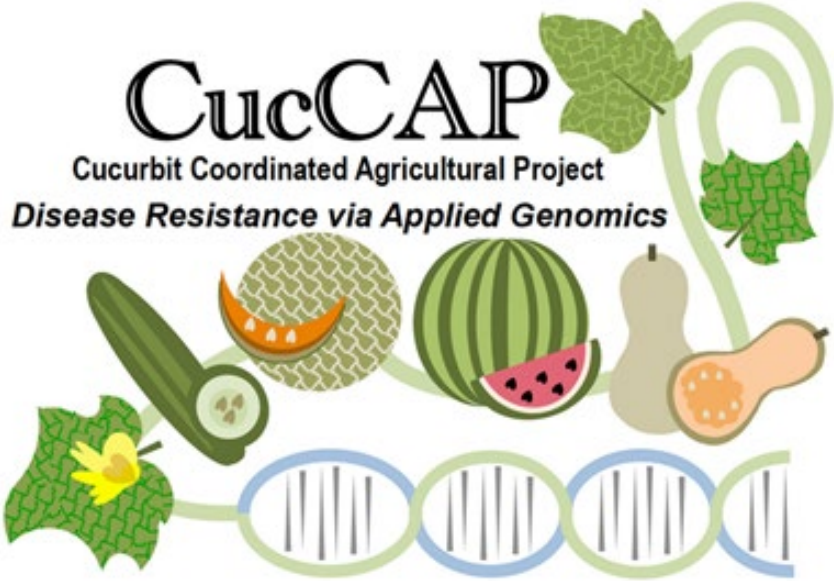
CucCAP2

Harnessing genomic resources for disease resistance and management in cucurbit crops – bringing the tools to the field



CucCAP2 Team Meeting

March 20-21, 2025

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AGENDA

CucCAP2 team meeting – March 20-21, 2025

*(**Note**: all times are U.S. Eastern Daylight Time)*

THURSDAY, MARCH 20

8:00-8:15 Arrival, welcome, Introduction of participants
8:15-8:30 Introduction to meeting, Overview of CucCAP accomplishments, Evaluating impact

Session I – Genomic Tools
Objective 1: Develop novel advanced bioinformatic, pan-genome, and genetic mapping tools for cucurbits.
- Develop high-resolution genotyping and advanced genome and pan-genome platforms for cucurbit species.
- Perform de novo genome assembly and pan-genome construction
- Develop breeder-friendly web-based databases for phenotypic, genotypic and QTL information.
- Perform seed multiplication and sequencing analysis of core collections of the four species, provide community resources for genome wide association studies (GWAS).
- [E/O] Provide access to cucurbit genomics tools and databases via the Cucurbit Genomics website (cucurbitgenomics.org) and genomics and bioinformatics workshops

8:30-9:00 Progress and accomplishments: bioinformatics platforms, databases, genomic analyses (Fei)
9:00-9:10 Discussion - Final priorities, data access and distribution
9:10-9:30 Status, distribution, and use of core panels – Overview and Discussion (seed stocks; resequencing; seed handling and distribution) (Grumet, Reitsma; Povilus, Harrison)

9:30 – 9:45 Break

Session II – Breeding for disease resistance
Objective 2. Perform genomic-assisted breeding to introgress disease resistance into cucurbit cultivars.
- Utilize genomic approaches to map resistance loci for key cucurbit diseases (QTL mapping, BSA, GWAS)
- Fine map and develop and verify molecular markers for efficient trait selection
- Introgress, pyramid, stack 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

9:45-11:00 **Watermelon**: Progress and accomplishments
Fusarium race 1 and 2, gummy stem blight, Phytophthora, powdery mildew, CYSDV, GCMMV, PRSV-W, ZYMV
(Levi, Branham, Kousik, Ling, McGregor, Reddy, Wechter)
11:00-11:15 Discussion

11:15-12:00 **Melon**: Progress and accomplishments
powdery mildew, CMV, CYSDV, Fusarium
(McCreight, Branham, Kousik, Wechter, Wintermantel)
12:00-12:10 Discussion

12:10-1:30 ***Lunch*** *Brainstorming- building on CucCAP progress*
- How to utilize knowledge and tools developed from CucCAP?

1:30-1:45 Report out from brainstorming sessions

1:45-2:15 **Cucumber**: Progress and accomplishments
downy mildew, Phytophthora, CGMMV
(Weng, Grumet, Keinath, Ling)

2:15-2:25 Discussion

2:25-3:15 **Squash**: Progress and accomplishments
C. moschata – powdery mildew, *Phytophthora*, *C. maxima – Phytophthora*,
C. pepo – powdery mildew, *Phytophthora*
(Mazourek, Hausbeck, Kousik, Meru, Smart)

3:15-3:25 Discussion

3:25-3:45 Break

Session III – Integrated disease management and economic analysis

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

- Perform multi-location, multi-isolate trials and pathogen population analyses
- Determine economic impacts of disease and control tools and valuation of crop attributes
- [E/O] Provide readily accessible disease management information and recommendations via multiple means including the CucCAP website (cuccap.org)

3:45-4:45 Progress and accomplishments
Multi-location trials, pathogen population analyses, economic analyses, delivery of disease information
(Quesada, Hausbeck, Keinath, Knuth, Kousik, Schulthies, Smart)

4:45-5:00 Discussion

Evening CucCAP Networking Dinner

FRIDAY, MARCH 22

8:00-8:15 Arrive

Session IV – Accomplishments and Impact

8:15-9:15 How best to summarize accomplishments?
Criteria for evaluating impact?
How to obtain information regarding impact (from who? What questions?)
Breakout groups:
Genomic and Bioinformatic Tools
Breeding
Integrated Disease Management

9:15-10:15 Report out from groups regarding accomplishments -
What criteria/what to measure? How to get feedback? Who to share information with?

10:15-11:00 Final details – funding, travel, logistics, Cucurbitaceae 2026
Wrap up discussions, feedback from external reviewers

CucCAP Team

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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 Association	George Szczepanski	Executive Director
California Melon Research Board	Steve Smith	Former Chair, California Melon Research Board
California Melon Research Board	Bart Fisher	Chair, California Melon Research Board President Fisher Ranch Corporation
Michigan Vegetable Council	Greg Bird	Executive Director
Pickle Packers International	John Cox	Executive Vice President
Swanson Pickles and Pickle Packers International	John Swanson	President Swanson Pickle Company; Research Board, Pickle Packers International
Seed Industry		
BASF	Mona Mazaheri Eben Ogundiwin	
Bayer Crop Science	Nischit Shetty	NAM Cucurbit Breeding Lead
East-West Seeds	Caleb Orchard Marilyn Hinlo Simon de Hoop	
Enza Zaden	Bart Kay Walter Verweij Tilly Elridge	Research Molecular Biology
Johnny's Selected Seeds	Lindsay Wyatt Rob Johnston	Squash and pumpkin breeder
Limagrain Vegetable Seeds/HM Clause	Kishor Bhattarai Peter Kraan	Research Discovery Manager, HM Clause, Vegetable Seeds Division
Origene America	Eyal Vardi	Founder and CEO
Sakata Seeds	Nihat Guner Jeff Zischke	Senior watermelon breeder
Syngenta Seeds Inc.	Matt Kinkade Sudarshana Padma	Team Lead, watermelon breeding
Taki Seeds	Yasushi Tokairin, Yamamoto Gaku Luis Maas	 R&D Director
United Genetics	Raquel Salaki Xuemei Zhang	

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CucCAP2 Project Objectives

Objective 1. Develop advanced bioinformatic, pan-genome, and genetic mapping tools for cucurbits.

1.1. Develop genomic and bioinformatic platforms for cucurbit crops: high-resolution genotyping platforms; advanced genome and pan-genome platforms; de novo genome assembly and pan-genome construction; breeder-friendly web-based database for phenotypic, genotypic and QTL information.

1.2 Perform seed multiplication and sequencing analysis of core collections of the four species, define phylogenetic relationships and population structure, provide community resources for genome wide association studies (GWAS).

[E/O] Maintain and enhance the Cucurbit Genomics Database (http://cucurbitgenomics.org/), providing publicly available tools to analyze and integrate genotype, phenotype, and pan-genome data.

Objective 2. Utilize genomic approaches to identify, map, and develop markers for resistances to priority diseases identified by cucurbit industries.

2.1. Map resistances and identify QTL for key cucurbit diseases: identify QTL by standard mapping, bulked-segregant analysis, GWAS, synteny; fine map, refine QTL

2.2. Develop and verify markers for MAS.

[E/O] Share QTL information and markers with scientific community and seed industry through publications, scientific and extension presentations, and collaborative research.

Objective 3. Introduce and pyramid/stack resistances into advanced breeding lines.

3.1. Introgress resistance alleles into advanced breeding lines.

3.2. Pyramid/stack resistances: multi-locus marker-assisted selection (MAS); genomic selection; MAGIC population development in watermelon.

[E/O] Provide breeding lines and testing results through germplasm releases, publications, scientific presentations, field trials, and web-based and face-to-face extension venues

Objective 4. Perform multi-location, multi-isolate trials of resistances to improve integrated disease management, assess economic impacts, and provide state-of-the-art disease control recommendations.

4.1. Perform disease management information and recommendations.

4.2. Perform multi-location, multi-isolate trials and pathogen population analyses: evaluate cucurbit cultivars and breeding lines for disease resistance; evaluate integrated disease management in cucurbits combining host resistance and chemical control; analyze pathogen populations to inform breeding and disease management.

4.3. Economic impacts of disease and gains from control tools and valuation of crop attributes: determine economic impacts of disease and control tools; estimate industry valuation of improvement in crop attributes.

[E/O] Maintain and update the CucCAP website (https://cuccap.org) which provides diagnostic and disease control information, disease alerts, links to forecasting tools and project related news. Distribute trial and economic data through publications, extension venues, and the CucCAP website.

Project Structure – Team Organization

Table 4. CucCAP Teams			
Team	**PD, PIs and Co-PIs**		**Institution[a]**
	PD: Rebecca Grumet (RG)		MSU
Watermelon	***Amnon Levi – Team Leader***	(AL)	ARS-SC
	Sandra Branham	(SB)	CLU
	Shaker Kousik	(SK)	ARS-SC
	Kai-Shu Ling	(KSL)	ARS-SC
	Cecilia McGregor	(CM)	UGA
	Umesh Reddy	(UR)	WVSU
	Pat Wechter	(PW)	CLU
Melon	***Jim McCreight – Team Leader***	(JM)	ARS-CA
	Shaker Kousik	(SK)	ARS-SC
	Pat Wechter	(PW)	ARS-SC
	Bill Wintermantel	(BW)	ARS-CA
Cucumber	***Yiqun Weng- Team Leader***	(YW)	ARS-WI
	Rebecca Grumet	(RG)	MSU
	Anthony Keinath	(AK)	CLU
	Kai-Shu Ling	(KL)	ARS-SC
Squash	***Michael Mazourek – Team Leader***	(MM)	CU
	Mary Hausbeck	(MH)	MSU
	Shaker Kousik	(SK)	ARS-SC
	Geoffrey Meru	(GM)	UFL
	Angela Linares Ramírez	(ALR)	UPR
	Christine Smart	(CS)	CU
Genomics/ bioinformatics	***Zhangjun Fei – Team Leader***	(ZF)	BTI
	Amnon Levi (watermelon)	(AL)	ARS-SC
	Mike Mazourek (squash)	(MM)	CU
	Pat Wechter (melon)	(PW)	ARS-SC
	Yiqun Weng (cucumber)	(YW)	ARS-WI
	Shan Wu	(SW)	BTI
Integrated Disease Management	***Lina Quesada - Team Leader***	(LQ)	NCSU
	Mary Hausbeck	(MH)	MSU
	Anthony Keinath	(AK)	CLU
	Melinda Knuth	(MK)	NCSU
	Shaker Kousik	(SK)	ARS-SC
	Jonathan Schultheis	(JS)	NCSU
	Christine Smart	(CS)	CU
	Daniel Tregeagle	(DT)	NCSU

[a]Institution abbreviations: ARS-CA (Salinas), SC (Charleston), WI (Madison); BTI-Boyce Thompson Inst; CLU-Clemson Univ; CU-Cornell Univ; MSU-Michigan St Univ; NCSU-North Carolina St Univ; UGA-Univ Georgia; UFL- Univ Florida; UPR-Univ Puerto Rico; WVSU-West Virginia St Univ

TEAM REPORTS

Genomics and Bioinformatics Team

Team members:

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Shan Wu (Boyce Thompson Institute)
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Rebecca Grumet (Michigan State University)

Objectives

Develop novel advanced bioinformatic, pangenome, and genetic mapping tools for cucurbits.

1.1. Develop genomic and bioinformatic platforms for cucurbit crops.

1.1.1. Development of high-resolution genotyping platforms for cucurbits.

Genome resequencing of the cucumber (388 accessions) and squash (207 *Cucurbita pepo* accessions) core collections has been completed. The average depths of cleaned sequences of cucumber and squash cores are 52.7× and 53.4×, respectively. For melon (384 accessions) and watermelon (372 accessions) cores, genome sequencing has been completed for 323 accessions of each species. In addition, we have completed genome resequencing for 26 *C. maxima* and seven *C. moschata* accessions.

The sequence data for cucumber, squash, melon and watermelon cores have been processed for SNP and small indel calling using the Gy14 genome (v2.1), MU-CU-16 genome (v4.1), 97103 genome (v2.5) and DHL92 genome (v4), respectively, as the references. Summary statistics of the called variants are presented in **Table 1**. Raw sequencing data and called variants have been shred with industry partners who have requested access. Biallelic variants with MAF >0.01 for the cucumber and squash core collections are publicly available for mining at CuGenDBv2 (http://cucurbitgenomics.org/v2/genotype). The remaining accessions in the melon and watermelon cores are currently undergoing sample collection and DNA preparation. Variant datasets will be updated accordingly once new sequences become available.

Table 1 Summary of genome sequencing of cucurbit core collections

	cucumber	**squash**	**melon**	**watermelon**
No. accessions	388	207	384	372
No. DNA prepared	388	207	323	323
No. sequenced	388	207	323	323
Average sequencing depth	52.7	53.4	53.6	48.6
No raw SNPs	5,332,225	5,007,376	21,022,493	11,042,203
No. biallelic SNPs with MAF>0.01	2,680,887	4,653,265	10,294,239	6,057,627
No raw indels	1,385,149	2,008,251	4,481,966	1,732,023
No. biallelic indels with MAF>0.01	526,218	1,298,579	1,540,406	1,195,826

1.1.2. Development of novel, advanced genome and pangenome platforms for cucurbit species.
For cucumber, we selected 27 accessions for PacBio HiFi sequencing, including five wild *Cucumis sativus* var. *hardwickii*, four Xishuangbanna (*C. sativus* var. *xishuangbannanesis*), and 18 cultivated (*C. sativus* var. *sativus*) cucumbers. Ten of these 27 accessions are from the core collection. HiFi sequences have been generated for all the 25 accessions, with an average sequencing depth of 32.2×.

For watermelon, we selected a total of 135 accessions for reference-grade genome development, including one *Citrullus naudinianus*, one *C. rehmii*, two *C. ecirrhosus*, five *C. colocynthis*, 16 *C. amarus*, nine *C. mucosospermus*, six *C. lanatus* var. *cordophanus*, seven landraces, and 88 cultivars. HiFi sequences have been generated for these 135 accessions, with an average sequencing depth of 30.3×. Additionally, ONT ultra-long reads and Hi-C sequencing data have been generated for ten of these accessions, including one *C. colocynthis*, three *C. amarus*, one *C. mucosospermus*, one *C. lanatus* var. *cordophanus*, and four cultivars.

For melon, we selected a total of 32 representative accessions for HiFi sequencing, including 15 *C. melo* ssp. *melo* and 17 *C. melo* ssp. *agrestis* accessions. These accessions originate from various regions: 13 from India/Pakistan, two from Turkey, four from Americas, and two from Africa, four from Central/West Asia, seven from East Asia, and one from Europe. HiFi sequences have been generated for these 33 accessions, with an average sequencing depth of 33.7×. Additionally, Hi-C data have been generated for eight accessions, and ONT ultra-long reads have been generated for one accession.

For squash, we selected eight accessions for HiFi sequencing, including two from *Cucurbita pepo* ssp. *texana* (also known as ssp. *ovifera*) and six from *C. pepo* ssp. *pepo*. HiFi sequences have been generated, with an average sequencing depth of 30.0×. We also generated HiFi sequences for *C. maxima* Rimu and *C. moschata* Rifu.

1.1.3. De novo genome assembly and pangenome construction
We have completed the assembly and annotation of chromosome-scale genomes for the 27 cucumber accessions. The assembled genome sizes range from 259.1 Mb to 302.1 Mb (average: 286.8 Mb) and N50 contig sizes from 5.25 Mb to 29.81 Mb (average: 16.26 Mb). The BUSCO completeness rate for these genome assemblies ranges from 96.4% to 98.8%, with an average of 98.36%. An average of 95.7% of the contigs (ranging from 90.3% to 98.5%) are assigned to the seven cucumber chromosomes. Protein-coding genes have been predicted in these genomes, along with 12 previously published chromosome-scale cucumber genomes (including eight cultivated, one Xishuangbanna and three wild *hardwickii*). The number of predicted genes ranges from 21,347 to 22,551, with an average of 21,870. The BUSCO completeness rate for genes predicted from each of these 39 cucumber genome assemblies ranges from 93.0% to 97.0%, with an average of 96.1%. Using the newly assembled AM716 ('WI7631') genome as the reference/backbone, large structural variants (SVs) have been identified across these 39 cucumber genomes (**Table 2**). A graph pangenome has been constructed using the AM716 genome and the identified SVs. By leveraging the constructed graph pangenome, SVs were then genotyped in the core collection using the resequencing short reads.

For watermelon, we have completed chromosome-scale genome assemblies and gene predictions

for all 135 accessions. The assembled genome sizes range from 368.6 Mb to 406.7 Mb (average: 377.5 Mb) and N50 sizes are all greater than 20 Mb (20.37-35.64 Mb; an average of 30.49 Mb). The BUSCO completeness rate for these genome assemblies ranges from 93.9% to 99.2%, with an average of 99.0%. An average of 99.2% of the contigs (ranging from 96.2% to 99.9%) are assigned to the 11 watermelon chromosomes. Notably, 1,162 (78.2%) of the assembled chromosomes contain telomeres on both ends, and 781 (52.6%) are gapless. Additionally, seven genome assemblies are telomere-to-telomere (T2T) and completely gapless. The number of predicted protein-coding genes ranges from 20,834 to 23,330 (average: 21,791). The BUSCO completeness rate of predicted genes across these 135 genome assemblies ranges from 94.1% to 96.5%, with an average of 95.9%. Using the newly assembled T2T gapless '97103' genome as the backbone, SVs were identified across the 135 watermelon accessions, as well as three previously published long-read assemblies (**Table 2**). The final SV dataset, along with the '97103' genome, was used to construct a *Citrullus* graph pangenome, which was further used to genotype these SVs in the core collection and additional accessions using the resequencing short reads (a total of 753 accessions, including 435 cultivars, 114 landraces, 12 *cordophanus*, 38 *mucosospermus*, 120 *amarus*, 33 *colocynthis* and 1 *rehmii*).

Table 2 Summary statistics of SVs identified in cucumber and watermelon across 39 and 138 genome assemblies, respectively.

SV size	Cucumber				Watermelon			
	Insertion		Deletion		Insertion		Deletion	
	Number	Total (bp)	Number	Total (bp)	Number	Total (bp)	Number	Total (bp)
20-50 bp	45,060	1,372,201	37,302	1,118,463	281,414	8,245,901	240,223	7,041,136
50-100 bp	14,728	1,002,103	10,915	738,924	62,573	4,254,586	55,405	3,789,248
100bp-1 kb	22,442	8,072,792	15,473	5,190,707	85,402	27,285,463	74,247	23,213,992
1-10 kb	15,598	54,927,090	6,954	23,047,659	63,348	222,301,442	36,663	118,733,794
>10 kb	2,134	38,411,368	1,286	25,259,944	10,959	304,306,832	1,492	20,001,261
Total	99,962	103,785,554	71,930	55,355,697	503,696	566,394,224	408,030	172,779,431

For melon, we have completed chromosome-level assemblies for 32 accessions. The assembled genome sizes range from 355.7 Mb to 387.0 Mb (average: 367.1 Mb) and N50 contig sizes from 10.48 Mb to 22.12 Mb (average: 14.38 Mb). The BUSCO completeness rate for these genome assemblies ranges from 96.6% to 98.8%, with an average of 98.3%. An average of 97.3% of the contigs (ranging from 95.0% to 100%) are assigned to the 12 melon chromosomes. Protein-coding genes were predicted from these assembled genomes, and the number of genes predicted in each genome ranges from 21,907 to 28,582 (average: 24,131). The BUSCO completeness rate for genes predicted across these 32 melon genomes ranges from 94.2% to 97.5%, with an average of 96.0%. A graph-based pangenome was constructed from these 32 genome assemblies and the resulting SVs were genotyped in the melon core collection using short sequencing reads.

For *Cucurbita* species, we have completed genome assemblies and gene predictions of eight squash (*C. pepo*) accessions, and *C. maxima* Rimu and *C. moschata* Rifu. The total assembled genome sizes of the eight *C. pepo* accessions range from 332.1 Mb to 384.0 Mb (average: 350.4 Mb) and N50 contig sizes from 3.51 Mb to 10.73 Mb (Average: 6.85 Mb). The BUSCO completeness rate for these genome assemblies ranges from 97.1% to 98.7% (average: 98.2%).

On average, 93.6% of the contigs (ranging 90.6% to 95.4%) are assigned to the 20 squash chromosomes. A total of 29,558 to 31,528 genes were predicted across these eight genomes (Average: 30,522), with the BUSCO completeness rate raging from 94.9% to 96.6% (Average: 96.0%). A graph-based pangenome was constructed from these 32 genome assemblies and the resulting SVs were genotyped in the squash core collection using short sequencing reads. Genome assembly and annotation statistics for *C. maxima* Rimu and *C. moschata* Rifu are provided in Table 3.

Table 3 Statistics of *Cucurbita* genome assemblies.

	***C. maxima* Rimu**	***C. moschata* Rifu**
Assembly size (bp)	350,631,597	311,872,014
Genome BUSCO completeness (%)	98.7	98.36
N50 (bp)	12,573,384	9,281,623
Chromosome size	333,304,442	294,885,981
Chromosome size %	95.06	94.55
No. genes	30,540	30,857
Gene BUSCO completeness (%)	98.76	98.51

1.1.4. Breeder-friendly web-based database for phenotypic, genotypic and QTL information
We have updated CuGenDB to version 2 (CuGenDBv2) and officially released CuGenDBv2 in April 2022. CuGenDBv2 currently hosts 34 reference genomes from 27 cucurbit species/subspecies belonging to 10 different genera. Protein-coding genes from all these 34 genomes (total: 919,903; average: 27,056) have been comprehensively annotated, and the annotated genes can be queried and extracted in the database. Genomic synteny blocks and syntenic gene pairs have been identified between any two and within each of the 34 cucurbit genome assemblies (595 pairwise genome comparisons). A total of 391,379 synteny blocks and 12,130,719 syntenic gene pairs (average: 31 per synteny block) have been identified between the 34 cucurbit genomes. The 'Synteny Viewer' module have been re-implemented in CuGenDBv2 to improve the efficiency in processing and displaying the large-scale synteny data.

A 'Genotype' module was newly developed in CuGenDBv2 providing a suite of functions that allow users to mine, analyze, extract, and download variants including SNPs and small indels from large-scale population genome sequencing projects. Currently variants (SNPs and small indels) called for cucumber and squash core collections and watermelon resequencing panel, and SNPs called from the GBS data generated under CucCAP1 for watermelon, melon, cucumber, *C. pepo*, *C. maxima* and *C. moschata* are available in the database for query and mining.

The 'Expression' module in CuGenDBv2 has been redesigned to provide a complete cucurbit gene expression atlas, using the publicly available cucurbit RNA-Seq datasets. Currently raw RNA-Seq data of a total of 221 projects, 1,513 distinct samples and 3,560 runs (or libraries) have been downloaded from NCBI and processed to derive expression values, which can be queried in CuGenDBv2 to display expression profiles of specific interesting genes in different tissues, development stages, and under different treatment conditions.

Phenotype data have been generated for melon and cucumber core collections. A total of 33

vegetative, flower and fruit characters and two disease resistance traits have been evaluated for the melon core collection, and for the cucumber core collection a combination of 15 external and internal characteristics have been collected for immature and mature fruit of plants grown in 2019 and 2021. Phenotype data and a tool to display the fruit images of cucumber core accessions are available in the database (http://cucurbitgenomics.org/v2/phenotype).

1.2 Perform seed multiplication and sequencing analysis of core collections of the four species, provide community resources for genome wide association studies (GWAS).

1.2.1. Seed multiplication of core collections

Cucumber (Weng)

Continued seed increase for the core collection with 388 accessions. As of March 8, 2025, seed increase of 372 accessions has been completed with 322 having >1000 seeds each and 66 with 100-1000 seeds per line. In the 2024 winter greenhouse season, seed increase was conducted for 35 lines with self-pollinations. Short-day treatment was applied for a few lines known to be photoperiod sensitive for flowering, which did not seem very effective. Seed increase for the remaining lines will be continued for the remaining lines in 2025 spring/summer. We are working with the USDA-NPGS Cucumis curator and plan to ship/deposit seeds of the core collection before the conclusion of the project.

Watermelon (Levi)

For watermelon, HM Clause have increased the seeds for 177 PI accessions in the core collection (1000 S3 seeds per accession). Following phytosanitary tests and procedures, the seeds were shipped to the USDA, ARS, U.S. Vegetable Laboratory (USVL), Charleston. The seeds packs of these 177 PIs are kept in seed room of the USVL. Additional 71 PIs were increased by HM Clause in Thailand during 2023, but seeds have not been shipped yet to USVL. Seeds of 39 PIs were provided by University of Georgia, Dept. of Horticulture to HM Clause to be self-pollinated and advanced to S3 in Thailand. At the USVL greenhouse, we have increased 24 *C. amarus* PIs (S2) to have 180-450 S3 seeds for each PI. We are continuing to increase these 24 PIs to have at least 500 S3 seeds for each accession. The final core collection should consist of 270 *Citrullus lanatus* PIs, 10 *Citrullus colocynthis* PIs, 21 *Citrullus mucosospermus* PIs, and 54 *Citrullus amarus* PIs (Total of 355 *Citrullus* spp. PIs).

Melon (McCreight)

Three companies assisted in advancing the melon core set: 259 of the 384 melon core lines were sent to three seed company cooperators; seed was obtained from 180 of those lines. United Genetics advanced 13 S0 lines to S1 and three S1 lines to S2. Nunhems advanced 13 S0 lines to S1. Sakata advanced 236 S2 lines to S3, with seed counts per line ranging from <100 to >3000, based on seed weight; only 57 lines produced 1,000 or more S3 seed; additional seed number estimates are in progress for most recent season. A MTRA (Material Transfer Research Agreement) was established with H.M.Clause to produce S3 seed of 50 accessions in 2025.

Squash (*Cucurbita pepo*) (Mazourek)

116 accessions have been inbred and >1000 seed is ready for transfer to Kathy Reitsma's team in Ames, IA. Another 88 accessions are with Linda Vista greenhouse in Costa Rica being increased in one last attempt to achieve 1000 of seed for these accessions. The final set will consist of 204

accessions which has been reduced due to attrition. We made a small distribution of this set to CucCAP colleagues in UGA for them to start screening this core population.

1.2.2. Plan for deposit of core population seeds with National Plant Germplasm System (NPGS)
CucCAP team members have worked with NPGS scientists to outline a procedure for deposit and distribution of core population seeds as described below:

CucCAP Core population seed distribution strategy

Goal: Make seeds of the re-sequenced inbred lines accessible to scientific and breeding communities for research and breeding

Core population size: ~250-400 lines per crop (cucumber, melon, watermelon, squash)

Lines: produced by single seed descent (2-3 generations) from single individual from initial source material (PI accession, cultivar, cultigen, breeding line); i.e., lines are derived from, but generally not equivalent to, respective initial sources

Genomic information: Each line has been/will be re-sequenced to 40-50x read depth. All original data, SNP and indel information will be made publicly available. Links will be established from NPGS to CuGenDB

Seed supply: lines will be multiplied to provide >1000 seed/line

Planned approach:

1. Seed (~1000/accession) will be provided to NPGS.
2. Seed to be submitted will be produced by companies or CucCAP Co-PIs in accordance with phytosanitary standards, and appropriate documentation will be provided.
3. CucCAP crop teams will assemble the collections of seed for their crop for submission to NPGS (or other germplasm repositories)
4. A small sample (50 seeds/line) will be submitted to Ft. Collins repository for long term storage
5. Seed is entered into the NPGS system with unique identifiers as part of the respective CucCAP Cores [e.g., local numbers, or CCCxxx (CucCAP core)]
6. Core lines will be linked to their respective original NPGS-GRIN source and/or cucurbit genomics database (CuGenDB) providing related phenotypic information and passport data for the original materials and/or core lines. Exact pedigree/selection process of sublines will be provided.
7. Seed will be distributed by NPGS until supplies are exhausted. NPGS will not be responsible for propagation.
8. Minimal seed will be provided to requestors (5-10 seed/line/request). Recipients can increase seed for their needs by self-pollination of the inbred CucCAP core lines.
9. Seed can be requested as a full set, or as specific lines.
10. If specific lines are running low, NPGS can alert the cucurbit community to see if it is possible to replenish supply for those lines.
11. Seed can be used without restriction for research and breeding, as per NPGS policy and will be distributed with a standard materials transfer agreement (SMTA). Documents accompanying the seed should state that the donor provides the germplasm to the NPGS free of any restriction on use, and without retaining or asserting any intellectual property rights.
12. A publication will be prepared indicating availability and how to request seeds.

Watermelon Team

Team members:

Amnon Levi (USDA, ARS)
Sandra Branham (Clemson University)
Shaker Kousik (USDA, ARS)
Kai-Shu Ling (USDA, ARS)
Cecilia McGregor (University of Georgia)
Umesh Reddy (West Virginia St University)
Pat Wechter (Clemson University)

Cecilia McGregor -UGA

1.2.1 Seed multiplication of core collections

Thirty-nine S_2 accessions (31 *C. amarus*, 7 *C. lanatus and 1 C. mucosospermus*) have been sequenced and sent for increase.

2.1 Map resistances and identify QTL for key cucurbit diseases

The WPop GSB1 (PI 482276 x Crimson Sweet) $F_{2:3}$ population is being bused to identify QTL associated with stem resistance to *S. citrulli*.

2.2. Develop and verify markers for MAS

We previously developed and/or validated KASP marker assays for selection of *Qgsb5.1* (syn. *ClGSB5.1*; Gimode et al., 2020), and *Qgsb7.1* (syn. *ClGSB7.1*; Gimode et al., 2020). These QTL are currently being introgressed into Crimson Sweet. We evaluated 5 BC_2F_3 and 5 $BC3F_3$ introgression lines as well as 1 line obtained from North Carolina State University (Rivera-Burgos et al., 2021) in the field. Sugar Baby, Crimson Sweet and Estrella were included as susceptible controls and UGA11 (selection from PI 482379), UGA81 (selection from PI 189225) and UGA 1081 (selection from PI 482276) were included as resistant controls. Plants were artificially inoculated with an *S. citrulli* isolate and leaf surfaces were kept wet using a mist system.

Three lines (9_BC_2, 62_BC_2 and 62_BC2) and NCSU-RIL-117 significantly lower gummy stem blight disease severity (AUDPC) than susceptible controls (Figure 1). The Crimson Sweet fruit size has been recovered in lines 177_BC_2, 9_BC_3, 35_BC_3, 177_BC_3 and 262_BC_3. Yield was not significantly different between the introgression lines and the susceptible controls.

References

Gimode, W., K. Bao, Z. Fei and C. McGregor (2021) QTL Associated with Gummy Stem Blight Resistance in Watermelon. Theor Appl Genet 134:573–584.

Rivera-Burgos, L.A., E. Silverman, N. Sari and T.C. Wehner. (2021) Evaluation of Resistance to Gummy Stem Blight in a Population of Recombinant Inbred Lines of Watermelon × Citron. HortScience 1:1–9.

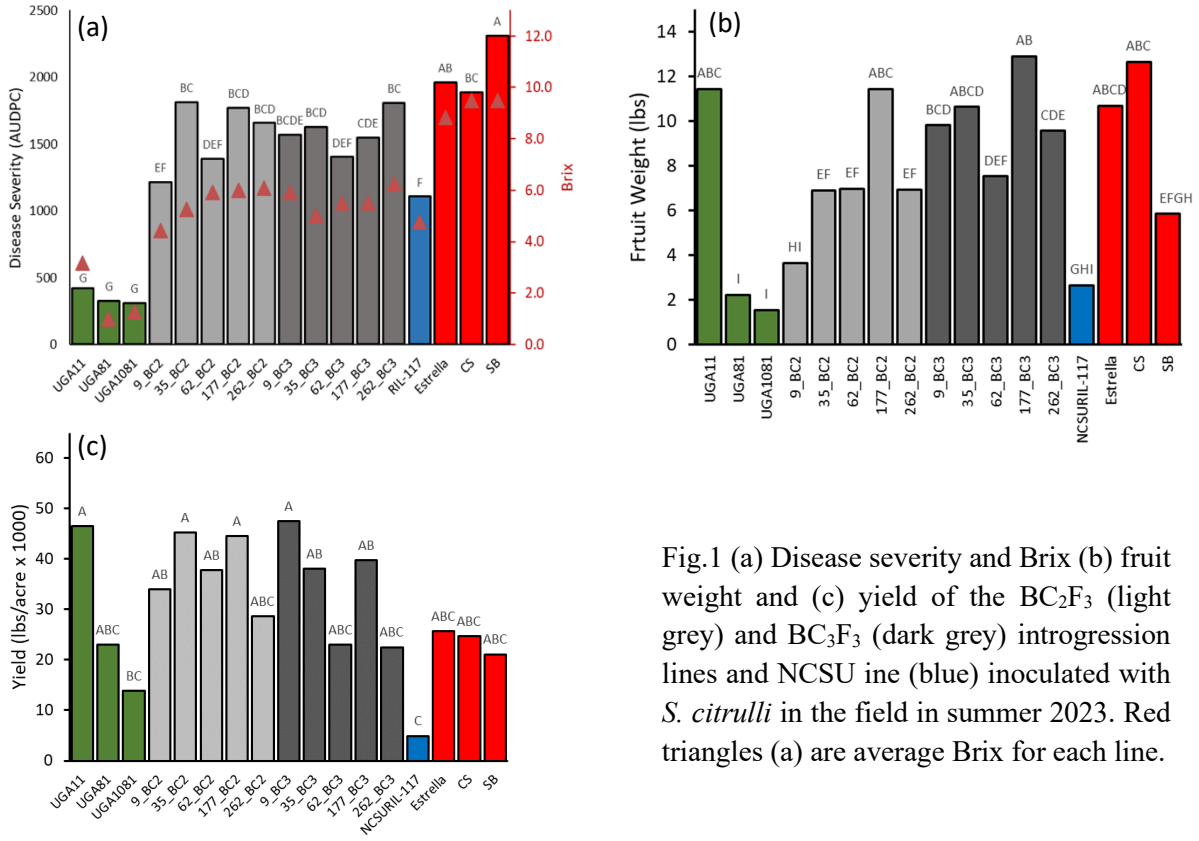

Fig.1 (a) Disease severity and Brix (b) fruit weight and (c) yield of the BC_2F_3 (light grey) and BC_3F_3 (dark grey) introgression lines and NCSU ine (blue) inoculated with *S. citrulli* in the field in summer 2023. Red triangles (a) are average Brix for each line.

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Venkat Ganaparthi (Graduate Student, Clemson Univ.)

Obj 2. Map and develop markers for disease resistance

2.1: Developing populations (P), phenotyping (Ph), QTL mapping (Q), Fine mapping (F)
-*Fon* race 2, Ph/Q

- Completed QTL mapping in the USVL246-FR2xUSVL114 RIL population and narrowed the QTL intervals found in the F2:3 population from the same cross. Developed KASP markers for four QTL and validated them in an independent interspecific (USVL246x'Sugar Baby') population. Ganaparthi et al. 2024 *Theoretical and Applied Genetics*.
- Completed disease screening (two replicated tests) of the *C. amarus* core collection for response to inoculation with *Fon* race 2 and used the phenotypes for GWAS and genomic predictions. Ganaparthi et al. 2023 *Plant Disease*.

-Downy mildew, Ph/Q

Completed disease screening (two replicated tests) of the *C. amarus* core collection for DM resistance and used the phenotypes for GWAS. Katuuramu et al. 2022. *Plant Disease*.

2.2: Develop marker (M), verify (V)

-Fon race 2, M/V

- KASP markers for Fon race 2 resistance were developed in the C. amarus 246x114 RIL population. An F2:3 interspecific population of USVL246-FR2 by 'Sugar Baby' was evaluated for response to inoculation with Fon race 2 in two replicated tests and the phenotypes used for QTL mapping and validation of the KASP markers. Ganaparthi et al. 2024. *Theoretical and Applied Genetics*.

-Powdery mildew race 2w, M/V

- XP-GWAS of powdery mildew race 2 resistance was completed for the USDA Citrullus core collection using historical data. KASP markers were designed for three regions of the genome with a significant signal. They were validated in two hundred accessions from the extremes of the distribution. Branham et al. 2025. *Scientific Reports*.

Obj. 3A. Introgress, pyramid/stack resistances into advanced breeding lines

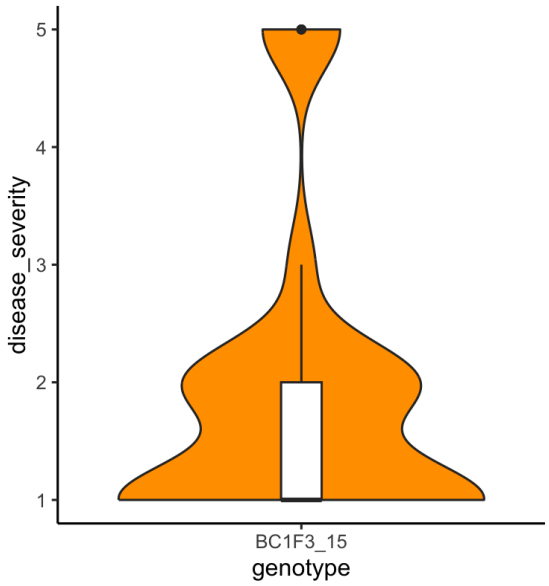
Develop breeding lines (B), introgress into cultivated (I), advanced lines (A), release to breeders (R)

-*Fon* races 1 and 2, AL/PW/SB

- Phenotypic and marker-based selections for Fon race 2 resistance were made from interspecific backcross populations of USVL246-FR2 with commercial cultivars 'Charleston Gray' and 'Crimson Sweet' as the recurrent parents (Table 1). We have the resistant haplotype in the homozygous state and have made several selections to develop advanced lines of red-fleshed watermelon with Fon race 2 resistance. We have also crossed USVL246 to 'All Sweet' to begin introgression into a another elite background (Table 1). The most advanced generation of all watermelon materials will be tested in a field trials in a 'hot' field naturally infested with Fon race 2 to evaluate yield and Brix in Spring 2025.

Table 1. Progress of introgression of *Fon* race 2 resistance into elite breeding lines

Crop	Current seed being generated	Number of plants (selections)
watermelon	BC3F2 (Crimson Sweet x 246)	5
watermelon	F2 (All Sweet x 246)	5
watermelon	BC1F4 (Charleston Gray x 246) x Charleston Gray	50



Obj. 3B. Using genomic selection approach to incorporate Fusarium wilt race 2 resistance into watermelon cultivars AB/VG/PW/AL/SB

Anju Biswas, Pat Wechter, Shaker Kousik, Sandra Branham, and Amnon Levi

Constructing and utilizing training populations for 'genomic selection' experiments
USVL246 x USVL114 (RIL), USVL252 x USVL119 (F3)
USVL246 x Sugar Baby (F3), USVL 252 x Sugar Baby (F3; F4; BC1;F2;F3)

Resistance to *Fusarium oxysporum* f. sp. *niveum* (Fon) race 2 in watermelon is a polygenic trait with moderate heritability. We evaluated genomic selection (GS) as an additional approach to quantitative trait loci (QTL) analysis/marker-assisted selection (MAS) for enhancing Fon race 2 resistance in elite watermelon cultivars. Our objectives were to: (1) assess the accuracy of genomic prediction (GP) models for predicting Fon race 2 resistance in a F2:3 versus a recombinant inbred line (RIL) population, (2) rank and select families in each population based on genomic estimated breeding values (GEBVs) for developing testing populations, and (3) determined how many of the most superior families based on GEBV also have all QTL associated with Fon race 2 resistance. Phenotyping data from two Fon race 2 tests and GBS-SNP data from genotyping-by-sequencing (GBS) for two populations (A F8/F9 RIL population: USVL246 FW-R2-resistant x USVL114 FW-R2-suceptible; A F2:F3 population: USVL252FW-R2-resistant x 244019-FW-R2-suceptible) were used, and parental line genome sequences were used as references. The GBLUP and Random Forest models tested here outperformed the parametric (GBLUP, Bayes B, Bayes LASSO) and three nonparametric AI (random forest, SVM linear, and SVM radial) models, producing correlations of 0.48 and 0.68 in the F2:3 and RIL population, respectively. Selection intensities (SI) of 10%, 20%, and 30% showed that superior

families with highest GEBV also comprise all QTL associated with Fon race 2 resistance (Branham et al. 2018; 2019), highlighting genomic prediction (GP) efficacy in improving elite watermelon cultivars with polygenic traits of disease resistance.

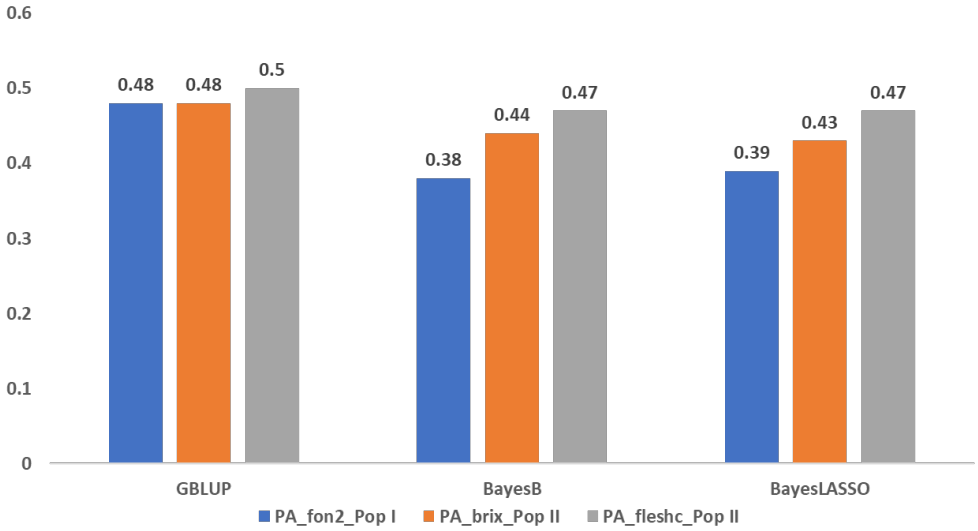


Figure 2. Predictive ability (PA) of GEBV for Fon race 2-resistance, brix and flesh color from different statistical models for a F2:F3 population: USVL252FW-R2-resistant x 244019-FW-R2-suceptible**.**

Genomic selection experiments for Fusarium wilt race 2-resistance and fruit quality traits at the USDA, ARS, U.S. Vegetable Laboratory and Clemson-Costal Research and Education Center (CREC), Charleston, SC (Summer 2023 and 2024).

Identifying Germplasm Resistant to Fusarium Wilt Race 3 and Developing Genetic Resources Useful for Incorporating the Resistance into Elite Watermelon Cultivars

Fusarium wilt race 3 has been rapidly emerging in recent years and is considered most virulent for the watermelon crop. *Fon* race 3 was recently reported in Florida and Georgia and could rapidly spread to other watermelon production areas in the USA and become a serious threat to the watermelon industry in coming years. There is an urgent need to evaluate the *Citrullus* spp. germplasm collections for resistance and identify genetic resources and gene loci useful in enhancing *Fon* race 3 resistance in watermelon cultivars.

We evaluated the *Citrullus amarus* PI collection (113 PIs) and performed a genome wide association (GWAS) study to identify gene loci associated with *Fon* race 3-resistance (using an isolate given to us by Dr. Nicolas Default at University of Florida; Gainesville).

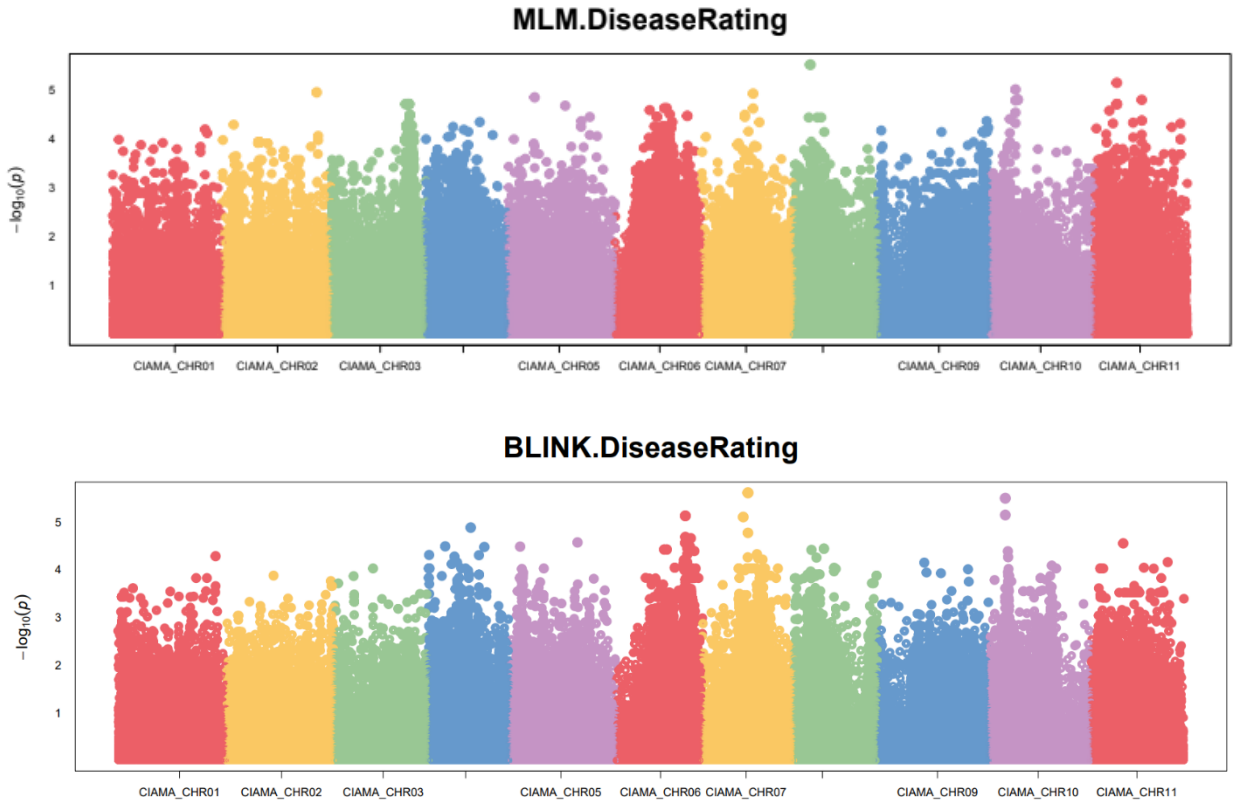


Figure 3. Preliminary analysis: Genome-wide association Manhattan plot using the MLM and BLINK models for *Fon* race 3 from 113 *C. amaraus* PIs showing putative QTN associated with Fon race 3-resistance on Chromosomes 6, 7, 8, 10, and 11.

Phytophthora fruit rot (PFR) and Powdery Mildew (PM) of watermelon

Shaker Kousik, Rahul Kumar, Amnon Levi; USDA, ARS, U.S. vegetable Laboratory (USVL), Charleston, SC

- Two F_2 populations (USVL531-MDR × Sugar Baby and USVL531-MDR × Calhoun Grey) were evaluated for resistance to Phytophthora fruit rot. The segregation ratio was 3 susceptible to 1 resistance for both the populations suggesting recessive trait.
- Data on seed type, flesh color, rind thickness, rind colo. for the two populations was also recorded for further analysis.
- Total DNA was extracted from the 100 samples from each of the two populations (USVL531-MDR × Sugar Baby and USVL531-MDR × Calhoun Grey) for DNA sequencing.
- Whole genome resequencing of (USVL531-MDR × Calhoun Grey) at 10X was done QTL seq analysis.
- Whole genome resequencing was done at 10X specifically for use in genomic prediction using models developed from the recombinant inbred line (RIL) population of (USVL531-MDR X USVL677).
- The two F_2 populations (USVL531-MDR × Sugar Baby and USVL531-MDR × Calhoun Grey) are also being screened for resistance to powdery mildew for further validating Kompetitive Allele-Specific PCR (KASP) markers developed using the RIL population.
- Three additional F_2 populations (USVL003-MDR X USVL677-PMS, USVL020-PFR X Dixie Lee, USVL020-PFR X PI 536464) developed using crosses of *Citrullus mucosospermus* (powdery mildew and Phytophthora fruit rot resistance source) X *C. lanatus* (susceptible) genotypes were rated for powdery mildew.
- Total DNA has been extracted from these F_2 plants for KASP marker analysis using KASP markers developed based on the RIL population (USVL531-MDR X USVL677-PMS) and another population using a different powdery mildew resistance source (USVL608-PMR X USVL677-PMS)
- A recombinant inbred line (RIL) population (F_{11}), derived from an interspecific cross between the resistant *Citrullus mucosospermus* genotype USVL531-MDR and susceptible *C. lanatus* genotype USVL677-PMS was used to identify quantitative trait loci (QTL) associated with powdery mildew (PM) and phytophthora fruit rot (PFR) resistance.
- A total of 183 RILs, along with their parents, were evaluated in two field trials in Charleston during summer and fall of 2023 for powdery mildew, phytophthora fruit rot, bitterness, and seed type.
- USVL531-MDR, consistently showed high levels of resistance to both PM and PFR, while USVL677-PMS, was highly susceptible.
- Total DNA was extracted from parents and whole genome resequencing of the 183 RIL lines was done at 20 X.
- *R/qtl2* and a high-density marker dataset (~400,000 SNPs) from whole-genome resequencing of the RIL lines (~20× coverage) was used for QTL mapping.
- Disease resistance for PM and PFR segregated independently within the RIL population, suggesting that these diseases are controlled by distinct genetic loci.

- Two QTL regions on chromosome 2, separated by approximately 13 Mb—one associated with PM resistance and the other with PFR resistance were identified. Two other QTLs on Chromosomes 5 & 6 were also associated with PFR resistance (Figure 1A, 2A, B).
- Genomic selection (GS) was applied for PFR resistance in the RIL population. A genomic estimated breeding value (GEBV) of 0.95 was observed using a Bayesian A model, with a five-fold cross-validation accuracy of 0.71, demonstrating the potential of GS for improving PFR resistance in watermelon (Table 1, Figure 3).
- Kompetitive Allele-Specific PCR (KASP) markers developed from QTL associated with PM resistance exhibited strong correlation with field phenotype (Figure 1A, B).

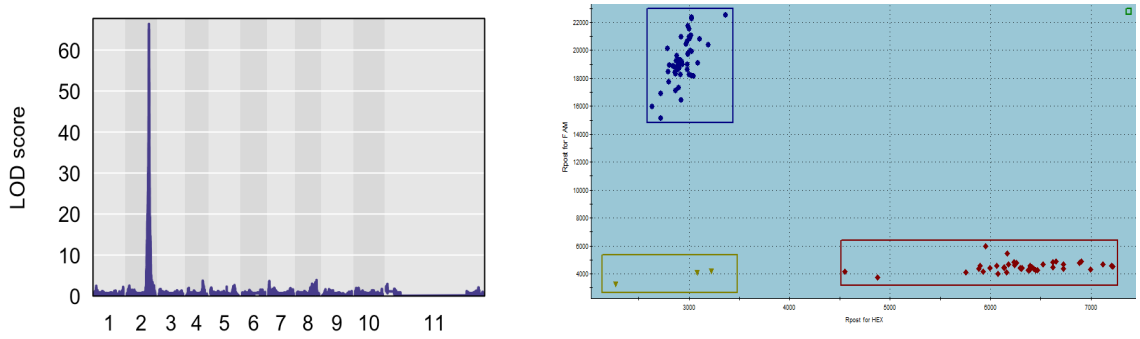


Figure 1. QTL mapping and KASP marker development for powdery mildew (PM). (A) A major QTL with a high LOD score of 70 was identified on chromosome 2. **(B)** KASP cluster plots displaying distinct genotype clusters for homozygous resistant (red), homozygous susceptible (blue), and control (blank water, yellow) samples. The KASP markers successfully differentiated between homozygous alleles. Genotypic and phenotypic data showed a 100% correlation between the KASP markers and the powdery mildew resistance phenotype.

A

B

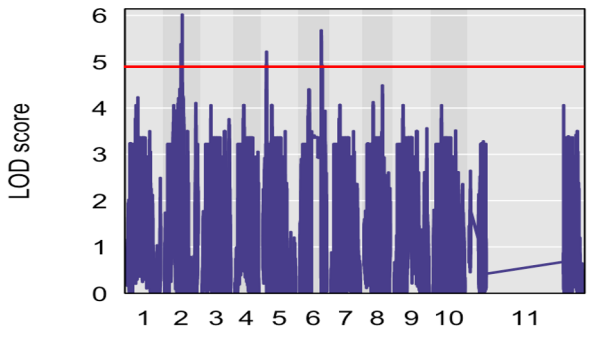


Figure 2. QTL mapping for phytophthora fruit rot in watermelon. (A) A QTL was mapped on chromosome 2 lesion size (diameter) formed inoculated with an agar plug of Phytophthora capsici grown on V8 juice agar and the fruit kept in high humidity (>95% RH) for five days (25 C). **(B)** Three QTLs were mapped on chromosome 2, 5, and 6 based on sporulation intensity rating on the lesion recorded on a 0-5 scale.

Table 1. Genomic Estimated Breeding Values (GEBVs) of six models: Bayesian Ridge Regression (BRR), Bayes A, Bayes B, Bayes C, Reproducing Kernel Hilbert Space (RKHS), and Bayesian LASSO (BL). Genomic selection was performed using the BGLR R-package, with Bayes A showing the highest GEBV among all models.

	Correlation	**MSE**	**MAE**
BRR	**0.91**	**1.44**	**0.99**
BayesA	**0.95**	**0.91**	**0.77**
BayesB	**0.92**	**1.4**	**0.97**
BayesC	**0.91**	**1.55**	**1.02**
RKHS	**0.89**	**1.8**	**1.11**
BL	**0.91**	**1.46**	**0.99**

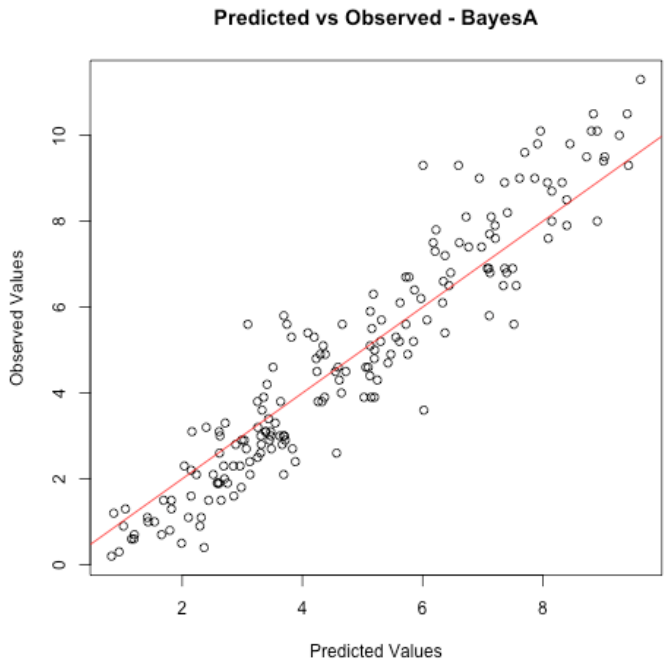


Figure 3. Scatter plot of predicted (x-axis) and observed (y-axis) disease lesion size values using the Bayes A model. The analysis showed a GEBV of 0.95 and a five-fold cross-validation accuracy of 0.71 for Bayes A.

Markers for Bitterness in Fruit Flesh

- QTL analysis using *R/qtl2* and a high-density marker dataset (~400,000 SNPs) from whole-genome resequencing of the RIL lines (~20× coverage) identified a major QTL on chromosome 1 for bitterness and KASP marker was developed for MAS (Figure 4A, B).

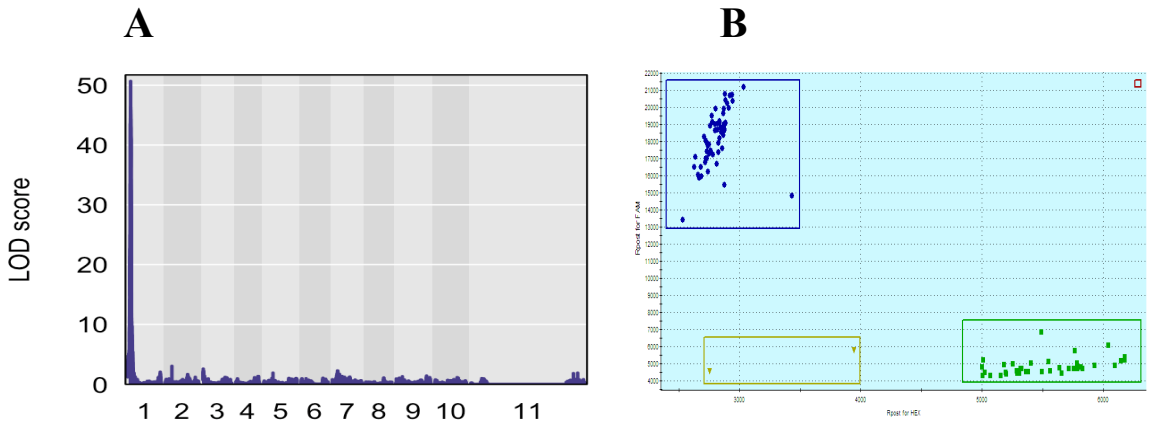


Figure 4. QTL mapping and KASP marker development for bitterness. (A) A major QTL associated with bitterness was identified on chromosome 1. **(B)** KASP cluster plots displaying distinct genotype clusters for homozygous non-bitter (green), homozygous bitter (blue), and control (yellow) samples. The KASP markers successfully differentiated between homozygous alleles.

Markers for Egusi Seed type

- QTL analysis using *R/qtl2* and a high-density marker dataset (~400,000 SNPs) from whole-genome resequencing of the RIL lines (~20× coverage) identified a major QTL on chromosome 6 (Figure 5 A) for egusi seed type and KASP marker was developed for MAS (Figure 5 B).

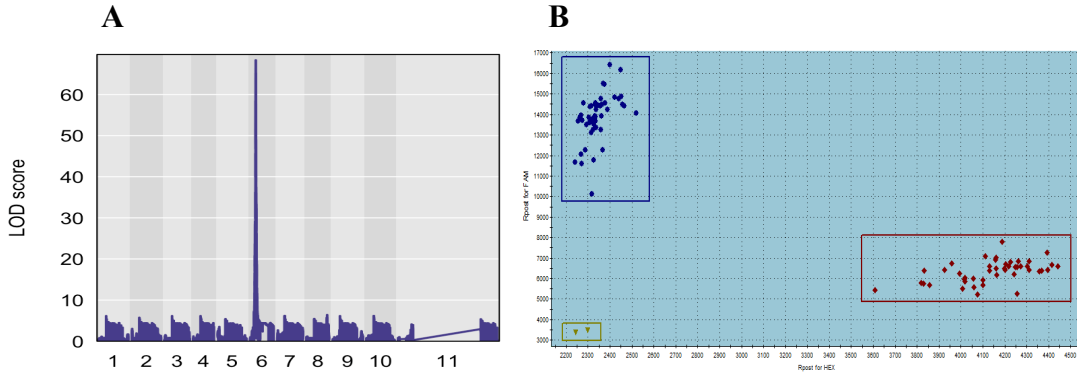


Figure 5. QTL mapping and KASP marker development for egusi seed type. (A) A major QTL associated with egusi seed was identified on chromosome 2. **(B)** KASP cluster plots showing distinct genotype clusters for homozygous non-egusi (red), homozygous egusi (blue), and control (yellow) samples. The KASP markers effectively distinguished between homozygous alleles. Genotypic and phenotypic data exhibited a 100% correlation between the KASP markers and the egusi seed phenotype.

Powdery Mildew of Watermelon (USVL608-PMR X USVL677-PMS)

- A *Citrullus lanatus* powdery mildew resistance source released by USDA ARS in 2018, and called USVL608-PMR was crossed with a susceptible genotype USVL677-PMS to develop F_1, F_2 and backcross populations.
- The populations were evaluated in the field and growth chamber for resistance to powdery mildew.
- Conventional inheritance studies indicated a dominant gene for resistance as the F2 populations segregated in a typical 3:1 ratio and the backcross population with the susceptible genotype segregated in a 1:1 ratio.
- USVL608-PMR was resistant in field and growth chamber compared to USVL677-PMS, Sugar Baby and Dixie Lee that were susceptible (Figure 6).
- To elucidate the genetic basis of resistance, bulked segregant analysis (BSA) was conducted on an F_2 population derived from a cross between resistant (USVL608-PMR) and susceptible (USVL677-PMS) genotypes.
- A 517-kb region on chromosome 2 was identified, containing eight resistance genes, including LOX, which catalyzes jasmonic acid biosynthesis and boosts reactive oxygen species (ROS) production via lipid peroxidation with potential to provide disease resistance.
- A tightly linked kompetitive allele specific PCR (KASP) marker was developed and validated across three F_2 populations (USVL608-PMR × USVL677-PMS, USVL608-PMR × Sugar Baby, USVL608-PMR × Dixie Lee), showing a 3:1 segregation ratio and 100% linkage to resistance.
- Marker-disease resistance linkage was further validated in the F_3 generation of all three populations (Figure 7) and an F_4 population was developed for further analysis and marker assisted breeding and selection for improved fruit quality traits and resistance.
- RNAseq analysis revealed the upregulation of *LOX*, JA, and ROS pathways post-inoculation, suggesting a *LOX*-mediated JA-ROS coordinated defense mechanism is potentially involved in powdery mildew resistance in watermelon. Further studies to elucidate the role of this LOX gene are in progress.
- The development of tightly linked KASP markers with powdery mildew resistance and a molecular understanding of disease resistance that worked in different susceptible backgrounds will be useful for developing commercial disease-resistant watermelon cultivars.

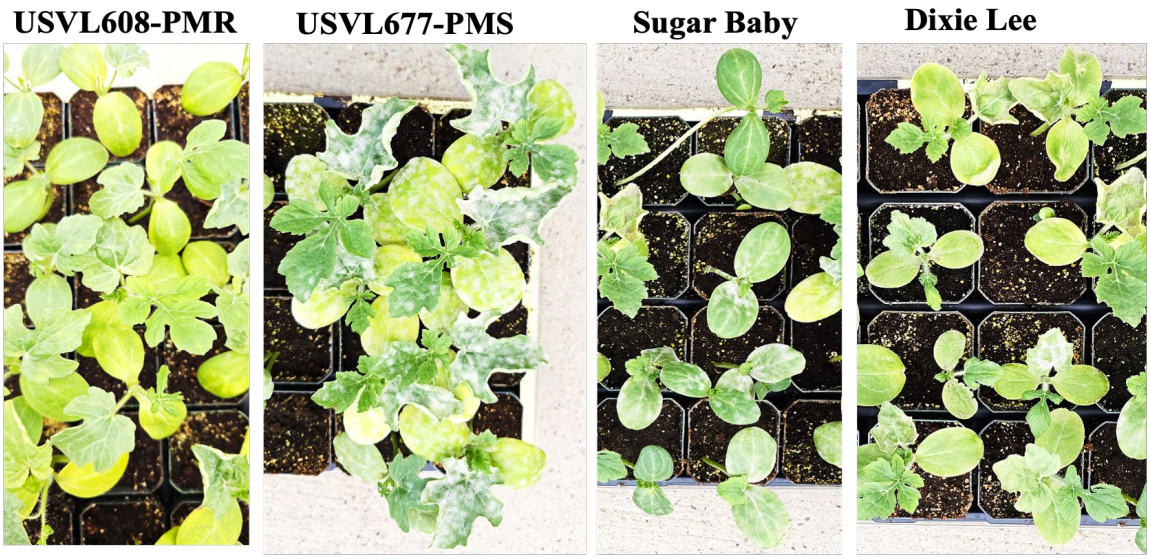


Figure 6. Powdery mildew development on susceptible genotype USVL677-PMS and commercial cultivars Dixie Lee and Sugar Baby compared to resistant USVL608-PMR.

Figure 7. Use of Marker assisted selection to develop resistant F3 progenies from crosses of USVL608-PMR with three susceptible genotypes USVL677-PMS, Sugar Baby and Dixie Lee.

- Microscopic observations over a time course study indicated significantly reduced powdery mildew development on USVL608-PMR compared to the susceptible USVL677-PMS (Figure 7). Powdery mildew symproms were visible to the naked eye 144 hours after inoculation.

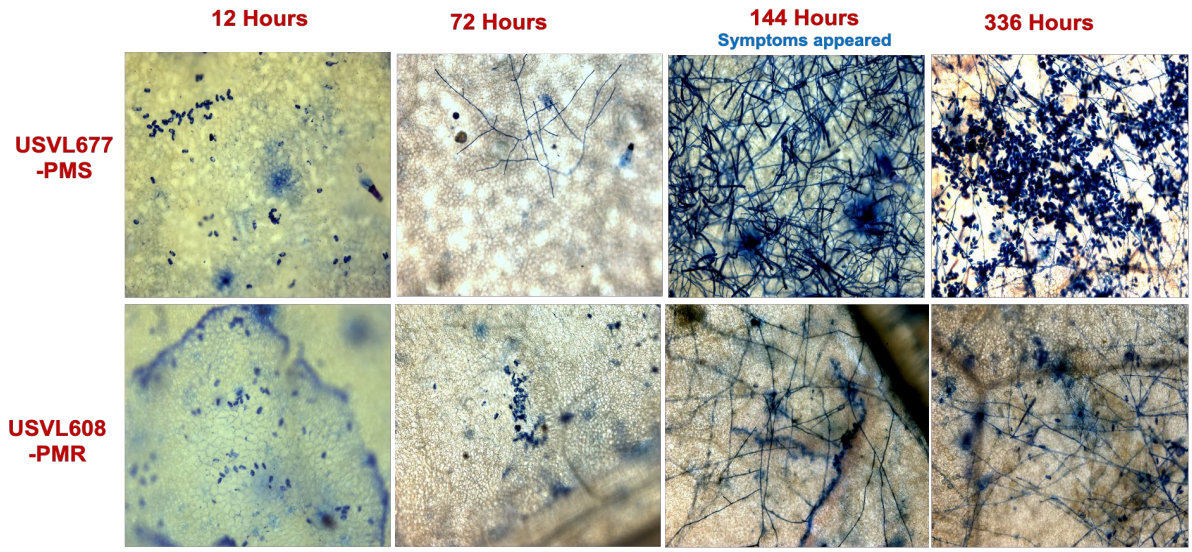


Figure 7. Microscopic observations of powdery mildew development on the susceptible e USVL677-PMS compared to the USDA ARS released resistant line USVL60-8-PMR. USVL608-PMR displayed exhibited reduced fungal growth.

Powdery Mildew of Watermelon (USVL278-PMR X USVL677-PMS)

- Another population developed using powdery mildew resistant USVL482-PMR and susceptible USVL 677-PMS was phenotyped in the field and growth chamber studies. USVL278-PMR is highly resistant to powdery mildew and exhibits a non-lobbed leaf phenotype, while USVL677-PMS is susceptible to powdery mildew and has a lobbed leaf phenotype. An F_2 population (USVL278-PMR × USVL677-PMS) was evaluated for powdery mildew resistance in both the field and a growth chamber (Figure 8).
- In the field, 50 plants each of USVL278-PMR, USVL677-PMS, F_1, and BCF_1S, along with 200 F_2 and 50 BCF_1R plants, were evaluated for powdery mildew resistance and leaf phenotype. Field evaluation results indicate that powdery mildew resistance is controlled by a single dominant gene, while the non-lobbed leaf phenotype is controlled by a single recessive gene.
- In the growth chamber, 226 F_2 plants, along with the USVL278-PMR and USVL677-PMS parents, were evaluated for powdery mildew resistance. The results indicate that powdery mildew resistance is controlled by a single dominant gene.
- Bulk segregant analysis (BSA) is being used for QTL mapping of powdery mildew resistance and the non-lobbed leaf phenotype. DNA bulks from resistant, susceptible, non-lobbed, and lobbed leaf lines. Sequencing is being conducted at the North Carolina State University Genomics Center (Figure 9).
- KASP markers will be developed for powdery mildew resistance and non-lobbed leaf phenotypes, and these markers will be validated in other populations as well.

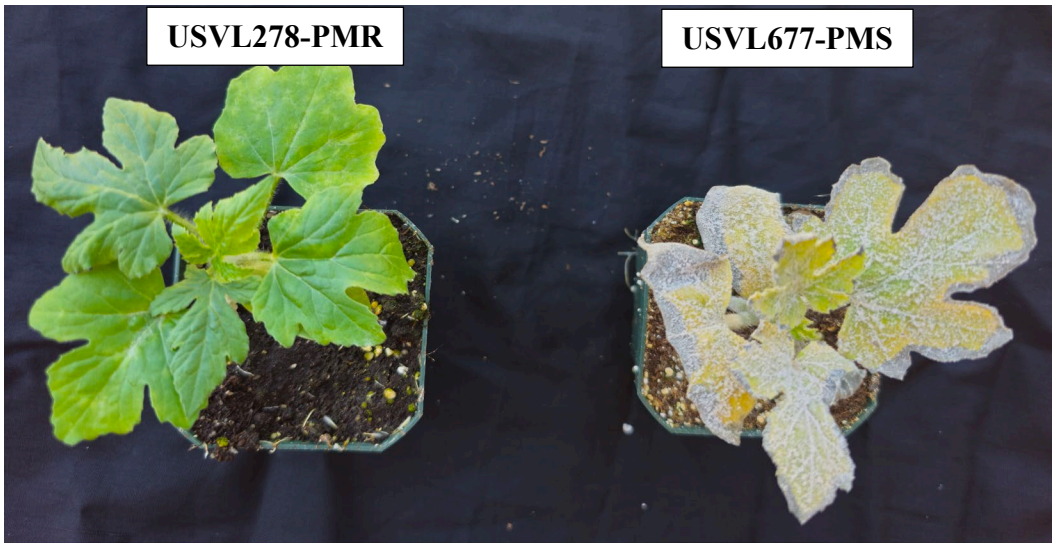


Figure 8: Phenotyping of USVL278-PMR and USVL677-PMS for powdery mildew resistance. Parents and their F_2 progenies were evaluated for powdery mildew resistance in the growth chamber. USVL278-PMR showed resistance to powdery mildew, while USVL677-PMS exhibited susceptibility. A 3:1 (Resistant : Susceptible) genetic ratio was observed in the F_2 population, indicating that powdery mildew resistance is controlled by single dominant gene. QTL and KASP marker analysis is ongoing.

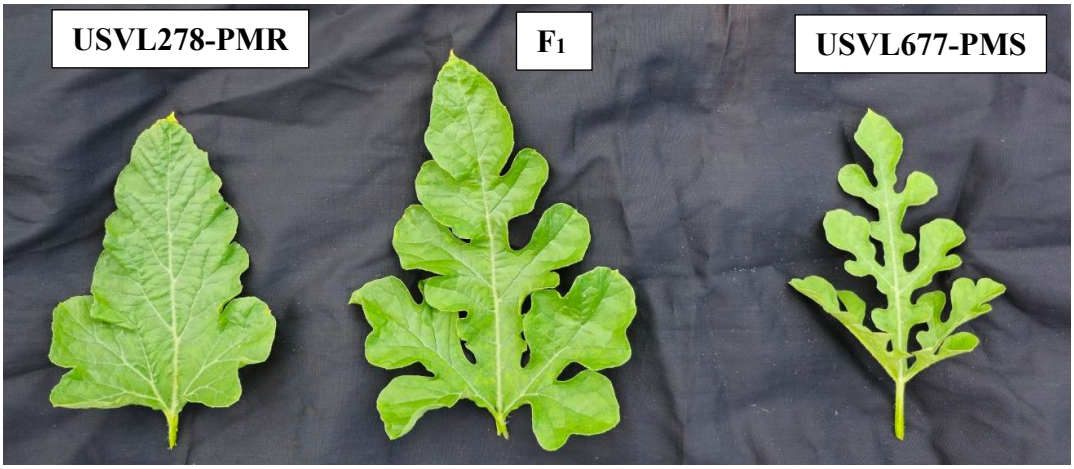


Figure 9: Phenotyping of USVL278-PMR and USVL677-PMS for leaf type. Parents and their progenies were evaluated for the leaf phenotype in the field. USVL278-PMR showed a non-lobbed phenotype, while USVL677-PMS exhibited lobbed leaf phenotype. A 1:3 (Non-lobed : lobed) genetic ratio was observed in the F_2 population, revealed that non-lobbed leaf phenotype is controlled by single recessive gene. QTL analysis is ongoing.

- Backcross (USVL278 X USVL677-PMS) X USVL677-PMS was also evaluated by phenotyping and the resistant lines were selected for advancing to the next generation to

develop a better quality non-lobed leaf type watermelon line with powdery mildew resistance and higher brix and good flesh quality.

Phenotyping RIL lines developed by North Carolina State University for resistance to powdery mildew (*Citrullus a*marus X *Citrullus lanatus* crossing blocks).

- A total of 140 recombinant inbred line (RIL) population developed by Todd Wehner at North Carolina State University using multiple parents, including PI526233, PI482374, PI482283, PI482342, PI189225, all sweet watermelon types, Charleston Grey, Sugar Baby, and Crimson Sweet were evaluated for resistance to powdery mildew.
- PI 526233, PI 482374, PI 482283, and PI 189225 exhibited resistance to powdery mildew, while the other parents were susceptible.
- Genotyping-by-sequencing (GBS) data is available for all the lines in this RIL population.
- The study will be repeated in the growth chamber in 2025.
- Genome-wide association studies (GWAS) and genomic selection will be performed for powdery mildew resistance using the available genotypic and phenotypic data.

Whole genome re-sequencing and analysis of 161 diverse watermelon accessions

Umesh Reddy, West Virginia State University

Future Directions

The variants identified through the comprehensive and high-coverage re-sequencing approach will be further utilized for genome-wide association studies (GWAS) in conjunction with various phenotypic data. This will enable the investigation of the genetic basis of important traits in watermelon, facilitating the identification of candidate genes and markers for breeding programs.

Among the RILs, RIL207, RIL195, RIL237, and RIL149 have demonstrated potential disease resistance, as indicated by negative random effect values, suggesting reduced pathogen susceptibility. By leveraging genomic data, GBLUP enabled the early selection of resistant lines using PACE assays. We aim to integrate genomic selection by generating F1, F2, and advanced crosses that combine multiple resistance alleles. The F1 crosses, including RIL257 × RIL299, RIL265 × RIL253, and RIL299 × RIL149, introduce genetic diversity while maintaining fruit quality. The F2 populations, such as Bush Sugar Baby × RIL27, Bush Sugar Baby × RIL207, Bush Sugar Baby × RIL242, and Bush Sugar Baby × RIL195, serve as key segregating populations for marker-assisted selection. The advanced crosses, such as (RIL207 × RIL195) × (RIL242 × RIL237), are designed to stack multiple resistance loci, enhancing durability against evolving pathogens while preserving fruit quality. These structured crosses effectively balance resistance traits and agronomic performance, ensuring a continuous pipeline of elite breeding materials.

Impacts of utilizing the CucCAP watermelon core collection

1) **GWAS to identify gene loci associated with watermelon root traits using 167 PIs (S3) of the CucCAP watermelon core collection**.

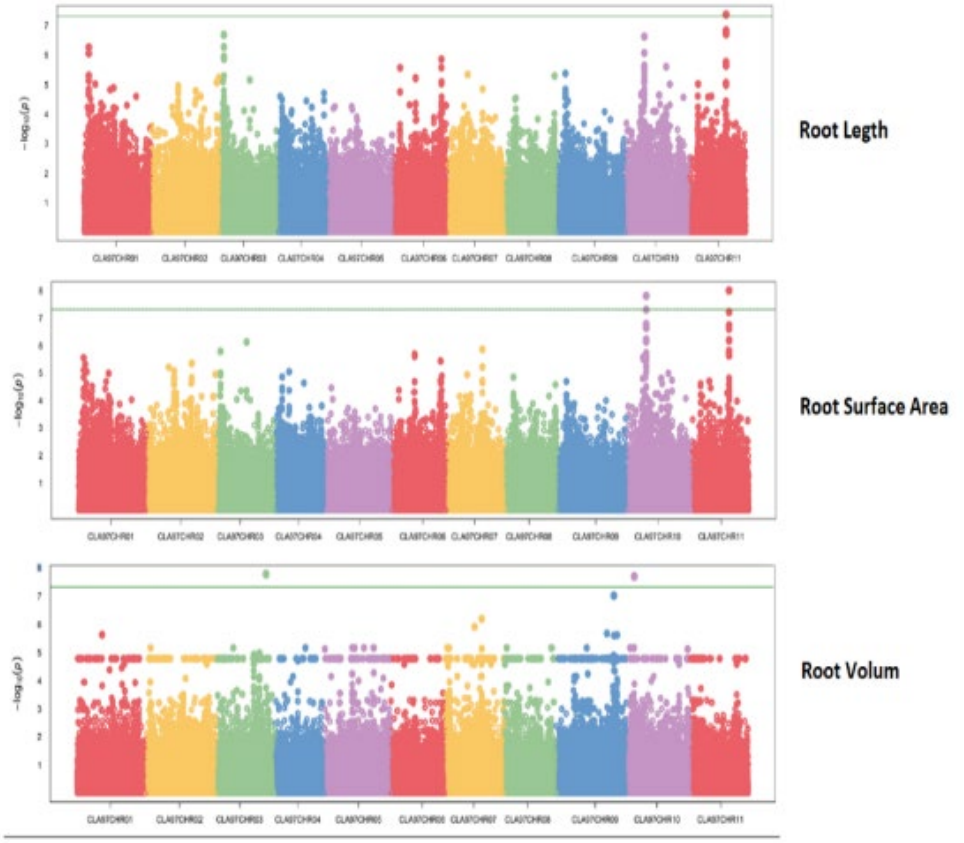


Figure 10. Genome wide association (GWAS) study of 167 *Citrullus lanatus* accessions reveling quantitative trait nucleotides (QTNs) associted with gene loci controlling root length, root diameter, and root surface area.

2. Development of a DArT marker diversity panel for watermelon

A. Levi, Z. Fei, C. McGregor, S. Kousik, U. Reddy, P. Wechter, and S. Branham

In collaboration with the USDA-ARS, the Breeding Insight Team at Cornell University is using the CucCAP watermelon Super-PanGenome data and core collection for the development of a diversity panel consisting of 3000 DArT markers covering large parts of the watermelon genome. A PCA plot of all Citrullus species (882 lines) using 13K markers is shown in Figure 11 shows clear distinction among the different species and subspecies. Validation of QTL and primers is in progress using different genetic populations of watermelon provided by the watermelon team.

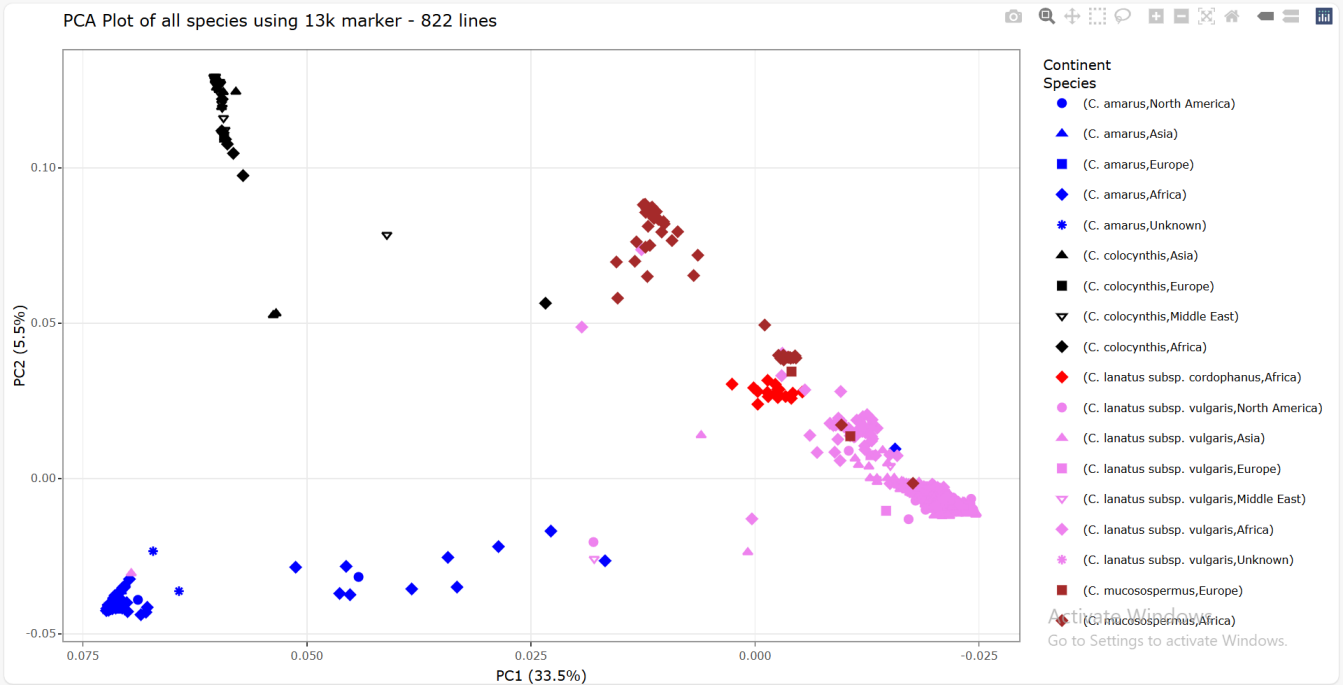


Figure 11. PCA plot of *Citrullus* species using DArT markers.

Melon Team

Team members:
Jim McCreight (USDA, ARS), Sandra Branham (Clemson University) Shaker Kousik (USDA, ARS), Pat Wechter (Clemson University), Bill Wintermantel (USDA, ARS)

Obj. 2. Map and develop markers for disease resistance

2.1 QTL mapping of resistances
2.1: Developing populations (P), phenotyping (Ph), QTL mapping (Q), Fine mapping (F)
-Powdery mildew, Ph, Q, F

- Completed QTL mapping in the MR-1xAY RIL population and narrowed the QTL intervals by adding KASP markers to the GBS data. Developed KASP markers for two major QTL and validated them in a set of unrelated cultivars. Branham et al. 2021.

-Fusarium, Ph, Q, F

- Completed QTL mapping in the MR-1xAY RIL population and narrowed the QTL intervals by adding KASP markers to the GBS data. Developed KASP markers for the single major QTL for races 1 and 2 and validated them in a set of unrelated cultivars. population. Branham et al. 2018.

-Downy mildew, Ph, Q, F

- Completed QTL mapping in the MR-1xAY RIL population and narrowed the QTL intervals by adding KASP markers to the GBS data. Developed KASP markers for the major QTL. Toporek et al. 2020 and 2023

2.2: Develop marker (M), verify (V)
-Powdery mildew, M, V

- KASP markers for powdery mildew race 1 resistance were developed in the MR-1xAY RIL population and were validated with a set of commercial cultivars.

-Fusarium, M, V

- KASP markers for Fusarium wilt races 1 and 2 resistance were developed in the MR-1xAY RIL population and were validated with a set of commercial cultivars.

-Downy mildew, M

- KASP markers for downy mildew mating groups 1 and 2 resistance were developed in the MR-1xAY RIL population. Toporek et al. 2020 and 2023

Obj. 3. Introgress, pyramid/stack resistances into advanced breeding lines
Develop breeding lines (B), introgress into cultivated (I), advanced lines (A), release to breeders (R)
-Fusarium wilt races 1 and 2/Powdery mildew race 1, B,I,A
Over the past 12 months we have continued with selections of more advanced lines from an initial four-way cross of MR-1 (resistant to Powdery mildew race 1, *Fusarium oxysporum* f. sp. *melonis* race 1 and race 2 and sulfur) x Top Mark x Charentais (Figure 1). Selections have been made following two breeding paths, one as backcrossed into Top Mark and on as backcrossed into Charentais. Selections have been made using a combination of KASP markers and phenotyping. We currently have BC2F3 and BC1F4 families possessing resistance alleles in the homozygous state for all traits. Additionally, we currently generating BC2F4 and BC1F5 seed

(Table 1). The families were also selected for horticultural traits such as fruit shape, flesh color, brix, flesh texture and netting. We have also made selections from the Charentais breeding path for autonomous selfing and growth habits in Controlled Environment Agricultural (CEA), hydroponic-based systems. All families were evaluated for horticultural traits in replicated field trials in fall 2024 and will also be evaluated in spring 2025. One of the Charantais-like lines (CP-2; Figure 2) had significantly higher brix than the commercial check, 'Athena' and maintains many of the positive horticultural attributes of Charantais (Figure 3). This advanced line has potential for commercial release.

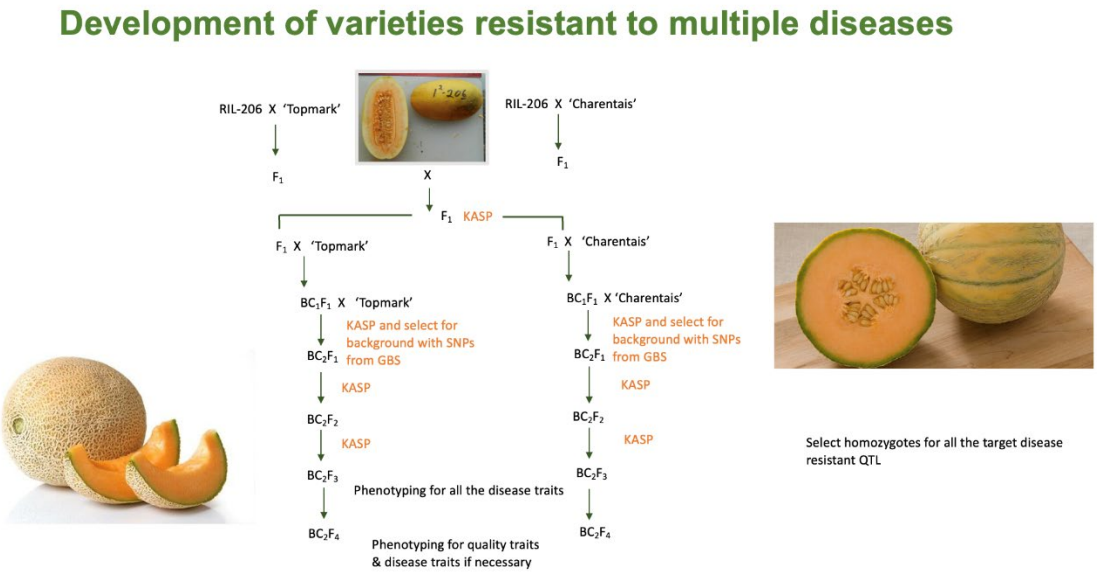
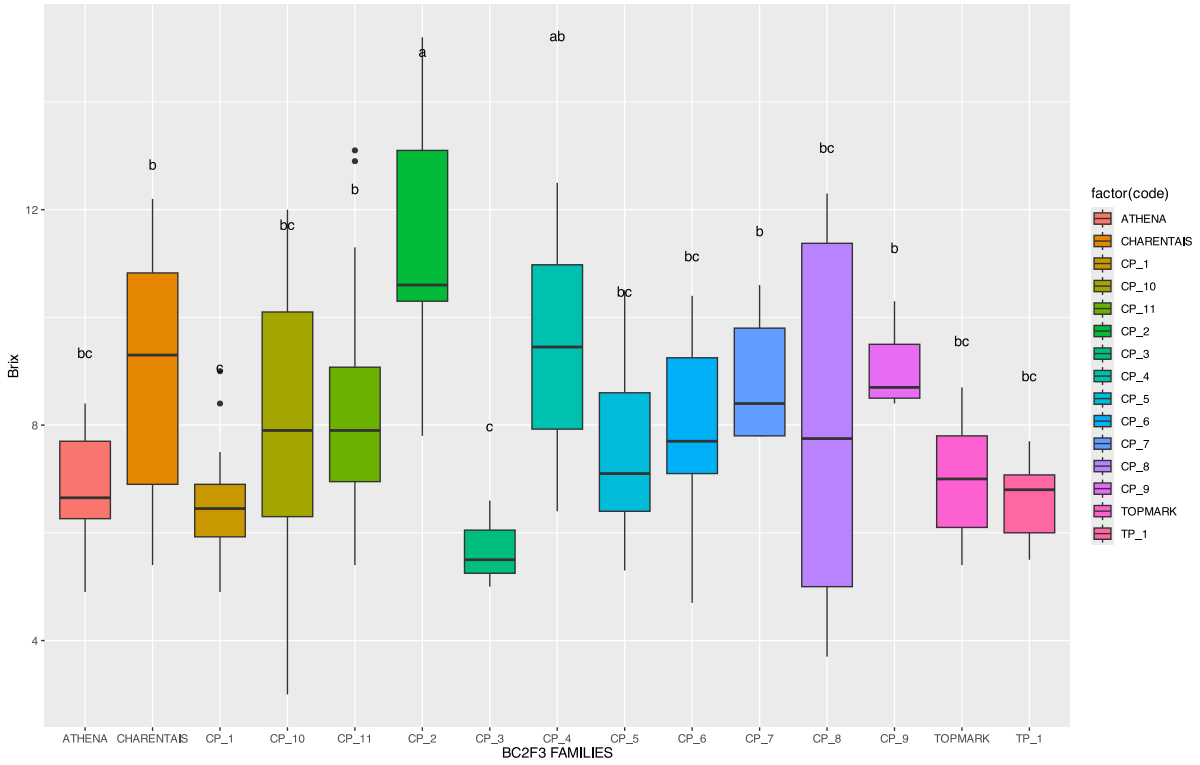
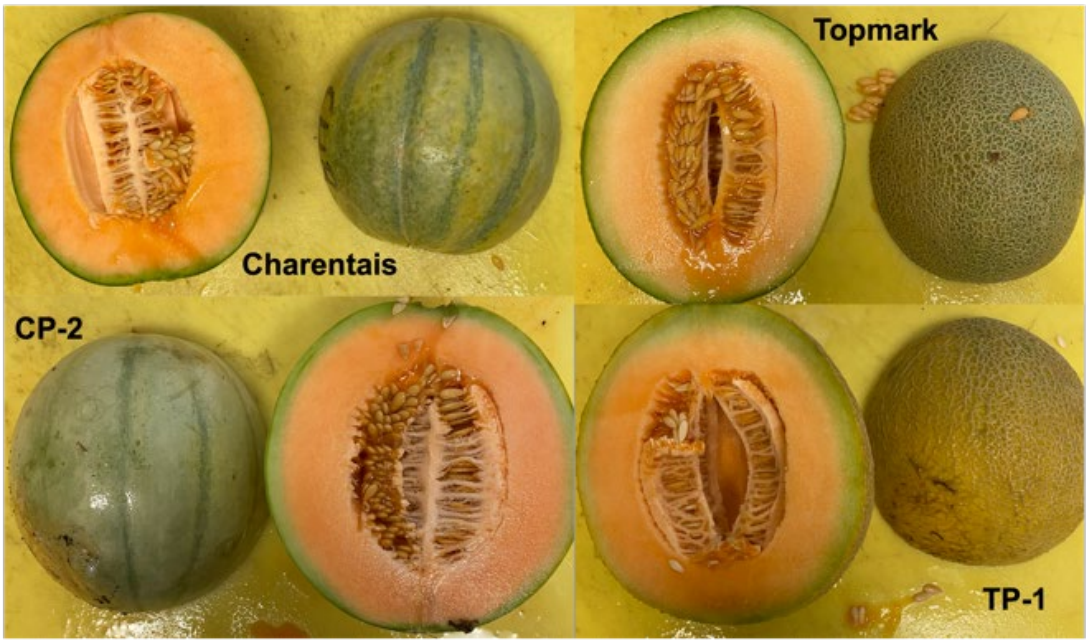


Table 1. Breeding progress for development of multi-disease resistant cantaloupe

Crop	Current seed being generated	Number of families (selections)
Melon	BC2F4 (Charentais x RIL-206)	90
Melon	BC2F4 (Topmark x RIL-206)	3
Melon	BC1F5 (Charentais x RIL-206)	5
Melon	F_1 [BC2F4 (Charentais x RIL-206) x BC2F4 (Topmark x RIL-206)]	6





Update on new virus threat from watermelon chlorotic stunt virus (WmCSV):
WmCSV emerged as a new threat in the Sonoran Desert cucurbit production region in 2023. The whitefly-transmitted virus is now well-established in the region and has become the most prevalent virus in the region, occurring in mixed infections with CYSDV and CCYV. Although WmCSV has not yet been identified in the Central Valley of California, Texas or the

Southeastern U.S., spread is anticipated to these regions based on the frequency at which viruses are introduced among production regions in the U.S. Breeding programs should look for strategies to incorporate sources of resistance to WmCSV into U.S. germplasm, particularly for watermelon and melon.

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1. Toporek SM, Branham SE, Keinath AP, Wechter WP. 2023. QTL Mapping of Resistance to *Pseudoperonospora cubensis* Clade 2, Mating Type A1, in *Cucumis melo* and Dual-Clade Marker Development. Theoretical and Applied Genetics 136(4): 91.
2. Branham SE, Kousik CS, Mandal M, Wechter WP. 2021. QTL mapping of resistance to powdery mildew race 1 in a recombinant inbred line population of melon. Plant Disease 105(12): 3809-3815.
3. Toporek S, Branham SE, Katawczik M, Keinath AP, Wechter WP. 2020. QTL Mapping of Resistance to *Pseudoperonospora cubensis* Clade 1, Mating Type A2, in *Cucumis melo*. Theoretical and Applied Genetics 134(8): 2577-2586.
4. 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. Theoretical and Applied Genetics 131(4): 829-837.

Cucumber Team

Team members:
Yiqun Weng (YW), USDA-ARS, University of Wisconsin Madison,
Rebecca Grumet (**RG**), Michigan State University
Kai-Shu Ling (**KL**), USDA-ARS Charleston, SC
Anthony Keinath (**AK**), Clemson University, SC

During the last year of the project (non-cost extension), since we have completed most of the research objectives, the cucumber team members are wrapping up the project focusing on data analysis and manuscript preparation. The following summarizes research activities and results obtained since the 2024 project meeting by team members.

1. Seed multiplication and deposit of cucumber core collection (Weng)
Continued seed increase for the core collection with 388 accessions. As of March 8, 2025, seed increase of 372 accessions has been completed with 322 having >1000 seeds each and 66 with 100-1000 seeds per line. In the 2024 winter greenhouse season, seed increase was conducted for 35 lines with self-pollinations. Short-day treatment was applied for a few lines known to be photoperiod sensitive for flowering, which did not seem very effective. Seed increase for the remaining lines will be continued for the remaining lines in 2025 spring/summer. We are working with the USDA-NPGS Cucumis curator and plan to ship/deposit seeds of the core collection before the conclusion of the project.

2. QTL mapping of DM resistance in WI7012A (Weng/ and Keinath).
WI7012 is an inbred line carrying introgression from the cucumber relative, *Cucumis hystrix* (2n=24) with DM resistance. A recombinant inbred line (RIL) population was developed from the cross between WI7012A (2n=14) and the susceptible 9930. A linkage map (531 SNP loci; 1010.4 cM) was constructed using DArT-Seq SNP genotyping of 146 RILs. In the 2024 field season, these RILs were phenotyped for responses to natural infection of the DM pathogen. Six DM resistance QTL were detected with *dm5.1* and *dm6.1* contributing major-effect to DM resistance (**Fig. 1**). This work suggests that Dm resistance in WI7012 is controlled by multiple QTL. Based on their positions, *dm2.1, dm6.1* and *dm7.*1 are novel QTL for DM resistance.

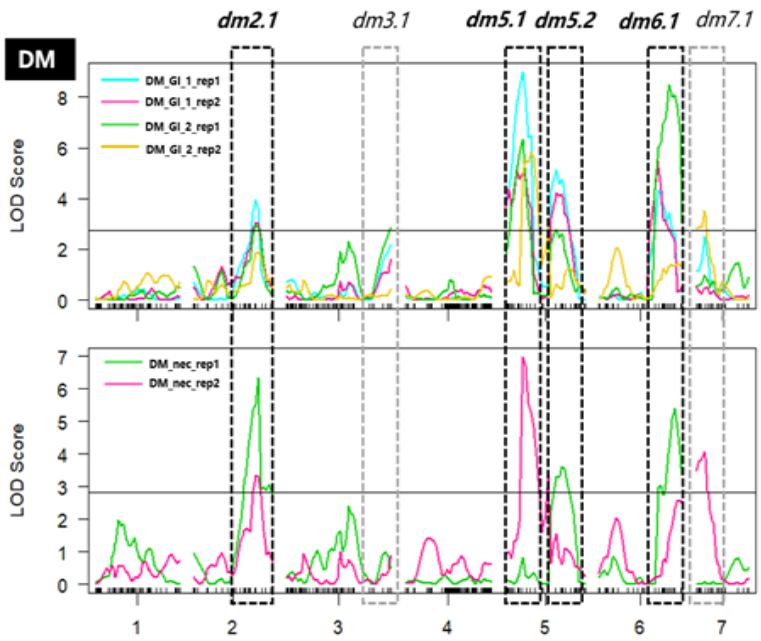


Fig. 1. LOD profiles of DM resistance QTL in WI7012A inbred lines based on phenotypic data of 147 RILs and 531 SNP markers.

3. CGMMV (Lin and Weng)

Cucurbit green mottle mosaic virus (CGMMV) is a seed-borne virus pathogen causing serious disease symptoms and losses in cucumber production. In 2024 we continued CGMMV screening of the cucumber core collection and a segregation population derived from the cross between CGMMV tolerant line WI7814.

Among the 177 accessions, 12 seemed tolerant, 24 and 137 exhibited intermediate tolerance, and 137 were highly susceptible (Fig. 2A). We performed GWAS for CGMMV resistance among 177 cucumber accessions with different models/approaches (Fig. 2B-D). No significant QTL was detected for CGMMV tolerance when kinship and population structure/PCs were considered.

Eighty-two F2 plants from the WI7814 population were phenotyped for CGMMV inoculation responses (Fig. 3A). Ninety-six F2 plants were genotyped with DArT-Seq. QTL analysis identified three peaks on Chromosomes 1, 3 and 6, but none was above the threshold (Fig. 3B). Overall, it seem more accurate phenotyping is needed to increase the reliability of QTL analysis in both biparental and natural populations.

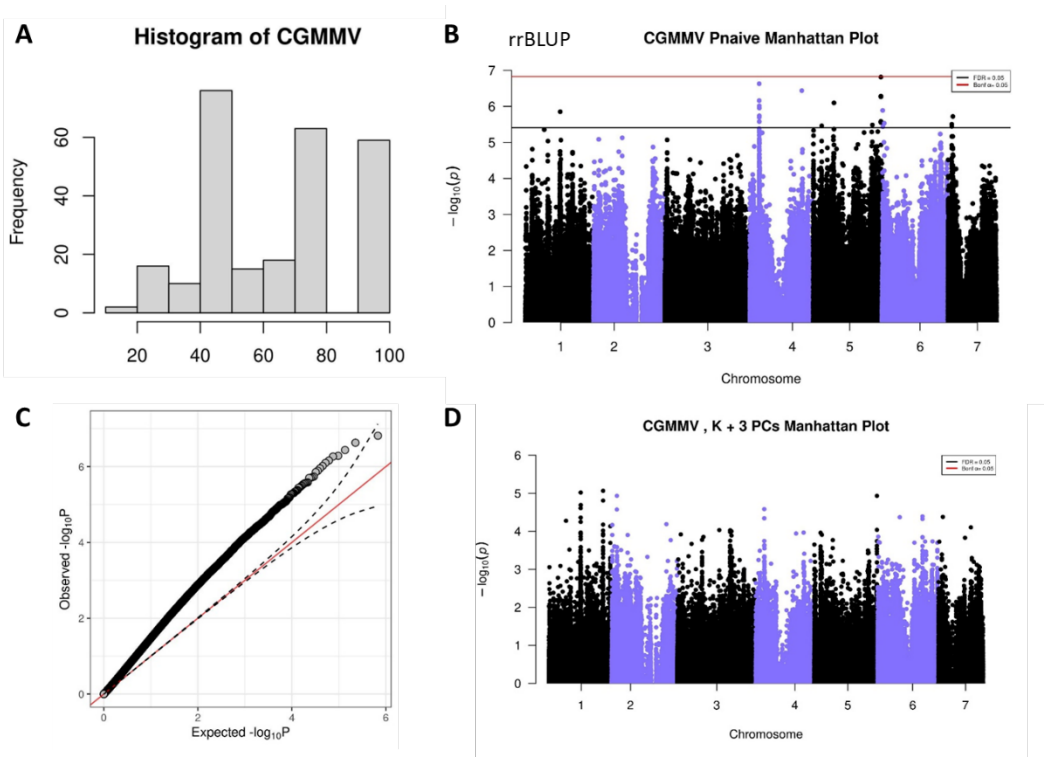


Fig. 2: Association analysis of CGMMV resistance among 177 cucumber accessions. A. Histogram of disease scores among 177 accessions. B-D: Manhattan plots and QQ plots.

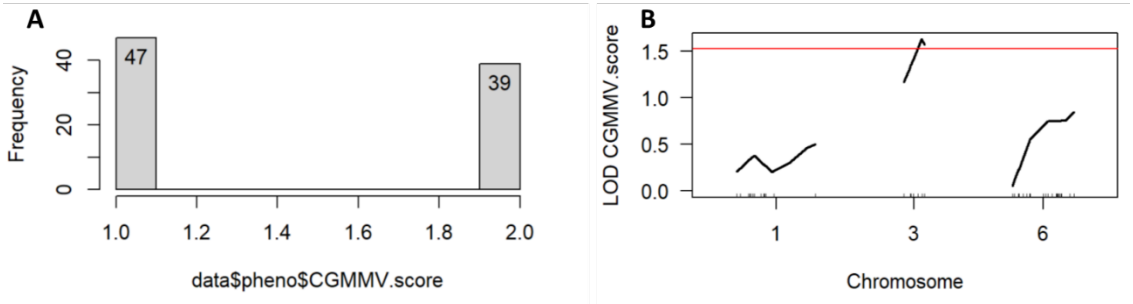


Fig. 3. Linage analysis of CGMMV tolerance in the cucumber line WI7814. A. Histogram of disease scores of 82 F_2 plants. B. LOD profile from QTL analysis.

3. GWAS of fruit traits in cucumber core collection (Grumet)

Phenotype-genotype association analysis was completed for quantitative analysis of 15 fruit quality traits for the cucumber core collection: mature fruit length, diameter, fruit shape index, carpel number, seed cavity, flesh thickness, hollowness, curvature, tapering, skin color, flesh color and netting; and young fruit shape index, curvature, tapering, skin color, and spine density as well as several lipid associated fruit surface traits (cuticle thickness, lipid droplet number and size). Genome-wide association studies (GWAS) were performed on these fruit traits using multiple models. Significant QTL were identified for all of the traits including several closely located SNPs for highly correlated traits, and several that were in close proximity to prior identified fruit quality QTL and candidate genes (Table 1). This work has been accepted for publication (Lin et al., 2025, Horticulture Research. https://doi.org/10.1093/hr/uhae340). GWAS also identified several QTL corresponding with genes previously implicated in cuticle or lipid biosynthesis, including the transcription factor SHINE1/WAX INDUCER1 (Rett-Cadman et al., 2024).

Table 1. Closely located significant cucumber fruit quality SNPs (PVE>2.5) identified for multiple GWAS models or traits, significance of allele effects, distance to previously identified fruit quality genes, and potential novel fruit-expressed candidate genes.

Trait	Model[1,2]	SNP Chr_Position[3]	P-value			PVE (%)				
			Farm CPU	BLINK	MMLM	F	B	M	Candidate gene[4] (**bold**-previously identified[reference], *italic*-novel candidate)	Distance from SNP to candidate gene
Diameter	B****	S1_7676265		7.41E-09			4.40			
L/D young	F****	S1_7676265	3.41E-10			3.01				
Young fruit G	F****	S1_9325655	3.81E-14			5.05				
Young fruit R	F****	S1_9325655	6.83E-14			5.85				
Netting	FB****	S1_10543542	3.11E-16	9.85E-13		9.10	15.62		*CsGy1G014660, extensin*	*21 kb*
Carpel number	B**	S1_10793141		7.05E-16			3.84		***CsGy1G014910*, CsCLV3 [16, 17]**	25.6 kb
Seed cavity	FB**	S1_10793807	1.69E-11	7.05E-16		4.88	3.84			23.9 kb
Carpel number	B****	S1_10809541		5.35E-09			4.52			8.2 kb
	F ns	S1_10810604	5.43E-10			4.51				7.1 kb
	F ns	S1_10811977	1.76E-09			14.22				5.7 kb
	FB**	S1_10811982	3.46E-20	7.81E-22		20.03	3.98			5.7 kb
Seed cavity	B****	S1_18954596		1.28E-08			10.44		*CsGy1G020250, Villin4*	*5.3 kb*
Hollowness	FB****	S1_18954596	4.11E-14	7.41E-10		12.24	13.62			*5.3 kb*
Diameter	F****	S1_18971536	2.66E-08			7.73				*1623 bp upstream*
Spine density	M*	S1_23527125			3.48E-08			11.00		
	B ns	S1_23539769		8.74E-09			6.92			
	F ns	S1_23565429	6.00E-11			4.17				
L/D mature	FM****	S2_3230903	4.49E-09		2.37E-08	7.70		21.02	*CsGy2G005630, WAT1-related protein*	*689 kb*
Curvature	B****	S2_3225700		2.11E-10			10.76			*694 kb*

	M****	S2_3228800			1.40E-11			23.63		*691 kb*
Diameter	B****	S2_11379931		5.99E-11			5.81		***CsGy2G011350*, CsTRM5 [18,19]**	151 kb
Curvature	B****	S2_12351085		5.55E-11			5.15			1.12 Mb
L/D mature	F****	S2_12445336	7.68E-09			3.10				1.22 Mb
L/D young	M****	S2_12446608			8.33E-09			18.50		1.22 Mb
Netting	FB****	S3_1615287	1.28E-15	1.69E-10		5.43	4.80			
Young fruit R	B ns	S3_4519392		1.54E-08			22.56			
Young fruit G	F ns	S3_4519392	8.31E-09			3.68				
Flesh color G	FBM***	S3_10983567	2.17E-14	4.27E-13	1.04E-09	3.70	32.23	32.23		
Spine density	BM****	S3_38703909		1.03E-13	6.14E-11		7.51	10.79	*CsGy3G041410, auxin responsive*	*1958 bp upstream*
L/D mature	F****	S4_20273647	3.09E-10			5.98			***CsGy4G016160*, CsPILS6 [20]/**	612 kb/*4.97 kb*
L/D young	F****	S4_20280932	4.39E-11			4.60			*CsGy4G015630, SCAR*	604 kb/*in exon*
L/D mature	B****	S4_20280932		3.13E-14			2.55			604 kb/*in exon*
Length	FM****	S4_20284337	1.29E-15		3.73E-08	10.57		2.52		601 kb/*in intron*
Curvature	B****	S4_20398766		2.44E-14			7.68			
	F****	S4_20409682	2.33E-13			3.27				
Tapering	FB****	S5_30760720	1.48E-08	9.40E-09		3.60	6.31			
Flesh thick	FB**	S6_684445	5.02E-18	2.98E-11		9.25	6.29			
Seed cavity	FB ns	S6_2746735	6.51E-12	6.86E-16		4.64	5.45			
Hollowness	F ns	S6_4888792	4.71E-09			4.60				
Diameter	B ns	S6_4904391		3.21E-08			7.60			
Mature fruit R	FBM ns	S6_13940065	5.66E-12	1.24E-13	8.50E-09	5.39	19.57	31.54		
Netting	FB ns	S7_5090216	8.64E-09	1.72E-08		3.61	3.88			

[1] – F-FarmCPU, B-BLINK, M-MLMM

[2] – Significance of allele effect ns, *,**,***,**** not significant, $P \leq 0.05, 0.01, 0.001, 0.0001$, respectively (data are shown in Supplementary Figure 3),

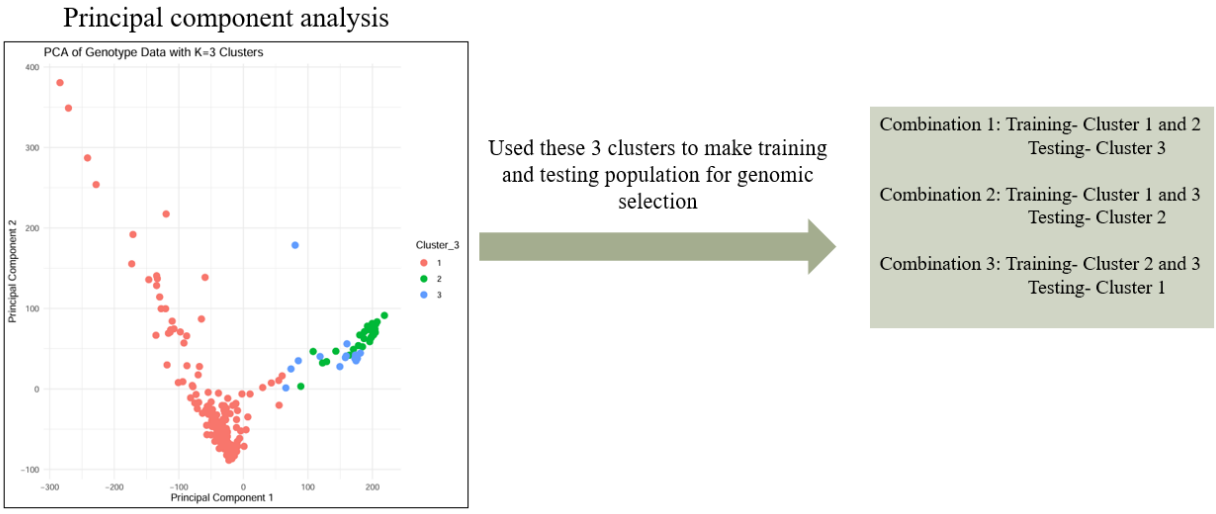
[3] – all locations according to Gy14 v. 2.1 (http://cucurbitgenomics.org/v2/)

[4] – **Bold – previously identified candidate gene**; *italic* – potential novel candidate gene

Squash Team

Florida: Geoffrey Meru
Michigan: Mary Hausbeck
New York: Michael Mazourek, Chris Smart
Puerto Rico: Angela Linares

Obj. 2. Map and develop markers for disease resistance
2.1 QTL mapping of resistances
2.1.4 Squash
- Powdery Mildew – *C. pepo (UF)*
Genomic selection for powdery mildew resistance in squash: The potential application of genomic selection for improvement of powdery mildew resistance in squash was evaluated. Genotype data consisting of 103,296 high-quality SNPs (i.e. 80% filtered VCF file) and phenotype data previously collected from a greenhouse disease screening in Florida were used for this study. PCA analysis revealed 3 primary clusters (k=3). The clusters were used to create different training and testing combinations for genomic prediction (Figure 1).
Figure 1 PCA analysis and cluster designation for genomic prediction



The Genomic Best Linear Unbiased Prediction (GBLUP) was used to predict the genomic estimated breeding values (GEBVs). GBLUP utilizes the genomic relationship matrix (computed from SNP data) to estimate GEBVs for each genotype, considering all genetic markers across the genome. A Genomic Relationship Matrix (GRM) was created using the VanRaden method, which accounts for the genetic similarities between individuals based on marker data. GEBVs were calculated for each trait, predicting the genetic potential for powdery mildew resistance, where negative GEBVs indicated better resistance. Genotypes were ranked to identify the top candidates for breeding. Overall, the best prediction accuracies were obtained when cluster 2 and cluster 3 were used to train the model and predict GEBV's for cluster1. Several accessions were consistently ranked as resistant across traits, which was generally consistent with previous GH observations (Figure 2).

Figure 2 GEBV's of top resistant accessions. Accessions marked in Asterix were consistently ranked as resistant across two or more traits.

Top 4th leaf

ID	UF Code	Trait	GEBV	Rank
*GT130	68	1	-25.40255238	1
*GT092	189	1	-18.72658635	2
*GT152	144	1	-15.32829743	3
*GT198	114	1	-11.3681455	4
GT144	115	1	-11.31940817	5
*GT091	188	1	-11.03095821	6
*GT094	192	1	-10.89099772	7
*GT086	179	1	-10.18843493	8
GT003	25	1	-9.752593881	9
*GT095	193	1	-9.472870056	10

Bottom 4th leaf

ID	UF Code	Trait	GEBV	Rank
*GT091	188	2	-17.56802581	1
GT093	190	2	-16.8637327	2
*GT095	193	2	-16.50600026	3
*GT094	192	2	-15.82249821	4
*GT161	168	2	-13.86056366	5
*GT086	179	2	-11.79019648	6
GT139	83	2	-11.52739488	7
*GT092	189	2	-11.21039896	8
GT070	142	2	-11.10555038	9
*GT198	114	2	-10.97153273	10

Stem above 4th leaf

ID	UF Code	Trait	GEBV	Rank
*GT152	144	3	-14.44885518	1
*GT092	189	3	-14.44846309	2
*GT130	68	3	-11.75699133	3
*GT091	188	3	-11.4065101	4
GT133	72	3	-10.14696028	5
*GT059	125	3	-9.456385623	6
GT126	62	3	-9.317920376	7
GT127	64	3	-8.887138253	8
GT183	16	3	-8.72091161	9
*GT025	70	3	-8.58109735	10

Stem below 4th leaf

ID	UF Code	Trait	GEBV	Rank
*GT130	68	4	-15.85165432	1
*GT092	189	4	-13.37686427	2
*GT152	144	4	-13.04190595	3
*GT091	188	4	-11.56959472	4
*GT059	125	4	-9.930570491	5
*GT198	114	4	-9.639456178	6
*GT025	70	4	-9.040175181	7
GT061	127	4	-6.966366937	8
GT083	176	4	-6.923830314	9
GT016	40	4	-6.691194655	10

Whole Plant

ID	UF Code	Trait	GEBV	Rank
*GT092	189	5	-27.14098692	1
*GT130	68	5	-19.40451887	2
GT167	191	5	-10.4940982	3
*GT095	193	5	-9.963803158	4
*GT161	168	5	-9.495916351	5
GT068	140	5	-8.611809111	6
GT131	69	5	-7.394511886	7
GT106	5	5	-7.341457093	8
GT090	187	5	-6.938460618	9
GT199	129	5	-6.696068706	10

Obj. 3. Introgress, pyramid/stack resistances into advanced breeding lines

3.4 Squash (*C. pepo, C. moschata*)

-Powdery mildew in C. moschata (CU)

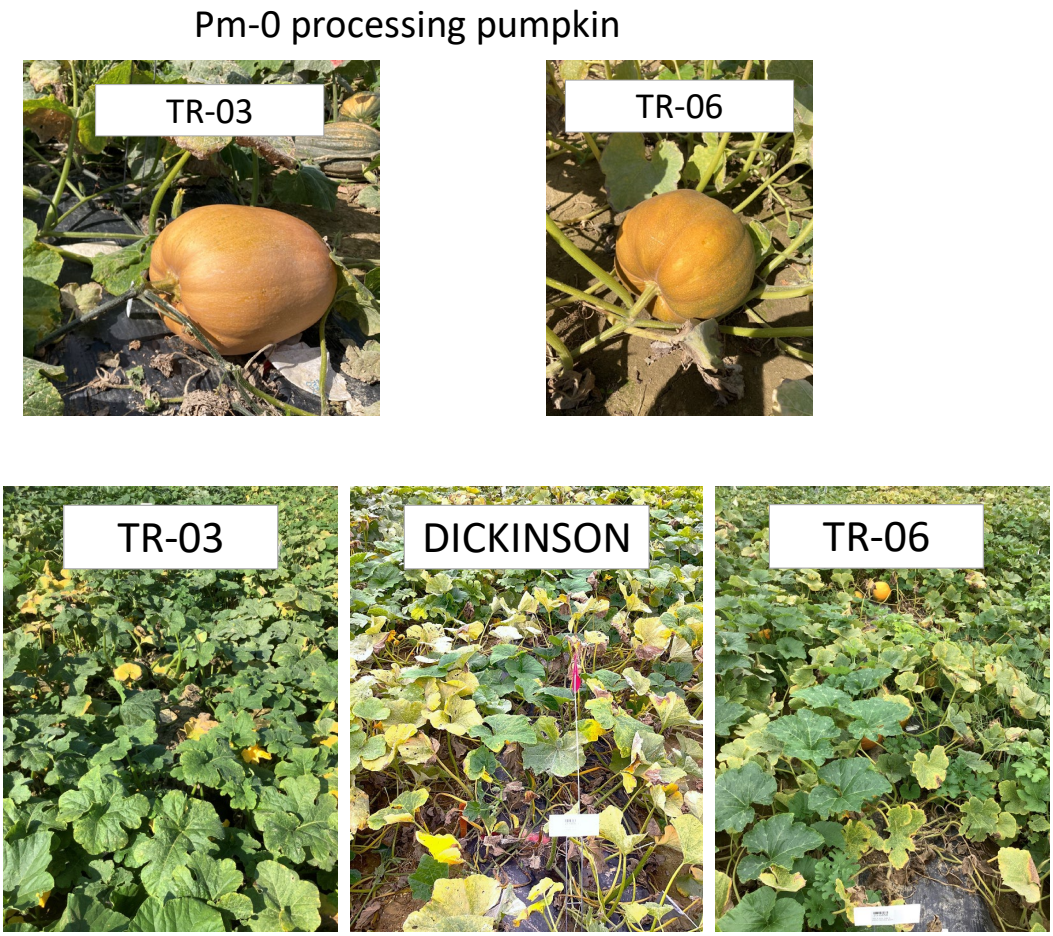
We have used the PM-0 marker from CucCAP I to introgress powdery mildew resistance into a Honeynut squash background. Unlike most winter squash, the full season nature of Honeynut has proven to run into powdery mildew pressure early enough in fruit development where it affects fruit quality by premature plant senescence. The Pm-0 marker allowed us to introgress PM resistance into Honeynut while simultaneously selecting for improved storage and fruit quality. Other traits were selected upon less stringently such as black rot resistance, earliness, and aesthetics.

Honeynut with mildew on petioles

***Pm-0* Honeynut with asymptomatic petioles**

***Pm-0* Honeynut fruit in the field**

A final PMR Dickinson hybrid was grown in 2024 with parental selection based on canning results from Libby Indermaur in the Smart Lab. The plants were healthy and productive, however they were also very attractive to deer. We plan a final trial evaluation on a fully fenced field in 2025 to determine if the hybrid cultivar is potentially commercially viable.



-P. capsici crown rot in C. pepo (UF)

We continued effort to introgress crown rot resistance from *C. moschata* into *C. pepo* background. Seedlings of 21 families segregating for resistance to *P. capsici* crown rot were screened in 2024. Among these, 4 families () were found to have promising resistance, with average crown rot DS of <1 (Table 1). The susceptible and resistant controls responded as expected.

Table 1. Response of 21 *C. pepo* x *C. moschata* families to segregating *P. capsici* crown rot.

Genotype	GH ID	D.S	Pedigree
SS49	115	0.25	49-37^{R}sib49-31^{R}
SS2721	93	0.33	(SS334-6/SS2535-22^{R})-11^{R}
SS3027	112	0.66	38-8/49-37^{R}
SS2722	49	0.90	SS1531-10/SS69-52-8^{R}
SS2567	39	1.48	SS69-52-8-3^{R}/SS2234-2
SS2879	108	1.86	SS2834-11/38-8
SS1531	48	1.95	SS1531-3^{R}
SS2857	124	2.24	38-13^{R}/67-5
SS2934	110	2.55	SS2838-A/38-8
SS2824	98	2.75	(EP/SS2535-( )^{R})-34^{R}/(334-6/SS2535-22^{R})-7^{R}
SS2871	118	2.75	SS2834-3/60-6
SS2525	36	2.91	SS2226-2/SS333-8-3^{R}
SS2883	127	3.07	SS2834-B/67-5
SS2844	101	3.35	SS2721-12^{R}(Tray 3 "1")/SS2721-4^{R}
MS41	46	3.82	F18/SS2535-20^{R}
SS2804	94	4.00	(SS2535-15^{R}/YC)-4/SS2535-( )^{R}
MS22	45	4.05	SS2453-10/SS2535-20^{R}
SS2854	123	4.15	YC/67-5
SS2654	91	4.19	(SS2535-19^{R}/YC)- ( )^{R}
SS2655	92	4.67	(SS2535-11^{R}/EP)- ( )^{R}
SS2858	125	4.97	EP/67-5
EP	EP	5	Susceptible control
BB	BB	5	Susceptible control
394	394	0.285714	Resistant control

Summary of identification of new sources of resistance (I), resistance QTL (Q), marker (M) development, and release of resistant lines (L) for cucurbit crop diseases

Disease	Crops	Species	I/Q/M	Publications
Alternaria *Alternaria cucumerina*	Melon	*Cucumis melo*	Q	Daley et al. 2017
Angular leaf spot *Pseudomonas syringae* pv. *lachrymans*	Cucumber	*Cucumis sativus*	M, gene	Wang et al. 2019
Anthracnose *Colletotrichum orbiculare*	Cucumber	*Cucumis sativus*	M, gene	Pan et al. 2018; Wang et al. 2019
Bacterial fruit blotch *Acidovorax citrulli*	Watermelon	*Citrullus amarus*[1]	Q	Branham et al. 2019b
Bacterial wilt *Erwinia tracheiphila*	Melon	*Cucumis melo*	I	Acharya et al. 2021
CCYV *Cucurbit chlorotic yellows virus*	Squash	*Cucurbita pepo*	I	Adeleke et al. 2024 Kavalappara et al. 2024
CYSDV *Cucurbit yellow stunting disorder virus*	Melon	*Cucumis melo*	Q	Tamang et al. 2021
CuLCrV *Cucurbit leaf crumple virus*	Squash Watermelon	*Cucurbita moschata, C. ecuadorensis, C. okeechobeensis* *Citrullus mucosospermus*	I I	Luckew et al. 2022 Luckew et al. 2025
Downy mildew *Pseudoperonospora cubensis*	Cucumber Melon Watermelon	*Cucumis sativus* *Cucumis melo* *Citrullus amarus*	Q,M, gene Q,M Q	Wang et al. 2016; 2018; 2019; Tan et al., 2022 Toporek et al. 2021; 2023 Katuuramu et al., 2022
Fusarium wilt *Fusarium oxysporum* f. sp. *melonis* f. sp. *niveum*	Melon Watermelon -Race 1 -Race 2	*Cucumis melo* *Citrullus amarus* *Citrullus lanatus* *Citrullus lanatus*	Q I,Q Q,M Q	Branham et al. 2018a Meru and McGregor 2016; Branham et al. 2019a Fall et al. 2018; Branham et al. 2018b Meru and McGregor, 2016

		Citrullus amarus	Q,M	Branham et al. 2017; 2020; Ganaparthi et al. 2023; 2024
Gummy stem blight *Stagonosporopsis* spp	Cucumber Watermelon	*Cucumis sativus* *Citrullus amarus*	M, gene I, Q	Wang et al. 2019 Gimode et al. 2019; 2021; Adams and McGregor, 2022; Rivera-Burgos et al. 2021; Natarajan et al. 2024
Phytophthora fruit rot *Phytophthora capsici*	Cucumber -young fruit -age-related Watermelon	*Cucumis sativus* *C. mucosospermus*	 L, Q, M Q L	 Grumet and Colle 2017; Lin et al. 2023 Lin et al. 2023 Kousik et al., 2023
Phytophthora crown, root rot *Phytophthora capsici*	Squash	*Cucurbita moschata* *Cucurbita pepo*	I Q	Kousik et al., 2021 Michael et al. 2021; Vogel et al., 2021
Powdery mildew *Podosphaera xanthii*	Cucumber Melon Squash Watermelon Bottle gourd	*Cucumis sativus* *Cucumis melo* *Cucubita pepo* *C. moschata* *Citrullus lanatus* *C. mucosospermus* *Lagenaria siceraria*	Q,M Q,M M, gene L Q,M L L	Liu et al. 2017; Wang et al. 2018 Branham et al., 2021 Holdsworth et al. 2016 Indermaur et al. 2025 Kousik et al. 2018; Mandal et al. 2020; Branham et al. 2025 Kousik et al., 2023 Kousik et al., 2018
PRSV *Papaya ringspot virus*	Watermelon Squash	*Citrullus amarus* *C. colocynthis* *Cucurbita moschata*	Q I Q,M	Branham et al., 2020 Levi et al. 2016 Shrestha et al., 2022
Target leaf spot *Corynespora cassiicola*	Cucumber	*Cucumis sativus*	M, gene	Wang et al. 2019
Whiteflies *Bemisia tabaci*	Squash Watermelon	*Cucurbita pepo* *Citrullus ecirrhosus*	I I	Luckew et al. 2022 Simmons et al. 2019
ZYMV *Zucchini yellow mosaic virus*	Watermelon Squash	*Citrullus amarus* *Citrullus lanatus* *Cucurbita moschata*	I,Q L Q,M	Guner et al. 2019 Levi et al. 2016; Levi and Ling 2017 Shrestha et al. 2021
[1] *Citrullus amarus* previously *C. lanatus* var. *citroides*				

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Integrated Disease Management Team and Personnel Working on Project

- Lina Quesada-Ocampo (NC State)
    - Yara Rosado (technician)
    - Mary Lorscheider (extension communicator)
    - Mariana Prieto (PhD student)
    - Sarah Cochran-Murray (PhD student)
- Mary Hausbeck (MSU)
    - Carmen M. Medina-Mora (technician)
    - John Spafford (graduate student)
    - David Perla (technician)
- Chris Smart (Cornell)
    - Colin Day (lab manager)
    - Libby Indermaur (PhD student)
    - Emma Nelson (PhD student)
- Anthony Keinath (Clemson)
    - Sierra Zardus
    - Anna Mothersbaugh
- Shaker Kousik (USDA-ARS)
    - Jennifer Ikerd
- Jonathan Schultheis (NC State)
    - Stuart Michel (Technician/MS Student)
    - Brandon Parker (Research Associate)
    - Baker Stickley (Research Assistant)
    - Cameron Roberts (Technical Support - Hourly)
    - Daphne Meyer (Technical Support - Hourly)
    - Lia Hunt (Technical Support - Hourly)
    - Nathaniel Wyschka (Technical Support - Hourly)
- Daniel Tregeagle (NC State)
    - Alice Kilduff (PhD Student)
- Melinda Knuth (NC State)

4.1. Disease management information and recommendations (Year 1-4).

CucCAP website: From Sept. 1, 2021 until Feb. 7, 2025, the CucCAP website was visited by 45,721 users including 46,623 new users with 49,827 sessions and 86,523 pageviews. A total of 857 news items were posted on the website. These posts were shared in a monthly newsletter sent to 160 subscribers and in posts on social media including Facebook with 1,049 followers, Twitter with 332 followers, and LinkedIn with 52 followers. Cucurbit disease factsheets and links to integrated pest management resources are maintained and updated annually on the website. Five of the top ten pages visited on the website were Cucurbit disease management factsheets in Spanish. The CucCAP website events calendar shared notices of regional commodity meetings, education sessions, and scientific meetings.

Quesada: Since the start of the project, Quesada has provided diagnostics and disease management recommendations for 38 cucumber, 67 watermelon, 18 melon, 25 squash, and 18 pumpkin samples submitted to the NC State Plant Disease and Insect Clinic. Quesada has also been involved in providing disease management recommendations through oral presentations, social media (Twitter: 7,665 (lab) + 4,090 (Quesada) followers, LinkedIn: 3,712 followers), and generating disease management resources such as the NC Agricultural and Chemicals Manual and the Southeastern US Vegetable Crop Handbook.

Smart: The 2024 field season in New York was fairly dry, and there were not as many outbreaks of *P. capsici* or other cucurbit diseases. There were three farms that had significant disease, and isolates were collected from those farms. Smart received 41 text messages and 21 email messages asking for diagnostic assistance with cucurbits. She visited 6 farms with cucurbit diseases and gave advice on cultural practices, the potential for future resistant cultivars, and fungicide efficacy.

Hausbeck: Hausbeck maintains a page dedicated to downy mildew (Downy Mildew News) which includes an early alert spore monitoring system that is updated weekly during the cucurbits growing season (late May to August) and keeps the scientific community and growers informed with current information about the disease. This page includes a weekly summary of the results from spore trapping used for tracking, monitoring, and management recommendations for the state and surrounding growing areas. This year's results corresponded to seven spore traps deployed in seven counties in Michigan's lower peninsula. Four were next to commercial cucumber fields, one was next to a commercial squash field, and two were in MSU research plots. The webpage includes a Michigan map that is updated as mildew symptoms are confirmed in the state, facts sheets, illustrative identification of mildew on cucurbits, and reference articles and links to main diseases threatening crop production of cucurbits.

Schultheis: Since the start of the project, Schultheis has been involved in cultivar evaluations on melon, zucchini, pumpkin, and watermelon. Cultivar and production recommendations for the industry are made annually in the Southeastern US Vegetable Crop Handbook. Additional research more recently has involved canary melons with respect to cultigen field evaluations, internal chemistry, and sensory evaluations as well as grower extension activities. Watermelon cultivar response to Fusarium wilt has been the main focus and this information has been conveyed regularly through oral and poster presentations.

4.2. Multi-location, multi-isolate trials and pathogen population analyses.

4.2.1 Evaluation of cucurbit cultivars and breeding lines for disease resistance (Year 1-2).

These objectives were completed in years 1-2.

4.2.2 Evaluation of integrated disease management in cucurbits combining host resistance and chemical control (Year 3-4).

Watermelon Fusarium wilt (Lead: Schultheis, Secondary Site: Keinath):

Two studies investigating the effect of fungicides and triploid watermelon cultivar tolerance to *Fusarium oxysporum* f. sp. *niveum* (FON) were conducted in 2023-2024 at two locations; Clayton, NC and Charleston, SC. In 2023, 12 treatments were replicated 4 times in a randomized complete block design. The treatments were combinations of triploid watermelon cultivars (Fascination, Eleanor, and Shoreline) and fungicide/grafting treatments; Proline at 5.7 oz/A, Propulse at 13.6 oz/A, Proline and Propulse at the aforementioned rates, grafting to Carolina Strongback rootstock, and a nontreated control. Cultivars Fascination and Eleanor received each level of the treatments whereas Shoreline only received the grafting and nontreated treatments due to space limitations in the field. The NC study was conducted at the Central Crops Research Station in Clayton, NC and all plants were grown on black plastic with drip fertigation in a field infested with races 1 and 2 of FON. Plots were 27.5 ft long with 10 feet between rows and 10 ft alleys between plots in the row. There were 10 plants per plot with 27.5 inches between plants. Pollenizers SP-7 and SP-7 grafted to Carolina Strongback rootstock were planted after triploid plants 1, 4, 7, and 10 in each plot. Plants were seeded on 27 March 2023 and were transplanted on 3 May 2023. Fungicides were applied to the corresponding plots through the drip tube on 4 May 2023; less than 24 hours after transplanting. An additional application of Proline at 5.7 oz/A was applied on 18 May 2023 (15 days after transplanting (DAT)) to the Propulse and Proline treatment plots. Disease incidence data were collected weekly for 8 weeks from 24 May to 12 July 2023. Yield data were collected over 4 harvests from 20 July to 11 August 2023. The SC study was conducted at the Coastal Research and Education Center in Charleston, SC. All plants were also grown on black plastic with drip fertigation in a field infested with races 1 and 2 of FON. Plots were 36 ft long with 9 ft between rows and 3 ft between plants in row for a total of 12 plants per plot. The same pollenizers were used at both locations. Plants at the SC location were seeded on 27 February 2023 and were transplanted on 5 April 2023. Fungicides were applied to the corresponding plots on 6 April 2023. The additional Proline application for the Proline and Propulse treatments was made on 20 April 2023 (15 DAT). Disease incidence data were collected weekly for 8 weeks from 25 April to 16 June 2023. Yield data were collected over 8 harvests from 19 June to 7 August 2023. Data were analyzed for the effect of treatment on disease incidence and the effect of treatment on yield in SAS 9.4 using PROC GLM and MIXED with Tukey's HSD for means separation for the NC study, and GLIMMIX using Fisher's LSD for the SC study.

The three grafted treatments had the lowest disease incidence at both locations with each treatment having 0% except for the grafted 'Eleanor' treatment at the SC location which had 0.6%. 'Shoreline' had the highest disease incidence at both locations with 95% in NC and 98.3% in SC. 'Eleanor' treated with Proline and Propulse (67.5%) had lower disease incidence than the nontreated 'Shoreline' (95%) in NC. At the SC location, 'Fascination' treated with Proline (47.2%) had less disease incidence than 'Eleanor' treated with Proline and Propulse (95%), 'Eleanor' treated with Propulse (92.5%), and the nontreated 'Shoreline' (98.3%). Marketable yield was mostly consistent with disease incidence. Treatments with the lowest disease incidence generally had the highest yields. The three grafted treatments had higher marketable yields than

all other treatments at both locations. Grafted ‘Fascination’ had the highest yield at the NC and SC locations at 45338 lb/A and 56139 lb/A, respectively. Nontreated 'Shoreline’ had the lowest marketable yield at both locations with 0 lb/A in NC and 916 lb/A in SC. The results suggest that grafting is a practical management strategy for growing watermelons in a field infested with races 1 and 2 of FON. Cultivar tolerance alone or when paired with fungicide treatments made no practical differences to disease incidence or marketable yield in these studies.

Disease Incidence (%) and Marketable Yield (lb/A) for FON Field Study in NC and SC, 2023						
Trt #	Cultivar	Treatment	Disease Incidence (%) NC	Marketable Yield (lb/A) NC	Disease Incidence (%) SC	Marketable YIeld (lb/A) SC
1	Shoreline	Nontreated	95 a	0 b	98.3 a	916 c
2	Fascination	Nontreated	87.5 ab	2819 b	68.1 bcd	7437 c
3	Eleanor	Nontreated	82.5 ab	4015 b	78.2 abcd	5416 c
4	Fascination	Proline 5.7 oz/A	95 a	3948 b	47.2 d	9554 bc
5	Eleanor	Proline 5.7 oz/A	70 ab	3972 b	73.5 abcd	7563 c
6	Fascination	Propulse 13.6 oz/A	72.5 ab	3128 b	56.5 cd	9428 bc
7	Eleanor	Propulse 13.6 oz/A	72.5 ab	7480 b	92.5 abc	1573 c
8	Fascination	Proline 5.7 oz/A + Propulse 13.6 oz/A	85 ab	4764 b	82.2 abcd	5947 c
9	Eleanor	Proline 5.7 oz/A + Propulse 13.6 oz/A	67.5 b	4478 b	95 ab	2828 c
10	Shoreline	Grafted (C. Strongback)	0 c	34317 a	0 e	42016 a
11	Fascination	Grafted (C. Strongback)	0 c	45338 a	0 e	56139 a
12	Eleanor	Grafted (C. Strongback)	0 c	39493 a	0.6 e	33832 ab

In 2024, 8 treatments were replicated 4 times as a 2 x 4 factorial using a randomized complete block design. The treatments were pairings of triploid watermelon cultivars, Cracker Jack and Fascination, and fungicide/grafting treatments; 2 applications of Miravis Prime at 15.4 oz/ac, 3

applications of Propulse at 13.6 oz/ac, grafting to Carolina Strongback rootstock, and a nontreated control. The NC study was conducted at the Central Crops Research Station in Clayton, NC and all plants were grown on black plastic with drip fertigation in a field infested with races 1 and 2 of FON. Plots were 36 ft long with 10 feet between rows and 10 ft alleys between plots in the row. There were 12 plants per plot with 3 ft between plants. Pollenizers SP-7 and SP-7 grafted to Carolina Strongback rootstock were planted after triploid plants 1, 4, 7, and 10 in each plot. Plants for both study locations were donated by Tri-Hishtil (Mills River, NC). Plants for the NC study were transplanted on 6 May 2024. Fungicides were applied to the corresponding plots through the drip tube on 7 May 2024; less than 24 hours after transplanting. A second and third application of Propulse at 13.6 oz/A occurred on 21 and 28 May 2024; 14 and 21 DAT, respectively. A second application of Miravis Prime at 15.4 oz/A occurred on 28 May 2024; 21 DAT. Disease incidence data were collected weekly for 7 weeks from 27 May 2024 to 8 July 2024. Yield data were collected over 3 harvests from 10 July to 3 August 2024. The SC study was conducted at the Coastal Research and Education Center in Charleston, SC. All plants were grown on black plastic with drip fertigation in a field infested with races 1 and 2 of FON. Plots were 36 ft long with 9 ft between rows and 3 ft between plants in row for a total of 12 plants per plot. The same pollenizers were used at both locations. Plants at the SC location were transplanted on 8 April 2024. Fungicides were applied to the corresponding plots through the drip tube on 9 April 2024; less than 24 hours after transplanting. A second and third application of Propulse at 13.6 oz/A occurred on 23 and 29 April 2024; 14 and 21 DAT, respectively. A second application of Miravis Prime at 15.4 oz/A occurred on 29 April 2024; 21 DAT. Disease incidence data were collected weekly for 7 weeks from 30 April to 11 June 2024. Yield data were collected over 4 harvests from 25 June to 16 July 2024. Data were analyzed for the effect of the interaction of cultivar and treatment on disease incidence and the effect of the interaction of cultivar and treatment on yield in SAS 9.4 using PROC GLIMMIX with Tukey's HSD for means separation for both studies.

No significant interaction of cultivar and treatment on disease incidence was found at either location. Numerically, the grafted treatments had the lowest disease incidence at both locations. Grafted 'Fascination' had the lowest disease incidence with 2.1% in NC and 0% in SC followed by grafted 'Cracker Jack' with 8.3% in NC and 3.1% in SC. The nontreated 'Cracker Jack' had the highest disease incidence at the NC location with 74.5%. The second highest incidence for NC was 'Cracker Jack' treated with Propulse at 71.6%. The nontreated 'Fascination' had lower disease incidence than all 'Cracker Jack' treatments other than the grafted treatment for the NC location. In SC, 'Cracker Jack' treated with Miravis Prime had the highest disease incidence at 99.5%. Nontreated 'Cracker Jack' had 97.7% incidence, and 'Cracker Jack' treated with Propulse had 97%. 'Fascination' with all treatments other than grafting had lower disease incidence than 'Cracker Jack'. There were no differences in marketable yield at the NC location for the effect of the cultivar and treatment interaction. Both grafted treatments had higher marketable yields than all other treatments at the SC location. Grafted 'Fascination' had a higher marketable yield than grafted 'Cracker Jack' in SC. Grafted 'Fascination' had the highest marketable yield at both locations with 34761 lb/A in NC and 45990 lb/A in SC. Nontreated 'Fascination' had the lowest yield at 6605 lb/A in NC and 'Cracker Jack' treated with Miravis Prime had the lowest yield at 903 lb/A in SC. The results suggest that grafting is a practical management strategy to reduce disease incidence and improve marketable yields when growing watermelons in a field infested with races 1 and 2 of FON. Cultivar tolerance alone or when

paired with multiple applications of Propulse or Miravis Prime made no practical differences in these studies.

Disease Incidence (%) and Marketable Yield (lb/A) for FON Field Study in NC and SC, 2024						
Trt #	Cultivar	Treatment	Disease Incidence (%) NC	Marketable Yield (lb/A) NC	Disease Incidence (%) SC	Marketable YIeld (lb/A) SC
1	Cracker Jack	Nontreated	74.5	9370	97.7	2596 c
2	Cracker Jack	Grafted (C. Strongback)	8.3	28322	3.1	33958 b
3	Cracker Jack	Miravis Prime 15.4 oz/A (2 app)	71.6	12792	99.5	903 c
4	Cracker Jack	Propulse 13.6 oz/A (3 app)	67.7	14599	97	2389 c
5	Fascination	Nontreated	61.2	6605	62.7	2291 c
6	Fascination	Grafted (C. Strongback)	2.1	34761	0	45990 a
7	Fascination	Miravis Prime 15.4 oz/A (2 app)	38.9	10724	60.7	7632 c
8	Fascination	Propulse 13.6 oz/A (3 app)	49.9	11141	67.4	5713 c

<u>Cucumber downy mildew (Lead: Hausbeck, Secondary Site: Quesada)</u>:

Quesada: This study investigates the management of downy mildew in cucumber crops at the Horticultural Crops Research Station in Clinton, NC. Experimental plots consist of single raised beds on 5-foot centers, covered with white plastic mulch, measuring 14 feet long, with 5-foot fallow borders on each end and nontreated guard rows on either side. Cucumbers were directly seeded on 1 August, with a 2-foot in-row spacing and two seeds per hill, then thinned to one plant per hill after emergence (7 plants per plot). Regular cultural practices, including irrigation and fertilization (N-P-K ratio of 4-0-8), were applied via drip tape. Twelve treatments, including three varieties and four fungicide programs, were tested in a randomized complete block design with four repetitions. Fungicide treatments were applied using a CO2-pressurized backpack sprayer equipped with a dual-nozzle handheld boom and TXVS-26 hollow cone nozzles,

delivering 40 gallons per acre at 40 psi. Disease severity per plot was assessed weekly. Data were analyzed using ARM software (Gylling Data Management, Brookings, SD) with analysis of variance (ANOVA) and Fisher's protected least significant differences (LSD) test to separate means.

Downy mildew was first detected on 29 August, with approximately 2% disease severity in the field. On 1 October, treatments 1 and 3 had the highest disease severity compared to all other treatments. Treatment 12 was the only treatment to have significantly lower disease severity than any nontreated variety. No phytotoxicity is observed in the experiment.

Trt #	Variety	Treatments and rate/Acre	Application Code[z]	Disease Severity[y] (%) 1 Oct	AUDPC[x]
1	Vlaspik	Nontreated	–	72.5 a[w]	12156.13 ab
		Howler Evo 1.25 lb/A	ACE		
		Dyne-Amic 0.375% v/v	ACE		
		Kocide 3000 1.25 lb/A	BDF		
3	Vlaspik	Dyne-Amic 0.375% v/v	BDF	62.5a	16807 a
9	Chaperon	Nontreated		46.3 b	9702.38 bc
		Orondis Opti 2.5 pt/A	AE		
		Kocide 3000 1.25 lb/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Howler Evo 1.25 lb/A	BF		
		Dyne-Amic 0.375% v/v	BF		
		Previcur Flex 1.2 pt/A	C		
		Kocide 3000 1.25 lb/A	C		
		Dyne-Amic 0.375% v/v	C		
		Zampro 14 fl oz/A	D		
		Howler Evo 1.25 lb/A	D		
2	Vlaspik	Dyne-Amic 0.375% v/v	D	45.0 b	8673.25 bcd
		Howler Evo 1.25 lb/A	ACE		
		Dyne-Amic 0.375% v/v	ACE		
		Kocide 3000 1.25 lb/A	BDF		
7	Citadel	Dyne-Amic 0.375% v/v	BDF	38.8 bc	10048 bc
5	Citadel	Nontreated	–	31.3 cd	8159.13 bcd
		Howler Evo 1.25 lb/A	ACE		
		Dyne-Amic 0.375% v/v	ACE		
		Kocide 3000 1.25 lb/A	BDF		
11	Chaperon	Dyne-Amic 0.375% v/v	BDF	31.3 cd	10293.13 bc
		Orondis Opti 2.5 pt/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Bravo Weather Stik 2 pt/A	BF		
		Previcur Flex 1.2 pt/A	C		
		Bravo Weather Stik 2 pt/A	C		
		Zampro 14 fl oz/A	D		
4	Vlaspik	Bravo Weather Stik 2 pt/A	D	30.0 cde	8379 bcd

		Orondis Opti 2.5 pt/A	AE		
		Kocide 3000 1.25 lb/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Howler Evo 1.25 lb/A	BF		
		Dyne-Amic 0.375% v/v	BF		
		Previcur Flex 1.2 pt/A	C		
		Kocide 3000 1.25 lb/A	C		
		Dyne-Amic 0.375% v/v	C		
		Zampro 14 fl oz/A	D		
		Howler Evo 1.25 lb/A	D		
6	Citadel	Dyne-Amic 0.375% v/v	D	22.5 de	8074.13 bcd
		Orondis Opti 2.5 pt/A	AE		
		Kocide 3000 1.25 lb/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Howler Evo 1.25 lb/A	BF		
		Dyne-Amic 0.375% v/v	BF		
		Previcur Flex 1.2 pt/A	C		
		Kocide 3000 1.25 lb/A	C		
		Dyne-Amic 0.375% v/v	C		
		Zampro 14 fl oz/A	D		
		Howler Evo 1.25 lb/A	D		
10	Chaperon	Dyne-Amic 0.375% v/v	D	22.5 de	5984.13 cd
		Orondis Opti 2.5 pt/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Bravo Weather Stik 2 pt/A	BF		
		Previcur Flex 1.2 pt/A	C		
		Bravo Weather Stik 2 pt/A	C		
		Zampro 14 fl oz/A	D		
8	Citadel	Bravo Weather Stik 2 pt/A	D	20 de	6256.13 cd
		Orondis Opti 2.5 pt/A	AE		
		Ranman 2.75 fl oz/A	BF		
		Bravo Weather Stik 2 pt/A	BF		
		Previcur Flex 1.2 pt/A	C		
		Bravo Weather Stik 2 pt/A	C		
		Zampro 14 fl oz/A	D		
12	Chaperon	Bravo Weather Stik 2 pt/A	D	17.5 e	4922.13 d

[z]Application code based on application date

[y]Disease rating based on percent necrotic foliage caused by *P. cubensis*, 4 weeks after planting.

[x]Area under disease progress curve AUDPC = $\sum_{i=1}^{n-1} \frac{y_i+y_{i+1}}{2} x(t_{i+1}-t_i)$

[w]Treatments followed by the same letter(s) within a column are not statistically different (P=0.05, Fisher's Protected LSD).

Hausbeck: The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. Treatment plots consisted of 20 ft rows with 5 ft buffers separating treatment plots. On 30 August, Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29 August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value (lb). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

Disease symptoms were initially observed on 23 August with incidence in the untreated control relatively low (1.0%). All treatments were more effective than the untreated control. On 29 August and 6, 12 and 19 September, all treatments similarly limited downy mildew symptoms compared to the untreated control. On 26 September and 4 August, all treatments limited downy mildew symptoms compared to the untreated control. On these dates and according to the AUDPC data, Cevya SC 5.0 fl oz + Activator 90 was less effective than all other treatments included in this study. The total yield did not differ between the untreated control and the treatments. Neither phytotoxicity nor product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-14 day intervals	Foliar Disease (%)[z]							Harvest Totals (lb)
	23 Aug	29 Aug	6 Sep	12 Sep	19 Sep	26 Sep	4 Oct	AUDPC[y]
Untreated	1.0 a[x]	6.3 a	16.3 a	18.8 a	31.5 a	38.8 a	65.0 a	1053.5 a	9.2 a
Orondis Opti SC 40.0 fl oz, apps ACE -alt- Ranman SC 2.75 fl oz + BWS[w] 32.0 fl oz, apps BDF	0.0 c	0.0 b	0.0 b	2.0 b	0.3 b	0.3 c	0.8 c	19.6 c	9.5 a
Zampro SC 14.0 fl oz + Activator 90 SL 0.25% V/V, apps A-D	0.5 b	0.0 b	0.0 b	0.5 b	2.0 b	0.8 c	0.5 c	26.4 c	8.1 a
Zampro SC 14.0 fl oz -alt- Cevya SC 5.0 fl oz + Activator 90 SL 0.25% V/V, apps A-D	0.0 c	0.0 b	0.5 b	2.0 b	0.0 b	1.0 c	2.0 c	32.0 c	8.8 a
Cevya SC 5.0 fl oz + Activator 90 SL 0.25% V/V, apps A-D	0.5 b	1.3 b	6.0 b	6.5 b	10.3 b	19.5 b	32.5 b	442.5 b	9.9 a

[z]Based on visual assessment foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo Weatherstik SC

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. Treatment plots consisted of 20 ft rows separated by 5 ft buffers on either side. On 30 August. Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29 August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value

(lb). Data was analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

Downy mildew symptoms were first confirmed in the plot on 23 August with 5% disease incidence in the untreated control; all treatments were more effective than the untreated control except for CX-10081 SC 64.0 (high rate) + Activator 90. On 29 August, 15.8% of the untreated control foliage exhibited downy mildew symptoms. On this date, CX-10081 SC 32.0 fl oz (midrate) + Activator 90 and CX-10081 SC 16.0 fl oz (low rate) + Activator 90 were not statistically different from the untreated control, but the other treatments were effective. On 6 and 12 September, all treatments significantly limited downy mildew compared to the untreated control. For each date, the standard fungicide program (Orondis Opti SC alt. Ranman SC + Bravo WeatherStik SC) was significantly more effective than the other treatments. On 19 September, all treatments were similar to the untreated control (41.3%), except for the standard fungicide program (3.3%) of leaves with downy mildew symptoms. On 26 September, downy mildew symptoms were observed on 53.8% of the untreated control. CX-10081 SC (low and medium rates) + Activator 90 were similar to the untreated control 53.8 % of downy mildew and the high rate of CX-1008 + Activator 90. The standard fungicide program significantly limited downy mildew to 1.8% of the foliage with downy mildew symptoms. On 4 October, all treatments were more effective than the untreated control, but the standard fungicide program was more effective than all other treatments. The mid-rate of CX-10081 SC + Activator 90 was more effective than the low rate. According to the AUDPC data, all treatments significantly limited disease compared to the untreated control and the standard fungicide program was most effective. The AUDPC data did not indicate a rate response for the CX-10081 + Activator 90 treatments. The total yield did not differ between the untreated control and the treatments. Neither phytotoxicity nor product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Foliar Disease (%)[z]							Harvest Totals (lb)
	23 Aug	29 Aug	6 Sep	12 Sep	19 Sep	26 Sep	4 Oct	AUDPC[y]
Untreated	5.0 a[x]	15.8 a	18.5 a	28.3 a	41.3 a	53.8 a	82.5 a	1460.3 a	23.6 a
Orondis Opti SC 40.0 fl oz, apps ACE -alt- Ranman SC 2.75 fl oz + BWS[w] 32.0 fl oz, apps BDF	0.0 c	0.0 c	0.0 c	0.0 c	3.3 b	1.8 c	0.3 d	36.9 c	26.6 a
CX-10081 SC 64.0 fl oz + Activator 90 0.125% V/V, apps A-D	3.0 ab	6.3 bc	10.8 b	16.0 b	40.0 a	40.0 b	67.5 bc	1082.0 b	26.1 a
CX-10081 SC 32.0 fl oz + Activator 90 0.125% V/V, apps A-D	2.0 bc	8.3 ab	12.3 b	18.8 b	38.8 a	41.3 ab	58.8 c	1087.0 b	27.6 a

CX-10081 SC 16.0 fl oz + Activator 90 0.125% V/V, apps A-D	2.0	bc	8.3	ab	11.0	b	17.5	b	35.0	a	46.3	ab	71.3	b	1131.4	b	24.6	a

[z]Based on visual assessment foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo Weatherstik SC

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. On 30 August. Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29 August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value (lb). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD), square root transformation was used when necessary.

Downy mildew symptoms were first confirmed in the plot on 23 August with 2.8% disease incidence in the untreated control; all treatments were more effective in limiting disease. On 29 August, the untreated control (9.8%) and the organic program (Howler EVO DF 2.5 lb + Dyne-Amic – alternated with Curezin XT SL + Dyne-Amic Dyne-Amic) (10.8%) were similar in downy mildew disease. On this dates, the standard fungicide program (Orondis Opti SC 2.5 pt alternated with Ranman SC 2.75 fl oz + Bravo WeatherStik alternated with Previcur Flex SL 1.2 pt + Bravo WeatherStik alternated with Zampro SC 14.0 fl oz + Bravo WeatherStik) and the modified standard fungicide program (Orondis Opti SC 2.5 pt + Curezin XT SL-alt- Ranman SC 2.75 fl oz + Curezin XT SL + Dyne-Amic SL -alt- Previcur Flex SL 1.2 pt + Curezin XT SL + Dyne-Amic SL-alt- Zampro SC 14.0 fl oz + Curezin XT SL + Dyne-Amic SL) significantly limited downy mildew incidence (<1.5%) compared to the untreated control and the other treatments. On 6 September, all treatments limited the disease (<10.3%) compared to the untreated control (18.5%). The organic program was not as effective as the standard fungicide program and was similar to Curezin XT SL + Salia. On 19 September, all treatments limited the disease (<11.3%) compared to the untreated control (41.3 %). The standard and the modified standard fungicide programs similarly limited downy mildew symptoms; the modified standard fungicide program was also similar to the organic program and Curezin XT SL + Salia.

According to the foliar disease incidence on 26 September and 4 October and the AUDPC data, all treatments limited downy mildew compared to the untreated control. However, the standard and the modified standard fungicide programs effectively limited downy mildew symptoms compared to the other treatments and the untreated control. The total yield did not differ between the untreated control and the treatments. Neither phytotoxicity nor product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Foliar Disease (%)[z]												AUDPC[y]		Harvest Totals (lb)	
	23 Aug		29 Aug		6 Sep		19 Sep		26 Sep		4 Oct					
Untreated	2.8	a[x]	9.8	ab	18.5	a	41.3	a	46.3	a	87.5	a	1380.1	a	35.0	a
Orondis Opti SC 2.5 pt, apps AE -alt- Ranman SC 2.75 fl oz + BWS[w], apps BF -alt- Previcur Flex SL 1.2 pt + BWS, apps CG -alt- Zampro SC 14.0 fl oz + BWS, apps DH	0.0	b	0.5	c	1.5	c	1.0	c	1.5	c	6.8	c	67.5	c	40.9	a
Orondis Opti SC 2.5 pt + Curezin XT[v] SL, apps AE -alt- Ranman SC 2.75 fl oz + Curezin XT SL + Dyne-Amic[u] SL, apps BF -alt- Previcur Flex SL 1.2 pt + Curezin XT SL + Dyne-Amic SL, apps CG -alt- Zampro SC 14.0 fl oz + Curezin XT SL + Dyne-Amic SL, apps DH	0.0	b	1.3	c	2.8	c	3.8	bc	2.5	c	4.5	c	111.9	c	40.6	a
Curezin XT SL + Salia SL 12.0 fl oz, apps A-H	0.3	b	6.0	b	5.5	bc	10.5	b	13.5	b	39.5	b	464.8	b	39.1	a
Howler EVO DF 2.5 lb + Dyne-Amic SL, apps ACEG -alt- Curezin XT SL + Dyne-Amic SL, apps BDFH	0.8	b	10.3	a	10.3	b	11.3	b	14.3	b	51.3	b	606.0	b	39.8	a

[z]Based on visual assessment of foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo Weatherstik SC, rate/A = 2.0 pt

[v]Curezin XT rate/A = 6.0 pt

[u]Dyne-Amic rate/A = 0.375% V/V

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. On 30 August. Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29 August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value (lb). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

Disease symptoms were initially observed on Aug 23. On this date, the downy mildew incidence was 3.0% in the untreated control and all treatments were similar except for Orondis Opti SC alt Ranman SC + Bravo WeatherStik (standard fungicide program) that did not exhibit disease symptoms. While disease increased on 29 August and 6 and 19 September, the standard fungicide program effectively limited downy mildew symptoms (>0.3%) whereas the other treatments were similar to the untreated control (16.0% - 43.8%). On 26 September, the two treatments that were significantly better than the untreated control included SA-0650120 XA (28 fl oz) and the standard fungicide program. Downy mildew reached 82.5% on the untreated control by the final rating date on Oct 4. Only the standard fungicide program was significantly limited at the end of conclusion of the trial based on the foliar disease rating and according to the AUDPC values. There were no statistical differences between the treated and untreated plots for the total yield. Neither phytotoxicity nor tank-mix incompatibility was observed.

Treatment and rate/A, application order, applied at 7–14-day intervals	Foliar Disease (%)[z]						AUDPC[y]	Harvest Totals (lb)
	23 Aug	29 Aug	6 Sep	19 Sep	26 Sep	4 Oct		
Untreated	3.0 a[x]	16.0 a	21.8 a	43.8 a	51.3 a	82.5 a	1501.3 a	38.1 a
Orondis Opti SC 40.0 fl oz, apps ACE -alt- Ranman SC 2.75 fl oz + BWS[w] 32.0 fl oz, apps BDF	0.0 b	0.0 b	0.0 b	0.3 b	0.0 c	1.8 b	9.5 b	43.3 a
SA-0650120 CS 28.0 fl oz, apps A-E	4.8 a	13.0 a	19.3 a	32.5 a	41.3 b	75.0 a	1241.8 a	36.8 a
SA-0650120 CS 55.0 fl oz, apps A-E	2.3 a	11.3 a	21.5 a	33.8 a	46.3 ab	81.3 a	1320.6 a	33.6 a
SA-0650120 CS 28.0 fl oz + Arius 250 SC 12.0 fl oz, apps A-C	3.0 a	14.8 a	20.8 a	31.3 a	48.8 ab	81.3 a	1333.3 a	39.1 a
SA-0650120 CS 41.0 fl oz, apps A-E	4.3 a	12.0 a	19.8 a	35.8 a	52.5 a	75.0 a	1355.4 a	36.6 a

[z]Based on visual assessment foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo Weatherstik SC

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. Treatment plots consisted of 20 ft rows separated by 5 ft buffers. On 30 August. Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29

August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value (lb). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

Downy mildew symptoms were confirmed in the plot on 23 August with disease at a 3% level in the untreated control. The disease progressed steadily on the untreated control throughout the evaluation period, reaching 78.8% at the final evaluation date (4 October). All fungicide treatments significantly limited the disease incidence compared to the untreated control at all evaluation dates. All fungicide treatments were similar to each other during the evaluation period based on the foliar disease incidence and the area under disease progress curve with the exception of 26 September when Orondis Opti SC 40.0 fl oz alternated with Ranman SC 2.75 fl oz + Bravo WeatherStik 32.0 fl oz was significantly more effective than the other treatments evaluated. According to the AUDPC data, all treatments were equally effective in limiting downy mildew compared to the untreated control. Based on the total harvest data, significant differences were not observed between the treatments and the untreated control and among the treatments. No phytotoxicity or product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Foliar Disease (%)[z]																	
	23 Aug		29 Aug		6 Sep		12 Sep		19 Sep		26 Sep		4 Oct		AUDPC[y]			
Untreated	3.0	a[x]	13.8	a	18.0	a	31.3	a	47.5	a	56.3	a	78.8	a	1503.8	a		
Orondis Opti SC 40.0 fl oz, apps ACEGI -alt- Ranman SC 2.75 fl oz + BWS[w] 32.0 fl oz, apps BDFHJ	0.0	b	0.0	b	0.0	b	2.3	b	0.3	b	0.0	c	1.8	b	23.4	b		
Orondis Opti SC 40.0 fl oz + Activator 90 0.125% V/V, apps A-H	0.0	b	0.3	b	0.8	b	2.8	b	7.3	b	3.0	b	1.0	b	102.1	b		
Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps AG -alt- Reason 500 SC 5.5 fl oz, apps BH -alt- Orondis Opti SC 40.0 fl oz, apps CI -alt- Zing SC 36.0 fl oz, apps DJ -alt- Zampro SC 14.0 fl oz, apps EK -alt- Gavel DF 2.0 lb, apps FM	0.3	b	0.0	b	0.3	b	5.5	b	12.5	b	6.0	b	3.8	b	185.8	b		

Orondis Ultra SC 8.0 fl oz, apps AG -alt- Gavel DF 2.0 lb, apps BH -alt- Zampro SC 14.0 fl oz, apps CI -alt- Reason 500 SC 5.5 fl oz + Badge SC 32.0 fl oz, apps DJ -alt- Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps EK -alt- Zing SC 36.0 fl oz, apps FM	0.0	b	1.8	b	1.3	b	4.8	b	14.3	b	11.0	b	0.0	b	234.1	b				
Latitude SC 29.0 fl oz + Activator 90 0.125% V/V, apps A-H	0.0	b	0.8	b	0.3	b	7.5	b	18.8	b	20.0	b	0.5	b	339.0	b				

[z]Based on visual assessment of foliage diseased
[y]Area Under the Disease Progress Curve
[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)
[w]BWS = Bravo WeatherStik SC

	Harvest (lb)											
Treatment and rate/A, application order, applied at 7-day intervals	3 Sep		10 Sep		12 Sep		17 Sep		19 Sep		Total (lb)	
Untreated	6.8	a[z]	9.3	a	1.2	a	10.6	ab	1.4	a	29.3	a
Ranman SC 2.75 fl oz + BWS[y] 32.0 fl oz, apps AG -alt- Reason 500 SC 5.5 fl oz, apps BH -alt- Orondis Opti SC 40.0 fl oz, apps CI -alt- Zing SC 36.0 fl oz, apps DJ -alt- Zampro SC 14.0 fl oz, apps EK -alt- Gavel DF 2.0 lb, apps FM	6.2	a	13.9	a	1.4	a	16.0	a	1.4	a	38.8	a
Orondis Ultra SC 8.0 fl oz, apps AG -alt- Gavel DF 2.0 lb, apps BH -alt- Zampro SC 14.0 fl oz, apps CI -alt- Reason 500 SC 5.5 fl oz + Badge SC 32.0 fl oz, apps DJ -alt- Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps EK -alt- Zing SC 36.0 fl oz, apps FM	5.1	a	10.2	a	1.7	a	14.1	ab	1.3	a	32.4	a
Orondis Opti SC 40.0 fl oz, apps ACEGI -alt- Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps BDFHJ	5.0	a	10.5	a	1.6	a	13.5	ab	1.7	a	32.2	a

Latitude SC 29.0 fl oz + Activator 90 0.125% V/V, apps A-H	4.7	a	7.9	a	1.4	a	8.9	b	1.7	a	24.5	a
Orondis Opti SC 40.0 fl oz + Activator 90 0.125% V/V, apps A-H	6.9	a	11.4	a	0.8	a	13.6	ab	1.5	a	34.3	a

[z]Column means with a letter in common are not significantly different (LSD t test; P=0.05)
[y]BWS = Bravo WeatherStik SC

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100 g=2.5, Oakville fine sand) previously planted to a cover crop. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on June 4. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on June 4 with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. 'Vlaspik' seed was planted on 18 July. Treatments were arranged in a randomized complete block design with four replicates. On 30 August. Quintec (6 fl oz/A) was applied to the foliage to protect from powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Downy mildew was visually assessed for the percentage of the leaf with downy mildew symptoms on 23, and 29 August; 6, 12, 19 and 26 September; and 4 October. Mature fruit (category 2B and over) were harvested on 3, 6, 10, 12, 17, and 19 September and all data combined for a total harvest value (lb). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

Downy mildew symptoms were confirmed in the plot on 23 August with disease at a 3% level in the untreated control. The disease progressed steadily on the untreated control throughout the evaluation period, reaching 78.8% at the final evaluation date (4 October). All fungicide treatments significantly limited the disease incidence compared to the untreated control at all evaluation dates. All fungicide treatments were similar to each other during the evaluation period based on the foliar disease incidence and the area under disease progress curve with the exception of 26 September when Orondis Opti SC 40.0 fl oz alternated with Ranman SC 2.75 fl oz + Bravo WeatherStik 32.0 fl oz was significantly more effective than the other treatments evaluated. According to the AUDPC data, all treatments were equally effective in limiting downy mildew compared to the untreated control. Based on the total harvest data, significant differences were not observed between the treatments and the untreated control and among the treatments. No phytotoxicity or product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Foliar Disease (%)[z]																	
	23 Aug		29 Aug		6 Sep		12 Sep		19 Sep		26 Sep		4 Oct		AUDPC[y]			
Untreated	3.0	a[x]	13.8	a	18.0	a	31.3	a	47.5	a	56.3	a	78.8	a	1503.8	a		
Orondis Opti SC 40.0 fl oz, apps ACEGI -alt- Ranman SC 2.75 fl oz + BWS[w] 32.0 fl oz, apps BDFHJ	0.0	b	0.0	b	0.0	b	2.3	b	0.3	b	0.0	c	1.8	b	23.4	b		
Orondis Opti SC 40.0 fl oz + Activator 90 0.125% V/V, apps A-H	0.0	b	0.3	b	0.8	b	2.8	b	7.3	b	3.0	b	1.0	b	102.1	b		
Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps AG -alt- Reason 500 SC 5.5 fl oz, apps BH -alt- Orondis Opti SC 40.0 fl oz, apps CI -alt- Zing SC 36.0 fl oz, apps DJ -alt- Zampro SC 14.0 fl oz, apps EK -alt- Gavel DF 2.0 lb, apps FM	0.3	b	0.0	b	0.3	b	5.5	b	12.5	b	6.0	b	3.8	b	185.8	b		
Orondis Ultra SC 8.0 fl oz, apps AG -alt- Gavel DF 2.0 lb, apps BH -alt- Zampro SC 14.0 fl oz, apps CI -alt- Reason 500 SC 5.5 fl oz + Badge SC 32.0 fl oz, apps DJ -alt- Ranman SC 2.75 fl oz + BWS 32.0 fl oz, apps EK -alt- Zing SC 36.0 fl oz, apps FM	0.0	b	1.8	b	1.3	b	4.8	b	14.3	b	11.0	b	0.0	b	234.1	b		
Latitude SC 29.0 fl oz + Activator 90 0.125% V/V, apps A-H	0.0	b	0.8	b	0.3	b	7.5	b	18.8	b	20.0	b	0.5	b	339.0	b		

[z]Based on visual assessment of foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo WeatherStik SC

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100g=2.5, Oakville fine sand) previously planted to cover crops. Preplant fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied and incorporated on 4 June. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 8 ft apart were formed on 4 June with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for plot irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation. Planting occurred 18 July from seed spaced 12in apart. The cultivar used for this experiment was 'Vlaspik'. Treatments were arranged in a randomized complete block design with four replicates. Treatment plots were 20 ft long separated by a 5 ft buffer. Quintec (6 fl oz/A) was applied to control the incidence of powdery mildew and Admire Pro (10.5 fl oz/A) was applied through the drip tape for insect control on 30 August. The treatments were applied on 1, 8, 16, 22 and 30 August; 5, 12 and 23 September; and 1 October using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Foliage was evaluated for disease severity on 23, and 29 August; 6, 12, 19 and 26 September; 4 and 7 October. Mature fruits (category 2B pickles and over) were harvested on 3, 6, 10, 12, 17, 19 and 26 September, the values of all the harvesting dates were summed into a total harvest value (lb). Data was analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).
On the initial assessment date, 23 August, the untreated control had a higher foliar disease percentage compared to all treatments. On 29 August; 6, 12, 19, and 26 September; 4, and 7 October all treatments had a lower foliar disease percentage compared to the untreated control. On the final assessment date, 7 October, the untreated control reached 81.3% of disease incidence while the rest of the treatments remained < 5.3% of disease incidence. According to the area under disease progress curve data (AUDPC), all the treatments were more effective controlling downy mildew compared to the untreated control. According to harvest data all treatments had a similar yield compared to the untreated control with two exceptions: Zampro and Previcur Flex both had higher yields than the untreated control. Phytotoxicity was not observed during the duration of the trial.

Treatment and rate/A, application order, applied at 7-day intervals	Foliar Disease (%)[z]										AUDPC[y]		Harvest Totals (lb)	
	23 Aug		29 Aug		6 Sep		12 Sep		19 Sep		26 Sep		4 Oct		7 Oct					
Untreated	3.3	a[x]	7.0	a	18.8	a	23.8	a	26.3	a	38.8	a	73.8	a	81.3	a	1346.3	a	14.8	b
Orondis Opti SC 2.5 pt, apps A-I	0.0	b	0.0	b	0.0	b	0.0	c	0.8	b	0.8	b	0.0	b	0.0	b	10.9	b	17.3	ab
Omega F 24.0 fl oz, apps A-I	0.5	b	0.3	b	0.3	b	1.8	bc	0.5	b	1.0	b	0.0	b	0.3	b	27.8	b	14.3	b
Zampro SC 14.0 fl oz, apps A-I	0.8	b	0.8	b	1.3	b	0.3	c	1.0	b	2.8	b	0.3	b	0.5	b	47.6	b	23.1	a
Orbus 4F 24.0 fl oz, apps A-I	0.3	b	0.3	b	2.5	b	2.8	bc	1.5	b	0.3	b	0.5	b	0.5	b	53.8	b	13.6	b
Previcur Flex SL 1.2 pt, apps A-I	0.3	b	0.5	b	1.0	b	1.0	bc	1.5	b	1.0	b	3.3	b	5.3	b	61.5	b	21.2	a
RenaZ SC 2.75 fl oz, apps A-I	0.3	b	0.5	b	1.8	b	2.8	bc	0.5	b	2.0	b	1.5	b	1.5	b	63.4	b	13.9	b
Elumin SC 8.0 fl oz, apps A-I	0.3	b	1.8	b	4.0	b	4.0	b	1.5	b	3.0	b	2.0	b	3.0	b	115.5	b	17.9	ab

[z]Based on visual assessment of foliage diseased

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

<u>Squash powdery mildew (Lead: Smart, Secondary Site: Hausbeck)</u>:

Smart: This objective was completed in year 3.

Hausbeck: The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100g=2.5, Oakville fine sand) previously planted to cover crops. Fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied prior to planting and incorporated on 4 June. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 16 ft apart were formed on 4 June with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for plot irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation during the evaluation period. Three week old 'Ultra' butternut squash seedlings were transplanted on 12 June. Treatments were arranged in a randomized complete block design with four replicates. Each replicate was 20 ft long with a 5 ft buffer between each plot in a row, with 20 seedlings planted 12 in. apart. Presidio (6 fl oz/A) was applied to control the incidence of Phytophthora blight on 6 June. The treatments were applied on 18, 25 July, 1, 8, 16, and 22 August using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-

fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Foliage was evaluated for disease severity using two parameters: percentage of foliage with sporulating lesions on 1, 8, 15, 22 and 29 August; and the percentage of foliage with necrotic lesions on 22, 29 August, and 3 September. Disease ratings were used to calculate the area under disease progress curve (AUDPC). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

On the first assessment date (1 August) the untreated control had 11.0% foliage with sporulating lesions. On 1 August all treatments had a lower percentage of sporulating lesions compared to the untreated with two exceptions, TebuStar + VM Agritech-001 alternated with Rally + VM Agritech-001, and VM Agritech-001 + Salia. On 8, 15, and 22 August all treatments had a lower percentage of sporulating lesions compared to the untreated control. On 8, 15, and 22 August the Luna Experience program, the Torino + Bravo WeatherStik program, and the Torino + VM Agritech-001 program were all amongst the programs with the fewest percentage of sporulating lesions. On the final assessment date (29 August) all programs had fewer sporulating lesions compared to the untreated with one exception, VM Agritech-001 + Salia. The Luna Experience program, the Torino + Bravo WeatherStik program, and the Torino + VM Agritech-001 program were the programs with the fewest percentage of sporulating lesions on the final rating date. According to AUDPC data all treatments had fewer sporulating lesions compared to the untreated control. The Luna Experience program, the Torino + Bravo WeatherStik program, and the Torino + VM Agritech-001 program were all the programs with the fewest percentage of sporulating lesions according to AUDPC data.

On the first assessment date for necrotic lesions (22 August) the untreated control had 31.3% foliage with necrotic lesions. This progressed to 85.0 % and 90.5% foliage with necrotic lesions on 29 August and 3 September, respectively. On 22 August all treatments had a lower necrotic lesion percentage compared to the untreated control with one exception, VM Agritech-001 + Salia. On 29 August and 3 September all programs had a lower necrotic lesion percentage compared to the untreated control with two exceptions, TebuStar + VM Agritech-001 alternated with Rally + VM Agritech-001, and VM Agritech-001 + Salia. According to AUDPC data all treatments had a lower necrotic lesion percentage compared to the untreated control with the exception of VM Agritech-001 + Salia. The Luna Experience program, the Torino + Bravo WeatherStik program, and the Torino + VM Agritech-001 program were all amongst the programs with the lowest percentage of necrotic lesions, according to AUDPC data. Neither phytotoxicity nor product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Sporulating Lesion (%)[z]										AUDPC[y]	
	1 Aug		8 Aug		15 Aug		22 Aug		29 Aug			
Untreated	11.0	a[x]	41.3	a	72.5	a	78.8	a	81.3	a	1670.4	a
[w]Luna Experience SC 17.0 fl oz + BWS[v], apps AF -alt- Quintec SC 6.0 fl oz + BWS, apps BG -alt- Vivando SC 15.4 fl oz + BWS, apps CH -alt- Torino SC 3.4 fl oz + BWS, apps DI -alt- Magister SC 36.0 fl oz + BWS, apps EJ	2.0	b	0.8	cd	1.3	c	0.5	d	8.8	c	55.1	d
Torino SC 3.4 fl oz + BWS, apps AE -alt- Quintec SC 6.0 fl oz + BWS, apps BF -alt- Aprovia Top EC 13.5 fl oz + BWS, apps CG -alt- Prolivo SC 5.0 fl oz + BWS, apps DH	0.0	b	0.0	d	4.5	c	8.5	d	15.0	c	143.5	d
Torino SC 3.4 fl oz + VM Agritech-001 SL 96.0 fl oz, apps AE -alt- Quintec SC 6.0 fl oz + VM Agritech-001 SL 96.0 fl oz, apps BF -alt- Aprovia Top EC 13.5 fl oz + VM Agritech-001 SL 96.0 fl oz, apps CG -alt- Prolivo SC 5.0 fl oz + VM Agritech-001 SL 96.0 fl oz, apps DH	0.0	b	1.8	cd	10.3	c	12.8	d	10.0	c	208.3	d
TebuStar EC 6.0 fl oz + VM Agritech-001 SL 96.0 fl oz, apps ACEGI -alt- Rally WSP 5.0 oz + VM Agritech-001 SL 96.0 fl oz, apps BDFH	3.8	ab	15.3	b	40.0	b	33.8	c	41.3	b	780.5	c
VM Agritech-001 SL 96.0 fl oz + Salia SL 12.0 fl oz, apps A-H	5.3	ab	13.0	bc	52.5	b	56.3	b	80.0	a	1150.6	b

[z]Based on visual estimation of the percentage of foliage with powdery mildew symptoms
[y]Area Under the Disease Progress Curve
[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)
[w]Treatment followed a 7-14 day spray schedule
[v]BWS = Bravo WeatherStik SC, rate 32.0 fl oz/A

The study was conducted at the Michigan State University Southwest Research and Extension Center near Benton Harbor, MI, on sandy soil (soil pH=6.1, CEC meq/100g=2.5, Oakville fine sand) previously planted to cover crops. Preplant fertilizer (nitrogen 100 lb/A, potassium 180 lb/A, sulfur 25 lb/A, and boron 2.0 lb/A) was applied and incorporated on 4 June. Raised plant beds (6 in.) covered with black polyethylene plastic and spaced 16 ft apart were formed on 4 June with a single drip tape (0.65 gpm/100 ft) installed under the plastic mulch for plot irrigation. Fertilizer (nitrogen 28%) was applied weekly at one gal/A/day through drip irrigation during the evaluation period. 3 week old 'Ultra' butternut squash seedlings were transplanted on 12 June. Treatments were arranged in a randomized complete block design with four replicates. Each replicate was 20 ft long with a 5 ft buffer between each plot in a row, with 20 seedlings planted 12 in. apart. Presidio (6 fl oz/A) was applied to control the incidence of phytophthora blight on 6 June. The treatments were applied on 18, 25 July, 1, 8, 16, and 22 August using a CO_2 backpack sprayer, and a broadcast boom equipped with three XR8003 flat-fan nozzles spaced 18 in. apart, calibrated at 35 psi, and delivering 50 gal/A. Foliage was evaluated for disease severity using two parameters: Percentage of foliage with sporulating lesions on 1, 8, 15, 22, and 29 August; and the percentage of foliage with necrotic lesions on 22, 29 August, and 3 September. Disease ratings were used to generate the area under disease progress curve (AUDPC). Data were analyzed using an analysis of variance (ANOVA) with means separation performed using Fisher's protected least significant difference (LSD).

On the first assessment date (1 August) the untreated control had 12.3% foliage with sporulating lesions. All programs had significantly less symptoms < 2.5 % than the untreated control, except for the program Bravo WeatherStik alternated with Luna Flex (7.8%) and Bravo WeatherStik alternated with Luna Experience (9.5%). On 8, 15 and 22 August, all the programs significantly reduced sporulating lesion percentage compared to the untreated control. On the final assessment date (29 August) the untreated control had 48.8% foliage with sporulating lesions. Three programs had a lower percentage of sporulating lesions on the final assessment date compared to the untreated control, the Quintec alternated with Prolivo alternated with Aprovia Top program, the Quintec alternated with Aprovia Top alternated with Torino program, and the Bravo WeatherStik alternated with Inspire Super program. According to AUDPC data all programs were more effective at reducing the number of sporulating lesions compared to the untreated control. On the first date of assessment for necrotic lesions percentage (22 August) the untreated control had 28.8% foliage with necrotic lesions. This developed into 91.3% and 89.8% foliage with necrotic lesions on 29 August and 3 September, respectively. All the treatments had significantly less necrosis than the untreated control on 22, 29 August, and 3 September. According to the AUDPC, all the program limited foliar necrosis compared the untreated control. Neither phytotoxicity nor product incompatibility was observed during the evaluation period.

Treatment and rate/A, application order, applied at 7-day intervals	Sporulating Lesion (%)[z] 1 Aug		8 Aug		15 Aug		22 Aug		29 Aug		AUDPC[y]	
Untreated	12.3	a[x]	42.0	a	76.3	a	92.0	a	48.8	a	1685.3	a
Quintec SC 6.0 fl oz + BWS[w] 2.0 pt, apps ADG -alt- Prolivo SC 4.0 fl oz + BWS 2.0 pt, apps BEH -alt- Aprovia Top SC 13.5 fl oz + BWS 2.0 pt, apps CFI	1.5	bc	1.3	c	0.3	d	4.8	c	16.3	bc	105.9	d
Quintec SC 6.0 fl oz + BWS 2.0 pt, app A -alt- Aprovia Top SC 13.5 fl oz + BWS 2.0 pt, apps BDF -alt- Torino F 3.4 fl oz + BWS 2.0 pt, apps CE	0.0	c	0.0	c	0.5	d	10.0	c	10.0	c	108.5	d
BWS 3.0 pt, apps ACEF -alt- Inspire Super SC 16.0 fl oz + Activator 90 XL 0.125% V/V, apps BD	2.5	bc	9.5	b c	12.3	b-d	13.0	c	13.8	bc	300.1	cd
Aprovia Top SC 13.5 fl oz, apps ACE -alt- Rally WSP 5.0 oz + BWS 2.0 pt, apps BDF	0.5	c	3.0	c	7.0	cd	21.3	bc	23.8	a-c	303.6	cd
BWS 3.0 pt, apps ACEF -alt- Aprovia Top SC 10.5 fl oz + Activator 90 XL 0.125% V/V, apps BD	2.3	bc	9.5	b c	16.5	b-d	36.3	b	40.0	ab	583.6	bc
BWS 3.0 pt, apps ACEF -alt- Luna Flex SC 12.8 fl oz + Activator 90 XL 0.125% V/V, apps BD	7.8	a-c	18.0	b	31.3	b	36.3	b	33.8	a-c	743.8	b
BWS 3.0 pt, apps ACEF -alt- Luna Experience SC 10.0 fl oz + Activator 90 XL 0.125% V/V, apps BD	9.5	ab	18.8	b	27.5	bc	36.3	b	38.8	ab	746.4	b

[z]Based on visual estimation of the percentage of foliage with powdery mildew symptoms

[y]Area Under the Disease Progress Curve

[x]Column means with a letter in common are not significantly different (LSD t test; P=0.05)

[w]BWS = Bravo WeatherStik SC

Squash Phytophthora blight (Lead: Hausbeck, Secondary Site: Smart):

Hausbeck: this objective was completed in year 3.
Smart: this objective was completed in year 3.

4.2.3 Analysis of pathogen populations to inform breeding and disease management (Yr 2-3).

Phytophthora capsici (Smart): 25 commercial and wild eggplant accessions were evaluated for resistance to Phytophthora fruit rot using two *P. capsici* isolates: one from eggplant and one from pumpkin. Isolate had an effect on fruit rot severity, with the eggplant isolate causing greater disease severity on the eggplant fruit than the isolate from pumpkin. Additionally, Smart collected 184 *P. capsici* isolates from 3 cucurbit fields in New York for downstream population genotypic and phenotypic analyses.

Pseudoperonospora cubensis (Quesada): This objective was completed in year 3.

4.3. Economic impacts of disease and gains from control tools and valuation of crop attributes (Year 1-4). (Tregeagle, Knuth)

4.3.1. Determine economic impacts of disease and control tools (Year 1-4).

Tregeagle: To gather additional information for the NC pickling cucumber budget, an interactive audience survey was conducted at the 36th annual Southeast Vegetable & Fruit Expo in Myrtle Beach, SC. Responses for questions on yield, prices received, and cost categories were solicited and audience members could respond using the Poll Everywhere platform. Unfortunately, in a session with ~20 participants, 7 members responded to the poll, and only 3 members provided substantive answers. Due to the small sample and lack of representativeness, the responses were not used for the budget.

Knuth: Working with PI Quesada on downy mildew cost analyses (Spring 2025). Set to complete June 2025. Two peer reviewed publications set to be developed.

Since May 2024, interviewing watermelon and cucumber growers in North Carolina, Virginia, and Michigan to develop partial budget analyses. Contacted 20 watermelon growers, 8 completed in-person interviews. Called three cucumber growers but was told to retry again in off-season for interviews. Set to complete partial budgets in June 2025. Peer reviewed publication for each budget is set to be developed.

Attended Southern Vegetable and Fruit Conference in Dec 2024; Attempted to attend Georgia Watermelon conference in Jan 2025 (cancelled travel due to snow in Georgia, South Carolina, and North Carolina).

4.3.2 Estimate industry valuation of improvement in crop attributes (Year 1-4).

Techniques identified in the existing literature were adapted to develop surveys for the three crop-pest pairs below. The cucumber/downy mildew survey was developed fully first, intending to be used as a test case to refine the survey contents, distribution methods, and statistical design, which will then be applied to the other crop-pest pairs.

MI – cucumber/downy mildew: The cucumber survey was approved by the NCSU IRB. In Oct 2023, Tregeagle and his graduate student, Kilduff, deployed the survey via the hub-and-spoke method to 60 cucumber and vegetable extension specialists and agents nationwide. By March, 2024 only 5 responses had been received: 4 from North Carolina and 1 from South Carolina. The survey had been designed to be robust to a potential small sample, with a minimum sample size of approximately 30 responses necessary for statistically significant results. However, the number of responses received fell far short of this threshold. To obtain a potentially valid sample size, an alternative, more time and labor intensive recruitment strategy would be necessary. Tregeagle did not have the time available to implement an alternative strategy and the survey objective was halted.

MI – squash/phytophthora: Attributes and levels for squash/phytophthora survey were developed from a review of current seed catalogs published by a variety of commercial seed distributors. It needs IRB approval before deployment.

NC – cucumber/downy mildew: See comment above for MI - cucumber/downy mildew.

NC – watermelon/fusarium: Attributes and levels for watermelon/fusarium survey were developed from a review of current seed catalogs published by a variety of commercial seed distributors. It needs IRB approval before deployment.

NY – squash/phytophthora: Smart has collected data on the value of winter squash in NY from producers and field scouts. The average price for winter squash in NY is $31.00 per cwt. Average yield in NY is 12 Tons/A with yields in 2022 ranging from 8-20 Tons/A. Average loss per year due to Phytophthora is 10%. In wet years losses will be higher, up to 35% (of total acreage) which would be 80-100% in some fields and 0-20% in other fields.

Attributes and levels for squash/phytophthora survey were developed from a review of current seed catalogs published by a variety of commercial seed distributors. It needs IRB approval before deployment.

SC – watermelon/fusarium: Attributes and levels for watermelon/fusarium survey were developed from a review of current seed catalogs published by a variety of commercial seed distributors. A complete draft survey for watermelon was developed. It needs IRB approval before deployment.

PUBLICATIONS,

RESOURCE MATERIALS

and

PRESENTATIONS

REFEREED PUBLICATIONS
(Items in bold added for 2025 report)

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BOOK CHAPTERS, THESES and DISSERTATIONS

Book Chapters

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159. Wintermantel, W.M. 2023. Cucurbit yellow stunting disorder virus. ecucurbitviruses.org (Emerging Viruses in Cucurbits Working Group website)
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SCIENTIFIC CONFERENCE and UNIVERSITY PRESENTATIONS

1. Adams, L., Josiah, S., Legendre, R., & McGregor, C. (2022). The Effect of Three Genetic Loci on Rind Thickness in Watermelon. HortScience, S291
2. Alzohairy, S.A., Moore, B.M., Hammerschmidt, R., Shiu, S., and Hausbeck, M.K. 2022. Lignin biosynthesis gene expression is associated with age-related resistance of winter squash to *Phytophthora capsici*. Cucurbitaceae 2022 Abstract Book. Naples, FL, 30 Oct-2 Nov.
3. Andreason, S. and Kousik, C.S. 2022. Detection of cucurbit leaf crumple virus infectious clones from the virus vector *Bemisia tabaci*. American Phytopathological Society Annual Meeting, Pittsburg, PA. August 2022.
4. Agudelo P., Corbin J., Desaeger J., Gorny A., Grabau Z., Guan Z., Hajihassani A., Mueller J., Quesada-Ocampo L. M., Rutter W., and Wadl P. 2022. Multi-state effort to contain and manage *Meloidogyne enterolobii* on vegetable crops. Cucurbitaceae, Naples, FL, November 2022.
5. Bhuiyan, M. Z. R., D'Arcangelo, K. N. and Quesada-Ocampo L. M. 2023. Populations of *Pseudoperonospora cubensis* Causing Downy Mildew in Squash and Cucumbers are Structured by Host Genotype. American Phytopathological Society Annual Meeting, Plant Health 2023, Denver, CO, August 2023.
6. **Biswas A, Sedler H, Massey L, Kousik S, Wechter P, Branham S, Levi. 2025. Genomic Prediction of Fusarium Wilt Race 2-Resistance and Brix Content in Watermelon. PAG annual meeting 2025, San Diego, CA**.
7. **Biswas, A. 2025. Leveraging Genomic Tools to Address Fusarium Wilt in Watermelon. SR-ASHS annual meeting, Dallas, TX, February 2025**
8. **Biswas A, Branham S, Ganaparthi V, Kousik S, Wechter P, Levi A. 2024. Predicting resistance to fusarium wilt (race 2) in citron melon (*Citrullus amarus*) using a genomic selection (GS) versus marker-assisted selection (MAS) approach in different population types. Plant and Animal Genome, San Diego, CA; January 2024.**
9. **Biswas A, Branham S, Ganaparthi V, Kousik S, Wechter P, Levi A. 2024. Utilizing Genomic Selection Approach for Enhancing Fusarium wilt race 2-resistance in Watermelon. Southern Region-American Society of Horticultural Sciences Conference, 2024.**
10. **Biswas A, Houston H, Massey L, Branham S, Wechter P, Levi A. 2024. Genome-Wide Association Analysis of Fusarium Resistance for Fon race 1 in *Citrullus lanatus*: Insights from the CucCAP Core Collection. National Association of Plant Breeders, Saint Louis, MO. 2024.**

11. **Biswas A, Houston H, Massey L, Kousik S, Branham S, Wechter P, Levi A. 2024. Enhancing Fusarium Wilt Race 2-Resistance and Brix Content in Watermelon through Genomic Selection. American Society of Horticultural Science Conference, Hawaii, 2024.**
12. **Biswas, A., Ganaparthi V., Wechter, P., Kousik, S., Branham, S., Levi, A. 2024. Utilizing genomic selection approach for enhancing fusarium wilt race 2 resistance in watermelon. Southern Region ASHS meeting 2024, Atlanta, GA.**
13. **Biswas, A., Ganaparthi V., Wechter, P., Kousik, S., Branham, S., Levi, A. 2024. Enhancing resistance to fusarium wilt (race 2) in watermelon cultivars (Citrullus Lanatus) using genomic selection (GS) versus marker assisted selection (MAS)approach. PAG, San Diego, CA.**
14. Biswas, A., V. Ganaparthi, S. Kousik, P. Wechter, A. Levi, and S. Branham. 2023. Genomic Selection (GS) Approach to incorporate Fusarium wilt race 2-resistance into Watermelon Cultivars. National Association of Plant Breeders, Greenville, SC July16-20.
15. Branham SE. 2023. Genomics-assisted vegetable breeding to develop new varieties for South Carolina. Clemson University, AGSC 4100/6100 Newman Seminar and Lecture Series
16. Branham SE, Ganaparthi V, Kousik S, Wechter WP, Park YH, Wehner T, Davis A, Tetteh A, Hammar S, Grumet R, Levi A. 2023. XP-GWAS and marker development for resistance to powdery mildew race 2W in watermelon (*Citrullus lanatus*). Plant and Animal Genome.
17. Branham SE. 2022. Marker-assisted vegetable breeding for production in the Southeastern US. Cornell University, School of Integrative Plant Science Spring Seminar Series.
18. Branham SE, Ganaparthi V, Kousik S, Wechter WP, Park YH, Wehner T, Davis A, Tetteh A, Hammar S, Grumet R, Levi A. 2022. XP-GWAS and marker development for resistance to powdery mildew race 2W in watermelon (*Citrullus lanatus*). Cucurbitaceae.
19. Branham, S.E., Wechter, W.P., Ling, K., Katuuramu, D.N., Levi, A. 2021. QTL mapping and pyramiding resistance to *Fusarium oxysporum* f. sp. *niveum* (races 1 and 2) and potyviruses in watermelon. Eucarpia Cucurbitaceae Symposium Proceedings.
20. Bhuiyan, M. Z. R., D'Arcangelo, K. N. and Quesada-Ocampo L. M. 2023. Populations of *Pseudoperonospora cubensis* causing downy mildew in squash and cucumbers are structured by host genotype. Phytopathology 113: S3.108.
21. Chanda, B., Ikerd, J.L., Adkins, S., Kousik, C.S. 2021. Understanding the disease resistance mechanism through RNA-Seq analysis of SqVYV-resistant watermelon. Annual Meeting of the American Phytopathological Society.
22. Chanda, B., Shamimuzzaman, M., Gilliard, A., and Ling, K.-S. 2021. Managing the spread of *Tomato brown rugose fruit virus* and *Cucumber green mottle mosaic virus* using chemical disinfectants. Plant Health -2021 annual meeting of American Phytopathological Society, on-line, August 2-6, 2021.
23. Chen FC 2022. Genetic architecture of the downy mildew resistance locus *dm4.1* in PI 330638 (WI7120). Cucurbitaceae 2022, Naples, FL
24. **Cochran-Murray, S., Miles. T., and Quesada-Ocampo, L. M. (2024) Evaluating a Recombinase Polymerase Amplification (RPA) assay for detection of *Phytophthora capsici* in on-farm surface water sources. (Plant Health). Phytopathology, July 2024.**
25. Cochran, S., Miles, T., Quesada-Ocampo L. M. (2024) Development of a Recombinase Polymerase Amplification (RPA) assay for rapid detection of *Phytophthora capsici*. American Phytopathological Society-Southern Division, Columbia, SC, February 2024**.**
26. Condo, I., Prieto-Torres, M., Quesada-Ocampo L. M. 2022. Monitoring populations in *Pseudoperonospora cubensis* using biosurveillance and molecular markers. Undergraduate Research and Creativity Symposium. North Carolina State University. Raleigh, North Carolina. July 2022

27. Culp C, Chen YC, Grumet R. 2022. Testing Cucumber Accessions for Phytophthora Fruit Rot Resistance. MSU Undergraduate Research Forum. East Lansing MI
28. D'Arcangelo, K. N. and Quesada-Ocampo L.M. 2021. Characterization of the population dynamics of alleles related to Carboxilic Acid Amide and Quinone Outside Inhibitor resistance in the host-adapted clades of *Pseudoperononspora cubensis* to facilitate crop-specific management of cucurbit downy mildew. Department of Entomology and Plant Pathology Seminar. Raleigh, NC, October, 2021.
29. D'Arcangelo, K. N., Rahman, A., Miles, T. D. and Quesada-Ocampo, L. M. 2021. Utilizing a population genetics approach to facilitate crop-specific management of the cucurbit downy mildew pathogen, *Pseudoperonospora cubensis*. Annual Southern Division American Phytopathological Society Meeting, Virtual Meeting. February, 2021. Phytopathology 111:S1.14
30. D'Arcangelo, K. N., Rahman, A., Miles, T. D., and Quesada-Ocampo, L. M. 2021. Distribution of alleles related to carboxylic acid amide and quinone outside inhibitor resistance in host-adapted clades of *Pseudoperonospora cubensis*. American Phytopathological Society Annual Meeting, Plant Health 2021, Memphis, TN, August 2021. Phytopathology 111:S2.114
31. D'Arcangelo, K. N., Rahman, A., Miles, T. D. and Quesada-Ocampo, L. M. (2020) Leveraging population genetics to develop disease control practices: a study in the crop-specific management of cucurbit downy mildew. Phytopathology 110: S2.203.
32. De Figueiredo Silva, F., Keinath, A. P., Kunkel, D. 2021. Economic impact of the foliar disease downy mildew under fungicide applications in cucumber production: a preliminary analysis. Southern Agricultural Economics Association Annual Meeting. February 2021. https://saea2021.org/schedule/
33. **Fabrizio J, Mazourek M. A genomic approach for a more sustainable pumpkin. 2024. PAG. San Diego, CA.**
34. **Fei Z. 2025. Pangenomes of horticultural crops. Jiansu Academy of Agricultural Science. Nanjing, Jiangsu. February 2025**
35. **Fei Z. 2025. Pangenomes of horticultural crops. Yazhouwan National Laboratory. Sanya, Hainan. February 2025**
36. **Fei Z. 2025. Pangenomes of horticultural crops. Chinese Academy of Tropical Agricultural Science. Haikou, Hannan. February 2025**
37. **Fei Z. 2025. Graph-based pangenome reveals structure variation dynamics during cucumber breeding. Plant & Animal Genome Conference. San Diego, CA. January 2025**
38. **Fei Z. 2025. Genomic analyses of wild watermelons provide insights into the origin and breeding history of dessert watermelon Plant & Animal Genome Conference. San Diego, CA. January 2025**
39. **Fei Z. 2024. Genome and pangenome analyses provide insights into watermelon origin and breeding. Agricultural Genomics Institute at Shenzhen. November 2024**
40. **Fei Z. 2024. Pangenomes of horticultural crops. International Symposium of Horticultural Plant Biology. Wuhan, China. October 2024**
41. **Fei Z. 2024. Genomic insights into the origin, domestication, and agronomic traits of watermelon. Michigan State University. April 2024**
42. Fei Z. 2024. Cucurbit Genomics Database (CuGenDB) v2: an updated database for cucurbit genomics. Plant & Animal Genome Conference. San Diego, CA. January 2024
43. Fei Z. 2023. Genomic basis of watermelon origin, domestication, and breeding. School of Plant Integrative Science, Cornell University. February 2023
44. Fei Z. 2023. Genomic basis of watermelon origin and domestication. Nanjing Forestry University. November 2023
45. Fei Z. 2023. Pan-genomes of fruit crops. 10th International Horticulture Research Conference. Guanzhou, China. November 2023

46. Fei Z.(2023. Genomic insights into watermelon origin and domestication. Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences. November 2023
47. Fei Z. 2023. Genomic basis of watermelon origin and domestication. Hunan Agricultural University. November 2023
48. Fei Z. 2023. Genomic insights into watermelon origin and domestication. Fruit Quality Biology/ Food Quality and Safety International Conference 2023. Hangzhou, China. November 2023
49. Fei Z. 2023. Genomic basis of watermelon origin and domestication. Shanghai Normal University. November 2023
50. Fei Z. 2023. Pangenomes of wild and dessert watermelons. VII International Symposium on Cucurbits. Zhengzhou, China
51. Fei Z (2023) Pan-genomes of horticultural crops. Nature Genetics & Plant Editorial Communities
52. Fei Z (2023) Genomic and pan-genomic basis of watermelon origin, domestication and breeding. Molecular Horticulture
53. Fei Z (2023) Genomic and pan-genomic basis of watermelon origin, domestication and breeding. National Engineering Research Center for Vegetables. Beijing, China
54. Fei Z. 2022. Genomic basis of watermelon origin, domestication, and breeding. The 9th International Horticulture Research Conference. Wuhan, China. November 2022
55. Fei Z. 2022. A super-pangenome of cultivated and wild watermelon species. Cucurbitaceae 2022. Naples, FL. October 2022
56. Fei Z. 2022. Genomic basis of watermelon origin, domestication, and breeding. University of North Carolina. October 2022
57. Fei Z. 2022. Genomic basis of watermelon origin, domestication, and breeding. Shandong Academy of Agricultural Sciences. October 2022
58. Fei Z. 2022. Genomic basis of watermelon origin, domestication, and breeding. The 2022 International Symposium of Horticulture and Plant Biology. Wuhan, China. August 2022
59. Fei Z. 2022. Genomic basis of watermelon origin, domestication, and breeding. BTI PGRP Summer Intern. July 2022
60. Fei Z (2021) Genomic analyses shed light on watermelon origin and the genetic history of domestication and agronomic traits. Zhejiang University
61. Fei Z (2021) Genomic analyses shed light on watermelon origin and the genetic history of domestication and agronomic traits. CSHL Plant Genomes, Systems Biology & Engineer
62. Fei Z. 2021. Genomic analyses shed light on the genetic history of watermelon domestication and agronomic traits. The 2021 Cold Spring Harbor meeting on Plant Genomes, Systems Biology and Engineering. December 2021
63. Fei Z. 2021. The origin, history and future of watermelon. BTI Breaking Ground series. November 2021
64. Fei Z. 2021. Genomic analyses provide insights into the genetic history of watermelon domestication and agronomic traits. The 7th Asia-Pacific Agrobiological Genome Symposium, Korea. November 2021
65. Frank A, Lin YC, Grumet R. 2022. Measurement and Analysis of Cucumber Fruit Curvature. MSU Undergraduate Research Forum. East Lansing MI
66. Gaines DD, Panicker GK, Henry K, Leonard K, Reddy UK. 2020. Evaluation of Grafted Watermelons (*Citrullus lanatus*) grown on a Heavy Soil with Organic Treatments for Their Biomass, Quality, Yield, and Adaptability. ASHS Annual Conference, 2020
67. Ganaparthi VR, Wechter WP, Levi A, Branham SE. 2024. *Citrullus amarus* as a source of disease resistance and introgression of Fusarium wilt resistance into cultivated watermelon. Cucurbit Genomics, Plant and Animal Genome.

68. Ganaparthi V, Wechter WP, Rennberger G, Levi A, Branham SE. 2022. QTL mapping and marker development for resistance to *Fusarium oxysporum* f. sp. *niveum* race 2 in an interspecific *Citrullus amarus/lanatus* population. Cucurbitaceae.
69. Ganaparthi V, Branham S, Levi A, Robinson S, Katawczik M, Wechter P. 2022. Mapping and Validation of QTLs Imparting Fon Race 2 Resistance in Watermelon. Cucurbitaceae, 2022, Naples, FL.
70. **Grumet R. 2025. Developing and leveraging applied genomics to facilitate breeding in cucurbit crops. Dept Plant Biology, Virginia Polytechnical Inst., Blacksburg, VA**
71. **Grumet R. 2025. Genomics informed breeding in cucurbit crops – the CucCAP experience. Plant and Animal Genome Conference, San Diego CA.**
72. **Grumet R, Lin Y-C, Rett-Cadman S. 2024. Mining the cucumber core collection for genetic control of fruit quality traits. Eucarpia Cucurbitacea, Vico Equense Italy.**
73. Grumet R. 2022. Grumet R. 2022. Leveraging applied genomics to increase disease resistance in cucurbit crops. Corteva Symposium, Cornell University. March 2022
74. Grumet R. 2022. Grumet R. 2022. Cucurbit germplasm - genomic tools and disease resistance. National Association of Plant Breeders. Ames Iowa. August 2022
75. Grumet R, Fei Z, Branham S, Levi A, Wechter WP, Weng Y, Wang Y, McCreight J, Mazourek M, Mansfeld BM, Lin Y-C (2021) Application of genomic tools for mapping and analysis of disease resistance traits in cucurbits: The CucCAP experience. XII Eucarpia Meeting on Cucurbit Genetics and Breeding. Virtual.
76. Grumet, R., Z. Fei, A. Levi, M. Maxourek, J.D. McCreight. J. Schultheis, Y. Weng, M. Hausbeck, S. Kousik, K.S. Ling, A. Linares-Ramirez, C. McGregor, L. Quesada-Ocampo, U. Reddy, C. Smart, P. Wechter, T. Wehner, L. Wessel-Beaver, and W.M. Wintermantel. (2020). The CucCAP project: Leveraging applied genomics to improve disease resistance in cucurbit crops. Acta Horticulturae 1294:101-114.
77. Hausbeck, M.K. 2023. Grower-Driven Research Leads to Integrated Disease Management. Departmental Seminar, Michigan State University, East Lansing, MI, 27 Apr.
78. Hausbeck, M.K., Harlan, B.R., Bello, J.C., and Kenny, G. 2021. Downy Mildew Management in Pickling Cucumbers. Agriculture Agri-Food Canada, Ontario, Canada. Virtual, Apr.
79. Heagy, K., T. Birdsell, and J. Schultheis. 2022. Effects of pumpkin spacing on fruit weight, quantity, and size. HortScience 57(9) Supplement (Part 2). S224 (Abstr.)
80. Heagy, K., T. Birdsell, and J. Schultheis. 2022. Effects of pumpkin spacing on fruit weight, quantity, and size. Watermelon Research and Development group, ASHS - Southern Region, New Orleans, LA. Feb. 11.
81. **Indermaur, E. J. and Smart, C. D. (2025) Multi-disciplinary approaches to manage diseases in processing pumpkin and rhubarb. Clemson University, Department of Plant and Environmental Sciences seminar. Clemson, SC, February 2025.**
82. **Indermaur, E. J., Day, C. T. C., DeBeer, C. E., Betaw, H., Herrmann, T. Q., Inzinna, G., Mazourek, M., Padilla-Zakour, O., and Smart, C. D. 2024. From field to can: assessing processing pumpkin breeding lines for disease resistance and canning quality (poster). Plant Health 2024. Memphis, TN. July 29, 2024.**
83. Indermaur, E. J., Day, C. T. C., and Smart, C. D. 2022. Biofungicides for organic management of powdery mildew in winter squash (poster). Cucurbitaceae. Naples, FL, October 2022.
84. **Kavalappara, S. R., Bag, S., Mcgregor, C., Luckew, A., Culbreath, A., & A. Simmons (2024) Evaluation of summer squash (*Cucurbita pepo* L) for resistance against emerging criniviruses. American Phytopathological Society-Plant Health 2024. Memphis, TN**

85. Katuuramu DN, Branham SE, Levi A, Wechter WP. 2021. Genome-wide association analysis of downy mildew resistance in a pre-breeding watermelon (*Citrullus amarus*) collection. Eucarpia Cucurbitaceae Symposium Proceedings.
86. Kelly B, Salcedo A, Rahman A, Wallace EC, Crouch JA, Quesada-Ocampo LM. 2022. Does a *Pseudoperonospora cubensis* cryptospecies population caused a cucurbit downy mildew epidemic in the U.S.? Undergraduate Research and Creativity Symposium. North Carolina State University. Raleigh, North Carolina. July 2022
87. Keinath, A. P. 2023. In-Field Food Crop Agent Training on Vegetable Diseases. In-service Training, Clemson Extension. September 26, 2023
88. Keinath, A. P. and Silva, F. D. 2021. Economic impacts of downy mildew and reduced fungicide efficacy on slicing cucumber. Canadian Reduced-Risk Strategy for Cucumber Downy Mildew Annual Meeting 2021.
89. Keinath, A. P., and Silva, F. D. 2021. Economic impacts of downy mildew and reduced fungicide efficacy on slicing cucumber. Plant Health 2021, American Phytopathological Society (virtual). https://events.rdmobile.com/Lists/Details/1179331
90. Kenny, G. 2020 Cucumber field data. Departmental seminar, Department of Plant Pathology, Michigan State University, East Lansing, MI. Virtual.
91. Kikway, I., Keinath, A. P., and Ojiambo, P. S. 2021. Field occurrence and overwintering of oospores of *Pseudoperonospora cubensis* in the eastern United States. Plant Health 2021, American Phytopathological Society (virtual). https://events.rdmobile.com/Lists/Details/1179538
92. Kilduff, A. and Tregeagle, D. 2023. Eureka! Or Sassy? Producer Valuations of Cucumber Traits. Department of Agricultural and Resource Economics, NC State University, Raleigh, NC, March 2023.
93. **Kousik, C.S. (2023). Existing and potential virus threats to the U.S. cucurbit industry: an overview. Annual Meeting of the American Phytopathological Society. August, 2023. Denver, Colorado.**
94. Kousik, C.S., Chanda, B., Mandal, M., Ikerd, J., Sudarshana, M., Turechek, W.W., Adkin, S. 2022. Identifying and Confirming Resistance to Whitefly-Transmitted Cucurbit Leaf Crumple Virus in Watermelon Using Infectious Clones. Cucurbitaceae 2022. Naples FL. Keynote talk.
95. Kousik, C.S., Chanda, B., Mandal, M., Ikerd, J., Sudarshana, M., Turechek, W.W., Adkin, S. 2022. Phenotyping resistance to whitefly-transmitted *Cucurbit leaf crumple virus* in watermelon using infectious clones and confirming resistance using dPCR. American Phytopathological Society Annual Meeting, Pittsburg, PA. August 2022. (Poster Presentation).
96. Kousik, C.S., Chanda, B., Mandal, M., Ikerd, J., Sudarshana, M., Turechek, W.W., Adkin, S. 2022. Developing resources for breeding watermelon varieties for resistance to whitefly- transmitted viruses. Southern Division American Phytopathological Society Annual Meeting, March 2022. Chattanooga, TN. (Virtual talk)
97. Kousik, C.S., Chanda, B., Suren, H., M., Ikerd, J., Turechek, W.W., Adkin, S. 2021. Advances in breeding for resistance to whitefly transmitted viruses in watermelon. Entomological Society of America Annual Meeting. Invited Virtual Talk. November 2022
98. Kousik, C.S. 2020. Breeding for resistance to whitefly transmitted viruses in watermelon. Presented at the Whitefly Symposium. Entomological Society of America Annual Meeting, November 2020.
99. **Kumar R, Shaik K, Ikerd J, Karthikeyan R, Kousik CS (2025) QTL Mapping and Development of KASP Markers for Phytophthora Fruit Rot and Powdery Mildew Resistance in Watermelon. Plant and Animal Genome conference 32 (PAG32), San Diego, USA, January 10-15.**

100. Kumar R, Shaik K, Ikerd J, Karthikeyan R, Kousik CS (2025) Watermelon Breeding for Diseases Resistance and Fruit Quality using QTL Mapping and Genomic Selection, Southern Region ASHS Annual Meeting, Las Colinas, Texas, United States, January 31- February 2.

101. Kumar R, Chanda, B., Adkins, S. and Kousik, C.S. 2024. Transcriptomic analysis of Watermelon-Squash Vein Yellowing Virus Interactions Reveals Elevated Expression of Callose and RNA Silencing genes in Resistant Genotype. Presented at the Plant and Animal Genome Conference, January 2024, SanDiego, CA**.**

102. Kumar R, Branham S. Wechter W. and Kousik C.S. (2024). KASP Marker Development for Powdery Mildew Resistance in Watermelon (*Citrullus lanatus*) using Bulk Segregant Analysis (BSAseq) and RNAseq. Presented at the Watermelon Research and development Group meeting held in conjunction with Southern Region American Society for Horticultural Science. February 2024, Atlanta, GA.

103. Kumar R, Reddy U, Karthikeyan R, and Kousik CS (2024). QTLs mapping and KASP Marker Development for Powdery Mildew Resistance in Watermelon (*Citrullus lanatus*). National Association of Plant Breeders, 21-25 July St. Louis, MO.

104. Landrón A, Linares AM. 2022. Screening for powdery mildew resistance in *Cucurbita moschata* in Lajas, Puerto Rico. Proceedings Cucurbitaceae 2022, November, 2022, Naples. Florida p.37

105. Landron A. and A. Linares Ramirez. 2022. Identification of the Powdery Mildew Causal Agent in *Cucurbita moschata* Duch. for Breeding Purposes in Lajas, Puerto Rico. American Society of Horticultural Sciences. Chicago, IL.

106. **Levi, A., Biswas, A. 2024. "Genomic Prediction of Resistance to Fusarium Wilt (*Fusarium oxysporum* f. sp. *niveum* race 2) in Watermelon Using Parametric and Non-Parametric Approaches" EucarpiaCucurbitacea 2024, Naples, Italy (Oral**)

107. Levi A. 2022. Challenges and progress in genetic research and in enhancing disease resistance in watermelon. South Korean Society of Plant Breeders and Geneticists.

108. Lin YC, Tang X, Weng Y, Fei Z, Grumet R. 2024. Identification of QTL Associated with Young Fruit Resistance to Phytophthora Fruit Rot in Cucumber. Plant Animal Genome Conf., San Diego CA

109. Lin YC, Weng Y, Fei Z, Grumet R. 2024. Genetic Analysis of Morphological Diversity for Fruit Quality Traits in the Cucumber Core Collection. Plant Animal Genome Conf., San Diego CA

110. Lin YC, Grumet R. 2023. QTL Mapping of Young Fruit Resistance to *Phytophthora capsici* in Cucumber. Plant Animal Genome Conference, San Diego CA

111. Lin YC, Rett-Cadman S, Grumet R. 2022. Phenotypic and Genetic Analysis of Fruit Morphological Traits for the USDA Cucumber Core Collection. American Society of Horticultural Sciences. Chicago, IL

112. Lin YC, Grumet R. 2022. QTL Mapping of Young Fruit Resistance to *Phytophthora capsici* in Cucumber. Cucurbitaceae 2022. Naples FL

113. Lin YC, Weng Y, Fei Z, Grumet R. (2021) Phenotypic analysis of the U.S. cucumber PI core collection for fruit morphological diversity. National Association of Plant Breeders Annual Meeting; August 18th, 2021; Virtual.

114. Lin YC, Grumet R (2021) QTL-seq of Young Fruit Resistance to *Phytophthora capsici* in Cucumber. 2020 American Society for Horticultural Science Annual Meeting; August 9th, 2020; Virtual

115. Luckew, A., Sari, N., Pandey, S., McAvoy, T., Simmons, A., Meru G & C. McGregor (2024) Evaluation of watermelon and *Citrullus* crop wild relatives for resistance to whiteflies and whitefly transmitted viruses. ASHS Annual Conference, Honolulu, HI

116. Luckew, A., Bag, S., Srinivasan, R., Dutta, B., Da Silva, A.L.B.R., Meru, G., and C.E. McGregor. 2022. Genome wide association study of *C. pepo* evaluated for whiteflies and their transmitted viruses. Cucurbitaceae, Naples, FL.
117. Luckew, A. and C.E. McGregor. 2022. Identifying resistance to whitefly transmitted viruses in Cucurbita. Cucurbitaceae, Naples, FL.
118. Luckew, A. and C.E. McGregor. 2022. Evaluation of Cucurbita germplasm for resistance to whitefly transmitted viruses. Southern Region American Society for Horticultural Science, New Orleans, LA.
119. Luckew, A. and C.E. McGregor. 2022. Evaluation of Cucurbita germplasm for resistance to whitefly transmitted viruses. Joint Southeastern Branch Entomological Society of America and American Phytopathological Society- Caribbean Division, San Juan, PR.
120. Mandal, M.K., Chanda, B., and Kousik, C.S. 2021. Identification of Powdery Mildew Resistant Marker in Watermelon by Metabolomics and Genomics Approach. Annual Meeting of the American Phytopathological Society.
121. Mandal M K, Thompson D, Harris R, CS. 2021. Bacterial Biocontrols in Sustainable Management of Phytophthora Crown and Fruit Rot in Pepper and Watermelon. Annual Meeting of the American Phytopathological Society.
122. Mazourek M. 2023. National Association of Plant Breeders Conference. "Culinary Driven Plant Breeding" July 17, 2023
123. Mazourek M. 2022. Combining Resistance with Quality in Squash. Asia Pacific Seed Association Cucurbinar. Sept 29, 2022.
124. Mazourek M, Frost E 2022. Combining Cucurbits for Downy Mildew Resistance and More. OSSI Webinar Series. May 11, 2022.
125. McGregor, C., Rijal, S. & A. Boettcher (2025) Marker Assisted Backcrossing for Gummy Stem Blight Resistance in Watermelon. Watermelon Research Working Group meeting at the Southern Region ASHS. Irving, TX
126. McGregor, C., Rijal, R., Boettcher, A. & J. Reyes (2024) Introgressing QTL from a Wild Relative to Improve Gummy Stem Blight Resistance in Watermelon. ASHS Annual Conference, Honolulu, HI
127. McGregor, C. (2024) Crop Germplasm Committees: An Opportunity for Value-added Research. ASHS Annual Conference, Honolulu, HI
128. Mcgregor, C. (2023). Citrullus germplasm with resistance to whiteflies and whitefly transmitted viruses. In American Society of Horticultural Science 2023 Annual Conference
129. McGregor CE (2022) Where the Wild Things Are: Using Crop Wild Relatives for Watermelon Improvement. Invited seminar in Department of Horticulture, Michigan State University (virtual)
130. McGregor CE, Rijal S. and S Josiah (2022) The Use of Citrullus Crop Wild Relatives in Watermelon Breeding. American Society for Horticultural Science, Chicago, IL
131. McGregor*, C., Luckew, A., Wang, E., Mathews, P., Carvalho, R., da Silva, A., . . . & R. Srinivasan (2020). Evaluation of Cucurbita germplasm for resistance to whiteflies and whitefly-transmitted viruses. Entomological Society of America national meeting (Virtual).
132. Meru, G. 2023. Squash Breeding and Genetics: Building Blocks for Success in a Genomics Era. Horticultural Sciences Department Seminar, Michigan State University, East Lansing, MI.
133. Meru, G., Fu, Y., Shrestha, S., Sabharwal, P., Thakur, S., Michael, V. 2023. Development and application of genomic tools for squash breeding and genetics. Annual meeting of the American Society of Horticultural Sciences, Orlando, Florida. August 2023

134. Meru, G. 2022. Advancing the cucurbit industry through a genomics-enabled breeding and extension program. Horticultural Sciences Department Seminar, University of Florida, Gainesville, FL.
135. Meru, G., Fu, Y., Michael, N. and Shrestha, S. 2022. Genomics-enabled breeding in squash: progress towards high -throughput application. 135th annual meeting of Florida State Horticultural Society, Sarasota, FL, June 5-7, 2022.
136. Meru, G., Michael, N., Acharya, S., Fu, Y., Shrestha, S. and Sabharwal, P. 2022. RNA-SEQ reveals potential defense mechanisms against *Phytophthora capsici* in squash. Cucurbitaceae 2022. Naples FL, Oct. 30- Nov. 2, 2022.
137. Meru G. 2021. Squash breeding and genetics: building blocks for success in a genomics era. Presented at the University of Georgia, Department of Horticulture, Spring 2021 semester seminar series, held virtually February 24, 2021
138. Michel, S. W., Schultheis, J. R., Keinath, A. P., and L. Quesada-Ocampo. 2025. 2024 Results for Managing Fusarium Wilt of Watermelon with Fungicides and Grafting in North and South Carolina. American Society of Horticultural Science Southern Region Annual Conference, Watermelon Research and Development group, Irving, TX, January 2024.
139. Michel, S. W., Schultheis, J. R., Stickley, B. E., Parker, B. K., Allan, M. C., Johanningsmeier, S. D., and P. Perkins-Veazie. 2025. Canary Melon Yield and Exterior and Internal Quality Results, 2024. American Society of Horticultural Science Southern Region Annual Conference, Irving, TX, January 2024.
140. Michel, S., J. Schultheis, A. Keinath, and L Quesada. 2024. Watermelon cultigen yield response to *Fusarium oxysporum* f. *niveum* incidence in North and South Carolina, USA. ASHS 2024 Conference, Honolulu, HI pp. 274-275 (abstr.).
141. Michel, S.*, J.R. Schultheis, A.P. Keinath, and L. Quesada-Ocampo. 2023. 2023 Results for Managing Fusarium Wilt of Watermelon with Cultivar, Fungicide, and Grafting in North and South Carolina. American Society of Horticultural Science Southern Region Annual Conference, Atlanta, GA. Feb 3.
142. Michel, S.*, J.R. Schultheis, B. Parker, and B. Stickley. 2023. 2023 Mini Watermelon Cultigen Yield and Quality Results for North Carolina. American Society of Horticultural Science Southern Region Annual Conference, Atlanta, GA. Feb 3.
143. Michel S., Schultheis J., Keinath A., and Quesada-Ocampo L. M. 2022. Incidence and yield response of seedless watermelon cultivars affected with Fusarium wilt. Cucurbitaceae, Naples, Florida, November 2022.
144. Michael, V.N.; Fu, Y.; Shrestha, S.; Meru, G. 2020. QTL mapping of Phytophthora crown rot resistance in squash. Presented at the 133rd Annual Meeting for the Florida State Horticultural Society, held virtually October 18 - October 20, 2020.
145. Mondal, S., Ando, K., Tamang, P., Fashing, P., Chen, C., Wintermantel, W.M., and McCreight, J.D. 2023. Advancement of CYSDV-resistant melon lines using marker-assisted selection. American Phytopathological Society, Annual meeting, August 12 – 16, Denver, Colorado.
146. Mondal S, Wintermantel WM, McCreight J. 2022. Development of CYSDV-resistant lines using marker-assisted selection. Cucurbitaceae 2022 Naples, FL
147. Mondal S, Chen C, Jenkins-Hladky LL, Wintermantel WM. 2022. Spatio-temporal accumulation of two closely related criniviruses in melon plants during co-infection. Annual Meeting of the American Phytopathological Society, Pittsburgh, PA, August 6-10, 2022
148. Mondal S, Wintermantel W, McCreight J. 2022. Advancement of CYSDV-resistant Melon using Marker-Assisted Selection. Annual Meeting of the American Phytopathological Society, Pittsburgh, PA, August 6-10, 2022

149. Natarajan P, Nimmakayala P, Lopez-Ortiz C, Rathnagiri A, Rivera-Burgos LA, Sari N, Wehner TC, Levi A, Tomason Y, Reddy UK. (2023) Whole-Genome Scanning Using QTL-Seq and GWAS for Gummy Stem Blight Resistance in Watermelon. Plant & Animal Genome Conference: PAG 30. January 13-18, 2023. San Diego, CA, USA.

150. Natarajan P, Nimmakayala P, Abburi V, Lopez-Ortiz C, Levi A, Wehner T, Reddy UK. (2022) Whole-Genome Scanning Using QTL-Seq and GWAS for Gummy StemBlight Resistance in Watermelon. Cucurbitaceae 2022. October 30-November 2, 2022. Naples, FL, USA.

151. Nelson, E. M., Herrmann, T. Q., Day, C. T. C., and Smart, C. D. Unraveling unique interactions between *Phytophthora capsici* and understudied hosts (poster). Plant Health 2024. Memphis, TN. July 30, 2024.

152. Pandey, S., Luckew, A., McAvoy, T., Meru, G., Simmons, A., & Mcgregor, C. (2023). Evaluation of Citrullus Genotypes for Resistance to Whitefly Transmitted Viruses. In Southern Region— American Society for Horticultural Science

153. Pandey, S., Luckew, A., McAvoy, T., Meru, G., and C.E. McGregor 2022. Evaluation of *Citrullus* genotypes for resistance to whitefly transmitted viruses. Southern Region ASHS annual meeting Oklahoma City, OK.

154. Parada Rojas C. H. and Quesada-Ocampo L.M. 2023. Improving Knowledge of Host Resistance Against Soilborne Vegetable Pathogens. Department of Entomology and Plant Pathology Seminar. Raleigh, NC, February, 2023.

155. Parada-Rojas C. H. and Quesada-Ocampo L. M. (2022) *Phytophthora capsici* populations structure by host, geography, and fluopicolide sensitivity. Phytopathology 112: S3.102.

156. Perkins-Veazie, P., M. Trandel, J. Schultheis and T. Birdsell. 2020. Pumpkin Postharvest: Stem Retention and Moisture with Storage. *HortScience*, 55(9S): S410-S411(abstr.).

157. Perla, D., Medina-Mora, C.M., Engfehr, C., and Hausbeck, M.K. 2023. Evaluating hard squash cultivars for susceptibility to powdery mildew and fruit rot. 12th International Congress on Plant Pathology, The International Society for Plant Pathology and the French Phytopathological Society. Lyon, France. 20 Aug-25 Aug.

158. Perla D., and Hausbeck M.K. 2022. Vegetable Disease Management using host resistance and fungicides. American Phytopathological Society North Central Division Meeting, Lincoln, NE, June 2022.2020-5132139

159. Perla, D.E, Hayden, Z.D., and Hausbeck, M. K. 2022. Commercial hard squash cultivars exhibit differences in resistance to Phytophthora fruit and crown rot. Cucurbitaceae 2022. Naples, FL, November 2022.

160. Perla, D.E., Hayden, Z.D., and Hausbeck, M.K. 2022. Assessment of hard squash cultivars for resistance to crown rot caused by *Phytophthora capsici* and sugar content. American Phytopathological Society North Central Division Meeting. Lincoln, NE, 21-23 Jul.

161. Perla, D. 2020. Evaluate strategies for management of Phytophthora blight *Phytophthora capsici* in Michigan processing squash. Departmental seminar, Department of Plant Pathology, Michigan State University, East Lansing, MI. Virtual

162. Peterson, A.M., Bello, J.C., Kenny, G., Perla, D., Uebbing, M., Hausbeck, M.K. 2022. Burkard spore traps for detection of *Pseudoperonospora cubensis* sporangia in cucurbit production. American Phytopathological Society Annual Meeting, Pittsburg, PA. August 2022

163. Prieto Torres M, Quesada-Ocampo L. M. (2024) Optimizing a mobile spore trapping system for detection of Pseudoperonospora cubensis, causal agent of cucurbit downy mildew. American Phytopathological Society, Caribbean Division Meeting 2024, Merida, Yucatán, Mexico, April 2024.

164. Prieto Torres M, Quesada-Ocampo L. M. (2024) Oxathiapiprolin fungicide resistance mutation occurrence over time in Pseudoperonospora cubensis samples from North Carolina. American Phytopathological Society, Plant Health 2024, Memphis, TN, July 2024.

165. Prieto Torres M. and Quesada-Ocampo L. M. 2024. Using biosurveillance for detection of Pseudoperonospora cubensis, causal agent of cucurbit downy mildew, in both research and commercial field settings. School of Integrative Plant Science seminars - Cornell, Geneva, NY. November, 2024

166. Prieto Torres M. and Quesada-Ocampo L. M. (2024). Using biosurveillance for detection of *Pseudoperonospora cubensis*, causal agent of cucurbit downy mildew. Department of Entomology and Plant Pathology Graduate Symposium. Raleigh, NC, November 2024

167. Prieto Torres M, Quesada-Ocampo L. M. 2024. Optimizing a mobile spore trapping system for detection of *Pseudoperonospora cubensis*, causal agent of cucurbit downy mildew. American Phytopathological Society, Plant Health 2024, Memphis, TN, July 2024.

168. Prieto Torres, M., and Quesada-Ocampo L. M. 2023. Monitoreo y biovigilancia en poblaciones de mildeo velloso en cucurbitáceas (*Pseudoperonospora cubensis),* en Carolina del Norte. I Simposio Internacional de Fitopatología y Microbiología Agrícola, Universidad Nacional Mayor de San Marcos, Peru, November 2023.

169. Prieto-Torres, M. and Quesada-Ocampo L. M. (2023) Monitoring oxathiapiprolin fungicide resistance mutations in *Pseudoperonospora cubensis* populations in North Carolina. Phytopathology 113: S3.18.

170. Prieto-Torres, M. and Quesada-Ocampo L. M. (2023) Monitoring for mutations related to oxathiapiprolin fungicide resistance in *Pseudoperonospora cubensis* populations. Phytopathology 113: S2.31

171. Prieto-Torres, M. and Quesada-Ocampo L. M. 2023. Monitoring for mutations related to oxathiapiprolin fungicide resistance in *Pseudoperonospora cubensis* populations. American Phytopathological Society-Southern Division, Durham, NC. February 2023.

172. Prieto-Torres, M. and Quesada-Ocampo L. M. 2022. Monitoring populations and fungicide resistance in *Pseudoperonospora cubensis* using biosurveillance and molecular markers. Cucurbitaceae, Naples, Florida, November 2022.

173. Purayannur S., Cano L.M., Bowman M.J, Childs K.L., Quesada-Ocampo L.M. 2021. Effectors of the cucurbit downy mildew pathogen *Pseudoperonospora cubensis*. Annual American Phytopathological Society Meeting, Virtual Meeting. August, 2021. Phytopathology 111:S2.7

174. Purayannur S., Cano L.M., Bowman M.J, Childs K.L., Quesada-Ocampo L.M. 2021. Differential expression of effector-encoding genes in two clades of the cucurbit downy mildew pathogen *Pseudoperonospora cubensis*. International Society for Molecular Plant-Microbe Interactions Congress eSymposia series. September 2021.

175. Purayannur, S., Cano, L. M., Bowman, M. J., Childs, K. L., and Quesada-Ocampo, L. M. (2020) Clade-specific RXLR effectorome of the cucurbit downy mildew pathogen *Pseudoperonospora cubensis*. Phytopathology 110: S2.6.

176. Quesada-Ocampo L. M. 2024. Population structure of *Pseudoperonospora cubensis*. FRAC-APS Pathogen Resistance Committee Workshop. Oomycete Fungicides. American Phytopathological Society Annual Meeting. Memphis, TN, July 2024.

177. Quesada-Ocampo L. M. 2023. Applied genomics for disease management in vegetable crops. Department of Plant Pathology, Gainesville, FL, November 2023.

178. Quesada-Ocampo L. M. 2023. Applied genomics for disease management in vegetable crops. Department of Botany and Plant Pathology, West Lafayette, IN, November 2023.

179. Quesada-Ocampo L. M., Xiang, L., Brown H., and Vijapurapu R. 2023. Evaluation of commercially available spore traps for detection of clade 1 and clade 2 downy mildew on cucurbits. NC State Chancellor Innovation Fund Meeting, Raleigh, NC, May 2023**.**
180. Quesada-Ocampo L. M. 2023. Translational research for detection and management of diseases of vegetable crops. NC Plant Sciences Initiative Senator Visit, Raleigh, NC, June 2023.
181. Quesada-Ocampo L. M. 2023. Translational research for detection and management of diseases of vegetable crops. NC Plant Sciences Initiative Partners Event, Raleigh, NC, May 2023.
182. Quesada-Ocampo L. M. 2023. Applied genomics for disease management in vegetable crops. Department of Biochemistry and Molecular Biology Seminar, Reno, NV, September 2023.
183. Quesada-Ocampo L. M. 2023. Applied genomics for disease management in vegetable crops. Department of Plant Pathology Seminar, University of Georgia, Athens, GA, March 2023.
184. Quesada-Ocampo L. M. 2023. Next generation technologies for plant pathogen detection. NC Plant Sciences Initiative State of the Union. North Carolina Plant Sciences Initiative. North Carolina State University, Raleigh, NC, February 2023.
185. Quesada-Ocampo L. M. 2022. Translational research for detection and management of diseases of vegetable crops. Universidad Nacional Mayor de San Marcos. Lima, Peru, November 2022.
186. Quesada-Ocampo L. M. 2022. Applied genomics for disease management in vegetable crops. Genetics and Genomics Academy Seminar, North Carolina State University, Raleigh, NC, November 2022.
187. Quesada-Ocampo L. M., 2022. Next generation technologies for plant pathogen detection. Commercializing Academic Research Showcase & Innovation Expo. North Carolina Plant Sciences Initiative. North Carolina State University, Raleigh, NC, November 2022.
188. Quesada-Ocampo L. M. 2022. Applied genomics for disease management in vegetable crops. Department of Plant Biology Seminar, University of Massachusetts, September 2022.
189. Quesada-Ocampo L. M. 2022. Disease management in vegetable crops. AgBiome seminar, Durham, NC, July 2022.
190. Quesada-Ocampo L. M. 2021. Translational strategies to improve management of re-emerging pathogens of vegetable crops. Australasian Plant Pathology Society, Australia, November 2021.
191. Quesada-Ocampo L. M. 2021. From the field to the lab and back: translational strategies to improve disease management in vegetable crops. Department of Entomology and Plant Pathology, NC State University, Raleigh, NC, September 2021.
192. Quesada-Ocampo L. M. 2021. From the field to the lab and back: translational strategies to improve management of cucurbit downy mildew. Agriculture Agri-Food Canada, Ontario, Canada, April 2021.
193. Quesada-Ocampo L. M. 2020. Leveraging population genetics, epidemiology, and genomics to improve management of re-emerging pathogens of vegetable crops. Department of Plant Pathology, Kansas State University, Manhattan, KS, November 2020.
194. Quesada-Ocampo L.M. 2020. Population genetics and epidemiology approaches for management of re-emerging pathogens of vegetable crops. Department of Plant Pathology, University of Minnesota, St. Paul, MN, October 2020.
195. Quesada-Ocampo L.M. 2020. From the field to the lab and back: translational strategies to improve disease control in vegetable crops. Department of Plant Pathology, Washington State University, Pullman, WA, September 2020.
196. Rett-Cadman S, Grumet R. 2024. Genome Wide Association Study of Cuticle and Lipid Droplet Properties of Cucumber Fruit. Plant and Animal Genome Conference, San Diego CA

197. Rett-Cadman S, Hammar S, Grumet R. 2023. Biochemical and Genetic Analyses of Cucumber Fruit Peel Lipid Droplets. Plant Animal Genome Conference. San Diego CA

198. Rett-Cadman S, Hammar S, Grumet R. 2022. Isolation and Characterization of Lipid Droplets in Cucumber Fruit. Cucurbitaceae 2022, Naples FL

199. Rijal, S. And C.E. McGregor. 2022. Marker-Assisted Breeding for Gummy Stem Blight Resistance in Watermelon. Cucurbitaceae, Naples, Florida.

200. Rijal S, McGregor CE. 2022.Watermelon improvement for gummy stem blight (GSB) resistance through marker-assisted introgression of resistance quantitative trait loci (QTL) from the wild relatives. Southern Region American Society for Horticultural Science, New Orleans, LA.

201. Rijal S, McGregor CE. 2022. Introgression of gummy stem blight (GSB) resistance QTL into elite watermelon cultivars. Joint Southeastern Branch Entomological Society of America and American Phytopathological Society- Caribbean Division, San Juan, PR. HortScience, S233

202. Rijal, S. 2022. Watermelon's Wild Friends: Introgressing Important Traits in a Favorite Fruit. IPBGG Research Seminar, UGA.

203. Rosado-Rivera Y. I., Adams M. L., D'Arcangelo K. N. and Quesada-Ocampo L. M. 2022. Downy mildew disease management of cucumber and squash in North Carolina. Cucurbitaceae, Naples, Florida, November 2022.

204. Sabharwal, P., Meru, G. 2024. Exploration of Novel Genetic Resistance to Powdery Mildew in Cucurbita pepo Using Genome-Wide Association Studies. XII Eucarpia, Nov 2024, Naples, Italy.

205. Sabharwal, P., Meru, G. 2024. GWAS analysis of USDA *Cucurbita pepo* germplasm for powdery mildew resistance. ASHS, Oct. 2024 Hawaii.

206. Sabharwal, P., Smart, C., Indermaur, L., Day, C.T., Mazourek, M., Inzinna, G., Hausbeck, M., Medina-Mora, C., and Meru, G. 2023. Evaluation of *Cucurbita pepo* germplasm for resistance to powdery mildew. Annual Conference, American Society for Horticultural Science. Orlando, FL. 31 Jul-4 Aug.

207. Salcedo, A., Parada-Rojas C. H., Purayannur S.,Quesada-Ocampo L. M. 2021. Accelerating Resistance Breeding in Cucurbits. CucCAP2 meeting, Virtual Meeting, October 2021

208. Schultheis, J., Pfefferkorn, S. Michel, B. Stickley, and B. Parker. 2024. Canary melons yield and quality evaluations in North Carolina, 2023. ASHS 2024 Conference, Honolulu, HI p. 275 (abstr.).

209. Schultheis, J., S. Michel, B.K. Parker, and B.E.Stickley. 2025. 2024 Standard Size Watermelon Cultigen Yield and Quality Results for North Carolina. American Society of Horticultural Science Southern Region Annual Conference, Watermelon Research Watermelon Research and Development group. Irving, TX.

210. Schultheis, J.R.*, S. Michel, B. Parker, and B. Stickley. 2023 Standard Size Watermelon Cultigen Yield and Quality Results for North Carolina. American Society of Horticultural Science Southern Region Annual Conference, Atlanta, GA. Feb 3.

211. Schultheis JR, Keinath A, Quesada-Ocampo L. 2022. Watermelon cultivar symptom plant incidence and yield response in fields in North and South Carolina containing *Fusarium oxysporum* f. sp *niveum*. Watermelon Research and Development group, ASHS - Southern Region, New Orleans, LA, Feb. 11. HortScience 57:S290

212. Schultheis, J.R. and K.D. Starke. 2022 Triploid watermelon standard size cultivar yield and quality results, North Carolina, 2021. Watermelon Research and Development group, ASHS - Southern Region, New Orleans, LA Feb. 11.HortScience 57:S290

213. Schultheis, J. and K. Starke 2021. Melon cultigens and their adaptation in the southeastern United States when grown in North Carolina (abstr.)

214. Shaonpius Mondal, K. Ando, P. Tamang, P. Fashing, W.M. Wintermantel, and J.D. McCreight. 2022. Advancement of CYSDV-resistant melon using marker-assisted selection. Cucurbitaceae 2022, October 30–November 2, 2022.

215. **Singh, G., Srinivasan, R., Mcgregor, C., Luckew, A., & G. Meru (2024) Evaluating resistance to whiteflies and whitefly-transmitted viruses in squash species and bridge lines. In Southeastern branch Entomological Society of America Annual meeting. Augusta, GA**

216. Singh, G., Luckew, A., Mcgregor, C., & Srinivasan, R. (2023). Harnessing host plant resistance: A promising approach to tackle whiteflies and viral diseases in squash. In Entomological Society of America, Annual Meeting. National Harbor, MD

217. Singh, G., Mcgregor, C., & Srinivasan, R. (2023). Screening newly-developed Squash (*Cucurbita* spp.) germplasm lines for resistance against whitefly-transmitted Begomovirus and Crinivirus mixed infection. In Entomological Society of America, Annual SEB meeting. Little Rock, Arkansas

218. Smart, C. D. 2024. The changing landscape of vegetable production and the impact of *Phytophthora capsici*. Oregon State University, Dept of Botany and Plant Pathology. Student invited seminar speaker. Corvallis, OR. October 3, 2024.

219. Smart, CD. American Phytopathological Society. 2023. Phytopathologist of Distinction talk. A passion for plant pathology: Pairing discovery with public engagement.

220. Smart CD. Colorado State University. 2023. Our veggies are dying: The intersection of climate, consumers and pathogens.

221. Smart CD. 2023. Cornell University Plant Pathology & Plant-Microbe Biology Section, School of Integrative Plant Science. 2023 Water-limited Agriculture; My Colorado Experience.

222. Sun H. 2024. Graph-based pangenome of the *Citrullus* genus provides insights into watermelon evolution and domestication. Plant & Animal Genome Conference. San Diego, CA. January 2024

223. Sun H. 2023. The *Citrullus* genus super-pangenome. BTI Monday Morning Seminar Series. March 2023.

224. Tan JY, Weng Y. 2022. Sequence variation in sigma factor binding protein1 (CsSIB1) contributes to downy mildew resistance in cucumber.' A presentation at 2nd Intl Symposium for Hort Plant Biol and Biotech (Nov 17-18, 2022, Beijing, China)

225. Toporek, S.M., and Keinath, A. P. 2021. Clade and mating type distribution and population structure of *Pseudoperonsopra cubensis* on *Cucumis melo* in the eastern United States. Plant Health 2021, American Phytopathological Society (virtual). https://events.rdmobile.com/Lists/Details/1179180

226. Trandel, M.A., S. Johanningsmeier, C. Gunter, J. Schultheis, and P. Perkins-Veazie, P. 2020. Cell wall architecture in grafted and non-grafted 'Liberty' watermelon with hollow heart. HortScience, 55(9S):S129 (abstr.).

227. Trandel, M.A., P. Perkins-Veazie, S. Johanningsmeier, J. Schultheis, and C. Gunter. 2020. The Backbone of Fruit: Cell Wall Polysaccharides in Grafted and Non-grafted 'Liberty' Watermelon at Varying Levels of Hollow Heart. HortScience, 55(9S): S423-S424 (abstr.)

228. Trandel, M.A. P. Perkins-Veazie, J. Schultheis, C. Gunter, and E. Johannes. (2020). Grafting watermelon onto interspecific hybrid squash reduces hollow heart. Acta Horticulturae II International Symposium of Vegetable Grafting. 1302:225-232.

229. Turechek, W.W. Adkins, S., Kousik, C.S., Smith, H. 2020. Towards Areawide Pest Management of Whitefly-Transmitted Viruses in Florida Vegetable Production Systems.

Presented at the Whitefly Symposium. Entomological Society of America Annual Meeting, November 2020.

230. Uebbing M.R., Hausbeck M.K. 2022. Managing Cucurbit Downy Mildew in Pickling cucumber using disease forecasters and fungicides. 2022. Department of Plant Soil and Microbial Sciences, Michigan State University, March 2022.

231. Uebbing M.R., and Hausbeck M.K. 2022. Using weather conditions to time fungicide application intervals for control of downy mildew on cucumber. 2022. American Phytopathological Society North Central Division Meeting, Lincoln, NE, June 2022. 2020-51181-3219

232. Wechter WP. 2025. Genomics in plants: 21st century answers to 21st century problems. College of Charleston, Department of Physics and Meteorology Seminar.

233. Weng Y, Dymerski R, Wang Y, Chen F, Fei Z, Grumet R. 2025. Phylogenomics and GWAS Provide Insights Into Selection History of Horticulturally Important Traits in Cucumber. Cucurbit Genomics workshop, Plant and Animal Genome Conference (PAG32) San Diego, CA

234. Weng, Y. 2025. Mutations disturbing chloroplast and mitochondrial biological processes as a source of stress tolerances for plant breeding. Plant Molecular Breeding workshop at the Plant and Animal Genome Conference (PAG32) San Diego, CA

235. Weng Y (2023) Marker-assisted QTL pyramiding expedites development of cucumbers with multiple disease resistances. Plant and Animal International Conference 30 (Jan 15, 2023, San Diego, CA)

236. Weng Y. 2023. 'Development of 3K SNP panel for targeted genotyping in cucumber.' An oral presentation at ISHS Cucurbits Symposium (online, June 12, 2023, Zhengzhou, China)

237. Weng Y. 2023. 'The USDA-ARS, UW-Madison Cucumber Breeding Program.' A seminar presentation at Tennessee State University, Nashville (October 23, 2023; Nashville, TN).

238. Weng Y (2022) Genetic basis of downy mildew resistance in cucumber. An invited talk on Cucurbinars 2022 organized by APSA (Asian and Pacific Seed Association) (Sept 30, 2022)

239. Weng Y . 2022. Cucumber, genetics, genomics and breeding research: my journey. 'Lecture Series for Post Graduate Students' organized by the Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India (Virtual, February 24, 2022).

240. Weng Y. 2022. Cucumber Breeding: All Things Considered. 'Global Connect Series Lectures' organized by the Dr. Y.S.R. Horticultural University, India (Virtual, April 20, 2022).

241. Weng, Y. 2022. The Gy14v2.0 pickling cucumber genome. Cucurbitaceae 2022 international meeting (Naples, FL, November 2, 2022)

242. Weng Y (2021). Disease resistances in cucumber. SIPS seminar. Cornell University, Ithaca, NY. Virtual.

243. Weng Y, Xu XW, Dymerski R, Wang YH, Copetti D, Luo MC, Fei ZJ, Sun HH, Qu SJ, Jiang N, Bostan H, Iorizzo M (2022) The US processing cucumber genome assembly Gy14v2.0. Cucurbitaceae 2022 (November 1, 2022, Naples, FL)

244. Wilds E., Purayannur S., Quesada-Ocampo L. M. 2022. Differential expression of two effector-encoding genes in Clade 1 and Clade 2 of the cucurbit downy mildew pathogen (*Pseudoperonospora cubensis*) Undergraduate Research and Creativity Symposium. North Carolina State University. Raleigh, North Carolina. July 2022.

245. Wintermantel, W.M. 2024. Emergence of watermelon chlorotic stunt virus as a new threat to melon and watermelon production in the southwestern United States. Plant Health 2024, Memphis, TN, August 2024. Poster presentation.

246. Wintermantel, W.M. 2024. Emergence of watermelon chlorotic stunt virus and its impact on virus population structure and infection dynamics in southwestern U.S. melon production. Cucurbitaceae 2024, Vico Equense, Italy, November 2024.

247. Wintermantel, W.M. 2023. A historical perspective of cucurbit virus emergence and impact in the United States. American Phytopathological Society, Annual meeting, August 12 – 16, Denver, Colorado.
248. Wintermantel, W.M., and Mondal, S. 2023. Competitiveness of whitefly-transmitted yellowing viruses can influence virus dominance in cucurbit crops. Southern Division American Phytopathological Society Annual Meeting, February 13-16, 2023, Durham, NC.
249. Wintermantel, W.M., and Mondal, S. 2023. Factors influencing epidemiology and spread of whitefly-transmitted cucurbit viruses in the US vary among production regions. International Congress of Plant Pathology, August 20-25, 2023, Lyon, France.
250. Wintermantel WM. 2022. Whitefly-transmitted virus infection patterns in mixed infections vary among three cucurbit production regions in the United States. International Symposium on Plant Virus Epidemiology. Madrid, Spain, June 2022
251. Wintermantel WM. 2022. Seasonal prevalence and spread of whitefly-transmitted viruses in California production regions. Cucurbitaceae 2022. Naples FL.
252. Wintermantel WM. 2022. Whitefly populations in the Central Valley of California Lead to introduction and establishment of whitefly-transmitted viruses in melon. Entomological Society of America.
253. Wintermantel WM. 2022. Emerging viruses threatening cucurbit crops. Annual Meeting of the American Phytopathological Society, Pittsburgh, PA, August 6-10, 2022
254. Wu S. (2023) Super-pangenome of wild and cultivated watermelons. Plant & Animal Genome Conference. San Diego, CA. January 2023.
255. Wu S (2022) Pan-genome of wild and cultivated watermelons. University of Georgia
256. **Yu D, Tan J, Hao N, Nguyen T, Keinath AP, Lin M, Sheehan M, Weng Y. QTL Mapping of Horticulturally Important Traits in a RIL Population Derived from an Alien Introgression Line in Cucumber. Plant and Animal Genome Conference (PAG32) San Diego, CA**
257. Zia, B., Levi, A., Simmons, A. and Ling, K.-S. 2023. Identification of SNPs associated with Cucumber green mottle mosaic virus resistance in watermelon. Plant Health 2023, Denver, CO, August 12-16, 2023.
258. Zia B, Weng Y, Chen F, Levi A, Cutulle MA, Ling K-S. 2022. Identification and characterization of genetic resistance in cucumber and watermelon to *Cucumber green mottle mosaic virus*. Cucurbitaceae 2022, Naples, FL, USA, October 30 - November 2, 2022
259. Zia B, Weng Y, Cutulle MA, Ling, KS (2022) Identification of genetic sources of resistance to the emerging *Cucumber green mottle mosaic virus* in cucumber lines (APS meeting 2022, Pittsburgh, PA)

EXTENSION/OUTREACH PRESENTATIONS

1. Adams ML, Quesada-Ocampo LM. 2021. Cucurbit Disease Identification and IPM. Piedmont Research Station Horticulture and Specialty Crops Field Day. Salisbury, NC, August 2021.
2. Baugher, N. and J.R. Schultheis. 2022. NC pollinizer research report. NC Watermelon Production meeting. Virtual, Feb. 7, https://gates.ces.ncsu.edu/2022/03/2022-watermelon-production-meeting-recording/
3. Birdsell T, Heagy K, Schultheis J. 2021. Pumpkin Cultivars to Consider Growing in North Carolina; Pumpkin Spacing Considerations: Effects on Yield, Size and Fruit Uniformity. North Carolina Vegetable Growers Association Ag Expo, Raleigh, Dec. 1Grumet R. 2021. The CucCAP2 project. BASF. January 2021.
4. Branham SE. 2024. Breeding Fon race 2 resistant watermelon using crop wild relatives. Giant Watermelon Growers Association Meeting.
5. Branham S. Clemson University Coastal Research and Education Center 2022 Field Day. Exhibited melon lines in the field, as well as pathogenicity assays in the greenhouse and growth chamber to 100+ individuals.
6. **Cochran S. and Quesada-Ocampo L. M. Molecular detection of *Phytophthora capsici*. Pickle Packers International Annual Meeting. Chicago, LI, October 2024.**
7. Collins, H., and Quesada-Ocampo L. M. Management of *Phytophthora capsici* on cucurbit crops. 36th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, SC, November 2023
8. Grumet R. 2023. Genetic mapping of resistance to Phytophthora fruit rot in cucumber. Pickling Cucumber Research Committee.
9. Grumet R., Weng Y. 2021. Breeding for disease resistance in pickling cucumber. Great Lakes Fruit, Vegetable, Farm Market Expo. December, 2021
10. Grumet R, Lin YC. 2020. Resistance of cucumber fruit to *Phytophthora capsici*. Pickle Packers International. Virtual conference, October 2020.
11. **Hausbeck, M.K. and Spafford, J.* 2024. Downy Mildew Update. Great Lakes Fruit, Vegetable and Farm Market Expo. Proceedings online at http://glexpo.org/sessions/2024/Tuesday/Morning/ Pickles%20and%20Vine%20Crops-Hausbeck.pdf**
12. **Hausbeck, M.K. 2024. Tips to manage those pesky water mold pathogens: Phytophthora and downy mildew. Southeast Michigan Vegetable Grower Winter Meeting. Monroe, MI, 20 Feb.**
13. **Hausbeck, M.K. 2025. Successful disease control of vine crops. Mid-Atlantic Fruit and Vegetable Convention, Hershey, PA, 28 Jan.**
14. **Hausbeck, M.K. 2025. Phytophthora crown and fruit rot of pumpkin. Mid-Atlantic Fruit and Vegetable Convention, Hershey, PA, 28 Jan.**
15. **Hausbeck, M.K. 2024. Management of powdery and downy mildew on cucurbits. New England Vegetable and Fruit Conference, Manchester, NH, 17 Dec.**
16. **Hausbeck, M.K. 2024. Phytophthora management in cucurbits. New England Vegetable and Fruit Conference, Manchester, NH, 17 Dec.**
17. **Hausbeck, M.K. and Spafford, J.* 2024. Downy Mildew Update. Great Lakes Fruit, Vegetable and Farm Market Expo. Grand Rapids, MI. 10 Dec. 174 attendees.**
18. Hausbeck, M.K. 2023. Phytophthora control: lessons learned in Michigan. Ontario Fruit and Vegetable Convention. Niagara Falls, ON, Canada, 22 Feb.
19. Hausbeck, M.K. 2023. Phytophthora management: What really works? The Ohio State University 76th Annual Celeryville Muck Crops School. Willard, OH, 4 Jan. 25 attendees.

20. Hausbeck, M.K. 2023. Southwest Hort Days: Phytophthora crown rot session. Benton Harbor, MI. 1 Feb. 20 attendees
21. Hausbeck, M.K. 2022. Developments in downy mildew and *Phytophthora capsici* control in pickling cucumber. Annual Meeting of the Pickle Packers International. Las Vegas, NV, October, 2022.
22. Hausbeck, M.K. 2022. Phytophthora Crown Rot and Fruit Rot on Cucurbits and Peppers. Syngenta Canada Fruit and Vegetable Webinar. Ontario, Canada. Virtual, 2 Feb. 70 attendees.
23. Hausbeck, M.K. 2022. Putting together a Phytophthora program that works. MSU Extension meeting. Oceana County, MI, Mar. 25 attendees.
24. Hausbeck, M.K. 2022. Developing Tools to Limit Phytophthora on hard squash. Michigan IMP Alliance EPA Crop Tour, Phytophthora stop. Oceana County, MI, 23 Aug. 20 attendees.
25. Hausbeck, M.K. and Uebbing, M. 2021. Downy Mildew: New Insights on Control. Great Lakes Farm, Fruit and Vegetable Expo. Grand Rapids, MI, 8 Dec 2021. 2020-51181-32139
26. Hausbeck, M.K. and Uebbing, M.R. 2021. Pickles in a pickle: Trying to outsmart *Pseudoperonospora cubensis*, the cucurbit downy mildew pathogen. Annual Meeting of the Pickle Packers International. Virtual, 19 Oct. 78 attendees.
27. Hausbeck, M.K. 2021. A Partnership to protect Michigan's Cucumber Industry. Farm Lane Society meeting, Virtual, 5 Mar.
28. Hausbeck, M.K. 2020. Management of Phytophthora Blight in Processing Squash. Great Lakes Farm, Fruit and Vegetable Expo. Virtual, 10 Dec. 167 attendees.
29. Hausbeck, M.K. 2020. Downy Mildew Management in Pickling Cucumbers. Great Lakes Farm, Fruit and Vegetable Expo. Virtual, 8 Dec. 174 attendees.
30. Hausbeck, M.K. 2020. Vegetable and Root Crop Field Day: Disease control of Vegetables. Sept, Virtual, 39 attendees. https://www.canr.msu.edu/events/oceana-research-tour-virtual-field-day
31. Hausbeck, M.K. 2020. 2021 Spray Program. Southeast Vegetable Meeting. Virtual, 4 Nov. 90 attendees.
32. Hausbeck, M.K. and Higgins, D.S. 2020. The Grounder, the Line Drive, and the Pop Fly: Fielding Three Very Different Vine Crop Diseases. Great Lakes Farm, Fruit and Vegetable Expo. Virtual, 9 Dec. 178 attendees.
33. Hausbeck, M.K. and Kenny, G. 2020. From the Field to the Lab and Back: Monitoring Fungicide Resistance in Cucurbit Downy Mildew. Pickle Packers International Annual Meeting. Virtual, 19 Oct. 78 attendees.
34. Hausbeck, M.K. and Kenny, G. 2020. From the Field to the Lab and Back: Monitoring Fungicide Resistance in Cucurbit Downy Mildew. Pickle Packers International Annual Meeting. Virtual, 19 Oct. 78 attendees.
35. Heagy, K. and Schultheis, J. R. 2022. UAV images and objective detection software: estimating pumpkin yield and fruit size. North Carolina Vegetable Growers Association Ag Expo. Raleigh, NC, November 29, 2022.
36. Higgins D, Hausbeck MK. 2021.Phytophthora Crown Rot and Fruit Rot, and Powdery Mildew for Fresh Market Growers. Great Lakes Farm, Fruit, and Vegetable Expo. Grand Rapids, 9 Dec. 115 attendees.
37. Hurry, N. and J. Schultheis. 2023. Pollinizer Options for Seedless Watermelon Production. 36th Annual Southeast Vegetable & Fruit EXPO, Watermelon Section. Myrtle Beach, SC., Nov. 27
38. Indermar L, Smart CD. 2023. Specialty crop tour. Geneva NY September 16, 2023. Current research on diseases of specialty crops at Cornell AgriTech**.**
39. Indermaur, E. J., Day, C. T. C., and Smart, C. D. 2023. Tools for managing powdery mildew in winter squash organically: cultivars & biofungicides. Empire State Producers Expo. Syracuse, NY,

February, 2023.

40. Indermaur, E. J., Day, C. T. C., and Smart, C. D. 2022. Winter squash cultivar evaluations for resistance to powdery mildew. Empire State Producers Expo. Syracuse, NY, February, 2022.
41. Katuuramu D. N. 2022. GWAS for Resistance to Cucurbit Downy Mildew in Watermelon. 2022 Watermelon Research & Development Group Annual Meeting.in South Carolina. Edisto REC Watermelon Field Day, Blackville, SC. July 14, 2022.
42. **Keinath, A. P. 2024. 2024 Cucurbit Disease Update. Cucurbit Grower Meeting, Edisto REC, Blackville, SC. Virtual presentation. Feb. 23, 2024.**
43. Keinath, A. P. 2023. 2023 Vegetable Disease Update: Downy Mildew on Cucumbers and Anthracnose on Peppers. Pee Dee Vegetable Meeting, Florence, SC. 2/28/2023
44. Keinath, A. P. 2023. 2023 Midlands Vegetable Disease Update: Downy Mildew, Black Rot, Black Spot, and Anthracnose. Midlands Spring Vegetable Meeting, Pelion, SC. 3/7/23
45. Keinath, A. P. 2023. Integrated management of Fusarium wilt on seedless watermelon. Clemson Coastal REC Field Day. Presented twice on 6/7/23. 94 attendees, 96% reported learning something new.
46. Keinath, A. P. 2023. The SC Grower Exchange: June 30, 2023 - with Dr. Anthony Keinath. Podcast. 6/30/23. Major topic was cucurbit downy mildew. https://open.spotify.com/episode/1RGY5V6c3mukTVZbj9thIM
47. Keinath, A. P. 2023. Fusarium Biology and Disease Management. Clemson Edisto REC Watermelon Field Day. 7/13/23
48. Keinath, A. P. 2023. How Much Does It Cost to Not Spray Watermelon? And Other Economic Impacts of Vegetable Disease Management. Virginia Tech Eastern Shore Agricultural Research and Extension Center Lunch and Learn. March 24, 2023.
49. Keinath, A. P. 2023. Tebuconazole Resistance in the Gummy Stem Blight Fungus in South Carolina. 35th Southeast Vegetable & Fruit Expo. November 29, 2022.
50. Keinath, A. P. 2023. 2023 Vegetable Disease Update: Downy Mildew on Cucumbers and Anthracnose on Peppers. Pee Dee Vegetable Meeting, Florence, SC. February 23, 2023.
51. Keinath, A. P. 2023. 2023 Midlands Vegetable Disease Update: Downy Mildew, Black Rot, Black Spot, and Anthracnose. Midlands Spring Vegetable Meeting, Pelion, SC. March 7, 2023.
52. Keinath, A. P. 2022. Management and Economics of Three Common Foliar Diseases on Cucumber and Leafy Greens. Long Island Ag Forum (virtual). January 18, 2022.
53. Keinath, A. P. 2022. All You Need to Know about Downy Mildew on Cucumbers for the 2022 Growing Season. Clemson Extension Cucurbit Pre-Plant Meeting (virtual). February 8, 2022.
54. Keinath, A. P. 2022. Reduced Sensitivity to Tebuconazole is Common in South Carolina Isolates of *Stagonosporopsis*, Causal Agent of Gummy Stem Blight. Watermelon Research and Development Group Annual Meeting (virtual). February 11, 2022.
55. Keinath, A. P. 2022. Cucurbit Disease Update with 2021 Clemson Trial Results. Clemson Extension Cucurbit Grower Meeting (virtual). February 17, 2022.
56. Keinath, A. P. 2022. Tebuconazole Resistance is Widespread in the Gummy Stem Blight Fungus Keinath, A.P. 2021. In-service training for Commercial Horticulture Agents on cucurbit downy mildew, 9/30/2021 and 10/26/2021, 4 agents.
57. Keinath, A.P. 2021. Advanced Master Gardener Training: Identifying Downy Mildew in the Field on Cucurbits and Basil, Completed, Demonstration, Attendees: 11, (October 5 and 13, 2021)
58. Keinath, A.P. 2021. "Management and Economics of Three Common Foliar Diseases on Cucumber and Leafy Greens," Long Island (NY) Ag Forum (virtual), January 18, 2022. Estimated Attendees: 95
59. Keinath, A.P. 2021. CU Cucurbit Grower Meeting (virtual). Cucurbit Disease Update with 2021 Clemson Trial Results, Presented, Clientele Groups, Estimated Attendees: 8, (February 17, 2022)

60. Keinath, A.P. 2021. CU Cucurbit Pre-Plant Meeting (virtual). All You Need to Know about Downy Mildew on Cucumbers for the 2022 Growing Season, Presented, Clientele Groups, Estimated Attendees: 20, (February 8, 2022)
61. Keinath, A.P. 2020 Watermelon Fungicide Trial Results: Foliar and Fruit Anthracnose and Foliar Gummy Stem Blight. 2021 Watermelon Research and Development Group Annual Meeting. Virtual Meeting, February 2021.
62. Keinath, A.P. 2021. Understanding Root Diseases of Vine Crops. 2021 Mid-Atlantic Fruit & Vegetable Conference. Virtual Meeting, February 2021. https://amr.swoogo.com/mafvc2021/sessions
63. Keinath, A.P. 2021. New seedless watermelon cultivars and Fusarium wilt. CREC Field Day in-field presentation, June 2021. https://news.clemson.edu/clemsons-coastal-rec-research-helps-improve-vegetable-prduction-in-south-carolina/
64. Keinath, A.P. 2021. Seedling date and fungicides to manage cucumber downy mildew. CREC Field Day in-field presentation, June 2021. https://news.clemson.edu/clemsons-coastal-rec-research-helps-improve-vegetable-production-in-south-carolina/
65. Keinath, A.P. 2021. Managing anthracnose and gummy stem blight on watermelon with fungicides in 2021. Southwest Indiana Melon Growers. Virtual Meeting, March 2021. https://ag.purdue.edu/arge/swpap/Documents/Tony.pdf
66. Keinath, A.P. and Silva, F.D. 2021. Economic Impact of Downy Mildew and Fungicide Resistance on Cucumbers. Clemson Hort Team Virtual Cucurbit Meeting, February 2021. https://ensemble.clemson.edu/hapi/v1/contents/permalinks/Nj39MtRo/view
67. Kumar R, Branham S., Wechter W., Kousik C.S. 2024. KASP Marker Development for Powdery Mildew Resistance in Watermelon (Citrullus lanatus) using Bulk Segregant Analysis (BSAseq) and RNAseq. Presented at the Watermelon Research and development Group meeting held in conjunction with Southern Region American Society for Horticultural Science. February 2024, Atlanta, GA.
68. Levi A. 2023. History, Genomic Tools and Enhancing Disease Resistance in Watermelon. Giant Watermelon and Pumpkin Grower Group. March 25th, 2023, Elkin, NC.
69. Levi A. 2023. Genetic research in watermelon. Tour of State agricultural leaders, Senators, Representatives, and Minister of Agriculture from Canada. The U.S. Vegetable Laboratory (USVL), Charleston SC.
70. Levi A. 2022. Presentation to Minister of Agriculture from Qatar. May 11th, 2022.
71. Ling, K.-S. 2022. An integrated approach to prevent emerging viral disease outbreak in greenhouse vegetable production. Canadian Greenhouse Conference, Niagara Fall, Canada, October 5-6, 2022)
72. Ling, K.-S. 2023. Managing the Emerging Cucumber Green Mottle Mosaic Virus on Cucurbit Crops. Emerging viruses in Cucurbits working group meeting, Durham, NC.
73. Mauch KE, Wintermantel WM. 2024. Updates on resources to combat emerging virus threats. the California Melon Research Board Symposium in San Diego, CA (January 11, 2024)
74. Mazourek M, Inzinna G, Fabrizio J, Fenn M. 2023. Peppers and Cucurbits. VBI Field days. Freeville and Ithaca, NY. August 28-29, 2023.
75. Mazourek M, Haga, ER, Jenny P, Mueller, K. 2023. Selecting High-quality Breeding Material. Part of Webinar Series: Practical Training for On-Farm and Collaborative Plant Breeding. Jan 17, 2023.
76. Mazourek M. 2022. Vegetable Breeding Institute Field Days. August 29-20, 2022. Ithaca and Freeville, NY.
77. Mazourek M. 2021. Winter Squash Background, Diversity and Breeding. Winter Squash Sagra. Culinary Breeding Network. January 25, 2021

78. **McGregor, C., Luckew, A., Sari, N., Pandey, S., Lutinya, J., Bag, S., Srinivasan, B., Luiz Biscaia Ribeiro, A., McAvoy, T., Simmons, A. M. & G. Meru (2025) Breeding for resistance to whitefly transmitted viruses (WTVs) in squash and watermelon. Southeast Regional Fruit & Vegetable Conference. Savannah, GA.**
79. McGregor, C. & G. Boyhan (2020) Breeding better Cucurbits. Vegetable & Specialty Crop News, September 2020: 16-17
80. **Meru, G. 2025. Genomic Tools in Vegetable Breeding. ASTA 64TH Vegetable & Flower Seed Conference. Feb. 2 Orlando FL**
81. Meru G. 2021. Progress towards breeding resilient cultivars for Florida. Presented at the Southeast Florida Extension Meeting, held virtually April 8, 2021.
82. Meru G. 2021. Progress towards breeding resilient cultivars for Florida. Presented at the Extension Field Day for Vegetable Growers in Miami-Dade County, held virtually February 18, 2021.
83. **Michel, S. W., Schultheis, J. R., Parker, B. K., and B. E., Stickley. 2025. Pumpkin Cultivar Results from the Upper Mountain Research Station, Laurel Springs, 2023. Virginia Pumpkin Growers Association Meeting, Galax, VA, Jan. 25.**
84. **Michel, S. W., Schultheis, J. R., Keinath, A. P., and L. Quesada-Ocampo. 2024. Evaluating Fungicides and Grafting as Management Practices for Fusarium Wilt of Watermelon in North Carolina. 38th Southeast Vegetable & Fruit Expo, Myrtle Beach, SC, 4 Dec.**
85. **Michel, S. W., Schultheis, J. R., Stickley, B. E., Parker, B. K., and M. C., Allan. 2024. Canary Melons as an Option for NC. 38th Southeast Vegetable & Fruit Expo, Myrtle Beach, SC, 3 Dec.**
86. Michel, S.*, J.R. Schultheis, A.P. Keinath, and L. Quesada-Ocampo. 2024. Management Results of Fusarium Wilt of Watermelon Using Cultivar, Fungicide, and Grafting. Tri-County North Carolina Vegetable Production Meeting, Online, February 2024.
87. Michel, S.*, J.R. Schultheis, A.P. Keinath, A. P., and L. Quesada-Ocampo. 2024. Management Results of Fusarium Wilt of Watermelon Using Cultivar, Fungicide, and Grafting. North Carolina Watermelon Production Meeting, Online, January 2024.
88. Michel, S., Quesada-Ocampo, L., Schultheis, J., and Keinath, A. 2023. Triploid Watermelon Cultigen Responses in a Field Infested with *Fusarium oxysporum* f. sp. *niveum*. 35th Southeast Vegetable & Fruit Expo, Raleigh, NC. 11/29/23
89. Michel, S., L. Quesada-Ocampo, J. Schultheis, and T. Keinath. 2023. Management Results of Fusarium Wilt in Watermelon Using Cultivar, Fungicide, and Grafting. 36th Annual Southeast Vegetable & Fruit EXPO, Watermelon Section. Myrtle Beach, SC., Nov. 27
90. Michel, S., J. Schultheis, A. Keinath, and L. Quesada-Ocampo. Triploid watermelon cultigen responses in a field infested with *Fusarium oxysporum* f sp. *niveum*. North Carolina Vegetable Growers Association Ag Expo. Raleigh, NC, November 29, 2022.
91. Michel S., Quesada-Ocampo, L. M., Schultheis J., and Keinath T. Triploid watermelon cultigen responses in a field infested with *Fusarium oxysporum* f.sp. *niveum*. 35th Annual Southeast Vegetable and Fruit Expo. Durham, NC, December 2022.
92. **Nelson, E. M. and Smart, C. D. 2024. Screening for Phytophthora capsici resistance in commercial and wild eggplant accessions in NY. Cornell Cooperative Extension Agriculture, Food, and Environmental Systems In-Service. Ithaca, NY, November 2024.**
93. Nelson E, Smart CD. 2023. Rain and Hail Insurance Company Tour. Geneva NY July 19, 2023. Phytophthora blight of vegetable crops.
94. Parker, B., S. Michel, B. Stickley, A. Pfefferkorn, and J. Schultheis. 2023 Standard Size and Mini Watermelon Cultivar Study Results 2023. 36th Annual Southeast Vegetable & Fruit EXPO, Watermelon Section. Myrtle Beach, SC., Nov. 27
95. **Prieto Torres, M., Quesada-Ocampo L. M. 2024. Biosurveillance and disease management for**

cucurbit downy mildew (*Pseudoperonospora cubensis*). Pickle Packers International Annual Meeting. Chicago, IL, October 2024.

96. Quesada-Ocampo L. M., Rosado-Rivera Y.I., and Prieto M. 2024. Cucurbit downy mildew management updates. 38th Annual Southeast Vegetable and Fruit Expo. Myrtle Beach, SC, December 2024.

97. Quesada-Ocampo L. M. 2024. Cucurbit downy mildew: pathogen surveillance and disease management. Pickle Packers International Annual Meeting. Chicago, LI, October 2024.

98. Quesada-Ocampo L. M. Vegetable Disease Management. 2024. NC State Extension Horticulture Program Team Statewide Agent Training. Raleigh, NC, August 2024.

99. Quesada-Ocampo L. M., Xiang L., Prieto M., Rosado Y., Collins H., Lorscheider M. New technologies for disease detection in cucurbit crops. NC Legislature field day. Clayton, NC, June 2023

100. Quesada-Ocampo L. M. 2023. Field monitoring of the cucurbit downy mildew pathogen: the next frontier. Pickle Packers International Spring Meeting. Raleigh NC, April 2023**.**

101. Quesada-Ocampo L. M. 2023. Management of watermelon diseases. North Carolina Watermelon Production Meeting. Virtual, February 2023.

102. Quesada-Ocampo L. M., Rosado-Rivera Y.I., and Prieto M. 2022. Management of downy mildew in cucurbit crops. 35th Annual Southeast Vegetable and Fruit Expo. Durham, NC, December 2022.

103. Quesada-Ocampo, L. M. 2021. Pickles in a pickle: trying to outsmart *Pseudoperonospora cubensis*, the cucurbit downy mildew pathogen. North Carolina Vegetable Growers Association Ag Expo. Wilmington, NC, November 2021.

104. Quesada-Ocampo L. M. and Hausbeck M. K. 2021. Pickles in a pickle: trying to outsmart *Pseudoperonospora cubensis*, the cucurbit downy mildew pathogen. Pickle Packers International Spring Meeting. Austin, TX, October 2021.

105. Quesada-Ocampo L. M. 2021. From the field to the lab and back: translational strategies to improve management of cucurbit downy mildew. Agriculture Agri-Food Canada, Ontario, Canada, April 2021.

106. Quesada-Ocampo L.M. 2021. Management of Fusarium wilt and anthracnose in watermelon. NC Watermelon Convention. Virtual meeting, February 2021.

107. Quesada-Ocampo L.M. 2021. Cultural and chemical control options for Phytophthora fruit rot of watermelon. NC Watermelon Convention. Virtual meeting, February 2021.

108. Quesada-Ocampo L.M. 2021. Never a dill moment when managing cucumber downy mildew. 2020 Eastern NC Certified Crop Adviser Training. Virtual Meeting, December 2020.

109. Quesada-Ocampo L.M. 2020. From the field to the lab and back: monitoring fungicide resistance in cucurbit downy mildew. Pickle Packers International Annual Meeting. Virtual Meeting, October 2020.

110. Schultheis, J.R., K. Heagy, and M. Knuth. 2025. Pumpkin Economic Considerations Based on Plant Spacing; Considerations for Standardization of Pumpkin Categories. Virginia Pumpkin Growers Association Meeting, Galax, VA, 25 Jan.

111. Schultheis, J.R.,S.D. Johanningsmeier, and P. Perkins-Veazie. 2025. 2025 Research/Industry Update; Canary Melon a NC Crop Option. New & Emerging Crops Program, Raleigh, NC, 6 Mar.

112. Schultheis, J.R., B.E. Stickley, S.W. Michel, S., B.K. Parker, M.C. Allan, P. Perkins-Veazie. 2024. Canary Melons as an Option for NC. 38th Annual Southeast Vegetable & Fruit EXPO, Myrtle Beach,, SC, Dec. 3. (Abstr.)

113. Schultheis, J.R., B.K. Parker, S.W. Michel, and B.E. Stickley. 2024 Standard and Mini

Sized Watermelon Cultivar Results. 2024. 38th Annual Southeast Vegetable & Fruit EXPO, Myrtle Beach,, SC, 4 Dec.

114. Schultheis, J.R., B.K. Parker, S.W. Michel, and B.E. Stickley. 2024 Standard and Mini Sized Watermelon Cultivar Results. 2024. 38th Annual Southeast Vegetable & Fruit EXPO, Myrtle Beach,, SC, Dec. 4.

115. Schultheis, J.*, A. Pfefferkorn*, S. Michel, B. Stickley, and B. Parker. 2023. New Zucchini Cultivar Options; What About Ideal Melons?; Canary Melons, a Potential New Crop for North Carolina. 36th Annual Southeast Vegetable & Fruit EXPO, Myrtle Beach, SC., Nov. 27. (50 attenders)

116. Schultheis, J.*, K.Heagy, and M. Knuth. 2023. Pumpkin Economic Considerations Based on Plant Spacing; Considerations for Standardization of Pumpkin Categories. 36th Annual Southeast Vegetable & Fruit EXPO, Myrtle Beach, SC., Nov. 27. (30 attenders)

117. Schulthies J. 2023. Watermelon variety trials. Watermelon Production Meeting (virtual).Feb. 17, 2023 (~ 65 in attendance)

118. Schulthies J. 2023. Watermelon cultivar update. Regional Watermelon Grower meeting, Turkey, NC Fe. 13 (~25 in attendance)

119. Schultheis, J., A. Pfefferkorn, S. Michel, B. Stickley, and B. Parker. 2023. New Zucchini Cultivar Options; What About Ideal Melons?; Canary Melons, a Potential New Crop for North Carolina. 36th Annual Southeast Vegetable & Fruit EXPO, 2023 Yearbook. Cucurbit Section. Myrtle Beach, SC., Nov. 27. (abstr.)

120. Schultheis, J., K.Heagy, and M. Knuth. 2023. Pumpkin Economic Considerations Based on Plant Spacing; Considerations for Standardization of Pumpkin Categories. 36th Annual Southeast Vegetable & Fruit EXPO, 2023 Yearbook. Cucurbit Section. Myrtle Beach, SC., Nov. 27. (abstr.)

121. Schultheis, J. and A. Keinath. 2023. Watermelon cultivar incidence and yield response in fields in North and South Carolina containing *Fusarium oxysporum* f. sp. *niveum*. Mar-Del Watermelon Association meeting. Cambridge, MD, February 3, 2023.

122. Schultheis, J. and S. Michel. 2023. Watermelon cultigen yield and quality results, North Carolina, 2022. Mar-Del Watermelon Association meeting. Cambridge, MD, February 3, 2023.

123. Schultheis, J. and S. Michel. 2022. Watermelon cultigen yield and quality results, North Carolina, 2022. North Carolina Vegetable Growers Association Ag Expo. Raleigh, NC, November 29, 2022.

124. Schultheis JR, Quesada-Ocampo L. 2022. Watermelon Cultivar Evaluations in Fields with Minimal or High Levels of Fusarium Wilt; Potential Fusarium Wilt Management Strategies, NC Watermelon Production meeting, Virtual, Feb. 7, https://gates.ces.ncsu.edu/2022/03/2022-watermelon-production-meeting-recording/

125. Schultheis J, Quesada-Ocampo LM, Keinath T. 2021. Watermelon cultivar evaluations with and without Fusarium wilt. North Carolina Vegetable Growers Association Ag Expo. Wilmington, NC, November 2021.

126. Schultheis, J.R. 2021. Hollow heart considerations and pollenizer cultivar comparisons. North Carolina Watermelon Growers Association. Virtual meeting, January, 2021. 65 attendees

127. Schultheis, J. R. and L. Quesada-Ocampo. 2021 Watermelon cultivar evaluations in fields with minimal or high levels of Fusarium wilt: Potential Fusarium wilt management strategies. North Carolina Vegetable Growers Association Ag Expo. Raleigh, NC, December 1 2021.

128. Smart, C. D. 2025. Update on fungicide resistance and disease management in New York. Empire State Vegetable Expo. Geneva, NY, 4 Feb.

129. Smart CD. 2024. Long Island Agricultural Forum. Riverhead NY, January 10, 2024. Vegetable disease management updates. 30 minute talk to 50 growers.

130. Smart CD. 2024. New York State Vegetable Growers Expo. Syracuse NY, January 23, 2024. Strategies to manage Phytophthora in cucurbits. 30 minute talk to 30 growers.

131. Smart, CD. 2023. Western NY vegetable disease discussions – primarily focused on *Phytophthora capsici*. September 20, 2023.

132. Smart, CD. 2023. Monroe County NY vegetable disease discussions – primarily focused on *Phytophthora capsici* September 27, 2023

133. Smart CD. 2023. Master Gardener plant disease talk and discussion. October 4, 2023. 1.5 hour talk to 40 people.

134. Smart CD. 2023. Cornell AgriTech Legislative Tour. October 13, 2023. 30 minute talk and 1 hour tour of greenhouses. 44 people

135. Smart, CD. 2023. NY Capital District vegetable disease discussions – primarily focused on *Phytophthora capsici* October 17, 2023

136. Smart CD. 2023. Hudson Valley vegetable, apple and hemp disease grower discussions. October 19, 2023. 3x1 hour visits to farms, 5 people per farm.

137. Smart CD. 2023. Western NY winter vegetable meeting. Eden, NY. Fungicide resistance, two case studies. 60 minute talk to 46 people.

138. Smart CD. 2023. Hudson Valley vegetable, apple and hemp disease grower discussions. October 19, 2023. 3x1 hour visits to farms, 5 people per farm.

139. Smart C. 2022. Winter Squash Cultivar Evaluations for Resistance to Powdery Mildew. 2022. NY State producers expo.

140. Smart, C.D., 2021. Western NY vegetable twilight meeting. August 3, 2021. *Cucurbit diseases of 2021.* 2 x 1 hour meetings with 30 growers and educators in each.

141. Spafford, J.* and Hausbeck, M. 2024. Using the weather to determine the days between sprays for downy mildew. Annual Meeting of Pickle Packers, Inc., Chicago, IL, 29-31 Oct.

142. Spafford, J.* and Hausbeck, M. 2024. 2024 Spore trapping and fungicide trial results for downy mildew in Michigan. Annual Meeting of Pickle Packers, Inc., Chicago, IL, 29-31 Oct.

143. Tregeagle D. 2023. Economic Outlook for Pickles and Overview of Cucumber Seed Trait Valuation Research. Pickle Packers International Annual Meeting. Raleigh, NC. Apr 20, 2023.

144. Tregeagle D. 2023. Developing a Pickling Cucumber Budget. Southeast Vegetable and Fruit Expo. Myrtle Beach, SC. November 27, 2023.

145. Toporek, S. M., and Keinath, A. P. 2021. Grafting to manage downy mildew on cantaloupe. CREC Field Day in-field presentation, June 2021. https://news.clemson.edu/clemsons-coastal-rec-research-helps-improve-vegetable-production-in-south-carolina/

146. Uebbing M.R. and Hausbeck M.K. 2022. Downy Mildew Update in Pickling Cucumber. Great Lakes Farm, Fruit and Vegetable Expo. Grand Rapids, MI, December 2022.

147. Uebbing M.R. and Hausbeck M. 2022. Using disease forecasters to time fungicide applications to control downy mildew in pickling cucumbers. MSU Pickle & Pepper Research Committee meeting. Grand Rapids, MI, December 2022.

148. Uebbing M.R. and Hausbeck M.K. 2022. Practical and effective strategies to keep downy mildew in check. Pickle Packers International 2022 Annual Meeting. Las Vegas, NV, October 2022.

149. Wechter W, Branham S. 2023. Clemson University Coastal Research and Education Center 2023 Field Day. Exhibited melon lines in the field.

150. Weng Y. 2024. 'Molecular Breeding for Pickling Cucumber Improvement.' An oral presentation at Pickle Packer International (PPI) 2024 Spring meeting (April 17, 2024, Louisville, KY)

151. Weng Y. 2024. 'Genetic and Molecular Insights into the Biotic and Abiotic Stress Tolerances in a Cucumber Leaf Color Mutant.' An oral presentation at Pickle Packer International (PPI) 2024 annual meeting (October 29, 2024, Chicago, IL)

152. Weng Y. 2024. 'The USDA-ARS and UW Madison Cucumber Improvement Program.' Field talk at Hancock Agriculture Research Station (Hancock, Wisconsin, 9/1/2023).

153. Weng Y . 2024. 'Updates on Molecular Mapping of Downy Mildew Resistances in Cucumber.' An outreach talk at Midwest Pickle Association annual meeting (December 10, 2024, Grand Rapids, MI).

154. Weng Y. 2024. 'Accelerate development of disease resistant varieties with molecular breeding in cucumber.' An outreach talk with cucumber industry stakeholders (February 22, 2024, Madison, WI)

155. Weng Y. 2023. 'QTL mapping of downy mildew resistances in cucumber – a update.' An outreach talk with cucumber industry stakeholders (December 20, 2023, online).

156. Weng Y. 2023. 'The USDA-ARS, UW-Madison Cucumber Breeding Program.' A seminar presentation at Tennessee State University, Nashville (October 23, 2023; Nashville, TN).

157. Weng Y. 2023. 'The USDA-ARS and UW Madison Cucumber Improvement Program.' Field talk at Hancock Agriculture Research Station (Hancock, Wisconsin, 9/1/2023).

158. Weng, Y. 2022. Genetic basis of downy mildew resistances in cucumber. Asia Pacific Seed Association. September 2022

159. Weng Y (2022) Development of pickling cucumber inbreds with multiple disease resistances conferred by a novel mutant. Pickle Packers international (PPI) annual meeting (October 19, 2022 Las Vegas, NV)

160. Weng Y. 2022. A cucumber leaf color mutation associated with biotic and abiotic stress tolerance. Pickle Packer International (PPI) annual meeting (Las Vegas, NV, October 19, 2022)

161. Weng Y (2022) Marker-assisted QTL pyramiding for multiple disease resistances in cucumber. Midwest Pickle Association annual meeting (December 6, 2022, Grand Rapids, MI)

162. Weng Y (2021) The Gy14v2.0 cucumber draft genome. Chinese Cucumber Breeders Association 2021 Annual Meeting and Variety Show. April 2021. Virtual.

163. Y, Chen FF, Tan JY (2020) Marker-assisted QTL pyramiding for downy mildew (DM) and phytophthora fruit rot (PFR) resistances in pickling cucumber. Pickle Packers International. Virtual conference, October 2020.

164. **Wintermantel, W.M. California Melon research Board, San Diego, CA, January, 2025. Online presentation to ca. 70 Board members growers and seed company personnel.**

165. Wintermantel WM. 2024. Monitoring the incidence of whitefly-transmitted viruses in melon fields, weeds and alternate crops in the Central Valley and Low Desert production regions. California Melon Research Board Symposium in San Diego, CA (January 11, 2024)

166. Wintermantel WM. 2024. The Emerging Viruses in Cucurbits Working Group and new viruses of concern for U.S. cucurbit production. American Seed Trade Association's 63rd Annual Vegetable & Flower Seed Conference in Monterey, CA (January 26-30, 2024)

167. Wintermantel W. 2022. California Melon research Board, January, 2022. Online presentation to ca. 70 Board members growers and seed company personnel.

168. Wintermantel W. 2022. University of California Extension, Melon and Tomato Crops Meeting, WSREC, Five Points, CA, October 12, 2022. Symptoms and biology of potentially invasive melon viruses.