3112 21050. Email: *winkj.szgl@ccf.co.at.*
209. **Wolff, David W.** Sakata Seed America, Inc., P.O. Box 1118, Lehigh Acres, FL, 33970-118. Ph.: (941) 369-0032 x13; FAX: (941) 369-7528. Email: *david.wolff@mci2000.com*. Watermelon breeding and genetics; molecular markers.
210. **Wu, Mingzhu** Hort. Inst. Xinjiang Acad Agric Sci, Nanchang Road NO. 38, Urumqi, Xinjiang, People's Rep. China. Ph.: 0991-4840311-2094.
211. **Wu, Wendy Y.** Know-You Seed Co., Ltd., 330 Kao Tan Village, Jen Wu Hsing Kaohsiung, 814, Taiwan, R.O.C. Ph.: 886-7-3719725; FAX: 886-7-3718510. Breeding and growing cucurbits (all).
212. **Yamanaka, Hisako** Yamato-Noen Co., Ltd. 100, Byodobo-cho, Tenri-City NARA, Japan 632. Ph.: 07436-2-1182. FAX: 07436-3-3445.
213. **Yorty, Paul** Qualiveg Seed Production, 3033 E., 3400 N., Twin Falls, ID, 83301. Ph.: 733-0077; FAX: (208)733-0077. Cucurbit breeding.
214. **Zhang, Jiannong** Melon Research Institute, Gansu University of Agriculture, Lanzhou, Gansu, 730070, P.R. China.
215. **Zhang, Xingping** Hollar Seeds, P.O. Box 106, Rocky Ford, CO, 80167. Ph.: (719) 254-7411; FAX: (719) 254-3539. Email: *hollarw@iguana.ruralnet.net.* Watermelon and melon genetics & breeding.

216. **Zitter, Thomas** Cornell Univ., Dept. Plant Pathology, 334 Plant Science Buil Ithica, NY 14853-5908. Ph.: (607) 255-7857; FAX: (607) 255-4471, E-mail: *taz1@cornell.edu.* Fungal and viral disease resistance.

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    - Zoran Susic

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Covenant and By-Laws of the Cucurbit Genetics Cooperative

ARTICLE I. Organization and Purposes

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

ARTICLE II. Membership and Dues

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

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

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

ARTICLE III. Committees

1. The Coordinating committee shall govern policies and activities of the CGC. It shall consist of six members elected in order to represent areas of interest and importance in the field. The Coordinating Committee shall select its Chairman, who shall serve as spokesman of the CGC, as well as its Secretary and Treasurer.

2. The Gene List Committee, consisting of five members, shall be responsible for formulating rules regulating the naming and symbolizing of genes, chromosomal alterations, or other hereditary modifications of the cucurbits. It shall record all newly reported mutations and periodically report lists of them in the Report of the CGC. It shall keep a record of all information pertaining to cucurbit linkages and periodically issue revised linkage maps in the Report of the CGC. Each committee member shall be responsible for genes and linkages of one of the following groups: cucumber, *Cucurbita* spp., muskmelon, watermelon, and other genera and species.

3. Other committees may be selected by the Coordinating Committee as the need or fulfilling other functions arises.

ARTICLE IV. Election and Appointment of Committees

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

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

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

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

ARTICLE V. Publications

1. One of the primary functions of the CGC shall be to issue an Annual Report each year. The Annual Report shall contain sections in which research results and information concerning the exchange of stocks can be published. It shall also contain the annual financial statement. Revised membership lists and other useful information shall be issued periodically. The Editor shall be appointed by the Coordinating Committee and shall retain office for as many years as the Coordinating Committee deems appropriate.

2. Payment of biennial dues shall entitle each member to a copy of the Annual Report, newsletters, and any other duplicated information intended for distribution to the membership. The aforementioned publications shall not be sent to members who are in arrears in the payment of dues. Back numbers of the Annual Report, available indefinitely, shall be sold to active members at a rate determined by the Coordinating Committee.

ARTICLE VI. Meetings

An Annual Meeting shall be held at such a 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 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 provision of the By-Laws or any other document that might be susceptible to a contrary interpretation:

1. The CGC shall be organized and operated exclusively for scientific and educational purpose.
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; or
- (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 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.

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Cucurbit Genetics Cooperative

Financial Statement

31 December 1998

Balance (31 December 1997)		**$3,428.57**
Receipts		
Dues and CGC back issue orders	$2,886.94	
Interest on savings	$111.94	
Total receipts		**$2,998.88**
Expenditures		
CGC Report No. 21 (1998)		
Printing	$1,799.53	
Mailing	$171.01	
Call for papers (Report No. 22)	$162.00	
Member/Subscriber Renewal notices	$76.95	
Bank fees & Adjustment Charges	$0.00	
Miscellaneous (envelopes, postage)	$27.00	
Total Expenses		**$2,747.67**
Balance (31 December 1998)		**$3,679.78**