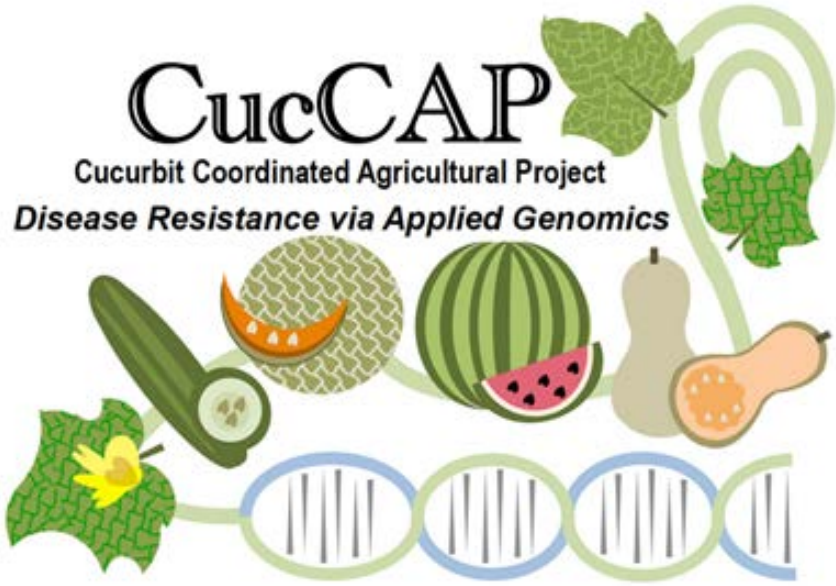
CucCAP:

Leveraging applied genomics to improve disease resistance in cucurbit crops



Third Annual CucCAP Team Meeting

April 4-5, 2018

Raleigh NC

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AGENDA

and

PARTICPANTS

AGENDA

Third annual CucCAP team meeting – April 4-5, 2018

Wednesday, April 4

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, videotaping (Grumet)

Session I – Genomic Tools

Objective I: 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 genomics and bioinformatics workshops

8:45-9:15 Overview of progress: bioinformatics platforms, website and workshops, GBS data and analysis
Fei, Reddy

9:15-10:00 Analysis of germplasm diversity, selection of functional panels
watermelon (Reddy, Levi)
melon (McCreight, Ando)
cucumber (Weng)
squash (Mazourek)

10:00-10:30 Discussion and Feedback from industry

10:30-10:45 Break

10:45-11:00 Cucurbitaceae 2018 – CucCAP meeting also? Travel grants, CucCAP branding
McCreight, Grumet

Session II – Breeding for disease resistance

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

11:00-12:00 Watermelon team report, questions, discussion
Levi, Kousik, Ling, McGregor, Wechter, Wehner,

12:00-1:00 Lunch
Watermelon team meeting – functional panel discussion
(other team meetings if desired)

1:00-1:45 Melon team report, questions, discussion
McCreight, Kousik, Wechter, Wintermantel

1:45-2:15 Cucumber team report, questions, discussion
Weng, Grumet, Wehner

2:15-2:45 Squash team report, questions, discussion
Mazourek, Wessel-Beaver, Smart

2:45-3:00 Break

Session III – Economic impact and disease control information

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

3:00-3:30 Socioeconomics team report, questions, discussion
Palma, Rivera

3:30-4:30 Extension team report, questions, discussion
Schulthies, Hausbeck, Linares, Quesada, Smart, Lorscheider

4:30-5:00 Discussion and feedback from industry

5:00-6:00 Working session I: Germplasm vulnerability (McCreight, Mazourek, leads)
Report from curators - status, needs of collections; potential interface with functional panels
Labate, Reitsma
Planning for vulnerability statement; timeline, questions for survey
McCreight, Mazourek

6:00 CucCAP Networking Dinner

Thursday, April 5

8:00-8:15 Arrive

8:15-9:15 Working session II: discussion of strategy moving forward
A. GBS and functional panels (Fei, lead)
publication, release of data, re-sequencing of panels, GWAS
providing germplasm supply (possible assistance from industry, PI stations)
B. Cucurbit disease resources, extension plans and industry needs (Quesada, lead)
What resources are needed

9:15-10:15 Working session III: Websites
A. Cucurbit genomics website (Fei, lead)
Feedback on tools and interfaces; suggestions for future tool development
B. CucCAP website (Lorscheider, lead)
Feedback on functionality, content, suggestions for improvement

10:15-10:30 Break

10:30-11:15 CucCAP II? Should we consider? Priorities? Strategies?
(phenotyping, germplasm supply, GWAS, SNP arrays, diseases (which), other traits)

11:15-12:00 Wrap up discussions, feedback from advisory board and external reviewers

CucCAP Team

Project Director

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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/Peter Kraan	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/ Nihat Guner	Director of Research, Vegetables, Sakata Seed
Syngenta Seeds Inc.	Matt Kinkade/Sandhu Ajay	Global Cucurbits Co-Lead, Syngenta Seeds
United Genetics Seeds Co.	Xuemei Zhang	Melon Breeder, United Genetic Seeds

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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)

(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 Facilty, we have set up the genotyping-by-sequencing (GBS) platform for the cucurbit species.

1.1.2. Sequence data processing/analysis

We have established a GBS data analysis pipeline based on TASSEL-GBS (http://www.maizegenetics.net/tassel).

1.1.3. ICuGI database development

We have re-implemented the ICuGI database (now named Cucurbit Genomics Database, and the new URL: http://cucurbitgenomics.org/) using the GMOD Tripal system (http://gmod.org/wiki/Tripal) and the Chado database schema (http://gmod.org/wiki/Chado). The newly designed and developed database was released in May 2017. Genome sequences of melon, watermelon Charleston Gray, cucumber Gy14, wild cucumber (*Cucumis sativus* var. *hardwickii* PI 183967), three *Cucurbita* species (*C. pepo*, *C. maxima*, *C. moschata*) and bottle gourd have been processed and added in the new database, besides those already in the previous database.

Genome syntenies between any two of the sequenced cucurbits have been identified and a synteny viewer have been implemented in the database. An "expression" module has been developed in the database using RNA-Seq datasets publicly available for cucurbit species, mainly collected from NCBI Sequence Read Archive (SRA). A set of tools to mine and analyze the RNA-Seq datasets, such as heatmap view of expression profiles and differential gene expression analysis, were implemented. The synteny viewer and the expression module have been packed as Tripal extension modules which can be implemented in other genomic databases developed using the Tripal system. We are currently working on developing a module for analyses of small RNA (sRNA) datasets. Development of tools and interfaces to analyze and integrate genotype and phenotype data are planned.

1.1.4 Community standardized nomenclature.
This has not begun.

1.1.5. Genomic, bioinformatics workshops
A workshop on the Cucurbit Genomics Database was held at the Solcuc2017 meeting in Sept. 2017 at Valencia, Spain. We are currently working with the BTI communication team to prepare a webinar on how to use the database. The video will be put on the database website.

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
We have finished GBS for all cucumber, melon, watermelon, *Cucurbita pepo* and *C. moschata* accessions collected from the USDA National Plant Germplasm System. Four 96-well plates of *C. maxima* samples were submitted to Cornell GBS facility in early March, 2018 and are currently under processing (Table 1). After removing accessions with insufficient reads and merging duplicated accessions, a total of 1,564 cucumber, 2,077 melon, 1,365 watermelon, 829 *C. pepo* and 191 *C. moschata* accessions have been genotyped. We have finished processing the GBS data and SNP calling for cucumber, melon and watermelon, while GBS data analysis for *C. pepo* and *C. moschata* is underway.

Table 1 Status of cucurbit GBS (March 13, 2018)

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	3/16/2017
10	3,10,17,46	384	cucumber	1/20/2017 & 2/2/2017	5/31/2017
11	50,51,52,53	384	melon	2/14/2017	5/5/2017
12	54,55,56,57	384	melon	2/22/2017	5/5/2017
13	58,59,60,61	384	melon	3/2/2017	5/5/2017

14	62,63,64,65	384	melon	3/16/2017	5/5/2017
15	66,67,68,69	384	melon	3/23/2017	5/5/2017
16	21,32,33,70	384	melon&watermelon	3/23/2017	5/31/2017
17	71,72,73,74	384	melon&squash	4/19/2017	6/13/2017
18	75,76,77,78	384	squash	5/31/2017	7/11/2017
19	22,23,79,80	384	squash	8/18/2017	9/25/2017
20	18,19,28,29	384	cucumber&melon	1/24/2018	3/5/2018
21	90	96	watermelon	2/8/2018	3/5/2018
22	91	96	watermelon	2/8/2018	3/5/2018
23	92	96	watermelon	2/8/2018	3/5/2018
24	93	96	watermelon	2/8/2018	3/5/2018
25	94	96	watermelon	2/8/2018	3/5/2018
26	81,82,83,84	384	C. maxima	3/1/2018	

Note: Those in yellow background are samples from mapping populations.

We obtained a total of 1.57, 1.71 and 0.88 billion GBS reads with expected barcodes for cucumber, melon and watermelon, respectively. From these reads, a total of 76,860,960, 54,192,089 and 34,621,369 unique tags were obtained, and 593,678, 743,545 and 388,298 tags with at least 10 reads were used for SNP calling for cucumber, melon and watermelon, respectively. A total of 113,854, 89,204 and 61,520 SNPs were called in cucumber, melon and watermelon, respectively, and 24,319, 27,835 and 25,739 SNPs were obtained by applying criteria of missing data rate < 0.5 and minor allele frequency (MAF) > 0.01.

A core collection selection strategy has been developed. Briefly, a total of ~400 accessions will be selected for each species. Around 300 accessions which represent the majority of the genetic diversity of the germplasm, based on the core collection analysis using GenoCore (Jeong et al., 2017, PLoS ONE 12:e0181420), will be selected. Another ~100 accessions with interesting traits and/or parents of mapping/breed populations will be selected. In the final core collection, if a selected line is known to be derived from a PI accession that is also in the final core collection, then the corresponding PI should be replaced with the most closely related one on the phylogenetic tree. Accessions in the final core collection whose genomes have already been resequenced should also be replaced by the most closely related ones on the phylogenetic tree, unless they harbor very interesting/important traits. Based on this strategy, a core collection of melon has been established, which contains 384 accessions. The melon core collection captures 98.96% of all allelic

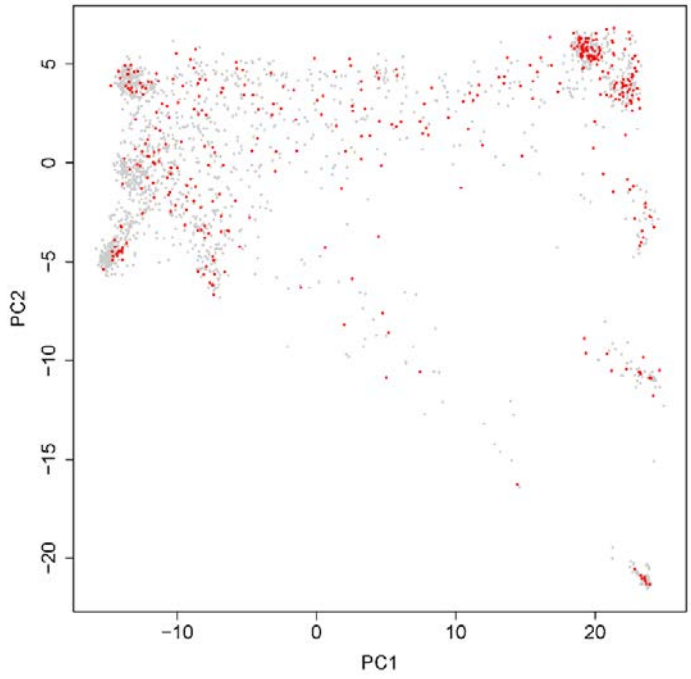


Figure 1. Principal component analysis of the melon core collection (red) and the entire collection (gray)

diversity in the melon germplasm we have genotyped. Principal component analysis (PCA) of the melon core collection showed similar pattern to that of the entire collection (Figure 1). Core collection section is currently underway for cucumber and watermelon.

1.2.2. Population genomics and GWAS analyses

Using SNPs called from the GBS data, we have performed population genomic analyses for cucumber, watermelon and melon accessions. Phylogenetic, PCA and population structure analyses have been done for accessions of cucumber, watermelon and melon. The results from these analyses for cucumber accessions are shown in Figure 2 as an example. Linkage disequilibrium (LD) decay patterns and population differentiation have also been investigated for these species.

We have collected historical phenotype data from the USDA National Plant Germplasm System for cucumber, watermelon and melon accessions. GWAS have been performed to identify SNPs and regions that are significantly associated with important agronomic traits. GWAS for cucumber anthracnose resistance is shown in Figure 3 as an example.

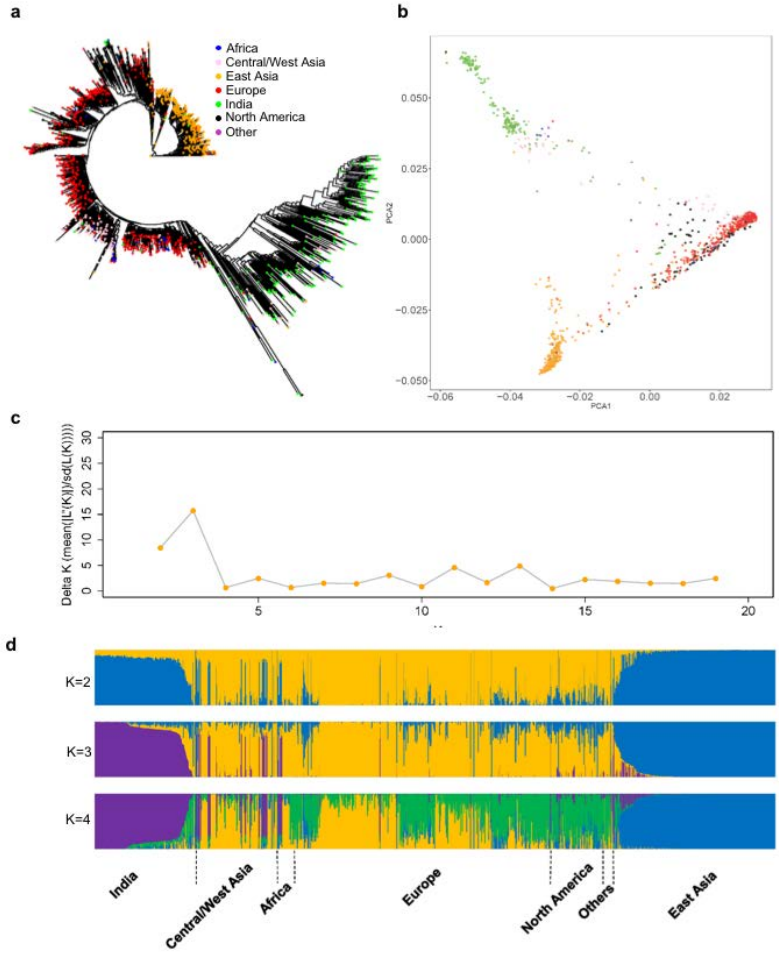


Figure 2. Phylogenetic and population genomic analyses of cucumber accessions. Unrooted neighbor-joining phylogenetic tree (a), principal component analysis (b) and population structure analysis (c and d) of cucumber accessions.

Manuscripts reporting the results from population genomics and GWAS analyses as well as core collection development are in preparation for watermelon, melon and cucumber. Analysis of the GBS data for *Cucurbita* species is underway.

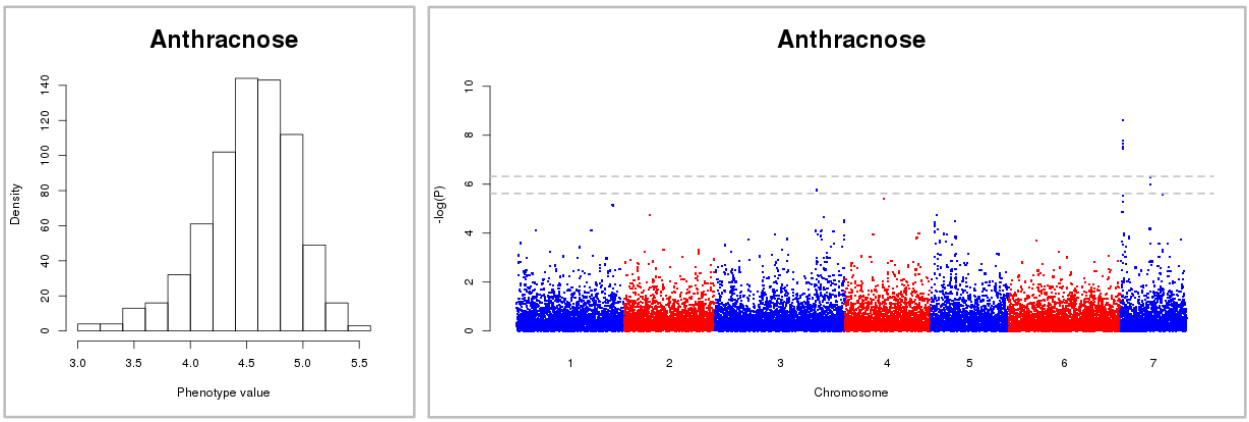


Figure 3. Frequency distribution of the anthracnose resistance trait (left) and Manhattan plot of GWAS result for anthracnose resistance in cucumber (right).

1.2.3 Genomic resequencing of core collections

We have been trying to identify cost-effective services for Illumina genomic library construction to accommodate our budget for genome resequencing of the core collections. We have submitted 43 DNA samples to Cornell Genomic Diversity Facility, which charges $33 for each library (http://www.biotech.cornell.edu/brc/genomic-diversity-facility/price-list). Additional $30 would be charged for each library to determine its concentration. For our samples, three randomly selected libraries were processed for concentration determination.

The libraries were pooled into two pools (21 samples in one pool and 22 in the other pool), and sent to Novegene for sequencing on a HiSeq X platform. We obtained 96 Gb and 88 Gb for the two pools, respectively. However, after processing with Trimmomatic to remove low quality sequences, only 73.6% of the reads and 59.6% of the bases were left. In addition, large variations of sequencing output are observed among different libraries (Figure 4). We are currently seeking other possible commercial services for library construction, with a backup plan that libraries will be made in our own or collaborator's labs.

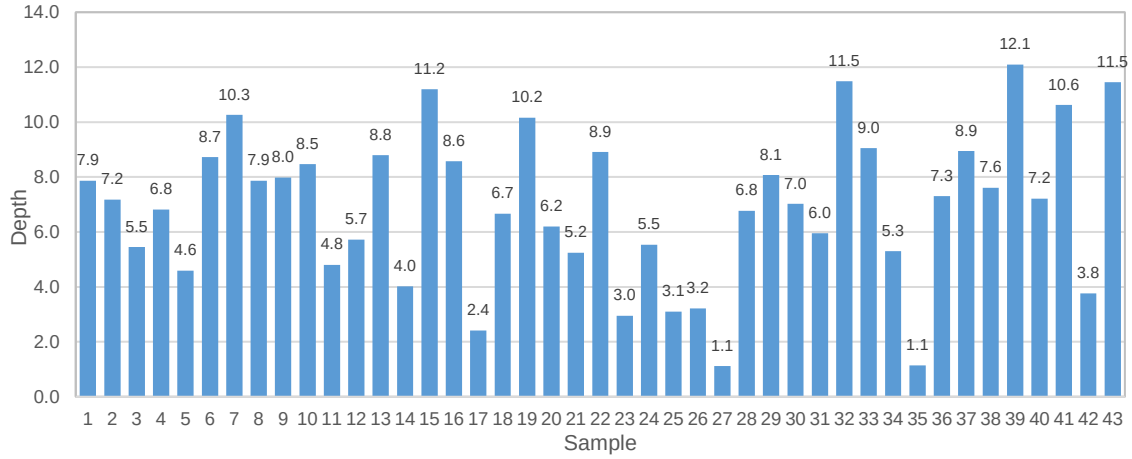


Figure 4. Depth of coverage for resequenced cucumber accessions.

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.

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: a) Evaluate a RIL population of watermelon (*Citrullus lanatus* × *C. amarus*) for resistance to gummy stem blight and fruit quality traits and b) Map GSB resistant genes through genome-wide association studies (GWAS).

Phenotyping: A watermelon GSB population was developed by intercrossing the most resistant accessions of *Citrullus* four times (I_4), followed by crossing with elite cultivars of watermelon (I_4F_1), followed by intercrossing without selection, while maintaining wild and elite types in the populations ($I_4F_1I_4$), followed by self-pollinations of plants at random ($I_4F_1I_4S_1$). The 300 RILs and 20 controls (10 PIs and 10 commercial

Figure 1. Greenhouse test for resistance to gummy stem blight

Figure 2. Gummy stem blight symptoms during the greenhouse test

cultivars) were evaluated for resistance to gummy stem blight in greenhouses at North Carolina State University in Raleigh, North Carolina (Figure 1 and 2), and in the field at the Horticultural Crops Research Station at Clinton, North Carolina (Figure 3). We inoculated plants with *S. cucurbitacearum* at a concentration of 5×10^5 spores/ml (Figure 4). To evaluate disease severity, we adopted an ordinal disease assessment scale (Gusmini et al. 2002). Plants were rated four times, in an experiment with, 2 locations, and 10 replications (at greenhouse and field). We also evaluated fruit quality in the gummy stem blight field trial. We also collected data of fruit shape, rind pattern and toughness, seed size and color, flesh color and intensity and hollow heart. We will identify RILs with high yield of excellent fruit quality.

Additionally, genomic DNA of gummy stem blight isolates collected from field outbreaks was extracted, and a PCR-based marker test for distinguishing the three morphologically identical, but genetically distinct species causing gummy stem blight was performed (Figure 4). We used three sets of primers, including *Db05* that produces a 216 to 224-bp fragment in all three species, *Db06* that produces a 283- to 289-bp in *S. citrulli* and a 268-bp and slightly fainter fragment in *S. cucurbitacearum*, and *Db01* that produces a 256- to 364-bp fragment in *S. citrulli* (Brewer et al. 2015). Two of the isolates were *S. cucurbitacearum* (syn. *Dydymella bryoniae*) and one isolate was *S. caricae*.

Genotyping: The 300 RILs will be planted in spring 2018, at greenhouses of NC State, to sample leaf tissue for DNA extraction. The DNA will be send for SNPs discovery through genotyping by sequencing (GBS) method at Cornell University. We expect to get several thousand of SNPs for the association analysis (GWAS).

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

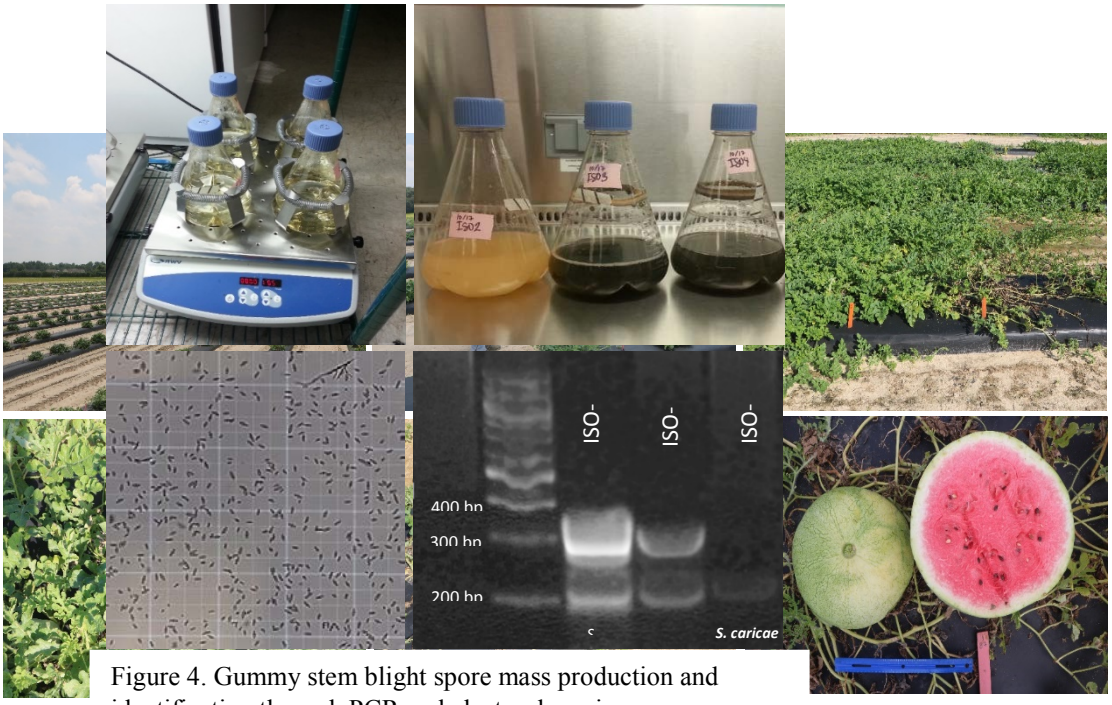


Figure 4. Gummy stem blight spore mass production and identification through PCR and electrophoresis

Figure 3. Field test for resistance to gummy stem blight


QTL Mapping, Marker Validation and Trait introgression of Gummy Stem Blight resistance in <u>Watermelon</u> *(<u>Cecilia McGregor and Winnie Gimode, University of Georgia, Athens, Georgia).</u>*

1.1 Population Development:

- WPop GSB1: PI 482276 x Crimson Sweet population of 225 $F_{2:3}$ lines. **Complete**
- Backcross population: WPop GSB 1BC: BCF_2 for PI 482276 x Crimson Sweet (recurrent) for trait introgression and marker validation. **In progress**
- WPop GSB2: PI 526233 x Sugar Baby population for 96 $F_{2:3}$ lines. **Complete** – This population will however not be phenotyped because the 'resistant' parent (PI 526233) has proven to be rather susceptible from the screens. This population has therefore been replaced with another population: WPop GSB2B: PI 189225 x Sugar Baby. **In progress**
- WPop GSB3: Backup population of resistant *C. amarus* (PI 482276) x susceptible *C. amarus*. **In progress**

1.2 Phenotyping

- GSB1 $F_{2:3}$ Population (6 plants x 225 lines = 1,350 plants) was phenotyped in walk-in growth chamber. Disease symptoms for each seedling were scored on a 0 – 5 scale. Parents and F1 and 4 other control genotypes were also included.
- All the parental lines and a subset (14 plants x 95 lines = 1330 plants) of the GSB1 population were also phenotyped in the field in Attapulgus (GA) in summer 2017. Natural infection was allowed to take place. The purpose of this was to compare field level resistance to what we observe in the growth chamber screens. A subset of the population was used due to space limitations at the field site.
- Generally, symptoms in the growth chamber screens were more severe than in the field. Correlation between the field and growth chamber screens was high for controls, but low for the population. We are screening more plants per line in the growth chamber for the population.

1.3 Genotyping

- At the 2016 meeting in East Lansing it was proposed that QTL-Seq could be used. Since we use QTL-Seq for other traits in our lab and had an extra spot for sequencing, we decided to include resistant and susceptible bulks (selected using growth chamber phenotypic data from 2 screens)

of WPop GSB 1 (PI 482276 x Crimson Sweet population). However, we did not detect any significant QTL.
- Genotyping-by-sequencing will be used for this population (WPop GSB1) and 2 plates of the WPop GSB1 have been sent to MSU for DNA extraction and quality checks and GBS at Cornell.

2. Goals for 2017-2018

- Complete phenotyping for GSB1, GSB2 in the growth chamber
- Field phenotyping for subset of GSB1 and parental lines
- Mapping of resistance to GSB for GSB1 population, KASP marker development.

Fusarium wilt races 1 and 2 resistance in watermelon (*Citrullus amarus*)
(Patrick Wechter, Sandra Branham, Melanie Katawczik, and Amnon Levi)

Fusarium oxysporum f. sp. *niveum* (Fon)*,* 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 race 2 of *Fon*.

Year 3 progress: 2.1.1; 2.2.1; 2.3.1

Development of Germplasm lines and Genetic Populations

- Seeds of *C. amarus* USVL246-FR2 and USVL252-FR2, both developed in our work, have been requested and disseminated to ten seed companies and numerous researchers for use in breeding programs and Fusarium studies.
- A recombinant inbred line (RIL) population has been generated from 225, single seed descent lines at the F_7-F_8 stage from a cross of *Fon* race 1 and 2 resistant *C. amarus* USVL246 by a susceptible *C. amarus* PI582114.
- Two reciprocal $F_{2:3}$ genetic populations USVL252-$_{FR2}$ x PI 244019-$_{S3}$; with resistance to both races of *Fon* and papaya ringspot virus (PRSV) have been developed. The first population includes 178 $F_{2:3}$ families, while the population derived from the reciprocal cross includes 220 $F_{2:3}$ families. These populations have been developed with the generous support of Sakata Seeds (Dr. Nihat Guner).

Genetic mapping of QTL associated with resistance to Fusarium wilt race 2

- DNA was isolated from 203 RIL families (USVL246 x PI582114) and 203 F_2:F_3 (USVL252 x PI 244019) and GBS sequencing was performed at Cornell University.
- Three rounds of *Fon* race 1 greenhouse inoculation / resistance assays were performed using the $F_{2:3}$ (USVL246 x PI582114) families.
- Two rounds of *Fon* race 2 greenhouse inoculation / resistance assays were performed using the $F_{2:3}$ (USVL252 x PI 244019), in separate experiments at the U.S. Vegetable Laboratory.

- Genotype and phenotype data have been analyzed and we have identified one major QTL for race 1 resistance on Chromosome 9, making this resistance unique from the currently available *Fon* race 1 resistance in *C. lanatus* and PI296341-FR.
- Genetic mapping with this population resulted in a saturated map with 2495 SNP markers.
- KASP analysis has begun on *Fon* race 2 and race 1 resistance QTL for better marker development.
- USVL252-FR2 and USVL246-FR2 have been crossed into Sugar Baby, Charleston Gray and Calhoun Gray.
- Backcrossing and selfing of the above into the recurrent parent have been performed.

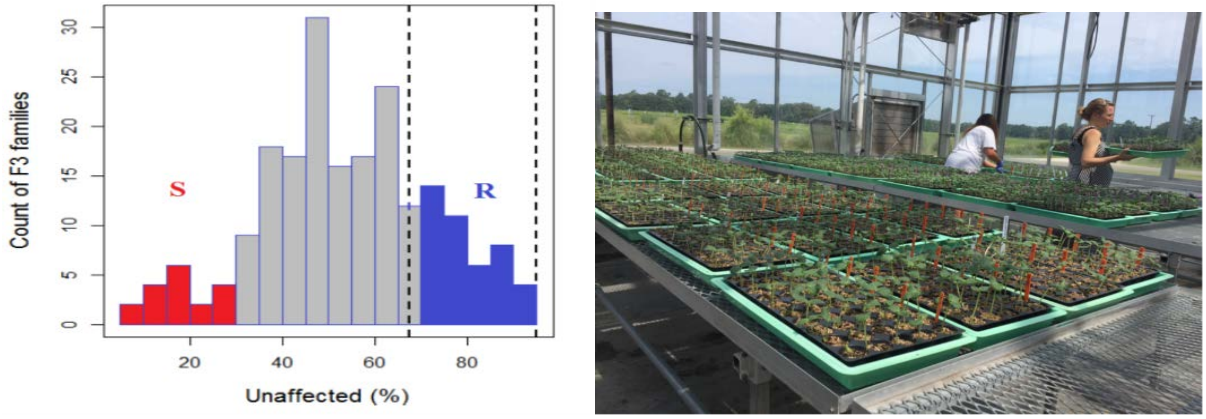


Figure 1. Distribution pattern of 220 $F_{2:3}$ families (USVL-252^{FR} x PI 244019-PRSV-R) for resistance to Fusarium wilt race 2 (left), following their evaluation in a greenhouse at the U.S. Vegetable Laboratory (right).

Converting QTL to SNP markers tightly linked to Fusarium wilt race 1 resistance in *C. lanatus*
(Sandra Branham, Patrick Wechter, Laura Massey, and Amnon Levi)

DNA of the resistant and susceptible parents and the F_2 plants of most resistant versus most susceptible $F_{2:3}$ families (Lambel et al. 2014) were submitted for whole genome resequencing. QTL-seq analysis of the bulks narrowed the known *Fon* race 1 resistance QTL interval on chromosome 1 of watermelon (Lambel et al. 2014). SNPs from the QTL were converted to Kompetitive Allele Specific PCR (KASP) primers and used to genotype the original $F_{2:3}$ population. A genetic map of these SNPs yielded several KASP markers tightly linked to *Fon* race 1 resistance (Figure 2). In collaboration with the HM.Clause team in Davis, California we will validate the KASP markers using advanced populations segregating for FW race 1 resistance. Also, we are testing 40 cultivars and PIs for *Fon* race 1 resistance and will use them to validate the KASP markers.

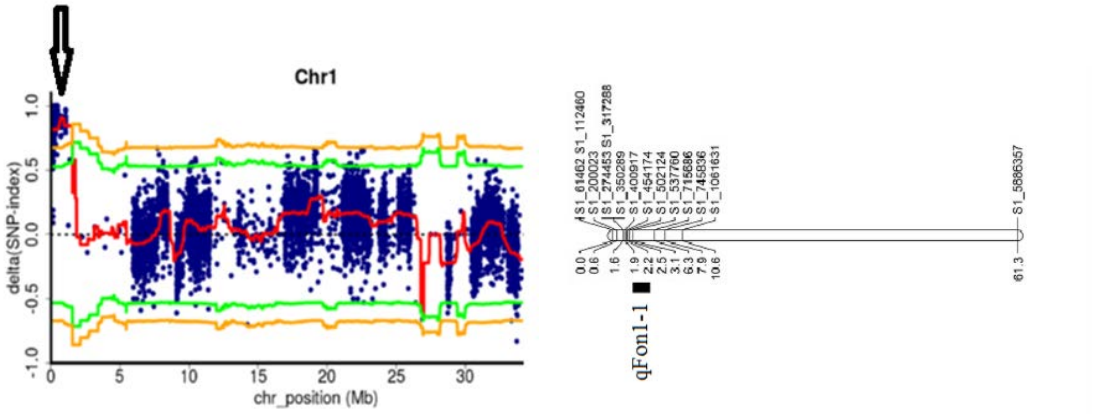


Figure 2. QTL-seq based on resequencing of resistant versus susceptible bulks identified SNPs tightly linked to Fusarium wilt race 1 and cover a small genomic region of 500 kb within a major QTL identified on Chromosome 1 (left) in *C. lanatus*. KASP markers tightly linked to Fusarium wilt race 1 resistance (qFon1-1) on chromosome 1 of watermelon (right). (Branham et al. unpublished data)

References:
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.

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

Branham, S.E., A. Levi, M.W. Farnham, 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.

Identifying QTL associated with Papaya ringspot virus (PRSV) resistance-
(*Amnon Levi and Kai-shu Ling, USDA, ARS, U.S. vegetable Laboratory (USVL), Charleston, SC*)

Several F_2 and BC_1 populations derived from the cross USVL-252^{FR} x PI 244019-PRSV-$R_{(S3)}$ were constructed with the help of Dr. Nihat Guner and team at Sakata Seeds. Two populations were evaluated for PRSV-resistance and soon be analyzed using GBS procedure for identification of QTL associated with the resistance.

What do you plan to do during the next reporting period to accomplish the goals?
-Complete GBS and QTL analysis of population segregating for FW race 2 resistance (Levi and Wechter).
-Complete validation of KASP markers tightly linked to FW race 1 resistance (Levi and Wechter).
-complete analysis of PRSV-resistance F2 and BC1 populations and identify QTL associated with resistance (Levi and Ling).

Powdery mildew of watermelon (*Shaker Kousik, Mihir Mandel and Jennifer*)

Powdery mildew (PM, *Podosphaera xanthii*) 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.A. We have developed USVL531-MDR which is resistant to powdery mildew and Phytophthora fruit rot and have provided the seeds of this germplasm lines recently to two seed companies (Voloagri and Syngenta) through a Materials transfer agreement (MTA). 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 F_2 plants for analysis. We will send out the 20 most susceptible and 20 most resistant F_2 lines and the parents for QTL-seq analysis.

Segregating populations (F_1, F_2, BCF_{1R}, BCF_{1S}) from cross of USVL003-MDR and USVL677-PMS were developed in 2016-2017. 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 PM will be conducted in 2018. Since resistance to Phytophthora fruit rot is complex we are developing recombinant inbred lines (RIL) of the cross between USVL531-MDR and USVL677-PMS.

Advancing Powdery mildew resistant inbred lines.
Fruit from F_2 plants from a cross of USVL531-MDR and USVL677-PMS with powdery mildew resistance, uniform red flesh and decent brix (>7) were collected and have been advanced till F_5 and further advancement to F_6 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. We completed assessment of fruit quality from F_4 and F_5 progenies that were homozygous for resistance to PM. We grew 6 lines from F_5 to obtain fruit and move to F_6 for further screening and advancement.

Release of pink to red fleshed powdery mildew resistant lines with broad resistance to isolates from across U.S.A.
We have developed and released four PM resistant lines with broad resistance to *P. xanthii* isolates from across the U.S.A. These lines: USVL608-PMR (powdery mildew resistant), USVL255-PMR, USVL313-PMR, and USVL585-PMR are watermelon (*Citrullus lanatus* var. *lanatus* (Thunb.) Matsum. & Nakai) germplasm lines that exhibit high levels of resistance to powdery mildew (PM) caused by *Podosphaera xanthii* (Castagne) U. Braun & Shishkoff (syn. *Sphaerotheca fuliginea*). Specifically, the hypocotyls, cotyledons and true leaves of these four PMR lines are highly resistant to powdery mildew compared to the susceptible watermelon line USVL677-PMS or cultivar 'Mickey Lee' on which severe powdery mildew and abundant development of conidia can be observed (Figure 1). The true leaves of these four PMR lines were also resistant to *P. xanthii* isolates from other states including; CA, FL, GA, NY, and SC. Each of these four PMR lines are uniform for various growth characteristics including, fruit size, shape and color with red to pink flesh (Figure 2) and brix content ranging from 6 to 8. Currently, commercial watermelon cultivars with powdery mildew resistance are rare. Hence, USVL608-PMR, USVL255-PMR, USVL313-PMR, and USVL585-PMR will be useful sources for incorporating resistance in commercially acceptable cultivars. These lines are fertile and can easily be crossed with commercial watermelon cultivars to develop new breeding populations.

We have also completed making crosses with these powdery mildew resistant lines (USVL608-PMR, USVL313-PMR, USVL585-PMR and USVL225-PMR) with USVL677-PMS and 'Dixie Lee' to develop populations for conducting inheritance studies in 2018 and developing resistant inbred lines with high

fruit quality. We have also completed collecting fruit quality on the four PM resistant lines at two locations (Charleston, SC and Fort Pierce, FL). We have also completed collecting PM resistance data in summer and fall of 2017 on these four PM resistant lines. A paper documenting the release of these four PM resistant watermelon lines was submitted for publication to HortScience in February 2018.

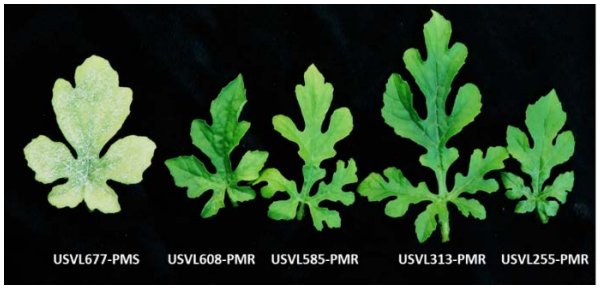


Figure 1. Reaction of powdery mildew resistant (PMR) lines (USVL608-PMR, USVL585-PMR, USVL313-PMR, USVL255-PMR) to *Podosphaera xanthii* isolate from Florida compared to susceptible line USVL677-PMS.

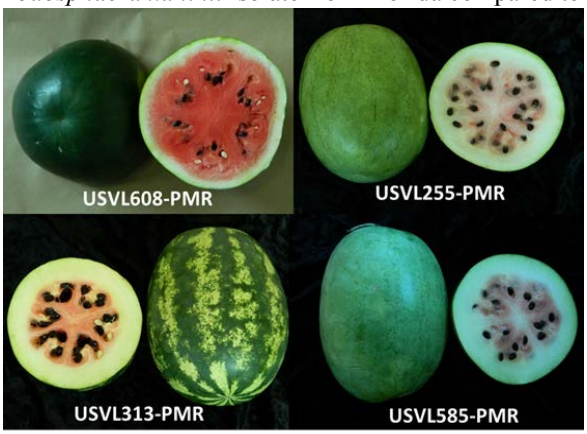


Figure 2. Fruit characteristics of USVL developed powdery mildew resistant (PMR) watermelon (*Citrullus lanatus* var. *lanatus*) germplasm lines USVL608-PMR, USVL255-PMR, USVL313-PMR and USVL585-PMR. USVL608-PMR has deep red flesh.

Whole genome resequencing of USVL531-MDR (PM resistant) and USVL677-PMS (PM susceptible) watermelon lines.

To identify SNPs between PM resistant and susceptible watermelon lines with either resistant (red flesh / white flesh) or susceptible (red fleshed) to powdery mildew (PM) pathogen *Podosphaera xanthii*, we resequenced three watermelon PI lines: USVL531-PMR (derived from PI 494531, white flesh), USVL608-PMR (PI 307608, red flesh) and USVL677-PMS (PI 269677, red flesh). Based on preliminary analysis we have identified 1176825 SNPs among the resistant and susceptible watermelon lines. Most of the sequenced reads mapped to the draft watermelon (*Citrullus lanatus*, 97103) genome sequence. Currently we are pursuing comparative analysis of our SNPs data with SNPs obtained from twenty already resequenced watermelon cultivar/PIs that have differential response to PM infection to identify candidate markers for PM resistance to be utilized for molecular breeding. In addition, the whole genome resequencing of the PM resistant and susceptible lines will help in analysis of transcriptome profiling data that we have generated using RNAseq during PM and resistant or susceptible host interactions.

Transcriptomic profiling of watermelon-powdery mildew (*Podosphaera xanthii*) resistant and susceptible interactions.

To gain a better understanding of the innate and activated molecular defense mechanisms involved during compatible (susceptible) and incompatible (resistant) powdery mildew-watermelon interactions, we conducted RNA-seq analysis.

The PM susceptible (USVL677-PMS) and resistant (USVL531-PMR) watermelon plants were inoculated with 10^5 conidia^{-ml} of *P.xanthii*. Symptom development was observed every day. In addition, leaf samples were collected for microscopy and for RNA extraction. RNA-seq profiling was done on leaf samples collected at 0, 1, 3, and 8 days post inoculation (DPI). The compatible interactions resulted in distinct plant gene activation (>2 fold unique transcripts, 335:191:1762 :: 1:3:8 DPI) as compared to incompatible interaction (>2 fold unique transcripts, 314:681:487 :: 1:3:8 DPI). Compatible interactions mostly involved pathogenesis events including carbohydrate metabolism, ethylene signaling and activation of stress responsive transcripts. Incompatible interaction results in activation of both TIR and CC-NBS-LRR mediated signaling events including induced transcripts of shikimate kinase, receptor kinase, ankyrin repeat containing protein and RIN4 like protein within 24 hr of PM infection. A detailed study on NBS-LRR genes activated during watermelon-PM interaction is under progress. A manuscript is in preparation and a poster of the study was presented at the American Phytopathological Society meeting in August 2017.

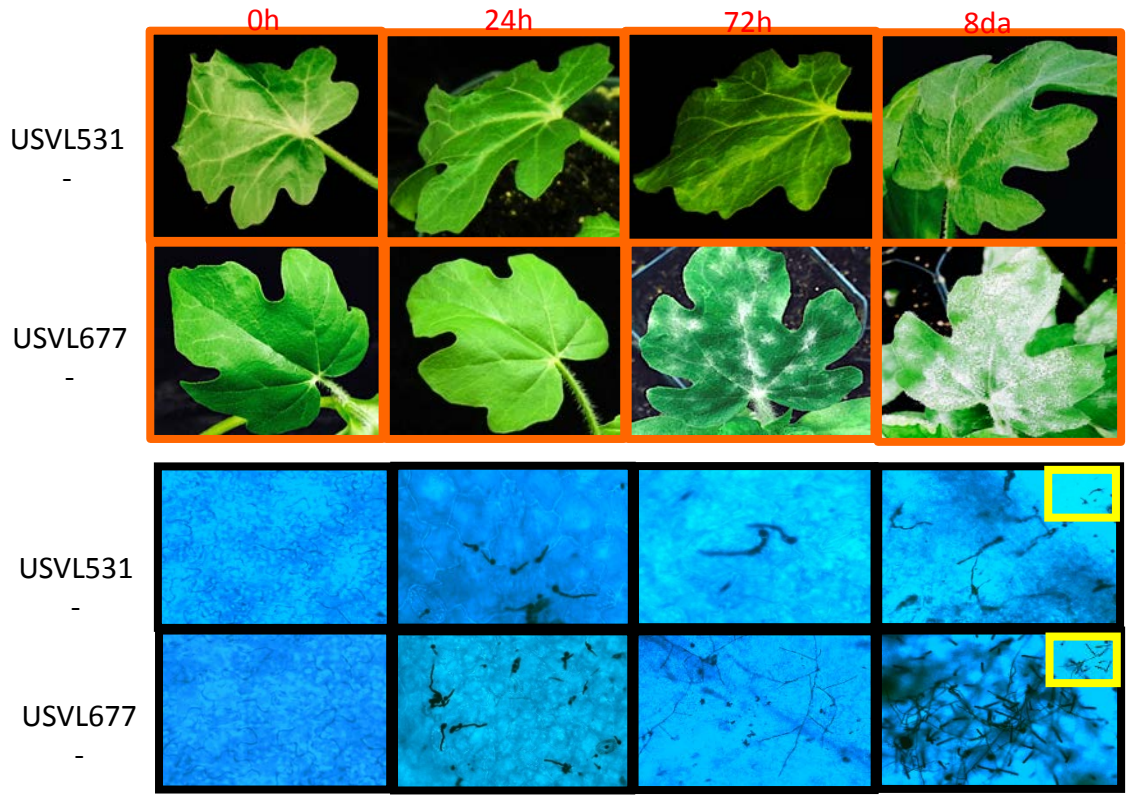


Figure 1. Time course of powdery mildew (PM) infection process in watermelon resistant (USVL531-MDR) and susceptible (USVL677-PMS) true leaves. PM conidia do germinate on leaves of the resistant line USVL531-MDR, however they do not develop rapidly or cause significant infection compared to the susceptible line USVL677-PMS where development of conidia can be observed by 8 days after inoculation. (Mandal et al. unpublished data).

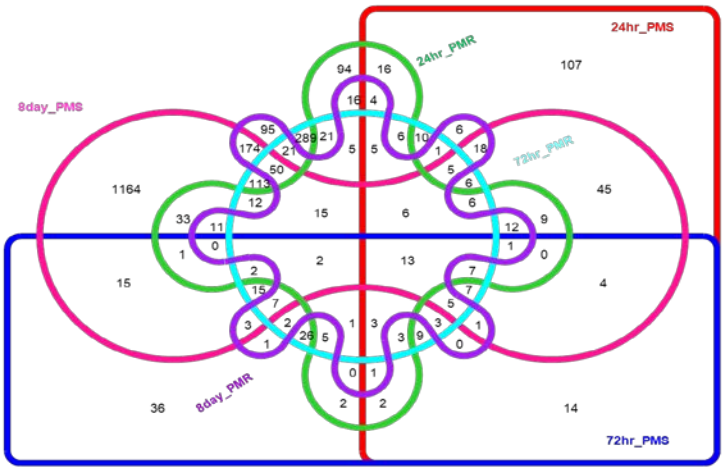


Figure 4. Venn diagram representing unique and overlapping differentially expressed genes (DEGs) in resistant (USVL531-PMR) and susceptible (USVL677-PMS) watermelon lines at 24hr, 72hr and 8 days post inoculation with *P. xanthii* conidia. (Mandal et al. unpublished data).

Additional research on powdery mildew as an offshoot of the CuCAP research

We hired a post-doctoral associate, Dr. Mihir Mandal through ORISE to help us with the molecular work on CuCAP project. Dr. Mandal has conducted the research on transcriptomic profiling and whole genome resequencing of the resistant and susceptible lines. During the process of our research on the CuCAP objectives on PM susceptible (USVL677-PMS) and resistant (USVL531-MDR) lines, we identified that melatonin could play a role in plant defense. To further study this we conducted additional research and the abstract of a manuscript that was recently submitted and is acceptable for publication (upon revisions) in *Journal of Pineal Research* and some additional details are presented below.

Since the 1950s, research on the animal neurohormone melatonin, has focused on its multi-regulatory effect on patients suffering from insomnia, cancer, and Alzheimer's. Previous studies on melatonin in plants have focused primarily on plant growth and development. However, studies on the physiological function of melatonin in host-pathogen defense mechanism are lacking. This study provides insight on the predicted biosynthetic pathway of melatonin in watermelon (*Citrullus lanatus*) and how application of melatonin, an environmental-friendly immune inducer, can boost plant immunity and suppress pathogen growth where fungicide resistance and lack of genetic resistance are major problems. We evaluated the effect of spray-applied melatonin and also transformed watermelon plants with the melatonin biosynthetic gene SNAT to determine the role of melatonin in plant defense. Increased melatonin levels in plants were found to boost resistance against the foliar pathogen *Podosphaera xanthii* (powdery mildew), and the soilborne oomycete *Phythophthora capsici* in watermelon and other cucurbits. Further, transcriptomic data on melatonin sprayed (1mM) watermelon leaves, suggests that melatonin alters the expression of genes involved in both PAMP and ETI mediated defenses. Twenty seven upregulated genes were associated with constitutive defense as well as initial priming of the melatonin induced plant resistance response. Our results indicate that developing strategies to increase melatonin levels in specialty crops such as watermelon can lead to resistance against diverse filamentous pathogens.

Phytophthora fruit rot of watermelon (*Shaker Kousik; USDA, ARS, U.S. vegetable Laboratory*)

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). The National Watermelon Association considered Phytophthora fruit rot its top research priority in 2017 as well. 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. However, based on this study it was difficult to assess the number of genes controlling resistance and hence we are in the process of developing a recombinant inbred line (RIL) population and are currently at the F_7 stage.

We completed growing out the F_3 families in summer-fall of 2018 (total 40 families, about 600 plants) and screened them for Phytophthora fruit rot. The data is being analyzed.

We have extracted DNA from parents and F_2 plants for GBS. However, since resistance to powdery mildew is a dominant trait we will pool the DNA from 20 most susceptible lines and 20 most resistant lines and send it out for sequencing. We will perform QTLseq analysis on the resulting data.

We will phenotype the populations from USVL003-MDR x USVL677-PMS for resistance to powdery mildew and Phytophthora fruit rot in 2018.

We completed experiments to determine the transcriptomic profile during *P. capsici* infection of resistant and susceptible genotypes. Advanced germplasm lines of USVL531-MDR, USVL0020-PFR, Charleston, Gray and Sugar Baby were grown in the field and fruit were harvested when mature. Fruit of each of these lines was inoculated with 10^4 zoospores/ml and maintained in a humid chamber (26 ± 1 °C >95%RH). Fruit rind samples were collected from individual fruit after 12h, 24h, 48h, 72h, and 96h after inoculation and immersed in liquid nitrogen to quench all the metabolomics processes. Rind samples were then processed for extraction of RNA and sent to Duke University Genomic center for RNA sequencing. Sequencing has been completed and we are currently analyzing the RNA-seq data.

We have identified three red fleshed (plants) with tolerance to Phytophthora fruit rot and high level of resistance to Powdery mildew (at the F_5 stage). These will be screened for resistance to both the diseases and advanced further to F_6

Our studies with melatonin have also shown that it can suppress the growth of Phytophthora capsici in culture plates. Our research has also indicated that 1000mM melatonin solution is capable of reducing development of Phytophthora fruit rot on cucumbers.

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**

2.1.1.1 CGMMV: **Watermelon with resistance to CGMMV: Year-3 progress (Ling and Levi)**

- **Developing segregating breeding populations of watermelon germplasm (*Citrulus colocynthis)* with CGMMV-resistance.**
  - *Cucumber green mottle mosaic virus* (CGMMV) is an emerging disease on watermelon and other cucurbit crops in North America (Ling et al., 2014; Tian et al., 2014). This seed-borne virus is contagious and poses a serious threat to the entire cucurbit industries in the U.S. In the last two years, through screening of the entire USDA watermelon germplasm, several lines from *Citrulus colocynthis* were confirmed to have some level of resistance/tolerance to CGMMV. Our focus in the last year was to develop segregating population of breeding lines for the inheritance of resistance study.
  - Through biological screening of the entire USDA watermelon germplasm (~1,400 accessions) through mechanical inoculation for CGMMV resistance, those plants with potential resistance based on symptom observation and appropriate lab tests (ELISA, PCR) were selected for self-pollination though single plant selection.
  - A repeat test on plants from seven accessions (including three *Citrulus lanatus* and four *C. colocynthis*) with potential resistance (tolerance) to CGMMV were conducted and resistance (tolerance) was confirmed on those *C. colocynthis* lines. Through single plant selection, S2 seeds were generated. One line was chosen to advance the seeds to S3, which will soon be released by ARS to the industry.
  - To study genetic inheritance of resistance, cross pollinations were made between the most resistance and a susceptible *C. colocynthis* line, as well as between the CGMMV-resistance *C. colocynthis* line and *C. lanatus* (cv. Charleston gray or Crimson Sweet). Currently, F1 and F2 seeds for *C. colocynthis* have been generated. Due to self-incomparability from hybridization between *C. colocynthis* and *C. lanatus,* only two families of F1 and BC1 seeds were generated.
  - Development of those seeds is an important milestone for the evaluation of inheritance of resistance in *C. colocynthis* to CGMMV.

- **Seed Transmissibility of Cucumber Green Mottle Mosaic Virus in Cucurbits and Seed Health Assays.**
- CGMMV is a seed-borne virus, but its mechanism of virus transmission through contaminated seeds have not be well characterized and the seed health test methods have not been optimized.
- In this study, through seedling grow-out or by mechanical inoculation to melon seedlings with CGMMV-contaminated seed extract, we determined that although seed transmission to seedlings through natural seeding grow-out process was fairly low, the mean of virus transmission to seedlings were more prevalent through mechanical inoculation of contaminated seed extract.
- Comparative evaluation of various seed health test methods showed that serological methods (ELISA, immunostrips) could produce reliable results for seed health if a good source of antibody was used. LAMP (isothermal amplification) was also sensitive for virus detection on seeds, but qRT-PCR results were poor and additional improvement is needed.

- **Genome sequencing of bottle gourd *(lagenaria siceraria)* and identification of SNPs associated with PRSV resistance.**
- In recent years, several cucurbit genomes (cucumber, melon, watermelon and squash) have been sequence. In corporation with Fei's group at Boyce Thompson Institute, we were able to obtain the genome sequence of bottle gourd using an advance selected line of *L. siceraria* with multiple virus resistance (Wu et al., 2017).

- Using genotyping-by-sequencing technology, we were able to identify SNPs associated with resistance to Papaya ringspot virus (PRSV)
- The molecular markers (CAPS, cleaved amplified polymorphic sequence) developed were shown to be useful for marker-assisted selection.

References:

1. Ling KS, Li R, Zhang W. 2014. First report of *Cucumber green mottle mosaic virus* infecting greenhouse cucumber in Canada. Plant Disease, 98:701.
2. 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.
3. Wu, S., Shamimuzzaman, M., Sun, H., Salse, J., Sui, X., Wilder, A.J., Wu, Z., Levi, A., Xu, Y., Ling, K.-S., Fei, Z. 2017. The bottle gourd genome provides insights into Cucurbitaceae evolution and facilitates mapping of a Papaya ringspot virus resistance locus. Plant Journal 92:963-975.

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

- Genotyped the available NPGS melon accessions and heirloom (n= 2,084) by GBS methods. Population structure, pattern of LD, and redundant accessions were analyzed using the genotype data
- Selected 384-member molecular-informed core population, i.e., functional panel or diversity panel, from the 2,084 based on molecular data analysis and historic importance.
  - Validated the utility of the diversity panel for identification of loci that determine quantitative and qualitative traits based on GWAS of 100-seed weight, fruit characteristics, and flower sex expression.
  - The panel was planted March 6 in a field in Imperial Valley for phenotyping, in particular with respect to those traits that define melon horticultural groups.
  - A manuscript is in preparation that will report results of population structure analyses using a suite of tools, LD decay, Core collection selections, and GWAS using historical and project-generated data.
- Analyses of GBS and endorna virus data of 42 *C. melo* ssp. *agrestis* var. *texanus* accessions collected in the U.S. and Mexico confirmed their unique identity among the 19 melon horticultural groups in the recently revised melon classification scheme.

(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

- GBS has been completed on 180 RIL lines derived from MR1 x AY.
- Two independent powdery mildew race 1 greenhouse assays were completed on the RILs.
- QTL analysis was performed and markers mapped to the genome.
- We have identified two major QTL and two minor QTL linked to powdery mildew race 1 resistance.
- There appears to be epistatic interactions between two of the QTL.

California Field Tests

Two replicated field tests of cucurbit powdery mildew race differentials subjected to natural infection.

- Imperial Valley. University of California, Desert Research and Extension Center, Holtville; watered March 9, 2017, disease reactions evaluated mid-June; melon race 1 present in the field
- Central Valley. University of California, Westside (Westside Research and Extension Center, Five Points; Planted 27 June, evaluated early to mid-September; infection insufficient for evaluation.

Fusarium Wilt resistance in MR1xAY RIL

- GBS has been completed on 180 RIL lines derived from MR1 x AY.
- Two independent Fusarium oxysporum f. sp. melonis (FOM) race 2 assays for resistance of the RILs were completed.
- Two independent Fusarium oxysporum f. sp. melonis (FOM) race 1 assays for resistance of the RILs were completed.
- QTL analysis was performed for each race, and a genetic map generated from the MR1 x AY cross.
- We have identified one major QTL and three minor QTL linked to Fom race 1 resistance.
- We have identified one major QTL associated with Fom race 2 resistance in melon.
- We have generated the most saturated SNP-based map to date of melon with 5663-binned markers.
- RILs were grown and fruit was processed and tested for carotenoids in collaboration with Dr. Li Li, ARS, Ithaca, NY.
- We have identified a major QTL for total carotenoids in the MR1 x AY RIL population.

CYSDV

- Planted in December 2017, 184 F2 PI 313970 x Top Mark for production of the F2:F3 generation in a greenhouse. The entire population was sequenced using GBS and is in the process of genetic analysis. Due to delays in female flower production, the material was planted in the field in Imperial Valley in early-March and will be sampled for DNA analysis using GBS and self-pollination in the field.
- Planted in January 2018, 184 F2 PI 313970 x TGR 1551 (PI 482420) for production of the F2:F3 generation in a greenhouse. DNA samples have been collected for GBS analysis.

CMV

- Advanced CMV-resistant lines (western U.S. shipping type cantaloupe, and honeydew) developed by M. Kyle-Jahn and H.M. Munger were increased 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. Virus resistance assays were initiated in March 2018. Due to limited seed supply, the material will be planted only at the UC Westside Research and Extension Center, Five Points, CA; planting date in late June 2018.

Additional Related Virus Information and Activity ***Cucurbit yellow stunting disorder virus*** (CYSDV) impacts production of melon and other cucurbit crops in the southwestern and southeastern US, and

Texas. Research has led to the advancement of germplasm for resistance to CYSDV, with reduced symptom development. Previous studies by our laboratory demonstrated reduced CYSDV titer early in symptom development correlates with decreased symptom development in plants. This allowed laboratory-based screening of selections in 2016, prior to field studies conducted in 2017. Further greenhouse evaluations of CYSDV have been delayed due to limits on whitefly populations and greenhouse renovations. Renovations have now been completed and we anticipate completion of greenhouse germplasm evaluations during the summer of 2018. Evaluations will involve whitefly inoculation of CYSDV followed by treatment of plants with imidocloprid to prevent whitefly buildup per APHIS regulations.

Cucurbit plants evaluated for virus infection in California during in 2017 demonstrated typical moderate levels of CYSDV incidence in spring melons. Fall production is not viable in most desert production regions due to this virus, but information from growers indicated lower than average levels of CYSDV incidence in spring/summer melons. CMV and *Watermelon mosaic virus* (WMV) were also present in Imperial County melon. Whitefly incidence in the San Joaquin Valley emerged late in the fall season, but no whitefly-transmitted viruses have been identified to date in cucurbit crops. San Joaquin Valley virus incidence was predominantly WMV, CMV, and limited *Cucurbit aphid-borne yellows virus* (CABYV). Through cooperation with extension and growers we will again monitor prevalent viruses affecting cucurbit production in the San Joaquin and Imperial Valleys of California during the 2018 growing season to determine level of potential virus threats as well as whether WMV continues to emerge as a growing production concern. This virus has the potential to produce fruit scarring and blemishes that can impact marketability.

Cucumber mosaic virus (CMV)**.** CMV has emerged as an increasing problem for melon production in western states, particularly in California and Arizona. Melon seed was received from the Cornell University breeding program in January after increase during the previous year in the Mazourek Lab. The 25 breeding lines are for evaluation of resistance to CMV, and adaptation and fruit quality. Seed was divided between the breeding and virology programs with 15 seeds of each line reserved for field evaluations and the remainder for replicated greenhouse experiments. A CMV isolate collected previously from infected melon plants in California has been maintained frozen at ARS, Salinas. All 25 lines are currently being evaluated against this isolate, with initial results anticipated by early April 2018. Seeds were sown and transplanted in a greenhouse, and will be inoculated by mechanical (rub) inoculation of cotyledons in March. Evaluation of plants will include visual symptoms and ELISA using commercial CMV antiserum. All tests are expected to be completed by late-May, allowing time for further increase of resistant germplasm this year.

RNA interference (RNAi) methods for control of whiteflies on tomato, melon, and cassava. Whiteflies and whitefly-transmitted viruses result in significantly decreased agricultural productivity throughout the world through reduced yields and plant longevity, yet little resistance exists to whitefly and only limited natural resistance is available to many virus diseases. The Wintermantel Lab in collaboration with the Fei Lab (BTI) sequenced the transcriptome (RNA used for gene expression) of the whitefly in response to transmission of *Cucurbit yellow stunting disorder virus* (genus *Crinivirus*, family *Closteroviridae*) and identified over 250 differentially expressed genes in response to virus infection of the melon source plant on which the whitefly fed. This information is being used to understand how these viruses interact with the whitefly vector and for development of RNA interference (RNAi), a method for specific elimination of the whitefly vector (and not other insects) in vegetable crops and cassava through another project involving team members Wintermantel, Ling, and Fei. A related collaborative project

involving W.M. Wintermantel and K-.S. Ling at USDA-ARS in Salinas, CA and Charleston, SC, respectively, in collaboration with Zhangjun Fei at the Boyce Thompson Institute in Ithaca, NY have been evaluating RNAi approaches for control of whitefly in other crops. The Wintermantel Lab has been conducting preliminary testing to evaluate performance of RNAi constructs effective on these other crops for efficacy in control of whitefly on melon. Research is in progress.

Virus Isolates. ARS-Salinas maintains isolates of CMV and CYSDV for research on evaluation and advancement of resistance in melon and other cucurbits. A new isolate of WMV is also being maintained, as this virus appears to be reemerging in California as a production threat.

2.2 Marker development and verification

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

- See 2.1.2.

Fusarium wilt

- See 2.1.2.

CYSDV

- No planned research for this period

CMV

- No planned research for this period. Will do 3'RNA seq in the next year pending confirmation of phenotypes.

2.3 Introgress resistance into advanced breeding lines

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

- See *2.1.2.*: CYSDV

Fusarium wilt

- We have begun making crosses of the best performing RILs with multiple resistances into Top Mark.

CYSDV

- Backcrossed resistant field selections from Fall 2016 in a greenhouse.

- Evaluated F_2 and S_1 from several backcross families of orange flesh and honeydew melon from crosses with 8 different resistance sources for reaction to natural infection in Imperial Valley in Fall 2017.
- CYSDV-resistant, single plant selections from F_2 and S_1 of backcross populations taken as vegetative cuttings for backcrossing and selfing in a greenhouse at Salinas and subsequent round of selection in fall 2019.

CMV

- Seeds of advanced CMV-resistant lines were increased for testing in Arizona and California.

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, Dymerski R), Grumet (Grumet R, Hammar S.) and Wehner (Wehner T., Silverman EJ) Labs

2017 progress

1. GBS of PI lines
GBS has been completed for 1234 cucumber accessions including plant introduction (PI) lines and historical cultivars or landraces of cultivated (*Cucumis sativus* var. *sativus*) and wild (*C. sativus* var. *hardwickii*) cucumber lines. Data analysis has been performed by the bioinformatics team to identify SNPs, determine minor allele frequency, perform phylogenetic, population genomic, and linkage disequilibrium (LD) analysis. This information is being used to establish a functional core population to capture ~99% of allelic diversity as well combined with representation of key disease resistance, fruit quality and agronomic features.

2. *Phenotyping of morphological traits and DM resistance in cucumber natural populations*
Four hundred and twelve cucumber lines were grown in the University of Wisconsin Hancock Agricultural Research Station (HARS) for collection of morphological data. Meanwhile, 352 cucumber

lines (2 reps, 6 plants per rep) were planted in North Carolina State University experimental field in summer 2017. Data for responses to DM natural infestation were collected.

2018 work plan

1. A core collection (384) are being selected using multiple criteria including GBS results to construct the GWAS panel.
2. Seed increase of cucumber lines by self-pollination for those without enough seeds or with high degree of heterozygosity.
3. Prepare GWAS panel lines for re-sequencing
4. Approximately 300 lines in the GWAS panel will be planted in 2018 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.
5. Prepare a manuscript describing cucumber diversity and establishment of functional panel.

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)

2017 progress

We aim to conduct QTL mapping of DM resistance from two resistant sources: PI 330628 (WI7120) and PI 197088. We previously identified two major-effect QTL *dm4.1* and *dm5.2* for DM resistance from WI7120 (Wang et al. 2016). Using the PI 197088×Coolgreen RIL population, we also identified 4 major- or moderate-effect QTL, *dm4.1, dm5.1, dm5.2*, and *dm5.3* for DM resistance in PI 190788; *dm5.3* is co-localized with *pm5.1* (syn. *CsMLO1* or *CsMLO8*, *pm-h*), which is a major-effect QTL for PM resistance in cucumber (Wang et al. 2017). We focused on three major-effect DMR QTL, *dm4.1*, *dm5.2* from WI7210 and *dm5.3* from PI 197088 for fine mapping.

F_2 and RIL plants carrying respective QTL regions were selected to backcross with the susceptible cucumber line 9930. Near isogenic lines (NILs) for each QTL were developed in the susceptible 9930 genetic background. We have completed marker-assisted development of NILs for *dm4.1* and *dm5.2*. Secondary F_2 populations from crosses between resistant and susceptible NILs were developed, which were genotyped for DM inoculation responses in both field and controlled environments. The development of NILs for *dm5.3* has been advanced to BC_2.

Through QTL analysis in the secondary F_2 populations, the *dm4.1* and *dm5.3* loci have been delimited to ~100 kb intervals on chromosomes 4 and 5, respectively.

2018 work plan

1. Narrow down the QTL region (1.5 LOD interval) of target QTL regions through continued 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.

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*

2017 progress:

1. *Initiate introgression and genetic analysis*.
   a. *Population development* BC_1 individuals showing resistance were backcrossed to Gy14; BC2 progeny were screened in the greenhouse in the fall 2017. Doubled haploid families derived from four PI 109483-53 lines were produced by Rijk Zwaan Seed from these plants were grown in the greenhouse and field in 2017and fruit tested for response to inoculation. Selected DH individuals were crossed with Gy14 to provide a second population for QTL analysis.
   b. Phenotyping. An F_2 population (n=400) of GY14 X PI109483-53B was tested in summer 2017. Fruit were harvested from each plant at approximately 4-6 day post-pollination (4-8 mm), and inoculated with *P. capsici*. Three sets of harvests were performed on the full population to provide replication in sampling dates, and at least 10 fruit per F_2 individual. The population exhibited a normal distribution for disease score; ~60 potentially resistant and potentially susceptible individuals were chosen for further testing. Three additional harvests were performed on those plants; the two groups of individuals performed as predicted, verifying the initial ratings as resistant or susceptible. DNA will be prepared from the 15-20 most resistant and most susceptible individuals for sequencing and subsequent QTL-seq analysis.

2. Field trial in P. capsici infested field. Field trials were performed in 2017 in a heavily *P. capsici*-infested site maintained in Geneva, New York by Dr. Chris Smart's group. Two methods of inoculation were tested: spray at fruiting time with zoospore suspensions, and incorporation of infested vermiculite into the soil between the rows. Overall infection rates were 22% and 39% of fruit harvested for the vermiculite and zoospore inoculations, respectively. Future work will test the breeding lines under development.

2018 work plan:

1. Phenotype young fruit of F_2 progeny from Gy14 x DH 109483-53-derived resistant lines for response to *P. capsici*.
2. Perform QTL-seq analysis on selected F2s from the summer 2017 (Gy x 109483-53) and spring 2018 (Gy14 x DH 109483-53) experiments.
3. Intercross BC progeny to increase resistance levels in a background with better fruit type, more uniform germination, and earlier female flower production.
4. Perform 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.

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

2017 progress:

1. QTL seq analysis. In preparation for QTL-seq, B. Mansfeld developed an R package, QTLseqr (no R packages are currently available), using two statistical approaches, QTL-seq and a tricube smoothed G statistic, G', to identify and assess statistical significance of QTL. QTLseqr, can import and filter SNP

data, calculate SNP distributions, relative allele frequencies, G' values, and log10(p-values). The source code is available at https://github.com/bmansfeld/QTLseqr. Since October it has been downloaded >600 times with an altmetric score in the top 5%. A manuscript describing the program has been submitted to Plant Genome.
2. Transcriptomic and metabolomic analysis of peels from ARR+ and ARR- cultivars. Work describing the transcriptomic and metabolomic analysis was published in 2017 (Mansfeld et al., Hort Res): Transcriptomic and metabolomics analyses of cucumber fruit peels reveal a developmental increase in terpenoid glycosides associated with age-related resistance to *Phytophthora capsici*.
3. Transcriptomic and microscopic analysis of the infection process is underway to determine the point at which infection is inhibited and compare responses between ARR+ (Poinsett) and ARR- (Gy14). The use of a second ARR+ line also helps to narrow candidate genes associated with ARR.

2018 work plan:
1. Phenotype Gy14 x Poinsett-derived DH population. The DH population provides a second population and season for QTL-seq analysis and also allows for replicated screening not possible with F2 plants, as only a single fruit per plant can be set per plant to avoid competition effects on development.
2. Perform QTL seq analysis for ARR. Compare results of transcriptome analysis with QTL seq analysis to help identify genomic regions of greater interest.
3. Complete transcriptomic and microscopic analysis of infection process.

Objective 2.3 Advanced line development for downy mildew resistance

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 *dm4.1* and *dm5.2* QTL from WI7120/PI 197088. In 2017-2018 period, homozygous lines carrying both *dm4.1* and *dm5.2* were developed. In 2017 summer trial, these plants were grown in the University of Wisconsin Hancock Agricultural Research Station for preliminary observations. The plants were also tested for DM inoculation responses in controlled environments.

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).

In 2017, 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). The RILs ranged from 2.0 to 8.0 for best rating (0-9 scale) for DM resistance. The RILs ranged from 2.7 to 8.0 for fruit quality rating (9-1). Five RILs had DM resistance of 2.0 to 4.3 and fruit quality of 5.0 to 8.0, making them suitable for use in crossing with elite breeding lines to develop resistant cultivars.

In 2018, we will evaluate sublines for high resistance to the new downy mildew in the field in North Carolina. The design will be a randomized complete block with 3 replications and 4 disease ratings. Sublines will be rated for fruit traits such as skin type (smooth, cracked, netted) and spine color (black, white). The RILs ranged from 2.0 to 8.0 for best rating (0-9 scale) for DM resistance. The RILs will be tested for traits that make them suitable for use in crossing with elite breeding lines to develop resistant cultivars.

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.

In 2017, we evaluated sublines for high resistance to the new downy mildew as well as fruit quality in the field in North Carolina. A total of 38 sublines were evaluated in a randomized complete block with 3 replications and 4 disease ratings. The RILs ranged from 2.0 to 8.0 for best rating (0-9 scale) for DM resistance. The RILs ranged from 2.7 to 8.0 for fruit quality rating (9-1). Five RILs had DM resistance of 2.0 to 4.3 and fruit quality of 5.0 to 8.0, making them suitable for use in crossing with elite breeding lines to develop resistant cultivars.

In 2018, we will evaluate sublines for high resistance to the new downy mildew as well as fruit quality in the field in North Carolina. Lines will be evaluated in a randomized complete block with 3 replications and 4 disease ratings. The RILs will be selected for traits that make them suitable for use in crossing with elite breeding lines to develop resistant cultivars.

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/PI 197088. Combine *dm3* into Gy14+*dm4.1*+*dm5.2* genetic background through marker assisted selection. 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.

In 2017, 54 lines (including checks) from the three populations (PI 197088 x Gy14, NC-25, or Poinsett 76) were tested for DM resistance (0-9 scale) and fruit quality (9-1 scale). The design was a randomized complete block with 3 replications and 4 disease ratings. Of those, 4 lines from Gy14, 3 lines from NC-25, and 2 lines from Poinsett 76 were advanced since they had resistance of 3 to 5 and quality of 5 to 7.

In 2018, lines (including checks) from the three populations (PI 197088 x Gy14, NC-25, or Poinsett 76) will be tested for DM resistance (0-9 scale) and fruit quality (9-1 scale). The design will be a randomized complete block with 3 replications and 4 disease ratings. The most resistant lines with high fruit quality will be advanced.

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.

   In 2017, we produced sublines (S2) and backcross lines (BC1S1) from PI 605996 x Poinsett 76 that will be tested for high resistance to DM as well as fruit quality.

   In 2018, we will produce sublines (S4) and backcross lines (BC1S3) from PI 605996 x Poinsett 76 for testing for high resistance to DM, as well as fruit quality.
4. Field screening of downy mildew resistance for the 300-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	ZF (BTI), RG (MSU)	X	X		
- squash	MM (CU)	X	X		
1.2.2. Population genetics and GWAS analysis	UR (WVSU), ZF (BTI)		X	X	X
- squash	MM (CU)				
(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	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)**				
2.2.4 Squash					
- powdery mildew	MM(CU), LWB(UPR)	RM	V		
- Phytophthora	MM (CU)			RM	V
- PRSV-W	MM(CU), LWB(UPR)		RM	V	
- CMV	MM(CU), LWB(UPR)		RM	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	Already exists				
- Phytophthora	MM (CU), CS (CU)	I	I	AR	AR
- PRSV-W	Already exists				
- CMV	Already exists				

Powdery mildew resistance in squash

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

Completed in 2017

Virus resistance in squash

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

We are investigating resistance derived from *C. ecuadorensis* by locating genomic regions that contain *C. ecuadorensis*-specific alleles within a panel of 86 *C. pepo* cultivars. We have defined *C. ecuadorensis*-specific alleles in this study as a set of 13,274 GBS SNP markers that are fixed variants between *C. ecuadorensis* and a phenotypically diverse set of heirloom *C. pepo* cultivars. To aid in the identification of C. ecuadorensis introgressions, we have genotyped 'Whitaker' using GBS, a *C. pepo* summer squash from Cornell that is resistant to PRSV and CMV, as well as powdery mildew and ZYMV. The pedigree of 'Whitaker' contains *C. ecuadorensis* and *C. okeechobeensis* subsp. *martinezii*, and therefore it contains several introgressions from each species within its genome. By using 'Whitaker' as a guide to common introgressions from *C. ecuadorensis*, we have tentatively identified a genomic region on chromosome 16 with a length of approximately 1 Mb that may be associated with resistance to PRSV.

The 20 *C. pepo* members of the cultivar panel that express PRSV resistance are homozygous for *C. ecuadorensis*-specific alleles within this genomic region. To bolster the cultivar panel, we are using GBS to genotype historical germplasm from the Cornell breeding program that has been phenotyped for PRSV and CMV resistance. 'Whitaker' has been used extensively in the breeding program, and thus these additional resources will aid in refining the genomic region associated with resistance. Additional sources of resistance have been incorporated to this historical germplasm, which will also be explored. Additionally, we are developing a 'Whitaker'-based mapping population to further refine and validate any identified genomic regions associated with resistance.

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

Inheritance of resistance to PRSV:

To date we have evaluated the following resistant x susceptible F2 populations: Nigerian Local x Taína Dorada (335 F2 plants evaluated), Menina x Taína Dorada (120 F2 plants evaluated) and Verde Luz x Menina (120 F2 plants evaluated). In addition, we have recently finished evaluating the F2 population cross between our two sources of PRSV resistance: Nigerian Local and Menina. Plants of each population were mechanically inoculated with PRSV and then scored for disease severity and tested with ELISA. DNA samples were collected from most of the F2 plants. DNA samples will be lyophilized and will be used only in the event that other approaches to development of a molecular marker for PRSV are not successful (they could be then used for bulk segregant analysis) . The most resistant plants (based on both symptom severity and ELISA) have been transplanted to the field for self-pollination (see below). Although data analyses of the inheritance studies are not complete, we can make some conclusions. Segregation ratios from the resistant x susceptible F2 populations varied, depending on the susceptible or resistant parent used in the cross. None of the populations segregated 1:3 (resistant:susceptible), indicating that there is not a single recessive gene for PRSV resistance as has been previously reported in the literature. When Menina and Nigerian Local were crossed, the F2 population clearly segregated for resistance, indicating that at least some gene or genes for resistance in these two genotypes are not allelic. Based on symptom severity, we saw a segregation of 215 resistant to 23 susceptible in the F2 (combined data from 4 greenhouse trials). Based on ELISA readings, we saw a segregation of 166 resistant to 72 susceptible. We tested two common 2-gene models, 15:1 and 13: 3 for goodness-of-fit. The null hypothesis of goodness-of-fit was rejected in each case, but not by very much. However, each of these models proposes a single dominant gene in each resistant genotype. But susceptible x resistance crosses have not produced resistant F1 plants as would be expected if Menina and Nigerian Local carried a dominant gene for resistance. These traditional inheritance studies are being carried out as an auxiliary study to the search for molecular markers. Therefore, the fact that these two sources of resistance carry separate genes for resistance will need to be considered when developing markers for resistance to PRSV.

Tropical pumpkin lines with resistance to PRSV and ZYMV:

Self-pollination of lines derived from the various resistant x susceptible F2 populations has continued. After each self-pollinated, the lines that have been advanced a generation are tested for resistance to PRSV and ZYMV via mechanical inoculations in the greenhouse. Highly and moderately susceptible lines are eliminated, and a single most resistant plant is transplanted to the field for another generation of self-pollination. This process was somewhat slowed because of Hurricane Maria in Sept 2017. All field plantings were destroyed. But to date we have 54 F3 families, 13 F5 families and 10 F6 families that have been selected for resistance to PRSV. For ZYMV we have 5 F3 families, 6 F5 families and 12 F6 families. In general, we have observed that it has been easier to select for resistance to ZYMV (which is known to be controlled by dominant genes). In the case of PRSV, many families identified as resistant in the F2, F3 or F4, later appear to be completely susceptible or continue segregating for resistance (again, suggesting that inheritance of resistance to PRSV is somewhat complex). The resistant families generated to date will be used to validate any PRSV markers that are developed.

Effect of PRSV and ZYMV on tropical pumpkin development and production:
A field trial in summer 2017 in Lajas, Puerto Rico was conducted to document the effect of PRSV and ZYMV on development and growth of tropical pumpkin. The study included resistant genotypes Nigerian Local and Menina along with 4 susceptible cultivars. There was a general trend for infected plants to flower later, although this effect was significant only for plants infected with both PRSV+ZYMV (double infection). Control plants produced an average of 3.4 fruits per plant, while plants infected with PRSV produced only 2.15 fruits on average. Plants infected with ZYMV or PRSV+ZYMV produced fewer fruits per plant compared to control plants, although the difference was not significant. Fruit yield (weight) was strongly impacted by PRSV, ZYMV and PRSV+ZYMV (double infection). Yields were almost 50% less in infected compared to control plants. We noted that fruit production in Menina was unaffected by virus infection (infected plants produced the same yield as control plants). However, yields in control plants of Nigerian Local were double that of PRSV or ZYMV infected plants, despite the fact that we never observed virus symptoms in this supposedly resistant genotype. Pulp thickness and % dry matter were unaffected by the presence or absence of virus. This is the first study that we know of to document the effects of these two potyviruses in tropical pumpkin at the field level.

"Resistant" lines as a source of virus inoculum:
Lines with a low score for symptom severity (score of 0 or 1, and thus classified as "resistant" for PRSV or ZYMV) can sometimes have high ELISA readings (we consider readings of >0.400 as positive for virus). We conducted a series of studies to determine whether sap from "resistant" lines (based on the line having few or no foliar symptoms) can infect susceptible genotypes. Our results indicate that plants of Nigerian Local and Menina inoculated with PRSV or ZYMV are not capable of infecting susceptible plants. In contrast, several of the "resistant" lines that we have developed are capable of infecting susceptible plants. These results support the practice of considering both foliar symptoms and virus titer (as indicated by ELISA) when evaluating for virus resistance.

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 F2'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. Last summer we will screened F2 individuals and found them to be asymptomatic when inoculated with *P. capsici* on the blight farm. We will repeat this screen in the greenhouse with F2:3 populations for QTL analysis. Work in the greenhouse will allow us to have more controlled inoculations with more aggressive strains of the pathogen.

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

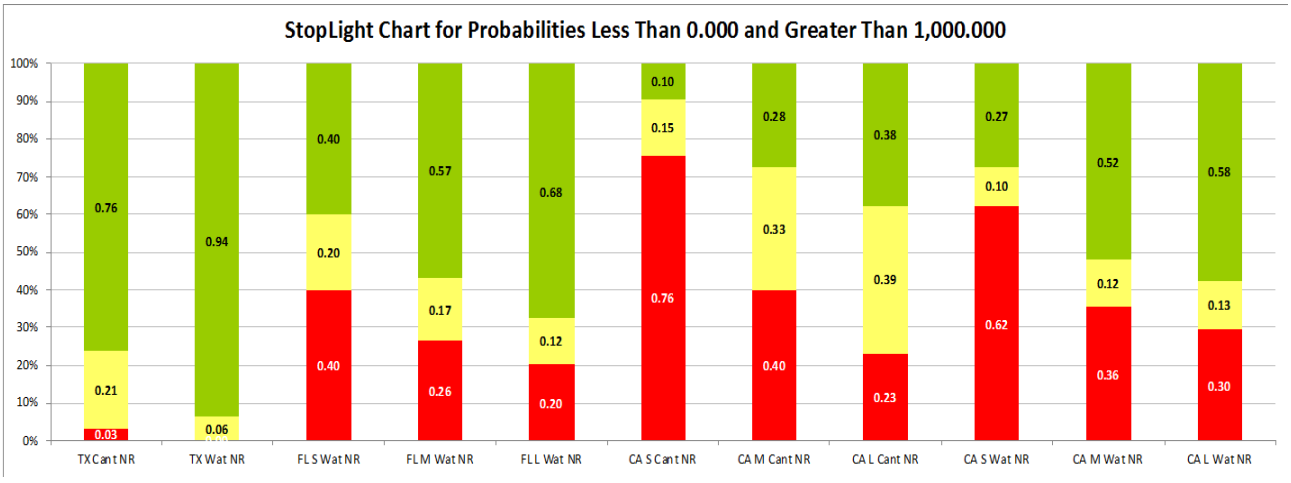
3.1.1. Define, parameterize, simulate, and validate production variables based on cucurbit production crop budgets

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 2018)
- Identify how the findings of the project impact representative farms (Spring 2018)
- Develop and validate all representative farms (Summer/Fall 2018)



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 has not changed as the timeline has progressed. The extension component 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 in conjunction with Mary Lorscheider, who the web manager for this project.

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 April 2017 through March 2018 regarding the objectives and their associated results or outputs. An pertinent extension or research activity inadvertently missed in previous reports has been included with this report.

3.2.1 Develop a centralized cucurbit disease website.

The CucCAP website was presented to the CucCAP team at the Annual meeting in March 2017. The team was able to view the website for 6 months and give feedback and suggestions for improvement. In June 2017, a monthly newsletter called the CucCAP Chronicle was initiated. The newsletter is designed to display news and events that are posted on the CucCAP website. The initial list of subscribers to the CucCAP Chronicle was the 21 members of the CucCAP team. Here is a link to previous installments of the CucCAP Chronicle: CucCAP Team Email Campaign Archive. In the future, we plan to post a link on the CucCAP website so visitors to our site can subscribe to the newsletter. Since June, we have posted news and events on the website. News posts include activities of the crop teams, announcements of recent publications, recent and upcoming presentations by CucCAP researchers at

scientific meetings, news of disease outbreaks during the growing season, and upcoming events on the CucCAP calendar. In addition to sharing news and events, the CucCAP website has been following and sharing news from lab websites and social media including news from the Quesada Vegetable Pathology lab at NC State, the Hausbeck Plant Pathology Research Lab at MSU, the Smart Lab at Cornell, the Cucurbit Genomics Database website and the Boyce Thompson Institute. News posts on the CucCAP website and social media generate traffic to the site. One of our goals for the future is to post short informative YouTube videos of activities of the CucCAP teams. Google analytics was set up to scan the CucCAP website for user data in September 2017. Ongoing activities in the CucCAP website include adding new publications with links to the site, scanning the site for broken links and repairing them, adding news and events to the calendar, and developing posts for social media including news posts with images and videos.

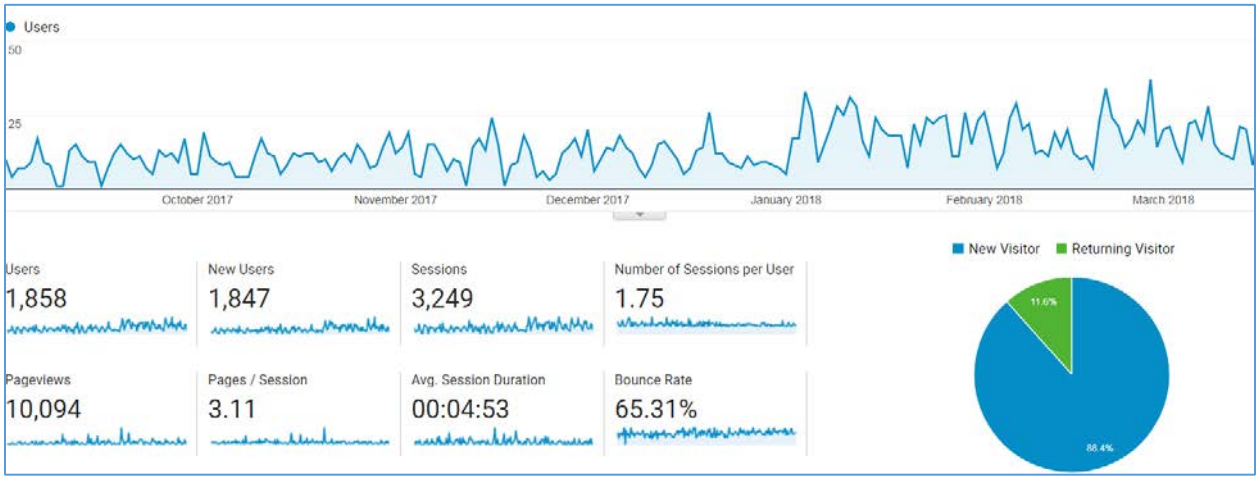


Figure 1: Google analytics user data for September 1, 2017 to March 15, 2018.

	Country	Users	% Users
1.	United States	977	52.27%
2.	India	120	6.42%
3.	China	67	3.58%
4.	Canada	52	2.78%
5.	Mexico	40	2.14%
6.	Germany	33	1.77%
7.	Spain	33	1.77%
8.	South Korea	30	1.61%
9.	Philippines	30	1.61%
10.	Iran	28	1.50%

Figure 2: Google analytics data, Country of website audience from September 1, 2017 to March 15, 2018.

Operating System	Acquisition			Behavior		
	Users ↓	New Users	Sessions	Bounce Rate	Pages / Session	Avg. Session Duration
	649 % of Total: 34.93% (1,858)	649 % of Total: 35.14% (1,847)	749 % of Total: 23.05% (3,249)	77.97% Avg for View: 65.31% (19.38%)	1.59 Avg for View: 3.11 (-48.82%)	00:00:54 Avg for View: 00:04:53 (-81.38%)
1. iOS	**321** (49.46%)	321 (49.46%)	369 (49.27%)	81.57%	1.41	00:00:33
2. Android	**305** (47.00%)	305 (47.00%)	353 (47.13%)	74.50%	1.72	00:01:17
3. Windows	**18** (2.77%)	18 (2.77%)	22 (2.94%)	68.18%	2.68	00:01:08
4. (not set)	**3** (0.46%)	3 (0.46%)	3 (0.40%)	100.00%	1.00	00:00:00
5. BlackBerry	**2** (0.31%)	2 (0.31%)	2 (0.27%)	100.00%	1.00	00:00:00

Figure 3: Google Analytics data, operating systems used by CucCAP website visitors.

3.2.2. Develop and post diagnostic resources and disease control information

Publications

1. Smart, C.D. and Lange, H. 2018. Fungus, water mold or bacteria:which is which in my vine crops? Proceeding of the 2017 Empire State Producers Expo, Syracuse, NY

3.2.3. Provide disease alerts and forecasting tools

Weekly conference calls, NCSU Vegetable Team (Quesada)**:** These calls occurred from June 7 to September 27 in 2016, and from April 4 to October 31 in 2017 .

Weekly conference calls, Cucurbit ipmPIPE (Hausbeck, Quesada, Smart)**:** These calls begin in May and continue through August and 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.

In 2017, Quesada provided diagnostics and disease management recommendations for 22 cucumber, 31 watermelon, 9 melon, 10 squash, and 6 pumpkin samples submitted to the NCSU Plant Disease and Insect Clinic. In 2016, Quesada provided diagnostics and disease management recommendations for 12 cucumber, 33 watermelon, 8 melon, 12 squash, and 9 pumpkin samples submitted to the NCSU Plant Disease and Insect Clinic. In 2015, Quesada provided diagnostics and disease management recommendations for 40 cucumber, 28 watermelon, 10 melon, 13 squash, and 11 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 Vegetable Crop Handbook. Smart diagnosed over 60 samples during the 2017 growing season, in addition to over 100 disease issues diagnosed via photo through email or text message. Of the cucurbits,

30 were pumpkin, 15 summer squash, 10 winter squash, and 5 cucumber. She also provides management recommendations through oral presentations and updates to regional extension educators (both conventional and organic).

Production guides

1. Southeastern Vegetable Extension Workers. Kemble J., Lewis Ivey M., Jennings K. M., and Walgenbach J. F., Eds. (2018) Southeastern US 2018 Vegetable Crop Handbook. Basil, cucurbits, hop, sweetpotato, and fungicide resistance tables (Quesada-Ocampo L. M. 10 total; Schultheis).
2. Quesada-Ocampo L. M., Meadows I., and Louws F. (2018) Disease control for commercial vegetables. North Carolina Agricultural and Chemicals Manual. Basil, cucurbits, hop, sweetpotato, and fungicide resistance tables (Quesada-Ocampo L. M. 10 total).

Web Content

1. Hausbeck, M.K., and Linderman, S.D. 2016. Managing *Phytophthora* on cantaloupe, muskmelon and watermelon. https://veggies.msu.edu/wp-content/uploads/2017/05/FS_Managing-Phytophthora-on-Melon.pdf.
2. Hausbeck, M., Krasnow, C., and Linderman, S. 2017. Phytophthora disease reported on winter squash and pumpkin, scout and treat now to preserve your crop. Michigan State University Extension News for Agriculture: Vegetables, 14 Jul. http://msue.anr.msu.edu/news/phytophthora_disease_reported_on_winter_squash_and_pumpkin.

Spanish Factsheets – Accessible on Website

1. Hausbeck, M.K. and S.D. Linderman. 2017. Monitoring and managing cucurbit downy mildew. *Spanish translation by Linares Ramírez, A.M. and M. Miranda.* 2018. Monitoreo y manejo del añublo lanoso en las cucurbitáceas. [Factsheet] https://cuccap.org/espanol/monitoreo-y-manejo-del-anublo-lanoso-de-las-cucurbitaceas/
2. Hausbeck, M.K., J. Morrice, and S.D. Linderman. 2016. Management of cucurbit downy mildew for home gardeners. *Spanish translation by Linares Ramírez, A.M. and M. Miranda*. Seda. 2018. Manejo del añublo lanoso de las cucurbitáceas para los agricultores. [Factsheet] https://cuccap.org/espanol/manejo-del-anublo-lanoso-de-la-cucurbitaceas-para-los-agricultores/.
3. Hausbeck, M.K. and S.D. Linderman. 2016. Managing *Phytophthora* on cantaloupe, muskmelon and watermelon. *Spanish translation by Linares Ramírez, A.M. and W. Seda. 2017.* Manejo de Phytophthora cantalupo, melón y sandía. [Factsheet] https://cuccap.org/espanol/manejo-de-phytophthora-en cantalupe-melon-y-sandia/
4. Hausbeck, M.K. and S.D. Linderman. 2016. Managing *Phytophtora* on cucumber. *Spanish translation by Linares Ramírez, A.M. and W. Seda.* 2017. Manejo de *Phytophthora* en pepino. [Factsheet] https://cuccap.org/espanol/manejo-de-phytophthora-en-pepino/
5. Hausbeck, M.K. and S.D. Linderman. 2016. Managing *Phytophthora* on summer squash and zucchini. *Spanish translation Linares Ramírez, A.M. and W. Seda*. 2017. Manejo de *Phytophthora* en calabaza de verano y calabacín. https://cuccap.org/espanol/manejo-de-phytophthora-en-calabaza de-verano-y-calabacin/
6. Hausbeck, M.K., C. Krasnow, and S.D. Linderman. 2016. Managing *Phytophthora* on Winter Squash and Pumpkin. *Spanish translation by Linares Ramírez, A.M. and M. Miranda*. 2017. Manejo de *Phytophthora* en calabaza de invierno y en calabaza. [Factsheet]. https://cuccap.org/espanol/manejo-de-phytophthora-en-calabaza-de-invierno-y-en-calabaza/
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10. Quesada-Ocampo, L. 2013. Anthracnose of Cucurbits. *Spanish translation by Miranda, M. and A. M. Linares Ramírez*. 2017. La actracnosis de las cucurbitáceas. [Factsheet]. https://content.ces.ncsu.edu/la-antracnosis-de-las-cucurbitaceas
11. Quesada-Ocampo, L. 2013. Cucurbit Downy Mildew. *Spanish translation by Linares Ramírez, A.M*. 2017. Añublo lanoso en las cucurbitáceas. [Factsheet]. https://content.ces.ncsu.edu/anublo-lanoso-en-cucurbitaceas
12. Quesada-Ocampo, L. and N. Miller. 2015. Fusarium Wilt of Watermelon. *Spanish translation by Linares Ramírez, A.M*. 2017. Marchitez de Fusarium en Sandia. [Factsheet]. https://content.ces.ncsu.edu/marchitez-de-fusarium-en-sandia

3.2.5. Field days and demonstration plots.

Quesada is evaluating commercial watermelon varieties for anthracnose resistance and 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 (winter squash and summer squash) and other vegetables.

Schultheis was involved in several cucurbit variety studies in 2017; 2 zucchini squash, 2 yellow summer squash, 2 watermelon (standard and mini size, 1 orange flesh melon, 4 specialty melons (piel de sapo, honeydew, canary, and galia), 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 field day ("Hort Expo") was held in Lajas, Puerto Rico on April 4, 2017 by Lineares Ramirez. Participants saw a field experiment that documented the effects of the two potyviruses (PRSV and ZYMV) that have the greatest impact on tropical pumpkin production in Puerto Rico. The field demonstration included both uninfected plants (controls) and virus-inoculated plants. Participants also learned about how plant breeders incorporate genetic resistance into new varieties that combine resistance and good horticultural traits. The field demonstration was also part of an experiment to determine whether evaluations for resistance made in the greenhouse correlate with evaluations made in the field. Assessments made in the greenhouse require much less space and are more economical. One hundred eighteen people attended (72 males, 46 females). Of these; 12 were students, 12 farmers, 15 researchers, 12 technicians, 38 agronomists, 10 agricultural agents and 19 others.

Publications from demonstration plots

1. 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 Reports 10: V076.
2. Adams M. L., Noel N. A., and Quesada-Ocampo L. M. (2017) Evaluation of fungicides for control of anthracnose on cucumber, Cleveland 2016. Plant Disease Management Reports 11: V099.
3. Adams M. L., Parada C. H., and Quesada-Ocampo L. M. (2017) Evaluation of fungicides for control of Phytophthora fruit rot of watermelon, Kinston 2016. Plant Disease Management Reports 11: V111.

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6. Adams M. L. and Quesada-Ocampo L. M. (2018) Evaluations of fungicides for control of powdery mildew on winter squash, Kinston 2017. Plant Disease Management Reports: submitted.
7. Lange, H.W., Smart, C.D. and Seaman, A.J. 2018. Evaluation of materials allowed for organic production on downy mildew of cucumber, 2017. Plant Disease Management Report. Volume 12.
8. 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.
9. Miller N., Adams M. L., and Quesada-Ocampo L. M. (2017) Evaluation of fungicides for Fusarium wilt of watermelon, 2016. Plant Disease Management Reports 11: V135.
10. Miller N., Adams M. L., and Quesada-Ocampo L. M. (2017) Evaluation of fungicides for control of Fusarium wilt of watermelon, Salisbury, NC, 2015. Plant Disease Management Reports 11: V134.
11. Noël N.A. and Quesada-Ocampo L. M. (2017) Tolerance of watermelon lines to cucurbit anthracnose, 2016. Plant Disease Management Reports 11: V062.
13. Noël N. A. and Quesada-Ocampo L. M. (2018) Tolerance of watermelon cultivars to cucurbit anthracnose, 2017. Plant Disease Management Reports: submitted.
14. Schultheis, J.R., K.D. Starke, and A.L. Wszelaki. 2018. 2016 North Carolina and Tennessee pumpkin cultivar evaluations. Horticulture Series No. 216. 38 pp.
15. Schultheis, J.R. and K.D. Starke. 2018. 2017 North Carolina watermelon standard and mini-size cultivar evaluations. Horticulture Series No. 221. 59 pp.
16. Schultheis, J.R. and K.D. Starke.2018. 2017 North Carolina orange flesh cultivar evaluations. Horticulture Series 220, 36 pp.
17. Schultheis, J.R. K.D. Starke, and A.L. Wszelaki. 2018. 2017 North Carolina and Tennessee pumpkin cultivar evaluations. Hort Research Series 219. 41 pp.

Cumulative CucCAP

PUBLICATIONS,

RESOURCE MATERIALS

and

PRESENTATIONS

PUBLICATIONS *(Current year in italics)*

REFEREED PUBLICATIONS
(total- 56; added this year-23)

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Branham SE, A Levi, MW Farnham, WP 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

Branham, S., L. Vexler, A. Meir, G. Tzuri, Z. Frieman, A. Levi, W.P. Wechter, Y. Tadmor and A. Gur. ***2017.*** *Genetic mapping of a major codominant QTL associated with β-carotene accumulation in watermelon. Mol. Breeding https://doi.org/10.1007/s11032-017-0747-0 .*

Branham SE, Levi A, Katawczik M, Fei Z, Wechter WP. ***2018.*** *Construction of a genome-anchored, high-density genetic map for melon (Cucumis melo L.) and identification of Fusarium oxysporum f. sp. melonis race 1 resistance QTL. Theor Appl Genet doi: 10.1007/s00122-017-3039-5*

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

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(total-23; added this year-7)

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.

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Book/Book Chapters

*Adkins, S.T., and Kousik, C.S. **2017**. Cucumber vein yellowing virus. Compendium of Cucurbit Diseases. American Phytopathological Society. 2017:143-144.*

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*McCreight, J.D. **2017.** Botany and culture, p. 1–9. In: A.P. Keinath, W.M. Wintermantel, and T.A. Zitter (eds.). Compendium of cucurbit diseases and insect pests, 2nd ed. APS Press, St. Paul, Minn.*

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*McCreight, J.D. and A.P. Keinath. **2017.** Crown blight of melons and crown decline of watermelon, p. 185–186. In: A. Keinath, W.M. Wintermantel, and T.A. Zitter (eds.). Compendium of cucurbit diseases and insect pests, 2nd ed. APS Press, St. Paul, Minn.*

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Many members of CucCAP contributed chapters to:

Grumet R, Katzir N, Garcia-Mas J. 2017. *Genetics and Genomics of Cucurbitaceae*. Plant Genetics and Genomics: Crops and Models. Vol. 20 Springer International Publishing. ISBN978-3-319-49330-5

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

Plant variety protection (PVP)

*Wechter, P., R. Hassell and A. Levi. **2018**. Plant variety protection (PVP) for 'Carolina Strongback' a watermelon rootstock with resistance to Fusrium wilt and root-knot nematodes.*

EXTENSION PUBLICATION, WEB CONTENT and OUTREACH RESOURCES

EXTENSION PUBLICATIONS
(total-43; added this year-14)

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.

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*Adams M. L., Parada C. H., and Quesada-Ocampo L. M. **2017.** Evaluation of fungicides for control of Phytophthora fruit rot of watermelon, Kinston 2016. Plant Disease Management Reports 11: V11*

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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.

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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.

*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.*

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*Lange, H.W., Smart, C.D. and Seaman, A.J. **2018.** Evaluation of materials allowed for organic production on downy mildew of cucumber, 2017. Plant Disease Management Report. Volume 12.*

*Miller N., Adams M. L., and Quesada-Ocampo L. M. **2017.** Evaluation of fungicides for Fusarium wilt of watermelon, 2016. Plant Disease Management Reports 11: V135.*

*Miller N., Adams M. L., and Quesada-Ocampo L. M. **2017.** Evaluation of fungicides for control of Fusarium wilt of watermelon, Salisbury, NC, 2015. Plant Disease Management Reports 11: V134.*

*Noël N.A. and Quesada-Ocampo L. M. **2017.** Tolerance of watermelon lines to cucurbit anthracnose, 2016. Plant Disease Management Reports 11: V062.*

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

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*Schultheis, J.R., K.D. Starke, and A.L. Wszelaki. **2018**. 2016 North Carolina and Tennessee pumpkin cultivar evaluations. Horticulture Series No. 216. 38 pp.*

*Schultheis, J.R. and K.D. Starke. **2018.** 2017 North Carolina watermelon standard and mini-size cultivar evaluations. Horticulture Series No. 221. 59 pp.*

*Schultheis, J.R. and K.D. Starke.**2018.** 2017 North Carolina orange flesh cultivar evaluations. Horticulture Series 220, 36 pp.*

Schultheis, J.R. K.D. Starke, and A.L. Wszelaki. ***2018.*** *2017 North Carolina and Tennessee pumpkin cultivar evaluations. Hort Research Series 219. 41 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
Coffey, M.D. and McCreight, J.D. ***2017****. Cucurbit Powdery Mildew: Melon Powdery Mildew Database at UC Riverside: powderymildew.ucr.edu.*
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
Hausbeck, M.K., and Linderman, S.D. ***2016.*** *Managing Phytophthora on cantaloupe, muskmelon and watermelon. https://veggies.msu.edu/wp- content/uploads/2017/05/FS_Managing-Phytophthora-on-Melon.pdf.*
Hausbeck, M., Krasnow, C., and Linderman, S. ***2017.*** *Phytophthora disease reported on winter squash and pumpkin, scout and treat now to preserve your crop. Michigan State University Extension News for Agriculture: Vegetables, 14 Jul. http://msue.anr.msu.edu/news/phytophthora_disease_reported_on_winter_squash_and_pumpkin.*

Spanish Factsheets

Hausbeck, M.K., C. Krasnow, and S.D. Linderman. 2016. Managing Phytophthora on Winter Squash and Pumpkin. Spanish translation by Linares Ramírez, A.M. and M. Miranda. ***2017.*** *Manejo de Phytophthora en calabaza de invierno y en calabaza. [Factsheet]. https://cuccap.org/espanol/manejo-de-phytophthora-en-calabaza-de-invierno-y-en-calabaza/*
Hausbeck, M.K. and S.D. Linderman. 2017. Monitoring and managing cucurbit downy mildew. Spanish translation by Linares Ramírez, A.M. and M. Miranda. ***2018.*** *Monitoreo y manejo del añublo lanoso en las cucurbitáceas. [Factsheet] https://cuccap.org/espanol/monitoreo-y-manejo-del-anublo-lanoso-de-las-cucurbitaceas/*

Hausbeck, M.K. and S.D. Linderman. 2016. Managing Phytophthora on cantaloupe, muskmelon and watermelon. Spanish translation by Linares Ramírez, A.M. and W. Seda. ***2017****. Manejo de Phytophthora cantalupo, melón y sandía. [Factsheet] https://cuccap.org/espanol/manejo-de-phytophthora-en cantalupe-melon-y-sandia/*

Hausbeck, M.K. and S.D. Linderman. 2016. Managing Phytophtora on cucumber. Spanish translation by Linares Ramírez, A.M. and W. Seda. ***2017.*** *Manejo de Phytophthora en pepino. [Factsheet] https://cuccap.org/espanol/manejo-de-phytophthora-en-pepino/*

Hausbeck, M.K. and S.D. Linderman. 2016. Managing Phytophthora on summer squash and zucchini. Spanish translation Linares Ramírez, A.M. and W. Seda. ***2017****. Manejo de Phytophthora en calabaza de verano y calabacín. https://cuccap.org/espanol/manejo-de-phytophthora-en-calabaza de-verano-y-calabacin/*

Hausbeck, M.K. and S.D. Linderman. 2017. Monitoring and managing cucurbit downy mildew. Spanish translation by Linares Ramírez, A.M. and M. Miranda. ***2018.*** *Monitoreo y manejo del añublo lanoso en las cucurbitáceas. [Factsheet] https://cuccap.org/espanol/monitoreo-y-manejo-del-anublo-lanoso-de-las-cucurbitaceas/*

Hausbeck, M.K., J. Morrice, and S.D. Linderman. 2016. Management of cucurbit downy mildew for home gardeners. Spanish translation by Linares Ramírez, A.M. and M. Miranda. Seda. ***2018.*** *Manejo del añublo lanoso de las cucurbitáceas para los agricultores. [Factsheet] https://cuccap.org/espanol/manejo-del-anublo-lanoso-de-la-cucurbitaceas-para-los-agricultores/.*

Quesada-Ocampo, L, 2013. Gummy Stem Blight of Cucurbits. Spanish translation by Linares Ramírez, A.M. and R. McPhail. ***2017****. Pudrición gomosa en las cucurbitáceas. [Factsheet] https://content.ces.ncsu.edu/pudricion-gomosa-del-tallo-en-cucurbitaceas*

Quesada-Ocampo, L. 2015. Cucurbit Powdery Mildew. Spanish translation by Linares Ramírez, A.M. ***2017****. Añublo polvoriento en las cucurbitáceas. [Factsheet] https://content.ces.ncsu.edu/anublo-polvoriento-en-cucurbitaceas*

Quesada-Ocampo, L. 2013. Anthracnose of Cucurbits. Spanish translation by Miranda, M. and A. M. Linares Ramírez. ***2017.*** *La actracnosis de las cucurbitáceas. [Factsheet]. https://content.ces.ncsu.edu/la-antracnosis-de-las-cucurbitaceas*

Quesada-Ocampo, L. 2013. Cucurbit Downy Mildew. Spanish translation by Linares Ramírez, A.M. ***2017****. Añublo lanoso en las cucurbitáceas. [Factsheet]. https://content.ces.ncsu.edu/anublo-lanoso-en-cucurbitaceas*

Quesada-Ocampo, L. and N. Miller. 2015. Fusarium Wilt of Watermelon. Spanish translation by Linares Ramírez, A.M. ***2017****. Marchitez de Fusarium en Sandia. [Factsheet]. https://content.ces.ncsu.edu/marchitez-de-fusarium-en-sandia*

Smart, C. 2017. The facts about Phytophthora blight. Spanish translation by Linares Ramírez, A.M. and R. McPhail. ***2017****. Infección de Phytophthora. [Factsheet]. https://cuccap.org/espanol/infeccion-de-phytophthora/*

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.

PRESENTATIONS

SCIENTIFIC CONFERENCES and UNIVERSITY PRESENTATIONS
(total- 84; added this year- 42)

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.

Alzohairy, S.A., Hammerschmidt, R., and Hausbeck, M.K. ***2017.*** *Characterization of the structural basis of winter squash fruit age-related resistance to Phytophthora capsici. American Phytopathological Society Annual Meeting, San Antonio, TX, 5-9 Aug. Poster*

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

Daley, J. and T. Wehner. ***2017****. Screening for bacterial fruit blotch resistance in watermelon fruit. Abstract and Poster. Crop Science Society of America, Tampa, FL.*

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

Fei, Z. ***2018****. Cucurbit Genomics Database for cucurbit genomics, genetics and breeding. PAG. January.*

Fei Z, Wu S. ***2017.*** *Cucurbit Genomics Database Workshop. The XIV Solanaceae and III Cucurbitaceae Genomics Joint Conference. September.*

Guo, S. ***2018****. Comparative population genomics reveals the evolution of fruit quality traits during watermelon domestication. PAG. January.*

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

Grumet R. ***2017.*** *The USDA-SCRI CucCAP project: Leveraging applied genomics to increase disease resistance in cucurbit crops. SCRI Advisory Board Meeting, Aug. 17, Traverse City MI*

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

Indermaur, E., J. Schultheis, and K. Starke. ***2018****. Galia specialty melon opportunities and evaluations. SR-ASHS, Jacksonville, FL, February.*

Kaur, N., Chen, W., Fei, Z. and Wintermantel, W.M. ***2017.*** *"Transcriptome changes occurred in the whitefly, B. tabaci MEAM1 in response to feeding on melon infected with the crinivirus, CYSDV," 3rd Hemipteran-Plant Interactions Symposium, Madrid. Spain. June 4-8, 2017.*

Kaur, N., Chen, W., Fei, Z. and Wintermantel, W.M. ***2017.*** *"Transcriptome changes occurred in the whitefly, B. tabaci MEAM1 in response to feeding on CYSDV-infected melon," American Phytopathological Society annual meeting, San Antonio, TX, August 5-9, 2017.*

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. ***2017****. Presented an invited seminar on "Progress and challenges in managing watermelon diseases". Department of Plant Pathology, University of Georgia Athens, GA, Aug. 2017. >50 attendees*

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. 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., 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., Ikerd, J.L. and Mandal, M.K. ***2017****. Long term monitoring of cucurbit powdery mildew (Podosphaera xanthii) races in Charleston, South Carolina. Presented at the Annual meeting of the American Phytopathological Society, San Antonio, TX August 2017. 503-P*

Kousik, C.S., Ikerd, J.L., and Mandal, M.K. ***2018****. Relative susceptibility of commercial watermelon varieties to powdery mildew. Presented at the Annual meeting of the Southern Division, American Phytopathological Society (SD-APS).Fayetteville, AR Feb 16-18, 2018.*

Kousik, C.S., Mandal, M.K., Ikerd, J.L., Adkins, S., and Turechek, W. ***2018.*** *Powdery mildew resistant watermelon germplasm lines USVL608-PMR, USVL278-PMR, USVL313-PMR and USVL585-PMR. Presented at the Watermelon Research and Development Group (WRDG) meeting. Southern Region ASHS, Jacksonville, FL. February 2018.*

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.

Krasnow, C.S., and Hausbeck, M.K. ***2016.*** *Age-related resistance of Cucurbita spp. fruit to Phytophthora capsici. Abstr. Phytopathology 106 (Suppl.):S1.5.*

Linares-Ramirez, A.M. 2016. Cucurbits: From to the field to the lab. Agricultural Experimental Station, University of Puerto Rico.

Ling, K.-S. ***2017.*** *Presented invited seminars on "Developing genome-guided strategies to manage viral diseases of cucurbit crops" in four institutions throughout China, including:*
Zhengzhou Fruit Research Institute,
Beijing Vegetable Research Center (China, Israel, and the U.S. Workshop on Cucurbit Research), Zhejiang Academy of Agricultural Sciences
Fujian Agricultural and Forestry University.

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)

*Mandal, M.K., Ikerd, J.L., Wallace, E.C., Rebbeca, G., Turechek, W., Quesada-Ocampo, L.M. and Kousik, C.S. **2017**. Population biology of the downy mildew pathogen on tolerant and susceptible cucumber in the southeastern United States. Presented at the Annual meeting of the American Phytopathological Society, San Antonio, TX August 2017. 563-P*

*Mandal, M.K., Suren, H. and Kousik, C.S. **2017**. Transcriptomic profiling of watermelon-powdery mildew (Podosphaera xanthii) interactions. Presented at the Annual meeting of the American Phytopathological Society, San Antonio, TX August 2017. 361-P*

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

*Mansfeld B, Grumet R. **2018.** QTLseqr: An R package for bulk segregant analysis with next generation sequencing. PAG XXVI, San Diego CA.*

*Mantooth, K.L., Ikerd, J.L., Mandal, M.K. and Kousik, C.S. **2017**. Potential sources of resistance to Phytophthora crown rot in Cucurbita maxima and Cucurbita moschata. Presented at the Annual meeting of the American Phytopathological Society, San Antonio, TX August 2017. 291-P*

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)

*Natwick, E.T., W.M. Wintermantel, R.L. Gilbertson, S.G. Blanco, and J.D. McCreight. **2017.** "Evaluation of potential new sources of melon host plant Resistance to the whitefly, Bemisia tabaci," 3rd Hemipteran-Plant Interactions Symposium, Madrid. Spain. June 4-8, 2017.*

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

*Patel, T. and T. Wehner. **2017**. Identification of new resistance sources and SNPs markers in watermelon for anthracnose (Colletotrichum orbiculare). Abstract and Poster. National Association of Plant Breeders, Davis, CA.*

*Perkins-Veazie, P., J. Schultheis, and T. Birdsell. **2018.** Butternut squash in the south: postharvest quality after curing. SR-ASHS, Jacksonville, FL, February.*

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

*Quesada-Ocampo LM. **2017**. From the field to the lab and back: translational strategies to improve disease control in vegetable crops. VIB-PSB-NC State Plant Sciences Workshop, Ghent, Belgium*

*Rivera-Burgos L. and T. Wehner. **2017**. Evaluation of gummy stem blight resistance in a recombinant inbred line watermelon population. Abstract and Poster. National Association of Plant Breeders, Davis, CA*

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.

*Smart, C.D. SUNY Potsdam November **2017**, Potsdam NY. Genomic approaches to understand and manage plant disease epidemics.*

*Smart, C.D. James Hutton Institute, August 10, **2017**, Dundee Scotland. Comparing sexual and asexual Phytophthora species.*

*Sui, X., Li, R., Wu, Z., Ling K.-S. **2018.** Seed transmissibility of Cucumber Green Mottle Mosaic Virus in cucurbits and seed health assays. Presented at the Watermelon Research and Development Group (WRDG) meeting. Southern Region ASHS, Jacksonville, FL. February 2018.*

*Trandel, M.A., P. Perkins-Veazie, J. Schultheis, C. Gunter, and E. Johannes. **2018.** Hollow heart formation in grafted and non-grafted watermelon. SR-ASHS, Jacksonville, FL, February.*

*Vogel, G., LaPlant, K., Reeves, E., Mazourek, M., Gore, M. and Smart, C.D. **2017.** Evaluation of Cucurbita pepo breeding lines with reduced susceptibility to root and crown rot caused by Phytophthora capsici. American Phytopathological Society. San Antonio TX August 2017*

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

*Wechter, P. **2017**. "Identification of quantitative trait loci associated with resistance to race 1 Fusarium wilt in Cucumis melo," American Phytopathological Society annual meeting, San Antonio, TX, August 5-9, 2017*

*Wechter, P. **2017**."Mapping Resistance to Alternaria Cucumerina in Muskmelon," Plant and Animal Genome meeting, San Diego, CA, January 14-18, 2017.*

*Weng Y. **2017**. Improve QTL detection power: cucumber downy mildew resistance. An invited talk at China Agricultural University (Beijing, China, July 111, 2017)*

*Weng et al. **2018.** Genetic architecture of downy mildew resistance in cucumber. Cucurbit workshop. Plant and Animal Genome Conference (Jan 9-13, 2018, San Diego, CA).*

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.

Wu S, Zhong Y, Grumet R, Levi A, Weng Y, Mazourek M, McCreight J, Katzir N, Garcia-Mas J, Fei Z. ***2017.*** *Cucurbit genomics database. Sol/Cuc Conference, Valencia, Spain*

Wu S. ***2018****. Cucurbita genome sequences provide insights into polyploid genome evolution and heterosis in interspecific hybrid. PAG. January.*

Yuhui, W., K. VandenLangenberg, T. C. Wehner and Y. Weng. ***2018.*** *Genetic architecture of downy mildew resistance in cucumber. Plant Animal Genome Conf., San Diego CA.*

Zheng Y. ***2018****. Cucurbit Genomics Database: Integration genetic and genomics resources for cucurbit breeding. PAG. January*

EXTENSION and OUTREACH PRESENTATIONS
(total- 130; added this year- 50)

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.

Ando, K. and J.D. McCreight. ***2017.*** *"Potential for production of Turkmen melons in California," National Association of Plant Breeders, Davis, CA, August 2017. 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., Jennings K.M., Monks D.W., Louws F.J., Jordan D.L., Schultheis J.R. 2015. Critical period for weed control in grafted and nongrafted triploid watermelon (Poster). North Carolina Crop Protection School. December 2, Cary, NC.

Bertucci M.B., Jennings K.M., Monks D.W., Louws F.J., Jordan D.L., Schultheis J.R. 2016. Effect of grafting on the critical period of weed control of triploid watermelon (Poster). North Carolina Crop Protection School. December 6, Cary, NC.

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.

Birdsell, T., J. Schultheis, and P. Perkins-Veazie. ***2017.*** *Butternut squash cultivar, production, harvest, and enterprise budget considerations. Annual North Carolina Vegetable Growers Association. Myrtle Beach, SC, November.*

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.

Grumet R. ***2017****. CucCAP: Leveraging applied genomics to increase disease resistance in cucurbit crops PPI Spring Meeting, April 19, Milwaukee WI*

Grumet R, Lin YC, Mansfeld B. ***2017****. Resistance of cucumber fruit to Phytophthora capsici. PCIC/PPI, Nov.1, Chicago IL*

*Grumet R, Lin YC. **2017.** Resistance to Phytophthora fruit rot in cucumber. 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. 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, 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.

*Hausbeck, M. **2018.** Phytophthora management for winter squash, cucumber and pepper. Grower Meeting, Hudsonville, MI, 21 Feb. 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 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.

*Indermaur, E., K. Starke, and J. Schultheis. **2017.** Galia and canary melon cultivar evaluation. Annual North Carolina Vegetable Growers Association. Myrtle Beach, SC, November.*

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.

*Kousik, C.S. **2017**. Presented information on Phytophthora fruit rot and powdery mildew of watermelon to the U.S. Secretary of Agriculture, Dr. Sonny Purdue and his team when they visited the U.S. Vegetable Laboratory, USDA, ARS in Charleston, SC. August 21, 2017.*

*Kousik, C.S. **2017**. Provided information to Sarah Mock, Washington D.C. Bureau Chief for RFD-TV on research being conducted on watermelon at the U.S. Vegetable Laboratory and details of the visit of Dr. Sonny Purdue to USVL. August, 21, 2017. The interview was aired by RFD-TV and is located at website: https://youtu.be/R4tHGZSJqRI*

*Kousik, C.S. **2018**. Best practices to reduce impact of Phytophthora. Southeast Regional Fruit and Vegetable Conference, Savannah, GA, January 2018. >100 attendees at the talk.*

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.

*Mandal M.K., Kousik, C.S. **2017**. Resistance Signaling in Watermelon using Genomics and Metabolomics. Invited talk to seed industry HM. Clause, (HARRIS MORAN and CLAUSE, LIMAGRAIN), Sacramento, Davis CA. June, 2017. >30 attendees.*

*Mandal, M.K. and Kousik, C.S. **2018**. Multidimensional approaches to study host-resistance signaling in cucurbits against diseases: from epidemiology to omics. Invited talk to USVL USDA-ARS, Charleston SC. January, 2018. >40 attendees*

*Mandal, M.K., Suren, H., Ikerd, J.L., and Kousik, C.S. **2018.** Molecular Dissection of Resistance Signaling during Compatible and Incompatible Watermelon- Powdery Mildew (Podosphaera xanthii) Interactions using RNA-Seq Approach. Presented at the Watermelon Research and Development Group (WRDG) meeting. Southern Region ASHS, Jacksonville, FL. February 2018.*

Mazourek M. 2017. Vegetable Breeding Institute Field Days. Freeville, NY. Aug 28, 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.

*McCreight, J.D. **2017**. "Agricultural Research Technology Center," Western Regional Seed Physiology Research Group, University of California, Davis, January 24, 2017.*

*McCreight, J.D. **2017**. AgKnowledge class annual visit to U.S. Agricultural Research Station, Grower-Shipper Association of Central California, Salinas, CA, June 2017.*

*McCreight, J.D. **2017**. Assisted Seed Central (http://www.seedcentral.org) hosting 100 persons from ag related companies with research updates and provided laboratory and greenhouse tours, Salinas, CA, April.*

*McCreight, J.D. **2017.** U.S. Plant Breeding: Lettuce, Spinach, Melon, and Sugar beet. Seed Central (an initiative of the Seed Biotechnology Center at the University of California Davis, and Seed Quest), Salinas CA, April.*

*McCreight, J.D. **2017**. Melon powdery mildew race variation in California. University of California, Cooperative Extension, Imperial County, 28th Annual Fall Desert Crops Workshop, Imperial, CA, December.*

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. 2015. New control options for Fusarium wilt in watermelon. 30th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, Dec.

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, Druffel A, Adams M, Quesada-Ocampo LM. **2017.** Control options for Fusarium wilt of watermelon. 32nd Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, NC, December*

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.

Ribera, Luis A. Trade impact talks:

*APHIS Project Kick-Off, Raleigh, North Carolina, January 31, **2017**.*

*C-FARE, Washington, DC, April 6, **2017**.*

*Viva Fresh 2017, Austin, Texas, April 21, **2017**.*

*Texas A&M AgriLife Program Planning Meeting, Rosenberg, Texas, May 9, **2017.***

*Texas International Produce Association, Mission, Texas, May 30, **2017**.*

*Moosejaw, Canada, June 27, **2017**.*

*Imperial Valley EDC, Calexico, California, August 15, **2017***

*Ag. Economics Extension Tailgate Workshop, College Station, Texas, September 30, **2017**.*

*Extension Outlook Conference, Stillwater, Oklahoma, October 20, **2017***

*Del Rio Economic Development Council, Del Rio, Texas, November 2, **2017**.*

*Imperial Valley EDC Annual Banquet, Calexico, California, November 16, **2017***

*29th Annual Texas Plant Protection Conference, Bryan, Texas, December 5, **2017**.*

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

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. **2017.** Perspectives and opportunities for growing orange flesh and specialty melons. Vine crops Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids,MI Dec. 2017*

*Schultheis, J. **2017.** The North Carolina pickling industry and use of parthocarpic fruiting types. Pickling Cucumber Session, Great Lakes Fruit, Vegetable and Farm Market Expo, Grand Rapids,MI, Dec.*

*Schultheis, J. **2018**. Melon varieties; orange flesh and various specialty melon opportunities. DelMar Vegetable meeting. City, DE, January 2018.*

*Schultheis, J. **2018.** A melon mix of specialty and cantaloupe types. Ontario Fruit and Vegetable Convention. Niagara Falls, ON Canada. February 2018*

*Schultheis, J. **2018.** The North Carolina pickling industry and use of parthenocarpic fruiting types. . Regional Pickling Cucumber meeting, Wilson Co., NC, March*

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

*Schultheis, J. and K. Starke. **2017**. Specialty melon opportunities. Annual North Carolina Vegetable Growers Association, Myrtle Beach, SC, November.*

*Schultheis, J. and K. Starke. **2017.** Watermelon production considerations; pollenizer and grafting. Annual North Carolina Vegetable Growers Association, Myrtle Beach, SC, November.*

Schultheis, J. and K. Starke. Standard size watermelon cultivar and quality results, North Carolina, 2017. Georgia Watermelon Association. Saint Simons Island, GA, January 2018.

*Schultheis, J. and K. Starke. **2018.** Standard size watermelon cultivar yield and quality results, North Carolina, 2017. 2018 Watermelon Research and Development Group Annual meeting, Jacksonville, FL, February.*

Schultheis, J.R. and K.D. Starke. ***2018.*** *Pollenizer placement considerations effects on watermelon (Citrullus lanatus) yield and quality over two growing seasons. Watermelon Research and Development Group Annual meeting, Jacksonville, FL, February.*

Schultheis, J. and K. Starke. ***2018.*** *Standard size watermelon cultivar yield and quality results, North Carolina, 2017. North Carolina Watermelon Association, Wrightsville, NC, March.*

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.

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.

Smart, C.D. ***2017.*** *Twilight discussion of cucurbit diseases. Western NY Field Days. Portland, NY, Aug 2017*

Smart, C.D. ***2017.*** *On-farm discussion of methods to control Phytophthora blight in summer squash. Seneca Falls NY, July 2017*

Smart, C.D. ***2017.*** *Role of cover crops in Phytophthora blight control. Northeast Cover Crops Council. November 2017*

Smart, C.D. and Lange, H. ***2018****. Fungus, Water Mold or Bacteria: Which is Which in My Vine Crops? NewYork State Producers Expo. January*

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.

Starke, K. and J. Schultheis. **2017.** *Honeydew, crisp flesh and piel de sapo melon options. Annual North Carolina Vegetable Growers Association. Myrtle Beach, SC, November.*

Starke, K.D. and J.R. Schultheis. ***2018.*** *Mini-watermelon cultivar yield and quality evaluations in North Carolina, 2017. Watermelon Research and Development Group Annual meeting, Jacksonville, FL, February.*

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.

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

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

*Weng Y. **2017.** "Genetic architecture of downy mildew resistances in cucumber". 2017 PPI Annual Meeting (Chicago, IL, Nov 1 2017)*

*Weng Y. **2017.** Genetic resources for cucumber breeding - a molecular perspective. PPI 2017 Spring Meeting (4-19-2017, Milwaukee, WI).*

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.

*Wessel-Beaver, L. and A.M. Linares Ramirez. **2017.** Dos Virus Importantes en la Calabaza: Mosaico Amarillo del Calabacín (ZYMV) y Mancha Anular de la Papaya (PRSV). Expo Hort, Lajas, PR 4 Abril. 118 attendees*