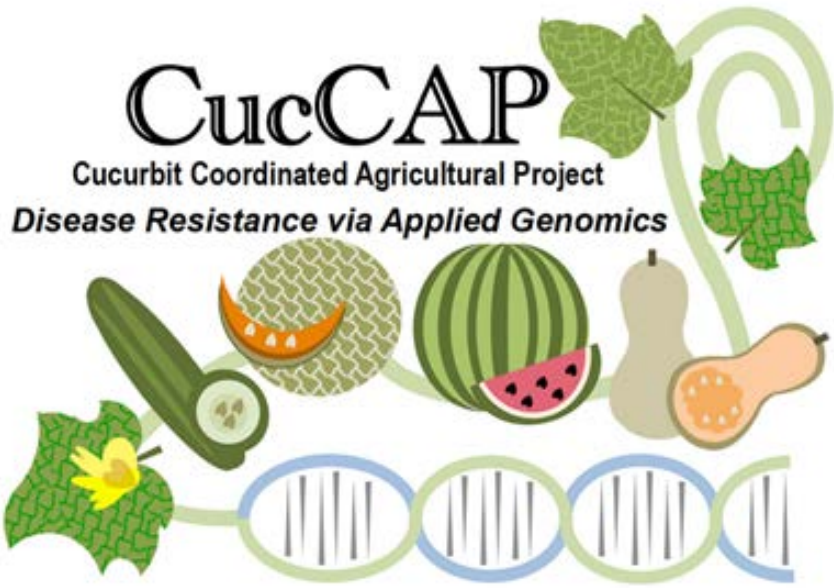
CucCAP:

Leveraging applied genomics to improve disease resistance in cucurbit crops



Second Annual CucCAP Team Meeting

March 27-28, 2017

Charleston SC

Table of Contents

AGENDA

and

PARTICPANTS

AGENDA

Second annual CucCAP team meeting – March 27-28, 2017

Monday, March 27

8:00-8:15 Arrival, welcome

8:15-8:30 Introductions
(team members, industry advisory board, external reviewers, germplasm curators, guests)

8:30-8:45 Overview of project progress, plans for meeting (Grumet)

8:45-9:15 Bioinformatics team report, questions, discussion (Fei et al)

9:15-9:45 Watermelon team report, questions, discussion (Levi et al)

9:45-10:00 Break

10:00-10:30 Melon team report, questions, discussion (McCreight et al)

10:30-11:00 Cucumber team report, questions, discussion (Weng et al)

11:00-11:30 Squash team report, questions, discussion (LaPlant et al)

11:30-12:00 Discussion: Cucurbit gene nomenclature (Weng lead)

12:00-1:00 Lunch

1:00-1:30 Extension team report, questions, discussion (Schultheis et al)

1:30-2:00 Socioeconomics team report, questions, discussion (Palma)

2:00-2:30 CucCAP website, overview, questions, discussion (Lorscheider)

2:30-2:45 Break

2:45-3:15 Views from the cucurbit industries – needs and concerns

3:15-3:45 Views from the seed industry

3:45-5:00 Breakout Session I - Websites
A. CucCAP website (Schulthies, Lorscheider leads)
B. ICuGI website (Fei lead)

Barbecue Dinner

Tuesday, March 28

8:00-8:15 Arrive

8:15-9:30 Breakout Session II
A. Core collections – selection criteria, obtaining germplasm
Sequencing strategy, Maintenance (Weng, Fei leads)
(curators, seed company reps, members of crop teams)
B. Cucurbit disease resources (Smart lead)
(commodity reps, extension, crop team members)

9:30-10:30 Breakout Sessions III
A. Cucurbit Crop Germplasm Committee, Cucurbit Vulnerability Statement
(McCreight lead)
(curators, seed company reps, members of crop teams)
B. Extension plans and industry needs (Schulthies lead)
(commodity reps, extension, socioeconomic, crop team members)

10:30-10:45 Break

10:45-12:00 Wrap up discussions, feedback from advisory board and external reviewers

CucCAP Team

Project Director

Rebecca Grumet, Professor, Department of Horticulture
1066 Bogue Street, Michigan St Univ., East Lansing MI 48824 (grumet@msu.edu)

Team Leaders

Watermelon (*Citrullus lanatus*)
Amnon Levi, Research Geneticist, Vegetable Research Laboratory
2700 Savannah Highway, USDA-ARS, Charleston SC 29414 (Amnon.levi@ars.usda.gov)

Melon (*Cucumis melo*)
Jim McCreight, Research Leader, US Agricultural Research Station
1636 E Alisal St, USDA-ARS, Salinas, CA 93905 (Jim.McCreight@ars.usda.gov)

Cucumber (*Cucumis sativus*)
Yiqun Weng, Research Geneticist, USDA-ARS and Associate Professor, Dept. Horticulture
1575 Linden Drive, Univ. Wisconsin, Madison, WI 53706 (Yiqun.weng@ars.usda.gov)

Squash (*Cucurbita spp*.)
Michael Mazourek, Assistant Professor, Department of Horticulture
248 Emerson Hall, Cornell University, Ithaca, NY 14853 (mm284@cornell.edu)

Genomics and Bioinformatics
Zhangjun Fei, Associate Professor, Boyce Thompson Institute for Plant Research
533 Tower Road, Cornell Univ., Ithaca NY 14853 (zf25@cornell.edu)

Socioeconomics
Marco Palma, Associate Professor, Department of Agricultural Economics
330D AGLS Building, Texas A&M Univ., College Station, TX 77843 (mapalma@tamu.edu)

Extension/Outreach
Jonathan Schultheis, Professor, Department of Horticulture
264 Kilgore Hall, North Carolina St. Univ., Raleigh, NC 27695 (jonathan_schultheis@ncsu.edu)

Co-PDs

Mary Hausbeck
Professor
Dept. Plant Soil and Microbial Sciences
Michigan State University East Lansing MI, 48824
hausbec1@msu.edu
(cucumber and extension/outreach teams)

Shaker Kousik
Research Plant Pathologist
USDA-ARS Vegetable Lab.
2700 Savannah Highway,
Charleston, SC 29414
shaker.kousik@ars.usda.gov
(watermelon, melon teams)

Kai-Shu Ling
Research Plant Pathologist
USDA-ARS Vegetable Laboratory
2700 Savannah Highway,
Charleston, SC 29414
Kai.ling@ars.usda.gov
(watermelon team)

Angela Linares Ramirez
Assistant Professor
Dept. Agronomy and Soils
University of Puerto Rico
Mayaguez PR 00681
angela.linares@upr.edu
(squash, extension/outreach)

Cecilia McGregor
Assistant Professor
Department of Horticulture
1119 Miller Plant Sciences
University of Georgia Athens, GA 30602
cmcgre1@uga.edu
(watermelon team)

Lina Quesada-Ocampo
Assistant Professor Vegetable Pathology
2510 Thomas Hall
North Carolina St. Univ.
Raleigh NC 27695
lmquesad@ncsu.edu
(watermelon, extension/outreach teams)

Umesh Reddy
Professor
Biology Department
133 Hamblin Hall
West Virginia St. Univ. Institute WV 25112
ureddy@wvstateu.edu
(genomics/bioinformatics)

Louis Ribera
Associate Professor
Dept. Agric. Economics
327C AGLS Building
Texas A&M University College Station, TX 77843
lribera@tamu.edu
(socioeconomics team)

Christine Smart
Professor Dept. Plant Path. & Plant-Microbe Biology
630 West North Street
NY State Agric. Exp. Sta.
Cornell University
Geneva NY 14456
cds14@cornell.edu
(squash, extension/outreach)

Pat Wechter
Research Plant Pathologist
USDA-ARS Vegetable Lab.
2700 Savannah Highway,
Charleston, SC 29414
Pat.wechter@ars.usda.gov
(watermelon, melon teams)

Todd Wehner
Professor
Department of Horticulture 222 Kilgore Hall
North Carolina St. Univ.
Raleigh NC 27695
tcwehner@gmail.com
(watermelon, cucumber)

Linda Wessel-Beaver Professor
Dept. Agronomy and Soils
Box 9030
University of Puerto Rico
Mayaguez PR 00681
lbeaver@uprm.edu
(squash team)

Bill Wintermantel
Research Plant Pathologist
USDA-ARS, US Agricultural Res. Station
1636 E Alisal St
Salinas CA 93905
Bill.Wintermantel@ars.usda.gov
(melon team)

Stakeholder Advisory Board		
Organization	**Representative**	**Position**
Commodity Groups - Growers, Shippers, Processors, Marketing		
National Watermelon Promotion Board	Mark Arney	Executive Director, National Watermelon Promotion Board
National Watermelon Association	Robert Morrissey	Executive Director, National Watermelon Association
California Melon Research Board	Milas Russell	Chair Elect, California Melon Research Board President, Sandstone Melon Company
California Melon Research Board	Steve Smith	Chair, California Melon Research Board Co-Owner Turlock Fruit Company
Pickle Packers International	Brian Bursiek	Executive Vice President, Pickle Packers International
Swanson Pickles and Pickle Packers International	John Swanson	President Swanson Pickle Company; Research Board, Pickle Packers International
Martin Farms (squash grower, shipper)	Mitch Beyler	Partner, John B. Martin and Sons Farms, Inc.
Stony Brook Wholehearted Foods (squash processor)	Greg Woodworth	Founder, Stony Brook Wholehearted Foods
Seed Industry		
Bayer Crop Science	Jovan Djordjevic/ Suren Baliji	Global R&D Lead, Melons and Watermelons, Bayer Crop Science
HM Clause	Kishor Bhattarai	Phytopathology Project Manager, HM Clause, Vegetable Seeds Division, Limagrain
Hollar Seed Company	Bruce Carle	Plant Breeder, Hollar Seed Company
Johnny's Selected Seeds	Rob Johnston/ Lindsay Wyatt	Chairman, Johnny's Selected Seeds
Monsanto	Nischit Shetty	NAFTA Cucurbit Lead for Monsanto Vegetable Seeds
Sakata Seeds	Jeff Zischke/ Benito Juarez	Director of Research, Vegetables, Sakata Seed
Syngenta Seeds Inc.	Jim Brusca/Matt Kinkade/Sandhu Ajay	Global Cucurbits Co-Lead, Syngenta Seeds
United Genetics Seeds Co.	Xuemei Zhang	Melon Breeder, United Genetic Seeds

Industry Participants:

Isabel Armas, Daniel Ludeking, Rijk Zwaan

Cucurbit Crop Curators

Robert Jarret - *Citrullus* spp.
USDA-ARS, Plant Genetic Resources Conservation Unit
1109 Experiment Station, Griffin GA 30223
Bob.Jarret@ARS.USDA.GOV

Joanne Labate – *Cucurbita* spp.
USDA-ARS, Plant Genetic Resources Unit, Geneva, NY 14456
joanne.labate@ars.usda.gov

Kathy Reitsma - *Cucumis* (*C. melo* and *C. sativus*)
USDA-ARS, North Central Regional Plant Introduction Station
Iowa State University, Ames IA 50011
Kathleen.Reitsma@ARS.USDA.GOV

External Evaluators

Allen Van Deynze
Director of Research at the UC Davis Seed Biotechnology Center
Department of Plant Sciences
Plant Reproductive Biology Extension Center Drive, Davis, CA 95616
avandeynze@ucdavis.edu

Nurit Katzir
Professor and Head of the Agricultural Research Organization Newe Ya‘ar Research Center (recently retired)
Newe Ya'ar Research Center, P.O.Box 1021, Ramat Yishay 30095, Israel
katzirn@volcani.agri.gov.il

Phil McClean
Director of the Genomics and Bioinformatics Program at North Dakota State University
Department of Plant Sciences, North Dakota State University, Fargo, ND 58105
phillip.mcclean@ndsu.nodak.edu

CucCAP PROJECT OBJECTIVES,

TIMELINES and METRICS

CucCAP PROJECT OBJECTIVES

Each objective includes integrated research and extension/outreach [E/O] approaches:

Obj. 1. Develop genomic approaches and tools for cucurbit species.

- Develop genomic and bioinformatic platforms for: genotyping by sequencing (GBS); sequence data processing and analysis; and genotype, phenotype and QTL databases
- Perform GBS analysis of PI collections and core populations of the four species to provide a community resource for genome wide association studies (GWAS) for current and future traits of interest
- [E/O] Provide access to cucurbit genomics tools and databases via the International Cucurbit Genome Initiative (ICuGI) website, and by genomics and bioinformatics workshops open to all members of the cucurbit scientific and breeding communities

Obj. 2. Perform genomic-assisted breeding to introgress disease resistance into cucurbit cultivars.

- Utilize genomic approaches to map resistance loci for key cucurbit diseases
- Develop and verify molecular markers for efficient trait selection and gene pyramiding
- Introgress resistances into advanced breeding lines
- [E/O] Provide web-based and face to face information via field trials, extension venues, and scientific meetings regarding breeding materials, markers, and breeding progress

Obj. 3 Perform economic impact analyses of cost of production and disease control and provide readily accessible information to facilitate disease control.

- Define, parameterize, simulate, and validate production variables based on cucurbit production crop budgets
- Use a risk-based simulation model to analyze economic potential of the disease resistant cucurbit cultivars
- [E/O] Develop a centralized cucurbit disease website, including content in English and Spanish, providing information about diagnostics and links to disease clinics; disease control recommendations; disease alerts and links to forecasting tools

Disease priorities identified by the cucurbit industries:

Table 1. Major disease threats to cucurbit crop production as identified by cucurbit industry stakeholders.

Disease	Identified as commodity funding priority[a]	Also affects:
Downy mildew	cucumber	melon, watermelon, squash/pumpkin
Fusarium wilt	watermelon	melon, cucumber
Gummy stem blight	watermelon	melon, cucumber, squash/pumpkin
Phytophthora rot	cucumber, watermelon, squash/pumpkin	melon
Powdery mildew	melon, watermelon, squash/pumpkin	cucumber
Viruses (CMV[b], CYSDV[c], PRSV-W[d], CGMMV[e]	melon[b,c], watermelon[d,e]	cucumber[c,e], squash/pumpkin[b,d]

Project Structure – Team Organization

CucCAP Teams			
Team	**PD, Co-PDs and Co-PIs**		**Institution[a]**
	PD: Rebecca Grumet	(RG)	MSU
Watermelon	***Team Leader: Amnon Levi***	(AL)	ARS-SC
	Shaker Kousik	(SK)	ARS-SC
	Kai-Shu Ling	(KSL)	ARS-SC
	Cecilia McGregor	(CM)	UGA
	Lina Quesada	(LQ)	NCSU
	Pat Wechter	(PW)	ARS-SC
	Todd Wehner	(TW)	NCSU
Melon	***Team Leader: Jim McCreight***	(JM)	ARS-CA
	Shaker Kousik	(SK)	ARS-SC
	Pat Wechter	(PW)	ARS-SC
	Bill Wintermantel	(BW)	ARS-CA
Cucumber	***Co-PD, Team Leader: Yiqun Weng***	(YW)	ARS-WI
	Rebecca Grumet	(RG)	MSU
	Mary Hausbeck	(MH)	MSU
	Todd Wehner	(TW)	NCSU
Squash	***Team Leader: Michael Mazourek***	(MM)	CU
	Christine Smart	(CS)	CU
	Linda Wessel-Beaver	(LWB)	UPR
Genomics/bioinformatics	***Team Leader: Zhangjun Fei***	(ZF)	BTI
	Umesh Reddy	(UR)	WVSU
	Amnon Levi (watermelon)	(AL)	ARS-SC
	Mike Mazourek (squash)	(MM)	CU
	Pat Wechter (melon)	(PW)	ARS-SC
	Yiqun Weng (cucumber)	(YW)	ARS-WI
Socioeconomics	***Team Leader: Marco Palma***	(MP)	TAMU
	Louis Ribera	(LR)	TAMU
Extension/Outreach	***Team Leader: Jonathan Schultheis***	(JS)	NCSU
	Lina Quesada (watermelon)	(LQ)	NCSU
	Mary Hausbeck (cucumber)	(MH)	MSU
	Jim McCreight (melon)	(JM)	ARS-CA
	Angela Linares Ramírez	(ALR)	UPR
	Christine Smart (squash)	(CS)	CU
	Zhangjun Fei (bioinformatics)	(ZF)	CU

[a]Institution abbreviations: ARS-CA (Salinas), SC (Charleston), WI (Madison); BTI-Boyce Thompson Inst; CU-Cornell Univ; MSU-Michigan St Univ; NCSU-North Carolina St Univ; TAMU- Texas A&M Univ; UGA-Univ Georgia; UNH-Univ New Hampshire; UPR-Univ Puerto Rico; WVSU-West Virginia St Univ

TIMELINE CHART

TIMELINE CHART					
Objective	**Personnel/Institution**	**Year**			
	(initials as in Table 3)	1	2	3	4
(a) Obj. 1. Develop common genomic approaches and tools for cucurbits					
1.1. Develop genomic and bioinformatics platforms					
1.1.1. Genotyping by sequencing	ZF (BTI)	X	X	X	
1.1.2. Sequence data processing/analysis	ZF (BTI)	X	X	X	X
1.1.3. ICuGI database development	ZF (BTI)	X	X	X	X
1.1.4 Community standardized nomenclature	YW (ARS-WI), AL (ARS-SC) JM (ARS-CA). MM (CU)		X	X	
1.1.5. Genomic, bioinformatics workshops	ZF (BTI), UR (WVSU), members of crop teams		X	X	X
1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)					
1.2.1. GBS of cucurbit species, establish molecular-informed core populations	ZF (BTI), RG (MSU)	X	X		
- watermelon	AL (ARS-SC)	X	X		
- melon	JM (ARS-CA)	X	X		
- cucumber	YW (ARS-WI),	X	X		
- squash	MM (CU)	X	X		
1.2.2. Population genetics and GWAS analyses	UR (WVSU), ZF (BTI)		X	X	X
- watermelon	AL (ARS-SC)		X	X	X
- melon	JM (ARS-CA)		X	X	X
- cucumber	YW (ARS-WI), RG (MSU)		X	X	X
- squash	MM (CU)		X	X	X
(b) Obj. 2. Genomic assisted breeding for disease resistance					
2.1 QTL map resistances:	Screen for resistance (**Sc**), develop populations **(P)**, phenotype (**F**), sequence **(S)**, QTL map **(Q)**				
2.1.1. Watermelon					
- CGMMV	KSL (ARS-SC), AL (ARS-SC)	Sc	Sc,P	P,F,S	S,Q
- Fusarium race 1	AL (ARS-SC), PW (ARS-SC)	FSQ	Q		
race 2	PW (ARS-SC), AL (ARS-SC)	PFS	PFSQ	FSQ	
- gummy stem blight	CM (UGA), TW (NCSU)	P	PFSQ	FQ	
- Phytophthora	SK (ARS-SC)	PFS	SQ		
- powdery mildew	SK (ARS-SC)	PFS	SQ		
- PRSV-W	AL (ARS-SC), KSL (ARS-SC)	PF	FSQ	FSQ	
2.1.2. Melon					
- powdery mildew	SK,PW (ARS-SC), JM (ARS-CA)	PF	PFS	FQ	FQ
- Fusarium	PW (ARS-SC)	PFS	PFS	PFSQ	
- CYSDV	JM (ARS-CA), WW (ARS-CA)	F	FS	FSQ	
- CMV	JM (ARS-CA), MM (CU)	P	F	SQ	
2.1.3. Cucumber					
- downy mildew	YW (ARS-WI), TW (NCSU)	PFS	SQ	SQ	
- Phytophthora	RG (MSU)	PF	PFSQ	SQ	
2.1.4 Squash					
- Phytophthora	MM (CU), CS (CU)	PF	PF	Q	
- PRSV-W	MM	PFQ	Q		
- CMV	MM	PFQ	Q		
2.2 Marker development and verification:	Refine map (**R**) develop marker **(M)**, verify **(V)**				
2.2.1. Watermelon					
- Fusarium race 1	AL (ARS-SC), PW (ARS-SC)	R	RV	V	V
race 2	PW (ARS-SC), AL (ARS-SC)			RM	RM
- gummy stem blight	CM (UGA), TW (NCSU)			RMV	V
- Phytophthora	SK (ARS-SC)			RM	V
- powdery mildew	SK (ARS-SC)			RM	V
- PRSV-W	AL (ARS-SC), KSL (ARS-SC)			RMV	V
2.2.2. Melon					
- powdery mildew	SK (ARS-SC)			RM	V
- Fusarium	PW (ARS-SC)	M	RM	RM	V
- CYSDV	WW (ARS-CA), JM (ARS-CA)			RM	V
- CMV	JM (ARS-CA), MM (CU)			RM	V

2.2.3. Cucumber - downy mildew - Phytophthora	 YW (ARS-WI), TW (NCSU) RG (MSU)	 RM	 RM	 V RM	 V V
2.2.4 Squash - powdery mildew - Phytophthora - PRSV-W - CMV	 MM(CU), LWB(UPR) MM (CU) MM(CU), LWB(UPR) MM(CU), LWB(UPR)	 RM	 V RM RM	 RM V V	 V
2.3. Introgress resistance into advanced breeding lines:	Develop breeding lines **(B),** introgress into cultivated **(I)**, advanced lines **(A)**, release to breeders **(R)**				
2.3.1. Watermelon - Fusarium race 1 race 2 - gummy stem blight - Phytophthora - powdery mildew - PRSV-W	 AL (ARS-SC), PW (ARS-SC) PW (ARS-SC), AL (ARS-SC) CM (UGA), TW (NCSU) SK (ARS-SC) SK (ARS-SC) AL (ARS-SC), KSL (ARS-SC)	 B B B B B	 I B B I I B	 IA I I I I I	 AR I I A A I
2.3.2. Melon - powdery mildew - Fusarium - CYSDV - CMV	 SK (ARS-SC), JM (ARS-CA) PW (ARS-SC) JM (ARS-CA), WW (ARS-CA) JM (ARS-CA)	 B B I I	 I B I I	 I I IA I	 IA IA IAR IA
2.3.3. Cucumber - downy mildew - Phytophthora	 YW (ARS-WI), TW (NCSU) RG (MSU)	 B B	 I B	 I I	 R I
2.3.4 Squash - powdery mildew - Phytophthora - PRSV-W - CMV	 Already exists MM (CU), CS (CU) Already exists Already exists	 I	 I	 AR	 AR
(b) Obj. 3. Economic impact analyses, disease control information					
3.1 Perform economic analysis, cost of production/disease control					
3.1.1. Define, parameterize, simulate, validate production variables	LR (TAMU), MP (TAMU)	X	X		
3.1.2. Estimate the potential economic impacts to the cucurbit industry	LR (TAMU), MP (TAMU)			X	X
3.2 Provide readily accessible information to facilitate disease control					
3.2.1. Develop a centralized cucurbit disease website	LQ (NCSU), JS (NCSU)	X	X		
3.2.2. Develop and post diagnostic resources and disease control information in English and Spanish; prepare diagnostic poster	LQ (NCSU), MH (MSU), CS (CU), ALR (UPR)	X	X X	X X	X
3.2.3 Provide disease alerts and forecasting tools		X	X	X	X
3.2.4. Field days and demonstration plots	Crop and extension teams	X	X	X	X

Status of resistance breeding for the priority cucurbit diseases at project outset.

Crop and disease	Sources of resistance	Elite germplasm for introgression	Field testing locations	Resistant parental line	Phenotypic data for GWAS	Segregating populations	Analysis of inheritance	QTL analysis segregating populations	Marker development	Introgression into cultivated types	Advanced breeding lines for release	Cultivars for release to farmer
Watermelon												
Fusarium race2 (Fus)	PI 482246-USVL246^{FR2}; PI 482252-USVL252^{FR2}	Standard: Charleston Gray Icebox: Sugar Baby	SC	X	x	X				x		
Fusarium race 1	Calhoun Gray		SC	x	x	X	**X**	**X**		X		
Gummy stem blight (GSB)	PI 482276-UGA1081; PI 526223-UGA157		NC, GA	x	x	X				X		
Phytophthora (Phyt)	PI 494531-USVL531MDR; PI 560003- USVL003MDR		SC, NC	x	x	X				X		
Powdery mildew (PM)			SC, NC	X		X	**X**			X		
CGMMV	Currently evaluating		GH[b]									
PRSV-W	PI 595203		SC	X	x	x	X					
Melon												
Powdery (PM)	MR-1	Cantaloupe: TopMark, Impac Honeydew: Green Flesh Honeydew or PMR Honeydew	CA1,2, AZ	x		X	X					
Fusarium (Fus)	MR-1		CA1	x		X	X			X	X	
CYSDV	PI 313970; TGR1551		CA1, AZ	X	x	X	**X**					
CMV	PI 161375; Freeman cucumber		CA1,2, AZ				X					
Cucumber												
Downy mildew (DM)	PI 197088; PI 330628	Slicer: Poinsett 76 Pickling: NC-25, GY14	WI, NC	X		X	**X**	**X**		X	X	
Phytophthora (Phyt)	PI 109483		MI, NY		**x**	X						
Squash												
Phytophthora (Phyt)	PI 211996; PI 483347; PI 634693	Butternut: Burpee Butterbush	NY	X			X					
Powdery (PM)	*C. martenezii*	Tropical pumpkin: Soler,Taina Dorada	PR	x			X	**x**	x	x	x	x
PRSV-W	Menina, Nigerian Local		PR	X			X			x	X	X
CMV	Menina, Nigerian Local		PR	x			x			x	X	X

PROJECT METRICS

Metrics to be used in CucCAP project evaluation
Short term metrics (1-2 years)
1. State of the art, genotyping by sequencing (GBS) and data analysis platforms are developed for cucurbit species. 2. GBS sequence data are obtained for 1000-1600 PIs for each of the four cucurbit crops. 3. Community-standardized cucurbit gene/trait descriptors and nomenclature are established. 4. Germplasm lines with resistance to *Fusarium* r.1,2, *Phytophthora*, powdery mildew, and PRSV are established for watermelon; for CYSDV in melon, and *Phytophthora* in cucumber. 5. Markers developed for KASP-based assay for downy mildew in cucumber and powdery mildew and ZYMV in squash. 6. Field trials and field days are held to test and demonstrate disease resistant materials (average 1/yr/crop). 7. Representative farms are developed for economic analyses for three locations for each of the four commodities. 8. The CucCAP Cucurbit Disease Extension Website is established. 9. Participation in outreach to 15-20 stakeholder groups per year via industry events and field days. 10. A Cucurbit Genomics and Bioinformatics workshop is delivered at PAG 2017 attended by members from at least 20 cucurbit research laboratories.
Medium term metrics (3-4 years)
1. Population structure analysis is performed and molecular-directed core populations are established for the four cucurbit crops. 2. Breeder-friendly databases to store and distribute genomic, phenotypic, and genotypic information and development of associated data analysis tools are implemented (www.icugi.org). Based on current traffic, at least 1000 unique visitors are expected per week. 3. GWAS analyses are performed for CGMMV, *Fusarium*, gummy stem blight, *Phytophthora* and PRSV-W in watermelon; CYSDV in melon and *Phytophthora* in cucumber. 4. QTL associated with CGMMV, *Fusarium* r.2, gummy stem blight, *Phytophthora*, powdery mildew, and PRSV in watermelon; CMV, CYSDV, *Fusarium* and powdery mildew in melon; downy mildew, *Phytophthora* in cucumber; and CMV, PRSV and powdery mildew in squash have been identified. 5. Molecular markers have been developed for *Fusarium* r.1 in watermelon; CMV, CYSDV, *Fusarium* and powdery mildew in melon; downy mildew in cucumber; and CMV, PRSV and powdery mildew in squash. 6. Breeding lines with resistance to *Fusarium* r.1,2 and PRSV in watermelon; CMV, CYSDV, *Fusarium* and powdery mildew in melon; downy mildew in cucumber; and *Phytophthora* in butternut squash are available to researchers and seed companies. 7. Cucumber lines carrying multiple disease resistances (downy mildew/powdery mildew/ZYMV) developed by marker assisted selection. 8. Field trials and field days are held to test and demonstrate disease resistant materials (average 2/yr/crop). 9. Cucurbit disease informational materials in English and Spanish are developed and posted on the CucCAP disease website for each of the priority diseases. 10. Stakeholders use website and social media tools to obtain information about disease outbreaks, diagnosis and control. Based on prior experience with cucurbit disease tracking and informational websites, 1000-2000 hits per week are expected during peak growing season. 11. Participation in outreach to 15-20 stakeholder groups each year via industry events and field days. 12. Representative farms are compared to information available through USDA agencies and Extension service budgets for accuracy, and inputs are used to develop stochastic economic feasibility model by region. 13. Scenarios developed using project findings are run through economic feasibility models. 14. The Cucurbitaceae 2018 conference is hosted, expected attendance of 200-250 international cucurbit scientists from public and private sector. 15. Cucurbit genomics workshops are delivered at PAG 2018, 2019 and Cucurbitaceae 2018; expected attendance at Cucurbitaceae 2018, 100-200 people. 16. 15 graduate students and 3 post-docs are trained in cucurbit genetics, genomics, disease and economic analysis. 17. 4-5 refereed articles are published by each crop group

Long term metrics
1. Sustainable data management, storage, and statistical analysis systems for cucurbit sequence, QTL, marker and phenotype data are available for the cucurbit research and breeding community
2. Sustainable community resources for cucurbit GWAS analysis are available for the four crops
3. Advanced breeding lines with resistance to Fusarium race 1,2, gummy stem blight, *Phytophthora*, powdery mildew, PRSV and GCMMV in watermelon; CMV, CYSDV, *Fusarium* and powdery mildew in melon; and combined downy mildew, powdery mildew, and ZYMV in cucumber.
4. Breeding lines with resistance to critical cucurbit diseases are used in breeding programs to improving/pyramiding resistance into commercial cucurbit cultivars
5. Markers developed from major QTL are used in breeding programs to improve disease resistance in commercial cucurbit cultivars
6. Markers are adopted by at least one fee for service genotyping lab serving the US breeding community
7. A sustainable web-based resource is available for information about cucurbit disease diagnosis and control
8. The cost and time frame for development of cucurbit cultivars with comprehensive disease resistance packages is reduced
9. Cucurbit producers experience reduced losses, improved crop quality and reduced input costs and labor due to increased disease resistance
10. There is reduced pesticide used to control cucurbit diseases.

TEAM PROGRESS REPORTS

and

PLANS FOR THE COMING YEAR

Genomics and Bioinformatics Team

Team members:

Zhangjun Fei (Boyce Thompson Institute)
Umesh Reddy (West Virginia St. Univ.)
Amnon Levi (USDA, ARS)
Yiqun Weng (USDA, ARS)
Michael Mazourek (Cornell University)
Pat Wechter (USDA, ARS)
Rebecca Grumet (Michigan State University)

Objectives Year 1

Develop common genomic approaches and tools for cucurbits

(a) Obj. 1. Develop common genomic approaches and tools for cucurbits	Personnel/Institution	Yr 1	Yr 2	Yr 3	Yr 4
1.1. Develop genomic and bioinformatics platforms					
1.1.1. Genotyping by sequencing	ZF (BTI)	X	X	X	
1.1.2. Sequence data processing/analysis	ZF (BTI)	X	X	X	X
1.1.3. ICuGI database development	ZF (BTI)	X	X	X	X
1.1.4 Community standardized nomenclature	YW (ARS-WI), AL (ARS-SC) JM (ARS-CA). MM (CU)		X	X	
1.1.5. Genomic, bioinformatics workshops	ZF (BTI), UR (WVSU), members of crop teams		X	X	X
1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)					
1.2.1. GBS of cucurbit species, establish molecular-informed core populations	ZF (BTI), RG (MSU)	X	X		
- watermelon	AL (ARS-SC)	X	X		
- melon	JM (ARS-CA)	X	X		
- cucumber	YW (ARS-WI),	X	X		
- squash	MM (CU)	X	X		
1.2.2. Population genetics and GWAS analyses	UR (WVSU), ZF (BTI)		X	X	X
- watermelon	AL (ARS-SC)		X	X	X
- melon	JM (ARS-CA)		X	X	X
- cucumber	YW (ARS-WI), RG (MSU)		X	X	X
- squash	MM (CU)		X	X	X

Work in progress and plans

1.1. Develop genomic and bioinformatic platforms for cucurbit crops

1.1.1. Genotyping by sequencing

In closely working with Cornell *Genomic Diversity* Facility, we have set up the genotyping-by-sequencing (GBS) platform for the four cucurbit species: watermelon, melon, cucumber and squash.

1.1.2. Sequence data processing/analysis

We have evaluated and compared the performance of TASSEL-GBS (http://www.maizegenetics.net/tassel) and GATK (https://www.broadinstitute.org/gatk/) in SNP calling using GBS data. Based on the results from this analysis we have established a GBS data analysis pipeline.

1.1.3. ICuGI database development

We are in the process of re-implementing the ICuGI database using the GMOD Tripal system (http://gmod.org/wiki/Tripal) and the Chado database schema (http://gmod.org/wiki/Chado). The implementation of the database is close to done. Genome sequences of melon, watermelon Charleston Gray and wild cucumber have been processed and included in the database. Genome syntenies between watermelon, melon and cucumber have been identified and a genome synteny browser have been implemented in the database. The database is currently run on an old development server (http://tripal.feilab.net/). We recently purchased a new high-end web server and the system is currently under configuration. The database will be moved to the new server once the configuration is done, and the link will be distributed to the CucCAP teams for suggestions and final tweaks.

1.1.4 Community standardized nomenclature.

This has not begun.

1.1.5. Genomic, bioinformatics workshops

A workshop on the ICuGI database has been scheduled at the Solcuc2017 meeting in Sept., 2017 at Valencia, Spain.

1.2. Perform GBS analysis of PI collections, establish core populations of the four species, and provide community resource for genome wide association studies (GWAS)

1.2.1. GBS of cucurbit species, establish molecular-informed core populations

Each crop team has grown PI seedlings and sampled leaf tissue for processing in the Grumet lab using high throughput DNA extraction protocols established at the outset of the CucCAP project. At this time, DNA has been prepared from the full PI collection for cucumber, along with additional lines representing different market classes and historical cultivars (1615 samples). The majority of the PI collection for watermelon (1344/1384 samples) also has been completed (as of 3/1/17); the remaining samples will be received and processed shortly. After quality checks, all samples were sent in 96-well format to Cornell for GBS, where GBS is performed in 384-plex format. At this time GBS data has been received for 26 plates (14 for cucumber; 12 for watermelon) and quality of this data has been evaluated. DNA preparations are currently underway for melon; 1900 samples have been received, 1520 (13 plates) have been processed and shipped. An additional 855 are in process and should be completed by late March. The squash PI collection spans three commercially important species. 165 accessions of *C. maxima* have been genotyped with a PstI digest. Tissue for 319 accessions of the *C. moschata* collection has been collected and is awaiting transfer to the Grumet lab for DNA preps. The entire available *C. pepo* collection is currently being planted and we expect to begin DNA preps in April.

Table 1 Status of cucurbit GBS

Batch	DNA plate No.	Multi-plex Level	Crop	DNA Submission Date	Data Release Date
1	8	96	cucumber	4/13/2016	7/12/2016
2	9	96	cucumber	5/2/2016	7/12/2016
3	11,12,13,14	384	cucumber	8/24/2016	10/18/2016
4	2,5,6,16	384	cucumber	9/23/2016	11/21/2016

5	1,4,7,15	384	cucumber	10/3/2016	11/21/2016
6	31,34,35,36	384	watermelon	10/19/2016	11/21/2016
7	37,38,39,40	384	watermelon	10/31/2016	1/3/2017
8	41,42,43,44	384	watermelon	11/4/2016	2/15/2017
9	49	96	melon	12/8/2016	
10	3,10,17,46	384	cucumber	1/20/2017 & 2/2/2017	
11	50,51,52,53	384	melon	2/14/2017	
12	54,55,56,57	384	melon	2/22/2017	
13	58,59,60,61	384	melon	3/2/2017	

1.2.2. Population genetics and GWAS analyses

We are waiting to get the GBS data for all samples of each species. All GBS data from each species will be processed together and SNPs called. The resulting SNPs will be used for population genomics analyses and for the analysis to identify core collections.

1.2.3 Genomic resequencing of core collections

During last year's annual meeting, we agreed to change our plan to genotype the core collection using whole genome resequencing instead of GBS. We were trying to identify cheap services for library construction and sequencing to accommodate our budget. For library construction, we identified Cornell Genomic Diversity Facility as our service provider, who charges $33 for each library (http://www.biotech.cornell.edu/brc/genomic-diversity-facility/price-list). For sequencing, we will use Novogene HiSeq X Ten system, which cost $18 per 100 Gb raw data.

Recently, we submitted 45 DNA samples to Cornell Genomic Diversity Facility for library construction. We expect to get the constructed libraries and sequences in about two months.

Watermelon Team

Team members:

Amnon Levi (USDA, ARS) Cecilia McGregor (Univ. Georgia)
Shaker Kousik (USDA, ARS) Pat Wechter (USDA, ARS)
Kai-shu Ling (USDA, ARS) Todd Wehner (North Carolina St. Univ.)

Overall objectives: Identifying quantitative trait loci (QTL) associated with resistance to major and emerging diseases, developing useful molecular markers and utilizing the genomic tools to incorporate resistance into watermelon cultivars.

Major diseases: Gummy stem blight, Fusarium wilt, Powdery mildew, Phytophthora fruit rot, Papaya ringspot virus (PRSV) and Cucumber green motile mosaic virus (CGMMV).

Objective	**Personnel/Institution**	**Year**			
	(initials as in Table 3)	1	2	3	4
(a) Obj. 1. Develop common genomic approaches and tools for cucurbits					
1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)					
1.2.1. GBS of cucurbit species, establish molecular-informed core populations	ZF (BTI), RG (MSU)	X	X		
- watermelon	AL (ARS-SC), TW (NCSU)	X	X		
1.2.2 Population genetics and GWAS analysis	UR (WSVU), ZF (BTI)		x	x	x
- watermelon	AL (ARS-SC)				
(b) Obj. 2. Genomic assisted breeding for disease resistance					
2.1 QTL map resistances:	Screen for resistance (**Sc**), develop populations **(P)**, phenotype (**F**), sequence **(S)**, QTL map **(Q)**				
2.1.1. Watermelon					
- CGMMV	KSL (ARS-SC), AL (ARS-SC)	Sc	Sc,P	P,F,S	S,Q
- Fusarium race 1	AL (ARS-SC), PW (ARS-SC)	FSQ	Q		
race 2	PW (ARS-SC), AL (ARS-SC)	PFS	PFSQ	FSQ	
- gummy stem blight	CM (UGA), TW (NCSU)	P	PFSQ	FQ	
- Phytophthora	SK (ARS-SC)	PFS	SQ		
- powdery mildew	SK (ARS-SC)	PFS	SQ		
- PRSV-W	AL (ARS-SC), KSL (ARS-SC)	PF	FSQ	FSQ	
2.2 Marker development and verification:	Refine map (**R**) develop marker **(M)**, verify **(V)**				
2.2.1. Watermelon					
- Fusarium race 1	AL (ARS-SC), PW (ARS-SC)	R	RV	V	V
2.3. Introgress resistance into advanced breeding lines:	Develop breeding lines **(B),** introgress into cultivated **(I)**, advanced lines **(A)**, release to breeders **(R)**				
2.3.1. Watermelon					
- Fusarium race 1	AL (ARS-SC), PW (ARS-SC)	B	I	IA	AR
race 2	PW (ARS-SC), AL (ARS-SC)	B	B	I	I
- gummy stem blight	CM (UGA), TW (NCSU)	B	B	I	I
- Phytophthora	SK (ARS-SC)	B	I	I	A
- powdery mildew	SK (ARS-SC)	B	I	I	A
- PRSV-W	AL (ARS-SC), KSL (ARS-SC)		B	I	I

Work in progress and plans

1.2. Perform GBS analysis of PI collections, establish core populations of the four species, and provide community resource for genome wide association studies (GWAS) *(Takshay Patel and Todd C. Wehner)*

1.2.1. GBS of cucurbit species, establish molecular-informed core populations

i. Objective*:* Develop molecular markers for high resistance to gummy stem blight (GSB) using genome-wide association studies (GWAS) in the USDA watermelon germplasm collection, and introgress GSB resistance into watermelon cultivars.

We are collecting and increasing *Citrullus* PI accessions, heirloom cultivars, and gene mutant type-lines. Seed increase of the 2000 PI accessions is being accomplished by seed companies, USDA scientists, and university researchers. Each is increasing 1 to 10 accessions per year using controlled pollination in greenhouse or field.

A list of the PI accessions and gene type-lines is being developed to use for the DNA sampling. The sampling protocol is from Michigan State University, and will involve 1000 PI accessions sampled at the seedling stage, with one plant per accession.

Genotyping: A group of 384 watermelon accessions are being selected to develop a core watermelon populations. The core watermelon population will be used to develop sequence-based molecular markers (SNPs) using the genotyping by sequencing (GBS) method at Cornell University. We expect to get several thousand of SNPs for the association analysis.

Association analysis: Collected phenotypic and genotypic data will be analyzed using R packages: SNPassoc, snpMatrix, GenABEL and pbatR. The result of the analysis will allow us to locate and identify SNP markers associated with GSB resistance.

Gene type lines

Sixty-two available accessions (red text indicates difficult to find) are index

Collection and seed increase of the watermelon gene type-lines will include all cultivars, breeding lines, and PI accessions in the gene mutant list at Cucurbit Genetics Cooperative. Examples include: PI 189225 (*db, Ar-2-1*), NC-517 (*C*), PI 482261 (*Ctr*), Bush Charleston Gray (*dw-1*), PI 595203 (*zym-CH, zym-FL*). Below is the list of 42 type lines.

Watermelon gummy stem blight resistance (Luis Rivera and Todd C. Wehner)

Objective: Develop molecular markers for high resistance to gummy stem blight (GSB) using genome-wide association studies (GWAS) in the USDA watermelon germplasm collection, and introgress GSB resistance into watermelon cultivars.

Phenotyping: The WmGsb population was developed by intercrossing the most resistant accessions of Citrullus four times (I4), followed by crossing with elite cultivars of watermelon (I4F1), followed by intercrossing without selection, while maintaining wild and elite types in the populations (I4F1I4), followed by self-pollinations of plants at random (I4F1I4S1). The 296 lines will be screened in the MAF greenhouse and the field at Clinton NC. Resistance will be rated several times on each plot, in an experiment having 2 years, 4 replications, and 2 locations (greenhouse and field).


2.1.1.1 CGMMV

Evaluating the watermelon PI collection for resistance to *Cucumber green mottle mosaic virus* (CGMMC) and conducting genome-wide association mapping to identify SNPs associated with CGMMV resistance (KS Ling, A Levi)

Cucumber green mottle mosaic virus (*CGMMV*) is an emerging disease on watermelon and other cucurbit crops in North America, including Canada and the United States (Ling et al., 2014; Tian et al., 2014). *CGMMV* is a tobamovirus, similar to *Tobacco mosaic virus* (TMV). This virus was first discovered in Europe and has caused serious epidemics in several Asian countries, like China, Japan, and Korea, and more recently in Australia and the Middle East (Jordan and Israel). It is a seed-borne virus. It is highly contagious and poses a serious threat to the entire cucurbit industries in the U.S. Currently, there is no known resistance sources available for watermelon and other cucurbits. Our primary objective has been to evaluate the entire USDA watermelon germplasm collection with the prospective of identifying and developing potential sources of resistance to CGMMV.

Due to its seed-borne nature and global seed trade *CGMMV* geographic distribution has been expanding rapidly and it became a major threat to all major cucurbit crops and the entire cucurbit industries in the U.S. and around world. The *CGGMV* has been identified as an emerging virus on cucumber, melon, watermelon and other cucurbit crops in Canada and the United States (Ling et al., 2014; Tian et al., 2014) and in Australia (http://www.nt.gov.au/d/cgmmv/).

- We have concluded the preliminary screening in a containment greenhouse of the entire USDA watermelon germplasm (~1,600 accessions) through mechanical inoculation, symptom observation and appropriate lab testing.
- Plants from seven accessions (including 3 *Citrulus lanatus* and 4 *C. colocynthis*) with potential resistance (tolerance) to *CGMMV* were selected based on symptom expression and lower virus titer in tests.
- Various number of seeds were collected from these selected plants.
- Secondary screening for resistance to *CGMMV* using seedlings generated from the S1 seeds (various number of seeds were collected from these selected plants) are underway and the results will be analyzed and presented at the project meeting.
- Resistant plants will be saved for selfing to produce S2 seeds. Cross pollination will be conducted to generate segregation populations for study genetic inheritance of the resistance.

- In addition to watermelon, to determine whether any of the USDA cucumber germplasm has resistance to *CGMMV*, we screened 174 core collection of cucumber germplasm. Unfortunately, none of the test materials was resistant to CGMMV. However, more cucumber germplasm collections are available for screening if needed.
- Furthermore, we also screened 18 rootstocks. Although *lagenaria siceraria* and *C. lanatus* genotypes were susceptible, several Cucurbita hybrids (*Cucurbita maxima* x *Cu. Moshata*) were resistant to *CGMMV*. These *CGMMV*-resistant rootstocks may be useful to protect grafted watermelon from *CGMMV* infection through root contacts in contaminated soil.
- Finally, seeds for approximately 200 accessions of *Cu. Maxima* and *Cu. Moshata* have been requested from the USDA-ARS germplasm resource centers and will be used to screen for resistance to *CGMMV*.

References:

Ling KS, Li R, Zhang W. 2014. First report of *Cucumber green mottle mosaic virus* infecting greenhouse cucumber in Canada. Plant Disease, 98:701.

Tian T, Posis K, Maroon-Lango CJ, Mavrodieva V, Haymes S, Pitman TL, Falk BW. 2014. First report of *Cucumber green mottle mosaic virus* on melon in the United States. Plant Disease 98:1163.

2.1.1.2- Fusarium race 1,2

Genetic mapping of QTL associated with resistance to Fusarium oxysporum races 1 and 2 in *Citrullus lanatus* var. *citroides*. (P. Wechter, S. Branham, and A. Levi)

Fusarium oxysporum f. sp. *niveum* which causes fusarium wilt of watermelon, is considered one of the most important diseases of watermelon production in the United States. There are currently no economical or even viable chemical control strategies or methods that can control this soil-borne pathogen. To date, only a few watermelon lines have been identified and reported as resistant or tolerant to this pathogen. Unfortunately, although some of these lines were reported more than twenty-five years ago, no commercial cultivar is available with resistance to the most serious of the races of this fungus, race 2.

Development of Germplasm lines and Genetic Populations

- Seeds of both *Citrullus lanatus* var. *citroides* USVL246-FR2 and USVL252-FR2, both developed in our work, have been requested and disseminated to eight seed companies and numerous researchers for use in breeding programs and fusarium studies. More than 4000 seeds were distributed in FY2016.
- F2:3 population (N = 173) derived from crossing the Fusarium wilt races 1 and 2 resistant *Citrullus lanatus* var. *citroides* line with the susceptible *Citrullus lanatus* var. *citroides* USVL114 line.
- Two hundred and twenty-five single seed descent lines have been taken to the F_6 stage from a cross of *Fusarium oxysporum* f. sp. *niveum* (*Fon*) race 1 and 2 resistant *Citrullus lanatus* var. *citroides* USVL246 by a susceptible *Citrullus lanatus* var. *citroides* PI582114. These will be carried to the recombinant inbred line (RIL) population (F_7+).
- Two reciprocal F2:3 genetic populations USVL252-FR2 x PI 244019 (S3; resistant to papaya ringspot virus PRSV) have been developed. The first population includes 178 F2:3 families, while the population derived from the reciprocal cross includes 195 F2:3 families. These populations have been developed with the generous support of Sakata Seeds (Dr. Nihat Guner).

Evaluating genetic populations and genetic analyses to identify QTL associated with resistance to Fusarium wilt races 1 and 2

- Two rounds of *Fon* race 2 greenhouse inoculation studies were performed
- DNA was isolated from 180 of the F_2 plants from this cross, and F_3 seed generated from each. All 180 of these DNAs have been sequenced using genotyping by sequencing (GBS) procedure.
- Genotype and phenotype data have been analyzed and we have identified one major and four minor QTL for race 2 resistance (Branham et al. 2016).
- Genetic mapping with this population resulted in a saturated map with 2495 SNP markers (Branham et al. 2016).
- $F_{2:3}$ lines have been assayed for resistance to *Fon* race 1.
- QTL associated with race 1 resistance have been identified and mapped to the genome.
- The two reciprocal F2:3 genetic populations USVL252-FR2 x PI 244019 will be evaluated for resistance for. Leaf samples were collected from all F2 plants for GBS-SNP analysis following their evaluation for resistance to Fusarium wilt races 1 and 2.

Breeding resistance in to watermelon cultivars

- USVL252-FR2 and USVL246-FR2 have been crossed into Sugar Baby, Charleston Grey and Calhoun Grey.
- Backcrossing (BC2F2) of the above into the recurrent parent have been performed.

References:

Branham S.E. A. Levi, M. Farnham and W.P. Wechter. 2016. A GBS-SNP-based linkage map and quantitative trait loci (QTL) associated with resistance to *Fusarium Oxysporum* F. Sp. Niveum Race 2 identified in *Citrullus lanatus* var. *citroides*. Theor. Appl. Genet. 130: 319-330.

2.2.1.1.Converting a Fusarium wilt race 1-resistance QTL to a DNA marker (S. Branham, P. Wechter, and A. Levi)

Year 2 progress: 2.1.1; 2.2.1; 2.3.1

Fusarium wilt (*FW*) race 1 is a major disease of watermelon throughout the United States. In a recent study (Lambel et al. 2014), we identified a major quantitative trait locus (QTL) on chromosome 1 of watermelon associated with resistance to *FW* race 1. There is a need to develop a SNP marker(s) for marker assisted selection (MAS) to precisely predict the presence of resistance in large genetic populations.

We have been developing genetic populations F1, F2, BC1R, BCS [Calhoun Gray (R) x Sugar Baby (S); or Calhoun Gray (R) x Black Diamond (S)] segregating for resistance to *FW* race 1.
To identify a tightly linked DNA marker, we performed QTL-seq analysis. We bulked the DNA of most resistant versus most susceptible F2 plants. The parent genomes and the resistant and susceptible bulked DNAs (Lambel et al. 2014) were re-sequenced. SNPs were called from genomic alignments and a delta-

SNP index was calculated as the frequency of the resistant allele in the susceptible bulk subtracted from the frequency in the resistant bulk.

QTL-seq analysis increased the resolution of the QTL on chromosome 1 from 6.5 Mb (Lambel et al. 2014) to 1.5 Mb. The resequencing data have been used for the construction of 20 KASP primers in this region. Of the 20 KASP primers, 10 are located in the area of highest association with resistance (0-500 kb) while the other 10 KASP primers are spread across regular intervals of the remainder of the major QTL (500 kb -1.5 Mb). The KASP primers will be used in a genetic analysis to identify the SNP which is most tightly linked to resistance to *FW* race 1 in watermelon.

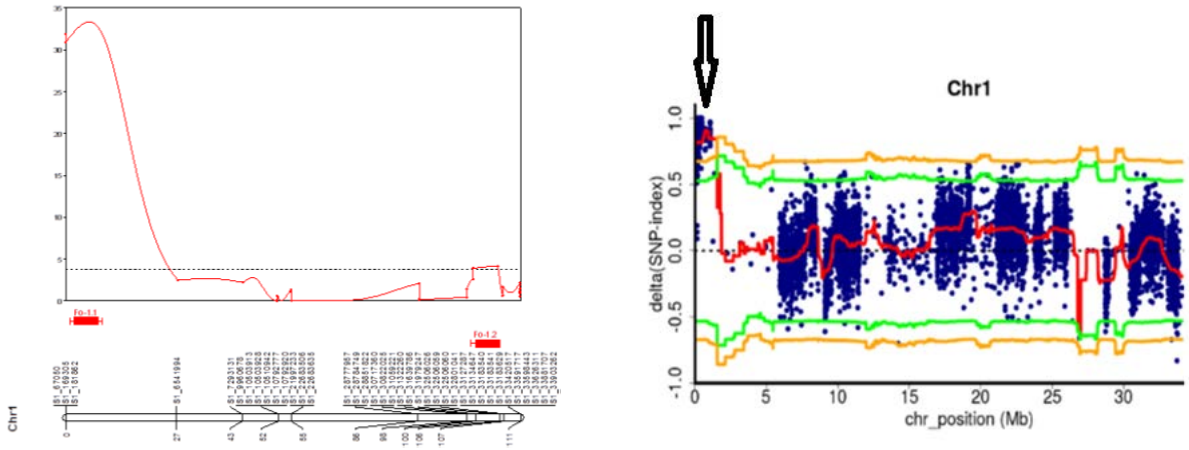


Figure 1. A major QTL associated with Fusarium wilt race 1, covering a chromosomal region of 6.5 Mb on the edge of chromosome 1 identified using GBS-SNPs (Lambel et al. 2014) (Left). QTL-seq based on resequencing of resistant versus susceptible bulks proved useful in identifying SNPs tightly linked to Fusarium wilt race 1 and cover a small genomic region of 500 kb within the major QTL on Chromosome 1 (Right).

Reference:

Lambel, S., B. Lanini, E. Vivoda, J.Fauve, W.P. Wechter, *K.R. Harris-Shultz, L. Massey*, and A. Levi. 2014. A major QTL associated with *Fusarium oxysporum* race 1 resistance identified in genetic populations derived from closely related watermelon lines using selective genotyping and genotyping-by-sequencing for SNP discovery. Theor. Appl. Genet. 127: 2105-15.

2.1.1.3. Gummy stem blight

QTL mapping, marker validation and trait introgression of Gummy Stem Blight resistance in watermelon. (C. McGregor)

Overview of objectives for project duration

Objectives	Year 1	Year 2	Year 3	Year 4
Population Development	X	X		
Phenotyping		X	X	
Sequencing		X		
QTL Mapping		X	X	
Refine Map			X	X
Marker Development			X	X
Marker Validation			X	X
Trait Introgression			X	X

1. Progress for Year 2

1.1 Population Development:

WPop GSB 1: PI 482276 x Crimson Sweet population of 220 $F_{2:3}$ lines. **Complete**

WPop GSB 2: PI 526233 x Sugar Baby population for 96 $F_{2:3}$ lines. **Complete**

WPop GSB 3: Backup population of resistant *C. amarus (*PI 482276) x susceptible *C. amarus*. **In progress**

1.2 Phenotyping

Phenotyping of gummy stem blight is very challenging, particularly when phenotyping a large number of plants. We tested several protocols spray and agar drop inoculation protocols in greenhouses/growth rooms/growth chambers. As expected, growth chambers gave the most constant results. The spray and drop methods gave comparible results, but the spray method takes less time when having to inoculate many plants. We secured space at the UGA Envirotron facility (Griffin, GA) which will enable us to carry out all screenings in growth chambers with complete temperature and humidity control. Population screening will start at this facility in April 2017. The parental lines and a subset of $F_{2:3}$ families will also be phenotyped in the field in Attapulgus (GA) in summer 2017. The purpose of this is to compare field level resistance to what we observe in the growth chamber screens. A subset is used due to space limitations at the field site.

1.3 Sequencing

Initially it was proposed that Genotyping-by-sequencing would be used for genotyping of the populations. However, at the 2016 meeting in East Lansing it was proposed that QTL-Seq should instead be used. In order to do QTL-Seq, phenotyping needs to be completed in order to select the lines that will make up the

resistant and susceptible bulks. All the leaf samples have been collected and are in the -80°C, ready for genotyping once phenotyping is complete.

1.4 QTL Mapping

See above

2. Conclusion and Future Work

Our schedule has changed somewhat due to the need to complete phenotyping before genotyping can start. However we are still confident that we can complete our project goals.

2.1.1.4. Phytophthora fruit rot of watermelon (S. Kousik)

Project metrics (time line) for research on Phytophthora fruit rot and powdery mildew of watermelon

- Develop germplasm lines with resistance to Phytophthora fruit rot and powdery mildew for watermelon: **Completed.**
- Develop populations for phenotyping resistance to Phytophthora fruit rot and powdery mildew of watermelon: **Completed**
- Sequence and map Phytophthora fruit rot and powdery mildew QTL in watermelon: **In progress.**
- Introgress Phytophthora and powdery mildew resistance into cultivated type watermelon: **In progress**
- Participation in outreach to stakeholder groups per year via industry events and field days. **Completed**

Phytophthora fruit rot of watermelon has been a major problem in watermelon growing areas in the Southeastern U.S. (FL, GA, SC, NC and VA). In recent years it has also become a problem in watermelon growing areas in Maryland (MD), Delaware (DE) and Indiana (IN) (Kousik et al., 2016). At the U.S. Vegetable Laboratory (USDA, ARS) in Charleston we have developed several germplasm lines with high levels of resistance to Phytophthora fruit rot. In these studies we used the germplasm line USVL531-MDR which was resistant to 20 different *P. capsici* isolates from across the U.S.A. Studies to determine inheritance of resistance to Phytophthora fruit rot using the same population described for powdery mildew (USVL531-MDR X USVL677-PMS) were conducted as USVL531 is resistant to both these diseases. Fruit from parents, F_1, F_2 and back cross populations were harvested when mature and placed on wire shelves in a walk-in-humid chamber. Each fruit was inoculated with a 7-mm agar plug from an actively growing colony of *Phytophthora capsici* as described before (Kousik et al., 2014a,b). Data on fruit rot was recorded five days after inoculation. Initial observations of the data indicated that inheritance to Phytophthora fruit rot is more complex than powdery mildew. We are currently compiling and analyzing the data from this study. As mentioned above, we have extracted DNA from parents and F_2 plants for GBS. Of the F_2 plants we self-pollinated 186 plants kept in a net house to generate $F_{2:3}$ populations for further evaluation. We will evaluate F_3 families in 2017. Similarly we will phenotype the populations from USVL003-MDR x USVL677-PMS for resistance to Phytophthora fruit rot in 2017.

Powdery mildew of watermelon (Shaker Kousik)

Powdery mildew of watermelon (*Citrullus lanatus*) continues to be a constant problem throughout the southeast. Our recent survey of watermelon researchers also indicated that powdery mildew was considered an important priority for research across the U.S. (Kousik et al., 2016). We have developed USVL531-MDR which is resistant to powdery mildew and Phytophthora fruit rot and have provided the

seeds of this germplasm line to many seed companies through and MTA. USVL531-MDR is an egusi type watermelon with white flesh and low brix (<2% TSS) and was derived from PI 494531 after five cycles of screening and selections. USVL677-PMS was derived from PI 269677 after five cycles of screening and selection for high levels of susceptibility to powdery mildew and Phytophthora fruit rot for use in genetic studies. A simple inheritance of resistance study on powdery mildew of watermelon caused by *Podosphaera xanthii* was conducted on the segregating population derived from the cross of USVL531-MDR x USVL677-PMS. A total of 713 plants were evaluated. Of these 66 plants were of the resistant parent (USVL531-MDR) and 81 plants of susceptible parent (USVL677-PMS). Of the segregating population, 112 were F_1, 311 F_2, 64 BCF_{1S} and 80 BCF_{1R}. All the plants were inoculated using a suspension (10^5 conidia^{-ml}) of powdery mildew conidia in sterile water plus 0.02% tween 20 as described before (Kousik et al., 2011). The powdery mildew isolate prevalent in the Charleston, SC area was used. This isolate behaves a melon Race 1 based on its reaction on melon (*Cucumis melo*) differentials. The isolate also is capable of causing powdery mildew on various watermelon cultivars including Mickey Lee, Dixie Lee and Crimson Sweet. Powdery mildew ratings on a 0-10 scale of increasing disease severity was recorded for hypocotyl, cotyledons and true leaves. Resistance to powdery mildew in cotyledons and true leaves appears to be a dominant trait in USVL531-MDR. We have completed extracting DNA from parents, and 180 F2 plants for GBS analysis. Of the F_2 plants we self-pollinated 186 plants kept in a net house to generate $F_{2:3}$ populations for further evaluation. We will evaluate F_3 families in 2017. Fruit from F_2 plants with powdery mildew resistance, uniform red flesh and decent brix (>7) were collected and have been advanced till F_4 and further advancement to F_5 is in progress. We conducted a progeny test on 23 red fleshed F_4 lines using 16 plants per line and identified several lines that are homozygous for resistance (Figure 1). Currently we are growing these in the greenhouse to get self-pollinated fruit to determine fruit quality and for advancing the line further to develop powdery mildew resistant inbred lines for release.

Segregating populations (F_1, F_2, BCF_{1R}, BCF_{1S}) from cross of USVL003-MDR and USVL677-PMS were developed in 2016. USVL003-MDR is resistant to powdery mildew and Phytophthora fruit rot whereas USVL677 is susceptible to both these diseases. USVL003 is an egusi type watermelon with white flesh and low brix and was derived from PI 560003 after five cycles of screening and selections. Studies on inheritance of resistance to powdery mildew and Phytophthora fruit rot will be conducted in 2017 spring and summer.

We have recently hired a graduate student (Ph.D.) through Clemson University who will be conducting her Ph.D. research project at USVL, USDA, ARS in Charleston, SC on breeding for resistance to powdery mildew of watermelon.

Figure 1. Progeny test of advanced watermelon progenies with red flesh and resistance to powdery mildew. Line # 8 (plants on left) in the figure is a homozygous highly susceptible line compared to line # 29 (on right) that is homozygous for resistance to powdery mildew

References

Kousik, C.S., Donahoo, R.S., Webster, C.G., Turechek, W.W., Adkins, S.T. and Roberts, P.D. 2011. Outbreak of Cucurbit Powdery Mildew on Watermelon Fruit Caused by *Podosphaera xanthii* in Southwest Florida. Plant Disease 95:1586.

Kousik, C.S., Ikerd, J., Wechter, W.P., Harrison, H., and Levi, A. 2012. Resistance to Phytophthora fruit rot of watermelon caused by *Phytophthora capsici* in U.S. Plant Introductions (PI). HortScience 47:1682-1689.

Kousik, C. S., Ikerd, J. L., and Harrison, H. F. 2014a. Development of pre- and postharvest Phytophthora fruit rot on watermelons treated with fungicides in the field. Plant Health Progress 15 (3):145-150. Online doi:10.1094/PHP-RS-14-0009.

Kousik, C.S., Ling, K., Adkins, S.T., Webster, C.G., Turechek, W. 2014b. Phytophthora fruit rot-resistant watermelon germplasm lines: USVL489-PFR, USVL782-PFR, USVL203-PFR, and USVL020-PFR. HortScience. 49:101-104.

Kousik, C. S., Brusca, J., and Turechek, W. W. 2016. Diseases and disease management strategies take top research priority in the Watermelon Research and Development Group members survey (2014 to 2015). Plant Health Progress. 17:53-58.

2.1.1.6 PRSV-W (A Levi, K-S Ling)

Identification of QTL associated with papaya ringspot virus (PRSV) in watermelon

Genetic populations F2:F3 have been generated using PRSV-susceptible *Clc* parent USVL252-FR2 crossed with the PRSV-resistant *Clc* parents PI 244017 (Pop 52-17) or PI 244019 (Pop 52-19) mentioned above. The genetic populations have been prepared with the generous help of Dr. Nihat Guner, Sakata Seeds). The populations are being prepared for evaluation for PRSV-resistance (as described by Ling et al. 2009). Leaf samples have been collected and following evaluation for PRSV resistance, DNA will be isolated and used in GBS analysis for identification of SNPs and QTL associated with PRSV-resistance.

Reference

Levi, A., J. Coffey, L.M. Massey, N. Guner, E. Oren, Y. Tadmor, and K.S. Ling. 2016. Resistance to papaya ringspot virus-watermelon strain (PRSV-W) in the desert watermelon Citrullus colocynthis. HortScience 51:4–7.

Melon Team

Team members:

Jim McCreight (USDA, ARS) Pat Wechter (USDA, ARS)
Shaker Kousik (USDA, ARS) Bill Wintermantel (USDA, ARS)
Michael Mazourek (Cornell Univ)

Table 4. TIMELINE CHART					
Objective	**Personnel/Institution**	**Year**			
	(initials as in Table 3)	1	2	3	4
(a) Obj. 1. Develop common genomic approaches and tools for cucurbits					
1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)					
1.2.1. GBS of cucurbit species, establish molecular-informed core populations - melon	JM (ARS-CA)	X	X		
1.2.2 Population genetics and GWAS analyses - melon	UR (WVSU), ZF (BTI) JM (ARS-CA)		x	x	x

1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)

1.2.1. GBS of cucurbit species, establish molecular-informed core populations

Melon

Melon accessions (n = 2,038) from the National Plant Germplasm System (NPGS) and additional heirloom melons were planted to collect leaf tissue for DNA isolation. A total of 22 plates will be send to Michigan State University (MSU) for extraction. To date, 21 plates have been sent; the last plate will be sent shortly. Four plates of high quality DNA have been sent thus far from MSU to Cornell for GBS analysis.

(b) Obj. 2. Genomic assisted breeding for disease resistance		Y1	Y2	Y3	Y4
2.1 QTL map resistances:	Screen for resistance (**Sc**), develop populations **(P)**, phenotype (**F**), sequence **(S)**, QTL map **(Q)**				
2.1.2. Melon - powdery mildew - Fusarium - CYSDV - CMV	 SK,PW (ARS-SC), JM (ARS-CA) PW (ARS-SC) JM (ARS-CA), WW (ARS-CA) JM (ARS-CA), MM (CU)	 PF PFS F P	 PFS PFS FS F	 FQ PFSQ FSQ SQ	 FQ

2.1.2. Melon

Powdery Mildew (Podosphaera xanthii) resistance in MR1xAY RIL

Charleston, South Carolina Race 1

- First round of phenotyping of *MR1xAY RIL* against Race 1 was completed in June 2016.
- Second round phenotyping of *MR1xAY RIL* against Race 1 was completed in March 2017.
- Total of 210 RIL lines were phenotyped
- Melon powdery mildew race differential lines confirmed the isolate was race 1 (Figure 1.)
- Three replications of four plants were evaluated in both rounds.
- First round was inoculated on May 16, 2016, and rated on May 27th and June 7th.
- Second round was inoculated January 17, 2017, and rated on February, and March 1, 2017.
  - Conidial suspension (10^5 conidia^{-ml} in distilled water with 0.02% tween 20)

  - Uniformly sprayed on the plants.
- First observation powdery mildew was recorded on hypocotyl, cotyledons and true leaves in first and second rounds. Mildew was also recorded for stems in the second round.
- Second observation recorded powdery mildew on upper true leaves.
- *MR1xAY RIL* populations will be phenotyped for resistance to powdery mildew race 2 during the fall of 2017.

Figure 1. Powdery mildew reactions on melon powdery mildew race differentials included in the assays of the *MR1xAY RIL* population. Top row from left to right: Iran H, 'PMR 45', 'PMR 5', and 'Edisto 47'. Bottom row from left to right: WMR 29, PI 414723, MR-1, and 'Védrantais'. Severe powdery mildew was only observed on leaves of Iran H and 'Védrantais', indicating that the isolate was race 1. (Charleston)

California and Arizona Field tests

Three replicated field tests planted; 138 RILs plus race differentials; subjected to natural infection.

- Imperial Valley, CA (University of California, Desert Research and Extension Center, Holtville)
  - watered March 4, 2016
  - Disease reaction evaluated mid-June
  - Variable plant stands (due reportedly to specific site conditions)
  - Virtually no powdery mildew due to abnormally high temperatures.
  - Plant and fruit data collected
- Yuma, AZ (Yuma Agricultural Research Center),
  - watered March 31
  - Disease reaction evaluated mid- to late June
  - Stands fairly uniform
  - CMV present in late April
  - Virtually no powdery mildew due to abnormally high temperatures.
  - Plant and fruit data collected
- Westside (Westside Research and Extension Center, Five Points)
  - Planting scheduled for early to mid-June

- Evaluation in early to mid-September
- Powdery mildew present; race identity not certain–either a unique race, or variant of race 5 (whereby 'PMR 45' had some mildew) (McCreight et al. 2012. Cucurbit powdery mildew of melon incited by *Podosphaera xanthii*: Global and western U.S. perspectives, p. 181–189. In: N. Sari et al. (eds.). Cucurbitaceae 2012, Proceedings of the Xth EUCARPIA meeting on genetics and breeding of Cucurbitaceae, Antalya (Turkey), October 15-18th, 2012).
- Plant and fruit data collected.
- ADDITIONAL
  Leafminers were uniformly distributed throughout the test. RILs and race differentials were qualitatively (susceptible or resistant) evaluated for leafminer infestation. MR-1 and PI 124111 were susceptible, but several powdery mildew race differentials exhibited resistance: PI 414724, PI 313970, PI 482420 (TGR 1551) and PI 482431 (TGR 1937). PI 313970 was previously reported resistant to leafminer, and PI 371795 was variable for resistance (Kennedy et al. 1978. J. Amer. Soc. Hort. Sci. 103:571–574). PI 414723 was derived form PI 371795 through selection for uniform reaction to melon aphid, *Aphis gossypii* (McCreight et al. 1992. Cucurbit Genet. Coop. Rpt. 15:51–52).

Fusarium Wilt resistance in MR1xAY RIL

- 205 RIL have now been generated from a cross of MR-1 x Ananas Yokneam.
- GBS has been completed on 90 RIL lines and we are currently waiting for data from an additional plate that will be provided in April 2017.
- *Fusarium oxysporum* f. sp. *melonis* (FOM) race 2 assays for resistance of the RILs. Two individual tests of 190 RIL were evaluated.
- QTL analysis will be performed as soon as data from the second GBS plate are available.
- New isolates of FOM race 1 are being tested for pathogenicity due to loss of virulent isolates at USVL.
- 150+ RILs have been grown in California and in South Carolina and evaluated for phenotype for future selection for introgression to U.S. western shipper-type cantaloupe.
- ADDITIONAL: 90 RIL lines were assayed for Alternaria leaf spot resistance, QTL were identified for resistance. (Daley et al. 2017. Phytopathology. DOI 10.1094/PHYTO-06-16-0246-R)
- ADDITIONAL: RILs will be tested for carotenoids in summer 2017 in collaboration with Dr. Li Li, ARS, Ithaca, NY.

CYSDV

- Planted PI 313970 and 'Top Mark' in a greenhouse for crossing and production of the F_2 for evaluation in fall 2017 in the field. DNA samples and cuttings will be collected from every plant in mid-September for QTL mapping and producing F_2:F_3 in a greenhouse at Salinas.
- ADDITIONAL related research on resistance in melon to sweetpotato whitefly
  - Third year of a field evaluation of resistance is planned for spring 2017 (late-April planting date).
  - Data from greenhouse studies of whitefly resistance in no-choice tests were analyzed.
  - Choice tests of whitefly resistance are planned to assess differences in antixenosis (non-preference) among sweetpotato whitefly-resistant sources.

CMV

- Increase advanced CMV-resistant lines (western U.S. shipping type cantaloupe, and honeydew) developed by M. Kyle-Jahn and H.M. Munger for assessment of CMV resistance in controlled-inoculation greenhouse tests and adaptation and fruit quality in field tests at three locations in Arizona and California.

Additional Related Virus Information and Activity

- The Wintermantel Lab maintains live and frozen stocks of *Cucumber mosaic virus*, (CMV), *Cucurbit yellow stunting disorder virus* (CYSDV), and other viruses common in the southwestern US production region. In addition, the lab maintains stocks of the whitefly, *Bemisia tabaci* MEAM1, and both green peach aphid (*Myzus persicae*) and melon aphid (*Aphis gossypii*).
- Testing of selected material from experimental trials by RT-PCR to determine prevalence of CYSDV and other common cucurbit viruses.
  Primers previously developed and confirmed effective in the Wintermantel Lab were used to test plant melon plants from summer CYSDV resistance evaluations for the presence of not only CYSDV, but also other viruses that are periodically associated with melons. This allowed determination of what other viruses may have contributed to severity in melon fields. Results demonstrated an abundance of CYSDV in late spring/early summer 2016 research trials from the desert, as well as additional prevalence of CMV and Squash vein yellowing virus in these melons. *Squash vein yellowing virus* (SqVYV) is an important pathogen of watermelon that emerged in California two years ago, but evidence to date suggests little if any impact on melon production. CMV and CYSDV, however, both have potential for significant impact on melon production and were both prevalent in trials, although the predominant symptoms were yellowing, caused by CYSDV.
  - CMV – 5/7 were positive
  - CYSDV – 7/10 were positive
  - SqVYV – 3/11 were positive
  - Potyviruses – 0/7 were positive (Checked with a general potyvirus primer set and also specifically for PRSV, ZYMV, and WMV.)
- Development and testing of TaqMan probes for quantification of CYSDV in melon.
  TaqMan probes were developed for detection and quantification of CYSDV. Probes were designed to an 81 nt region within the RNA dependent RNA polymerase (RdRp) gene of CYSDV RNA1. Evaluation demonstrated reliable detection of CYSDV and a linear relationship with the amount of CYSDV present in starting material (Figure 2), but await more robust evaluation from new field and greenhouse tests.

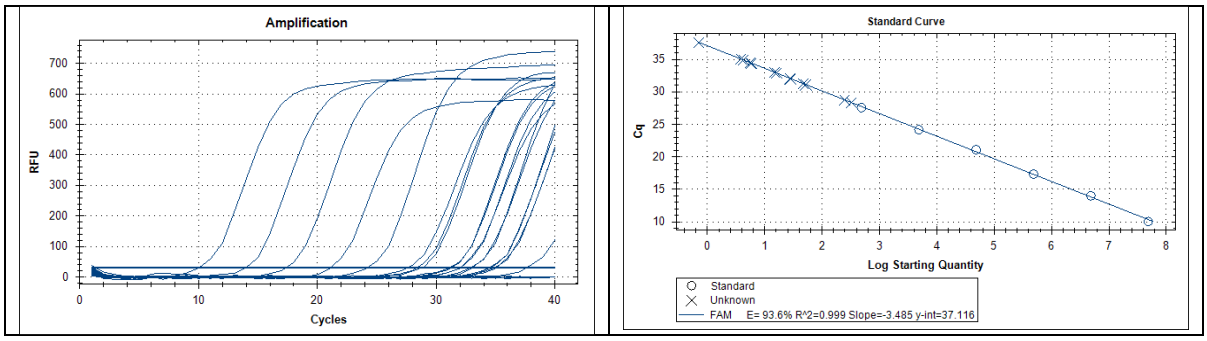


Figure 2. The assay was performed with SuperScript III Platinum One-Step Quantitative RT-PCR System (Life Technologies) for use with TaqMan probes. The standard curve range is from 10^2 - 10^7 copies. Samples graphed with standards were randomly selected from experiments to evaluate linearity.

2.2 Marker development and verification:	Refine map (**R**) develop marker **(M)**, verify **(V)**				
2.2.2. Melon					
- powdery mildew	SK (ARS-SC)			RM	V
- Fusarium	PW (ARS-SC)	M	RM	RM	V
- CYSDV	WW (ARS-CA), JM (ARS-CA)			RM	V
- CMV	JM (ARS-CA), MM (CU)			RM	V

Powdery Mildew

- No planned research for this period

Fusarium wilt

- See 2.1.2.

CYSDV

- No planned research for this period

CMV

- No planned research for this period

2.3. Introgress resistance into advanced breeding lines:	Develop breeding lines **(B),** introgress into cultivated **(I)**, advanced lines **(A)**, release to breeders **(R)**				
2.3.2. Melon					
- powdery mildew	SK (ARS-SC), JM (ARS-CA)	B	I	I	IA
- Fusarium	PW (ARS-SC)	B	B	I	IA
- CYSDV	JM (ARS-CA), WW (ARS-CA)	I	I	IA	IAR
- CMV	JM (ARS-CA)	I	I	I	IA

Powdery Mildew

- Planted three replicated field tests of 138 MR-1 x AY RILs at three locations in California (Imperial Valley and San Joaquin Valley) and Yuma, Arizona. There was scant powdery mildew infection in Imperial Valley and Yuma in June 2016. Powdery mildew was present in the San Joaquin Valley (Five Points) in September that appeared to be a variant of race 5, based on the reactions of 12 commonly used cucurbit powdery mildew race differentials.
- Forty-four North America-originated *C. melo* var *texanus* accessions (Decker-Walters et al. 2002. DOI 10.1007/s00606-002-0191-3) were evaluated for resistance to powdery mildew in a greenhouse to an unverified race (but where either race S or SD has mostly been present year-round for many years). All were susceptible with one exception that showed resistant phenotype with resistant blisters (McCreight. 2001. Cucurbit Genet. Coop. Rpt. 24:22.). We will self and cross the accessions with 'Top Mark' to further characterize the genetic basis of resistance. The *texanus* endornaviruses will also be characterized and compared with previous results form this Salinas lab (see Sabanadzovic et al. 2016).
- ADDITIONAL
  We have consulted with M. Pitrat about the correct/current horticultural nomenclature for the *texanus* accessions (Decker-Walters et al. 2002. DOI 10.1007/s00606-002-0191-3), as they were not considered in the recent revision of melon horticultural classification (Pitrat. 2016. DOI 10.1007/7397_2016_10).

Fusarium wilt

- See 2.1.2.

CYSDV

- Backcrossed resistant field selections from Fall 2015 for selfing and backcrossing in the greenhouse.
- Evaluated S_1 from several different backcross families for resistance to natural infection in Imperial Valley in Fall 2016.
- CYSDV-resistant single plant selections from S_1 of several backcross populations taken as vegetative cuttinsg for backcrossing in a greenhouse at Salinas and subsequent selection in fall 2017.

CMV

- Increase of advanced CMV-resistant lines for testing in Arizona and California is underway.

1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)

1.2.1. GBS of cucurbit species, establish molecular-informed core populations

Melon accessions held by North Central Plant Germplasm Resources Center, Ames, Iowa will be grown in a greenhouse at Salinas and sampled for GBS beginning late in year 1 and continuing through year 2.

Completing production of 200 RILs of MR-1 x Ananas Yokneam (MR1xAY). Seed of each RIL will be produced for remaining studies, including GBS on ~190 RIL for identification of high-quality SNPs for use in QTL analysis and mapping. Finished generation of one hundred and seventy-five F_7 or greater MR1xAY RIL. Will have completed 200 F_7 or greater lines by the end of 2016. Seed has been distributed for powdery mildew screens and fruit quality assessment. Seed being increased for 2017 screens.

Performed GBS of 89 MR1xAY RILs and have identified 2200, high-quality SNPs that have been used to identify 2 QTLs linked to Alternaria leaf blight resistance and to generate a high-density map of MR-1 x AY.

Will perform GBS with another 95 RILs and identify high-quality SNPs from the sequencing data. Will begin the Fusarium assays for Race 1 and 2. Will repeat powdery mildew tests and begin QTL analysis and mapping of Powdery mildew resistance.

Cucumber Team

Team members:
Yiqun Weng (USDA, ARS)
Rebecca Grumet (Michigan St. Univ.)
Todd Wehner (North Carolina St. Univ.)

Objectives	Personnel/Institution	2016	2017	2018	2019
1. Develop genomic approaches and tools					
1.2. GBS PI lines; establish GWAS core	ZF (BTI), RG (MSU) YW (ARS-WI)	X X	X X		
1.2.1. GBS of cucurbit species, establish molecular-informed core populations - cucumber	ZF (BTI), RG (MSU) YW (ARS-WI)	X X	X X		
1.2.2 Population genetics and GWAS analysis - cucumber	UR (WSVU), ZF (BTI) YW (ARS-WI), RG (MSU)		x	x	x
2. Genomic assisted breeding					
2.1 QTL map resistances	Sc=Screening, P=populations, F=phenotyping, S=sequence (S), Q=QTL				
2.1.3. Cucumber - downy mildew - Phytophthora	YW (ARS-WI), TW (NCSU) RG (MSU)	PFS PF	SQ PFSQ	SQ SQ	
2.2 Marker development and verification	R=Refining map, M=develop marker, V= verification				
2.2.3. Cucumber - downy mildew - Phytophthora	YW (ARS-WI), TW (NCSU) RG (MSU)	RM	RM	V RM	V V
2.3. Advanced breeding line development	B=breeding line, I=introgression, A=advanced, R=release				
2.3.3 Cucumber - DM - PFR	YW (ARS-WI), TW (NCSU) RG (MSU)	B B	I B	I I	R I

Objective 1.2 GBS of PI collection, establish GWAS core
Personnel: Weng (Wang Y, Tan J, Madera AR, Haider KR), Grumet (Grumet R, Hammar S.) and Wehner (Wehner T., Silverman EJ) Labs

<u>2016-2017 progress</u>
1. GBS of PI lines
DNA samples of 1,520 plant introduction (PI) lines and historical cultivars or landraces of cultivated (*Cucumis sativus* var. *sativus*) and wild (*C. sativus* var. *hardwickii*) cucumber lines have been sent to the Genomics team at Boyce Thompson Institute, Cornell University for genotyping by sequencing. Among them sequencing of 1,420 samples has been done. Data analysis is underway.

2. *Phenotyping of morphological traits and DM resistance in cucumber natural populations*
Three hundred cucumber lines were grown in the University of Wisconsin Hancock Agricultural Research Station (HARS) for collection of morphological data. One hundred cucumber lines (2 reps, 8 plants per rep) were planted in North Carolina State University experimental field in summer 2016. Data for responses to DM natural infestation were collected.

2017-2018 work plan

1. A core collection (384) will be selected pending GBS data analysis from Bioinformatics team.
2. Seed increase of the 384 PI lines
3. The 384 lines will be planted in 2017 field season at HARS for phenotypic data collection. The same set of materials will be grown in North Carolina State University fields for collecting data for responses to natural DM infestation.

Objectives 2.1 and 2.2: QTL mapping, marker development for DM and PFR resistances

A. Fine mapping of DM resistance in cucumber (Weng and Wehner Labs)

2016-2017 progress

We aim to conduct QTL mapping of DM resistance from two resistant sources: PI 330628 (WI7120) and PI 197088. Previous QTL mapping studies have identified 4 QTL, *dm2.1*, *dm4.1*, *dm5.2* and *dm6.1* for DM resistance from WI7120 which together could explain 62-76% phenotypic variations. Among them, *dm4.1* and *dm5.2* were major-effect QTL (Wang et al. 2016). Using the PI 197088 × Coolgreen RIL population, 11 QTL for DM resistance were identified including *dm1.1, dm2.1, dm2.2, dm3.1, dm3.2, dm4.1, dm5.1, dm5.2, dm5.3, dm6.1* and *dm6.2*, Among them, *dm5.2* and *dm5.3* are major-effect QTL. The four DMR QTL detected in WI7120 seem to be consistent with the corresponding ones detected in PI 197088 but their contributions to the total observed phenotypic variations are different. The dm5.3 QTL in PI 197088 is also closely linked with, but not the same as *pm5.1* (syn. *CsMLO1* or *CsMLO8*, *pm-h*), which is a major-effect QTL for PM resistance in cucumber.

We focused on three major-effect DMR QTL, *dm4.1*, *dm5.2* from WI7210 and *dm5.3* from PI 197088 for fine mapping. F2 and RIL plants carrying respective QTL regions were selected to backcross with the susceptible cucumber line 9930. Backcross derivatives (BC1, BC2) carrying target regions were selected with molecular markers.

2017-2018 work plan

1. Narrow down the QTL region (1.5 LOD interval) of target QTL regions through fine genetic mapping and GWAS; identify candidate genes for *dm4.1* and *dm5.2*.
2. Growth chamber and field evaluation of DM resistance of the NILs (Wisconsin and North Carolina).

B. QTL mapping of *Phytophthora capsici* resistance in cucumber (R Grumet lab - B Mansfeld, Y-C Lin; in collaboration with C. Smart)

B.1 Young fruit resistance to *P. capsici*

2016-2017 progress:

1. *Testing promising PI 104983-derived families with multiple P. capsici isolates.* S_6 families were grown in the field in summer 2016. Young fruit were harvested and tested for resistance to four isolates of *P. capsici* obtained from various crops (cucumber, pumpkin, pepper and bean) from locations in Michigan and New York: OP97; 10193; SP98; Bartley's1 and NY 0664-1. The isolates were originally provided by Mary Hausbeck (MSU) or Chris Smart (Cornell). Prior tests had been done with isolate OP97, originally isolated from cucumber in Michigan. Despite differences in severity among the different isolates, the relative disease rankings of the different lines were consistent, suggesting that the resistance is not isolate-specific. The rate of disease development was markedly reduced in PI 104983-53B with symptoms largely limited to the region of inoculation.
2. *Germplasm release*. An S_6 progeny line with young fruit resistance to *P. capsici*, PI 104983-53B, exhibited as reduced or delayed infection with little or no mycelial growth and sporulation at 5 days post inoculation (mean score 3-4/9 vs. 7-8/9 for susceptible controls), was prepared for release for breeding purposes (Colle and Grumet, 2017). Seed has been requested by, and provided to, three companies.
3. *Initiate introgression and genetic analysis – population development*. Crosses were made in the greenhouse in spring 2016 between resistant S_5 generation, PI 109483-53B (B) plant plants and the susceptible, sequenced pickling cucumber breeding line, Gy14 (G). In summer 2016, F_1 (G x B and B x G) plants were self-pollinated to produce segregating F_2 progeny and were backcrossed to GY14. Reciprocal F_1 progeny were planted in the field in summer of 2016 and compared to parental genotypes. The F_1 progeny had intermediate phenotypes for infection by *P. capsici* relative to the parents, suggesting quantitative inheritance. There were not differences between the reciprocal crosses. Backcross progeny were tested in the greenhouse in Fall 2016 and BC_1 individuals showing resistance were backcrossed again to Gy14. Doubled haploid families derived from four PI 109483-53 lines were produced by Rijk Zwaan for future analysis.
4. *Field trial in P. capsici infested field.* Field trials in a heavily *P. capsici*-infested site maintained in Geneva, New York are being performed by Dr. Chris Smart (Cornell University). The primary purpose of the trial in 2016 was to establish effective inoculation conditions. Two methods were tested: spray at fruiting time with zoospore suspensions, and incorporation of infested vermiculite into the soil between the rows. Inoculations were applied twice during the season. The soil incorporation method was more effective than spraying with zoospores in establishing cucumber fruit infection.

2017-2018 work plan:

1. Screen F_2 progeny from PI-derived resistant lines x Gy14, phenotyping for response to *P. capsici* to initiate inheritance and QTL analyses.
2. Intercross BC progeny to increase resistance levels in a background with better fruit type, more uniform germination, and earlier female flower production.
3. Characterize resistance in the PI-derived double haploids and initiate crossing with Gy14.
4. Initiate GWAS analysis for resistance to *P. capsici* using GBS data for cucumber PI accessions and data from prior *P. capsici* screening of the cucumber PI collection.
5. Field trial in *P. capsici* infested field. Further work is needed to establish effective screening conditions in the field. Tests this year will be performed with planting densities used by commercial pickling cucumber producers for machine harvest.

B2. Age-related resistance (ARR) to *P. capsici*

2016-2017 progress:

1. *QTL seq analysis*. Fruit from F_2 progeny (n=355) of lines that do and do not express ARR were phenotyped for response to *P. capsisi*. Pools of resistant and susceptible individuals were sequenced using Illumina Hi-Seq paired-end sequencing. QTL seq analysis is currently in progress.
2. *Transcriptomic and metabolomic analysis of peels from ARR+ and ARR- cultivars.* A manuscript describing the transcriptomic and metabolomic work has been submitted for publication (Mansfeld et al.). Genes uniquely upregulated in resistant age ARR+ fruit were associated with defense and/or specialized metabolism. Untargeted metabolomic analysis identified ions uniquely abundant in resistant 'Vlaspik' 16 dpp peel extracts; the most abundant of which had relative mass defects consistent with terpenoid glycosides.

2017-2018 work plan:

Continue QTL seq analysis for ARR from F_2 populations of Gy14 × Poinsett and Gy14 × Vlaspik. Screen additional F_2 progeny to increase population size. Compare results of transcriptome analysis with QTL seq analysis to help identify genomic regions of greater interest.

Objective 2.3 Advanced line development for downy mildew resistance

2016-2017 Progress:

1. Marker-assisted QTL pyramiding (Weng and Wehner Labs)

Our objective is to develop a new version of the elite pickle cucumber inbred line Gy14 with improved DM resistance to the post-2014 DM strain. We focused on marker-assisted pyramiding of the two major-effect QTL (*dm4.1* and *dm5.2*) of DM resistance from WI7120 into Gy14

genetic background. Crosses were made between Gy14 and plants carrying *dm2.1*, *dm4.1* and *dm5.1* QTL from WI7120. In 2016-2017 period, we have advanced the backcrosses to BC3F1 using marker-assisted selection. In 2016 summer trial, these plants were grown in the University of Wisconsin Hancock Agricultural Research Station for preliminary observations.

2. Breeding line development for DM resistance

2.1. RIL development and evaluation of DM resistance (Wehner lab: T Wehner, EJ Silverman)

The RILs population was developed in 2007 by a cross PI 197088 (HR) × Coolgreen (S). A total of 200 F_2 lines were generated and self pollinated in the greenhouse in 2009. The RILs have been tested in 7 years of field evaluations under high disease intensity. The 2017 population contains 146 lines; 71 at S12 generation, 35 at S11 generation, 32 at S10 generation, and 8 at the S9 generation. Several lines are being recovered and advanced for use in genetic studies.

In 2016, we evaluated for high resistance to the new downy mildew in the field in North Carolina. The design was a randomized complete block with 3 replications and 4 disease ratings. Lines were also rated for fruit traits such as skin type (smooth, cracked, netted) and spine color (black, white).

2.2 Inbreds with resistance and quality (Wehner lab: TC Wehner and EJ Silverman)

The population PI 197088 (HR) × Poinsett 76 (MR) contains 72 lines. The plants have been self pollinated in the greenhouse 8 generations and tested in the field for evaluation of yield, quality and resistance. We recovered 9 lines of the 72 that did not advance to S8 in the past greenhouse cycle. We were not able to recover 3 lines last greenhouse cycle and these lines are in the S7 generation. Lines in S6 and S7 are being tested in the field for yield, earliness and quality for release to the industry.

We selected and self-pollinated sub-lines from 41 lines that are at the S8 to S9 generation in the greenhouse in 2016. The lines were evaluated for high resistance to the new downy mildew, as well as fruit quality, in the field in North Carolina. The most resistant lines were crossed in the greenhouse using parents that had intermediate fruit quality, with the objective of improving fruit quality among the highly resistant lines.

2017-2018 work plan (Weng and Wehner Labs)

1. Continue marker-assisted backcrossing in Gy14 genetic background for pyramiding of *dm4.1* and *dm5.2* QTL from WI7120. Conduct field and greenhouse screening tests to evaluate DM resistance and performance of horticulture traits.
2. Develop inbred cucumber populations. Three populations (PI 197088 × Gy14, NC-25, or Poinsett 76) are being developed for inbred development of pickling and slicing type. Eight to 10 lines each have been selected with yield, earliness, quality and resistance. They will be released to industry for use cultivar development. In 2016, we advanced the most resistant families that also had acceptable fruit quality by self pollination in the greenhouse. There were 3 populations of 8, 9 or 10 families each (S1 to S4 generation) to make 1 or 2 sublines each. The resulting 50 families were tested for high resistance to the new downy mildew in

the field in North Carolina. The design was a randomized complete block with 3 replications and 4 disease ratings. Lines were also evaluated for fruit quality. Lines were evaluated for fruit quality on a 1 to 9 scale (1=poor, 9=excellent). A total of 3 lines were selected based on field data collected in 2016. The selected lines were self pollinated and also cross pollinated in pairs in fall 2016 to develop more highly resistant cucumber populations with better fruit quality.

3. Identify new sources of resistance. A new population derived from PI 605996 (HR) × 'Poinsett 76' is being developed to provide new sources of high resistance to downy mildew. The F_2 progeny will be self-pollinated and the S1 lines tested in the field for high resistance to natural disease incidence of downy mildew at the Clinton, NC research station. In addition to resistance, lines will be selected for yield, earliness and quality.

4. Field screening of downy mildew resistance for the 384-line GWAS panel.

Squash Team

Team members:

Michael Mazourek (Cornell Univ.) Angel Linares (Univ. Puerto Rico)
Linda Beaver (Univ. Puerto Rico) Chris Smart (Cornell Univ.)

Objective	**Personnel/Institution**	**Year**			
	(initials as in Table 3)	1	2	3	4
(a) Obj. 1. Develop common genomic approaches and tools for cucurbits					
1.2. Perform GBS analysis of PI collections, establish core populations, provide community resource for genome wide association studies (GWAS)					
1.2.1. GBS of cucurbit species, establish molecular-informed core populations - squash	ZF (BTI), RG (MSU) MM (CU)	X X	X X		
1.2.2. Population genetics and GWAS analysis - squash	UR (WVSU), ZF (BTI) MM (CU)		X	X	X
(b) Obj. 2. Genomic assisted breeding for disease resistance					
2.1 QTL map resistances:	Screen for resistance (**Sc**), develop populations **(P)**, phenotype (**F**), sequence **(S)**, QTL map **(Q)**				
2.1.4 Squash - Phytophthora - PRSV-W - CMV	 MM (CU), CS (CU) MM MM	 PF PFQ PFQ	 PF Q Q	 Q	
2.2 Marker development and verification:	Refine map (**R**) develop marker **(M)**, verify **(V)**				
2.2.4 Squash - powdery mildew - Phytophthora - PRSV-W - CMV	 MM(CU), LWB(UPR) MM (CU) MM(CU), LWB(UPR) MM(CU), LWB(UPR)	 RM	 V RM RM	 RM V V	 V
2.3. Introgress resistance into advanced breeding lines:	Develop breeding lines **(B),** introgress into cultivated **(I)**, advanced lines **(A)**, release to breeders **(R)**				
2.3.4 Squash - powdery mildew - Phytophthora - PRSV-W - CMV	 Already exists MM (CU), CS (CU) Already exists Already exists	 I	 I	 AR	 AR

1.2.1. GBS of cucurbit species, establish molecular-informed core populations - squash

The *Cucurbita* collection includes three commercially important species and several wild species, yet is one of the smaller crop focused collections in cucurbits. We plan to perform GBS on most of genus. *In C. maxima*, 165 accessions have already been genotyped by sequencing with PstI. About 319 accessions of *C. moschata* and 800 accessions of *C. pepo* are being prepared for DNA extraction. Of the wild species, we have performed GBS on *C. okeechobeensis* and are preparing *C. ecuadorensis* and *C. lundelliana.* All species other than *C. maxima* will be genotyped using ApeKI digests. While using different restriction enzymes will confound comparisons between species, the most interesting accessions will be resequenced and thereafter comparative studies will be unaffected.

Powdery mildew resistance in squash

2.2.4.1 Marker development and verification (Mazourek lab –K. LaPlant)

Powdery mildew is a major fungal disease on squash and pumpkins (*Cucurbita spp*) in the USA and throughout the world. Genetic resistance has been achieved in cultivated species through the introgression of a major resistance gene from the wild species *Cucurbita okeechobeensis* subsp. *martinezii*. Today, this gene, *Pm-0*, is used extensively in breeding, and is found in nearly all powdery mildew-resistant *C. pepo* and *C. moschata* commercial cultivars. The region containing the resistance allele was refined to a final candidate interval of 76.4 kb. Studies are currently underway to validate markers in this region and explore gene candidates by exploring gene expression in powdery mildew challenged materials using RT-PCR and QuantSeq.

We have shared a CAPS marker in the presumed causative locus and the sequence polymorphism of course could be converted to other platforms (Holdsworth et al., 2016). This marker has been reported to predict resistance perfectly in other breeding programs within *Cucurbita pepo* but was not effective for some parties in *C. moschata*. Though greenhouse inoculations, we confirmed that the marker does predict resistance effectively in *C. moschata* when the petioles of the plants are evaluated. We cannot rule out the possibility that other groups are using alternative genetics.

Virus resistance in squash

2.1.4.3, 2.1.4.4. Mapping resistance (M. Mazourek lab-K. LaPlant)

We are using an introgression mapping approach similar to that for powdery mildew resistance, above, to identify introgressions from the sources of resistance. Initially, we were focused on the *C. moschata* sources of resistance, 'Nigerian Local' and 'Menina', however resistance may also be derived from *C. ecuadorensis*. Accordingly, we are looking more broadly for shared introgressions and are aware that introgressions may be from divergent sources. Germplasm in the CU and UPR breeding programs has focused on the *C. moschata* sources of resistance and may be increasingly important as we seek to characterize resistance from these sources for support of the UPR germplasm and bolster the limited numbers of cultivars with resistance that are available for evaluation. We have identified and genotyped 43 cultivars with reported resistance to ZYMV, 27 cultivars with reported resistance to WMV, 13 with reported resistance to PRSV, and 10 with reported resistance to CMV. We will bolster these populations with historical materials from our breeding programs and classical genetic populations.

2.3.4.3, 2.3.4.4. Introgress resistance into advanced breeding lines (L. Beaver, A. Linares labs – M. Miranda, W. Seda)

Populations for studies of inheritance of PRSV and ZYMV resistance and for development of potyvirus resistant lines:

We have continued to develop PRSV and ZYMV resistant x susceptible populations (F1, F2, and some backcrosses). Cultivars of tropical pumpkin (*C. moschata*) widely used in Puerto Rico are being used as susceptible parents. Nigerian Local and Menina are being used as resistant parents. We have generated sufficient seed of F2 populations with the local cultivars Verde Luz

and Taina Dorada, breeding line TP411, and temperate cultivar Waltham. The F1, F2 and BC populations of Nigerian Local x Soler and Menina x Soler still need to be made and additional F1 seed is needed of some populations. Sufficient F2 seed of the resistant x resistant cross of Nigerian Local x Menina has been made with the purpose of determining if these two sources of resistance are allelic.

Study of inheritance of PRSV resistance:

We have initiated the study of inheritance of PRSV resistance in the F2 population Nigerian Local x Taína Dorada. A total of 100 F2 plants have been evaluated using a number of scoring techniques. Although those data have not been analyzed, we used symptom severity as a basis to select a group of the most resistant and most susceptible F2 plants to transplant to the field for self-pollination. Because of weather conditions, we were only able to self-pollinate five lines, including two that showed few symptoms as they matured in the field. We noted that no F2 plant was as symptom-free as the resistant parent Nigerian Local. Another group of 100 F2 plants from this same population are currently being tested. Again, we have not observed an F2 plant as resistant as Nigerian Local. The most resistant F3 or F4 lines derived from this and other populations will later be used to validate resistance markers that are expected to be developed by other members of the Squash Team.

Methods for evaluating potyvirus (PRSV and ZYMV) resistance in *C. moschata*:

Ideally the plant breeder would like to be able to reliably phenotype a seedling for disease resistance as soon as possible after inoculation with ZYMV or PRSV. Results from a greenhouse-based test for resistance must also be strongly correlated with field results. Since carrying out a small preliminary study that was reported on at Cucurbitaceae 2016 (Wessel-Beaver et al., 2016) we have conducted a series of experiments focusing on the development of reliable protocols for phenotyping for potyvirus resistance.

Using ELISA, we measured virus titer in the first 4 leaves of inoculated seedlings (cotyledons at approximately 5 days post seeding), evaluating leaf samples as each leaf expanded. The genotypes used had a known range of resistance from highly resistant (Menina and Nigeriam Local) to intermediate resistance to highly susceptible. Four separate runs were conducted (in different months). There was a very marked difference in results for PRSV and ZYMV. Differences among genotypes could be differentiated for ZYMV very early on: in either the 1st or 2nd expanding leaf. We also noted that visual symptoms of virus susceptibility (mosaic, mottling, leaf deformation) could also usually be observed, especially by the time the 2nd leaf was expanding. The situation for PRSV was very different. Genotypes could not usually be differentiated until sampling the 4th leaf (sometimes in the 3rd). Very vague symptoms (light mottling) could sometimes be observed earlier in susceptible genotypes, however symptoms were much more obvious and easier to classify once the 4th leaf emerged.

In March to July 2016 we conducted a trial that began in the greenhouse by inoculating seedlings (PRSV, ZYMV) of genotypes with a range of known resistance or susceptibility. Plants were evaluated for virus symptoms and ELISA in the greenhouse (3 weeks post-seeding), then transplanted to the field at 4 weeks. The individual plants were monitored for virus symptoms

and sampled for ELISA at 10 and 14 weeks post-seeding (6 and 10 weeks post-transplant). In general, Spearman (rank) correlations between ELISA results at different dates were lower than expected. For PRSV, $r = 0.48$ ($p<0.001$) between ELISA readings in the greenhouse and 5 weeks later (10 weeks post-seeding) for the same plants in the field. The correlation was not significant between the greenhouse readings and field readings taken 14 weeks post-seeding ($r = 0.26$ [$p=0.063$). Results for ZYMV were similar: $r = 0.54$ ($p<0.001$) and $r = -0.14$ (NS) between readings in the greenhouse and the 1st and 2nd field ELISA tests, respectively. We are currently repeating this study (transplanted to the field Feb 2017).

We also wanted to determine if leaves from multiple apices from a single plant should be sampled when evaluating resistance at the field level. We sampled two newly-expanded leaves from plants that had been inoculated in the greenhouse. We conducted ELISA tests on 10 and 14 week old plants (6 and 10 week post-transplant). At 10 weeks plants were flowering. At 14 weeks many plants had fruits beginning to mature. For both PRSV and ZYMV rank correlations between the two samples from a plant were high ($r = 0.81$ for PRSV and $r = 0.66$ for ZYMV, both with $p<0.001$). We are currently repeating this study as well and intend on taking more samples per plant.

<u>Evaluation of resistant parents Nigerian Local and Menina:</u>
Although our impression is that Nigerian Local and Menina have been used in the commercial seed industry as sources of resistance to PRSV and ZYMV, the reality is that there is little or no documentation in the literature about these genotypes except concerning their performance in seedling tests. We conducted a field trial in spring-summer 2016 to study how well plants of Nigerian Local and Menina, inoculated with either PRSV or ZYMV, maintain their resistance when transplanted to the field. In the case of plants inoculated with either PRSV or ZYMV, Nigerian Local remained symptom-free in the field and produced ELISA readings similar to the non-inoculated control plants. Menina also remained symptom-free, but in some cases plants inoculated with PRSV produced ELISA readings similar to other genotypes with symptoms and intermediate levels of resistance/susceptibility. In the case of ZYMV, ELISA readings for Menina were similar to the non-inoculated control plants. In general, both of the genotypes are excellent sources of resistance to both PRSV and ZYMV. We are currently repeating this trial and expect to document what, if any, impact PRSV and ZYMV have on yield of the two resistant genotypes. In a greenhouse study we found that even though potyvirus-inoculated Menina and Nigerian Local remain symptom-free and have low virus titer (as determined by ELISA), side-by-side observations of inoculated and uninoculated 3-week-old plants clearly show an effect of virus infection. Inoculated plants (especially of Menina) were slightly more chlorotic and less developed than control plants.

Phytophthora blight resistance in butternut squash

2.1.4.2 Mapping resistance and breeding new butternut squash with resistance to Phytophthora blight
and 2.3.4.2 Introgress resistance into advanced breeding lines (M. Mazourek)

We are self-pollinating F1's between a mildew resistant bush butternut breeding line and Phytophthora blight resistant *C. moschata* accessions PI 211996, PI 483347. Crosses with PI 634693 and this breeding line were unproductive and this population has been put on hold accordingly. This summer we will screen F2 individuals to found them to be asymptomatic when inoculated with *P. capsici* on the blight farm. We will create F2:3 populations for QTL analysis by crossing them with a powdery mildew resistant bush butternut developed by Mazourek. *Phytophthora* resistant, bush squash will be crossed to a high quality parent for further breeding and validation of QTL from the initial F2:3 populations.

Economics Team

Team members:
Marco Palma (Texas A&M Univ.)
Lius Rivera (Texas A&M Univ.)

(b) Obj. 3. Economic impact analyses, disease control information					
3.1 Perform economic analysis, cost of production/disease control					
3.1.1. Define, parameterize, simulate, validate production variables	LR (TAMU), MP (TAMU)	X	X		
3.1.2. Estimate the potential economic impacts to the cucurbit industry	LR (TAMU), MP (TAMU)			X	X

3.1 Perform economic analysis, cost of production/disease control

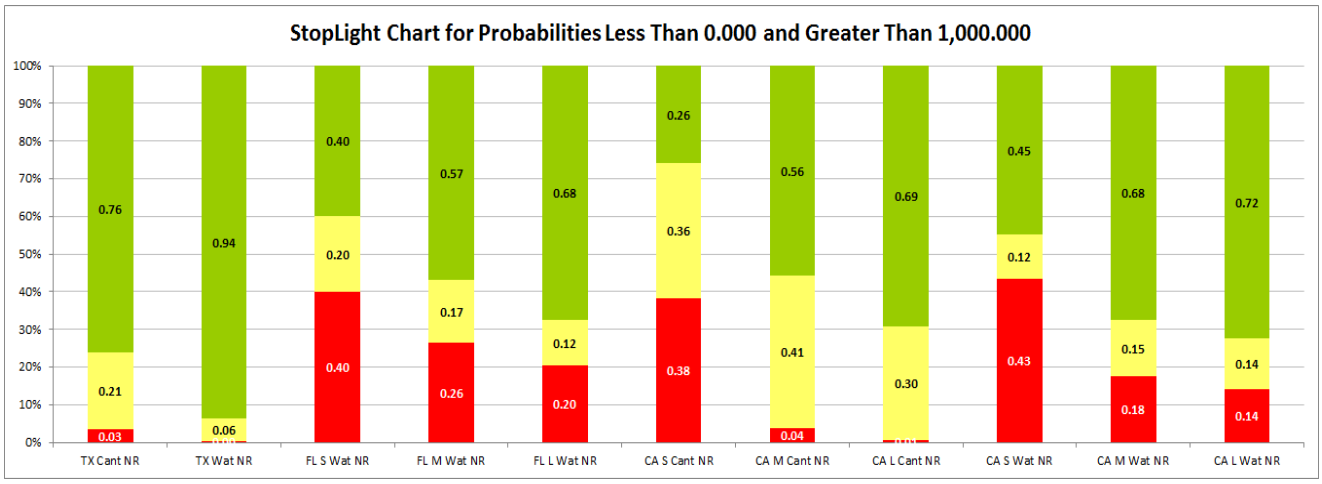
3.1.1. Define, parameterize, simulate, and validate production variables based on cucurbit production crop budgets

Completed:

- Macro and micro economic variables were collected to develop the economic model, such as interest rates, input costs, production windows and existing crop budgets.
- Graduate students were selected to work on the project and were trained on how to collect data to develop representative farms.
- Faculty and graduate students have IRB clearance to collect information from producers.
- Developed 11 representative farms in California (3 watermelon and 3 cantaloupe), Florida (3 watermelon) and Texas (1 watermelon and 1 cantaloupe)

In progress:

- Identify facilitators to develop representative farms in the Northeast region (Spring 2017)
- Develop and validate all representative farms (Summer/Fall 2017)



Extension/Outreach Team

Team members:
Jonathan Schultheis (N. Carolina St.Univ.)
Mary Hausbeck (Michigan St. Univ.)
Angela Linares (Univ. Puerto Rico)
Jim McCreight (USDA, ARS)
Lina Quesada (N. Carolina St. Univ.)
Chris Smart (Cornell Univ.)
Linda Wessel Beaver (Univ. Puerto Rico)

(b) Obj. 3. Economic impact analyses, disease control information					
3.2 Provide readily accessible information to facilitate disease control					
3.2.1. Develop a centralized cucurbit disease website	JS (NCSU)	X	X		
3.2.2. Develop and post diagnostic resources and disease control information in English and Spanish; prepare diagnostic poster	LQ (NCSU), MH (MSU), CS (CU), ALR (UPR)	X	X X	X X	X
3.2.3 Provide disease alerts and forecasting tools		X	X	X	X
3.2.4 Provide diagnostic and disease management assistance.	LQ (NCSU), MH (MSU), CS (CU)	X	X	X	X
3.2.5. Field days and demonstration plots	Crop and extension teams	X	X	X	X

3.2. Provide readily accessible information to facilitate disease control

As reported in the initial report, the extension component of this grant will be used to communicate the grant's goals, progress, results and its applications. The extension component reaches beyond those directly involved in the grant, such as breeders, seed company personnel, allied industry partners, growers, and other interested persons. Leadership for extension by commodity is provided mainly by Mary Hausbeck (cucumber), Lina Quesada (watermelon), Chris Smart (squash), and Jim McCreight (melon). The focus is on aspects related to disease. Linda Wessel-Beaver and Angela Lineares are the lead persons that will provide translation of documents from English to Spanish. Jonathan Schultheis complements these lead plant pathology PIs with pertinent cultural management information. He is also providing leadership with respect to the development of Cucurbit CAP webpage.

Many extension activities actively incorporate both stakeholders and extension personnel via field days, extension workshops, and commodity meetings at the local, state, national, and international levels. Specifically, the information which follows provides updates for June 2016 through March 2017 regarding the objectives and their associated results or outputs.

3.2.1 Develop a centralized cucurbit disease website.

A website developer and manager was hired in fall 2016 and the website has been under development for the past several months. There have been inputs during the website's development from CucCAP team leaders, the CucCAP Extension team, and specific input from the Project Leader, Rebecca Grumet and Lina Quesada. Quesada designed the logo for the project which is featured on the website. The Webpages on the CucCAP website include pages

describing the overall CucCAP project, work of each of the seven teams, contact information for CucCAP team members and their lab or institution, links to the Cucurbit Genomics Database (http://www.icugi.org) housed at Cornell University, links to forecasters including the Cucurbit Downy Mildew IPMpipe (http://cdm.ipmpipe.org/) and Melcast (http://melcast.ceris.purdue.edu/), links to diagnostic labs at Land Grant Universities, links to Plant Pathology & Extension factsheets or webpages for disease diagnosis, links to vegetable production guides, links to crop field trials, links to commodity organizations, and links to other disease management resources. Time sensitive information and location specific information including disease alerts, upcoming meetings or events, pesticide information and current articles about cucurbit diseases will be available in menus on the main page and footer of the site. The website is ready to be launched with a permanent address in March 2017. The main website address will be www.cuccap.org. Additional addresses to the site are www.cucurbitcap.org and www.cucurbitaceaecap.org. After review by the entire CucCAP team, the site will go public in April 2017. At that time, search engines will start indexing the website and analytics will be reported for purposes of understanding and optimizing usage of the CucCAP website.

3.2.2. Develop and post diagnostic resources and disease control information

Publications

1. Krasnow, C.S., and Hausbeck, M.K. 2017. Evaluation of winter squash cultivars for resistance to Phytophthora root rot, 2015. Plant Disease Management Reports 11:V028. Online.
2. Krasnow, C.S., and Hausbeck, M.K. 2016. *Phytophthora capsici*: Pathogen biology and management strategies. Pages 2-5in: *Phytophthora capsici* Session Summaries, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, MI, Dec. Online at http://glexpo.com/summaries/2016summaries/Phytophthora.pdf.
3. Hausbeck, M.K., Krasnow, C.S., and Linderman, S.D. 2016. Managing *Phytophthora* on winter squash and pumpkin. Online at https://veggies.msu.edu/extension-publications/#FactSheets.
4. Hausbeck, M.K., and Linderman, S.D. 2016. Managing *Phytophthora* on summer squash and zucchini. Online at https://veggies.msu.edu/extension-publications/#FactSheets.
5. Hausbeck, M.K., and Linderman, S.D. 2016. Managing *Phytophthora* on cucumber. Online at https://veggies.msu.edu/extension-publications/#FactSheets
6. Smart, C.D. and Lange, H. (2016) *Cucurbit Downy Mildew Update.* Article for the VegEdge newsletter February 2016
7. Smart, C.D. and Lange, H. (2016) *Vine Crop Update.* Proceedings of the 2016 Empire State Producers Expo, Syracuse, NY.
8. Schultheis, J.R., A.C. Thornton, and W.B. Thompson. 2016. Evaluating pickling cucumber plant populations to maximize yield for once-over mechanical harvest in the southeastern United States. Acta Hort. (ISHS) 1123:69-78.

3.2.3. Provide disease alerts and forecasting tools

Weekly conference calls, NCSU Vegetable Team (Quesada)**:** These calls began June 7 and continued through September 27.

Weekly conference calls, Cucurbit ipmPIPE (Hausbeck, Quesada, Smart)**:** These calls began in May and continued through August and will include plant pathologists from the eastern US.

Smart has active facebook and twitter accounts, and is also active in the Cornell Vegetable alerts blog (which sends messages to vegetable extension educators). As soon as diseases of cucurbits are first reported in NY, she alerts growers through these avenues. Additionally, any new advances made through CucCAP are also shared through these methods.

3.2.4 Provide diagnostic and disease management assistance.

Since the project started, Quesada has provided diagnostics and disease management recommendations for 12 cucumber, 33 watermelon, 7 melon, 12 squash, and 9 pumpkin samples submitted to the NCSU Plant Disease and Insect Clinic. Since the last report, Quesada has provided diagnostics and disease management recommendations for 3 cucumber, 22 watermelon, 5 melon, 8 squash, and 5 pumpkin samples submitted to the NCSU Plant Disease and Insect Clinic. Quesada has also been involved in providing disease management recommendations through oral presentations and generating disease management resources such as the NC Agricultural and Chemicals Manual and the Southeastern US 2016 Vegetable Crop Handbook.

Smart diagnosed over 100 samples during the 2016 growing season, in addition to over 100 disease issues diagnosed via photo through email or text message. She also provides management recommendations through oral presentations and production guides (both conventional and organic).

Production guides

1. Southeastern Vegetable Extension Workers. Kemble J., Lewis Ivey M., Jennings K. M., and Walgenbach J. F., Eds. (2017) Southeastern US 2017 Vegetable Crop Handbook. (Quesada & Schultheis, one of several co-authors)
2. Quesada-Ocampo L. M., Ed, (2017) Disease control for commercial vegetables. North Carolina Agricultural and Chemicals Manual.

3.2.5. Field days and demonstration plots.

Quesada recruited a part-time graduate student (Nicholas Noel) that evaluating commercial watermelon varieties for anthracnose resistance. Quesada and Noel are collaborating with Wehner, also on the watermelon team, who has a graduate student focusing on the genetic basis of disease resistance to anthracnose in watermelons. Quesada also supported demonstration plots to evaluate fungicides for disease control and combinations of tolerant varieties and fungicide applications.

Smart has yearly demonstration plots at the Phytophthora blight farm with variety trials for squash and other vegetables. She also has cucurbit downy mildew trials on research farms in

Geneva NY.

Schultheis was involved in several cucurbit variety studies in 2016; 2 zucchini squash, 2 butternut squash, 2 watermelon, 1 melon, 2 parthenocarpic pickling cucumber and 1 pumpkin. These trials were open to the industry and extension agents to evaluate for yield, quality and potential diseases. Representatives from multiple seed companies visited the studies and interacted.

A 1.5 day agent in-service training organized by Schultheis and focused on butternut squash and watermelon crops in August in Salisbury, NC. Cultural and disease management were featured at this in service training.

Publications from demonstration plots

1. Lange, H.W., Smart, C.D. and Seaman, A.J. 2017. Evaluation of materials allowed for organic production on downy mildew of cucumber, 2016. Plant Disease Management Report. Volume 11
2. Lange, H.W., Smart, C.D. and Seaman, A.J. 2017. Evaluation of materials allowed for organic production on powdery mildew of zucchini, 2016. Plant Disease Management Report. Volume 11
3. Schultheis, J.R., W.B. Thompson, and K.D. Starke. 2017. 2015 Yellow and zucchini squash cultivar evaluations. Dept. Horticultural Science. Horticulture Series #213. 26 pp.
4. Schultheis, J.R. and K.D. Starke. 2017. 2016 Zucchini squash cultivar evaluations. Dept. Horticultural Science. Horticulture Series #214. 12 pp.
5. Schultheis, J.R. and K.D. Starke. 2017. 2016 North Carolina melon cultivar evaluations. Dept. Horticultural Science. Horticulture Series #216. 32 pp.
6. Schultheis, J.R., W.B. Thompson and K. Starke. 2016. 2015 Triploid Watermelon Booklet. Hort. Res. Series 214. 41 pp.
7. Schultheis, J.R., W.B. Thompson and K. Starke. 2016. 2015 North Carolina melon cultivar evaluations. Hort. Research Series 211. 31 pp.

Oral and Poster Presentations

Extension and Industry Venues

Invited seminars

1. Smart, C.D. A tale of two *Phytophthora*: life with and without sex. Michigan State University, East Lansing, MI, March 2, 2017.
2. Smart, C.D. Multiplex detection for vegetable diseases. National Plant Diagnostic Network National meeting. Crystal City, VA, March 10, 2016.

Invited talks

1. Quesada-Ocampo L. M. Cucurbit disease management. Commercial vegetable grower symposium. Henderson, NC, February 2017.
2. Quesada-Ocampo L. M. Disease identification on vegetables. Certified Crop Advisor Training. Smithfield, NC, December 2016.

3. Quesada-Ocampo L. M. Fungicides and host resistance for cucurbit downy mildew management. 31st Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, December 2016.
4. Quesada-Ocampo L. M. Management of cucumber downy mildew using fungicides and host resistance. Pickle Packers International Annual Meeting. Charleston, SC, October 2016.
5. Schultheis, J.R. A perspective on melons; some North Carolins cultivar results and some "food" for thought. Eastern Cantaloupe Growers Association. Nashville, TN, 16 February 2017.
6. Schultheis, J.R. and T. Birdsell. Butternut squash production. Winter Vegetable Conference and Trade Show. Asheville, NC, 8 February 2017.

Oral presentations

1. Bertucci, M.B., K.M. Jennings, D.W. Monks, J.R. Schultheis, W.B. Thompson, F.W. Louws, D.L. Jordan, N.A. Basinger, S.C. Smith, M.D. and Waldschmidt. Early season crop development, yield, and fruit quality of standard and mini watermelons grafted to several cucurbit rootstocks. Watermelon Research Group, Mobile, AL. February 2017.
2. Harlan, B., and Hausbeck, M.. 2017. Vegetable diseases and control strategies. Michigan Agribusiness Association Meeting, Lansing, MI, 11 Jan. 60 attendees.
3. Hausbeck, M. 2017. A smorgasbord of vegetable diseases is on today's menu. MSU Extension and AgBioResearch State Council Meeting, Lansing, MI, Mar. 30 attendees.
4. Hausbeck, M. 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Vegetable Growers' Meeting, East Aurora, NY, 15 Feb. 40 attendees.
5. Hausbeck, M. 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Syngenta Meeting, East Lansing, MI, 9 Feb. 75 attendees.
6. Hausbeck, M. 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Wisconsin Fresh Fruit and Vegetable Conference, Wisconsin Dells, WI, 23 Jan. 40 attendees.
7. Hausbeck, M. 2016. Soilborne *Phytophthora capsici* on vine crops: Update and implications, Extension Specialist Breakfast Meeting via Zoom videoconference, East Lansing, 16 Jun. 15 attendees.
8. Krasnow, C., and Hausbeck, M. 2016. *Phytophthora capsici*: Fungicide programs and crop resistance. *Phytophthora capsici* Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, Dec. 55 attendees.
9. Hausbeck, M. 2016. *Phytophthora capsici*: Pathogen biology. *Phytophthora capsici* Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, Dec. 25 attendees.
10. Krasnow, C., and Hausbeck, M. 2016. Orondis: a new tool for controlling Phytophthora blight on pepper and squash. Syngenta Meeting, Lansing, MI, Feb. 75 attendees.
11. Krasnow, C., and Hausbeck, M. 2016. Phytophthora blight: management strategies for pepper and squash. Southwest Hort Days, Benton Harbor, MI, Feb. 35 attendees.
12. Krasnow, C., and Hausbeck, M. 2016. Rots and blights of vegetables. Bay Area Growers Extension Meeting, Bay City, MI, Jan. 40 attendees.
13. Meadows I., Mauney C., and Quesada-Ocampo L. M. Agent training on disease diagnostics and management in vegetable crops. Extension Conference. Raleigh, NC, November 2016.
14. Miller N. F. and Quesada-Ocampo L. M. Evaluation of a new fungicide for management of Fusarium wilt of watermelon. NCSU Masters Symposium, Raleigh, NC, November 2016.

15. Miller, N., M. Adams, and L.M. Quesada-Ocampo. Evaluation of a new fungicide for management of Fusarium wilt of watermelon. Watermelon Research Group. Mobile, AL, February 2017.
16. Schultheis, J.R. and K.D. Starke. Pollenizer placement considerations effects on watermelon (*Citrullus lanatus*) yield and quality. Watermelon Research Group, Mobile, AL. Feb. 2017
17. Smart, C.D. Understanding and controlling diseases of cucurbits. Crop Consultant Meeting, December 1, 2016 Syracuse NY.
18. Smart, C.D. Why is the *Phytopthora* blight from important? New York State Ag Experiment Station Task Force, October 10, 2016.
19. Smart, C.D. Field walk and discussion of diseases of cucurbits and other crops. Western NY Field Days. Portland, NY, Aug 31, 2016.
20. Smart, C.D. Vegetable disease management (1.5 hour discussion with growers and educators). Willsboro, NY, Aug 4, 20116
21. Smart, C.D. Vegetable disease management (1.5 hour discussion with growers and educators). Canton, NY, Aug 3, 2016.
22. Smart, C.D. How the NY Farm Bureau helped established the *Phytophthora* blight farm. Midwest Farm Bureau visit to NYSAES, June 24, 2016.
23. Starke, K.D. and J.R. Schultheis. Watermelon (*Citrullus lanatus*) yield and quality response to grafted versus non-grafted plants, 2016. Watermelon Research Group, Mobile, AL. February 2017.
24. Starke, K.D., B. Thompson, C. Jiang, and J. Schultheis. Planting density influences mini-watermelon yield and quality. 2016. VII International Symposium on Seed, Transplant and Stand Establishment of Horticultural Crops, Pretoria, South Africa, September 2016.

Posters

1. Birdsell, T.E., J.R. Schultheis, and P. Perkins-Veazie. Yield and quality response of butternut cultigens in NC. February 2017.

Webinars

1. Smart, C.D. Vegetable Diseases (for beginning growers), March 15, 2017. This was a 1.5 hour webinar.
2. Smart. C.D. Managing cucurbit downy mildew in organic systems in the northeast. December 6, 2016. 1.5 hour webinar with 135 participants.
3. Smart, C. D. Vegetable Diseases (for beginning growers), March 16, 2016. This was a 1 hour webinar.

Cumulative CucCAP

PUBLICATIONS,

RESOURCE MATERIALS

and

PRESENTATIONS

REFEREED PUBLICATIONS, BOOK CHAPTERS and CONFERENCE PROCEEDINGS

Refereed Publications

Ando K, Carr KM, Colle M, Mansfeld BN, Grumet R. 2015. Exocarp properties and transcriptomic analysis of cucumber (*Cucumis sativus)* fruit expressing resistance to *Phytophthora capsici*. PloS One 10: e0142133, doi:10.1371/journal.pone.0142133

Branham, S.E. A. Levi, M.W. Farnham and W.P. Wechter. 2016. A GBS-SNP-based linkage map and quantitative trait loci (QTL) associated with resistance to *Fusarium oxysporum* f. sp. *Niveum* race 2 identified in *Citrullus lanatus* var. *citroides*. Theor Appl Genet DOI 10.1007/s00122-016-2813-0

Carlson, MO, Gazave, E, Gore, MA, and Smart, CD. 2017. Temporal genetic dynamics of an experimental, biparental field population of *Phytophthora capsici*. *Frontiers in Genetics* 8:26. Doi: 10.3389/fgene.2017.00026

Cohen, Y., K. M. VandenLangenberg, T. C. Wehner, P. S. Ojiambo, M. Hausbeck, L. M. Quesada-Ocampo, A. Lebeda, H. Sierotzki, and U. Gisi. 2015. Resurgence of *Pseudoperonospora cubensis*: the causal agent of cucurbit downy mildew. Phytophathology 105: 998-1012.

Grumet R, Colle M. 2017. Cucumber (*Cucumis sativus*) breeding line with young fruit resistance to infection by *Phytophthora capsici*. HortScience. In press.

Holdsworth WL, LaPlant KE, Bell DC, Jahn MM, Mazourek M. 2016. Cultivar-Based Introgression Mapping Reveals Wild-Species Derived *Pm-0* The Major Powdery Mildew Resistance Locus in Squash. PLOS ONE. e0167715.

Daley, J., S. Branham, A. Levi, R. Hassell, and P. Wechter. 2017. Mapping resistance to *Alternaria cucumerina* in *Cucumis melo*. Phytopathology. DOI 10.1094/PHYTO-06-16-0246-R

Dhillon, N.P.S., S. Sanguansil, R. Schafleitner, Y.-W. Wang, and J.D. McCreight. 2016. Diversity among a wide Asian Collection of bitter gourd landraces and their genetic relationships with commercial hybrid cultivars. J. Amer. Soc. Hort. Sci. 141:475–484. 10.21273/JASHS03748-16

Dhillon, N.P.S., S. Sanguansil, S.P. Singh, M.A.T. Masud, P. Kumar, L.K. Bharathi, H. Yetisir, R. Huang, D.X. Canh, and J.D. McCreight. 2016. Genetic resources of minor cucurbits. In: R.G. Grummet, N. Katzir, and J. Garcia-Mas (eds.). Genetics and Genomics of the Cucurbitaceae. Springer Science+Media, New York.

Dhillon, N.P.S., S. Phethin, S. Sanguansil, and J.D. McCreight. 2017. Early staminate flowering monoecious lines have potential as pollenizers for gynoecious hybrid bitter gourd cultivars Pak. J. Agri. Sci. 54:27–33. DOI 10.21162/PAKJAS/17.4354

Kousik, C. S., Brusca, J., and Turechek, W. W. 2016. Diseases and disease management strategies take top research priority in the Watermelon Research and Development Group members survey (2014 to 2015). Plant Health Progress. 17:53-58.

Kousik, C. S., Ikerd, J., and Mandal, M. 2016. First report of fruit rot of ridge gourd (*Luffa acutangula*) caused by *Sclerotium rolfsii*. Plant Health Progress. 17:13-14. doi:10.1094/PHP-BR-15-0048.

Lebeda, A., E. Křístková, B. Sedláková, J.D. McCreight, and M.D. Coffey. 2016. Cucurbit powdery mildews: methodology for objective determination and denomination of races. European Journal of Plant Pathology 144:399–410. DOI 10.1007/s10658-015-0776-7

Levi, A., J. Coffey, L.M. Massey, N. Guner, E. Oren, Y. Tadmor, and K.S. Ling. 2016. Resistance to papaya ringspot virus-watermelon strain (PRSV-W) in the desert watermelon *Citrullus colocynthis*. HortScience 51:4–7.

Levi, A., R.K. Harris-Shultz and K. Ling. 2016. USVL-370, a Zucchini yellow mosaic virus–resistant Watermelon Breeding Line. HortScience 51:107–109.

Levi, A., Simmons, A.M., Massey, L.M., Coffey, J., Wechter, W.P., Jarret, R.L., Tadmor, Y., Nimmakayala, P., Reddy, U. 2017. Genetic diversity in the desert watermelon *Citrullus colocynthis* and its relationship with *Citrullus* species as determined by high-frequency oligonucleotides-targeting active gene markers. Journal of the American Society for Horticultural Science. 142:47–56.

McCreight, J.D., W.M. Wintermantel, and E.T. Natwick. 2017. Host plant resistance in melon to sweetpotato whitefly in California and Arizona. Acta Hort. (in Press).

McCreight, J.D., W.M. Wintermantel, E.T. Natwick, J.W. Sinclair, K.M. Crosby, and M.L. Gómez-Guillamón. 2017. Recessive resistance to *Cucurbit yellow stunting disorder virus* in melon TGR 1551. Acta Hort. (In Press).

Meru, G. and C. McGregor. 2016. Genotyping by sequencing for SNP discovery and genetic mapping of resistance to race 1 of *Fusarium oxysporum* in watermelon. Scientia Horticulturae 209: 31-40.

Naegele R. P., Quesada-Ocampo L. M., Kurjan J. D, Saude C., and Hausbeck M. K. (2016) Regional and temporal population structure of *Pseudoperonospora cubensis* in Michigan and Ontario. Phytopathology 106: 372-379.

Natwick, E., M.I. Lopez, W.M. Wintermantel, J.D. McCreight, O. Batuman, and R.L. Gilbertson. 2016. Watermelon whitefly insecticide efficacy trial, 2015. Arthropod Management Tests (2016) 41 (1): tsw088. DOI: https://doi.org/10.1093/amt/tsw088

Nimmakayala, P., Y. Tomason, V.L. Abburi, A Alvarado, T Saminathan, V.G. Vajja, G. Salazar, G. Panicker, A. Levi, W.P. Wechter, J.D. McCreight, A. Korol, Y. Ronin, J Garcia-Mas, and U.K. Reddy. 2016. Genome-Wide Differentiation of Various Melon Horticultural Groups for Use in GWAS for Fruit Firmness and Construction of a High Resolution Genetic Map. Frontiers in Plant Science 22 September 2016 http://dx.doi.org/10.3389/fpls.2016.01437

Niu, X. X. Zhao, K. Ling, A. Levi, Y. Sun, M. Fan. 2016. The FonSIX6 gene acts as an avirulence effector in the
Fusarium oxysporum f. sp. *niveum* - watermelon pathosystem. Nature Scientific Reports 6:28146 DOI: 10.1038/srep28146

Pan, Y.P., Qu, S.P., Bo, K.L., Gao, M.L., Haider, K.R., Weng, Y. 2017. QTL mapping of domestication and diversifying selection related traits in round-fruited semi-wild Xishuangbanna cucumber (*Cucumis sativus* L. var. *xishuangbannanesis*). Theor Appl Genet (provisionally accepted)

Sabanadzovic, S., R. Valverde, J.D. McCreight, W.M. Wintermantel, and N. Aboughanem-Sabanadzovic. 2016. *Cucumis melo* endornavirus: Genome organization, host range and co-divergence with the host. Virus Research 214:49–58

Schultheis, J.R., A.C. Thornton, and W.B. Thompson. 2016. Evaluating pickling cucumber plant populations to maximize yield for once-over mechanical harvest in the southeastern United States. Acta Hort. (ISHS) 1123:69-78.

Summers, C.F., Adair, N., Gent, D.H., McGrath, M.T., and Smart, C.D. (2015) *Pseudoperonospora cubensis* and *P. humuli* detection using species-specific probes and high definition melt curve analysis. *Canadian Journal of Plant Pathology* 37:315-330. DOI: 10.1080/07060661.2015.1053989 Thies, J.A., J.J. Ariss, C.S. Kousik, R.L. Hassell, and A. Levi. 2016. Resistance to Southern Root-knot Nematode (*Meloidogyne incognita*) in Wild Watermelon (*Citrullus lanatus* var. *citroides*) Populations. Journal of Nematology 48:14–19.

Summers, C.F., Gulliford, C.M., Carlson, C.H., Lillis, J.A., Carlson, M.O., Cadle-Davidson, L., Gent, D.H., and Smart, C.D. (2015) Identification of genetic variation between obligate plant pathogens *Pseudoperonospora cubensis* and *P. humuli* using RNA sequencing and genotyping-by-sequencing. *PLoS ONE* 10(11): eD143665. DOI: 1D.1371/journal.pone.D143665

Tabima JF, Everhart SE, Larsen MM, Weisberg AJ, Kamvar ZN, Tancos MA, Smart CD, Chang JH, Grünwald NJ. 2017. Microbe-ID: An open source toolbox for microbial genotyping and species identification. *PeerJ* 4:e2279; DOI 10.7717/peerj.2279

VandenLangenberg, K. and T. C. Wehner. 2016. Downy mildew disease progress in resistant and susceptible cucumbers tested in the field at different growth stages. HortScience 51: 984-988.

Wallace E., Adams M., and Quesada-Ocampo L. M. (2015) First report of downy mildew on buffalo gourd (*Cucurbita foetidissima*) caused by *Pseudoperonospora cubensis* in North Carolina. Plant Disease 99: 1861.Wallace E., Choi Y. J., Thines M., and Quesada-Ocampo L. M. (2016) First report of *Plasmopara* aff. *australis* on *Luffa cylindrica* in the United States. Plant Disease 100: 537.

Webster, C.G., Turechek, W.W., Li, W., Kousik, C.S. and Adkins, S. 2017. Development and evaluation of ELISA and qRT-PCR for identification of Squash vein yellowing virus in cucurbits. Plant Disease 101:178-185.

Wechter, W.P., McMillan, M.M., Farnham, M.W., and Levi, A. 2016. Watermelon germplasm lines USVL246-FR2 and USVL252-FR2 tolerant to Fusarium oxysporum f. sp. niveum race 2. HortScience 51:1065-1067.

Wintermantel, W.M., Gilbertson, R.L., McCreight, J.D., and Natwick, E.T. 2015. Host-specific relationship between virus titer and whitefly transmission of *Cucurbit yellow stunting disorder virus*. Plant Disease 100: 92-98. http://dx.doi.org/10.1094/PDIS-11-14-1119-RE

Withers S., Gongora-Castillo E., Gent D., Thomas A., Ojiambo P., and Quesada-Ocampo L. M. (2016) Using next-generation sequencing to develop molecular diagnostics for *Pseudoperonospora cubensis*, the cucurbit downy mildew pathogen. Phytopathology 106: 1105-1116.

Zhang G, Ren Y, Sun H, Guo S, Zhang F, Zhang J, Zhang H, Jia Z, Fei Z, Xu Y, Li H (2015) A high-density genetic map for anchoring genome sequences and identifying QTLs associated with dwarf vine in pumpkin (*Cucurbita maxima* Duch.). BMC Genomics 16:1101

Conference Proceedings

Grumet, R., Z. Fei, A. Levi, J.D. McCreight, M. Mazourek, M. Palma, J. Schultheis, Y. Weng, M. Hausbeck, S. Kousik, K.-S. Ling, C. McGregor, L. Quesada-Ocampo, A.L. Ramirez, U. Reddy, L. Ribera, C. Smart, P. Wechter, T. Wehner, L. Wessel-Beaver, and W. Wintermantel. 2016. CucCAP - Developing genomic resources for the cucurbit community, p. 222–226. In: E.U. Kozik, and H.S. Paris (eds.). Cucurbitaceae 2016, XIth Eucarpia Meeting on Genetics and Breeding of Cucurbitaceae, Warsaw, Poland.

Lebeda, A., E. Křístková, B. Sedláková, and J.D. McCreight. 2016 Initiative for international cooperation of researchers and breeders related to determination and denomination of cucurbit powdery mildew races, p. 148–152. In: E.U. Kozik, and H.S. Paris (eds.). Cucurbitaceae 2016, XIth Eucarpia Meeting on Genetics and Breeding of Cucurbitaceae, Warsaw, Poland.

Levi, A., A. Simmons, K. Ling, Y. Tadmor, P. Nimmakayala, and U.K. Reddy. 2016. Utilizing Genetic Diversity in the Desert Watermelon *Citrullus colocynthis* for Enhancing Watermelon Cultivars for Resistance to Biotic and Abiotic Stress. p. 105-108. In E.U. Kozik and H.S. Paris (eds).

Cucurbitaceae 2016, XIth EUCARPIA Meeting on Genetics and Breeding of Cucurbitaceae, Warsaw, Poland.

McCreight, J.D., W.M. Wintermantel, and E.T. Natwick. 2016. New Sources of Resistance to CYSDV in Melon, p. 61–65. In: E.U. Kozik, and H.S. Paris (eds.). Cucurbitaceae 2016, XIth Eucarpia Meeting on Genetics and Breeding of Cucurbitaceae, Warsaw, Poland.

Miranda-Vélez, M, L. Wessel-Beaver, Jose C. Verle-Rodrigues and W. Seda-Martínez. 2016. Effect of leaf position on the assessment of resistance to *Papaya ringspot virus* and *Zucchini yellow mosaic virus* in tropical pumpkin. Proceedings of the 41st meeting of the Sociedad Puertorriqueña de Ciencias Agrícolas, November 18, 2016, Corozal, Puerto Rico. p. 57.

Wessel-Wessel-Beaver, L. and J. C. V. Rodrigues. 2016. Sources of variation in ELISA tests used to quantify ZYMV and PRSV resistance in *Cucurbita moschata*. In E.U. Kozik and H.S. Paris, Eds: Cucurbitaceae 2016, Proceedings of Cucurbitaceae 2016, the XIth EUCARPIA meeting on Genetics and Breeding of Cucurbitaceae, July 24-28, Warsaw, Poland pp. 170-173.

Book/Book Chapters

Many members of CucCAP have contributed chapters to:

Grumet, R, Katzir N, Garcia-Mas J (eds.). ***Genetics and Genomics of the Cucurbitaceae***. Springer Science+Media, New York.

2016. Most available as electronic publication

2017. Print publication in process.

Bai Y, Zhang Z, Fei Z. 2016. Databases and bioinformatics for cucurbit species. Chapter 14. DOI 10.1007/7397_2016_27

Dhillon, N.P.S., S. Sanguansil, S.P. Singh, M.A.T. Masud, P. Kumar, L.K. Bharathi, H. Yetisir, R. Huang, D.X. Canh, and J.D. McCreight. 2016. Gourds: Bitter, bottle, wax, snake, sponge and ridge. Chapter 7. DOI 10.1007/7397_2016_24

Grumet R, Colle M. Genomic analysis of cucurbit fruit growth. Chapter 18. DOI 10.1007/7397_2016_4

Grumet R, Garcia-Mas J, Katzir N. Cucurbit genetics and genomics – a look to the future. Chapter 21.

Levi A, Jarret R, Kousik S, Wechter WP, Nimakayala, Reddy U. Genetic resources of watermelon. Chapter 5.

McCreight, J.D. 2016. Cultivation and Uses of Cucurbits. Chapter 1. DOI 10.1007/7397_2016_2

Naegele RP, Wehner TC. 2016. Genetic resources of cucumber. Chapter 4. DOI 10.1007/7397_2016_15

NImmakayala P, Saminathan T, Abburi VL, Yadav LK, Tomason Y, Levi A, Weng Y, Reddy UK. Comparative genomics of the Cucurbitaceae. Chapter 12.

Weng Y. 2016. The cucumber genome. Chapter 9. DOI 10.1007/7397_2016_6

Other

Weng Y., Wehner, T. C. 2017. Cucumber Gene Catalog 2017. Cucurbit Genet Coop 2017 issues 34-35

EXTENSION and OUTREACH RESOURCES and PRESENTATIONS

DISEASE CONTROL and EXTENSION RESOURCES

Adams M. L., Noel N. A., and Quesada-Ocampo L. M. (2016) Evaluation of fungicides for control of downy mildew on cucumber, Clayton 2015. Plant Disease Management Report. 10: V084.

Adams M. L. and Quesada-Ocampo L. M. (2016) Evaluation of fungicides for control of powdery mildew of winter squash, Cleveland 2015. Plant Disease Management Report. 10: V076.

Adams M. L. and Quesada-Ocampo L. M. (2016) Evaluation of fungicides for control of downy mildew on cucumber, Cleveland 2015. Plant Disease Management Report. 10: V085

Adams M. L. and Quesada-Ocampo L. M. (2016) Evaluation of fungicides for control of downy mildew on cucumber, Kinston 2015. Plant Disease Management Report. 10: V086

Hausbeck, M. 2016. Downy mildew spends a decade damaging cucumbers. Vegetable Grower News 50(5):16-17.

Kemble J., Quesada-Ocampo L. M., Lewis Ivey M., Jennings K. M., and Walgenbach J. F., Eds. (2015). Southeastern Vegetable Extension Workers. Southeastern US 2015 Vegetable Crop Handbook

Krasnow, C., Hausbeck, M., Bryant, A., Morrison, W.R. III, Werling, B., Quinn, N., Szendrei, Z., and Buchanan, A. 2015. Diseases and insects in Michigan cucurbits and their management. Michigan State University Extension Bulletin E3276.

Kousik, C.S. and Ikerd, J.L. 2016. Evaluation of watermelon varieties for tolerance to powdery mildew and Phytophthora fruit rot, 2014. Plant Disease Management Report 10:V082

Kousik, C.S. and Ikerd, J.L. 2016. Evaluation of fungicide rotations for management of Phytophthora fruit rot of watermelon, 2015. Plant Disease Management Report 10:V083

Krasnow, C.S., and Hausbeck, M.K. 2017. Evaluation of winter squash cultivars for resistance to Phytophthora root rot, 2015. Plant Disease Management Reports 11:V028. Online.

Krasnow, C.S., and Hausbeck, M.K. 2016. *Phytophthora capsici*: Pathogen biology and management strategies. Pages 2-5in: *Phytophthora capsici* Session Summaries, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, MI, Dec. Online at http://glexpo.com/summaries/2016summaries/Phytophthora.pdf.

Lange, H.W., Smart, C.D. and Seaman, A.J. 2016. Evaluation of fungicides allowed for organic production on downy mildew of cucumber, 2015. Plant Disease Management Report. Vol. 10

Lange, H.W., Smart, C.D. and Seaman, A.J. 2017. Evaluation of materials allowed for organic production on downy mildew of cucumber, 2016. Plant Disease Management Report. Volume 11

Lange, H.W., Smart, C.D. and Seaman, A.J. 2017. Evaluation of materials allowed for organic production on powdery mildew of zucchini, 2016. Plant Disease Management Report. Volume 11

Quesada-Ocampo L. M., Ed, (2015) Disease control for commercial vegetables. North Carolina Agricultural and Chemicals Manual.

Quesada-Ocampo L. M. Watermelon downy mildew reported in North Carolina. Extension Plant Pathology Portal. June 17, 2016.

Quesada-Ocampo L. M. Cucumber downy mildew reported in North Carolina. Extension Plant Pathology Portal. June 1, 2016

Quesada-Ocampo L. M. Keep an eye out for gummy stem blight in watermelons. Extension Plant Pathology Portal. May 5, 2016

Quesada-Ocampo L. M., Ed, (2016) Disease control for commercial vegetables. North Carolina Agricultural and Chemicals Manual.

Quesada, Schultheis among other authors. Southeastern Vegetable Extension Workers. Kemble J., Lewis Ivey M., Jennings K. M., and Walgenbach J. F., Eds. (2017) Southeastern US 2017 Vegetable Crop Handbook.

Quesada-Ocampo L. M., Ed, (2017) Disease control for commercial vegetables. North Carolina Agricultural and Chemicals Manual.

Schultheis, J.R., W.B. Thompson, and K.D. Starke. 2017. 2015 Yellow and zucchini squash cultivar evaluations. Dept. Horticultural Science. Horticulture Series #213. 26 pp.

Schultheis, J.R. and K.D. Starke. 2017. 2016 Zucchini squash cultivar evaluations. Dept. Horticultural Science. Horticulture Series #214. 12 pp.

Schultheis, J.R. and K.D. Starke. 2017. 2016 North Carolina melon cultivar evaluations. Dept. Horticultural Science. Horticulture Series #216. 32 pp.

Schultheis, J.R., W.B. Thompson and K. Starke. 2016. 2015 Triploid Watermelon Booklet. Hort. Res. Series 214. 41 pp.

Schultheis, J.R., W.B. Thompson and K. Starke. 2016. 2015 North Carolina melon cultivar evaluations. Hort. Research Series 211. 31 pp.

Smart, C. 2016. Vegetable diseases. Webinar. Mar. (1 hr)

Smart, C.D. and Lange, H. (2016) *Cucurbit Downy Mildew Update.* Article for the VegEdge newsletter February 2016

Smart, C.D. and Lange, H. (2016) *Vine Crop Update.* Proceedings of the 2016 Empire State Producers Expo, Syracuse, NY.

Web Content

Anthracnose of cucurbits: http://content.ces.ncsu.edu/anthracnose-of-cucurbits

Cucurbit downy mildew: http://content.ces.ncsu.edu/cucurbit-downy-mildew

Cucurbit powdery mildew: http://content.ces.ncsu.edu/cucurbit-powdery-mildew

Fusarium wilt of watermelon: http://content.ces.ncsu.edu/fusarium-wilt-of-watermelon

Gummy stem blight of cucurbits: http://content.ces.ncsu.edu/gummy-stem-blight-and-phoma-blight-on-cucurbits

Hausbeck, M.K., Krasnow, C.S., and Linderman, S.D. 2016. Managing *Phytophthora* on winter squash and pumpkin. https://veggies.msu.edu/extension-publications/#FactSheets

Hausbeck, M.K., and Linderman, S.D. 2016. Managing *Phytophthora* on summer squash and zucchini. https://veggies.msu.edu/extension-publications/#FactSheets.

Hausbeck, M.K., and Linderman, S.D. 2016. Managing *Phytophthora* on cucumber. https://veggies.msu.edu/extension-publications/#FactSheets

Webinars

Smart, C.D. Vegetable Diseases (for beginning growers), March 15, 2017. This was a 1.5 hour webinar.

Smart C.D. Managing cucurbit downy mildew in organic systems in the northeast. December 6, 2016. 1.5 hour webinar with 135 participants.

Smart, C. D. Vegetable Diseases (for beginning growers), March 16, 2016. 1 hour webinar.

EXTENSION and OUTREACH PRESENTATIONS

Adams M. L. and Quesada-Ocampo L. M. 2016. Managing fungal diseases in cucurbits. NC Watermelon Convention. Wrightsville Beach, SC, Mar.

Adams M. L. and Quesada-Ocampo L. M. 2015. Managing fungal foliar diseases in cucurbits. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, Dec.

Arteman, L. T.C. Wehner, and J.R. Schultheis. 2015. Evaluation of parthenocarpic pickling cucumbers for North Carolina production. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, SC. Dec.

Bertucci, M., K. Jennings, D. Monks, D. Jordan, F. Louws, and J. Schultheis. 2015. Competitiveness of grafted watermelon plants versus nongrafted watermelon plants at various times of weedy and weed-free intervals. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, SC. Dec.

Bertucci, M.B., K.M. Jennings, D.W. Monks, J.R. Schultheis, W.B. Thompson, F.W. Louws, D.L. Jordan, N.A. Basinger, S.C. Smith, M.D. and Waldschmidt. 2017. Early season crop development, yield, and fruit quality of standard and mini watermelons grafted to several cucurbit rootstocks. Watermelon Research Group, Mobile, AL. February 2017.

Chacko, N. J.-B. Mou, and M.D. Coffey. 2016. Powdery mildew race variation in California. California Melon Research Board, Annual Meeting, San Diego, CA, Jan.

Grumet, R. 2015. Update on resistance to *Phytophthora capsici* in cucumber. PPI Annual Meeting October 30, 2015, Fort Worth, TX

Grumet, R. 2015. Introduction to CucCAP: Leveraging applied genomics to increase disease resistance in cucurbit crops. Pickling Cucumber Commodity Meeting, Grand Rapids, Dec.

Grumet, R. and M. Colle. 2015. Development of genetic stocks for cucumber fruit resistance to *Phytophthora capsici*. Pickling Cucumber Commodity Meeting, Grand Rapids, Dec.

Grumet, R. 2016. Introduction to CucCAP: Leveraging applied genomics to increase disease resistance in cucurbit crops. California Melon Research Board, Annual Meeting, San Diego, CA, Jan.

Grumet R, Mansfeld B, Lin Y-C. 2016. Genetic characterization and development of breeding materials for resistance of young cucumber fruit to infection by *Phythophthora capsici.* Pickling Cucumber Commodity Meeting, Grand Rapids, Dec.

Harlan, B., and Hausbeck, M.. 2017. Vegetable diseases and control strategies. Michigan Agribusiness Association Meeting, Lansing, MI, 11 Jan. 60 attendees.

Hausbeck, M. 2015. The downy mildew report. Pickling Cucumber Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, MI, Dec. 144 attendees.

Hausbeck, M. 2015. Downy mildew research. Pickling Cucumber Commodity Meeting, Grand Rapids, Dec. 30 attendees.

Hausbeck, M.K. 2015. Ten years of downy mildew in Michigan. Pickle Packers International Inc Annual Meeting, Fort Worth TX, Oct. 30 attendees.

Hausbeck, M.K., and Cook, A. 2015. The downy mildew report. Pages 9-14 in: Pickling Cucumber Session Summaries, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, MI, Dec. Online.

Hausbeck, M. 2016. The downy mildew report. Syngenta Meeting, Lansing, MI, Feb. 120 attendees.

Hausbeck, M. 2016. Soilborne *Phytophthora capsici* on vine crops: Update and implications, Extension Specialist Breakfast Meeting via Zoom videoconference, East Lansing, 16 Jun. 15 attendees

Hausbeck, M. 2016. *Phytophthora capsici*: Pathogen biology. *Phytophthora capsici* Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, Dec. 25 attendees.

Hausbeck MK, Goldenhar K. 2016. Downy mildew prevention and control. Pickling Cucumber Commodity Meeting, Grand Rapids, Dec.

Hausbeck MK, Golenhar K, Bello JR. 2016. Downy mildew: What's next? Pickling Cucumber Commodity Meeting, Grand Rapids, Dec.

Hausbeck, M. 2017. A smorgasbord of vegetable diseases is on today's menu. MSU Extension and AgBioResearch State Council Meeting, Lansing, MI, Mar. 30 attendees.

Hausbeck, M. 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Vegetable Growers' Meeting, East Aurora, NY, 15 Feb. 40 attendees.

Hausbeck, M. 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Syngenta Meeting, East Lansing, MI, 9 Feb. 75 attendees.

Hausbeck M 2017. Managing Phytophthora crown and fruit rot in cucurbit crops. Wisconsin Fresh Fruit and Vegetable Conference, Wisconsin Dells, WI, 23 Jan. 40 attendees.

Kousik, C.S. 2016. Progress and challenges in managing Phytophthora fruit rot of watermelon. Indiana Horticultural Congress, Indianapolis, IN. January. 45 attendees (at the talk)

Kousik C.S. 2016. Managing Phytophthora fruit rot of watermelon. Georgia Watermelon Association, St. Simmons, GA. January. Over 100 attendees

Kousik, C.S. 2016. Breadth of resistance of USVL developed Phytophthora fruit rot resistant germplasm lines to *Phytophthora capsici* isolates from across USA. Watermelon Research and Development Group meeting. San Antonio, TX. Feb >50 attendees

Kousik, C.S. 2016. Chaired and organized Watermelon Research and Development Group meeting. San Antonio, TX. Feb >50 attendees, 26 talks.

Kousik, C.S. 2016. Progress and challenges in managing Phytophthora fruit rot of watermelon. U.S. Vegetable Laboratory Seminar. Charleston, SC. March

Kousik, C.S. 2017. Chaired and organized Watermelon Research and Development Group meeting. Mobile, AL. February 2017. >65 attendees, 38 talks.

Kristie, M., Ikerd, J.L., Mandal, M., Hassell, R., and Kousik, C.S. 2017. Development of Phytophthora crown rot (*Phytophthora capsici*) resistant rootstocks of Cucurbita maxima and *C. moschata* for watermelon grafting. Presented at the Watermelon Research and Development Group meeting. Mobile, AL. February 2017.

Krasnow, C., and Hausbeck, M. 2016. Progress in cucumber downy mildew control. Southwest Hort Days, Benton Harbor, MI, Feb. 35 attendees.

Krasnow, C., and Hausbeck, M. 2016. *Phytophthora capsici*: Fungicide programs and crop resistance. *Phytophthora capsici* Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids, Dec. 55 attendees.

Krasnow, C., and Hausbeck, M. 2016. Orondis: a new tool for controlling Phytophthora blight on pepper and squash. Syngenta Meeting, Lansing, MI, Feb. 75 attendees.

Krasnow, C., and Hausbeck, M. 2016. Phytophthora blight: management strategies for pepper and squash. Southwest Hort Days, Benton Harbor, MI, Feb. 35 attendees.

Krasnow, C., and Hausbeck, M. 2016. Rots and blights of vegetables. Bay Area Growers Extension Meeting, Bay City, MI, Jan. 40 attendees.

Levi, A. S. Steck, M. Horry, R.L. Jarret, P. Wechter, S. Kousik, B. Ward, G. Miller, R. Hassell, and A. Keinath. 2017. An overall small root system in watermelon cultivars indicates a need to improve

their lateral fibrous root capacity. Presented at the Watermelon Research and Development Group meeting. Mobile, AL. February 2017.

Mandal, M.K., Kousik, C.S. and Ward, B. 2016. Molecular dissection of resistance signaling in watermelon fruit through metabolomics and transriptomic approach. Watermelon Research and Development Group meeting. San Antonio, TX. Feb >50 attendees

Mandal, M.K., Ikerd, J.L., Shrestha, S. Battiste, A., Boroujerdi, A., Ward, B., Kousik, C.S. 2017. 1H NMR and HPLC-based metabolite profiling of watermelon varieties. Presented at the Watermelon Research and Development Group meeting. Mobile, AL. February 2017.

McCreight, J.D. 2015. Melon host plant resistance to powdery mildew and CYSDV. Fall Desert Crops workshop, sponsored by the University of California ANR Cooperative Extension, Imperial County, and University of Arizona Cooperative Extension, Yuma County. El Centro, CA, Oct.

McCreight, J.D. and E.T. Natwick. 2016. Evaluation and breeding of new sources of host plant resistance to CYSDV and sweetpotato whitefly biotype B. California Melon Research Board, Annual Meeting, San Diego, CA, Jan.

McCreight, J.D. and E.T. Natwick. 2017. Evaluation and breeding of new sources of host plant resistance to CYSDV and sweetpotato whitefly biotype B. California Melon Research Board, Annual Meeting, San Diego, CA, Jan. 4, 2017.

McGregor, C.E. 2016. Advances in Watermelon Breeding. Southeast Regional Fruit & Vegetable Conference, 8-10 January 2016, Savannah, GA .

Meadows I., Mauney C., and Quesada-Ocampo L. M. 2016. Agent training on disease diagnostics and management in vegetable crops. Extension Conference. Raleigh, NC, November 2016.

Miller N. F. and Quesada-Ocampo L. M. 2016. Evaluation of a new fungicide for management of Fusarium wilt of watermelon. NCSU Masters Symposium, Raleigh, NC, November 2016.

Miller, N., M. Adams, and L.M. Quesada-Ocampo. 2017. Evaluation of a new fungicide for management of Fusarium wilt of watermelon. Watermelon Research Group. Mobile, AL, February 2017.

Miller N. F. and Quesada-Ocampo L. M. 2015. New control options for Fusarium wilt in watermelon. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, Dec.

Quesada-Ocampo L. M. 2015. Diagnostics and management of cucurbit downy mildew. Pickle Packers International Annual Meeting. Fort Worth, TX, Oct.

Quesada-Ocampo L. M. 2016. Downy mildew and *Phytophthora* control in cucurbits. NC Watermelon Convention. Wrightsville Beach, NC, Mar.

Quesada-Ocampo L. M. 2016. Cucurbit downy mildew management, diagnostics, and pathogen populations. Pickle Packers International Spring Meeting. Raleigh, NC, Apr.

Quesada-Ocampo L. M. 2016. Downy mildew updates for cucurbits. Southeast Regional Fruit and Vegetable Conference. Savannah, GA, Jan.

Quesada-Ocampo L. M. 2016. Disease identification on vegetables. Certified Crop Advisor Training. Smithfield, NC, December 2016.

Quesada-Ocampo L. M. 2016. Fungicides and host resistance for cucurbit downy mildew management. 31st Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, December 2016.

Quesada-Ocampo L. M. 2016. Management of cucumber downy mildew using fungicides and host resistance. Pickle Packers International Annual Meeting. Charleston, SC, October 2016.

Quesada-Ocampo L. M. 2017. Cucurbit disease management. Commercial vegetable grower symposium. Henderson, NC, February 2017.

Schultheis, J.R. and S. Johnson. 2015. Grafted versus nongrafted watermelon studies using bare ground or plasticulture production methods. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, SC. Dec.

Schultheis, J.R. 2016. Grafted vs. nongrafted watermelon studies. NC Watermelon Convention. Wrightsville Beach, NC, Mar.

Schultheis, J.R. and W.B. Thompson. 2016. Watermelon yield and fruit size response to grafted versus non-grafted transplants in plasticulture and bare ground production systems. Watermelon Research Group, San Antonio, TX, Feb.

Schultheis, J.R. and W. B. Thompson. 2016, Watermelon cultivar yield and quality trial results, North Carolina, 2015. 2016. Watermelon Research Group, San Antonio, TX, Feb.

Schultheis, J.R. 2017. A perspective on melons; some North Carolina cultivar results and some "food" for thought. Eastern Cantaloupe Growers Association. Nashville, TN, 16 February 2017.

Schultheis, J.R. and T. Birdsell. 2017. Butternut squash production. Winter Vegetable Conference and Trade Show. Asheville, NC, 8 February 2017.

Schultheis, J.R. and K.D. Starke. 2017. Pollenizer placement considerations effects on watermelon (*Citrullus lanatus*) yield and quality. Watermelon Research Group, Mobile, AL. Feb. 2017

Smart, C. 2015. Disease problems common during the 2015 growing season. Twilight meeting, Eden Valley, NY.

Smart, C. 2016. Disease update. Western NY Vegetable Growers meeting. Lockport, NC, Mar.

Smart, C. 2016. Managing cucurbit diseases. Empire State Producers Expo. Jan.

Smart, C.D. 2016. Understanding and controlling diseases of cucurbits. Crop Consultant Meeting, December 1, Syracuse NY.

Smart, C.D. 2016. Why is the *Phytopthora* blight from important? New York State Ag Experiment Station Task Force, October 10, 2016.

Smart, C.D. 2016. Field walk and discussion of diseases of cucurbits and other crops. Western NY Field Days. Portland, NY, Aug 31, 2016.

Smart, C.D. 2016. Vegetable disease management (1.5 hour discussion with growers and educators). Willsboro, NY, Aug 4, 20116

Smart, C.D. 2016. Vegetable disease management (1.5 hour discussion with growers and educators). Canton, NY, Aug 3, 2016.

Smart, C.D. 2016. How the NY Farm Bureau helped established the *Phytophthora* blight farm. Midwest Farm Bureau visit to NYSAES, June 24, 2016.

Smart, C. and Lange, H. 2016. *Vine Crop Update 2015.* Proceedings of the 2016 Empire State Producers Expo, Syracuse, NY.

Starke, K.D. and J.R. Schultheis. 2016. Watermelon (*Citrullus lanatus*) yield and quality response to grafted versus non-grafted plants, 2016. Watermelon Research Group, Mobile, AL. February 2017.

VandenLangenberg K, Wehner T. 2015. High resistance over the production season to the new downy mildew in cucumber. PPI Annual Meeting (October 30, 2015, Fort Worth, TX)

Wallace E. C. and Quesada-Ocampo L. M. 2015. Controlling downy mildew in cucumber. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, Dec.

Weng, Y. 2015. QTL Mapping for downy mildew resistance in WI7120 cucumber. PPI Annual Meeting (October 30, 2015, Fort Worth, TX)

Wang Y, Haider KR, Weng Y. 2016. Pyramiding Downy Mildew Resistance Genes into Elite US Processing Cucumber with Marker-assisted Selection. Pickling Cucumber Commodity Meeting, Grand Rapids

Wechter, W. P., S.E. Branham, S. Lambel, N. Guner, and A. Levi. 2017. Towards the identification of quantitative trait loci and development of molecular markers linked to Fusarium wilt resistance in watermelon. Presented at the Watermelon Research and Development Group meeting. Mobile, AL. February 2017.

SCIENTIFIC CONFERENCES and UNIVERSITY PRESENTATIONS

Alzohairy, S., and Hausbeck, M. 2015. Transcriptomic profiling of *Cucurbita* species to characterize the age-related resistance against *Phytophthora capsici*. Page 19 in: Proceedings of the 1st International Soilborne Oomycete Conference, Duck Key, FL, 8-10 Dec. Abstract.

Daley, J., S. Branham, A. Levi, R. Hassell, and P. Wechter. 2017. Mapping resistance to Alternaria cucumerina in muskmelon. Plant & Animal Genome XXV ConferenCe. https://pag.confex.com/pag/xxv/meetingapp.cgi/Paper/25467

Fei, Z. 2016. Genome sequencing provide insights into watermelon evolution, domestication and important agronomic traits. Dept. of Plant Biology, Cornell University. March

Fei, Z. 2016. Genome sequencing provide insights into watermelon evolution, domestication and important agronomic traits. College of Horticulture, Shandong Agric. Univ. April

Fei, Z. 2016. Genome sequencing provide insights into watermelon evolution, domestication and important agronomic traits. College of Food Science and Engineering, Hefei University of Technology. May

Fei, Z. 2016. Genome sequencing provide insights into watermelon evolution, domestication and important agronomic traits. Texas A&M University. September, 2016

Fei, Z. 2016. Genome sequencing of sweetpotato wild progenitors. Institute of Vegetables and Flowers, CAAS. April, 2016

Fei, Z. 2016. Genome sequencing provide insights into watermelon evolution, domestication and important agronomic traits. Nanjing Agricultural University. July, 2016

Fei, Z. 2017. Genome variation elucidates evolution and domestication of fruit ripening and quality traits in watermelon. PAG. January, 2017

Grumet, R. 2016. Introduction to CucCAP - developing genomic resources for the cucurbit community. Plant and Animal Genome Conference. San Diego, CA. https://pag.confex.com/pag/xxiv/webprogram/Paper18951.html

Hausbeck, M. 2015. Rots and blights of vegetables. Pages 71-79 in: Proceedings of the Lower Mainland Horticultural Improvement Association/Pacific Agriculture Show Horticultural Growers' Short Course,

Kousik, C.S. and Ikerd, J.L. 2015. Reaction of Phytophthora fruit rot resistant germplasm lines to a broad range of *Phytophthora capsici* isolates from across United States of America. International soilborne Oomycete conference, Duck Key, FL. December

Kousik, C.S. 2016. Breeding rootstocks of cucurbit vegetable crops for resistance to biotic and abiotic stress. (Invited presentation). Platinum Jubilee Celebrations, Indian Horticultural Congress. November 15, 2016. (>300 attendees at the talk).

Kousik C.S., Egel D., Ji P., and Quesada-Ocampo L. M. (2016) Fungicide rotation schemes and Melcast for managing Phytophthora fruit rot of watermelon in Southeastern United States. Phytopathology. 106: S4.68.

Kousik, C.S., Ikerd, J.L., and Mandal, M.K. 2016. Breadth of resistance of Phytophthora fruit rot resistant watermelon germplasm to *Phytophthora capsici* isolates from across United States of America. Phytopathology S4.40 (Abstract)

Kousik, C.S. Pingsheng Ji and Quesada-Ocampo, L.M. 2015. Fungicide rotation schemes for managing Phytophthora fruit rot of watermelon across Southeastern United States (NC, SC, GA). International soilborne Oomycete conference, Duck Key, FL. December

Krasnow, C., and Hausbeck, M. 2015. Using directed fungicide applications to manage Phytophthora fruit rot of processing squash. Page 23 in: Proceedings of the 1st International Soilborne Oomycete Conference, Duck Key, FL, 8-10 Dec. Abstract.

Mandal, M.K., Ikerd, J.L., Soorni, A. and Kousik, C.S. 2016. Molecular dissection of resistance signaling in watermelon fruit through transcriptomic approach. Phytopathology S4.153 (Abstract)

Mansfeld B, Colle M, Grumet R. 2017. Genome-wide SNP discovery and identification of age-related resistance loci in cucumber by QTL-seq. PAG XXVI, San Diego CA.

Mazourek M, Holdsworth WL, Hernandez C, LaPlant KE. 2016. Making up for lost time in Cucurbita molecular breeding. Plant and Animal Genome Conference. San Diego, CA.

McCreight, J.D., W.M. Wintermantel, and E.T. Natwick. 2015. Evaluations of melon germplasm reported to exhibit host plant resistance to sweetpotato whitefly. Entomological Society of America, Annual Meeting, Minneapolis, MN, Nov. abstract

McCreight, J.D., W.M. Wintermantel, and E.T. Natwick. 2016. Expression of Host Plant Resistance in Melon to Sweetpotato Whitefly in the Desert Southwest United States. XXV International Congress of Entomology, Orlando, FL, Sep. abstract

Miller N. F. and Quesada-Ocampo L. M. (2016) Evaluation of fungicides for management of Fusarium wilt of watermelon. Phytopathology. 106:S4.2

Miranda-Vélez, M, L. Wessel-Beaver, Jose C. Verle-Rodrigues and W. Seda-Martínez. 2016. Effect of leaf position on the assessment of resistance to *Papaya ringspot virus* and *Zucchini yellow mosaic virus* in tropical pumpkin. Proceedings of the 41st meeting of the Sociedad Puertorriqueña de Ciencias Agrícolas, November 18, 2016, Corozal, Puerto Rico. p. 57. (abstract)

Noel N. and Quesada-Ocampo L. M. (2016) Fungicide resistance and host susceptibility of *Colletotrichum orbiculare* infecting cucurbit crops in North Carolina. Phytopathology. 106:S4.36

Rahman A. and Quesada-Ocampo L. M. (2016) Early detection and quantification of *Pseudoperonospora cubensis* airborne sporangia using real-time PCR. Phytopathology. 106:S4.16

Schultheis, J.R. and W.B. Thompson. 2016. Watermelon cultivar yield and quality trial results, North Carolina, 2015. HortScience. 51(9):S37

Schultheis, J.R. and W.B. Thompson. 2016. Watermelon yield and fruit size response to grafted versus non- grafted transplants in plasticulture and bare ground production systems. HortScience. 51(9):S38

Smart, C.D. A tale of two *Phytophthora*: life with and without sex. Michigan State University, East Lansing, MI, March 2, 2017.

Smart, C.D. Multiplex detection for vegetable diseases. National Plant Diagnostic Network National meeting. Crystal City, VA, March 10, 2016.

Starke, K.D., B. Thompson, C. Jiang, and J. Schultheis. Planting density influences mini-watermelon yield and quality. 2016. VII International Symposium on Seed, Transplant and Stand Establishment of Horticultural Crops, Pretoria, South Africa, September 2016.

Wallace E. C. and Quesada-Ocampo L. M. (2016) *Pseudoperonospora cubensis* on commercial and non-commercial cucurbits in North Carolina: population structure determine by simple sequence repeats (SSRs). Phytopathology. 106:S4.12

Wallace E. C. and Quesada-Ocampo L. M. 2016. Genetic structure of *Pseudoperonospora cubensis* populations infecting commercial and non-commercial cucurbits in North Carolina. XIth Eucarpia Cucurbitaceae Proceedings

Wintermantel WM, J.D. McCreight, and E.T. Natwick. 2016. Epidemiology of Cucurbit yellow stunting disorder virus (CYSDV) and associated whitefly-transmitted viruses in the US Southwest and

development of CYSDV resistant melon. Paper presentation at 2nd International Whitefly Symposium, February 14-19, Arusha, Tanzania.

Wintermantel WM, J.D. McCreight, and E.T. Natwick. 2016. Reservoir hosts of Cucurbit yellow stunting disorder virus and development of resistant melon. 13th International Plant Virus Epidemiology Symposium. Avignon, France, June 6-10, 2016.