Cucurbits 2015

V ISHS International Symposium

Programme and Book of Abstracts

Organization:

ISHS International Society for Horticultural Science

GOBIERNO DE ESPAÑA MINISTERIO DE ECONOMÍA Y COMPETITIVIDAD

CSIC Consejo Superior de Investigaciones Científicas

Universidad Politécnica de Cartagena

Instituto Murciano de Investigación y Desarrollo Agrario y Alimentario imida

TABLE OF CONTENTS

WELCOME p_3
COMMITTES p_5
PROGRAMME p_7
KEYNOTE PRESENTATIONS p_15
SESSIONS p_27
POSTERS p_71
AUTHOR INDEX p_129

WELCOME

Dear Colleagues and Friends,

We are glad to welcome you to the V International Symposium on *Cucurbits 2015* held from 22 to 26 June 2015 in Cartagena, Spain, under the auspices of the International Society for Horticultural Science (ISHS). This periodic event, previously held in Australia (2005) and China (2009), takes place in an ideal place for a botanic family as *Cucurbitaceae*. With a total production of 223,668 t of melon in 2013, out of which 87% were exported, the Region of Murcia stands as the second largest exporter of melon in Europe. Its privileged location in the Mediterranean coast and unique climate makes Murcia a great place to hold this event.

In addition, there are a number of national research groups working on different aspects of this crop (agronomy, improvement, physiology, pathogens, post-harvest and so forth), most of which are represented in the organizing and scientific committees, and the programme speakers. These groups gather scientists from the three public institutions of the Region of Murcia with the greatest relevance in agricultural research (IMIDA, UPCT and CEBAS-CSIC).

Our programme includes circa 100 oral and poster presentations organised from individual paper submissions on the following topics:

1. Genetics and Breeding
2. Genomics and Biotechnology
3. Crop Production, Physiology and Management
4. Biotic Stresses and Abiotic Stresses
5. Fruit Quality and Post-Harvest

This event gathers scientists and experts from research and industry worldwide. Participating groups will have the opportunity not only to present their work in a specialized forum of high scientific level, but also to build relationships with other researchers and private companies to further develop their research practice.

The organizing committee is delighted to organise this unparalleled symposium and will do its best to make *Cucurbits 2015* an enjoyable and meaningful experience that will live on in the memories of the audience.

We wish you a successful Symposium,

The Conveners,

María L. Gómez Guillamón
IHSM-UMA-CSIC, Spain

Francisco Pérez Alfocea
CEBAS-CSIC, Spain

COMMITTES

CONVENERS

María L. Gómez Guillamón
IHSM-UMA-CSIC, Spain

Francisco Pérez Alfocea
CEBAS-CSIC, Spain

Organizing Committee

María Dolores Bernal
Independent Technical Advisor, Spain

Francisco Pérez Alfocea
CEBAS-CSIC, Spain

Alfonso Albacete Moreno
CEBAS-CSIC, Spain

María del Puerto Sánchez
CEBAS-CSIC, Spain

José A. Franco
UPCT, Spain

Juan A. Fernández
UPCT, Spain

Josefa López Marín
IMIDA, Spain

Margarita Pérez Jiménez
IMIDA, Spain

Juan Carlos Gázquez Garrido
Fundación Cajamar, Spain

Cristina Soriano Carpena
CEBAS-CSIC, Spain

Cristina Martínez Andújar
CEBAS-CSIC, Spain

Ascensión Martínez
CEBAS-CSIC, Spain

Perla Gómez Di Marco
UPCT, Spain

Encarna Aguayo
UPCT, Spain

Francisco del Amor Saavedra
IMIDA, Spain

Scientific Committee

José A. Franco
UPCT, Spain

Francisco Artés Hernández
UPCT, Spain

María Luisa Guillamón
IHSM-UMA-CSIC, Spain

Miguel Aranda
CEBAS-CSIC, Spain

Josefa López Marín
IMIDA, Spain

Amnon Levi
USDA-ARS, United States

Yaakov (Kobi) Tadmor
Volcani Center, Israel

Xingfang Gu
Chinese Academy of Agricultural Sciences, China

Nebahat Sari
Çukurova University, Turkey

Encarna Aguayo
UPCT, Spain

Juan A. Fernández
UPCT, Spain

Francisco Pérez Alfocea
CEBAS-CSIC, Spain

Ana Garcés
CITA, Spain

Belén Picó
COMAV-UPV, Spain

James D. McCreight
USDA-ARS, United States

Catherine Dogimont
INRA, France

Alfredo Lacasa Plasencia
IMIDA, Spain

Juan Antonio Torés
EELM-CSIC, Spain

PROGRAMME

CUCURBITS 2015

V ISHS International Symposium on Cucurbits 2015

22 - 26 June 2015 • Cartagena (Spain)

PROGRAMME	
MONDAY 22	
8:30 - 10:00	Registration
10:00 - 10:30	Welcome Alejandro Pérez Pastor *Director of the Higher Technical School of Agricultural Engineering of the Technical University of Cartagena (UPCT)* Daniel Leskovar *Chair of the ISHS Section Vegetables, Quality Production Systems, Leafy Green and Non-Root Vegetables - ISHS Representative* María L. Gómez-Guillamón IHSM-UMA-CSIC, Spain. *Convener - CSIC Representative* Francisco Pérez-Alfocea CEBAS-CSIC, Spain. *Convener - CSIC Representative*
10:30 - 16:30	**ORAL SESSION 1 – GENETICS AND BREEDING** **Chair: Yaakov Tadmor** **Co-Chair: James D. McCreight**
10:30 - 11:10	Keynote speaker: Nurit Katzir, ARO, Israel *Unraveling genetic factors that underlie melon fruit quality traits by using NGS-based QTL mapping*
11:10 - 11:50	Keynote speaker: Emilio Sarria, Rijk Zwaan, Spain *Global challenges for the future of watermelon breeding*

11:50 - 12:10	*S1.1 Revealing the identity of the watermelon 'Y' locus* Yaakov Tadmor
12:10 - 12:30	*S1.2 Cucurbita rootstocks : From random crosses to rational breeding* Roni Cohen
12:30 - 12:50	*S1.3 Lycopene biosynthesis key genes expression and related hormone in different ploidy watermelon* Liu Wenge
12:50 - 13:10	*S1.4 Appraisals on the utility of pumpkin cross combinations as the rootstocks of grafted melon* Zhilong Bie
13:10 - 15:10	***Lunch***
15:10 - 15:30	*S1.5 Origin Of The Dessert Watermelon, Citrullus Lanatus* Harry S. Paris
15:30 - 15:50	*S1.6 Status of bitter gourd breeding at AVRDC - The World Vegetable Center* Narinder P.S. Dhillon
15:50 - 16:10	*S1.7 Molecular Mapping and Candidate Gene Analysis for Numerous Spines on the Fruit of Cucumber* Zhang Shengping
16:10 - 16:40	***Refreshment break***
16:40 - 18:30	Poster Session
19:00 - 22:00	Social Events - Tour around the historic centre of Cartagena - Group picture - Cocktail at 'Edificio CIM' offered by the Universidad Politécnica de Cartagena (UPCT)

TUESDAY 23	
9:00 - 12:30	**ORAL SESSION 2 – GENOMICS AND BIOTECHNOLOGY** **Chair: Catherine Dogimont** **Co-Chair: Rafael Perl-Treves**
9:00 - 9:40	Keynote speaker: Zhangju Fei, Boyce Thompson Institute for Plant Research, Unites States *Genomics of watermelon*
9:40 - 10:20	Keynote speaker: José Blanca, COMAV, Spain *The genome of Cucurbita pepo, a tool for breeders*
10:20 - 10:40	*S2.1 Development of ZYMV-Resistant Watermelon Lines Using Genomic Tools* Amnon Levi
10:40 - 11:30	***Coffee break***
11:30 - 11:50	*S2.2 Plant-pathogen interactions controlled by the Fom-1-Prv locus of melon* Rafael Perl Treves
11:50 - 12:10	*S2.3 Functional analysis of Mlo genes in powdery mildew resistance in melon* Catherine Dogimont
12:10 - 12:30	*S2.4 Effects of Genotypes and Irradiation Doses on Haploid Embryo Induction and Plant Production in Bottle Guard [Lagenaria siceraria (Malign) Stanley]* Nebahat Sari
12:30 - 18:40	**ORAL SESSION 3 – CROP PRODUCTION, PHYSIOLOGY AND MANAGEMENT** **Chair: Warley Marcos Nascimento** **Co-Chair: Roni Cohen**
12:30 - 13:10	Keynote speaker: Yiqun Weng, USDA-ARS, University of Wisconsin, United States *Cucumber applied genomics – where we are five years after release of cucumber draft genome*

13:10 - 13:20	Announcement of Cucurbits 2018, U.S. James D. McCreight
13:20 - 15:20	***Lunch***
15:20 - 16:00	Keynote speaker: Manuel Jamilena, Universidad de Almería, Spain *Agronomic traits regulated by ethylene in zucchini squash: from sex determination to postharvest quality of fruit*
16:00 - 16:30	*S3.1 Using computerized image analysis for evaluation of squash seed quality* Invited speaker: Warley Marcos Nascimento
16:30 - 16:50	*S3.2 Decreasing the temperature in the greenhouse does not necessarily reduce the yield of cucumber* Hans-Peter Klaering
16:50 - 17:10	*S3.3 Melon production in the Province of Murcia (SE Spain)* Juan A. Fernández
17:10 - 17:30	*S3.4 Evaluation of two potential Cucumis spp. resources for grafting melons* Belén Picó
17:30 - 18:00	***Refreshment break***
18:00 - 18:20	*S3.5 Pollen drying and storage for hybrid seed production of cucumber (Cucumis sativus)* Endah Retno Palupi
18:20 - 18:40	*S3.6 Isolation and characterisation of ethylene insensitive mutants from a collection of Cucurbita pepo L.* Cecilia Martínez
18:40 - 20:00	Poster Session

WEDNESDAY 24	
8:00 - 20:00	Full day technical visit - Field visit to 'Agrícola Perichán' (cucumber growing in greenhouse) - Field visit to 'Pozo Sur' (watermelon growing under open field conditions) - Field visit and processing facilities of 'Procomel' (market leader in the cultivation and commercialization of melon)
THURSDAY 25	
9:00 - 13:30	**ORAL SESSION 4 – ABIOTIC AND BIOTIC STRESSES** **Chair: Menahem Edelstein** **Co-Chair: Belén Picó**
9:00 - 9:40	Keynote speaker: Daniel Leskovar, Texas A&M University, United States *G×E×M strategies for melons in water-limited environments*
9:40 - 10:20	Keynote speaker: Miguel Aranda, CEBAS-CSIC, Spain *Cucurbit viruses in the Mediterranean Basin: Old friends and new threats*
10:20 - 10:40	*S4.1 Preventing entry of pharmaceuticals (carbamazepine) into the food chain by using grafted plants* Menahem Edelstein
10:40 - 11:00	*S4.2 Approach for determination and denomination of cucurbit powdery mildew races* Ales Lebeda
11:00 - 11:30	***Coffee break***

11:30 - 11:50	*S4.3 Effectiveness and mechanism of rootstock grafting to increase cucumber salt tolerance* Yuan Huang
11:50 - 12:10	*S4.4. Effect of saline priming in Cucurbita ficifolia Bouché seeds on germination parameters and synthesis of proline* Jorge Leonardo Olave Vera
12:10 - 12:30	*S4.5 Improving Cucumber Water Stress Tolerance in Saudi Arabia by Grafting* Abdulaziz Rabeh Alharbi
12:30 - 12:50	*S4.6 Host plant resistance in melon (Cucumis melo L.) to sweetpotato whitefly in California and Arizona* James Donald McCreight
12:50 - 13:10	*S4.7 Transmission efficiency of Cucumber Green Mottle Mosaic Virus via seeds, soil, pruning and irrigation water* Gu Qinsheng
13:10 - 13:30	*S4.8 Determination of Drought Tolerance Levels of Some Melon Genotypes Via Physiological Methods* Ozer Ayse
13:30 - 15:30	**Lunch**
15:30 - 19:20	**ORAL SESSION 5 – FRUIT QUALITY AND POST-HARVEST** **Chair: Harry S. Paris** **Co-Chair: Nebahat Sari**
15:30 - 16:10	Keynote speaker: Jordi García-Más, CRAG, Spain *Application of genetic and genomic tools for the characterization of valuable agronomic traits in melon*
16:10 - 16:50	Keynote speaker: Antonio Monforte, IBMCP, Spain *The genetic control of fruit morphology in Cucumis melo L.*
16:50 - 17:10	*S5.1 Effects of pasteurization and storage time on watermelon juice quality enriched with L-citrulline* Encarna Aguayo

17:10 - 17:30	*S5.2 Molecular and biochemical mechanisms for the formation of aroma volatiles in cucurbit fruit* Efraim Lewinsohn
17:30 - 18:00	***Refreshment break***
18:00 - 18:20	*S5.3 Physicochemical characteristics of twelve pumpkin varieties grown in UK* Marcin Glowacz
18:20 - 18:40	*S5.4 Variation in glucose, α- and β-carotene and lutein content during storage time in winter squash "type butternut"* Fernanda Isabel Zaccari Veiga
18:40 - 19:00	S5.5 *Uv-C Light Preserves Quality Of Minimally Processed Watermelon Cylinders* Perla Gómez Di Marco
19:00 - 19:20	S5.6 *Butternut squash fruit Cucurbita moschata Duch. conditioning by saline silage* Sanin Ortiz Grisales
19:20	ISHS Business Meeting
21:00	Gala Dinner
FRIDAY 26	
9:00 - 12:30	**TECHNICAL WORKSHOP 'NEW TENDENCIES IN VEGETABLE GRAFTING' (*)** Organizer: Juan Carlos Gázquez Garrido, Estación Experimental de Cajamar Las Palmerillas
9:00 - 9:10	Introduction
9:10 - 9:40	*ROOTOPOWER: Past, present and future in the field of rootstock research* Francisco Pérez-Alfocea, CEBAS-CSIC

9:40 - 10:15	***Section I. Latest developments of grafting techniques*** El Plantel Nursery. David Sánchez Lorden Natural Green Nursery. Miguel Ángel Zorrilla Lozano
10:00 - 10:15	Discussion
10:15 - 10:45	Coffee break
10:45 - 12:30	***Section II. Cucurbitaceae and Solanaceae rootstocks***
10:45 - 11:00	*Present situation and future perspectives in Cucurbitaceae rootstocks* Alfonso Giner Martorell, Fundación Cajamar Comunidad Valenciana
11:00 - 11:30	*Present situation and future perspectives in Solanaceae rootstocks* Alfredo Lacasa Plasencia, IMIDA
11:30 - 12:10	Main views from different private companies • Monsanto / Toon Van de Ven • Syngenta / Luis Ortega Fernández • Intersemillas / Claudio Vidal • Procomel / Juan Peñalver Pardo
12:10 - 12:30	**Discussion**
	Closing
	(*) Simultaneous interpreting English↔Spanish will be provided
12:30 - 12:45	Concluding Remarks and Symposium Closing Convener: Francisco Pérez-Alfocea. CEBAS-CSIC, Spain
13:00 - 16:00	Melon tasting in Torre Pacheco under the auspices of the City Hall of Torre Pacheco and lunch offered by the Organizing Committee

KEYNOTE PRESENTATIONS

Unraveling genetic factors that underlie melon fruit quality traits using next-generation-sequencing-based QTL mapping
Nurit Katzir

Global challenges for the future of watermelon breeding
Emilio Sarria Villada

Genomics of watermelon
Zhangjun Fei

The genome of Cucurbita pepo, a tool for breeders
José Blanca

Cucumber Applied Genomics: Where We Are Five Years After Release of Cucumber Draft Genome
Yiqun Weng

Agronomic traits regulated by ethylene in zucchini squash: from sex determination to postharvest quality of fruit
Manuel Jamilena

G×E×M strategies for melons in water-limited environments
Daniel Leskovar

Cucurbit viruses in the Mediterranean Basin: Old friends and new threats
Miguel Aranda

Application of genetic and genomic tools for the characterization of valuable agronomic traits in melon
Jordi García-Mas

The genetic control of fruit morphology in Cucumis melo L.
Antonio Monforte

Unraveling genetic factors that underlie melon fruit quality traits using next-generation-sequencing-based QTL mapping

Vitaly Portnoy[1], Navot Galpaz[1], Galil Tzuri[1], Itay Gonda[1], Zhangjun Fei[2], Omer Barad[3], Merav Kenigswald[1], Shery Lev[1], Rotem Harel-Beja[1], Adi Doron-Faigenboim[4], Einat Bar[1], Uzi Saar, Yimin Xu[2], Nadia Lombardi[2], Linyong Mao[2], Chen Jiao[2], Guy Kol[2], Ya'akov Tadmor[1], Yosef Burger[1], Efraim Lewinsohn[1], Arthur Schaffer[4], James Giovannoni[2], Nurit Katzir[1]

[1]Department of Vegetable Research, ARO, Newe Ya'ar Research Center, Ramat Yishay 30095, Israel; [2]Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, NY 14853, USA; [3]NRGENE, 3 Golda Meir St. Park HaMada, Ness Ziona 7403648, Israel; [4]Department of Vegetable Research, ARO, Volcani Center, Bet Dagan 50250, Israel

Fruit quality is determined by taste, aroma, color, texture, nutritional value and shelf life. Single-gene resolution QTL mapping was achieved in two projects aiming at the identification of the genetic factors affecting the metabolic pathways that underlie fruit quality traits in melon (*Cucumis melo* L.). In both projects we used next generation sequencing (NGS) coupled with unique genetic materials to attain ultra-high resolution mapping. The first project was based on the transcriptome analyses of 79 Recombinant Inbred Lines (RIL) of a melon population derived from a cross between PI414723 and 'Dulce'. The second project was based on genotyping by sequencing (GBS) analyses of 140 F_3 plants of the 'Noy Amid' x 'Dulce' population. Genotyping in both projects was conducted using *ca*. 60,000 SNP markers. Phenotyping and metabolic profiling included over 100 fruit quality trait descriptors of taste, aroma, color and appearance in the first project, while ethylene and formation of the abscission zone were the focus of the second project. QTLs for fruit pH, fruit length, flesh color and volatile levels were located to within 1-9 genes of the causative genes that underlie them. This clearly demonstrates the high resolution and accuracy of the mapping strategy. Novel candidate genes that control fruit aroma, color and ethylene emission were identified and functionally or genetically analyzed. The NGS-based QTL mapping at single-gene resolution, using relatively small-size populations, highlights the potential of this approach for one-step gene cloning and precise marker-assisted breeding.

Key words: *Cucumis melo*, RIL population, RNA-seq

Global challenges for the future of watermelon breeding

Emilio Sarria Villada

Prebreeder Watermelon. Rijk Zwaan Ibérica SA

The world’s population is forecast to grow by 75 million people each year until 2050. One of the most important challenges for the coming decades will be to feed the world’s population. Depending on the predictions, food production has to double or triple in the next decades. This international trend demands significant investments in plant research, plant breeding, as well as plant production sectors.

The increase of arable land surface seems to be the easiest solution. However, the best agricultural lands are already in use and water resources will be limited in the future. Under this scenario, the new watermelon varieties should perform under poor soil conditions due to the increase of their tolerance to abiotic stresses like drought, salinity or extreme temperature ranges.

The incidence of pathogens and pests has noticeably evolved in recent years. Globalization has increased threats from new transboundary pests and diseases. Watermelon production areas face similar phytosanitary problems, and growers need to handle with the incidence of anthracnose, powdery mildew, fusarium, among other diseases, and pests such as aphids, spider mites and whiteflies.

Watermelon fruit quality is essential for consumers and it is a key trait for the watermelon breeding programs. Sugar content, flesh firmness and the characteristic aroma and flavour have to be improved in modern varieties. Fruit quality should be stable even when watermelon consumption areas are far away from the production areas.

In addition, consumption habits are continuously changing, together with the population structure and lifestyle. Some of the most crucial changes are the fast ageing of the population, the reduction of the household size and the lack of time for food’s preparation. All these trends are influencing the watermelon market not only by promoting the consumers’ preference for smaller watermelon fruits, but also for the increase of fresh-cut market.

Key words: pest, disease, fruit quality.

Genomics of watermelon

Zhangjun Fei[1,2], Honghe Sun[1,3], Linyong Mao[1], Yi Zheng[1], Chen Jiao[1], Pat Wechter[4], Kai-shu Ling[4], Yaakov Tadmor[5], Nurit Katzir[5], Umesh Reddy[6], Padma Nimmakayala[6], Shaogui Guo[3], Amnon Levi[4], Yong Xu[3]

[1] Boyce Thompson Institute, Cornell University, Ithaca, NY 14853, USA
[2] USDA Robert W. Holley Center for Agriculture and Health, Ithaca, NY 14853, USA
[3] National Engineering Research Center for Vegetables, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China.
[4] USDA, ARS, U.S. Vegetable Laboratory, 2700 Savannah Highway, Charleston, SC 29414, USA
[5] Department of Vegetable Research, Agricultural Research Organization,
Newe Ya'ar Research Center, Ramat Yishay, 30095, Israel
[6] Department of Biology, West Virginia State University, Institute, WV 25112, USA

Abstract. Watermelon, *Citrullus lanatus* subsp. *vulgaris*, is an important and valuable vegetable crop throughout the world. Genomic resources of watermelon have been generated during the past several years. *De novo* assembly and analysis of the genome of an East Asian ecotype, 97103, have provided valuable information regarding watermelon genome content and structure, and illustrated an evolutionary scenario for the origin of the eleven watermelon chromosomes that were derived from a seven-chromosome paleohexaploid eudicot ancestor. The genomes of an American ecotype, Charleston Gray, and a wild watermelon (*C. lanatus* subsp. *lanatus*), PI 296341-FR, were also *de novo* assembled recently in very high quality. Comparative analysis of these genomes identified sequence changes in genes that are related to several important agricultural traits such as defense response and fruit quality. Finally, the genomes of 20 watermelon accessions representing three different *C. lanatus* subspecies, *C. lanatus* subsp. *lanatus*, *C. lanatus* subsp. *mucosospermus*, and *C. lanatus* subsp. *vulgaris,* were resequenced. Analysis of this resequencing dataset identified a large number of sequence polymorphisms and revealed the extent of genetic diversity and the population structure of watermelon germplasm. Genomic regions that were preferentially selected during domestication were identified and they were enriched with genes known to be related to important selected traits. Many disease resistance genes were found to be lost during domestication. All together, these genome sequences have helped us to better understand the watermelon genome evolution and domestication, and provide a valuable resource with great potential for genome manipulation, trait discovery and allele mining.

Keywords: watermelon, genome, evolution, domestication, comparative genomics

The genome of Cucurbita pepo, a tool for breeders

Jose Blanca[1], Javier Montero Pau[1], Cristina Esteras[1], Peio Ziarsolo[1],
Aureliano Bombarely[3], Lukas Muller[3], Carlos Martí[1], Cristina Roig[1],
Antonio Monforte[2], Pedro Gómez4[4], Manuel Jamilena[4],
Joaquín Cañizares[1] y Belén Picó[1]

[1] COMAV, UPV, 46022, Camino de Vera s/n-Valencia, Spain
[2] IMBCP-CSIC, 46022, Camino de Vera s/n-Valencia, Spain
[3] Boyce Thompson Institute, 533 Tower Road, Ithaca, New York 14853-1801, U.S.A.
[4] Universidad de Almería, Carretera de Sacramento s/n, 04120, Almería, Almeria, Spain

Next Generation Sequencing technologies are revolutionary tools that for the plant breeders are both an opportunity and a challenge. These technologies have been applied to develop genomic tools for the the Cucurbita community. In C. pepo the transciptome was assembled and used as a reference to look for SNPs that formed the basis of a genetic map in a F2 of C. pepo subsp. pepo. In this map several QTLs were mapped. In the next phase, a high quality zucchini genome has been assembled, from Illumina reads, resulting in 263 Mb assembled with an N50 of 1,73 Mb.

Both the genome and the transciptome are available at cucurbigene.net. The genome has been anchored to a genetic map of 9350 markers generated from a F8 RIL population in a GBS genotyping. This genomic effort is coordinated with the sequencing of the C. maxima and C. moschata genomes by other groups. To complement the static view of the genome, genomic sequences of 60 selected C. pepo varieties has been produced by GBS. Also the transciptome of 96 Cucurbita accessions, representing the variation of the five cultivated species (C.pepo, C.maxima, C.moschata, C.argyrosperma, and C.ficifolia) and most of the wild types of the genus has been sequenced and its variation analysed. These genomic tools provide a valuable insight into the Cucurbita genetic variation and can be used as extremely valuable tools by the Cucurbita breeders.

Key words: genome, Cucurbita pepo, genetic map, GBS

Cucumber Applied Genomics: Where We Are Five Years After Release of Cucumber Draft Genome

Yiqun Weng

USDA-ARS, Vegetable Crops Research Unit, Horticultural Department,
University of Wisconsin, Madison, WI 53706, USA

The first cucumber draft genome (North China fresh market type inbred line 9930) was released in 2009 (Version 1.0). Since then, due to the use of next generation sequencing technologies, seven high-density SSR- or SNP-based cucumber genetic maps have been constructed with mapped loci ranging from 700 to more than 12,000, which have helped improve the Gy14 (North American pickling cucumber) and 9930 draft genome assemblies. The current Gy14 assembly (V1.5) contains 198.2 Mbp covering ~54% of the 367 Mbp cucumber genome. The genome sequences and molecular markers have greatly facilitated molecular mapping and gene cloning in cucumber. Approximately 50 simply inherited genes have been molecularly tagged and several have been cloned. Many QTLs for horticulturally or evolutionarily important traits have also been identified. Molecular marker-based phylogenetic studies have provided new insights into the genetic diversity and population structural of worldwide cucumber collections. Comparative analysis has established syntenic relationships at both chromosomal and DNA sequence levels among cucumber and its relatives, which has increased our understanding of chromosome evolution in the genus *Cucumis*. This knowledge will help more efficient introgression of alien chromatins from cucumber relatives into cucumber. While these rapidly accumulating genetic and genomics resources provide powerful tools for accelerating classical cucumber breeding, to maximize of power of applied genomics in cucumber improvement, we need to develop a better draft genome assembly and improve the genome annotation. We need more mutants through mutagenesis to understand gene functions, and develop efficient functional genomics tools (for example, genetic transformation, virus-induced gene silencing etc.) for function validation of candidate genes.

Key words: cucumber, applied genomics, genetic mapping, physical mapping, molecular markers

Agronomic traits regulated by ethylene in zucchini squash: from sex determination to postharvest quality of fruit

Manuel Jamilena

Agrifood Campus of International Excellence (CeiA3) and Research Center in Agri-food Biotechnology (BITAL). Department of Biology and Geology. University of Almería, La Cañada de San Urbano s/n. 04120 Almería, Spain.

Ethylene is a gaseous plant hormone that regulates many agronomic traits in zucchini and other cucurbit crops, including sex expression and sex determination, fruit set, parthenocarpy and early fruit development, as well as ripening and postharvest fruit performance. In plant cells ethylene is synthesized from S-adenosylmethionine in two simple steps regulated by ACS and ACO enzymes, both encoded by multigenic families. Ethylene is perceived by a set of receptors, which, bound to the hormone, are able to initiate a signaling cascade that results in the induction of ethylene regulated genes. Both ethylene receptors and some signaling factors are negative regulators of ethylene action, and many of them are also members of multigenic families with redundant functions. Our group has identified and characterized many of the genes involved in the biosynthesis, perception and signaling of ethylene in zucchini squash. The ability to assess ethylene production and sensitivity in different plant organs at diverse stages of development, and the availability of molecular tools and mutants for ethylene production and sensitivity, has allowed the role of this hormone in different development processes to be studied. It has been demonstrated that the induction of female flowering in squash is regulated by the induction of ethylene biosynthesis but also by a downregulation of the ethylene negative regulators *CpETRs* and *CpCTRs* in the apical shoot and floral meristems. The andromonoecious phenotype in squash is not only dependent on a single mutation in the ethylene biosyntheis gene *CpACS27,* as has been observed in melon and cucumber, but also on another non-identified gene. The stability of monoecy in squash and other cucurbits is also regulated by more than one gene. The analysis of ethylene production and gene expression in ovary/fruits of parthneocarpic and non parthenocarpic zucchini genotypes indicated that ethylene regulates fruit set and parthenocarpy in squash and that the abortion of unpollinated fruits in non-parthenocarpic varieties was always concomitant with a peak of ethylene production at 3 days post-anthesis, which may be used as a selection criterion for parthenocarpy. Lastly, during the post-harvest storage of fruit, ethylene and ethylene genes are induced concomitantly with the development of postharvest chilling injury (PCI). In fact, in the most cold tolerant varieties, and under treatments that alleviate PCI, fruit reduces ethylene production and the expression of ethylene biosynthesis and signaling genes.

Key words: ethylene biosynthesis and signalling genes, sex determination, sex expression, fruit set, parthenocarpy, postharvest chilling injury

G×E×M strategies for melons in water-limited environments

Daniel I. Leskovar, Sat Pal Sharma, Kevin Crosby, Astrid Volder

Texas A&M AgriLife Research, Texas A&M University, Uvalde, TX 78801, USA

Open field irrigated agriculture in arid to semiarid regions of the world is seriously affected by frequent and severe droughts, limited water resources, and increased regulations restricting surface and underground water use. Integrated strategies for melon (*Cucumis melo* L.**)** production can be applied to increase water savings without reducing marketable yields and product quality. These include selecting high-efficiency irrigation systems, allowing plants to experience water stress to a degree that does not impact profit levels, choosing cultivars with drought tolerance, and growing them in adapted environments. A series of experiments were conducted to investigate the impact of multiple environments with different soil types and climatic conditions, and deficit irrigation strategies (50% crop evapotranspiration, ET_c) on melon genotypes. Studies examined leaf gas exchange, root and shoot growth, yield stability, quality and water productivity responses of three melon cultivars, Mission (cantaloupe; *reticulatus* type), Da Vinci (Tuscan; *reticulatus* type) and Super Nectar (honeydew; *inodorus* type). Genotypic evaluations for yield stability and component traits were conducted in three distinctive Texas locations. Mission was the most stable and average performing cultivar for marketable yield across all environments. The late maturing cv. Super Nectar was more sensitive to drought stress possibly due to a decrease in leaf area and photosynthetic rates; while early maturing cvs. Mission and Da Vinci escaped severe water deficit, and sustained leaf water status through improved root growth and leaf gas exchange adjustments. This presentation will also discuss the potential trait associations between yield, root length intensity, leaf area, and photosynthetic rates of melon cultivars grown under deficit irrigation.

Key words: crop evapotranspiration, deficit irrigation, leaf gas exchange, minirhizotron, root depth, water use efficiency

Cucurbit viruses in the Mediterranean Basin: Old friends and new threats

Miguel Juárez[1], Mona A. Kassem[2], Blanca Gosalvez[2],
Pedro Gómez[2], Manuel Miras[2], Miguel A. Aranda[2]

[1]Universidad Miguel Hernández, E-03312-Orihuela, Alicante, Spain
[2]Plant Pathology Group, CEBAS-CSIC, E-30100-Murcia, Spain

Virus-induced diseases cause major economic losses in many crops, including cucurbits. Based on our surveys in Southeaster Spain carried regularly since 2000, the predominant virus in cucurbit open-field crops is the polerovirus *Cucurbit aphid-borne yellows virus* (CABYV), which is ubiquitous and can be detected with very high frequencies in plants showing yellowing symptoms. Potyviruses like *Watermelon mosaic virus* (WMV) and *Papaya ringspot virus* (PRSV) followed CABYV in importance. In greenhouse crops or in open areas with large whitefly populations, *Cucurbit yellow stunting disorder virus* (CYSDV, genus *Crinivirus*) and *Cucumber vein yellowing virus* (CVYV, genus *Ipomovirus*) are widespread and cause significant problems. Available information suggests that the epidemiological situation in other Mediterranean countries is essentially similar, with local differences on the prevalence and, to a lesser extent, species composition of viral populations. However, it appears that the greatest threats for cucurbits production come from the introduction of new viruses or the evolution of current ones. Very clear examples found in our work are the recent identification in Spain of *Moroccan watermelon mosaic virus* (MWMV, genus *Potyvirus*) and *Tomato leaf curl New Delhi virus* (ToLCNDV, genus *Begomovirus*) affecting severely cucurbit crops, and the substitution of "classical" types of WMV for "emerging" types.

Key words: virus, disease, evolution, CABYV, CYSDV, potyvirus, begomovirus

Application of genetic and genomic tools for the characterization of valuable agronomic traits in melon

Jordi Garcia-Mas

IRTA, Centre for Research in Agricultural Genomics CSIC-IRTA-UAB-UB,
08193-Barcelona, Spain

Melon has become an interesting model for the study of fruit ripening, sex determination and phloem transport, among other important processes. The availability of the sequence of the melon genome together with several genetic and genomic resources provides useful tools to assist in melon breeding programs. We have combined the use of a melon near isogenic line (NIL) population and genomic resources to gain insight into important traits such as climacteric fruit ripening, resistance to *Cucumber Mosaic virus* (CMV) and the accumulation of sugars in fruits. An overview will be presented on the status of the characterization and cloning of some QTLs involved in the control of these traits.

Keywords: Cucumis melo, near isogenic line, sugar content, climacteric ripening, Cucumber mosaic virus, fruit quality

The genetic control of fruit morphology in *Cucumis melo* L.

Antonio José Monforte

Instituto de Biología Molecular y Celular De Plantas (IBMCP)
UVP-CSIC Ingeniero Fausto Elio S/N, 46022 Valencia, Spain

Wild melons can be found in both African and Asian continents. Typical wild melon fruit are very small (30-50 g), round or oval and without edible flesh. After domestication, melon varieties were develop after intensive diversification resulting in an impressive range of fruit morphology variability, ranging from the tens of grams of wild melons to several kilograms, and the shape may be round, oblate, ovate, elliptical to extremely elongated. By comparing several mapping studies, we hypothesize that specific regions on chromosomes I, II, III, VIII and XI that harbour the genes that may explain the phenotypic diversity found in melon germplasm. Melon members of the gene families of the tomato Quantitative Trait Loci (QTL) FASCIATED (YABBY family), CNR/FW2.2 (Cell Number Regulator family) SlKLUH/ FW3.2 (cytochrome P450 of the 78A class family), and LOCULE NUMBER (WOX family) and OVATE (Ovate family proteins, OFP), and SUN (IQ domain family) were identified in the melon genome, and their co-localization with major melon fruit morphology QTLs was investigated. QTLs for fruit weight co-localized frequently with members of the CNR/FW2.2 and KLUH/FW3.2 families, whereas members of OFP family members did it with fruit-shape QTLs. Thus, those three gene families are strong candidates to be responsible of the melon fruit morphology diversity.

Key words: QTL, comparative genomics, fruit shape, fruit weight, domestication

SESSIONS

GENETICS AND BREEDING 01

GENOMICS AND BIOTECHNOLOGY 02

CROP PRODUCTION, PHYSIOLOGY AND MANAGEMENT 03

BIOTIC STRESSES AND ABIOTIC STRESSES 04

FRUIT QUALITY AND POST-HARVEST 05

Oral Sessions

GENETICS AND BREEDING

01

S1. GENETICS AND BREEDING

S1.1 **Tadmor, Yaakov**

Revealing the identity of the watermelon ‘Y’ locus

S1.2 **Roni Cohen**

Cucurbita rootstocks : From random crosses to rational breeding

S1.3 **Wenge, Liu**

Lycopene biosynthesis key genes expression and related hormone in different ploidy watermelon

S1.4 **Zhilong Bie**

Appraisals on the utility of pumpkin cross combinations as the rootstocks of grafted melon

S1.5 **Paris, Harry S.**

Origin Of The Dessert Watermelon, *Citrullus Lanatus*

S1.6 **Dhillon, Narinder, P.S.**

Status of bitter gourd breeding at AVRDC - The World Vegetable Center

S1.7 **Zhang Shengping**

Molecular Mapping and Candidate Gene Analysis for Numerous Spines on the Fruit of Cucumber

S1.1

Revealing the identity of the watermelon ‘Y’ locus

Yuval Sa’ar, Ayala Meir, Uzi Sa’ar, Fabián Baumkoler, Shachar Ohali, Galil Tzuri, Arthur, A., Schaffer[1], Efraim Lewinsohn, Nurit Katzir, Vitaly Portnoy, Joseph Burger and Ya'akov Tadmor

Cucurbit section, Newe Yaar Research Center, ARO, Ramat Yishay, Israel
[1] - Volcani Center, ARO, Rishon LeZion, Israel

Mutations of the *CRTISO* gene in several plant species cause the accumulation of pro-lycopene and are associated with deleterious pleiotropic effects. Orange and salmon yellow watermelons accumulate pro-lycopene as their major pigment without any visual effects on plant performance or on etiolated plantlets color. Previous genetic studies indicated that the ‘Y’ locus has three alleles: ‘Y’ (red flesh), which is dominant to ‘y^o’ (orange flesh) that is dominant to ‘y’ (salmon yellow flesh). We used RNA-Seq of developing fruit of red, orange and salmon yellow flesh color to identify a unique SNP in the 3’ region of watermelon’s CRTISO gene. This SNP caused the alteration of a highly conserved leucine of the alpha helix motif at the C-terminus of the CRTISO protein. This amino acid alteration bends the alpha helix causing an inactivation of pro-lycopene isomerization in fruit chromoplasts in a specific manner. Both orange and salmon yellow fruit carry the same allele indicating that ‘Y’ locus has only two alleles and the intensity difference between orange and salmon yellow is governed by additional loci. We used the watermelon’s CRTISO SNP to develop a reliable DNA marker for fruit coloration. The identified SNP can serve to generate pro-lycopene accumulating fruit in various species via genome editing, without the pleotropic effects related to all other known CRTISO mutations.

Key words: watermelon, flesh color, carotenoids, carotenoid isomerase, pro-lycopene

S1.2

Cucurbita rootstocks: From random crosses to rational breeding

Roni Cohen[1], Menahem Edelstein[1] Rita Grosch[2] and Dietmar Schwarz[2]

[1]Department of Vegetable Crops, Agricultural Research Organization,
Newe Ya'ar Research Center, Ramat Yishay 30-095, Israel.
[2] Leibniz Institute for Vegetable and Ornamental Crops, Theodor Echtermeyer Weg 1,
14979 Großbeeren, Germany

Cucurbits can be grafted onto rootstocks from the same species or on rootstocks from another cucurbit species. Most of the commercial cucurbits, however, are being grafted on inter-specific *Cucurbita* rootstocks produced mainly by crossings between *C. maxima* and *C. moschata*. The reason for using the inter-specific rootstocks is not clear. The non-proved paradigm is that such rootstocks will be more vigorous, resulting in better yields and high-level resistances. On one hand, this is what the breeding companies claim and what they basically test. On the other hand, seed yields and quality of such inter-specific crosses are low, thus making seed production not efficient.

In the current study, we evaluated the response of melon grafted onto 15 *Cucurbita* rootstocks, under field and greenhouse conditions, to various root temperatures and to soil-borne pathogens. The rootstock collection used consisted of five hybrids and their respective *C. maxima* and *C. moschata* parents, enabling comparing the contribution of the parents to the performance of their respective inter-specific hybrids.

The results showed that, in most cases, there was no advantage of the inter-specific rootstocks over one or both of their respective parents. Using parental accessions or intraspecific *Cucurbita* hybrids, selected to answer defined obstacles in a particular growing environment, may lead to more precise and economical rootstock breeding.

S1.3

Lycopene biosynthesis key genes expression and related hormone in different ploidy watermelon

Dou Jun-Ling, Liu Wen-Ge*, Zhao Sheng-Jie, Lu Xu-Qiang, He Nan,
Zhu Hong-Ju, Gao Lei

Zhengzhou Fruit Research Institute, CAAS, Zhengzhou, Henan, China, 450009

In order to analysis the correlations between lycopene accumulation and biosynthesis genes expression in different ploidy and flesh color watermelon fruit, lycopene contents and expression of five key genes (PSY, PDS, ZDS, CRTISO, LCYb) during watermelon fruit development were measured. In the same time, the differences between genes expression and hormones(GA, ABA) in roots, stems, leaves of different ploidy watermelon was researched. The main results are as follows:

1. The content of lycopene was increased rapidly at 25d in fruit after pollination.The lycopene content was higher in autotriploid than in diploid or autotetraploid.

2., the expression of PSY in five genes was the highest in fruit whole growth period. The expression of LCYb in red flesh watermelon was the lowest in all genes, especially at 25d after pollination, while its expression in the yellow flesh watermelon was lower than that of PSY, this suggests the importance of LCYb in color control and lycopene synthesis.

3. The highest expression of all five genes in the root, stem and leaf were almost appeared on flowering period. And only the PSY expression in diploid was higher than polyploidy, the expression of other genes in diploid was lower than polyploidy.

4. The GA content was showed the trend of ‘increase-decrease’ in the whole period, and the negatively correlation with the lycopene. There was the positively correlation between ABA and lycopene in diploid watermelon, and not the tendency in polyploidy watermelon.

Key words: watermelon, lycopene, polyploidy, gene expression, endogenous hormone

S1.4

Appraisals on the utility of pumpkin cross combinations as the rootstocks of grafted melon

Yong Liu, Qiusheng Kong, Zhilong Bie*

College of Horticulture and Forestry Sciences, Huazhong Agricultural University/Key
Laboratory of Horticultural Plant Biology, Ministry of Education, Wuhan, P R China
*Email: biezhilong@hotmail.com

Melon (*Cucumis melo*. L) is one of the most important horticultural crops in terms of its planting scale and economic value on the world. Grafting is an efficient method to overcome the obstacle caused by soil-borne diseases in melon production. However, majority of the rootstocks were found to have negative effects on the fruit quality of grafted melon, which greatly limited the utilization of grafted melon in melon production. As a result, breeding high quality rootstock varieties specifically for melon is of great importance in commercial melon production. In this study, we created 13 interspecific hybrids of *C. maxima* and *C. moschata* and 12 intraspecific hybrids of *C. moschata.* The widely cultivated melon cultivar *Elizabeth* was used as scion, two popular commercial rootstock varieties of melon were used as the controls, and the non-grafted *Elizabeth* plants were also included to evaluate the grafting on melon performances. We measured the yield and fruit quality of grafted melon plants, as well as the hypocotyl thickness and length of the cross combinations and their tolerances to low temperature. After two years' appraisals, we selected three combinations, namely, B11 (*C. maxima* × *C. moschata*), B21 (*C. moschata* × *C. moschata*), and B24 (*C. moschata* × *C. moschata*), which had better comprehensive performance than the controls and non-grafted melon. This study not only provided better rootstocks for grafted melon production, but also highlighted the important role of pumpkin in the rootstock breeding specific for melon.

Keywords: melon, grafting, pumpkin, rootstock, breeding

S1.5

ORIGIN OF THE DESSERT WATERMELON, *CITRULLUS LANATUS*

Harry S. Paris

Agricultural Research Organization, Newe Ya‘ar Research Center,
P. O. Box 1021, Ramat Yishay 30-095, Israel

The dessert watermelon, *Citrullus lanatus*, is familiar and well-liked by almost everyone. However, among cucurbit genera, *Citrullus* has been the most confused etymologically and taxonomically. Moreover, its geographic origin, history, and evolution under domestication have been widely misunderstood. *Citrullus*, in northern medieval Latin, designated watermelon but is itself a diminuitive of *citrium*, a word which appears in a recipe from the 4th-century Latin cookbook of Apicius and designated the citron watermelon. The word *citrullus* was actually first used in southern Latin, designating a then new arrival to Europe, the much smaller but green-skinned cucumber (*Cucumis sativus* L.), modern Italian *cetriolo*. The colocynth of northern Africa, the citron watermelon of southern Africa and, more recently, the egusi watermelon of western Africa, have variously been considered as ancestors of the dessert watermelon. However, crosses of dessert watermelons with colocynths result in progenies with markedly lower fertility, with citrons have massive preferential segregation, and with egusis succeed only in one direction, suggesting that each of these constitutes a separate species. On the other hand, wild watermelons have repeatedly been encountered in Sudan, especially along the Nile River and its major tributaries. Moreover, seeds and images of *C. lanatus* have been found in tombs of ancient Egyptian royalty. Jewish instructional codices indicate that sweet dessert watermelons were common in Israel during Roman times. *C. lanatus* was therefore very likely first domesticated and cultivated in northeastern Africa and selection for sweetness succeeded by no later than the second century CE.

Keywords: *Citrullus lanatus*, evolution under domestication, geographic origin, Mishna, Sudan, watermelon

S1.6

Status of bitter gourd breeding at AVRDC – The World Vegetable Center

Narinder P.S. Dhillon[1], Supannika Sanguansil[1],
Ray-Yu Yang[2], Peter Hanson[2]

[1] AVRDC – The World Vegetable Center, East and Southeast Asia, Bangkok, Thailand
[2] AVRDC – The World Vegetable Center, Shanhua, Taiwan

Bitter gourd (*Momordica charantia* L.) is an economically and nutritionally important vegetable in South and Southeast Asia. AVRDC – The World Vegetable Center's bitter gourd breeding program began in 2010 to develop improved cultivars that meet the needs of growers and consumers. Breeding targeted development of high yielding open-pollinated lines with superior fruit quality and high concentrations of antidiabetic compounds, disease and insect resistance, early maturity, and capacity to set fruit under high temperatures. The breeding approach was to build and select within a genetically superior and broad-based germplasm base derived from elite commercial cultivars and diverse disease-resistant AVRDC genebank accessions. Eight improved lines of bitter gourd with yields and fruit quality comparable to commercial hybrids were distributed to the breeders in private and public sector for incorporation into their breeding programs in 2014. Lines resistant to powdery mildew (*Podosphaera xanthii*) were developed and tested successfully in multi-country trials in Asia; lines resistant to leaf spot (*Cercospora* spp., *Alternaria* spp.) and anthracnose (*Colletotrichum* spp.) have been identified. Two cycles of recurrent selection have been carried out in populations segmented by major fruit market types and created by crossing unrelated bitter gourd cultivars and genebank accessions followed by selection for high yield, fruit quality and disease resistance. A research project funded by BMZ (Federal Ministry for Economic Cooperation and Development) Germany led to the identification of bitter gourd lines with high and stable concentrations of antidiabetic compounds and an assessment of the contribution of these antidiabetic effects to human health where bitter gourd is eaten as part of a balanced diet.

Key words: *Momordica charantia*, breeding, disease resistance, phytonutrient

S1.7

Molecular Mapping and Candidate Gene Analysis for Numerous Spines on the Fruit of Cucumber

Sheng-ping Zhang[1,3] · Shu-lin Liu[1,3] · Han Miao[1] · Min Wang[1]·
Pan-na Liu[1] · Todd C. Wehner [2,*]· Xingfang Gu[1,*]

[1] Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences,
Beijing 100081
[2]Department of Horticultural Science, North Carolina State University, Raleigh,
NC 27695-7609, USA
[3] These authors contributed equally to this work.
[*] Correspondence author, with e-mail: guxingfang@caas.cn, and todd_wehner@ncsu.edu

Number of spines on the fruit is an important quality trait in cucumber. The inheritance and identification of molecular markers for fruit spine density gene will provide a basis for breeding and lay the foundation for gene cloning. Cucumber inbred lines NCG-122 with numerous spines and NCG-121 with few spines were used for genetic analysis and gene mapping in this study. Genetic analysis showed that numerous spines in NCG-122 was qualitative, and a single recessive nuclear gene (*ns*) controlled this trait. Few spines was dominant to numerous spines. In the preliminary genetic mapping of the *ns* gene, eight SSR markers were found to be linked to *ns* which was mapped to chromosome 2 (Chr.2) of cucumber. The closest flanking markers SSR22338 and SSR11596 were linked to the *ns* gene with genetic distances of 10.2 and 1.7cM, respectively. 130 pairs of new SSR primers and 28 pairs of Indel primers were developed based on the sequence information in the preliminary mapping region of *ns*. Fifteen SSR markers and two Indel markers were identified to be linked to the *ns* gene after analysis on the F_2 mapping population using the new molecular markers. The two closest flanking markers, SSRns-127 and SSR04219, were 0.7 and 2.4 cM from *ns*, respectively. The physical distance between SSRns-127 and SSR04219 was 266.1Kb containing 27 predicted genes. Csa2G285390 was speculated as the probable candidate gene for numerous spines. The accuracy of the closest linked marker to the *ns* gene, SSRns-127, for MAS breeding was 95.0%.

Keywords *Cucumis sativus* L.; numerous fruit spines; SSR marker; Indel marker; gene mapping

Oral Sessions

02

GENOMICS AND BIOTECHNOLOGY

S2. GENOMICS AND BIOTECHNOLOGY

S2.1 Amnon Levi

Development of ZYMV-Resistant Watermelon Lines Using Genomic Tools

S2.2 Rafael Perl Treves

Plant-pathogen interactions controlled by the *Fom-1-Prv* locus of melon

S2.3 Dogimont Catherine

Functional analysis of *Mlo* genes in powdery mildew resistance in melon

S2.4 Nebahat Sari

Effects of Genotypes and Irradiation Doses on Haploid Embryo Induction and Plant Production in Bottle Guard [Lagenaria siceraria (Malign) Stanley]

S2.1

Development of ZYMV-Resistant Watermelon Lines Using Genomic Tools

Amnon Levi and Kai-shu Ling

USDA, ARS, U.S. Vegetable Laboratory, 2700 Savannah Highway,
Charleston, South Carolina 29414

The aphid-transmitted potyviruses of watermelon, including papaya ringspot virus (PRSV), watermelon mosaic virus (WMV), and zucchini yellow mosaic virus (ZYMV) cause serious damage to watermelon crops throughout the world. The United States Plant Introduction (PI) 595203 is resistant to ZYMV-FL and ZYMV-CH and the resistance is conferred by a single recessive gene. In a previous study, we identified the eukaryotic elongation factor eIF4E allele of PI 595203 as closely associated with ZYMV-resistance. We developed two cleaved amplified polymorphic sequences (CAPS) markers within eIF4E linked (6 cM) and a sequence characterized amplified region (SCAR) marker linked (8 cM) to the ZYMV-FL resistance gene locus. The objective of this study was to incorporate the ZYMV-resistance into watermelon cultivars using phenotyping and genotyping (MAS) criteria in a backcross breeding and a recurrent selection scheme. We were able to develop BC3F6 and BC4F5 watermelon breeding lines with sufficient fruit quality and ZYMV-resistance. The watermelon genome contains several gene sequence with high similarity to the eIF4e. Still, the eIF4e (watermelon sequence Cla019623) located on chromosome 3 of the watermelon genome (locus=Chr3:7767735:7770583; www.icugi.org) proved useful for incorporating ZYMV-resistance from PI 595203 into the genomic background of watermelon cultivars.

S2.2

Plant-pathogen interactions controlled by the *Fom-1-Prv* locus of melon

Golan Miller, Arie Amitzur, Michael Normantovich and Rafael Perl-Treves

Faculty of Life Sciences, Bar Ilan University, Ramat Gan 5290002, Israel

We cloned the genomic locus for melon resistance towards *Fusarium oxysporum* f.sp. *melonis* (FOM) races 0 and 1, and the papaya ring spot virus (PRSV). The adjacent *Prv* and *Fom-1* genes encode proteins of the NBL (nucleotide binding site–leucine rich repeat) family; *Prv* carries an extra NB domain, and both have alternative, differentially expressed splice variants. We report extensive allelic polymorphism in the locus, indicative of diversifying selection. The genes' expression patterns were studied using a promoter-reporter system in transgenic melon roots using the "composite plant" system. In addition, the endogenous transcripts were quantified by RT-PCR, to evaluate possible induction by the respective pathogens in resistant *vs*. susceptible melon genotypes. To characterize the melon-FOM interaction, we compared the colonization of melon genotypes by a GFP-expressing FOM strain. In susceptible melons, the fungus readily colonized the vascular tissue, while the xylem of resistant seedlings remained clean. In our quest for possible fungal proteins that could interact with Fom-2 we isolated FOM homologs of *secreted in xylem* (six) genes that, in f.sp. *lycopersici*, were encode Avr factors. Two such homologs were found, but their distribution among FOM races did not fit the "gene for gene" model. We performed a proteomic analysis of the xylem sap of melon plants that were infected with FOM-0. A total of 513 melon protein and 9 fungal proteins could be annotated against the melon and FOM genomes, respectively. Many of the melon proteins appeared to be induced by inoculation.

Key words: melon, Fusarium oxysporum, PRSV, resistance genes, proteomics

S2.3

Functional analysis of *Mlo* genes in powdery mildew resistance in melon

S. Elbelt[1], N. Giovinazzo[1], V. Sarnette[1], M. Bardin[2], C. Troadec[3], , A. Bendahmane[3], C. Dogimont[1]

[1] INRA, UR1052 Génétique et Amélioration des Fruits et Légumes, Domaine St Maurice - Allée des Chênes CS 60094, 84143 Montfavet Cedex, France
[2] INRA, UR407 Pathologie végétale, Domaine St Maurice - Allée des Chênes CS 60094, 84143 Montfavet Cedex, France
[3] INRA, UMR1165 Unité de Recherche en Génomique Végétale, 2, rue Gaston Crémieux, CP5708, 91057 Evry Cedex, France

Powdery mildew is one of the most damageable diseases in *Cucurbitaceae* crops. Two fungal species, *Podosphaera xanthii* and *Golovinomyces cichoracearum* are the main causal agents. Powdery mildews are ascomycete, obligate biotroph fungi. They thus require host plant genes for their infection cycle. These genes involved in host plant susceptibility are promising targets for powdery mildew resistance. Among them, members of the *Mlo* family are used by powdery mildews in a conserved mechanism across plant species.

In this work, we aim to investigate the function of *Mlo* genes in the interaction between melon and cucurbit powdery mildews, with the aim of creating new, broad spectrum resistance sources to these pathogens.

We identified 15 *Mlo* genes that are well conserved across the three *Cucurbitaceae* species, melon, cucumber and watermelon. Phylogenetic analysis identified 5 members as candidates for powdery mildew susceptibility. Among these genes, *CmMLo2* was shown to be highly overexpressed upon powdery mildew infection. To validate the function of the genes, we used a TILLING approach. We identified a *Cmmlo2* non sense mutant in a melon mutagenized population. This mutant exhibited a complete resistance to *G. cichoracearum* and a partial resistance to several strains of *P. xanthii.* In parallel, we carried out an allele mining approach to search for natural diversity of *CmMLO* genes in a melon collection.

In this work, we demonstrated the involvement of *Mlo* genes from melon in susceptibility to two powdery mildew species and created novel alleles of resistance, not found in the natural diversity.

Key words: *Cucumis melo*, *Golovinomyces cichoracearum, MLO, Podosphaera xanthii,* resistance, TILLING

S2.4

Effects of Genotypes and Irradiation Doses on Haploid Embryo Induction and Plant Production in Bottle Guard [*Lagenaria siceraria* (Malign) Stanley]

Pakize Gok Guler[1], Nebahat Sari[2], Mahmut Yegul[1],
Yaprak Kantoglu[3], Burak Kunter[3], Halit Yetisir[4]

[1]Plant Protection Research Institute, Ministry of Food Agriculture and Livestock, Adana-Turkey
[2]Dept. of Horticulture, Fac. of Agric., Univ. of Cukurova, Adana-Turkey
[3]Turkish Society for Atomic Energy, Eskisehir Road 9th km, Ankara-Turkey
[4]Dept. of Horticulture, Fac. of Agric., Univ. of Erciyes, Kayseri-Turkey

Cultivated *Lagenaria siceraria* (Malign) Stanley is commonly known as the white-flowered gourd. It has been grown annually and it is a monocious, vigorous climber species and five wild perennial diocious species and the fruits are generally eaten as a vegetable. The mature fruit is often scooped out and the skin used as containers, bowl, music instrument, decorative purposes or in some cases, fishing floats. Shoots, tendrils and leaves are also cooked and the seeds are removed for oil extraction or for use in cooking. Furthermore, *L. siceraria* is used as rootstocks for watermelon against soil-born diseases and adverse soil conditions. Lagenaria type rootstocks have high level graft affinity with watermelon. This study was conducted at Department of Horticulture, Faculty of Agriculture, University Cukurova and Turkish Society for Atomic Energy for obtention of Lagenaria haploids. Induction of parthenogenetic haploid embryos by pollination of irradiated pollen with different doses (50, 75, 100, 125, 150, 175 and 200 Gray gamma rays of Co^{60}) in 4 bottle gourd genotypes (Adana, Birecik, Spain and Cyprus) was investigated.

According to the results, pollination with 50 and 75 Gray doses of pollens had a positive effect on haploid embryo induction. After pollination with irradiated pollens, embryos with different shape were rescued, cultured and converted to intact plants under tissue culture conditios. The genotypes had important effect on induction of haploid embryo by irradiated pollen techniques. 75 plants from Adana genotype, 10 plants from Birecik genotype, 121 plants from Spain genotype, 141 plants from Cyprus genotype and totaly 347 plants were produced from this research.

Key Words: Irradiated pollen, pollen germination, haploid embryos, haploid plants

03

CROP PRODUCTION, PHYSIOLOGY AND MANAGEMENT

S3. CROP PRODUCTION, PHYSIOLOGY AND MANAGEMENT

S3.1 **Nascimento, Warley Marcos**

Using computerized image analysis for evaluation of squash seed quality

S3.2 **Klaering, Hans-Peter**

Decreasing the temperature in the greenhouse does not necessarily reduce the yield of cucumber

S3.3 **Juan A. Fernández**

Melon production in the Province of Murcia (SE Spain)

S3.4 **Pico, Belen**

Evaluation of two potential Cucumis spp. resources for grafting melons

S3.5 **Endah Retno Palupi**

Pollen drying and storage for hybrid seed production of cucumber (*Cucumis sativus*)

S3.6 **García, Alicia**

Isolation and characterisation of ethylene insensitive mutants from a collection of *Cucurbita pepo* L.

S3.1

Using computerized image analysis for evaluation of squash seed quality

[1,3] Warley Marcos Nascimento, [1] Patrícia Pereira da Silva,
[2,3]Júlio Marcos-Filho, [2] Francisco Guilhien Gomes Junior

[1]Embrapa Vegetables, CP 0218, 70359-970 Brasília-DF; Brazil, E-mail: warley.nascimento@embrapa.br; [2]USP/ESALQ - Depto. Produção Vegetal, Av. Pádua Dias, 11, 13418-900 Piracicaba-SP, Brazil; [3]Bolsista de Produtividade em Pesquisa, CNPq.

For some crops, such as vegetables, there are few tests standardized for seed vigor determination and this has a fundamental importance for the Brazilian seed industry growing. The objective of this study was to verify the effectiveness of a computerized image analysis of 'Brasileirinha' squash (*Cucurbita moschata*) seedling compared to the other vigor tests. Six seed lots were produced at Embrapa Vegetables, Brasília – DF, Brazil, from 2006 to 2012. Seed quality was evaluated using the Seed Vigor Imaging System (SVIS®), first count, germination, seedling emergence, cold test and accelerated aging with the use of saturated NaCl. Seed mass was also determined. The SVIS® provided data on the index of vigor, uniformity of development and growth of seedlings at three days after sowing under optimum conditions. The seed lots with high vigor through the different tests have better evaluation on SVIS®, indicating the sensitivity of SVIS® on the seed vigor. This system may be an interesting alternative to obtain reliable information about the physiological potential of squash seeds.

Keywords: *Cucurbita moschata*, analysis of seedlings, physiological potential

S3.2

Decreasing the temperature in the greenhouse does not necessarily reduce the yield of cucumber

Hans-Peter Klaering

Leibniz Institute of Vegetable and Ornamental Crops Grossbeeren/Erfurt e.V.,
Grossbeeren, Germany

Decreasing the set point for heating considerably reduces heat energy consumption, and hence CO_2 emissions, in greenhouse plant production. However, growers worry about a decline in yield, especially in cucumber. Therefore, the constraints of ecological and economic feasibility involved were investigated in two experiments in autumn/winter. The set points for heating at night/day were 10/12, 14/16 and 18/20 °C resulting in mean temperature over the treatment period of 13, 16 and 19 °C, respectively, each in two greenhouse cabins. Crop photosynthesis was measured using the cabins as open chambers. Surprisingly, no difference in photosynthesis among the treatments could be observed. Plants responded to decreasing temperature mainly with a dramatic decrease of the fruit growth rate and a delay in the harvest. Total yield, however, was not affected by low night temperature as long as daytime temperature rose to the range above 20 °C. Under those conditions, obviously enough sinks for assimilates were available due to the high fruit load and the relative low photosynthesis at low light conditions in autumn. Leaves grew slower but senescence was delayed. It seems to be possible to produce cucumbers at low temperatures. However further research is necessary in particular concerning the effect of the diurnal course of temperature on fruit growth.

Keywords: Fruit growth, open chamber, photosynthesis

S3.3

Melon production in the Province of Murcia (SE Spain)

Juan A. Fernández[1], Maria Dolores Bernal[2],
Josefa López-Marín[3], Francisco Pérez-Alfocea[4]

[1]Departamento de Producción Vegetal, UPCT, Paseo Alfonso XIII 48, 30203 Cartagena, Spain, [2]Ingeniero Técnico Agrícola, C/ Emilio Zurano, 28, 30700, Torre Pacheco, Spain, [3]Departamento de Hortofruticultura, IMIDA, 30150 La Alberca (Murcia), Spain, [4]Department of Plant Nutrition, CEBAS-CSIC, E-30100-Murcia, Spain

The province of Murcia is one the second producer of melon in Spain with nearby 6,000 ha producing around 220,000 t per year. Production is concentrated in the period from late spring to summer, being the type ‘Piel de Sapo’ the most commonly used for national consumption. However, the types ‘Galia’, ‘Cantaloup’ and ‘Amarillo’ are also grown, which production is principally exported to the EU. Melon is normally grown in semi-protected conditions with different types of protection such as low tunnel, floating polypropylene cover or mulching, which permits different degrees of earliness and continued production in the season. For low tunnels, there is a tendency to use perforated plastic to reduce condensation and improve illumination within the tunnel. The most widely used mulching plastic is the transparent with the principal aim of increasing soil temperature and therefore to bring forward harvesting. The mulch is normally left on the ground at the end of the growth cycle since it is difficult to recycle, causing a negative effect on the environment. Emerging biodegradable materials for mulching might be an alternative solution to polyethylene. Our results have shown that they do not adversely affect earliness and productivity to any great extent and so their future use seems assured. In general, the producers of melon have strengthened the economy by increasing exports, because of the high quality of the product, while that the scarce availability of water, which differs from year to year, will lead to higher cultivation cost, since alternative sources will be necessary.

Key words: mulching, low tunnel, floating cover, earliness, biodegradable films

S3.4

Evaluation of two potential Cucumis spp. resources for grafting melons

Carmina Gisbert[1], Najet Gammoudi[1], Francecs Xavier Sorribas[2], María Belén Picó[1]

[1]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV-UPV),
Universitat Politècnica de València, Camino de Vera s/n, 46022 Valencia, Spain
[2]Dept. Enginyeria Agroalimentària i Biotecnologia, -Universitat Politècnica de Catalunya,
Esteve Terradas 8, Edifici D4. 08860 Castelldefels, Barcelona

Cultivation of *Cucumis melo* is hampered by soil stresses. Grafting is used to overcome these limitations. Different cucurbits belonging to several genera have been used as rootstocks for melons: *Cucurbita, Lagenaria, Luffa*, etc. However, negative effects on fruit quality appear in some rootstock-scion combinations. The selection of new resistant rootstocks that do not cause this negative impact in quality is necessary to improve melon cultivation. In this work, we evaluated two rootstocks, closer genetically to melon scions than those usually employed : a) an F1 hybrid between a commercial melon (*C. melo* subspecies *melo* var *inodorus* market class Piel de Sapo) and one exotic accession (*C. melo* subspecies *agrestis* var. *chinensis*) with resistance to *Monosporacus cannonballus*, the causal agent of melon vine decline, and with a certain level of tolerance to *Fusarium oxysporum* f sp. *melonis* race 1.2, that causes *Fusarium* wilt, and b) an accession of *Cucumis metuliferus*, highly resistant to *M. cannonballus*, *F. oxysporum* 1.2 and *Meloidogyne* spp. Grafting compatibility of these two selected genotypes with commercial melons was good. All grafted plants displayed higher vigour and earlier flowering than ungrafted plants. Fruits from plants grafted onto *C. metuliferus* showed similar quality than those from ungrafted/selfgrafted plants. However, fruits from plants grafted onto the F1 (*inodorus* x *chinensis*) had lower brix degree than the ungrafted controls. The resistance to soil borne pathogens found in *C. metuliferus* and the good performance regarding plant development and fruit quality of the scions indicate that this species is a promising rootstock for melons.

S3.5

Pollen drying and storage for hybrid seed production of cucumber (*Cucumis sativus*)

Endah Retno Palupi[1], Rotua Melisa Sidabutar[1], Karyadi Wanafiah[2]

[1]Department of Agronomy and Horticulture, Bogor Agricultural University, Bogor, Indonesia
[2]East West Seed Indonesia, Purwakarta, West Java, Indonesia

One of the major problems in hybrid seed production of cucurbits is the low pollen production and low pollen viability. The research was conducted during March to September 2012 at Production Farm of East West Seed Indonesia Ltd. in Jember, East Java, Indonesia. The research material was cucumber male parental variety, i. e. KE014. The research was arranged in completely randomized design and was carried out in three steps. The first step was aimed to investigate the declining pollen moisture content related to viability during pollen drying up to 24 hours. The second step was aimed to study the maintenance of pollen viability during storage whereas the third step was to study the effectiveness of stored pollen for hybrid seed production. The result showed that pollen moisture content decreased significantly during the first eight hours of drying from 12.05% to 6.71% while the viability increased from 10.16% to 25.60%. Prolonged pollen drying up to 24 hours did not substantially reduce the moisture content. Pollen that had been dried for 8 hr was able to maintain its viability during 56 days storage. The dried and then stored pollen was effective for hybrid seed production, resulted in 20.5-25.7 % fruit set and 77.9-87.0% seed set, higher than fruit set and seed set of the undried but stored pollen of 5.2% and 35.7% respectively. Weight of 1000 grain seed were similar of all treatments, however, seed germination of those from dried and stored pollen was slightly higher (98.36-99.63%) than those of undried and stored pollen (95.58%).

Key words: fruit set, moisture content, pollen drying, pollen viability, seed set.

S3.6

Isolation and characterisation of ethylene insensitive mutants from a collection of *Cucurbita pepo* L.

Alicia García[1], Susana Manzano[1], Cecilia Martínez[1], Zoraida Megías[1], Juan Carlos Gázquez[2], Manuel Jamilena[1]

[1]Agrifood Campus of International Excellence (CeiA3) and BITAL. Department of Biology and Geology. University of Almería. La Cañada de San Urbano s/n. 04120 Almería, Spain.
[2]Fundación Cajamar. Estación experimental Las Palmerillas. Santa María del Águila (El Ejido). 04710 Almería Spain.

Ethylene is a plant hormone that controls many physiological and developmental processes in plants. In zucchini squash (*Cucurbita pepo* L.), it regulates important aspects such as sexual expression, monoecy stability, senescence and flowers abscission, parthenocarpy, and postharvest fruit quality, including chilling injury. The identification and characterization of ethylene-insensitive mutants will be a great advance not only for *C. pepo* functional genomics, but also to generate agronomic interesting traits for breeding programs in *Cucurbita* species.

We have developed a mutant collection of approximately 3000 M2 families in the zucchini genetic background MUC-16. Here we report the phenotyping of seedlings in the complete collection, including the response of etiolated seedlings to ethylene. The proportion of families with mutant phenotypes at the seedling stage, including albinos, alterations in the morphology and number of cotyledons, and in the leaf color and shape, was similar or higher than in other EMS collections in cucumber and melon, indicating that the quality of the *Cucurbita* collection is excellent. By using the triple response assay in etiolated seedlings, we have detected four partially ethylene insensitive M2 families. The phenotyping of ethylene-sensitive and insensitive adult plants of these four families indicates that the mutants are not only affected in seedling ethylene sensitivity, but are also altered in sex determination, sex expression, and fruit set and parthenocarpy.

Key words: zucchini squash, EMS, ethylene, triple response.

Oral Sessions

BIOTIC STRESSES AND ABIOTIC STRESSES

04

S4. BIOTIC STRESSES AND ABIOTIC STRESSES

S4.1 **Edelstein Menahem**

Preventing entry of pharmaceuticals (carbamazepine) into the food chain by using grafted plants

S4.2 **Lebeda Ales**

Approach for determination and denomination of cucurbit powdery mildew races

S4.3 **Yuang Huang**

Effectiveness and mechanism of rootstock grafting to increase cucumber salt tolerance

S4.4 **Olave Vera, Jorge Leonardo**

Effect of saline priming in Cucurbita ficifolia Bouché seeds on germination parameters and synthesis of proline

S4.5 **Alharbi, Abdulaziz Rabeh**

Improving Cucumber Water Stress Tolerance in Saudi Arabia by Grafting

S4.6 **McCreight, James Donald**

Host plant resistance in melon (*Cucumis melo* L.) to sweetpotato whitefly in California and Arizona

S4.7 **Gu Qinsheng**

Transmission efficiency of Cucumber Green Mottle Mosaic Virus via seeds, soil, pruning and irrigation water

S4.8 **Ozer Ayse**

Determination of Drought Tolerance Levels of Some Melon Genotypes Via Physiological Methods

S4.1

Preventing entry of pharmaceuticals (carbamazepine) into the food chain by using grafted plants

Edelstein, M[1]., Ben-Hur, M[2]., Ju-Young, Y[1]., Bernstein, N[2]., Nasser, A[2]., Baumkoler, F[1]. and Gerstl, Z[2].

[1]Department of Vegetable Crops, Agricultural Research Organization, Newe Ya'ar Research Center, P. O. Box 1021, Ramat Yishay 30-095, Israel.
[2]Institute of Soil, Water and Environmental Sciences, ARO, the Volcani Center, P.O. Box. 6, Bet Dagan 50-250, Israel.

The entry of pharmaceuticals into the food chain is of concern due to their increased presence in soils and water sources. It may be possible to limit their uptake into the edible portions of plants by grafting them onto appropriate rootstocks. The purpose of this study was to compare the uptake of carbamazepine, a conservative and ubiquitous pharmaceutical, among *Cucurbita* accessions, for identification of potential rootstocks that prevent carbamazepine uptake. Seven accessions were planted in perlite and drip irrigated with a 10 or 500 µg/L carbamazepine solution. The experiment was carried out for 30 days in 4 replicates. The EC, pH and carbamazepine concentration were determined in both the irrigation water and drainage, and also in the plant sap exudate. At the end of the growing period, the dry weights of the shoot and roots were measured. No significant effect was found in plant development for any accession at either of the two concentrations. At the higher carbamazepine concentration, an increase in its concentration in the sap exudate was observed, i.e., carbamazepine was transported to the above ground parts of the plant. Differences in the transport of carbamazepine to the canopy were observed among the accessions tested; at 10 µg/L of carbamazepine, two accessions exhibited reduced carbamazepine transport to the shoots, whereas at 500 µg/L all accessions exhibited reduced carbamazepine transport. Hence, these accessions can be used as potential biological barriers to prevent the penetration of carbamazepine to the edible portion of grafted plants.

Key words: carbamazepine, fruit safety, plant uptake, rootstock.

S4.2

Approach for determination and denomination of cucurbit powdery mildew races

Aleš Lebeda[1*], Eva Křístková[1], Božena Sedláková[1],
James D. McCreight[2], Michael D. Coffey[3]

[1] Palacký University, Faculty of Science, Department of Botany, Šlechtitelů 11, 783 71,
Olomouc-Holice, Czech Republic [*] E-mail: ales.lebeda@upol.cz
[2] U.S. Department of Agriculture, Agricultural Research Service,
1636 E. Alisal St., Salinas, CA 93905, USA
[3] University of California, Department of Plant Pathology and Microbiology,
3206 Webber Hall, Riverside, CA 92521, USA

Cucurbit powdery mildew (CPM), a disease on field and greenhouse cucurbit crops worldwide, is caused most frequently by two obligate erysiphaceous ectoparasites (*Golovinomyces orontii s.l.*, *Podosphaera xanthii*) that are highly variable in pathogenicity and virulence. Various, independent systems of CPM race determination and denomination are used worldwide, having to date been differentiated on different cultivars or lines of melon (*Cucumis melo* L.).

We briefly review historical perspectives and the current state of understanding of the virulence variation of the two CPM pathogens at the pathogenic race level, their differentiation and designation. Furthermore, we propose for use by the international CPM research, breeding, seed and production community new tools to enhance research, communication and management of CPM.

Our newly proposed package consists of five components: 1) a set of 21 differential genotypes of *Cucumis melo* L. for the identification of CPM races; 2) a triple-part, septet code for meaningful, concise designation of CPM races; 3) protocols for maintenance of CPM isolates, differential genotypes, and laboratory assays; 4) rules and principles of practical application of this system in breeding, seed production and cucurbit growing, and a proposal for a race denomination suitable for practical application; 5) crucial activities leading to the implementation and running of new tools for CPM research and management. The five components of this package have equal importance, forming a compact system, and none of them can be omitted.

Keywords: *Golovinomyces orontii s.l.*, *Podosphaera xanthii*, *Cucumis melo*, virulence variability, race-specificity, septet code

S4.3

Effectiveness and mechanism of rootstock grafting to increase cucumber salt tolerance

Yuan Huang, Jin Zhu, Ai Zhen, Zhixiong Liu, Bo Lei, Mengliang Niu,
Junjun Xie, Jingyu Sun, Haisun Cao, Zhilong Bie*

College of Horticulture and Forestry Sciences, Huazhong Agricultural University/Key
Laboratory of Horticultural Plant Biology, Ministry of Education, Wuhan, P R China
*Email: biezhilong@hotmail.com

Soil salinity is a major constraint to crop production in the world. Grafting has been widely used to avoid the serious crop loss caused by infection of soil-borne diseases aggravated by successive cropping. This practice is now rapidly spreading and expanding over the world. The effectiveness and mechanism of rootstock grafting to increase cucumber salt tolerance has been investigated by our research group. The results showed that salt tolerant rootstock grafting can increase salt tolerance of cucumber, either by short- term or long- term experiment. The physiological mechanism is related to limited transport of Na^+ from rootstock to scion, increased antioxidant system and photosynthesis, as well as higher osmotic adjust capacity. Scanning ion-selective electrode technique and X-ray microanalysis demonstrated that Na^+/H^+ antiporter system of salt tolerant pumpkin rootstock was sufficient to exclude Na^+, and the highly vacuolated root cortical cells of pumpkin roots could sequester more Na^+, limit the radial transport of Na^+ to the stele and thus restrict the transport of Na^+ to the scion. The genes that regulate Na^+ uptake and transport will be identified through RNA-Seq and bioinformatics, as well as transformation of model plants. The transgenic of salt tolerant pumpkin rootstock will also be established in future.

Key words: rootstock, cucumber, NaCl stress, Na^+ uptake, antioxidant system

S4.4

Effect of saline priming in *Cucurbita ficifolia* Bouché seeds on germination parameters and synthesis of proline

Olave, J.[1, 2] y Santander, C.[1, 2]

[1]Centro de Investigación y Desarrollo en Recursos Hídricos (CIDERH)
[2]Facultad de Recursos Naturales Renovables, Universidad Arturo Prat, Iquique, Chile
E-mail: jorge.olave@ciderh.cl

In northern Chile production and quality of cucurbits is affected by salinity water and soil. Therefore Cucurbita ficifolia is an option as salinity tolerant rootstock. The aim of this study was to determine the effect of saline priming in seeds of *Cucurbita ficifolia* on the parameters of germination and synthesis of proline. The assay was performed in the Soil-Water-Plant laboratory of CIDERH. Seeds were primed with two salt solutions of 300 and 600 mM/L of NaCl for 96 hours at 20 ± 1 ° C. Subsequently primed and non-primed seeds were put to germinate for 88 hours in Petri dishes in four solutions of germination (DG): 0, 25, 50 and 75 mM/L of NaCl. Per treatment were sown 100 seeds divided into ten repetitions. The parameters evaluated were: germination percentage and speed, length and speed of growth of the radicle, and germination rate priming effect (GIPr) and per dissolution of germination (GIDg) as biochemical parameter was determined proline synthesis at 88 hours of germination. The results showed an advance and uniform germination of primed seeds. The highest GIPr was obtained with the priming of 300 mM/L (+ 107%) referred to control; instead the GIDg, there were no significant differences obtained. In regard to Proline there is no interactive effect between priming and DG. The results obtained indicate that the seed of *C. ficifolia* priming with 300 mM/L (28.65 mS/cm = Ψs: -1.33 MPa) has tolerance to the salinity conditions evaluated, with a synthesis of 2,96 µmol Proline g/fw.

Key Words: *Cucurbita ficifolia*, salinity, rootstock, proline

S4.5

Improving Cucumber Water Stress Tolerance in Saudi Arabia by Grafting

Abdulaziz R. Al-Harbi[1], Francisco Pérez-Alfocea[2],
Abdulrasoul M. Al-Omran[3], Mahmoud A. Wahb-Allah[1]

[1]Department of Plant Production, College of Food and Agricultural Sciences, King Saud University, Saudi Arabia, [2] Department of Plant Nutrition, CEBAS-CSIC, E-30100-Murcia, Spain, [3]Department of Soil Science, College of Food and Agricultural Sciences, King Saud University, Saudi Arabia

Water scarcity is a major limiting factor for crop productivity in arid and semi-arid areas. Grafting elite commercial cultivars onto selected vigorous rootstocks is considered as a useful strategy to alleviate the impact of environmental stresses. This study aims to investigate the feasibility of using grafting to improve fruit yield and quality of cucumber under water stress conditions. Two cucumber cultivars (*Cucumis sativus* L.) Alosama F_1 and Alwaled F_1 were grafted onto Affyne (*Cucumis sativus* L.) and Shintoza A90 (*Cucurbitamaxima x C. moschata*) rootstocks. Non-grafted plants was used as control. All genotypes were grown under three surface drip irrigation regimes: 50, 75 and 100% of the crop evapotranspiration (ETc),which represent high-water stress, moderate-water stress and non-water stress conditions, respectively. Yield and fruit quality related traits were analyzed and assessed. In comparison to the non-grafted plants, the best grafting treatment under water stress was cultivar Alosama F_1 grafted onto Shintoza A90 rootstock. It had an overall improved yield and fruit quality under water stress owing to an increase in total fruit yield (by 27% , from 4.815 kg plant^{-1} in non-grafted treatment to 6.149 kg plant^{-1} in grafted treatment under moderate -water stress), contents of total soluble solid (13%), titratable acidity (39%) and vitamin C (33%). The positive effects of grafting on plant growth, productivity, and water use efficiency support this strategy as an useful tool for improving water stress tolerance in greenhouse grown cucumber in KSA.

Keywords: Cucumber, Grafting, Saudi Arabia, Water stress, Surface drip irrigation.

S4.6

Host plant resistance in melon (*Cucumis melo* L.) to sweetpotato whitefly in California and Arizona

James D. McCreight, William M. Wintermantel
U.S. Department of Agriculture, Agricultural Research Service,
Salinas, CA 93905, USA

Eric T. Natwick
University of California ANR, Cooperative Extension Imperial County,
Holtville, CA 92250, USA

Sweetpotato whitefly (MEAM1 cryptic species of *Bemisia tabaci*; SPWF) feeding severely impacts fall season melon yield and quality in the lower deserts of California and Arizona. Melon accessions PI 313970 and TGR 1551 (PI 482420) have been reported to exhibit host plant resistance (HPR) to SPWF. Potentially higher levels of HPR to SPWF were observed in *ad hoc* comparisons of numbers of adults per leaf on six melon accessions, PI 313970, TGR 1551, 'Impac', and 'Top Mark' in a naturally infested field test at Holtville, CA in fall 2012. Replicated field tests at Holtville in fall 2013 and spring 2014 (when SPWF populations are lower than in the fall) compared SPWF infestation of five (PI 116482, PI 123689, PI 124107, PI 124431, PI 145594) of the six accessions with PI 313970, TGR 1551, TGR 1937 (PI 482431), 'Top Mark' and 'Impac'. Few significant differences were found among the entries for numbers of adults, eggs, crawlers, red eyes, or nymphs per cm^2 leaf area during either season. Though there were significant ($P<0.05$) differences among the entries for number of adults per cm^2 leaf area at seven weekly sampling dates in fall 2013, none of the accessions had consistently fewer adults than 'Impac' or 'Top Mark'. There were few differences among the entries in spring 2014 for numbers of adults per cm^2 leaf area. PI 116482 had the most, and PI 145594, PI 313970 and TGR 1937 had the fewest adults on average.

Key words: biotype B, CYSDV, host plant resistance

S4.7

Transmission efficiency of Cucumber Green Mottle Mosaic Virus via seeds, soil, pruning and irrigation water

Li Junxiang , Gu Qinsheng

Henan Key Laboratory for Fruit and Cucurbit Biology,Zhengzhou Fruit Research Institute,
Chinese Academy of Agricultural Sciences
Correspondent author: guqinsheng@caas.cn

Cucumber green mottle mosaic virus (CGMMV) infects grafted watermelon frequently and widely in China. Investigating the transmission modes and their efficiency is urgently needed to understand the factors contributing to epidemiology of this viral disease. In the present study, we found that the occurrence of CGMMV in bottle gourd seed production base reached 100%, while the contamination rate and transmission rate were 100% and 0.92% respectively. The bottle gourd plants showed obvious mottle symptom on leaves starting 36 days after seed sowing. The long latent period of CGMMV in seedlings implies a potential risk to use contaminated seeds in the production of grafted watermelon. This virus could overwinter in soil with debris of infected plants and the infection rate of CGMMV from contaminated soils was 10.3%. CGMMV could be transmitted from infected watermelon plants to healthy ones by pruning at least to the ninth plant during the whole growing season. The transmission distance was 1.32~1.98m （the second next to infected plant）by dipping irrigation and 1.98~2.64m (the third next to infected plant) by flooding irrigation. This study suggested that contaminated seeds, contaminated soil, pruning and irrigation transmitted CGMMV at different efficiency, all contribute to the epidemiology of CGMMV .

Key words: *Cucumber green mottle mosaic virus* · Seed · Soil · Pruning · Water · Transmission rate

S4.8

Determination of Drought Tolerance Levels of Some Melon Genotypes Via Physiological Methods*

Ayse OZER[1], Mehmet HAMURCU[2], Onder TURKMEN[1],
Nebahat SARI[3], Ilknur SOLMAZ[3]

[1]Dept. of Horticulture, Fac. of Agric.,Univ. of Selcuk, Konya-Turkey
[2]Dept. of Soil Science and Plant Nutrition, Fac. of Agric.,Univ. of Selcuk, Konya-Turkey
[3]Dept. of Horticulture, Fac. of Agric.,Univ. of Cukurova, Adana-Turkey

Flora extending from Anatolia to Japan, Turkey is among the secondary melon genetic centers of important plant genetic resources. In recent years, global climate change and environmental factors such as drought are limiting the efficiency of melon yield. In our research we made two different scanning and determined levels of drought tolerance in melon genotypes; in the climate-controlled greenhouse of Selcuk University, Faculty of Agriculture, with perlite environment and climate-controlled room under controlled conditions in water culture. In the pre-scanning step of this work, we have used 192 melon genetic resources which are own to Cukurova University, Faculty of Agriculture, Department of Horticulture's Cucurbit genetic resources collection. In controlled greenhouse, seeds were planted drought and control groups. Drought has been applied to the plants with the PEG 6000 into mixing Hougland solution. The results obtained from the pre-screening stage were analyzed by weighted rating calculations. In the second year's private screening, we have used 20 melon genotypes (drought-tolerant 10 and sensitive 10). As well as control (Hoagland solution) groups, drought groups were formed by mixing PEG 6000 into Hoagland solution. In melon seedlings, root and shoot length, fresh and dry weight, number of leaves was calculated and Relative Water Content, Leaf Water Potential Measurements, EC, 0-5 scale values were measured. Results were evaluated by calculating the weighted ratings. From within 192 melon accessions, the most tolerant genotypes to drought was Kav248 and the most sensitive genotype was Kav20 were selected.

Key words: Drought tolerance, melon, physiological parameters

Oral Sessions

FRUIT QUALITY AND POST-HARVEST

05

S5. FRUIT QUALITY AND POST-HARVEST

S5.1 **Aguayo, E.**

Effects of pasteurization and storage time on watermelon juice quality enriched with L-citrulline

S5.2 **Lewinsohn Efraim**

Molecular and biochemical mechanisms for the formation of aroma volatiles in cucurbit fruit

S5.3 **Marcin Glowacz**

Physicochemical characteristics of twelve pumpkin varieties grown in UK

S5.4 **Zaccari Veiga, Fernanda Isabel**

Variation in glucose, α- and β-carotene and lutein content during storage time in winter squash “type butternut”

S5.5 **Perla Gómez Di Marco**

Uv-C Light Preserves Quality Of Minimally Processed Watermelon Cylinders

S5.6 **Ortiz Grisales Sanin**

Butternut squash fruit *Cucurbita moschata* Duch. conditioning by saline silage

S5.1

Effects of pasteurization and storage time on watermelon juice quality enriched with L-citrulline

E. Aguayo[1*], M.P. Tarazona-Díaz[2]

[1]*Postharvest and Refrigeration Group. Technical University of Cartagena (UPCT). Paseo Alfonso XIII, 48. 30203. Cartagena, Spain. Institute of Plant Biotechnology.*
[2]*Department of Food Engineering, Jorge Tadeo Lozano University, Bogotá, D.C, Colombia.*
**e-mail: encarna.aguayo@upct.es*

Watermelon juice has gained increasing popularity among consumers as a rich natural source of functional compounds such as lycopene and L-citrulline. This amino acid is an excellent candidate to reduce muscle soreness. Watermelon juice enriched with L-citrulline is presented as an industry opportunity for the sport drink sector. However, the application of conventional thermal pasteurization can degrade those functional compounds. Effects of pasteurization at 80 °C for 40 s (PW-40s) or 90 s (PW-90s) and storage (4 °C for 30 days) on watermelon juice enriched with L-citrulline was studied. Before pasteurization, initial lycopene content was 14.65 ± 0.30 mg/kg reducing to 10.50 ± 0.06 in PW-40s and 10.10 ± 0.08 mg/kg in PW-90s after 30 days. Initial enriched citrulline content was 15.68 ± 0.05 g/L which decreased to 12.38 ± 0.03 in PW-40s and 12.04 ± 0.09 g/L in PW-90s treatment after 30 days of storage. Pathogenic bacteria (*Salmonella* spp., *Listeria monocytogenes* and *Escherichia coli*) were not detected during storage. However, mesophilic growth was high at 7.9 log cfu/g for PW-40s and 6.5 log cfu/g for PW-90s. The sensory quality (appearance) determined the shelf-life at 25 d for PW-40s and only 15 d for PW-90s. The use of higher temperatures of pasteurization is necessary to obtain a safe watermelon juice but this needs to be balanced with reduced times to maintain functional and sensory parameters which are easily thermodegradated.

Keywords: *Citrullus lanatus,* firmness, sensorial parameters.

S5.2

Molecular and biochemical mechanisms for the formation of aroma volatiles in cucurbit fruit

Efraim Lewinsohn[1], Itay Gonda[1], Einat Bar[1], Rachel Davidovich-Rikanati[1], Vitaly Portnoy[1], Shery Lev[1], Galil Tzuri[1], Rotem Harel-Beja[1], Navot Galpaz[1], Shiri Freilich[1], Mwafaq Ibdah[1], Mingyun Huang[2], Zhangjun Fei[2], James J. Giovannoni[2],Joseph Burger[1], Arthur A. Schaffer[3], Ya'akov Tadmor[1], and Nurit Katzir[1]

[1] Institute of Plant Sciences, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay, 30095, Israel
[2]Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, NY 14853, USA
[3] Institute of Plant Sciences, The Volcani Center, Agricultural Research Organization, P.O. Box 6, Bet Dagan, 50250, Israel

Many of the volatiles that affect the full flavor of fruits are derived from the degradation of nutritionally important metabolites such as carotenoids, essential amino acids and essential fatty acids. Cucumber aroma is mainly based on fatty acid derived compounds while watermelon aroma is augmented by carotenoid-derived volatiles. Pumpkin aroma consists both of fatty acid and carotenoid-derived volatiles, augmented by sulfur derivatives. Melons display a high polymorphism in their aroma and the largest assortment of volatiles among the cucurbit fruits. Generally, climacteric melon varieties are characterized by higher volatile levels than in non-climacteric varieties. The major volatiles present in climacteric melon varieties are esters, while in non-climacteric varieties alcohols and aldehydes are dominant. Orange-fleshed varieties contain β-ionone and β-cyclocitral, potent odor compounds derived from the degradation of β-carotene, while green- and white-fleshed varieties lack these compounds. Sesquiterpenes are mainly accumulated in rinds and their levels and composition vary according to the variety examined. The degradation of essential amino acids (mainly L-phenylalanine, the branched-chain amino acids and L-methionine) is a key factor in imparting the unique aroma of melons. An increasing number of enzymes and genes involved in aroma formation in cucurbit fruits have been identified and characterized. They include lipoxygenases, hydroperoxide lyases, alcohol dehydrogenases, alcohol acetyltransferases, carotenoid cleavage dioxygenases, sesquiterpene synthases, amino acid aminotransferases and a methionine gamma lyase. Integrating genomic, transcriptomic, enzymatic and metabolomical data has contributed to our understanding of the formation of aroma volatiles in melon and in other fruits.

Key words: aroma, fruit quality, volatiles

S5.3

Physicochemical characteristics of twelve pumpkin varieties grown in UK

Marcin Glowacz[a], Peter Waldock[b], Gerard Bishop[c],
Richard Colgan[a], Debbie Rees[a]

[a] Natural Resources Institute, University of Greenwich, Kent, ME4 4TB, UK
[b] Growing Earth Consultancy Ltd, East Sussex, TN22 1DN, UK
[c] East Malling Research, Kent, ME19 6BJ, UK

In the United Kingdom, pumpkins are mainly used for Halloween decoration. In recent years, the interest in their utilisation as food products has increased. There is, however, only limited information available in the literature, on postharvest practices aiming to reduce quality loss of pumpkins during storage. Knowledge of differences among varieties will help growers in understanding their storage potential. The goal of this research was to investigate physicochemical characteristics - visual quality (skin and flesh colour, presence of rots), texture (whole fruit firmness, skin strength, flesh hardness), and composition (mineral analysis, sugar content) in twelve pumpkin varieties, *i.e.* Becky, Cinnamon Girl, Flynn, Gomez, Harvest Moon, Jack Sprat, Magician, Mars, Paintball, Racer, Small Sugars and Spitfire - to find those that correlate with quality maintenance during storage. Better storability of pumpkins was found to be associated with higher whole fruit firmness and dry matter content. Furthermore, poor storing varieties, *e.g.* Magician and Flynn, had lower magnesium and phosphorus content, which could be related with weaker cell walls strength, and thus reduced flesh hardness. Substantial differences were also found in the flesh colour, especially in *a** value, ranging from 2.7 (pale yellow) to 17.8 (orange) in Flynn and Jack Sprat varieties, respectively. Visual quality, however, did not correlate with pumpkins storability. More detailed biochemical analyses are still needed to better define key components influencing the storage potential of pumpkins.

Key words: storage quality, colour, texture, mineral content, sugar composition

S5.4

Variation in glucose, α- and β-carotene and lutein content during storage time in winter squash “type butternut”

Fernanda Zaccari[ab], María Cristina Cabrera[b], Ali Saadoun[bc]

[a]Poscosecha de Frutas y Hortalizas. Departamento de Producción Vegetal. Facultad de Agronomía. Universidad de la República (UdelaR). Av. Eugenio Garzón 780. CP 12900. Montevideo, Uruguay. fzaccari@fagro.edu.uy [b]Nutrición y Calidad de Alimentos. Facultad Agronomía. UdelaR. [c]Fisiología y Nutrición. Facultad de Ciencias. UdelaR.

Winter squash, “type butternut pumpkin”, is an interesting source of high quality nutrients, but after 4 to 6 months of storage there are physiological processes that can modify the content of these compounds. The aim of this work was to determine the variation in valuable nutrients during the storage of squashes. Content of total glucose, α- and β-carotene and lutein were determined in raw pulp squash, “type butternut” (AtlasF1, Sakata) at harvest (0), 2, 4 and 6 months of storage (14 °C, 80% RH) from the whole fruits. Increasing carotenoids content was observed in raw pulp during the storage from 0 until 4 months. Lutein content was higher (79.7 µg) at 2 months, while α-carotene (33.7 mg) and β-carotene (37.6 mg) were higher at 4 months of storage. Total glucose increased by 72% in the second month of storage and then decreased significantly by 46% and 80% at 4 and 6 months respectively compared with the content at 0 month fresh raw pulp. At 6 months, was lower in total glucose (0.8 times) and carotenoids higher (0.7 times) than harvest, in the dry matter content. These results show that storage significantly affects nutrient content in squashes, and that the nutritional value depends on the time of storage. This information is useful to a better understanding about the nutritional quality and composition of this food.

Key words: *Cucurbita moschata*, postharvest, carotenoids, total glucose

S5.5

UV-C LIGHT PRESERVES QUALITY OF MINIMALLY PROCESSED WATERMELON CYLINDERS

Francisco Artés-Hernández[1,2*], Perla A. Gómez[2], Pedro A. Robles[1],
Alejandro Tomás-Callejas[3], Mariano Otón[2] and Francisco Artés[1,2]

[1] Postharvest and Refrigeration Group. Department of Food Engineering. Technical University of Cartagena. Paseo Alfonso XIII, 48. 30203. Cartagena, Murcia, Spain.
[2] Institute of Plant Biotechnology. Technical University of Cartagena. Campus Muralla del Mar. 30202. Cartagena, Murcia, Spain.
[3] R&D Salads and Healthy Snacking. Chiquita Brands International, Inc. /Fresh Express.
607 Brunken Ave., Salinas CA 93901. USA.
* To whom correspondence should be addressed: fr.artes-hdez@upct.es

Watermelon (*Citrullus lanatus*) is usually minimally processed as cubes, being edge-cut damage a remarkable defect. To avoid such disorder, processing as cylinders and using UV-C as sanitizing tool can be an interesting alternative to preserve quality during shelf life. The effect of UV-C radiation on overall quality, microbial growth, phenolics content and lycopene concentration of watermelon cylinders (2.7 cm ϕ) of several lengths (1, 2, 4 and 8 cm) were analyzed. After harvesting, fruits were washed (150 µL L^{-1} NaClO), precooled and processed at 8ºC. Once removed the skin, fruits were manually cut as cylinders, exposed to 4.79 kJ UV-C m^{-2} and packaged in polypropylene packages under passive modified atmosphere. UV-C untreated cylinders were used as control. After 7 days at 5ºC, O_2 partial pressure was higher for the longest cylinders (17.9 kPa for 8 cm vs 11.2 kPa for 1 cm) with the lowest CO_2 partial pressure (2 kPa for 8 cm vs 3.4 kPa for 1 cm), indicating a higher respiration rate for the smaller sizes. A better sensory quality in 8 cm cylinders for both, control and UV-C treated, was observed. However, microbial growth was better controlled and phenolics content better maintained (≅6 mg CAE 100 g^{-1} fw) in UV-C treated samples. Lycopene content did not significantly decrease in any treatment. As conclusion, watermelon minimally processed as cylinders pretreated with 4.79 kJ UV-C m^{-2} can be stored for up to 7 days at 5ºC without noticeable quality changes.

Key words: *Citrullus lanatus*; fresh-cut; postharvest; lycopene; phenolics

S5.6

Butternut squash fruit *Cucurbita moschata* Duch. conditioning by saline silage

Sanín Ortiz Grisales

Ph.D. Associate Professor. Facultad de Ciencias Agropecuarias. Universidad Nacional de Colombia. Palmira, Valle del Cauca, Colombia. Corresponding author: sortizg@unal.edu.co

To test the stability of postharvest solid wet fruit pulp Butternut squash Cucurbita moschata Duch., by silage technology three treatments with sodium chloride (T1 = 3, T2 = 4 t3 = 5%) was used. With 16, 17 and 19% moisture removal respectively of wet solid before ensiling. After 21 days of anaerobic fermentation, the final product was stable with: 18.6, 19.2 y 20.7% of dry matter (DM); pH on 3.66, 3.64 y 3.65 respectively without significant differences ($P<0,05$); Crude Protein on 13.2, 12.9 y 12.9% and Neutral detergent fiber (NDF) on de 23.8, 19.5 y 18.6% respectively without significant differences ($P<0,05$). The average volatile fatty acids was 6.6% with 0.34; 1.99 y 0.87% to acetic, lactic and butyric respectively. All values of control microbial growth (mesophilic aerobes, molds, yeasts, total coliforms, clostridial spores, *Escherichia coli* and *Salmonella*) were expressed under the provisions of the Colombian Technical Standard. The silage saline 5% sodium chloride is the ideal technique to preserve and store the butternut squash fruit.

Key words: Squash, pumpkins, cucurbits, fleshy fruits, postharvest conditioning, anaerobic fermentation, bovine supplement, Dry matter in fruit.

POSTERS

P1.1

New tools for breeding cantaloup melons: First Introgression line collection of makuwa melons into Charentais genetic background

Gorka Perpiñá-Martín[1], Cristina Esteras-Gómez[1],
Antonio J Monforte[2] María Belén Picó-Sirvent[1]

[1]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV-UPV),
[2] Instituto de Biología Molecular y Celular de Plantas (IBMCP), Consejo Superios de Investigaciones Científicas (CSIC), Universitat Politècnica de València,
Camino de Vera s/n, 46022 Valencia, Spain

A large number of Single Nucleotide Polymorphisms (SNPs) have been developed recently in melon, representing a resource that facilitates the development of new breeding populations. Introgression Lines (ILs) collections are suitable to the study of quantitative traits and, especially, to introduce new exotic genetic variability into modern cultivars. We have developed a new ILs collection, employing the Japanese cultivar “Ginsen makuwa”, subsp. *agrestis* var. *conomon* as exotic donor parent and the French Charentais-type cultivar “Vedrantais”, subsp. *melo* var. *cantalupensis* as recurrent parent. Successive backcrosses and selfing generations (BC2, BC3, BC3S1, BC3S2 and BC4S1) were genotyped with SNPs uniformly distributed throughout the melon genome by Sequenom MassARRAY and High Resolution Melting assays. In each generation, plants with higher recurrent genome, but representing the whole makuwa genome in the whole population, were selected. The final ILs population covered nearly 100% of the donor genome. Fruit quality traits were assessed and *Quantitative Trait Loci* (QTLs) could be mapped for some of these traits. Some QTLs involved in sugar content, fruit shape, flesh firmness and flesh color showed consistent effects across generations. Some of these QTLs coincide with previously reported QTLs, but some of them map in genomic regions where QTLs were not reported before. Remarkably, some makuwa introgressions were associated with an increase in fruit sugar content. Some of the ILs displayed combined phenotypes interesting for cantaloup breeding, such as delayed climacteric associated to a higher sugar content.

Key words: cantalup melons, Introgression lines, makuwa, quality traits.

P1.2

A new introgression line collection to improve Piel de sapo melons

Gabriel Castro[1], Gorka Perpiñá[1], Cristina Esteras[1],
Antonio J Monforte[2,] María Belén Picó[1]

[1]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV-UPV),
[2] Instituto de Biología Molecular y Celular de Plantas (IBMCP), Consejo Superios de
Investigaciones Científicas (CSIC), Universitat Politècnica de València,
Camino de Vera s/n, 46022 Valencia, Spain

Melon (*Cucumis melo*) is an economically important species worldwide with a large number of cultivars displaying an impressing phenotypic and genotypic variation. However, only a fraction of this variability is exploited in modern breeding. Among those, "Piel de sapo" (PS) market class cultivar (belonging to the *inodorus* botanic group) is one of the most widely cultivated, producing non-climacteric and elliptic fruits with green with dark green spots skin and white to cream sweet juicy flesh. In order to introduce new exotic variation into PS modern cultivars, we have developed new introgression lines (ILs) in the "Piel de sapo" genetic background, including chromosome segments from an Asian exotic *dudaim* cultivar (*C.melo* subsp *agrestis* var. *dudaim*). *Dudaim* melons develop small round fruits with a certain climacteric behaviour, characterized by a yellow rind with ochre stripes, a non-sweet white flesh, and a complex aromatic profile, that results in a sweet fragrance. Successive backcrosses and selfing generations were genotyped with a set of SNPs uniformly distributed throughout the melon genome. In each generation, plants with higher recurrent genome, but representing the whole *dudaim* genome in the whole population, were selected. Fruit quality traits were assessed and *Quantitative Trait Loci* (QTLs) could be mapped for some of these traits. Some QTLs involved in rind and flesh color, climacteric ripening, aroma, fruit shape and size were found. Some of the observed phenotypes could be interesting for the development of new Piel de sapo types, which may contribute to the diversification of this market class.

Key words: Piel de sapo melons, Introgression lines, *dudaim*, quality traits.

P1.3

Tolerance to ToLCNDV in *Cucurbita* spp.

Cristina Sáez[1]*; Cecilia Martínez[2]*; María Ferriol[3]; Susana Manzano[2]; Manuel Jamilena[2]; Carmelo López[1]; Belén Picó[1]

[1]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV-UPV),
Universitat Politècnica de València, Camino de Vera s/n, 46022 Valencia, Spain.
[2]Agrifood Campus of International Excellence (ceiA3). Department of Biology and Geology.
University of Almería. La Cañada de San Urbano s/n. 04120 Almería, Spain.
[3]Instituto Agroforestal mediterráneo, Universitat Politècnica de València,
Camino de Vera s/n, 46022 Valencia, Spain.
* These authors have contributed equally to this work

Tomato leaf curl New Delhi virus (ToLCNDV) is a bipartite begomovirus (Geminiviridae) first reported in India and neighboring countries. A severe outbreak of ToLCNDV in Zucchini (*Cucurbita pepo*) occurred in Southern Spain in 2012. Mechanical inoculation and natural infection with *Bemisia tabaci,* in Almeria, were used to screen part of the COMAV´s *Cucurbita* core collection that represents the variation in the four main cultivated species. The tolerance was assessed by symptomatology and by a PCR-based diagnostic method that allows the detection of the two viral components in a single reaction. Mechanical transmission of ToLCNDV was confirmed in all the species. Severe symptoms were found 15 and 21 days after mechanical and natural inoculation, respectively, in *C. pepo*, in all accessions belonging to the Zucchini morphotype and to other morphotypes of the subsp. *pepo,* subsp *ovifera* and even in the wild relative *C. fraterna*. *Cucurbita maxima* and *C. ficifolia* were also highly susceptible. The only species showing tolerance was *C. moschata*. Instead of curling, which was typically observed in most *Cucurbita* species, in *C. moschata* we observed mosaic and mottling, which suggest a differential response of this species. Under natural infection a few *C. moschata* accessions remained asymptomatic and no virus was detected in the plant apex. Under mechanical inoculation, ToLCNDV symptoms were mild and delayed in these accessions and they were PCR positive. Some of the more tolerant accessions came from India, the country in which this virus was firstly reported, as was also previously shown for tolerant melons.

Key words: ToLCNDV, zucchini, squash, resistance, mechanical inoculation, whitefly transmission

P1.4

The genotype analysis of watermelon in the BC_7 population

GAO Lei, LIU Wen-ge, ZHAO Sheng-jie, Lu Xu-qiang, HE Nan,
ZHU Hong-ju, DOU Jun-ling

Zhengzhou Fruit Research Institute, CAAS, Zhengzhou, Henan, China, 450009

Years of cultivation and selection targeting yield and desirable fruit qualities have narrowed the genetic base of watermelon, resulting in a major bottleneck in watermelon improvement. However, wild watermelon has many perfect agronomic traits, excavation and making full use of excellent genes of wild watermelon germplasm resources, is an important way to improve watermelon qualities. With wild watermelon called A69 as donor parent and cultivation watermelon called 203Z as recurrent parent, In the BC_7 population, there were lots of fruit characters variation, such as different flesh colors, sour, bitter, firmness flesh, low sugar, and so on. Some of variant lines were chosen and marked by SSR and genotyping by GGT. A total of 178 SSR markers amplified with 99 selected primers for showing polymorphism between the parental lines A69 and 203Z were used for analysing genotype in the BC_7 population. There were 11 variant lines which had different flesh firmness were chosen for analysing genotype. We found that every variant line had 1-2 exogenous wild segments which probably had something to do with flesh firmness, however, so far, we have not known which gene existed in exogenous wild segments, which needs further study.

Key words: watermelon, BC_7 population, SSR marker, genotype

P1.5

Survey of InDel Markers based on *Citrullus lanatus* Genome Related to Gummy Stem Blight in Watermelon

Hye-Eun Lee, Soo-Jin Kim, Yun-Chan Huh, Yul-Kyun Ahn, Do-Sun Kim

Vegetable Research Division, National Institute of Horticultural & Herbal Science, RDA,
Suwon 440-706, Korea

Watermelon (*Citrullus lanatus*) is an important vegetable crop in the world and contains various health promoting compounds including many antioxidants such as lycopene and beta-carotene. Genetic diversity of cultivated watermelon is very narrow, which is one of major factors limiting the improvement of watermelon breeding program. Gummy stem blight (*Didymella bryoniae* (Auersw.)) is one of the most destructive diseases and causes crown blight, defoliation and fruit rot, resulting in severe production loss in watermelon. Insertion/deletion (InDel) markers, important molecular markers for genetic studies are frequent sequence variation in the plant genome. This study was performed to develop InDel markers related to gummy stem blight resistance from two watermelon lines, one susceptible and the other resistant to gummy stem blight. Sequence information from two different lines were compared and 40 primer pairs from InDels that differ in two lines were designed. High resolution melt (HRM) analysis was conducted using the primers with two gummy stem blight resistant and one susceptible lines. A total of 10 candidate InDel primers were detected melt temperature difference, respectively. These InDel markers can be useful for developing disease resistance-related markers and, therefore, beneficial to watermelon breeding program.

Key words: gummy stem blight, InDel, molecular marker, watermelon

P1.6

Breeding Development of ‘Longsheng’Series Watermelon

X.Q. Wang*, Y.H. Jia, Y.K. Fu, H.B. You

Horticultural Branch of Heilongjiang Academy of Agricultural Sciences,
Harbin150069, P. R. China
* xiqingwang100@163.com

Horticultural Branch of Heilongjiang Academy of Agricultural Sciences devoted to watermelon breeding from 2000. We have bred more than 10 watermelon varieties until now, and 5 watermelon varieties have been registered in Heilongjiang province and ‘Longsheng No. 1’ passed country examination in 2014. ‘Longsheng No. 1’ ‘Longsheng No. 2’ and ‘Longsheng No. 4’ are small watermelon varieties with an average fruit size 2.4 kg. ‘Longsheng No. 1’ and ‘Longsheng No. 4’ have a red fresh and ‘Longsheng No. 2’ has a yellow fresh. Their fresh have higher soluble solids content about 12.8%. They were suitable for protected cultivation in spring and with a resistance to *Fusarium wilt*, *Anthrax* and other disease. The yield on 667 m^2 is 4 000 kg in trellis cultivation and 3100 kg in open filed cultivation. ‘Longsheng No. 3’ and ‘Longshengxiyue’ fruit for open field cultivation. Their fruit are round and have a better toughness fit for transportation. The weight of ‘Longsheng No. 3’ and LongShengxiyue’ is 8-10kg. The fruit shape is round and with flower leather. The fresh is red and the center soluble solids content is 12%-13%. They have a good resistance to *Fusarium wilt.* ‘Longsheng’ series watermelon is suitable for cultivation in cold area of china.

Keywords: watermelon, breeding development, ‘Longsheng’

P1.7

Identification of *Micro-trichome*, a homeodomain-leucine zipper gene involved in multicellular trichome development in *Cucumis sativus*

Junlong Zhao, Junsong Pan, Yuan Guan, Huanle He, Hongli Lian, Run Cai

School of Agriculture and Biology, Shanghai Jiao Tong University, Shanghai 200240, China

The regulatory genes involved in unicellular trichome development in *Arabidopsis thaliana* have been intensively studied, but genes regulating multicellular trichome development in plants remain unclear. Cucumber trichomes are characterized as representative multicellular and unbranched structures, and are classified to two types, the majority are glandless and the minority are glandular. The *Micro-trichome* (*Mict*), a critical gene encoding a class I homeodomain-leucine zipper (HD-Zip) transcription factor involved in multicellular trichome development, was identified using map-based cloning in cucumber. Genetic analysis indicated that the *Mict* acts as a single dominant nuclear gene. A 2649-bp genomic deletion spanning the first and second exons, occurred in this HD-Zip gene of the *mict* mutant. Leaf trichome number counts between wild type and *mict* indicated that *Mict* represses trichome spacing. The *Mict* is strongly expressed in trichomes, specifically at the apical cell of trichome in cucumber. Overexpression of the *Mict* in *A. thaliana gl1* mutant, *gl3egl3* double mutant, *lmi1* mutant and Col-0 wild type line failed to restore or influence trichome phenotypes, preliminarily deducing that *Mict* regulates multicellular trichome development distinctly from genes regulating unicellular in *A. thaliana*.

Key words: cucumber, multicellular trichome, homeodomain-leucine zipper gene, map-based cloning.

P1.8

Recessive resistance to *Cucurbit yellow stunting disorder virus* in melon

James D. McCreight, William M. Wintermantel
U.S. Department of Agriculture, Agricultural Research Service, Salinas, CA 93905, USA

Eric T. Natwick
University of California ANR, Cooperative Extension Imperial County, Holtville, CA 92250, USA

Jonathan W. Sinclair, Kevin M. Crosby
Texas, A&M University, College Station, TX, USA

María Luisa Gómez-Guillamón
Experimental Station 'La Mayora,' C.S.I.C., 29750, Algarrobo-Costa, Málaga, Spain

Cucurbit yellow stunting disorder virus (CYSDV) reduces melon (*Cucumis melo* L.) fruit quality and yield in many parts of the world. CYSDV and its vector, sweetpotato whitefly (MEAM1 cryptic species of *Bemisia tabaci*; SPWF) are a devastating combination in the Sonoran Desert areas of California and Arizona in the USA, and Sonora and Baja California Norte, Mexico. Host plant resistance of melon to CYSDV and SPWF are high priorities for sustainable melon production in affected production areas. High-level resistance to CYSDV exhibited by TGR 1551 (PI 482420) appeared to be controlled by a dominant gene in controlled inoculation, greenhouse tests in Spain. Mean CYSDV symptom severity rating of F_1 TGR 1551 x Dulce did not significantly differ from those of TGR 1551, but the F_2 distribution suggested a recessive gene for resistance to CYSDV in controlled inoculation, greenhouse tests in Texas. TGR 1551 clearly expressed recessive genetic resistance in open field tests in Imperial Valley, California where the mean symptom severity ratings of 'Impac' and 'Top Mark' and the F_1 progeny from crosses with TGR 1551 were not significantly different, and both differed from TGR 1551; the F_2 and respective testcrosses confirmed recessive resistance to CYSDV. TGR 1551 subsequently expressed recessive resistance in subsequent greenhouse tests in Spain. PI 313970 expressed recessive resistance to CYSDV in a naturally infected test in California.

Key words: CYSDV, Cucumis melo

P1.9

Pinpointing genes underlying the quantitative trait loci of ripening characteristics in melon: ethylene, abscission zone and color

Merav Kenigswald[1,3], Elazar Fallik[2], Galil Tzuri[1], Vitaly Portnoy[1], Sharon Alkalai-Tuvia[2], Yaacov Pertzean[2], Uzi Saar[1], Fabian Baumkeler[1], Joseph Burger[1], Amnon Lers[2] and Nurit Katzir[1]

[1]Department of Vegetable Research, Agricultural Research Organization, Newe Ya'ar Research Center, Ramat Yishay, 30095 Israel
[2] Department of Postharvest Science of Fresh Produce, Agricultural Research Organization, The Volcani Center, Bet Dagan, 50250 Israel.
[3] Robert H. Smith, Faculty of Agriculture, Food and Environment, Hebrew University of Jerusalem, Israel.

Consumers' preferences determine directions of breeding of melon (*Cucumis melo L*) varieties in terms of taste, texture, appearance and shelf life. As part of the breeding effort, we crossed two melon varieties that differ in ripening patterns to create the research population: Noy-Amid, a Yellow Canary type (var*. inodorus*, non-climacteric) was crossed with Dulce, an American Cantaloupe type (var. reticulatus, climacteric). F_2 and F_3 populations were grown and phenotyped for ethylene emission, formation of abscission zone and additional fruit traits. Genotyping by sequencing was performed on 140 plants of F_3, F_1 and the parental lines, using ca. 60,000 reliable SNP markers. High resolution QTL mapping allowed for the identification of candidate causative genes involved in ethylene biosynthesis, abscission zone formation and additional traits. The accuracy of the mapping strategy was supported by the precise mapping of a QTL for orange flesh color into the locus of the known gene that regulates the orange color of fruit flesh (*CmOr*).

Key words: Genotyping by sequencing, GBS, *Cucumis melo*

P1.10

Gene Effect Evaluation of Fruit Characters and Their Related to Shelf Life in A Cross between Thai melon and Cantaloupe

Arak Tira-umphon, Somkiet Sripongprapai

School of Crop Production Technology, IAT, SUT, Nakhon Ratchasima 30000, Thailand

Shelf-life and its related characters are the key important quantitative traits closely related to the fruit quality in Thai melon and cantaloupe. It also can be used to evaluate the marketing operation, transportation and especially, for their varieties improvement. However, the genetic effect of them has not been well studied. Therefore, a cross between Thai melon "RML1" (*Cucumis melo* L. var. *conomon*) and cantaloupe "KML370" (*Cucumis melo* L. var. *cantalupensis*) was studied. The generation mean analysis of the six populations showed variety of gene actions. The additive genetic effects were the key regulator of fruit weights and fruits width. The dominant genes had effects on fruit weight of and disease percentage. Furthermore, the fruit weight was positively correlated to the fruit width and the fruit length. But it was negatively correlated to the disease percentage, Moreover the positive correlation between shelf-life and the fruit length was found.

Key words: Generation Mean Analysis, Shelf-life, Thai melon*, Cucumis melo L. var. conomon,* Cantaloupe, *Cucumis melo L. var. recticularis*

P1.11

Fruit and Seed Size in Some Mini Watermelon Lines

Nebahat Sari[1], Ilknur Solmaz[1], Seher Pamuk[1], Bora Cetin[1], Munevver Gocmen[2], Ismail Simsek[2]

[1]Dept. of Horticulture, Fac. of Agric., Univ. of Cukurova, Adana-Turkey
[3]Antalya Tarim Seed Company, Antalya-Turkey

Watermelon is an important vegetable species in terms of production amount and commercial value in Turkey. Watermelons are grouped according to fruit size as icebox, mini, medium, large and very large. In this study we measured 10 seeds with 4 replications of 13 mini watermelon lines according to following characters: seed weight, seed diameter, seed length and seed thickness. We also measured the fruit weight, fruit length and fruit diameter of these lines. All data were analyzed with Costat statistical program.

According to the research results; it was determined that each parameters was statistically significant at a significance level of 1%. Line 19 had the heaviest seed (0.051 g/1 seed), line 10 had the lightest (0.0033 g/1 seed) seed weight. The highest seed width, length and thickness were measured in line 19; the lowest data were obtained from line 10, 14, 15 and 29 in terms of seed diameter; line 10 in terms of seed size and thickness.

In case of fruit weight except line 4 all 13 mini watermelon lines used in this study were in the same statistical group. Line 4 had 160 grams of fruit weight, while other lines fruits ranged from 966.67 to 1540 grams. Fruit diameter have been identified between 6.50 cm and 19.88 cm; fruit diameter values of the lines showed similar results with fruit weight; 12 lines in the same statistical group with values between 11.77-13.75 cm, while line 4 came in last with 6.80 cm value.

Key Words: Fruit and seed weight, length and diameters

P1.12

Inheritance of resistance to *Podosphaera xanthii* in melon accessions AM55-1 and C-AC-15

Elaíne Welk Lopes Pereira Nunes[1], Eva Maria Martínez Pérez Martinez[3],
Fernando Antônio Souza de Aragão[2], Glauber Henrique de Sousa Nunes[1],
María Belén Picó-Sirvent[3]

[1]Universidade Federal Rural do Semi-árido (UFERSA), Mossoró, Brazil
[2]Empresa Brasileira de Pesquisa Agropecuária, EMBRAPA-CNPAT, Fortaleza, Brazil
[3]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV), Universitat Politécnica de Valencia, Valencia, Spain

Powdery mildew is a severe disease caused by the fungus *Podosphaera xanthii* (Px) that reduces the melon production around the world. Genetic resistance is available in melon, but the reported alleles do not confer total resistance to all the pathogen races. In this study, the inheritance of the resistance of two new resistant sources was investigated. The accessions AM55-1 and C-AC-15 (exotic types from India and Brazil respectively) were crossed with the susceptible cultivar 'Véndrantais'. Different derived populations (F_1, F_2, BC_1 and BC_2) and nine differential cultivars were screened under artificial inoculation conditions. Plants were artificially inoculated by depositing a small amount of conidia on the second true leaf of each plant. Fifty days after inoculation, the plants were scored according to the level of sporulation of the fungus. Four phenotypic classes were defined (1-4). Plants in classes 1 and 2 were considered resistant, and those in classes 3 and 4, where the infection progressed, were considered susceptible. The reactions of the differential cultivars demonstrate that the inoculated fungus belonged to Px race 2Fr. The observed resistance/susceptibility segregation ratios indicated a monogenic and dominant inheritance in AM55-1A and two independent genes with epistatic interaction in C-AC-15.

Key words: *Cucumis melo*, powdery mildew, physiological race, epistasis, genetic control.

P1.13

Morphological and molecular characterization of new melon germplasm resistant to *Podosphaera xanthii*

Elaíne Welk Lopes Pereira Nunes[1], Anânkia Ricarte de Oliveira[1], Eva Maria Martínez Pérez, Martinez[3], Glauber Henrique de Sousa Nunes[1], María Belén Picó-Sirvent[3]

[1]Universidade Federal Rural do Semi-árido (UFERSA), Mossoró, Brazil
[2]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV), Universitat Politécnica de Valencia, Valencia, Spain

Powdery mildew, mainly caused by the biotrophic fungus *Podosphaera xanthii*, is a devastating disease of cucurbits worldwide. The use of resistant cultivars is a main strategy to control this disease. The objective of the present work was to evaluate a highly variable collection of melon accessions for resistance to *P. xanthii.* In the first experiment fifty-six melon accessions were screened. These were selected from a larger melon core collection, representing different geographical origins and most of the botanic groups within *Cucumis melo* subspecies *agrestis*. Artificial inoculation under greenhouse conditions was conducted in Valencia, Spain. In the second experiment fifteen selected melon accessions were screened for resistance to races 1 and 5 in Mossoró, Rio Grande do Norte State, Brazil. The accessions C-AC-02, C-AC-09, C-AC-15, C-AC-34, and AM55-1 were highly resistant in both experiments. These were morphological and molecularly characterized with SSRs and SNPs markers. The accessions C-AC-02, C-AC-09, C-AC-15, and C-AC-34 (all landraces from Brazil) exhibited characteristics of the botanic group *momordica,* while the Indian accession AM55-1 fitted to the *acidulus* group. The molecular characterization confirmed the morphological results. The accessions identified may be useful as sources of resistance in breeding programs against *P. xanthii* in Brazil and Spain.

Key words: *Cucumis melo*, powdery mildew, microsatellites, Single nucleotide polymorphisms, physiological races, resistance.

P1.14

Characterization of some melon (*Cucumis melo* L.) pure lines and their hybrid combinations and resistance to *fusarium oxysporum f. sp. melonis*

Ahmet Secim[1], Buse Özdemir[2], Tugce Ozsan[2], A. Naci Onus[2]

[1]Gento Seed Company, [2]Akdeniz Univ., Faculty of Agr., Antalya, Turkey

This study was performed to determine the morphological characters of some melon (*Cucumis melo* L.) pure lines and their hybrid combinations as well as their resistance to *Fusarium oxysporum f. sp. melonis*. During hybridization of the research, 20 pure lines of plant material each of with high heterosis, representing the cantaloupe, charentais, and kirkagac melon types, belong to Gento Vegetable Seeds Company, were employed. All genotypes were infected with *fusarium* isolates, among the resistance lines of two cantaloupe types and one kirkagac type melons were defined as male parents and were hybridized. As a result of hybridization; 30 cantaloupe types and 2 kirkagac types hybrids were obtained. Morphological characterizations of these hybrids were conducted on 26 different traits such as date of flowering, plant characteristics, fruit characteristics, leaf characteristics and pomological fruit characteristics. In addition to morphological characterization, 4 yield specialties and 2 heterosis of yield specialties were also studied on hybrid varieties, pure lines and commercial hybrid varieties. While heterosis variations were found to be between -24.59% to 70.71% in hybrids productivity comparing to parents, the heterobeltiosis percentages were found to be between -40.15% and 50.87%.

Key words: *Cucumis melo* L., *fusarium oxysporum f. sp. melonis*, morphological characterization, heterosis, breeding.

P1.15

Screening of *Cucurbita* germplasm for ToLCNDV resistance under natural greenhouse conditions

Cecilia Martínez[1], Susana Manzano[1], Zoraida Megías[1], Alicia García[1], Rafael Garrido[1], Harry S. Paris[2], Manuel Jamilena[1]

[1]Agrifood Campus of International Excellence (CeiA3) and BITAL, Department of Biology and Geology, University of Almería, La Cañada de San Urbano s/n. 04120 Almería, Spain.
[2]A.R.O., Newe Ya'ar Research Center, P. O. Box 1021, Ramat Yishay 30-095, Israel

In 2012, a new severe disease started to affect zucchini and other cucurbit crops in SE Spain. The identified causative agent was Tomato Leaf Curl New Delhi Virus (ToLCNDV), a begomovirus with a bipartite genome of single-stranded DNA that was previously reported to affect various crop species of the *Solanaceae* and *Cucurbitaceae* in India.

To identify sources of resistance to this new virus in *Cucurbita*, we performed a screening of 142 accessions under natural infection with viruliferous whiteflies in a greenhouse at Almería, Spain. The entries were mostly *C. pepo* and *C. moschata*, selected from the germplasm banks at the University of Almería in Spain (BSUAL), the U.S. Department of Agriculture, and the Newe Ya'ar Research Centre in Israel. Symptoms to ToLCNDV were assessed by a scale ranging from 0 to 4 in two replications of 6-8 plants at 21, 28 and 35 days post inoculation (dpi). In the most promising entries, the level of tolerance was also assessed by a PCR-based diagnostic method to identify the presence of the virus in the apex of the plants at 28 and 35 dpi.

Most of the inoculated accessions were very susceptible to the ToLCNDV. Severe symptoms were found in most *C. pepo* accessions at 35 dpi, but five accessions showed some of tolerance, expressed as a delay in the appearance of symptoms and their reduced incidence. Two *C. moschata* accessions were found to be resistant as they remained asymptomatic, and accumulated no virus in the plant apex during the entire essay.

Key words: *Cucurbita moschata*, *Cucurbita pepo*, ToLCNDV, symptoms, PCR

P1.16

Genetic diversity of fruits of chilacayote (*Cucurbita ficifolia* Bouché) by the AFLP technique

Araceli Moya-Hernández, Elsa Bosquez-Molina,
Alejandra Serrato-Díaz, Gerardo Blancas-Flores

Department of Biotechnology. Universidad. Autónoma Metropolitana Unidad Iztapalapa,
México

Cucurbita ficifolia Bouché is a wild crop known in Mexico as "chilacayote" whose fruits are used as food. The fruits show a pericarp and seeds of different color. Recent studies report that this species has remarkable hypoglycemic properties. However, there is not any report which shows if the hypoglycemic properties depend on the phenotypic characteristics. The objectives of this study were: 1) Evaluate the phenotypic characteristics of *C. ficifolia* of different growing areas through a molecular differentiation. 2) Determine if the aqueous extracts of the fruits from different regions have the same hypoglycemic effect. In order to achieve the first objective, young and fresh leaves of chilacayote from the states of Hidalgo, Tlaxcala, Michoacán, Puebla and Mexico State were collected. DNA samples were analyzed through AFLP (Amplified fragment length polymorphism). A binary matrix of presence-absence was built, and a dendrogram was obtained with the UPGMA method (Unweighted Pair Group Method with Arithmetic Mean). For the second objective, an aqueous extract from the fruits was obtained and 500 mg extract / kg was administered to male mice of 35 g (strain CD-1). Glibenclamide (20 mg / kg) was used as positive control and an isotonic saline (4 ml per kg) as control. The molecular results showed an 89.4-98.5% of similarity among samples and their relationships are associated with the geographical region to which they belong. It was also found that the fruits of all regions showed higher hypoglycemic activity than the glibenclamide.

Key words: *Cucurbita ficifolia*, AFLP, hypoglycemic activity

P1.17

Evaluation of Genetic Relationships among Hungarian and Turkish Melon (*Cucumis melo*) Accessions by SSR Markers

Csaba Szamosi[1], Ozhan Simsek[2], Yildiz Aka-Kacar[2],
Ilknur Solmaz[2], Nebahat Sari[2]

[1]Rijk Zwaan Seed Company, Antalya-Turkey
[2]Dept. of Horticulture, Fac. of Agric., Univ. of Cukurova, Adana-Turkey

Molecular diversity and genetic relationships among the most typical Hungarian and Turkish melon accessions were analysed using SSR markers. A total of 30 melon accessions were characterized by fifteen SSR primers for melons.

Seventeen SSR primers generated a total of 69 bands across the 30 melon accessions, of which 66 were polymorphic. The sizes of the bands ranged from 112 to 237 bp. The pair-wise genetic distances (GD) for the 30 melon accessions, based on fifteen SSR markers that gave amplification, ranged from 0.28-0.96. Accessions “Kav 13” and “Kav 173” showed the largest genetic distance (0.28), while the accessions “Kav 30” and “Kav 39” (two Kirkagac type accessions from different geographic origin) were the most similar genotypes (0.96) in the germplasm.

Based on the pair-wise genetic distances obtained by SSR marker results, Hungarian accession S6 showed 62% similarity with the Turkish genotype “Kav 16” and 50 % with “Kav 13”. Clustering dendrograms based on the genetic distance matrix produced by NTSYS-PC program indicated genetic relationships among melon accessions of the different countries. Accessions were divided into two main groups (I-II). Within these groupings, three sub clusters, two within cluster I and one within cluster II, were defined. The obtained data showed that the investigated germplasm contained high genetic variability.

Key words: *Cucumis melo* L., genetic relationship, molecular markers, SSR

P1.18

A simple assay for resistance to cucumber black root rot and screening *Cucurbita* genetic resources for resistant rootstock

Koichiro Shimomura[1], Mitsuhiro Sugiyama[1], Yoichi Kawazu[1],
Yosuke Yoshioka[2], Norio Nishimura[1]

[1] NARO Institute of Vegetable and Tea science, kusawa360, Ano, Tsu, Mie, 514-2392, Japan
[2] Faculty of Life and Environmental Sciences, University of Tsukuba, 1-1-1 Tennodai,
Tsukuba, Ibaraki, 305-8572, Japan

Cucumber black root rot caused by the fungal phytopathogen *Phomopsis sclerotioides* is a serious soil-borne disease of open-field cultivation in Japan. Grafting is one of the most effective control methods for suppressing outbreaks of soil-borne disease (e.g., Fusarium wilt) in cucumber, and the cucumber scion is usually grafted on pumpkin rootstock. In Japan, *Cucurbita moschata* is mostly used as rootstock because of its high disease resistance and ability to produce bloomless cucumber fruit. However, no bloomless-type rootstock cultivar resistant to black root rot has been reported, only the bloom-type rootstock cultivar *C. ficifolia*. Here, we report the development of a simple assay for evaluating disease severity and screening *C. moschata* rootstock genetic resources for resistance to cucumber black root rot. Two weeks after sowing, soil was removed from the roots of seedlings. Then, the seedlings were transplanted into a mixture of *P. sclerotioides*, wheat bran, and sterilised potting soil, and grown in a phytotron at 25°C. During field assays, it usually takes a few months before typical symptoms appear to evaluate disease severity. In our method, disease severity can be evaluated approximately 3 weeks after inoculation with *P. sclerotioides*. We evaluated disease severity in approximately 100 accessions of *C. moschata*. We observed differences in disease severity among the accessions, but no accessions demonstrated the same or higher resistance to black root rot than *C. ficifolia*. Further screening of genetic resources will be required to find *C. moschata* accessions with high resistance to this disease.

Key words: black root rot, *Cucurbita moschata*, grafting, *Phomopsis sclerotioides*, rootstock

P1.19

Identification of QTL associated with fruit traits in linkage groups II and IV of a RIL melon population derived from 'TGR-1551'

Paola Beraldo-Hoischen, María Luisa Gómez-Guillamón,
Ana I. López-Sesé

IHSM-La Mayora, CSIC-UMA, 29750-Algarrobo-Costa, Málaga, Spain

A melon RIL population (F7:F8), derived from the Zimbabwean and multi-resistant accession 'TGR-1551' and the Spanish cultivar 'Bola de Oro', was characterized in order to detect QTL associated with vegetative, phenologic, and fruit traits. Means, standard deviations, pair-wise correlation, and ANOVA were estimated from data recorded in two growing seasons. Fifty-six QTL were detected for the 21 traits recorded during both years in eleven out of the twelve linkage groups (LG) of melon genetic map. Twenty-one and eleven of these QTL were found in LGII and IV, respectively, and they were involved mainly in fruit and ovary traits. Concretely, in LG II the QTL identified explained between 12.5 and 37.5% of the phenotypic variation observed, showing LOD scores from 2.51 to 9.93 (2.5-3 of LOD threshold). The QTL associated with fruit length, female corolla diameter, and shape of both ovary and fruit, showed more than 25% of the phenotypic variation observed in those characters. In linkage group IV, the eleven QTL detected showed percentages of phenotypic variation explained ranging from 11.6 to 26.8%, with LOD scores between 3.07 and 7.63 (2.5-2.9 of LOD threshold). More than 20% of the phenotypic variation observed for these characters was explained by the QTL associated with length and weight of fruits.

Key words: fruit shape, length, ovary, quantitative trait loci, recombinant inbred line

P1.20

Studies on in Vitro Culture and Plant Regeneration of Unfertilized Ovary of Pumpkin

Ziyang Min [1], Han Li [1], Tian Zou [1], Long Tong [1],
Juan Cheng [1] , Xiaowu Sun [1,2*],

([1]College of Horticulture,Hunan Agricultural University,changsha,Hunan 410128,china;
[2]Hunan Province Melon Research Institute,Shaoyang, Hunan 422001,china)
Corresponding author: Xiaowu Sun E-mail: sunxiaowu2007@126.com

Using unfertilized ovaries of pumpkin as explants, effects of different combinations and concentrations of growth regulators, genotypes, embryo sac development stages, disinfection methods and duration of high temperature pretreatments on embryoid induction via in vitro culture were determined to establish a regeneration system of unfertilized ovaries of pumpkin. The results showed that: the mediums of MS+ 4.0 mg•L^{-1}2, 4-D+0.5 mg•L^{-1} NAA+1.0 mg•L^{-1}6-BA and MS+0.04 mg•L^{-1}TDZ achieved higher induction rates of 19.8% and 20.1% respectively compared to other mediums examined, with the TDZ-induced method easier in operation. Among the 6 pumpkin varieties tested, two varieties (Xue feng mi ben and E yu nan gua) with stronger growth had higher embryoid induction rates and were more suitable to be used as experiment materials. The operation of slicing and then sterilizing the ovaries picked in the bloom day decreased the cavernous callus formation effectively and increased the embryoid induction rate. Treatments with darkness and heat shock (35°C) for 5 days could help ovary turn green and induce embryoid. When moved to hormone-free MS medium, the cotyledon embryos developed to regenerated seedlings and survived after transplantation. There were 7 regenerated plantlets with the chromosomal number of n=x=22 and average number of chloroplast in stomatal guard cell was 4.28, which indicated that they were haploid plants.

Key words: embryoid, pumpkin, plant regeneration, unfertilized ovary

P1.21

Genetic diversity analysis of Iranian melons (*cucumis melo* L.) accessions using ISSR markers

Abdolali Shojaeiyan, Masoud Maleki, Sajad Rashidi-Monfared

Department of Horticultural Science, Tarbiat Modares University, Tehran, Iran

Melon (*Cucumis melo* L.) is one of the old vegetables in Iran, so Iran is a center of genetic diversity. In this study to assessment genetic diversity within and between 27 accessions used ISSR markers. A total of 23 ISSR primers were screened and based on degree of polymorphism, 10 ISSR primers were selected for the study. To appraise genetic population structure was applied GeneAlex software. Polymorphic information content and marker index are estimated to find distinction power of markers. High value of these was related to $(AG)_8T$ primer. Polymorphism percent mean was 51.6%. Molecular variation analysis used to calculation share percentage of genetic diversity within and between accesstions showed which 31% of total variation is related to the variation of between accesstions and 69% of total variation into accessions. Use of ISSR marker along with polyacrylamide gel could reveal genetic diversity inside and between accessions.

Key words: melon, *Cucumis melo*, genetic diversity, ISSR. molecular markers

P1.22

Assessment of genetic diversity using ISSR markers in Iranian snake melon (*Cucumis. melo* var. *flexuosus*)

Abdolali Shojaeiyan, Narges Dastranji, Mohsen Falahati-Anbara

Department of Horticultural Science, Tarbiat Modares University, Tehran, Iran

Landraces, due to the compatibility of that during the time, have obtained the desirable traits of genes. Iran appears to be one of the centers of diversity in snake melon. With regard to the economic importance of this plant as well as the little attention that has been focused on, it is necessary to assess genetic studies such as genetic variation in the case of this plant, especially the local landraces. In this study, the genetic variation within and between accessions of 16 snake melon using 10 ISSR primers were evaluated. A total of 93 bands were identified with an average of 8.2 polymorphic bands per primer. The average level of polymorphism was 82.95%. The average of polymorphic information contents and marker index was 0.34 and 2.58 respectively. Genetic diversity within accessions was 85% while it was 15% between accessions. Cluster analysis was carried out by UPGMA method and Nei's genetic distance coefficient. Cluster analysis classified the accessions into 5 major groups.

Key words: Cluster analysis, *Cucumis melo* var. *flexuosus*, Genetic diversity, ISSR markers, snake melon

P2.1

Pleiotropic effects of *CmACS7* on fruit growth and quality parameters in melon (*Cucumis melo*)

Marina Martos-Fuentes[1], Juan Antonio Lizarzaburu[2], Encarna Aguayo[3], Cecilia Martínez[4], Manuel Jamilena[4]

[1]Instituto de Biotecnología Vegetal. Universidad Politécnica de Cartagena, Spain.
[2]Bayer Crop Science Vegetable Seeds, 30593 La Palma-Cartagena, Spain.
[3]Dept. Ingeniería de Alimentos y del Equipamiento Agrícola, ETSIA.
Universidad Politécnica de Cartagena, Spain.
[4]Agrifood Campus of International Excellence (CeiA3) and BITAL,
Department of Biology, University of Almería, 04120 Almería, Spain.

CmACS7 is a sex determination gene that is known to be involved in the biosynthesis of ethylene at very early stages of pistillate flower developmet in melon, promoting so the arrest of stamen during the development of female flowers, and resulting in monoecious plants. Loss-of-function mutations for *CmACS7* reduce the production of ethylene in pistillate flowers, which results in hermaphrodite flowers and andromonoecious plants. In this paper we compare fruit growth and quality in monoecius and andromonoecious isogenic lines of 5 different genotypes of Galia and Cantaloupe melon types. Results demonstrate that the gene not only regulates sex determination but also other fruit growth parameters. The mutation that causes andromonoecy and reduces ethylene in female flowers promoted a reduction in fruit set, fruit weight and number of total and viable seeds, as well as an alteration of fruit shape in the five genotypes analyzed, although in some genotypes the monoecy stability was reduced, concomitantly with a loss of significant differences between isogenic lines. The gene mutation, however, had no effect on fruit quality parameters such as total soluble solids, fruit pH and titratable acidity. To assess whether these pleiotropic effects of the gene are associated with ethylene biosynthesis, we have analyzed the production of ethylene in the ovary/fruit of unpollinated flowers during the days immediately after anthesis, confirming a higher induction of ethylene in the monoecious isoline. Results are discussed in relation to ethylene production and autoregulation of ethylene biosynthesis in flowers and fruits.

Key words: fruit set, seed quantity and quality, fruit quality, Cantaloupe, Galia

P2.2

Efficient production of *eyfp*-expressing *Cucumis melo* diploid plants using different type of explants

García-Almodóvar R.C.[1], Gosalvez.B.[1], Aranda. M.A. [1] and Burgos L.[2]

[1]Grupo de Patología Vegetal. Departamento de Biología del Estrés y Patología.
[2]Grupo de Biotecnología de Frutales. Departamento de Mejora Vegetal.
CEBAS-CSIC. Apartado de Correos 164, 30.100-Murcia, Spain.

Melon (*Cucumis melo* L.) is consensually considered as a recalcitrant species for genetic transformation. Additionally, many works describe that regenerated transgenic plants are polyploids. Here we studied the effect of using different type of explants from the proximal portion of the BGV-130 melon seeds on the transformation efficiency and the ploidy status of regenerated transformed plants. EHA105 strain of *Agrobacterium tumefaciens* containing the pMOG800 vector harboring the *eyfp* reporter gene and the selectable kanamycin resistance *npt*II was used in transformation experiments. Highest *eyfp* expression was found in hypocotyl slices, followed by cotyledon explants from the most proximal part of the seed (closer to the root meristem), though the former regenerated poorly. Positive EYFP buds were recovered with transformation efficiencies from 2.5% to 6% depending on the explant used. On the other hand, escapes (buds that didn´t show fluorescence) were easily identified and discarded. These results indicated that *EYFP* could be an effective reporter gene to identify and recover transgenic buds in melon. Additionally, using quiescent seeds and the cotyledon explants from the proximal parts of the seed allowed the recovery of more than 80% of diploid plants. The methodology developed is efficient enough to be used to produce transgenic plants harboring all types of transgenes, including those designed for genome editing by directed mutagenesis.

Keywords: transformation efficiency; transgenic buds; ploidy status; melon.

P2.3

Proteomic Analysis of Roots of Watermelon Seedlings

Zhang Man, Yang Xing-ping*, Xu Jin-hua, Liu Guang,
Yao Xie-feng, Li Ping-fang

Institute of Vegetable Crops, Jiangsu Academy of Agricultural Sciences,
Nanjing 210014, P.R.China

To understand the function of differential expression proteins in roots of watermelon seedlings, proteins of watermelon roots at different development stages were studied using proteomics technique. A comparative study with differences in protein group analysis of watermelon roots was carried out by using two-dimensional gel electrophoresis. There were 12 differentially expressed protein spots identified by Electrophoresis and MALDI-TOF/TOF analysis. These proteins were involved in protein biosynthesis (16.7%), metabolism (33.3%), plant defense (33.3%) and GA signaling (8.3%). Expression profile of 12 protein spots was differential, of these, 4 proteins were up-regulated, 2 down-regulated and 6 differentially-regulated. Four candidate proteins were further investigated using quantitative real time PCR in mRNA level. Expression changes of Jasmonate-induced protein 1 gene and MAP kinase gene in mRNA level were consistent with that in proteome changes, while the expression of Gibberellin receptor GID1L2 gene and Jasmonate-induced protein 2 gene was related with transcriptional regulation. This work provided a theoretical basis for further studying the molecular mechanism of watermelon root development.

Key words: gene expression; proteomics; root development; watermelon rootstocks

P2.4

The molecular identification and detection of *Fusarium oxysporum* f. sp. *momordicae*

Chen Zhendong[1, 2], Wen Junli[1], Huang Rukui[1, 2], Qin Jian[1], Li Qiqin[3]

(1)Vegetable Research Institute, Guangxi Academy of Agricultural Sciences, 174 Daxue Road, Nanning, Guangxi 530007, China; (2)Guangxi Crop Genetic Improvement and Biotechnology Lab, 174 Daxue Road, Nanning, Guangxi 530007, China; (3) College of Agriculture, Guangxi University,100 Daxue Road, Nanning, Guangxi 530005, China

Fusarium wilt caused by *Fusarium oxysporum* f. sp. *momordicae* Sun & Huang (*FOM*) is a serious soil-born disease of bitter gourd (*Momordica charantia* L.). The identification of *FOM* isolates were based on morphometrics and pathogenicity on the host plant. But these conventional methods are time-consuming and laborious. In order to establish a rapid, sensitive and accurate method to identify and detect *FOM* isolates, we analyzed the genomic DNA polymorphism of 24 *F. oxysporum* f. spp. of *cucurbitaceae* isolates by random amplified polymorphic DNA (RAPD) PCR fingerprinting with 320 arbitrary primers and obtained a unique 519 bp fragment $S58_{-519}$ from *FOM* isolates. We designed a pair of specific SCAR primers F1/R1 to convert this RAPD marker $S58_{-519}$ into a stable SCAR marker RS_{-256}. The RS_{-256} was specific for identifying *FOM* isolates, the detection sensitivity for this specific marker was 1 $pg·\mu L^{-1}$ of pathogen genomic DNA, and 100 conidia per gram in soil. The SCAR-PCR based method could detect the *FOM* in the tissues of infecting bitter gourd seedling before the symptom appearance, and thus provides a method to identify the *FOM* without host inoculation tests.

Key words: Bitter gourd; *Fusarium oxysporum* f. sp. *momordicae*; Molecular marker; Identification; Detection

P2.5

Differential Responses of Proteomes by Foliar Application of Plant Defence Activators in Melon and Korean Melon Seedling

Hwang, MR[1], Kim, HM[1], Choi, HG[2], Kwon, JK[2], Kang, NJ[3*]

[1]*Gyeongsang National University, Jinju 660-701, Korea*
[2]*Protected Horticulture Research Station, NIHHS, RDA, Pusan 618-800, Korea*
[3]*Insti. of Agric. & Life Sci., Gyeongsang National University, Jinju 660-701, Korea*

This study was conducted to obtain basic information on proteomic responses of melon and Korean melon seedlings treated by 2, 6-dichloroisonicotinic acid (INA) and methyl jasmonate (MeJA). Foliar application of INA and MeJA-induced alterations in protein expression in the melon and Korean melon leaves were detected by two dimensional electrophoreses, and 48 protein spots showing altered expression were selected. Among the selected protein spots, 9 protein spots were up-regulated and 20 spots down-regulated in melon. In Korean melon, 8 protein spots were up-regulated and 11 spots down-regulated. Out of 48 differentially expressed protein spots, 40 protein spots were identified using mass spectrometry (MALDI-TOF-TOF) and NCBI protein database. Among the identified proteins, some proteins are known to be involved in various stress responses, but the others are not directly involved in stress responses. Also, proteins from the photosynthesis, sulfer metabolism, and respiration, aminoacid metabolism were identified.

Key words: INA, Korean melon, MeJA, Melon, Proteomics

P2.6

Analysis of ABC genes during melon ripening

Jorge Corbacho and Maria C. Gomez-Jimenez

University of Extremadura, Avda de Elvas s/n, 06006 Badajoz, Spain

The ATP-binding cassette (ABC) transporter superfamily is the largest transporter gene family responsible for transporting specific molecules across lipid membranes in all living organisms. Although the superfamily of ABC proteins plays key roles in the physiology and development of plants, the functions of members of this family mostly remain to be clarified, especially in crop plants. Thus, analysis of this family in melon (*Cucumis melo* L.) will be helpful in the design of strategies for functional analysis. Here, we identified 14 putative ABC genes from charentais melon fruit and analyzed their phylogenetic relationships. Gene expression analysis revealed that they are differentially regulated dependent on tissue and developmental stage. Moreover, we have investigated their temporal expression patterns during melon ripening using quantitative real-time PCR. Our results indicate that 4 ABC genes (*CM-ABCF1*, *CM-ABCF4*, *CM-ABCG23* and *CM-ABCE2*) were up-regulated during melon ripening. Of these, the expression of one ABC gene, *CM-ABCG23*, was reduced in ethylene-suppressed antisense ACC oxidase fruit, suggesting that this gene is potentially regulated by ethylene. Our analysis provides novel information for the ABC genes during ripening and lays a foundation for future analysis of their hormonal regulation.

Key words: ABC transporter, ethylene, melon, ripening

P2.7

Early transcriptomic events involved in melon mature-fruit abscission

Jorge Corbacho[1], Félix Romojaro[2], Jean-Claude Pech[3],
Alain Latché[3], Maria C. Gomez-Jimenez[1]

[1]University of Extremadura, Avda de Elvas s/n, 06006 Badajoz, Spain
[2]CEBAS-CSIC, Campus de Espinardo, PO Box 164, 30100 Murcia, Spain
[3]UMR990 INRA/INP-ENSA Toulouse, F-31326 Castanet-Tolosan, France

Mature-fruit abscission in fleshy-fruit is a genetically controlled process with mechanisms that, contrary to immature-fruit abscission, has not been fully characterized. Here, we use pyrosequencing to characterize the transcriptomes of melon abscission zone (AZ) at three stages during AZ-cell separation in order to understand abscission control at an early stage of AZ-activation. The results show that by early induction of abscission, the melon AZ exhibits major gene induction, while by late induction of abscission, melon AZ shows major gene repression. Analysis of gene-expression from these AZs reveal that a sequential induction of cell-wall-degrading genes is associated with the upregulation of genes involved in endo and exocytosis, and a shift in plant-hormone metabolism and signaling genes during abscission. This is accompanied by transcriptional activity of small-GTPases and synthaxins together with tubulins, dynamins, V-type ATPases and kinesin-like proteins potentially involved in abscission signaling. Early events are potentially controlled by down-regulation of MADS-box, AP2/ERF and Aux/IAA transcription-factors, and up-regulation of homeobox, zinc finger, bZIP, and WRKY transcription-factors, while late events may be controlled by up-regulation of MYB transcription-factors. Overall, the data provide a comprehensive view on abscission in fleshy-fruit, identifying candidate genes and pathways associated with early induction of fruit abscission. Our comprehensive gene-expression profile will be very useful for elucidating gene regulatory networks of the fruit abscission in fleshy-fruit.

Key words: expressed sequence tags, mature-fruit abscission, melon, pyrosequencing, transcriptomic comparative

P3.1

To set or not to set: new tools to study the control of cucumber fruit set

Yulia Shnaider, Yariv Brotman and Rafael Perl-Treves

Faculty of Life Sciences, Bar Ilan University, Ramat Gan 5290002, Israel

Understanding the developmental control of fruit set is an important challenge. In cucumber, fruit set is governed by several hormones, including gibberellin, cytokinin and auxin, and is also affected by assimilate supply and previous fruit load. We have produced transgenic cucumbers that express reporter genes under the control of the Exp, ARR5 and DR5 promoters, reported to respond to gibberellin, cytokinin and auxin, respectively. Specific expression patterns were observed in ovaries and ovules of cucumber at different stages, and we try to correlate these with ovary developmental fates. To determine the possible role of metabolite supply in fruit set, we monitored the transcript levels of sugar-metabolism genes in the ovaries, including ovary-specific invertases, as well as a fruit-set related galactosyl transferase. Finally, metabolomic analysis of ovaries has been initiated, to look at changes in primary and secondary metabolites, hormones and lipids during cucumber fruit set.

Key words: cucumber, fruit set, metabolomics, hormone reporter genes

P3.2

Biochemical changes in pumpkin hybrid seeds at different stages of maturation

[1]Patrícia P. da Silva, [2]Denise C. F. S. Dias, [1]Warley M. Nascimento

[1]Embrapa Hortaliças, CP 0218, 70359-970 Brasília-DF, e-mail:
warley.nascimento@embrapa.br; [2]Universidade Federal de Viçosa - MG

This study aimed to evaluate the biochemical changes of pumpkin hybrid seeds obtained from fruits harvested at different maturity stages (15, 30, 45, 60 and 75 days after anthesis - DAA). In every stage, thirty fruits were harvested: fifteen fruits had their seeds extracted immediately and the other fifteen fruits were stored for twenty days in plastic boxes and, after this period, had their seeds extracted. After seed processing and drying, the following determinations were made: seed moisture content, germination, first count, electrophoretic profile analysis of heat-resistant proteins (Late Embryogenesis Abundant - LEA) and activity of antioxidant enzymes (peroxidase and ascorbate peroxidase). Seeds from fruits harvested at 30 DAA showed high concentration of antioxidant enzymes and low concentration of LEA proteins, demonstrating themselves were immature and that the desiccation possibly caused damage in their cell membranes. Thus, there was increased activity of antioxidant enzymes by the accumulation of reactive oxygen species (ROS), leading the seeds not to resist the oxidative damage. The reduction in germination and seed vigor was caused possibly by the high concentration of antioxidant enzymes and low concentration of LEA proteins.

Keywords: *Cucurbita máxima, Cucurbita moschata*, Late Embryogenesis Abundant, antioxidant enzymes

P3.3

Influence of quantity and disposition of pollinated flowers on production of squash hybrid seed

[1,3] Warley Marcos Nascimento, [1]Graziele P. Lima, [2]Ricardo Carmona,
[1]Patrícia Pereira da Silva, [1]Raquel Alves de Freitas

[1]Embrapa Vegetables, CP 0218, 70359-970 Brasília-DF; Brazil,
E-mail: warley.nascimento@embrapa.br;
[2]UnB - Depto. Agronomia, Brasília, DF, Brazil
[3]Bolsista de Produtividade em Pesquisa, CNPq.

The low seed production of local squash hybrid from Brazilian pure lines has contributed for an increasing of seed import, mainly from Japan. A field trial was carried out at Embrapa Vegetables, Brasília, DF, Brazil, to evaluated the effects of quantity and disposition of pollinated flowers in the production and physiological quality of hybrid seeds of 'Jabras', a tetsukabuto type squash. The experimental design was randomized, using three replicates of 20 plants/plot and six treatments, pollinating the following flowers: first; first and second; only first, second and third; only second; second and third; and only third. The pollination of the first or second flower, independently of their location, resulted in the highest seed production of squash hybrid due to the higher fruit set.

Keywords: *Cucurbita máxima*, *Cucurbita moschata,* Pollination, fruit set

P3.4

Diurnal temperature variation significantly affects cucumber fruit growth

Hans-Peter Klaering, Angela Schmidt

Leibniz Institute of Vegetable and Ornamental Crops Grossbeeren/Erfurt e.V., Grossbeeren, Germany

Decreasing the temperature in heated greenhouses significantly reduces CO_2 emission. However, growth of the plants may be decreased with major implications for yield. The thermophile cucumber is known to be very sensitive to low temperature. In particular fruit growth is considerable decreased. Nevertheless, reports show that cucumber can be grown successfully at low night temperature. In order to explain this phenomenon, the effect of the diurnal temperature variation on fruit growth was investigated in a growth chamber experiment. The temperature in three chambers during the light and dark phase was 16/16 °C, 19/13 °C, and 11 °C during the dark phase with an increase to 25 °C during the middle of the light phase, respectively. All treatments resulted in a daily average of 16 °C. Introducing the diurnal temperature variation considerably increased fruit growth compared to cultivation at 19/13 °C, where it was still greater than at constantly 16 °C. Related to fruit dry matter, this sequence was preserved although fruit dry matter content was less at variable than at constant temperature. Total biomass and water uptake however, appeared to be unaffected by the treatments because leaf and especially root dry matter were greater at constant than at variable temperature. Summarising, diurnal temperature variations affect dry matter allocation to the plant components but not dry matter growth. Short daily periods with high temperature can mitigate the negative effect of low night temperature on fruit growth and yield.

Keywords: Biomass, dry matter allocation, dry matter content, root

P3.5

A new training method to reduce wilting from cucumber black root rot (*Phomopsis sclerotioides*)

Takayuki Yamaguchi

Iwate Agricultural Research Center, Kitakami Iwate, Japan

In Japan, the incidence of damage caused by cucumber black root rot (*Phomopsis sclerotioides*) has been increasing. To protect against this disease, a soil fumigant such as a chloropicrin is often used. These soil disinfectants can only be applied after harvesting. Therefore, damage caused by this disease cannot be avoided during crop production. *P. sclerotioides* fungi were infected into cucumber roots grafted onto the squash *Cucurbita moschata*. The grafted roots exhibited reduced water absorption ability. As a result, the plants wilted and eventually died.

However, some plants had many healthy roots. These plants did not wilt, even if the fungus infected their roots. Therefore, we modified the training strategy such that it was stopped at an earlier time to promote new root production. This new training method can reduce grafted plant wilting, even after *P. sclerotioides* infection. We inferred that stopping training increases meristem and root production, and therefore reduce wilting.

It is necessary to stop the training before grafted cucumber plants begin to wilt. To examine this, we used plants in the *Cucumis* genus as indicators of wilting. *Cucumis* plants wilted more than one month earlier than *C. moschata* plants with grafted cucumber roots. Based on the results of this comparison, plant wilting in response to cucumber black root rot can be effectively reduced using this new training method.

Key words: cucumber black root rot, *Phomopsis sclerotioides,* disease control, *Cucumis*

P3.6

Evaluation of the *Cucumis sativus* Ontogeny in Warm Tropical Regions under Open Field, Low, Medium and High-Cost Greenhouses

Salcedo G.A[1]; Reca J.[2], Pérez-Saiz, M.[2] and Lao M.T.[3]

[1]Experimental Center of Agroplasticulture, University of Guayaquil.
Ecuador Faculty of Development Science Av. Delta s/n. Ecuador
[2]Department of Engineering, Higher Engineering School, University of Almería,
Agrifood Campus of International Excellence (CeiA3).
Ctra. Sacramento s/n. 04120 Almería, Spain
[3]Department of Agronomy, Higher Engineering School, University of Almería,
Agrifood Campus of International Excellence (CeiA3).
Ctra. Sacramento s/n. 04120 Almería, Spain
Corresponding author: mtlao@ual.es

In the warm coast of Ecuador, cucumbers grown in soil systems and open fields present very low yields due to the long period of heavy rainfall and the existence of a large number of pests and diseases. The cultivation under protection and the soilless system could be a solution that would increase the yields. The ontogeny of the cucumber *Cucumis sativus* cv Diamante has been evaluated. The trial was held from October 3rd to December 13th. Four plots of 2400 m^2 each, 3 under protection structures: multi-tunnel type with 5 tunnels of 8 m wide with different cost: high cost (100%) with soilless system, medium and low cost in soil system (50% and 30% respectively) and open field. In all plots the same cultural techniques were used. To study the morphological behaviour, plant height (cm), stem diameter (cm), number of leaves, width (cm) and the length of the leaves (cm), their dry and fresh weight (g) were measured. To study their productive performance the following parameters were evaluated: number of flowers, number of fruits per plant, fruit diameter (cm), reducing sugars (ºBrix) and crop yield (kg m^{-2}). The results allow us to conclude that the morphological behaviour of the cucumber plants grown under different structures of protection is significantly better than those growing in open field. The highest yield (3.3 kg m^{-2}) has been obtained under the high cost structure in soilless system and the lowest yield (2.7 kg m^{-2}) in open field, in soil system.

Keywords: food security, soil system crop, soilless system crop, fertigation

P3.7

Evaluation of the *Cucumis sativus* yield by direct seeding *versus* the nursery in warm tropical regions, in open field and greenhouse

Salcedo G.A[1]; Reca J.[2], Pérez-Saiz, M.[2] and Lao M.T.[3]

[1]Experimental Center of Agroplasticulture, University of Guayaquil.
Ecuador Faculty of Development Science Av. Delta s/n. Ecuador
[2]Department of Engineering, Higher Engineering School, University of Almería,
Agrifood Campus of International Excellence (CeiA3).
Ctra. Sacramento s/n. 04120 Almería, Spain
[3]Department of Agronomy, Higher Engineering School, University of Almería,
Agrifood Campus of International Excellence (CeiA3).
Ctra. Sacramento s/n. 04120 Almería, Spain
Corresponding author: mtlao@ual.es

The intensive production of cucumber is associated, among other techniques, with planting seedlings and with a subsequent transplanting. The aim of this study is to compare the crop response of the *Cucumis sativus* cv Diamante depending on the germination system used. A split plot design was established: direct seeding or planting seedlings and subsequent transplantation in both the greenhouse and the open field in order to evaluate the yield production. A trial was carried out in Vinces Los Ríos (Ecuador) (Latitude 1° 33′ 22″ N and Longitude 79° 45′ 56″ W). For the seedling, multi-alveolar trays of 12x6 *loculi* were used along with mixed substrate of peat and compost (50:50), enriched with humus. The irrigation was carried out through nebulizers’ 47.6 L h^{-1}; 3 daily irrigations were applied, 5 minutes each. The transplant was performed in 11 days when the seedling had 3 true leaves. In the case of direct sowing, one seed per hole was deposited and the drip irrigation was conducted with emitters of 2 L h^{-1}. 1 daily irrigation lasting 30 minutes was also applied. The parameters evaluated were the percentage of germination, the plant height (cm), the stem diameter (cm), the number of leaves, the width (cm) and the length of the leaves (cm), the number of flowers, the number of fruits per plant, the fruit diameter (cm) and the crop yield (kg m^{-2}). No significant differences were found in the germination percentage (around 99%), but changes in the ontogeny behavior and the yield have been found.

Key words: germination, yield, ontogeny behavior

P3.8

Agronomic performance of different cultivars of melon in the SE Spain

López-Marín, J., Pérez-Jiménez, M., A., Gálvez, A., del Amor, F.M.

Dep. Hortofruticultura. IMIDA. 30150. La Alberca. Murcia. Spain.

Melon (*Cucumis melo* L) is a cucurbit with a high economic impact, and also a well-known and valued product in Europe. Spain is the fifth most important melon producer worldwide; production that is mostly concentrated in Castilla la Mancha, Andalusia, Murcia, Extremadura and the Valencian Community areas. Cultivars belonging to Piel de sapo or Amarillo types (*Cucumis melo* var. *inodorus*) are the most popular in the Spanish market. Change consumer preferences and market conditions suggest that growers provide new melon varieties and marketing services that guarantee consistently high quality products. The aim of this work was to evaluate the quality and production of five cultivars, Galia traditional (Cyro), Galia with white flesh (3574), turkey type (Natalya), Harper type (Caribbean gold RZ), Galia with orange flesh (6804), in the SE of Spain. Fruits were harvested after the maximum growth was achieved. The following parameters were studied: soluble solids, total titratable acidity, º Brix, pH, firmness, color and average mass of the fruit. Although Galia with orange and white flesh showed an agronomic behaviour similar to Cyro, the firmness was lower in the new cultivars of Galia, the results of the rest of analysed parameters were similar. The evaluation of the performance in the field showed that these news cultivars are good as Cyro. On the other hand Natalya had a good adaptation to the cultivation cycle and the production was similar to previous studies conducted in Turkey.

Keywords: *Cucumis melo* L., varieties, Piel de sapo, Galia, Mediterranean conditions.

P3.9

Effects of microtunnel and polypropylene spunbonded nonwoven covering on yield and quality of melon plants

López-Marín, J., Gálvez, A., Pérez-Jiménez, M., del Amor, F.M.

Dep. Hortofruticultura. IMIDA. 30150. La Alberca. Murcia. Spain.

In the last years Spain has been compelled to strengthen its competitiveness due to the increase in the horticultural production in countries from the Mediterranean Region, including Morocco, Egypt or Turkey, and the easy export to the European Union (EU). Intensive horticulture uses various ways of protected areas for growing the plants and for the cultivation of vegetables in all seasons. Many of the most important crops of the Region of Murcia (SE Spain) are grown semi-protected in microtunnels, agrotextiles, and others.

The goal of this experiment was to evaluate yield and precocity in watermelon (*Citrullus lanatus*) in response to a temporary protection system; polypropylene spunbonded nonwoven (PP) and a plastic microtunnel (MP). Fruits were harvested after the maximum growth was achieved and the following parameters were studied: temperature, soluble solids, total titratable acidity, ºBrix, pH, firmness, color and average mass of the fruit. Two harvesting were carried out. In the MP treatment the watermelons were harvested 15 days before than PP. Although the total production was similar in PP and MP, the weight of fruit was higher with PP than with MP. The rest of the results of the analyzed parameters were similar in both treatments.

Keywords: agrotextile, precocity, semi-protected crop, *Citrullus lanatus*

P3.10

A Study on Exogenous Spermidine Improving Resistance to Powdery Mildew in Melon Seedlings

LI Xiao-ling, LIU Chang-ming, LIU Lian-hong, YANG Rui-ping, ZHENG Jun-xian, MO Yan-ling, Wu Mei-mei, ZHANG Xian,YANG Jing-jie

College of Horticulture, Northwest A & F University, Yangling, 712100, China

To gain further understanding about the physiological and biochemical effects of spermidine (Spd), the effect of Spd on induced resistance to powdery mildew in susceptible Cucumis melon variety ‘066’ , ‘0544’ and resistance variety ‘Yuntian-930’ seedlings was conducted. The activities of superoxide dismutase (SOD), peroxidase (PPO), catalase (CAT), polyphenol oxidase (PPO), as well as chlorophyll a, chlorophyll b, total chlorophyll, carotenoid, hydrogen peroxide(H_2O_2) and malondialdehyde (MDA) content were assayed in melon leaves after treated with Spd and inoculated with powdery mildew. The results show that: (1) The activities of four defence enzymes and the content of cytochrome in melon leaves inoculated with powdery mildew were all raised at first, and then decreased. Furthermore, the content of MDA went up observably. (2) Meanwhile, Spd mitigated the reduction of defence enzymes and the content of cytochrome, and reduced the content of MDA and the disease index, and 1.0 mmol/L Spd had the best effects. (3) Foliar-spraying Spd made the content of H_2O_2 in melon leaves go up whether if inoculated powdery mildew or not. One idea is that H_2O_2 may act as a kind of transport signals for the induction resistance to powdery mildew by Spd in melon. In summary, the results indicated that Spd mitigate the powdery mildew stress which cause reduction of defence enzymes activities and cytochrome content, increase plants photosynthetic capacity, and decrease disease index observably, then increase melon resistance to powdery mildew.

Key words: spermidine; Cucumis melon; powdery mildew; defence enzymes; chlorophyll

P3.11

Responses of Grafting on Plant Growth, Photosynthesis and Sugar Metabolism in Melon（*Cucumis melo* L.）

Qiushi Fu, Xinying Zhang, Huaisong Wang*

Institute of Vegetables and Flowers Chinese Academy of Agricultural Sciences,
Beijing, 100081, China
Qiushi Fu: fuqiushi@caas.cn; Huaisong Wang: wanghuaisong@caas.cn

The aim of the current work was to explore the influences of grafting on melon plant growth, photosynthesis performances and sugar metabolism including sugar levels in both source (leaf), phloem sap and sink tissues (fruit), related enzyme activities (acid invertase, neutral invertase, sucrose synthase and sucrose phosphate synthase) and gene expressions during fruit development. Pumpkin ‘Jingxin 3’ was used as rootstock for melon (‘IVF117’) in this experiment. The results showed that grafting significantly increased leaf area expansion, average single fruit weight and unit area yield. The net photosynthetic rate, transpiration rate, stomatal conductance and intercellular CO_2 concentration of grafted melon were significantly higher than those of own-rooted melon at later stage of fruit development. Total sugar levels in leaves (source), phloem sap (flow) and mesocarp tissues (sink) increased during fruit development. The primary contributors to the soluble sugar pools in leaves and mesocarp tissues were both sucrose and hexoses (glucose and fructose). Stachyose was found as the most important component of the phloem sap extracts, followed by sucrose and raffinose. The levels of fructose, glucose, sucrose and total sugar content in leaf and mature melon fruit decreased by grafting, acid invertase (AI) and netutral invertase (NI) activities of mature melon fruit increased and sucrose synthase (SS) activities and sucrose phosphate synthase (SPS) activities of mature melon fruit decreased by grafting. Gene expressions (AI, NI, SS, SPS) of grafted melon fruit were a little lower than those in own-rooted melon fruit. These were possibly the primary reasons for the decrease in sugar content of grafted melon fruit.

Keywords: grafting, plant growth, photosynthesis, sugar metabolism, responses, melon

P3.12

Physiological and Biochemical Responses of Muskmelon Plants with Leaf Yellowing Symptom

Hee Ju Lee[1,2], Sang Gyu Lee[1], Sung Kyeom Kim[1], Chang Sun Choi[1],
Won Byoung Chae[1], Changhoo Chun[2,3*]

[1]Vegetable Research Division, National Institute of Horticultural and Herbal Science,
Suwon 440-706, Korea
[2]Department of Plant Science, College of Agriculture and Life Sciences, Seoul National University,
Seoul 151-921, Korea
[3]Research Institute of Agriculture and Life Sciences, Seoul National University,
Seoul 151-921, Korea

This study was carried out to investigate the growth parameters, net photosynthetic rate, root activity, and sugar contents of muskmelon plants with leaf yellowing symptom. The growth characteristics were not significantly different between the normal plants and the plants showing yellowing symptom. However, the root length of control was 1,197 cm, but that of plant showing yellowing symptom was significantly low as 696 cm. The root amount was higher in control (10.3 cm^3) than the plant showing yellow symptom (7.0 cm^3). The net photosynthetic rate of the diseased plants showed 4.1 $\mu mol\ CO_2 \cdot m^{-2} \cdot s^{-1}$ which was one third of the readings observed for the uninfected plants (12.4 $\mu mol\ CO_2 \cdot m^{-2} \cdot s^{-1}$). The root activity of the plant with leaf yellowing symptom was 0.3 $mg \cdot g^{-1}$, approximately a half that tested for the normal plant (0.5 $mg \cdot g^{-1}$).

The contents of glucose, fructose, and sucrose in leaves were higher in plants with leaf yellowing symptom than normal plants, while sugars of stems, fruits, and roots were slightly low in plants with leaf yellowing symptom. These results indicated that the occurrence of yellowing symptom in muskmelon were closely related with root growth and the higher sugar contents of leaves in yellowing symptom than control may be due to poor translocation of free sugars produced in leaves to other organs.

Key words: photosynthesis, root activity, root growth, sugar content

P3.13

Effect of Liquid Fertilizer on Growth and Development in Organic Cucumber (Cucumis sativus L.) Cultivation.

Nan-hee An, Jung-Rai Cho, Jae-Hun Shin, Jung-hun Ok,
Eun-Jung Han, Seok-cheol kim

Division of Organic agriculture, National Academy of Agricultural Science,
RDA, WanJu-gun, 565-851, Republic of Korea

Organic cucumber (Cucumis sativus L.) growers are using farm-made liquid fertilizer (LF) made with organic materials to supply the nutrients in Korea. But farm-made liquid fertilizers are not systemic like chemical fertilizer and pesticide in formulation methods and usage, and their effect were very variable according to cultural condition. This study was conducted to evaluate the effect of liquid fertilizer on growth and development in organic cucumber. According to application method of liquid fertilizer, the experiment plot was designed as follows; NF : no-fertilizer, LF 500: liquid fertilizer solution which produced using bone meal and rice bran by adding dry yeast and molasses diluted 500 folds. The effect of soil chemical properties after application of LF was few of change. The difference on the plant height of cucumber between NF and LF was no significant, but fresh weight of stem and root were higher in LF treatment. In conclusion, the application of liquid fertilizer increased the growth of cucumber.

Key words: Organic liquid fertilizer, Bone-meal, Rice-bran, Cucumber

P3.14

Integrated management of downey mildew and powdery mildew of cucumber(Cucumis sativus L.) using resistant variety, micro-climatic control and organic materials

Yong-Ki Kim, Eun-Jung Han, An-Nan Hee, Sung-Jun Hong, Jon-Ho Park, Chang-Ki Shim, Min-Jeong Kim, Jong-Won Park, Seok-Cheol Kim

Organic Agriculture Division, NAAS, RDA 166 Nongsaengmyeong-ro Iseo-myeon Wanju-gun Jeollabuk-do, Republic of Korea.

In cucumber, Powdery mildew, downy mildew, *Fusarium* wilt, damping-off and scab largely occur in Korea. Of them, Powdery mildew and downy mildew cause severe damage in the cultivation of cucumber. In this study, the effect of ventilation-fan installation, application of nitrogen fertilizer(urea), phosphorous, alternative application of chemicals, and application timing of chemicals on the development of Powdery mildew and downy mildew. In addition, disease resistance of 88 varieties of cucumber was screened against powdery mildew of cucumber. Downey mildew and powdery mildew were reduced remarkably by of ventilation-fan installation. Ventilation-fan installation reduced relative humidity in plastic film house by 6.4% and reduced downey mildew and powdery mildew. Foliar application of nitrogen fertilizer (urea) alone and mixed with chemicals showed good control effect against downey mildew of cucumber. It was conformed that phosphorous acid suppressed spore formation and germination of powdery mildew pathogen, and finally reduced disease incidence of powdery mildew. When dimethomorph was sprayed 7day-intervals three times 3day-before, just the day and 2day after disease onset, disease incidence was 72.9, 61.8 and 23.7%, respectively. Thus, to control effectively downey mildew of cucumber, preventive application of control agents should be needed. Of 88 cucumber varieties used, there were no highly resistant varieties against powdery mildew and only 10varieties showed moderate resistance against the disease. Based on above-described results, we think that cultivation of cucumber resistant varieties, ventilation-fan installation, phosphorous acid and optimal time application of chemicals can be used to control effectively downey mildew and powdery mildew of cucumber.

Key word: *Pseudoperonospora cubensis*, *Sphaerotheca fuligenea,* ventilation fan, Phosphorous acid, application time, resistant variety

P3.15

Control efficacy of crude extracts from spicy vegetables on several pests of cucumber (*Cucumis sativus* L.)

Eun-Jung Han, Jae-Pil Choi, Young-Sil Yun, Nan-Hee An, Yong-Ki Kim, Sung-Jun Hong, Jon-Ho Park, Chang-Ki Shim, Min-Jeong Kim, Seok-Cheol Kim

Organic Agriculture Division, NAAS, RDA 166 Nongsaengmyeong-ro Iseo-myeon Wanju-gun
Jeollabuk-do, Republic of Korea.

According to the increase of consumers' interest in safety of agricultural produces, the demand for development of environment-friendly techniques for plant protection has increased in Korea. Especially, farmers who grow organically cucumber have suffered due to insect pests, such as thrips, whiteflies and aphids. In this study, we developed the new method for extracting active compounds from spicy vegetables and evaluated their control efficacy against western flower thrips, *Frankliniella occidentalis* (Pergande), sweet potato whitefly, *Bemisia tabaci* (Gennadius) Mediterranean species and cotton aphid, *Aphis gossypii* (Glover). Spicy vegetables tested were garlic, leek, ginger and red pepper (plant and seed). To get the plant extracts, each spicy vegetable was dipped in fermented alcohol (concentration of 30%) or boiled water.

Extracts obtained from spicy vegetables with solvents were diluted ten-fold and hundred-fold and treated against western flower thrips, cotton aphid and two-spotted spider mite. As a result, extracts from garlic and leek with fermented alcohol showed highest control effect on western flower thrips (control value: 96%, mortalities: 100%). The highest mortality (95%) of sweet potato whiteflies was recorded in extracts from ginger with boiled water. The highest mortality (76%) of cotton aphid was recorded in extracts from red pepper seed with fermented alcohol. These results show the crude extracts from spicy vegetables can be promising materials for new botanical insecticides and further study will be needed for the insecticidal substances of crude extracts.

Key words: cotton aphids, plant extracts, spicy vegetable, sweet potato whiteflies, western flower thrips

P3.16

Pollen germination and viability in watermelon *(Citrullus lanatus)* genotypes with different levels of ploidy.

Elena Lima-Cabello, Juan de Dios Alché Ramirez

Estación Experimental del Zaidín. Spanish Council for Scientific Research (CSIC).
Profesor Albareda 1, 18008 Granada. Spain.

Ploidy plays an important role in plant morphology and physiology, and is also an important tool to create genetic and morphological variation. Production of genetic variants is in many cases focused to the generation of traits of interest, as are the absence, diminution of the number of seeds in fruits or their reduction in size and/or density. However, such modifications often alter sexual reproductive behaviour of plants, resulting in poor fertilisation and low fruit setting rates. We have analysed the frequencies of pollen viability and ability to germinate in watermelon (*Citrullus lanatus*). Three diploid lines, their tetraploid counterparts and a triploid line were examined. Male flowers at blooming stage were collected and the number of anthers of each flower registered, as well as their size and histological characteristics. Pollen viability, as per membrane integrity and presence of esterases, was estimated by using the fluorescein diacetate (FDA) fluorochromatic stain. Pollen samples were germinated in Petri dishes, each one containing freshly prepared medium. Pollen tube lengths were also recorded at different times after the onset of the culture. The results obtained are discussed as regard to the involvement of the ploidy level in the generation of effective germination, and the potential effect in fertilisation.

Acknowledgements: this work was funded by an ERDF/CSIC programme (RECUPERA2020-3.1.4.), and projects P2010-AGR6274 y P2011-CVI7487 (CEICE, Junta de Andalucía) and BFU2011-22779 (MINECO), also participated by ERDF. The authors thank D. Nicolás for technical assistance.

Key words: Cucurbit, FDA, ploidy, pollen germination, tube-growth, viability.

P4.1

Identification of QTLs for *Fom* race 1.2 resistance using a genotyping by sequencing approach

Ramon Botet [1,2], Ana Garcés-Claver[1], José Mª Álvarez[1]

[1]Agrifood Research and Technology Centre (CITA).
Avda. Montañana, 930. 50059, Zaragoza, Spain.
[2]Laboratory of Genetics, Wageningen University and Research (WUR),
P.O. Box 16, 6700 AA, Wageningen, The Netherlands
Corresponding author. E-mail: agarces@cita-aragon.es.
Tfno: +34976716560. Fax: +34976716335

Fusarium wilt of melon (*Cucumis melon* L.), caused by *Fusarium oxysporum* Schlecht. f. sp. *melonis* Snyd. & Hans. (*Fom*) is an important disease spread worldwide. Race 1.2, subdivided into pathotype 1.2y (Yellow) and 1.2w (Wilt), overcomes all resistance genes described and could become a serious threat to this crop cultivation. The development of cultivars exhibiting enhanced resistance to *Fom* race 1.2 is an important objective of breeding programs.

Partial resistance to *Fom* race 1.2 was studied using a recombinant inbred line (RIL) population derived from a cross between cv. 'Piel de Sapo', a highly valuable cultivar, and 'BG-5384', a partially resistant line. Artificial inoculations were performed with a yellow strain and a wilt one and two environments, growth chamber and greenhouse. Genotyping was carried out by using genotyping-by-sequencing approach. Genotypic data for 2625 single nucleotide polymorphism (SNP) markers on twelve chromosomes were used for the association analysis, revealing polygenic control with 10 different small effect QTLs. Those showed to be environment specific, probably due to a high RIL –environment interaction, and pathotype specific in most cases. These results match with previously reported research. Further work will be made on fine-mapping regions of interest and determining the molecular basis of such a complex resistance.

Key words: disease resistence, genotyping by sequencing, melon, RILs, QTLs.

P4.2

Race-specificity in interactions between *Cucumis melo* germplasm and *Pseudoperonospora cubensis*

Aleš Lebeda[1]*, Eva Křístková[1], Božena Sedláková[1],
Jana Štěpánková[1], Mark. P. Widrlechner[2]

[1] Palacký University in Olomouc, Faculty of Science, Department of Botany,
Šlechtitelů 11, 783 71, Olomouc-Holice, Czech Republic; *E-mail: ales.lebeda@upol.cz
[2] Iowa State University, Departments of Horticulture and of Ecology,
Evolution and Organismal Biology, Ames, Iowa 50011, USA.

Pseudoperonospora cubensis, the causal agent of cucurbit downy mildew, is one of the most economically important plant pathogens. Muskmelon (*Cucumis melo*) is seriously affected by *P. cubensis*. Within *C. melo*, several genotypes resistant to *P. cubensis* have been described; however, we lack detailed experimental studies focused on deciphering variation in this host-pathogen interaction. This study aims to describe race-specific variation in interactions between *C. melo* germplasm and isolates of *P. cubensis*.

Under controlled inoculation, 52 accessions of *C. melo* were studied for resistance/susceptibility to 8 isolates of *P. cubensis*. The plant material was obtained from the USDA Plant Introduction Station, Iowa, Ames, USA. Pathogen isolates originated from the Czech Republic (7 isolates) and France (1 isolate) and represented 8 distinct pathotypes as determined following Lebeda and Widrlechner (2003). Collectively, 8 different race-specific reaction patterns were recorded. Most of *C. melo* accessions (in total 39) were highly susceptible to all isolates. None of screened *C. melo* accessions expressed complete resistance to all isolates. Only accession PI 315410 (VIR 5682) was found to be highly resistant to 7 of the 8 *P. cubensis* isolates. The study: a) confirmed the race-specificity of interactions between *C. melo* and *P. cubensis*, b) established a sound framework for the development of a system to determine and classify *P. cubensis* races, and, in turn, c) should foster further broad screening of *C. melo* germplasm with a likelihood of detecting more effective sources of resistance to important pathotypes and races of *P. cubensis*.

Key words: cucurbit downy mildew, muskmelon, breeding, resistance

P4.3

Evaluation of *C. moschata* x *C. maxima* rootstocks against ToLCNDV

María Ferriol[1], Cristina Sáez[2], Carmina Gisbert[2],
Carmelo López[2], Belén Picó[2]

[1]Instituto Agroforestal Mediterráneo, Universitat Politècnica de València.
[2]Institute for the Conservation and Breeding of Agricultural Biodiversity (COMAV-UPV),
Universitat Politècnica de València, Camino de Vera s/n, 46022 Valencia, Spain

Tomato leaf curl New Delhi virus (ToLCNDV) was firstly detected in Spain in 2012-2013. Currently, it causes major economic losses in zucchini (*Cucurbita pepo*), and until now no resistant or tolerant sources have been found in this species. Although in general less harmful, this begomovirus also infects other *Cucurbita* species, such as *C. maxima* and *C. moschata*, whose hybrids are commonly used as rootstocks for grafting watermelons and melons. In the present study, we have screened a selection of *C. maxima* and *C. moschata* accessions and their corresponding hybrids against ToLCNDV using mechanical inoculation. Symptoms were scored at 15 and 30 days post inoculation (dpi), and the Vulnerability Index (VI) was calculated. ToLCNDV was detected by PCR. At 30 dpi, all the *C. moschata* accessions had lower VIs than the *C. maxima* accessions, which were more susceptible (9 to 72% and 46 to 90%, respectively). This is consistent with previous studies that show higher levels of resistance in some accessions of *C. moschata*. All accessions were ToLCNDV positive by PCR. Most of the evaluated hybrid progenies showed severe infections similar, or even more severe, to those found in the *C. maxima* parentals (ranging from 71 to 100%). The great aggressiveness of this virus and the high susceptibility of the assayed hybrids can make the production of rootstocks difficult. Furthermore, the use of susceptible rootstocks to ToLCNDV can contribute to increase the severity of the infection in scions. Therefore the development of new rootstocks derived from selected resistant *C. maxima* accessions might minimize this effect.

Keywords: *Cucurbita maxima*, *Cucurbita mochata*, mechanical inoculation, rootstock, ToLCNDV

P4.4

Identification of aphid resistance and correlation with physical characters of leaf in watermelon plant at seedling stage

Zhang Xian, Wu Mei-Mei, Yang Xiao-Zhen, Wang Yong-Qi,
Liu Lian-Hong, Li Xiao-Ling.

College of Horticulture, Northwest A&F University, Yangling 712100, Shaanxi, P. R. China

Watermelon is one of the most economically important agricultural crops all over the world. *Aphis gossypii Glover* is one of the major pests to feed on watermelon, not only resulting in a loss in yield and quality, but also promoting plant viruses spread as an important vector. To excavate excellent, anti-aphid watermelon germplasms, 21 germplasms were authenticated by combining of field and laboratory test. According to the results, the aphid resistance in field test was roughly consistent with that in laboratory test. And watermelon germplasms with different resistance to aphid were identified including'ZXG01018' and 'Zhenmu 4'with moderate resistance, 'ZXG00960' and 'M08' with low resistance, '134' and 'Y1-1' with sensitivity, 'Y1-3', 'Zhong10 haikang' and 'Jinmeiren1' with high sensitivity to aphid. Compared to susceptive germplasms ('Zhong 10 haikang', '148'), the stomata density of resistant germplasms ('Zhenmu 4', 'KY-2') were significantly lower, but the density of leaf hair and the content of leaf epidermis wax in resistant germplasms were markly higher. According to the correlation analysis, the index of aphids susceptibility was significantly, positively correlated with stomata density, but negatively correlated with the density of leaf hair and the content of leaf epidermis wax. In summary, the density of stoma and leaf hair and the content of leaf epidermis wax could be as indicators for estimating aphid resistance of watermelon germplasms.

Key words: watermelon; identification of aphid resistance; physical characteristics; correlation analysis

P4.5

Influence of temperature on powdery mildew development in TGR-1551

Paola Beraldo-Hoischen, Ana I. López-Sesé

IHSM-La Mayora, CSIC-UMA, 29750-Algarrobo-Costa, Málaga, Spain

Several plants of ‘TGR-1551’, a Zimbabwean melon accession resistant to races 1, 2 and 5 of *Podosphaera xanthii*, and the susceptible Spanish cultivar ‘Bola de Oro’ were inoculated with powdery mildew race 2 at two different temperatures (18-22ºC and 25-30ºC) in order to study the plant-pathogen interaction. Fungal development was evaluated at microscopic level through several parameters such as the number of penetrated points, detected by callose accumulation with the double aniline-blue-calcofluor staining technique, at 48, 72, 96 and 120 hours post inoculation (hpi), as well as the number of conidiophores at 120hpi stained with an ink/acetic acid solution. The melon accessions ‘PMR 45’ and ‘WMR 29’, susceptible and resistant to race 2 respectively, were used as control lines at 48 and 120hpi. At low temperature, ‘TGR-1551’ showed a non-resistant phenotype since the number of penetration points increased with time, as it is also observed for susceptible lines. Likewise, a high number of conidiophores were detected, although in lower quantities than in the susceptible lines. At high temperature, however, most of fungal conidias deposited on ‘TGR-1551’ plants stopped its development at germ tube or primary hyphae stage, and no conidiophores were observed at 120hpi. A similar behavior was recorded for ‘WMR 29’. The susceptible melon lines, ‘Bola de Oro’ and ‘PMR 45’, showed a great fungal development at both temperatures, being the greatest values observed at high temperature. This environmental factor might be affecting significantly the resistance of several melon genotypes to powdery mildew.

Key words: callose, conidia, *Cucumis melo*, *Podosphaera xanthii*, powdery mildew

P4.6

Cucurbit-infecting viruses in Brazil

Mirtes F. Lima[1]; Valter Oliveira[1]; Geovani Bernardo Amaro[1]

[1]Embrapa Vegetables, Caixa Postal 218 CEP 70.351-970, Brasília,DF

Viral diseases are one of the main causes of economic losses in cucurbit production in Brazil. During 2008-2015, a survey was performed in open-field of watermelon (*Citrullus lanatus* Thunb. (Matsui & Nagai), melon (*Cucumis melo* L.), cucumber (*C. sativus* L.), pumpkin (*Cucurbita* spp.), chayote (*Sechium edule* Swartz) and gherkin (*C. anguria* L.). More than 700 leaf samples were collected from symptomatic plants in 25 counties of nine Brazilian states and the Federal District. Samples were screened by dot-ELISA and DAS-ELISA tests using polyclonal antibodies to investigate the occurrence of *Papaya ringspot virus*-type watermelon (PRSV-W), *Watermelon mosaic virus* (WMV) and *Zucchini yellow mosaic virus* (ZYMV) (genus *Potyvirus*; family *Potyviridae*), *Cucumber mosaic virus* (CMV; genus *Cucumovirus;* family *Comoviridae*), *Zucchini lethal chlorosis virus* (ZLCV; genus *Tospovirus*; family *Bunyaviridae*) and *Melon yellowing-associated virus* (MYaV; genus *Carlavirus*; family *Betaflexiviridae*). Serological tests results indicated that more than 50% of samples were virus-infected. PRSV, WMV and ZYMV were the most prevalent viruses detected in all cucurbit species, while CMV, MYaV and ZLCV were found in a low percentage of the samples. MYaV occurred mostly in melon samples and ZLCV in watermelon and pumpkin plants. The occurrence of multiple infections with two or more viruses in the same plant was very common, especially combined with PRSV-W. These data confirm the economic importance and the widespread incidence of cucurbit-infecting viruses in Brazil and made the need in developing efficient strategies for disease management in the field.

P4.7

Design and validation of an infectious clone of ToLCNDV, an emergent virus in South-East Spain

Dina Cifuentes[1], Josefina Contreras[1], Miguel A. Aranda[2], César Petri[1]

[1] Departamento de Producción Vegetal, Universidad Politécnica de Cartagena,
30203-Cartagena, Murcia, Spain
[2] Departamento de Biología del Estrés y Patología Vegetal, CEBAS-CSIC,
30100, Murcia, Spain

Tomato leaf curl New Delhi virus (ToLCNDV) (family *Geminiviridae*, genus *Begomovirus*) is an important pathogen that strongly affects tomato and cucurbits production. Original from the Indian Subcontinent, it has been recently detected in Spain causing severe epidemics in cucurbit crops. ToLCNDV genome consists of two single-stranded circular DNA molecules, denominated DNA-A and DNA-B, of approximately 2.7 kb each. Partial dimeric DNA-A and DNA-B clones were constructed in a binary vector and used to agroinoculate zucchini (cv. 'Brillante') and pumpkin (cv. 'Avalon') plants. Symptoms were observed in plants of both species at 100% and 50% frequency for zucchini and pumpkin plants, respectively. First symptoms appeared 7 days post-inoculation, and they were clearly observed at 14 days post-inoculation. Visual observation was confirmed by molecular techniques, such as molecular hybridization and qPCR.

Keywords: zucchini, emerging disease, *Begomovirus,* resistance, *Cucurbitaceae*

P5.1

Chemical sanitizers and UV-C radiation for maintaining the microbiological and organoleptic quality of fresh-cut Galia melon

A.C. Silveria[1], F. Artés[2,3] and E. Aguayo[2,3*]

[1]Vegetable Production Department, Postharvest Division. Agronomy Faculty.
Avenida Garzón 780, CP 12300, Montevideo, Uruguay.
[2]Postharvest and Refrigeration Group. Technical University of Cartagena (UPCT).
Paseo Alfonso XIII, 48. 30203. Cartagena, Spain.
[3]Institute of Plant Biotechnology. UPCT. Campus Muralla del Mar, s/n. 30202.
*e-mail: encarna.aguayo@upct.es

Disinfection is one of the main steps to obtain proper microbial quality and extended shelf-life in fresh-cut fruits and vegetables. New sanitizers, less harmful for the ecosystem, are replacing chlorine. The effects of the UV-C (4.8 kJ m^{-2}), peracetic acid (PAA, 80 mg L^{-1}), hydrogen peroxide 30% w/v (H_2O_2, 50 mg L^{-1}), chlorine dioxide (ClO_3, 3 mg L^{-1}), acidified sodium chlorite (ASC, 200 mg L^{-1}) and a sodium hypochlorite control (NaOCl, 150 mg L^{-1}) in fresh-cut Galia melon was studied. Melon pieces were stored at 5°C during 10 days. Respiration rate (RR) during the first three days was of 4 to 5 mg CO_2/kg h although all treatments increased CO_2 emission at the end of storage (8 to 11 mg CO_2/kg h). The highest RR was obtained in melon pieces washed with ClO_3 whilst the lowest RR measured was in UV-C treated melon. This treatment also showed the lowest ethylene emission (in the range of 0.4 to 0.8 µL kg^{-1} h^{-1}) for all treatments. After 10 days of storage, the use of PAA, H_2O_2 and UV-C treated melon showed lower microbial loads (6 log cfu g^{-1}) of 1 to 1.5 log cfu g^{-1} lower than the others treatments. The ASC and ClO_3 were less effective on Enterobacteriaceae control. The sensory parameters were not negatively affected for any treatments and all them scored above limits of marketability. Melon UV-C-treated obtained the best overall quality and firmness retention. This treatment was considered as the optimum to provided better quality and 10 days of shelf-life at 5ºC.

Keywords: *minimally processed, disinfection methods, microbial growth, sensory parameters*

P5.2

1-MCP as Active Packaging to Keep Quality of Fresh-Cut Watermelon

E. Aguayo[1,2*], E. Gómez[1], A.C. Silveria[3], and F. Artés[1, 2] V.H. Escalona[4]

[1]Postharvest and Refrigeration Group. Technical University of Cartagena (UPCT).
Paseo Alfonso XIII, 48. 30203. Cartagena, Spain.
[2]Institute of Plant Biotechnology. UPCT. Campus Muralla del Mar, s/n. 30202.
[3]Vegetable Production Department, Postharvest Division. Agronomy Faculty.
Avenida Garzón 780, CP 12300, Montevideo, Uruguay.
[4]Centre of Postharvest Studies, Fac. Agricultural Sciences, University of Chile,
P.O. Box 1004, Santa Rosa 11315, La Pintana, Santiago, Chile.
**e-mail: encarna.aguayo@upct.es*

Fresh-cut watermelon is a relatively new product in Spain, with great consumer acceptation. However, this product suffers a rapid deterioration resulting in juice leakage, loss of texture and colour. The use of 1-methylcyclopropene (1-MCP) at two concentrations (0-control, 0.5 and 1 µL L^{-1}) applied to cut watermelon was studied. 1-MCP was provided in two different ways: T1, the exposure to a continuous flow inside glass jars for 24 h at 5 ºC followed by the modified atmosphere packaging (MAP) or T2, applied directly inside the tray (active MAP) for 8 days at 5ºC. The use of 1-MCP reduced respiration rate during the first two days (2 to 7 mg CO_2/kg h) although all the treatments increased CO_2 emission at the end of the storage (10 to 8 mg CO_2/kg h). 1-MCP did not affect firmness, maintaining 2.1 to 2.8 N during storage (all treatments). Psychrotrophic load was in the range of 3.5 to 2.8 log cfu/g for fresh-cut watermelon stored glass jars (T1) and 2.4 to 2.2 log cfu/g for those packaged from the beginning in MAP (T2). The main 1-MCP effect was the reduction of cosmetic damages (changes in translucency). At day 8, panelists scored the overall fresh-cut watermelon quality as 5.83 ± 0.44 for control and 7.00 to 6.33 for 1-MCP treatments. The use of 1-MCP at 0.5 µL L^{-1} applied as active MAP obtained the best sensory evaluation.

Keywords: *Citrullus lanatus,* firmness, sensory quality.

P5.3

Effects of Nano Silver and Modified Atmosphere Storage on Extension storage limit of Cucumber Fruit (*Cucumis sativus* L.)

Jeng-Jung Shyr, Sheng-Feng Peng and Nur Azida Binti Piakong

Department of Horticulture, National Ilan University,
1, Sheng-Loung Rd., I-Lan, Taiwan, 26041, R.O.C.

Storage of cucumber is generally less than 14 days at room temperature as visual and sensory quality deteriorate rapidly. Nano silver is proven to safely and effectively kill over 650 types of bacteria and molds. The aim of this study is to prolong the storage limit of cucumber by using modified atmosphere (MA) storage, precooling, low moisture content package, and nano silver. Cucumbers were packed by low density polyester (0.03mm, 0.05mm, and 0.08mm of thickness) or high density polyester (0.01m of thickness) bags and stored at 13 ℃. Corrugated paper was used to absorb the condensed water in the bags. For sterilize microbial, 50, 250, and 500mg/L nano silver solutions were painted on the inside surface of corrugated paper which was directly contacted to the surface of cucumber. Quality characteristics including color, texture, decay, and chilling injury symptom were checked every week during storage. Results showed that 0.01mm high density polyester bag is good for the low temperature storage of cucumber. Precooling did not show benefit for the storage of it. The combination of nano silver solution painted corrugated paper and MA storage showed the best results for prolong the storage limits of cucumber to 4 weeks at 13℃.

Keywords: cucumber, modified, atmosphere, storage, nano, silver

AUTHOR INDEX

A. Bendahmane, 43
A. Naci Onus, 86
A.C. Silveria, 125, 126
Abdolali Shojaeiyan, 93, 94
Abdulaziz R. Al-Harbi, 59
Abdulrasoul M. Al-Omran, 59
Adi Doron-Faigenboim, 17
Ahmet Secim, 86
Ai Zhen, 57
Alain Latché, 101
Alejandra Serrato-Díaz, 88
Alejandro Tomás-Callejas, 69
Aleš Lebeda, 56, 119
Ali Saadounbc, 68
Alicia García, 52, 87
Amnon Lers, 81
Amnon Levi, 6, 9, 19, 40, 41
Ana Garcés-Claver, 118
Ana I. López-Sesé, 91, 93, 94, 122
Anânkia Ricarte de Oliveira, 85
Angela Schmidt, 105
An-Nan Hee, 115
Antonio José Monforte, 12, 15, 20, 26, 73, 74
Araceli Moya-Hernández, 88
Arak Tira-umphon, 82
Aranda. M.A., 96
Arie Amitzur, 42
Arthur Schaffer, 17, 31, 66
Astrid Volder, 23
Aureliano Bombarely, 20
Ayala Meir, 31
Ayse OZER, 62
Belén Picó, 6,10,11,20,50,73,74,75,84,85,120
Blanca Gosalvez, 24
Bo Lei, 57
Bora Cetin, 83
Božena Sedláková, 56, 119
Burak Kunter, 44
Burgos L., 96
Buse Özdemir, 86
C. Dogimont, 43
C. Troadec, 43
Carlos Martí, 20
Carmelo López, 75, 120
Carmina Gisbert, 50, 120
Cecilia Martínez, 10, 52, 75, 87, 95
César Petri, 124
Chang Sun Choi, 113
Changhoo Chun, 113
Chang-Ki Shim, 115, 116
Chen Jiao, 17, 19
Chen Zhendong, 98
Choi, HG, 99
Cristina Esteras-Gómez, 20, 73, 74
Cristina Roig, 20
Cristina Sáez, 75, 120
Csaba Szamosi, 89
Daniel I. Leskovar, 23
Debbie Reesa, 67
del Amor, F.M., 109, 110
Dietmar Schwarz, 32
Dina Cifuentes, 124
Do-Sun Kim, 77
DOU Jun-ling, 76
E. Gómez, 126
Efraim Lewinsohn, 13, 17, 31, 66
Einat Bar, 17, 66
Elaíne Welk Lopes Pereira Nunes, 84, 85
Elazar Fallik, 81
Elena Lima-Cabello, 117
Elsa Bosquez-Molina, 88
Emilio Sarria Villada, 15, 18
Encarna Aguayo, 5, 6, 12, 65, 95, 125, 126
Endah Retno Palupi, 10, 46, 51
Eric T. Natwick, 60, 80
Eun-Jung Han, 114, 115, 116
Eva Křístková, 56, 119
Eva Maria Martínez Pérez, 84, 85
Fabian Baumkeler, 81
Fabián Baumkoler, 31
Félix Romojaro, 101
Fernanda Zaccariab, 68
Fernando Antônio Souza de Aragão, 84
Francecs Xavier Sorribas, 50
Francisco Artés, 6, 69, 125, 126
Francisco Artés-Hernández, 69
Francisco Guilhien Gomes Junior, 47
Francisco Pérez-Alfocea, 7, 13, 14, 49, 59
Gabriel Castro, 74
Galil Tzuri, 17, 31, 66, 81
Gálvez, A., 109, 110
GAO Lei, 76
García-Almodóvar R.C., 96
Geovani Bernardo Amaro, 123
Gerard Bishopc, 67
Gerardo Blancas-Flores, 88
Glauber Henrique de Sousa Nunes, 84, 85
Golan Miller, 42
Gorka Perpiñá-Martín, 73, 74
Gosalvez.B., 96
Gu Qinsheng, 12, 54, 61
Guy Kol, 17
H.B. You, 78
Haisun Cao, 57
Halit Yetisir, 44
Han Li, 92
Han Miao, 37
Hans-Peter Klaering, 10, 48, 105
Harry S. Paris, 8, 12, 35, 87
HE Nan, 76
Hee Ju Lee, 113
Honghe Sun, 19
Hongli Lian, 79
Huaisong Wang, 112
Huang Rukui, 98
Huanle He, 79

Hwang, MR, 99
Hye-Eun Lee, 77
Ilknur SOLMAZ, 62
Ismail Simsek, 83
Itay Gonda, 17, 66
Jae-Hun Shin, 114
Jae-Pil Choi, 116
James D. McCreight, 6, 7, 10, 56, 60, 80
James Giovannoni, 17, 66
Jana Štěpánková, 119
Javier Montero Pau, 20
Jean-Claude Pech, 101
Jeng-Jung Shyr, 127
Jin Zhu, 57
Jingyu Sun, 57
Joaquín Cañizares, 20
Jonathan W. Sinclair, 80
Jong-Won Park, 115
Jon-Ho Park, 115, 116
Jordi Garcia-Mas, 25
Jorge Corbacho, 100, 101
Jose Blanca, 20
José Mª Álvarez, 118
Josefa López-Marín, 49
Josefina Contreras, 124
Joseph Burger, 31, 66, 81
Juan A. Fernández, 5, 6, 10, 46, 49
Juan Antonio Lizarzaburu, 95
Juan Carlos Gázquez, 5, 13, 52
Juan Cheng, 92
Juan de Dios Alché Ramirez, 117
Jung-hun Ok, 114
Jung-Rai Cho, 114
Junjun Xie, 57
Junlong Zhao, 79
Junsong Pan, 79
Kai-shu Ling, 19, 41
Kang, NJ, 99
Karyadi Wanafiah, 51
Kevin M. Crosby, 23, 80
Kim, HM, 99
Koichiro Shimomura, 90
Kwon, JK, 99
Lao M.T., 107, 108
Li Junxiang, 61
Li Ping-fang, 97
Li Qiqin, 98
Li Xiao-Ling, 111, 121
Linyong Mao, 17, 19
LIU Chang-ming, 111
Liu Guang, 97
LIU Lian-hong, 111
LIU Wen-ge, 76
Long Tong, 92
López-Marín, J., 109, 110
Lu Xu-Qiang, 33
Lukas Muller, 20
M. Bardin, 43
M.P. Tarazona-Díaz, 65
Mahmoud A. Wahb-Allah, 59
Mahmut Yegul, 44
Manuel Jamilena, 10, 15, 20, 22, 52, 75, 87, 95
Manuel Miras, 24
Marcin Glowacza, 67
María Belén Picó-Sirvent, 50, 73, 74, 84, 85
Maria C. Gomez-Jimenez, 100, 101
María Cristina Cabrerab, 68
Maria Dolores Bernal, 49
María Ferriol, 75, 120
María Luisa Gómez-Guillamón, 80, 91
Mariano Otón, 69
Marina Martos-Fuentes, 95
Mark. P. Widrlechner, 119
Masoud Maleki, 93
Mehmet HAMURCU, 62
Menahem Edelstein, 11, 32
Mengliang Niu, 57
Merav Kenigswald, 17, 81
Michael D. Coffey, 56
Michael Normantovich, 42
Miguel A. Aranda, 24, 124
Miguel Juárez, 24
Min Wang, 37
Mingyun Huang, 66
Min-Jeong Kim, 115, 116
Mirtes F. Lima, 123
Mitsuhiro Sugiyama, 90
MO Yan-ling, 111
Mohsen Falahati-Anbara, 94
Mona A. Kassem, 24
Munevver Gocmen, 83
Mwafaq Ibdah, 66
N. Giovinazzo, 43
Nadia Lombardi, 17
Najet Gammoudi, 50
Nan-Hee An, 116
Narges Dastranji, 94
Narinder P.S. Dhillon, 8, 36
Navot Galpaz, 17, 66
Nebahat SARI, 62
Norio Nishimura, 90
Nur Azida Binti Piakong, 127
Nurit Katzir, 7, 15, 17, 19, 31, 66, 81
Olave, J., 58
Omer Barad, 17
Onder TURKMEN, 62
Ozhan Simsek, 89
Padma Nimmakayala, 19
Pakize Gok Guler, 44
Pan-na Liu, 37
Paola Beraldo-Hoischen, 91, 122
Pat Wechter, 19
Patrícia Pereira da Silva, 47
Pedro A. Robles, 69
Pedro Gómez, 20, 24
Peio Ziarsolo, 20

Pérez-Jiménez, M., 109, 110
Pérez-Saiz, 107, 108
Perla A. Gómez, 69
Peter Hanson, 36
Peter Waldockb, 67
Qin Jian, 98
Qiusheng Kong, 34
Qiushi Fu, 112
Rachel Davidovich-Rikanati, 66
Rafael Garrido, 87
Rafael Perl-Treves, 9, 42, 102
Ramon Botet, 118
Ray-Yu Yang, 36
Reca J., 107, 108
Richard Colgana, 67
Rita Grosch, 32
Roni Cohen, 8, 9, 30, 32
Rotem Harel-Beja, 17, 66
Rotua Melisa Sidabutar, 51
Run Cai, 79
S. Elbelt, 43
Sajad Rashidi-Monfared, 93
Salcedo G.A, 107, 108
Sang Gyu Lee, 113
Sanín Ortiz Grisales, 70
Santander, C., 58
Sat Pal Sharma, 23
Seher Pamuk, 83
Seok-Cheol Kim, 115, 116
Shachar Ohali, 31
Shaogui Guo, 19
Sharon Alkalai-Tuvia, 81
Sheng-Feng Peng, 127
Sheng-ping Zhang, 37
Shery Lev, 17, 66
Shiri Freilich, 66
Shu-lin Liu, 37
Somkiet Sripongprapai, 82
Soo-Jin Kim, 77
Sung Kyeom Kim, 113
Sung-Jun Hong, 115, 116
Supannika Sanguansil, 36
Susana Manzano, 52, 75, 87
Takayuki Yamaguchi, 106
Tian Zou, 92
Todd C. Wehner, 37
Tugce Ozsan, 86
Umesh Reddy, 19
Uzi Sa’ar, 31
Uzi Saar, 17, 81
V. Sarnette, 43
V.H. Escalona, 126
Valter Oliveira, 123
Vitaly Portnoy, 17, 31, 66, 81
Wang Yong-Qi, 121
Warley Marcos Nascimento, 9, 10, 47, 104
Wen Junli, 98
William M. Wintermantel, 60, 80
Won Byoung Chae, 113
Wu Mei-Mei, 121
X.Q. Wang, 78
Xiaowu Sun, 92
Xingfang Gu, 6, 37
Xinying Zhang, 112
Xu Jin-hua, 97
Y.H. Jia, 78
Y.K. Fu, 78
Yaacov Pertzean, 81
Yaakov Tadmor, 7, 8, 19
YANG Jing-jie, 111
YANG Rui-ping, 111
Yang Xiao-Zhen, 121
Yang Xing-ping, 97
Yao Xie-feng, 97
Yaprak Kantoglu, 44
Yariv Brotman, 102
Yi Zheng, 19
Yildiz Aka-Kacar, 89
Yimin Xu, 17
Yiqun Weng, 9, 15, 21
Yoichi Kawazu, 90
Yong Liu, 34
Yong Xu, 19
Yong-Ki Kim, 115, 116
Yosef Burger, 17
Yosuke Yoshioka, 90
Young-Sil Yun, 116
Yuan Guan, 79
Yuan Huang, 12, 57
Yulia Shnaider, 102
Yul-Kyun Ahn, 77
Yun-Chan Huh, 77
Yuval Sa’ar, 31
Zhang Man, 97
ZHANG Xian, 111
Zhangjun Fei, 15, 17, 19, 66
ZHAO Sheng-jie, 76
ZHENG Jun-xian, 111
Zhilong Bie, 8, 30, 34, 57
Zhixiong Liu, 57
ZHU Hong-ju, 76
Ziyang Min, 92
Zoraida Megías, 52, 87

www.cucurbits2015.org

Sponsors:

Procomel s.l. el Abuelo de los melones
UNIGENIA BIOSCIENCE
SAKATA®
syngenta®

HM • CLAUSE
RIJK ZWAAN
Pozo Sur
Perichán
Seminis®

f SéNeCa(+) Agencia de Ciencia y Tecnología Región de Murcia
MINISTERIO DE ECONOMÍA Y COMPETITIVIDAD
INIA Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria
AC2014-00011-00
Ayuntamiento de Torre Pacheco
FUNDACIÓN cajamar
MELÓN de TORRE PACHECO