

National Plant Disease Recovery System (NPDRS)

2020 Research Progress Reports

March 1, 2021

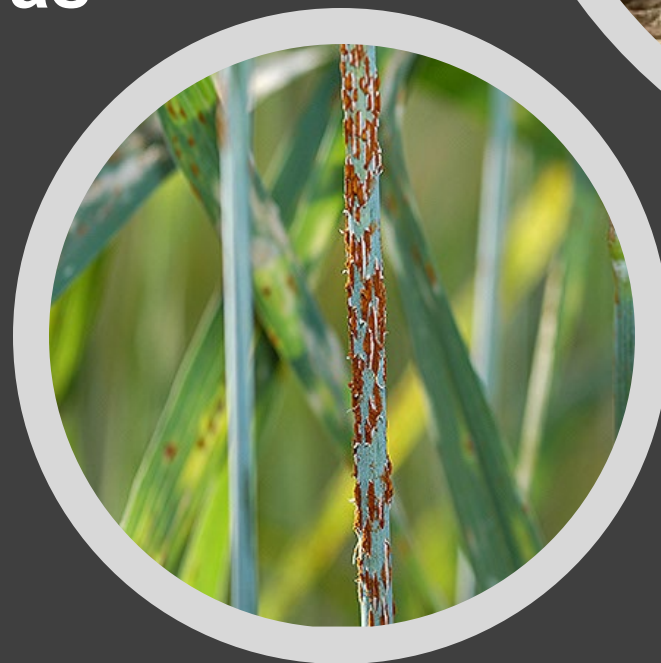
Tim Widmer, USDA-ARS
(tim.widmer@usda.gov)

<https://www.ars.usda.gov/crop-production-and-protection/plant-diseases/docs/npdrs/>



The NPDRS Program

- Called for in Homeland Security Presidential Directive Number 9 (HSPD-9) which was issued in February of 2004
- Oversight by ARS
- Consists of two parts:
 - **Recovery Plans:**
www.ars.usda.gov/crop-production-and-protection/plant-diseases/docs/npdrs/
 - **Research**



Dr. Jo Anne Crouch

Mycology and Nematology Genetic Diversity and Biology Laboratory:

Beltsville, MD

joanne.crouch@usda.gov

Problem: Tools & resources to accurately identify Downy Mildews of cereals/grasses very limited, especially the foreign pathogens**



****The PI has requested a hold on viewing their presentation at this time. If you would like further information, please contact them directly.**

Dr. Christopher Dunlap

Crop Bioprotection Research Laboratory: Peoria, IL
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Novel approaches to controlling laurel wilt and Fusarium dieback in avocados.



Dr. Christopher Dunlap,
Crop Bioprotection Research Unit
National Center for Agricultural Utilization
Research,

In collaboration with our state partners
and local growers



Dr. Daniel Carrillo,
TREC- University of Florida

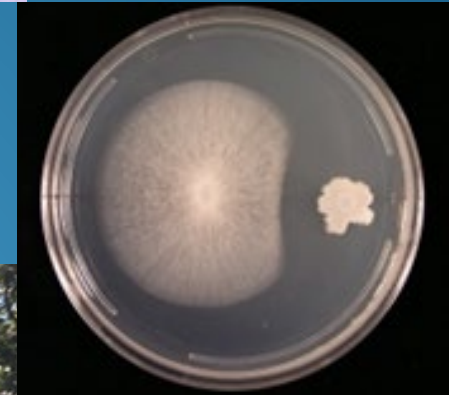


Questions?
Christopher.Dunlap@USDA.gov



Research and Accomplishments

- Evaluated and developed entomopathogens for use against ambrosia beetles, which are now routinely used by growers during phytosanitation procedures.
- Identified antifungal antagonists against the plant pathogens. Identified two new *Paenibacillus* species and *B. velezensis*.
- Developed experimental foam formulations to improve delivery of biocontrol agents to the target.



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BIOCONTROL
Solutions for IPM



Dr. William Rutter

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Developing resources to manage Guava
Root-Knot Nematode
(*Meloidogyne enterolobii*)

William Rutter

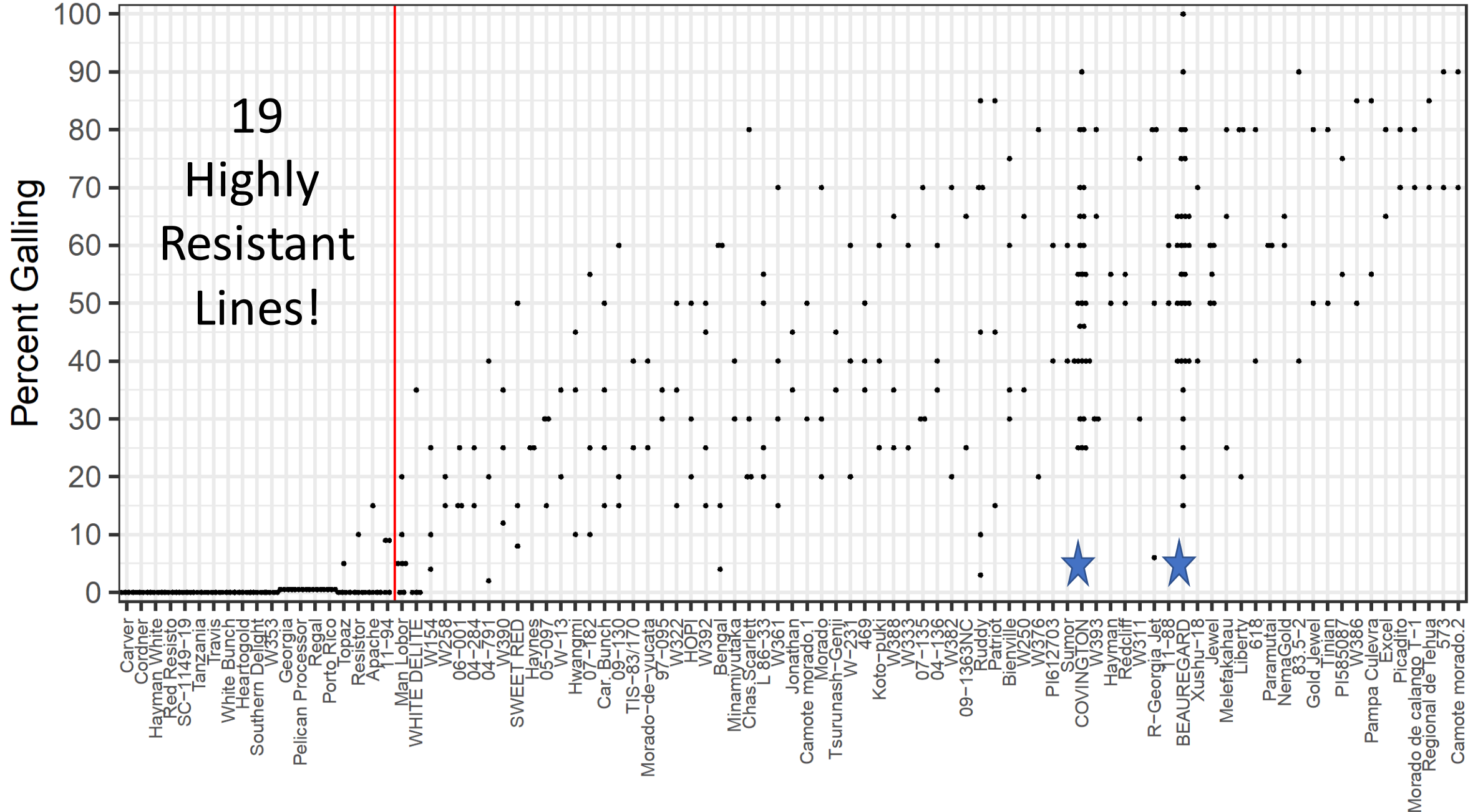
USDA-ARS

Charleston, SC

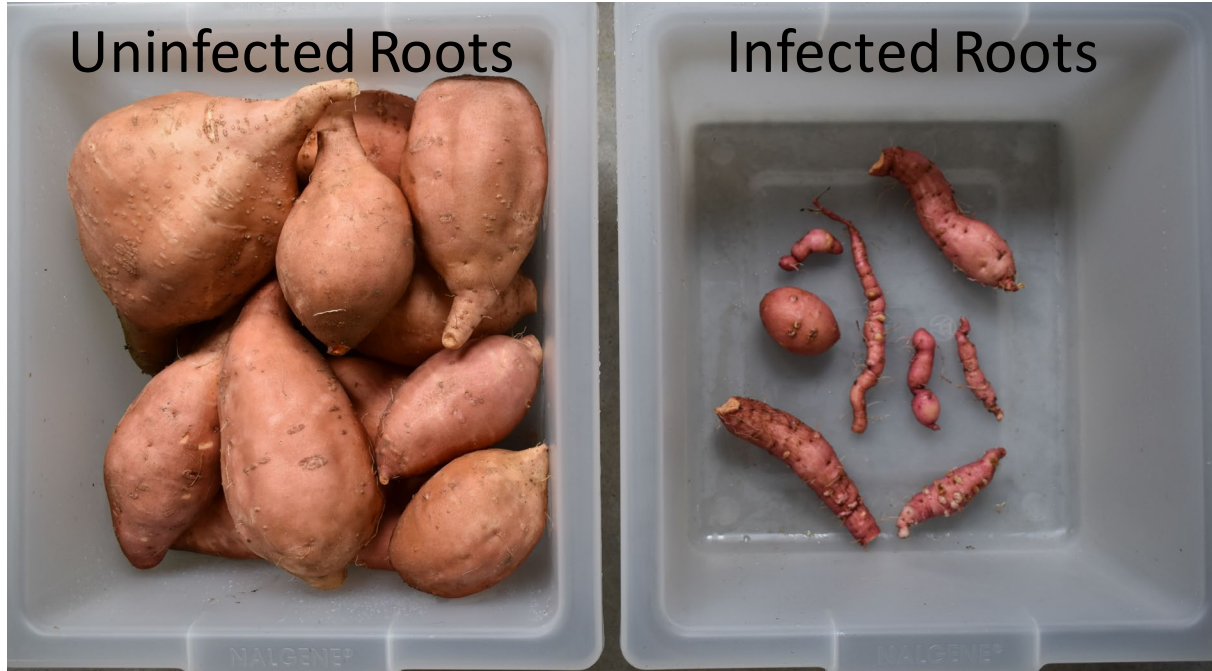
Identifying *M. enterolobii* resistant Sweetpotato



Identifying *M. enterolobii* resistant Sweetpotato



A new Method for Detecting *M. enterolobii* in Sweetpotato

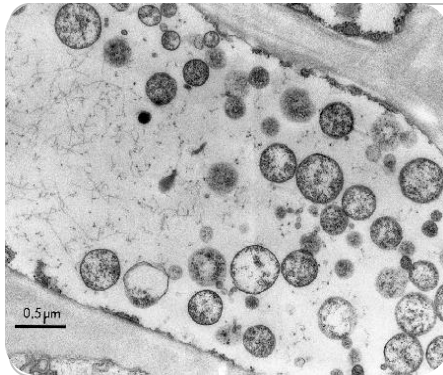


Dr. Yan Zhao and Dr. Wei Wei

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yan.zhao@usda.gov wei.wei@usda.gov



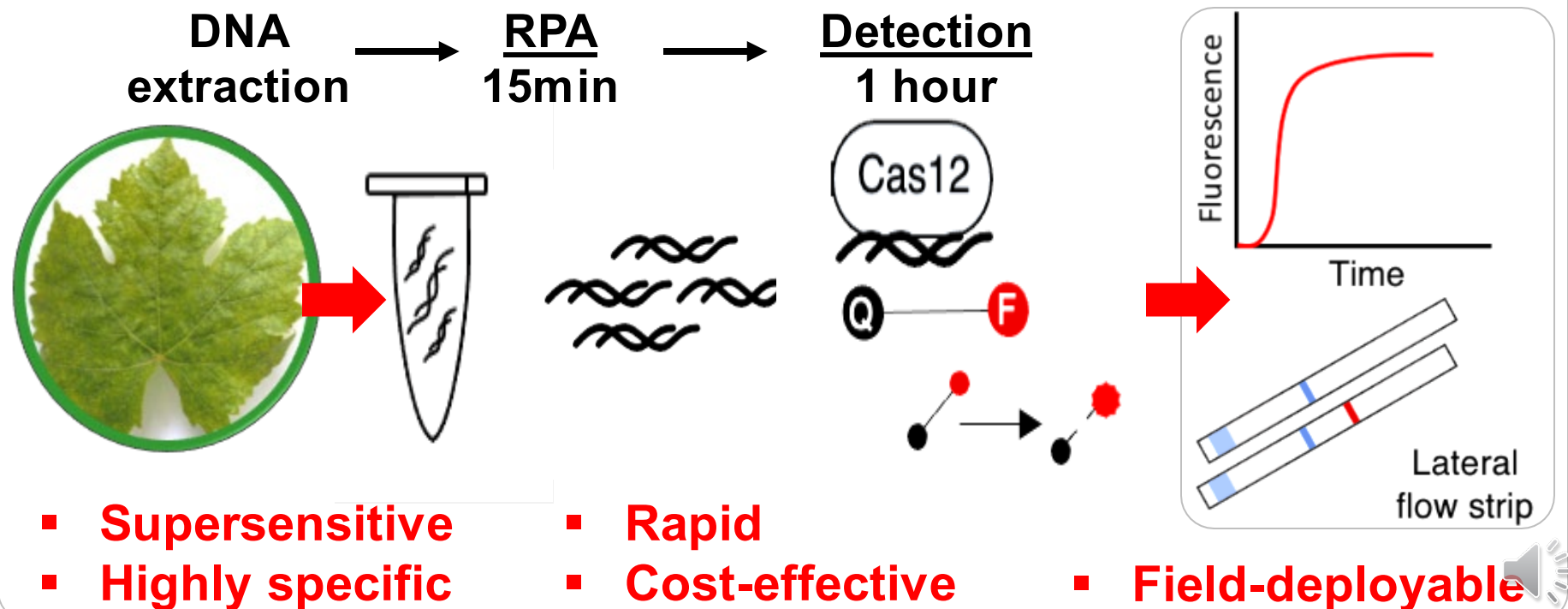
Developing CRISPR/Cas12a-based Technologies for Early Detection of Exotic Phytoplasmas



Phytoplasmas

- Phloem-inhabiting bacteria without a cell wall
- Cause numerous diseases in agricultural crops
- Six species are quarantine pests

CRISPR/Cas12a-based Detection



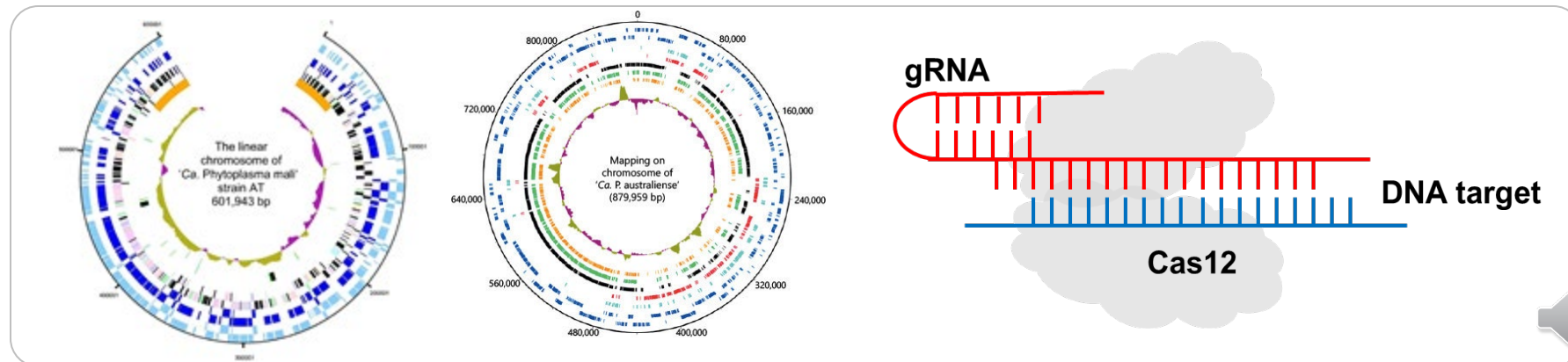
Developing CRISPR/Cas12a-based Technologies for Early Detection of Exotic Phytoplasmas



Apple proliferation disease
caused by '*Ca. Phytoplasma mali*'
(Photo credit: Osler/DBADP, Univ. of Udine, Italy)



Grapevine yellows disease
caused by '*Ca. Phytoplasma solani*'
(Photo credit: Fabio Quaglino, Univ. of Milan, Italy)



Dr. Scott Adkins

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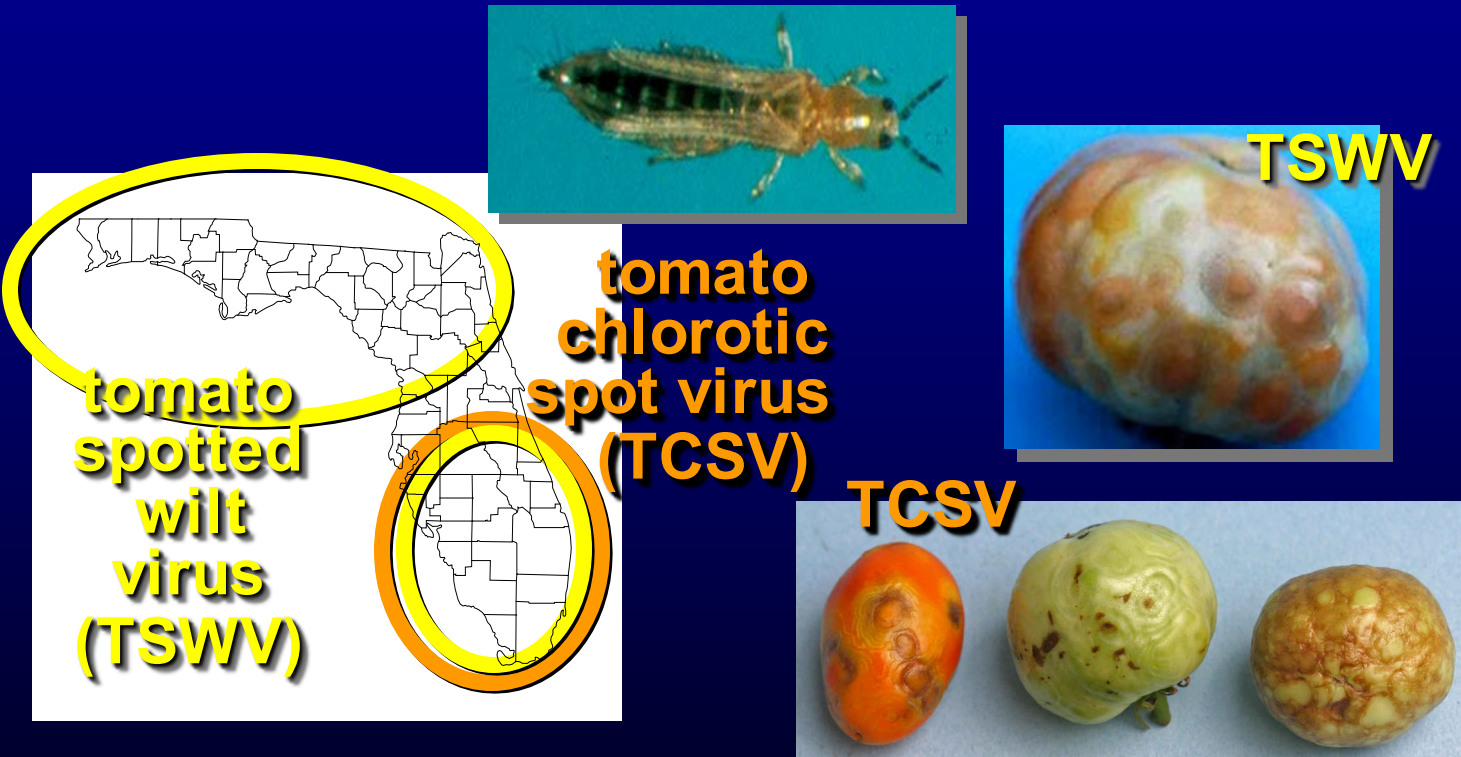


Tomato Resistance-Breaking Tospoviruses

Scott Adkins, USDA-ARS, Fort Pierce, FL

Ozgur Batuman & Salih Yilmaz, UF, SWFREC, Immokalee, FL

Tong Geon Lee & Samuel Hutton, UF, GCREC, Wimauma, FL



TSWV and TCSV management by resistance



TSWV
R gene: - Sw-5 Sw-5

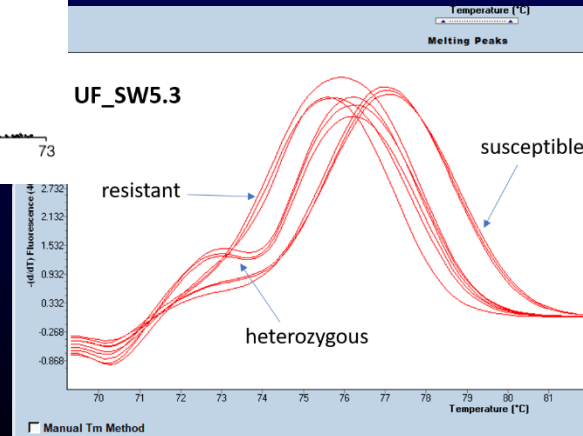
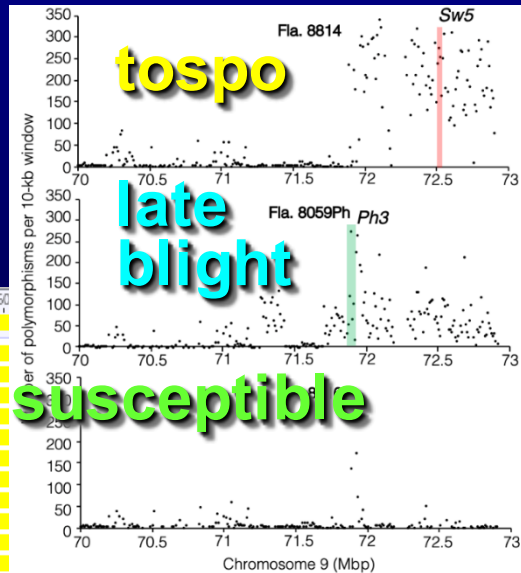
TSWV isolates able to overcome Sw-5 resistance in tomato identified in 2016 for the first time in California



Tomato Resistance-Breaking Tospoviruses

- Planting Sw-5 tomato in Florida and Puerto Rico for TSWV & TCSV:
- 1) Tools/protocols for detecting resistance-breaking TSWV & TCSV
 - 2) Tools/protocols for detecting tomato tospovirus resistance genes
 - 3) Analyze resistant tomato cultivars in Florida and Puerto Rico

TSWV & TCSV sequences are similar



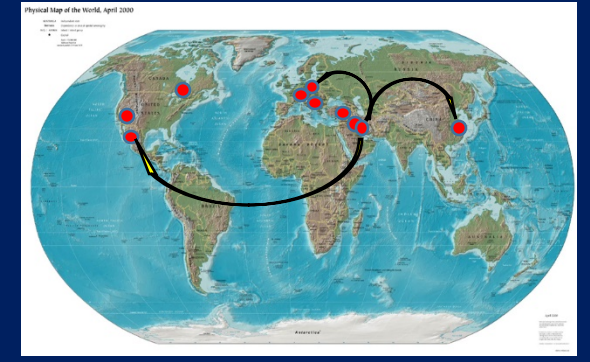
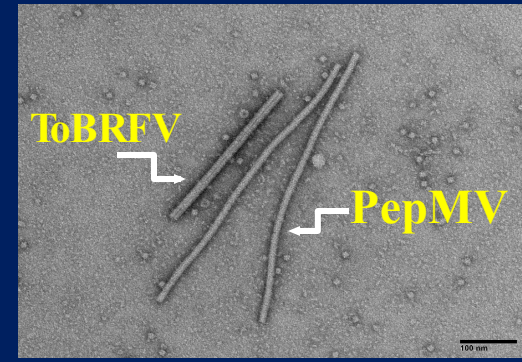
Dr. Kai Ling

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Managing emerging Tomato brown rugose fruit virus through sensitive detection, effective disinfection and improved immunity

-Kai-Shu Ling, USDA-ARS, Charleston, SC-



Objectives:

- To evaluate selected disinfectants for field application and seed treatment.
- To optimize real-time PCR useful for seed health assays.
- To conduct genetic and genomic analysis of novel resistance to ToBRFV in tomato.

Progress and Accomplishments

1. Effective disinfectants identified and recommended to growers.
2. Developed a sensitive Real-time PCR useful for seed health testing.
3. Screened tomato germplasm and identified new sources of resistance to ToBRFV.

Need for research

1. Improving methods of application for effective disinfectants to achieve disease management in tomato productions.
2. Understanding the genetic basis of resistance and molecular marker development.
3. Developing genetic materials that are useful in tomato breeding for resistant to ToBRFV.

Publications:

Chanda, B., Shamimuzzaman, M., Gilliard, A., and Ling, K.-S. 2021. *Virology Journal* 18:7.

Chanda, B., Rivera, Y., Nunziata, S.O., Galvez, M.E., Gilliard, A.C., Ling, K.-S. 2020. *Microbiology Resource Announcements*. 9(29):e00630-20.

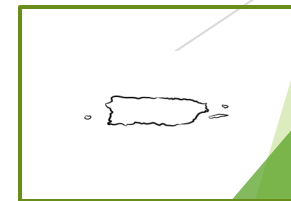
Dr. Bob Jarret

Plant Genetic Resources Conservation Unit: Griffin, GA
bob.jarret@usda.gov

Screening the ARS *Capsicum*
Germplasm Collection for
Tobamoviruses**



**The PI has requested a hold on
viewing their presentation at this time.
If you would like further information,
please contact them directly.



Dr. Ricardo Goenaga

Tropical Crops and Germplasm Research Laboratory: Mayaguez, P.R.
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Highly sensitive qPCR screening of the U.S. cacao germplasm collection in Puerto Rico for presence of the emergent Cacao mild mosaic badnavirus (CaMMV) previously restricted to the Trinidad Gene Bank collection.

INTRODUCTION:

- The NPGS living cacao germplasm collection comprises strategically representative accessions belonging to the 10 genetic cacao groups, and is the only world collection planted in an RCBD.
- During 1943, two virus-like symptom phenotypes were observed for the first time in cacao trees in Trinidad and Tobago and symptoms attributed to two strains of a suspect viral disease, referred to as Trinidad cacao virus (TCV) disease.
- These strains represent two new badnaviruses, named *Cacao mild mosaic virus* (CaMMV) and *Cacao yellow vein banding virus* (CYVBV), making them the first cacao-infecting badnaviruses known in the Western Hemisphere.
- During 2019-2020, symptoms reminiscent of TCV, now known to be associated with CaMMV or CYVBV, were observed in a commercial field in Puerto Rico, and several clones housed in the USDA germplasm collections in Mayaguez and Miami quarantine greenhouse.
- Quantitative PCR (qPCR) and PCR assays that target the viral movement protein (MP) have been developed based on CaMMV and CYVBV sequences (1 genome each), the only available isolates. A SNP genotyping tool has been developed to identify accessions by genetic group affiliation, and genotype analysis of virus-infected trees is underway to aid in identifying germplasm with apparent resistance or tolerance, and potentially, link historical origins of CaMMV with genetic group.

OBJECTIVES:

1. Screen the USDA cacao germplasm collection in Mayaguez, PR, and the cacao quarantine greenhouse in Miami, FL and any symptomatic trees observed in the Trinidad and CATIE-Costa Rica collections for CaMMV/CYVBV using qPCR to determine badnavirus distribution and simultaneously guide replacement of infected clones with uninfected trees, and removal of infected commercial trees;
2. Confirm identity of badnaviral species in representative samples found positive for CaMMV or CYVBV presence by PCR amplification, cloning, and DNA sequencing of MP;
3. Genotype cacao samples using cacao SNPs analysis found to be CaMMV or CYVBV-infected



Highly sensitive qPCR screening of the U.S. cacao germplasm collection in Puerto Rico for presence of the emergent Cacao mild mosaic badnavirus (CaMMV) previously restricted to the Trinidad Gene Bank collection.

RESULTS AND DISCUSSION

1. Screen USDA cacao germplasm collection in Mayaguez, PR, Miami cacao quarantine greenhouse, and Trinidad cacao genebank for CaMMV/CYVBV.
 - a. Amplification with qPCR primers designed to detect CaMMV-Trinidad (only known isolates);
 - b. Positive samples – verified CaMMV by PCR amplification with CaMMV-T original MP primers; **Results:** Phylogenetic analysis revealed not one but three CaMMV clades (**Fig. 1**). **Conclusion:** There is genomic variability among Mayaguez, Brazil and Trinidad CaMMV isolates.
 - c. Re-designed and validated modified MP-PCR primers to account for all CaMMV variants: **Results:** Re-designed primers amplified all CaMMV variants. **Conclusion:** Development of a much more powerful test for CaMMV.
 - d. Re-run Miami & Mayaguez samples again with previously re-design primer combination (to account for false negatives in 1st run). **Results:** Positive detection was greater with new re-designed primer combination. Is the virus endemic? TBD.
 - e. Validation of CYVBV-T with 8 isolates from Trinidad (2020). Primer testing was halted due to budget constraints.
2. In the Quarantine Miami greenhouse: selected samples from plants showing virus-like symptoms were subject to Illumina DNA sequencing and RNAseq: **Results:** No CaMMV /badnavirus detected. In DNA reads, no DNA-virus found; in RNA reads: polerovirus-like sequences detected. Whether representative of a complete polerovirus genome will require further study. New virus??
3. SNP discovery analysis using the raw sequencing data from collection genotypes is pending additional funding. Do cacao genetic groups differ in their susceptibility to badnaviruses?

IMPACT OF DELIVERABLES

- 1) Developed/validated improved qPCR and PCR detection of CaMMV and three groups of variants, are now recognized through this research (**Fig. 2**).
- 2) Development of highly useful assay for virus-indexing and managing USDA cacao germplasm collections.
- 3) Positive impact on improving current regulatory testing capacity to aid APHIS-PPQ decision-making.

Figure 1. Phylogenetic analysis of CaMMV movement protein (MP) resolved three additional groups of clades of the virus, a result that agreed with the results of pairwise distance analysis (see Clades 1-4). Sequences from the current study are highlighted in blue = commercial farms, Puerto Rico, red = USDA germplasm collection, Mayaguez, Puerto Rico, or green = Gene Bank in Trinidad.

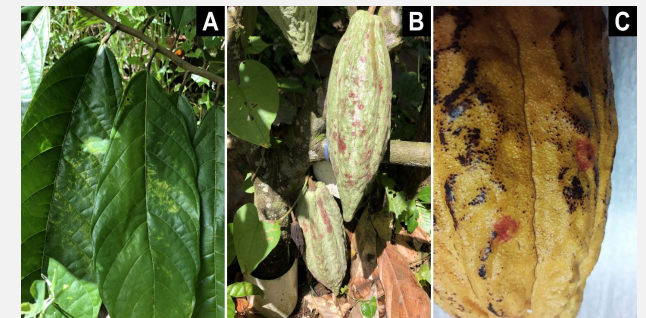
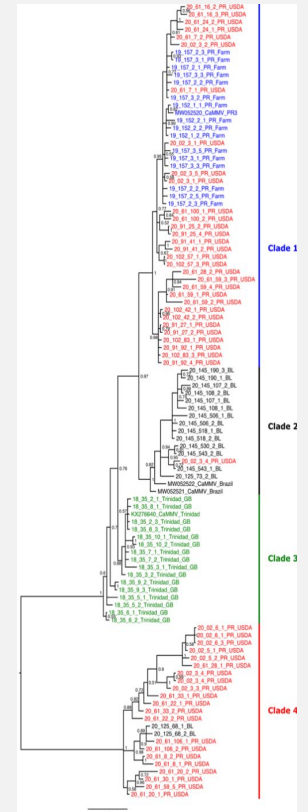


Figure 2. CaMMV-like symptoms in Puerto Rico.

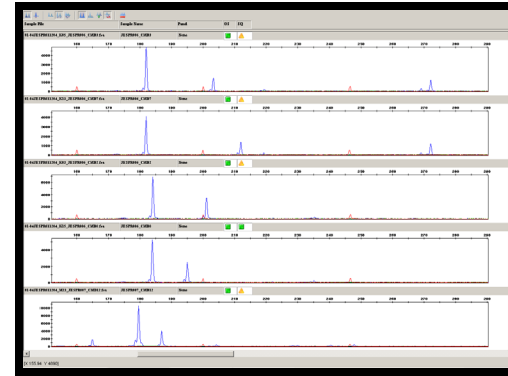
Dr. Jodi Scheffler

Crops Genetics Research Unit: Stoneville, MS

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National and international collaborations to proactively combat threats to U.S. cotton. Partnered with Pakistani scientists to mitigate the effects of **Cotton Leaf Curl Virus (CLCuV) a virus transmitted by whiteflies.**



DNA markers for marker assisted selection. Can breed without having the disease present and can also decrease the number of years for development from ten years to six!

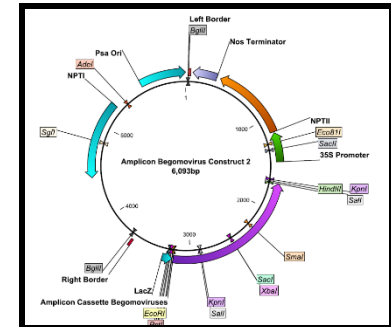
Infected plants (left) and resistant (right)

Created diagnostic tests to detect then identify and track the virus.

Have already used the tests on new viruses found in the U.S., but so far not found.

Developed advanced cotton lines. Provided seed to U.S. public breeders and breeding companies and breeders in China, India, Brazil and Australia. Seed is available on request.

In 2021, more improved resistant elite cotton lines will be available.



Using RNAi, CRISPR and other emerging technologies to develop plants with their own self protection mechanisms.

Emerging Threat **Cotton Leaf Roll Dwarf Virus (CLRDV)**. In 2017, a variant of this virus, which causes Cotton Blue Disease in Brazil, was detected in the U.S. Took advantage of Brazil's experience to get a jump on tackling CLRDV in the U.S.



By 2019 the virus was found in ten states across the cottonbelt.

Cotton Inc. organized a Task Force to tackle CLRDV

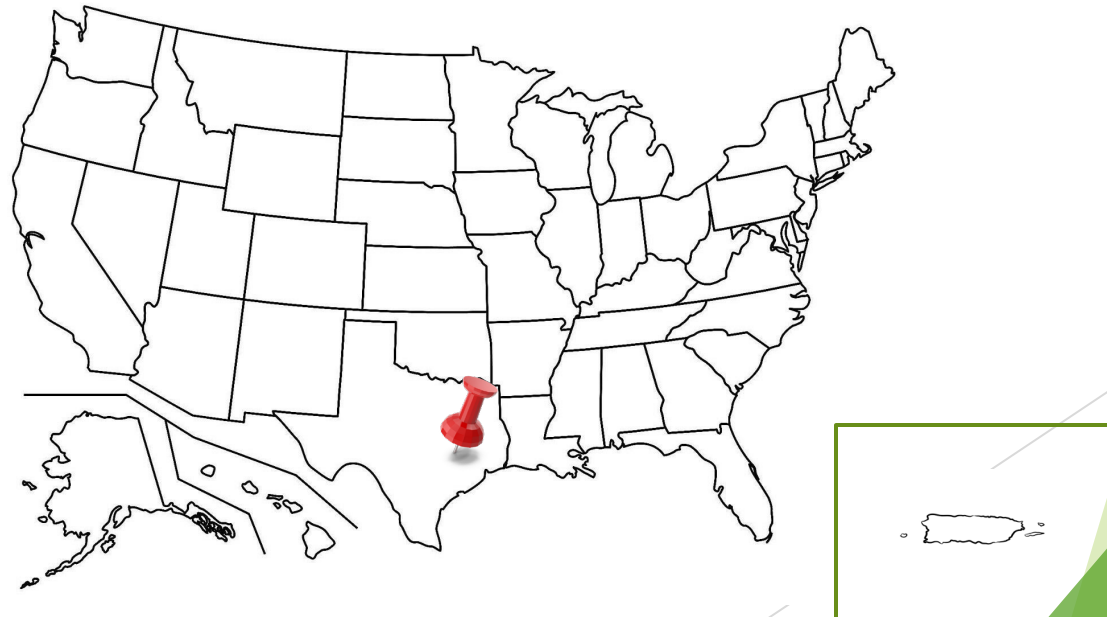
- Research to understand the best ways to mitigate the effects of CLRDV
- Develop cheap and effective diagnostic tests
- Identify resistant cotton germplasm, so far best candidates have come from the USDA Cotton Germplasm Collection and originated in Africa
- Breed resistant cotton varieties

Phylogenetic study of CLRDV samples collected across the cottonbelt, indicates a single main point of origin that spread into other states.



Dr. Joshua Udall

Crop Germplasm Research Unit: College Station, TX
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Resistance to Fusarium wilt Race 4 (FOV4) identified from the U.S. National Cotton Germplasm Collection

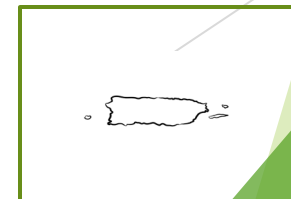
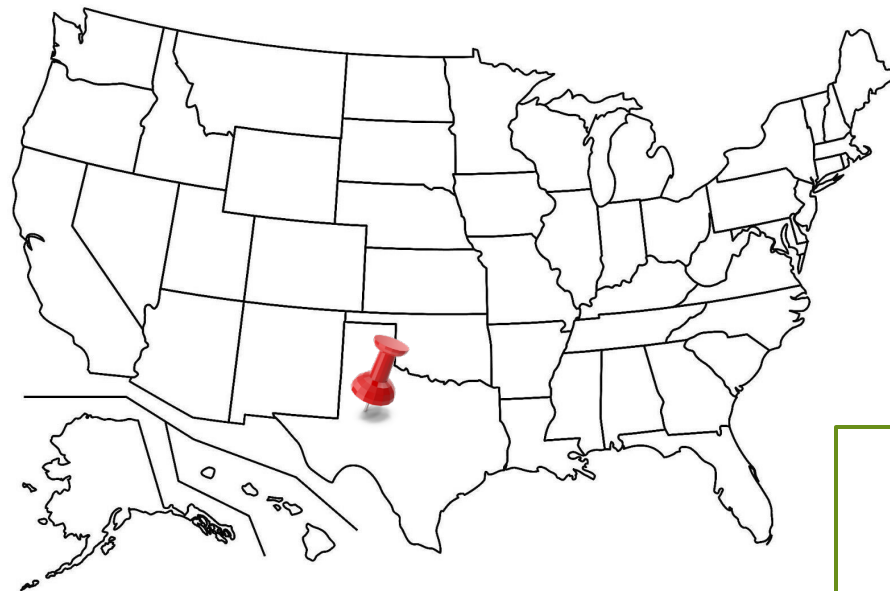


Figure 1. A. FOV4 in San Joaquin Valley (photo credit: Dr. Bob Hutmacher, University of California). B. FOV1 in Georgia (photo credit Dr. Peng Chee, University of Georgia). C. FOV4 in El Paso County Tx (photo credit Dr. Jason Woodward)

- ~10,000 accessions are available in the Collection
- ~2,000 accessions screened by multiple collaborators using differing methods to search for FOV4 tolerance/resistance
- ONE (1) accession identified as tolerant/resistant to FOV4 in highly replicated field studies

Dr. Mauricio Ulloa

Plant Stress and Germplasm Development Research Unit: Lubbock, TX
mauricio.ulloa@usda.gov





Unraveling population shift of *Fusarium* wilt race 4 (FOV4) fungi-strains and their interaction for overcoming tolerance/resistance in cotton

- The Fungus *Fusarium oxysporum* f. sp. *vasinfectum* race 4 (FOV4) adversely impacts cotton production causing plant wilt and death. FOV4 is an inoculum density-dependent disease, and, so far, resistant cultivar is the only management control.

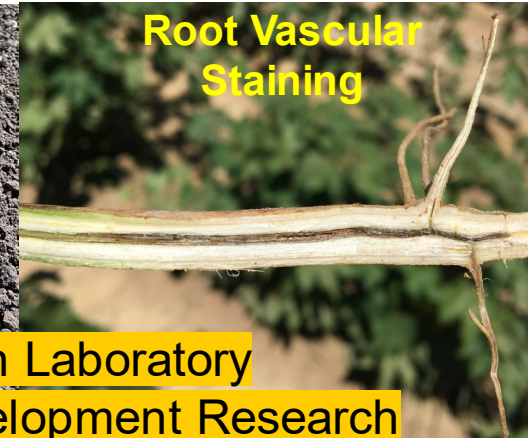
➤ Previous and Ongoing Research

- Identified new sources of FOV4 resistance in Upland and Pima cotton
- Developed new Upland and Pima cotton progeny or breeding lines with high resistance to FOV4.
- Publicly release Upland and Pima germplasm lines with high resistance to FOV4.
- Preliminary characterization of current *Fusarium oxysporum* f. sp. *vasinfectum* isolates from cotton in the San Joaquin Valley of California and El Paso Texas Valley.

Seedling Mortality



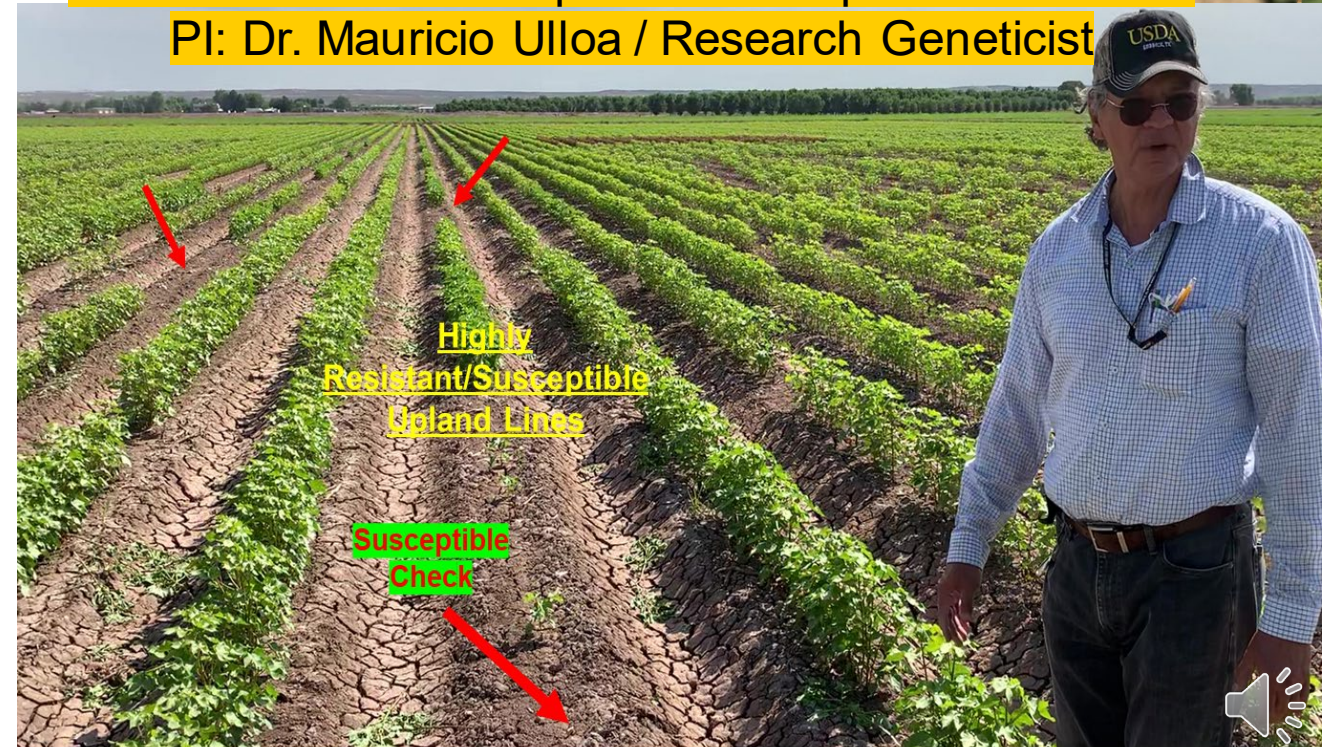
Root Vascular Staining



Cropping System Research Laboratory

Plant Stress and Germplasm Development Research

PI: Dr. Mauricio Ulloa / Research Geneticist



➤ **With the support of the NPDRS program, we are going to further identify and characterize emerging devastating *Fusarium* strains in different soil types and infected cotton plants from evaluation sites in California and Texas**

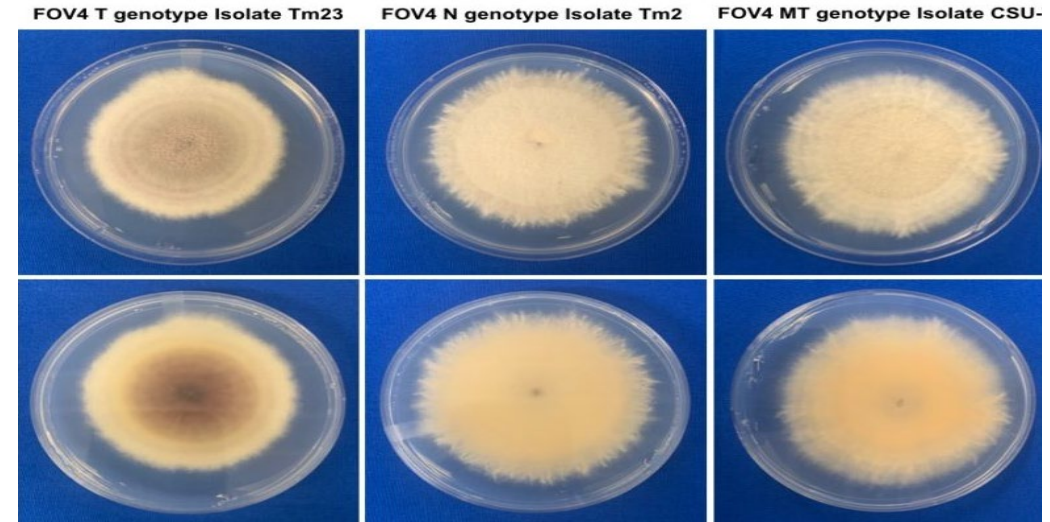
➤ So far, a preliminary FOV molecular characterization study identified diversity/variability within FOV4 strains and confirmed the presence of two (T and N) strains of FOV4 (VCG 0014i) in California cotton fields and possibly population shift in some fields due to selective pressure towards the N strains

➤ Seedling assays to assess pathogen infection reveals differences in isolate's virulence or aggressiveness and the complexity of FOV4, wilt disease and plant resistance mechanisms.

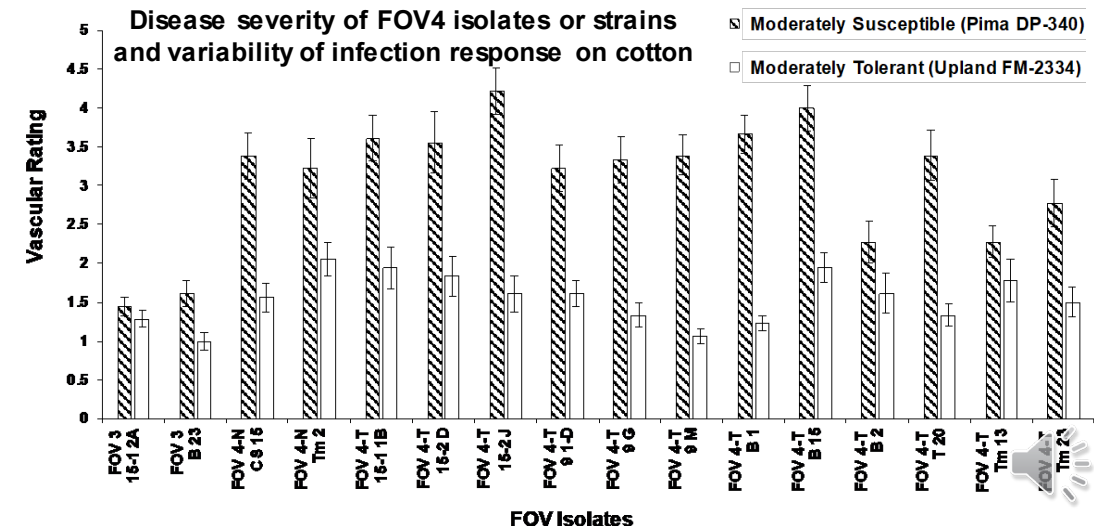
➤ Overall, results from this and previous studies suggest that the FOV4 populations identified to date in far-west Texas vary from those found in California.

➤ **DNA sequencing or blueprint-information generated from this project will help us to identify and distinguish these new FOV4 variants and to develop new diagnostic tools and assays for Soil FOV Quantification and Breeding Resistant Varieties.**

Simple variability can be observed on growth and pigmentation when fungus grows on media

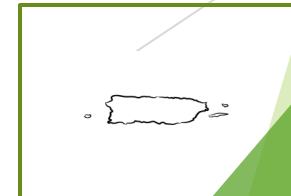


Diaz, J., Garcia, J., Lara, C., Hutmacher, R. B., Ulloa, M., Nichols, R. L., Ellis M. L. 2020. Characterization of current *Fusarium oxysporum* f. sp. *vasinfectum* isolates from cotton in the San Joaquin Valley of California and Lower Valley El Paso Texas. Plant Disease Journal. <https://doi.org/10.1094/PDIS-05-20-1038-RE>



Dr. Glen Hartman

Soybean/Maize Germplasm, Pathology, and Genetics Research Unit: Urbana, IL
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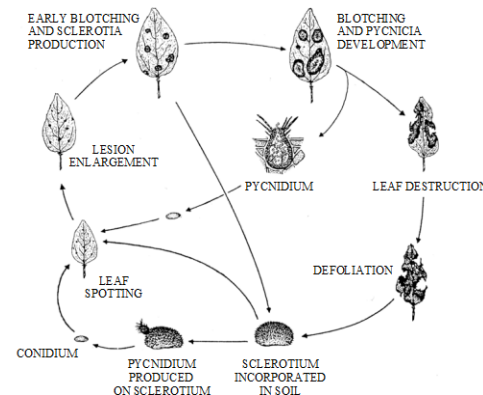
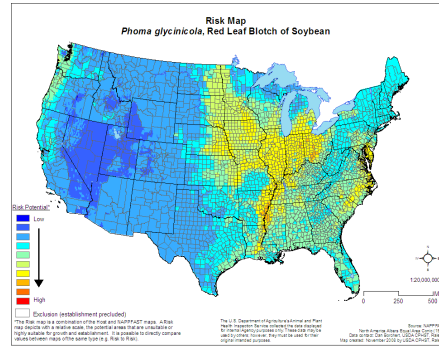
An Exotic Foliar Fungal Disease - Red Leaf Blotch of Soybean

Background

- The disease occurs only in Sub-Saharan African countries on soybean and a native legume plant, *Neonotonia wightii*
- Based on the APHIS Recovery Plan developed in 2009, distribution in the USA if introduced could become widespread from the south to the northern areas of production

Symptoms and signs

- Leaf lesions are most noticeable (lesions on petioles, pods, and stems also occur; not known to be seed borne)
- Lesions progress from small red-brown spots to larger leaf blotches
- Older lesions contain fungal structures including sclerotia (survival structures) and pycnidia (spore-producing structures)



Issues/problems

- Yield losses of 50% reported in several African countries
- With more recent information about the disease and conducive epidemic environments, the potential risk to soybeans in the USA needs updating even though there is a lack of detailed research on distribution, spread, fungal variability, and management in Africa

Disease management

- Fungicides may be effective for controlling RLB, but questions about efficacy, application timing, and registrations remain unknown
- Biological and cultural management may aid in alleviating disease pressure, but research in this area is lacking



Evaluation of Soybean Genotypes for Resistance to RLB

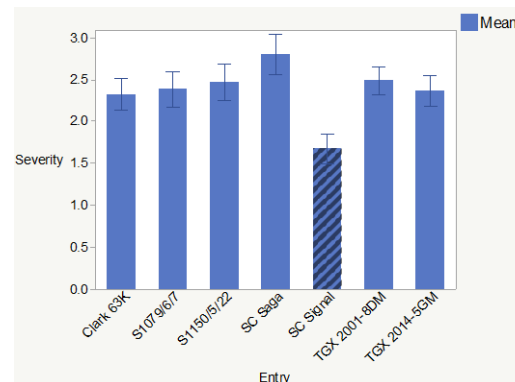
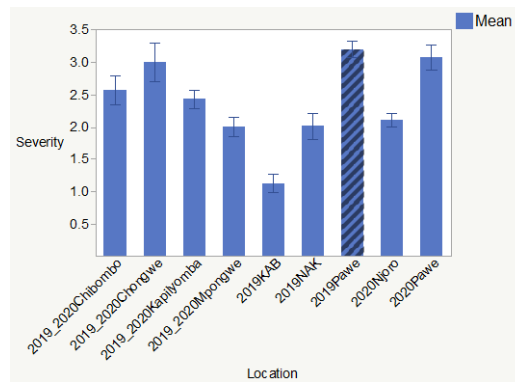
- Until now, there has been little concerted effort to evaluate soybean genotypes for resistance to RLB
- One report screened soybean germplasm in the USA (ARS Foreign Disease-Weed Science Research Unit) and concluded that all 23 soybean genotypes tested (representing 90% of the genes present in public U.S. materials) were susceptible

Research Objective

- Evaluate red leaf blotch resistance in the field in breeding lines and cultivars developed in Africa

Acknowledgements

- ARS - National Plant Disease Recovery System
- Soybean Innovation Laboratory (SIL)
- Field cooperators with SIL



Materials and Methods

- Nine locations were evaluated for RLB resistance in the Pan African Trials (PAT); the PAT is part of a USAID Feed the Future Initiative funded project to the Soybean Innovation Lab
- A total of 69 entries were evaluated; all locations had a minimum of 30 entries
- Seven entries were common among locations

Summary

- Disease severity differed by local and entry
- Top bar graph shows Uganda with the lowest level of disease; Ethiopia with the highest
- Lower bar graph shows cultivar SC Signal with the lowest severity (commercially available cultivar developed in Zimbabwe)
- Our mandate is to continue to screen more germplasm to find sources of resistance that are more complete



Dr. Shuxian (Susan) Li

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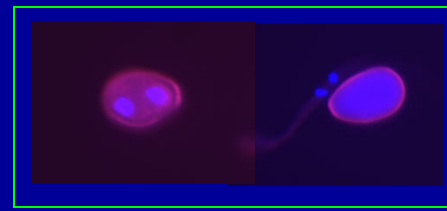
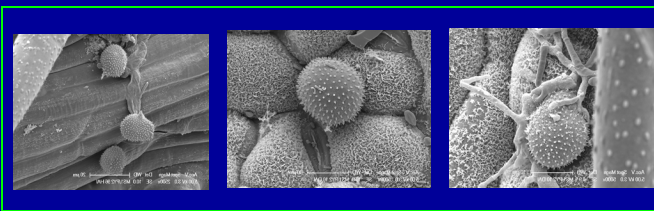
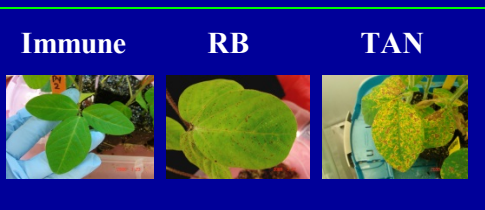
Recovery and Preservation of *Phakopsora pachyrhizi* Collection from Southern US: Meeting the Needs for Soybean Rust Research

Shuxian Li

USDA, ARS, Crop Genetics Research Unit
Stoneville, Mississippi 38776, USA



- Soybean rust (SBR) is one of the most economically important soybean foliar diseases caused by the fungal pathogen *Phakopsora pachyrhizi*.
- Yield losses from 13% to 90% due to SBR have been reported.
- SBR has the potential to cause major economic damage to U.S. soybean production.
- The causal agent has a broad host range, an airborne nature, and diverse and complex virulence pattern.
- Developing soybean cultivars with resistance to different isolates of *P. pachyrhizi* are needed to combat the emerging potential threat of soybean rust in the U.S.



[shuxian.li @usda.gov](mailto:shuxian.li@usda.gov)

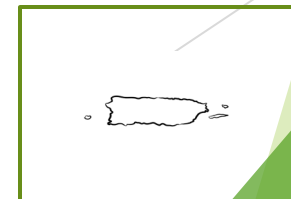
- Collections of plant pathogens are crucial for phytopathological research and breeding for host resistance to diseases.
- **Objective for phase I research:** Recover stored *P. pachyrhizi* isolates
- **Accomplishments during the pandemic in 2020:**
 - Fifteen isolates were recovered using the heat-shock method (Bonde et al. (2006) or Tween-water soaking technique.
 - Isolate MS 06-1 was used to identify the *Rpp6* gene in 2012.
 - A Florida isolate was reported to defeat *Rpp 1* and *Rpp6* genes previously.
- **Ongoing research:**
 - Confirm the pathogenicity of recovered isolates by inoculating a panel of differentials with known resistance (*Rpp*) genes and susceptible plants.
 - Set up long-term storage.



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Dr. Kelly Chamberlin

Wheat, Peanut, and Other Field Crops Research Unit: Stillwater, OK
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Breeding for Resistance to Peanut Smut

- **What is peanut smut?**

- Fungal disease of peanuts
- No above ground symptoms; Nuts (seed) replaced with fungal spores
- No control method; Highly dispersive and easily spread
- Not found outside of Argentina and Brazil

- **Why are we worried about peanut smut?**

- 100% incidence in Argentina, up to 50% yield loss
- Threat to global peanut production (\$47 B in 2020) and thus U.S. peanut production (\$1.13 B in 2019)
- U.S. stakeholder requested action

- **What is the plan?**

- USDAARS scientists are working with INTA, Argentina scientists to:
 - Identify sources of smut resistance through screening
 - Incorporate smut resistance into peanut for the U.S.
 - Identify and deploy markers for selecting resistance
 - Develop high-throughput methods for phenotyping and detection
 - Determine the variability of pathogen population



Accomplishments to Date:

- Identified 13 sources with near immunity over 3 years of phenotyping U.S. germplasm in Argentina
- Conducting crosses to incorporate smut resistance into cultivars for production in the U.S.
- Advancing breeding populations for resistance screening and cultivar development
- Resistance marker development nearly complete

- **Impact**
 - **Protection of the U.S. peanut crop, valued at \$1.13 B in 2019**
 - **Resistant germplasm available to peanut breeding programs**
 - **Molecular markers for use in peanut breeding programs**



Dr. Shyam Tallury

Plant Genetic Resources Conservation Unit: Griffin, GA
shyam.tallury@usda.gov

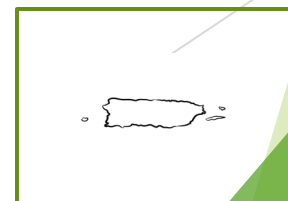
Development and validation of
a molecular diagnostic assay
for the detection of peanut
clump virus (PCV) and Indian
peanut clump virus (IPCV)**



**The PI has requested a hold on
viewing their presentation at this time.
If you would like further information,
please contact them directly.

Dr. Shahryar Kianian

Cereal Disease Lab: St. Paul, MN
shahryar.kianian@usda.gov



Understanding and combating increased virulence to oat crown rust (*Puccinia coronate* f. sp. *avenae*)

Shahryar F. Kianian

USDA-ARS Cereal Disease Lab



- ✓ Oat crown rust is the most widespread and damaging disease of oat worldwide.
- ✓ Moderate to severe epidemics can reduce grain yield by 10 to 40%.
- ✓ In 2014 yield losses due to this disease in Minnesota was reported at 50% and in South Dakota as 35.

Oat crown rust isolates are becoming substantially more virulent

“Resistance is futile”?

- 100+ seedling resistance genes identified in oat
- 3 years effective lifespan
- innumerable races
- Low apparent fitness cost to virulence
- No negative associations between virulences
- Abundant sexual recombination on common buckthorn

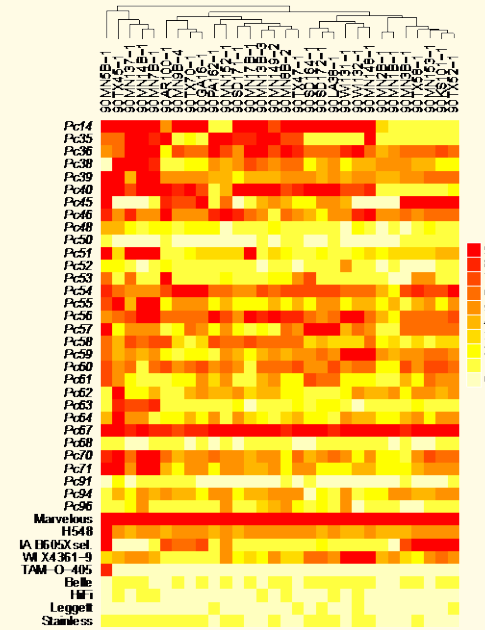
Entry 191- BT1021-1-1 X O/CI1712-5-131



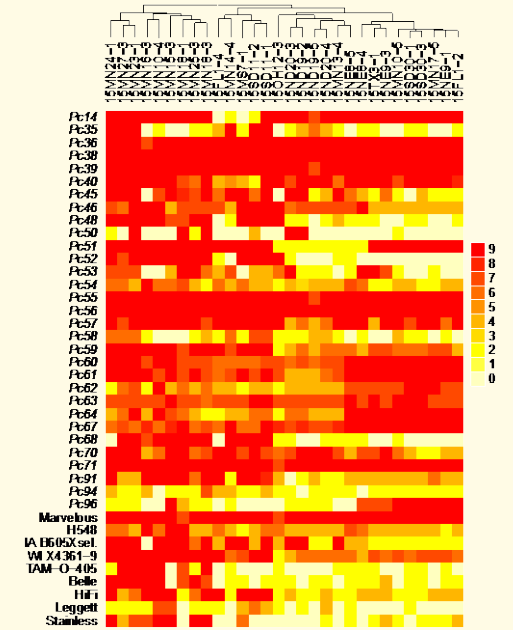
Entry 147- BT1020-1-1 X O/CI8000-4-66



1990 *Pca* Isolates



2015 *Pca* Isolates



Dr. Les Szabo

Cereal Disease Lab: St. Paul, MN
les.szabo@usda.gov



Genotyping of Critical Wheat Stem Rust Pathogen Stains.

Les J. Szabo, St. Paul, MN

- Wheat Stem Rust
 - Historically the most devastating disease of wheat.
 - Caused by the fungal pathogen *Puccinia graminis*.
 - Recently re-emerged as serious threat to wheat production in Africa, Western Asia and Southern Europe.
 - Ug99 race group (Africa)
 - TKTTF race group
 - TTRTF race group
 - These new strains of *P. graminis* are a threat wheat production in the U.S.



Infected wheat field in Kenya

Genotyping of Critical Wheat Stem Rust Pathogen Stains.

Les J. Szabo, St. Paul, MN

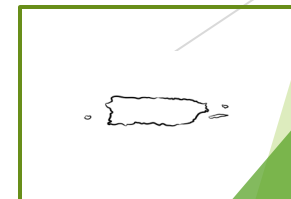
- Objective: Develop genotyping tools and characterize U.S. and global population.
 - Developed high-throughput SNP chips.
 - Genotyped over 2,500 samples.
 - Defined the major genetic groups in the U.S. and global populations.
- Objective: Develop rapid molecular diagnostic tools.
 - Developed rapid molecular assays for the U.S. and global populations.
 - Assays are being used as part of an international surveillance program for wheat stem rust pathogen.



Isolate	RACE	Clade	MLG	Pgt Core SNP Markers																
				A101	A105	A106	A107	A109	A111	A119	A121	A126	A127	A128	A129	A130	A131	A133	A134	A135
				C/A	C/T	T/G	T/C	G/C	A/G	T/C	A/G	G/A	G/A	C/G	T/C	G/A	G/T	C/A	C/T	
04GE0156/704	TRTSE	I	04-AB1	CA	CT	TG	TC	GC	AG	CC	AG	GA	AA	CG	CC	TC	GA	GT	CA	TT
09N1108-3	JRCXC	II	09-AB2	CA	CC	GG	CC	GC	GG	CC	AG	AA	AA	CG	CC	TC	GG	GT	CA	TT
06TE0354-1	TKTTF	III-A	06-AB3	CA	TT	TG	TC	GC	GG	TC	AA	GA	GA	GG	TC	TC	GA	TT	CA	TT
14GE0189-1	TRTTF	III-B	04-AB4	CA	CT	TG	CC	CC	GG	CC	AA	AA	AA	CG	CC	TC	GG	GG	CA	TT
13GE1113-1	TKTTF	III-A.1	04-AB5	CC	CC	TT	TT	GG	GG	TC	AG	GA	AA	GG	TC	TT	GG	GG	CC	CT
13GE1027-3	TKTTF	III-A.2	04-AB6	CA	CT	TG	TC	GC	GG	TC	GG	GG	GA	CC	TT	TT	GG	GG	CC	CT
14GE1104-1	TKTTF	III-B	04-AB7	AA	CT	TG	TC	CC	AA	TT	AG	GA	GA	GG	TC	TT	GG	GG	CC	CT
13GE1026-1	PKPTF	III-C	04-AB8	CA	CT	TG	TC	GC	AG	TT	AG	GG	AA	CG	TC	TT	GA	GG	CC	CC
13GE1021-1	TKTTF	IV-D	04-AB9	CA	CT	TG	TC	GC	AG	TC	AG	GA	GA	CG	TC	TT	GA	GT	CA	CT
13GE1016-5	TRTTF	III-C.1	04-AB10	AA	CC	TT	TC	CC	AG	TC	AA	GA	GA	GG	TC	GA	GG	CC	CT	CT
13GE1029-1	TRTTF	III-C.2	04-AB11	AA	CT	TG	TC	CC	AG	TC	AA	GA	AA	CG	CC	TC	AA	GG	CA	CT
14GE0189-1	TRTTF	III-F	04-AB14	CC	CT	TG	TC	CC	GG	TC	AG	GA	AA	CG	TC	TC	GA	GG	CC	CT
13GE1024-1	TRTTF	III-A	04-AB17	AA	TT	TG	CC	CC	AA	CC	AG	GG	AA	GG	CC	TC	GG	GT	CA	CT
13GE0152-2	TRTTF	III-B	04-AB18	CA	TT	TT	CC	CC	AG	TC	AG	GA	AA	CG	TC	TC	CA	GG	CC	CT
680317a	HFLG	III-A	04-AB15	CA	TT	TG	CC	CC	GG	CC	AA	GA	AA	GG	TC	TC	AA	TT	AA	TT
2700102A	RCRS	III-B	04-AB16	AA	CT	GG	TC	CC	GG	CC	AG	AA	AA	GG	CC	CC	CA	GA	TT	AA
910540a	TRCS	III-C	04-AB17A	AA	TT	GG	CC	CC	GG	CC	AA	AA	GA	GG	CC	CC	AA	TT	AA	TT

Dr. Bob Bowden

Hard Winter Wheat Genetics Research Unit: Manhattan, KS
robert.Bowden@usda.gov



Breeding Resistant Wheat Varieties to Stem Rust Using Marker-Assisted Selection

Robert Bowden and Mary Guttieri, USDA-ARS, Manhattan, KS
Amir Ibrahim, Texas A&M University, College Station, TX



Summary of Problem: Wheat crops in the US are threatened by new exotic virulent races of stem rust, such as the Ug99 group. New durably resistant germplasm is needed that also has elite agronomic characteristics.

Research Objectives:

1. Determine rust resistance reactions to stem rust, stripe rust, and leaf rust diseases for advanced breeding lines in the Southern Plains at the Castroville, TX hot-spot for wheat rusts.
2. Develop high-yielding, high-quality winter wheat germplasm lines adapted to the Great Plains region with durable resistance to stem rust, stripe rust, and leaf rust diseases.

Relevance of the Objectives to NPDRS Program Priorities

Wheat is the most widely grown crop in the Great Plains region. New races of all three rust species threaten the sustainable production of wheat crops. Durably resistant varieties are within reach through cooperation of USDA-ARS, Texas A&M University, and others.



PROGRESS REPORT

Castroville Screening Nursery, 2021



Lines Screened

- Winter Wheat: 16,334
- Spring Wheat: 2,421
- Oats: 1,548
- Barley : 114

Germplasm Development



Durable, Quantitative Resistance Breeding

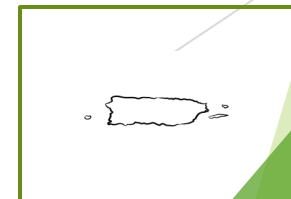
- Four lines with durable SR resistance from 'Kingbird'
- *Sr2, Sr9b, Sr12, Sr57, Sr58*

Gene Pyramid Breeding

- Elite backgrounds: TAM114, TAM205, TX13M5625, Smith's Gold, Showdown, KS090387K-20
- *Sr22, Sr26, Sr35, Sr38, Sr57, Sr58*

Dr. David Marshall

Plant Science Research Unit: Raleigh, NC
david.marshall@usda.gov



Stacking Ug99 Stem Rust Resistance with Other Resistances in Wheat – David Marshall, Raleigh, NC

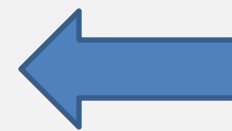
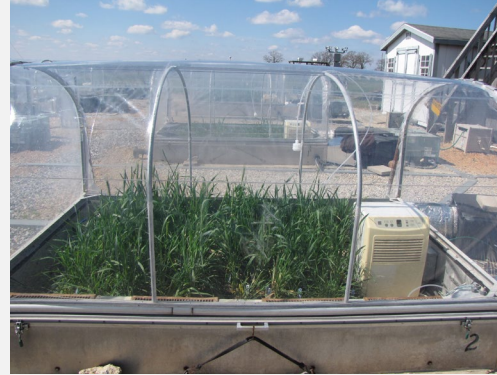
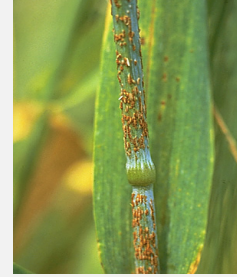
IMPORTANCE:

Rusts and other wheat diseases are global problems.

Genetic resistance is the most cost-effective disease management for farmers.

KEY OBJECTIVES:

- Identify effective, long-lasting resistance to three wheat rusts.
- Combine those resistances with resistance to powdery mildew and Fusarium head blight.
- Breed those combined resistances into diverse wheat backgrounds and market classes.



RESULTS

APPROACH:

- National & International
- Controlled screening
- Molecular markers
- Phenotyping & genotyping
- Breeding & selection

Dr. Matthew Rouse

Cereal Disease Lab: St. Paul, MN
matthew.rouse@usda.gov



Rouse: Wheat resistance to Ug99

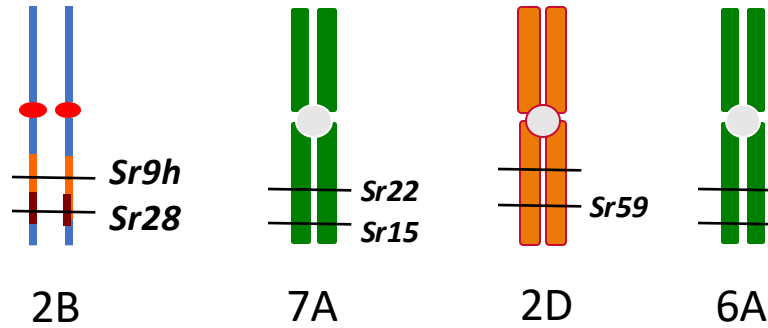
2007 Ug99 Resistance Loci

- 19 resistance genes,
- 5 with markers

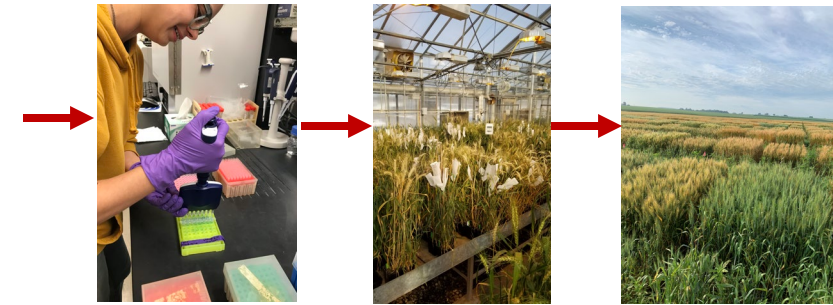
2020 Ug99 Resistance Loci

- 43 resistance genes
- 39 with markers

Linkage Blocks of Ug99 resistance genes



- | | | | |
|-------------|-----------|-----------|-----------|
| • Linkert | • Linkert | • 7 lines | • 6 lines |
| • Bolles | • Lang-MN | • UMN | • UMN |
| • Advance | • Prevail | • SDSU | • SDSU |
| • Forefront | | | • NDSU |



- Marker-assisted backcrossing
- BC₄-derived fixed +/- lines
- Yield trials in collaboration with breeders

Field Screening of Spring Wheat and Barley in Africa

Impact

- 1500+ spring wheat lines
- 200+ spring barley lines
- 7 US universities
- 4 private companies
- Recent resistant varieties 'MN-Torgy', 'SY-Longmire'



UMN variety 'Linkert' with Ug99 resistance – 833,900 acres in Minnesota and North Dakota in 2018



Dr. Yue Jin

Cereal Disease Lab: St. Paul, MN
yue.jin@usda.gov



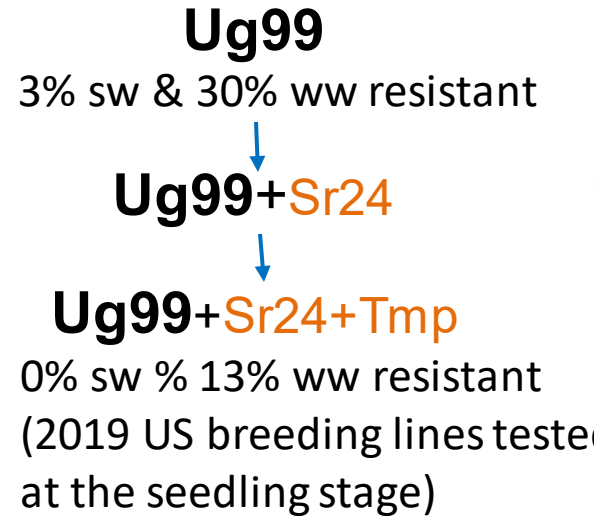
Stem rust surveillance to monitor Ug99 and other significant virulence

Y. Jin, USDA-ARS Cereal Disease Lab, St. Paul, MN

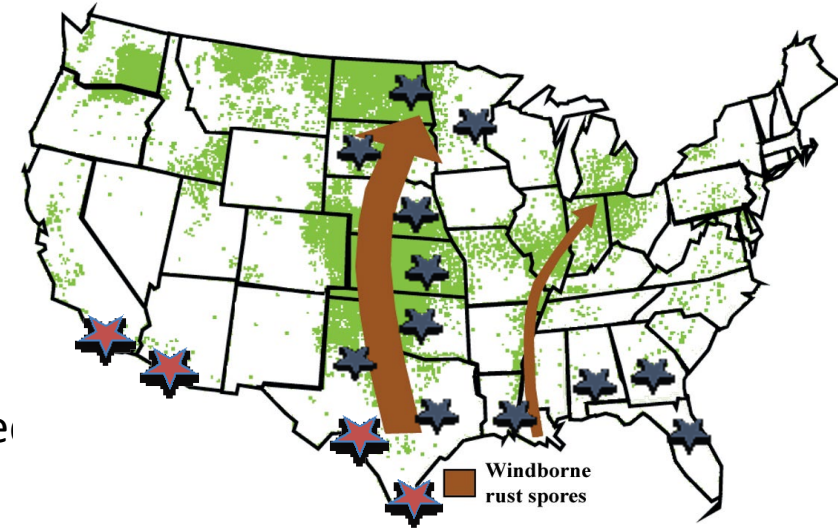
Stem rust of wheat:



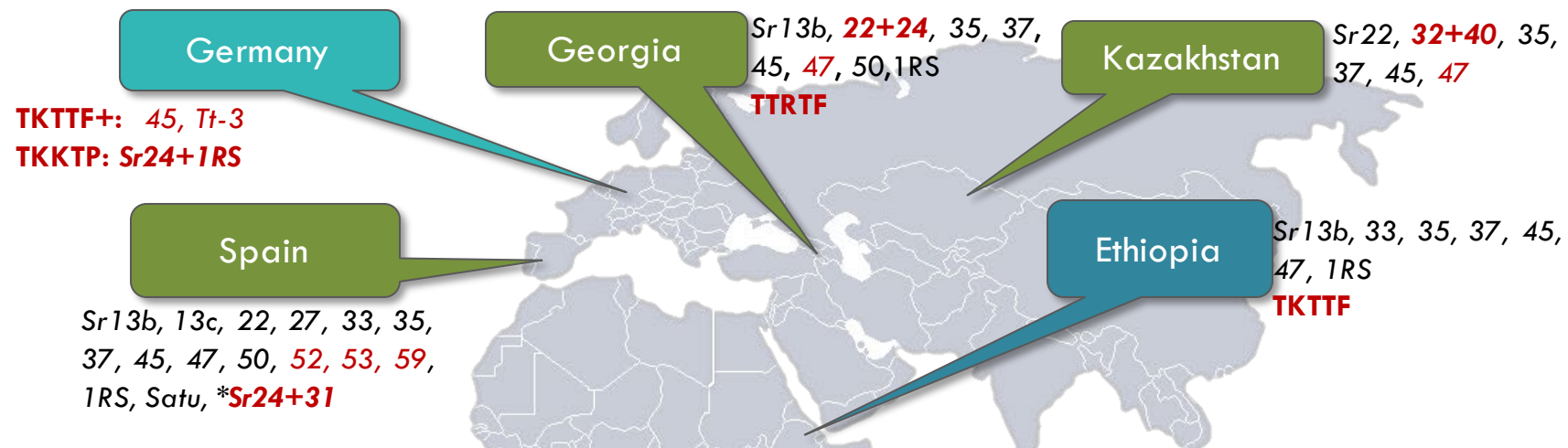
Ug99 race group:



Ug99 sentinel plots in US:



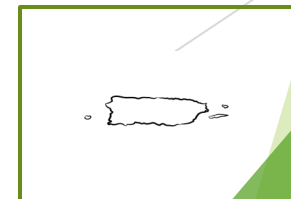
Detection of non-Ug99 races that have caused epidemics/outbreaks:
(in close collaborations with D. Luster and P. Olivera)



Dr. Doug Luster

Foreign Disease - Weed Science Research Unit: Fort Detrick, MD

doug.luster@usda.gov



Preliminary screening and storage of exotic cereal rust accessions in BSL3 containment

Douglas G. Luster Foreign Disease-Weed Science Research Unit, Fort Detrick, MD

Cereal rust pathogens are evolving new forms and threatening the world's food security

Stem rust of wheat:



- Foreign rust collections are received during the growing season at the ARS Ft. Detrick MD BSL-3 Plant Pathogen Containment Facility, recovered, screened and archived.
- Selected accessions are shipped during the Winter Containment season to the ARS Cereal Disease Laboratory, St. Paul MN for intensive screening, pathotyping and genotyping
- 2019 to 2020: over 320 sample receipts from 9 countries in Africa, Europe, and Asia recovered, screened and archived.

NPDRS FY 2018 Funding: “Rapid detection of *Phytophthora ramorum* (Sudden Oak Death) in nursery irrigation water”

Douglas G. Luster Foreign Disease-Weed Science Research Unit, Fort Detrick, MD

Problem: Detection of Sudden Oak Death in infested nurseries takes 10 days to 2 weeks

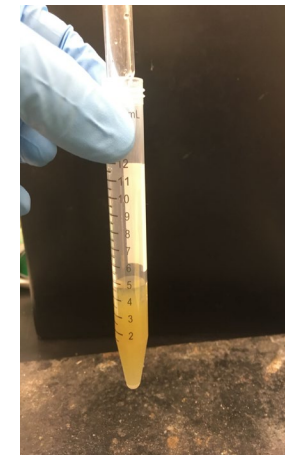
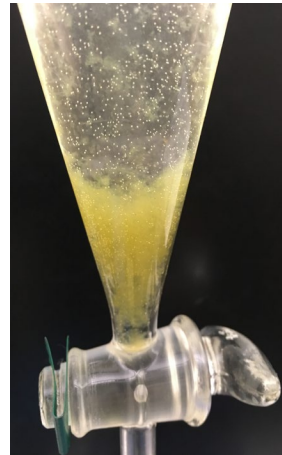
Mock Nursery Irrigation Retention Pond

National Ornamental Research Site
Dominican University, San Raphael CA



Rapid Sampling Strategy:

Flocculation of *P. ramorum* propagules from water samples



Objective: Rapid, efficient recovery and detection of *Phytophthora ramorum* from nursery irrigation water in 24 hrs

Mr. Gary Peterson

Foreign Disease - Weed Science Research Unit: Fort Detrick, MD

gary.peterson@usda.gov



Wheat blast

Wheat blast is an emerging fungal disease once limited to South America but recently reported in Bangladesh and Zambia with disease Losses of 30-100%.

Wheat blast has not been reported in North America

USDA ARS is currently screening U.S. wheat germplasm for disease resistance ARS Biosafety Level-3 Plant Containment Facility at Fort Detrick Maryland.

ARS Foreign Disease Weed Science Research Unit (FDWSRU) in Cooperation with Kansas State University and Asociación de Productores de Oleaginosas y Trigo (ANAPO) established a wheat blast screening nursery in La Paz, Bolivia

NPDRS is providing funding for the testing of U.S. wheat lines, identified at FDWSRU as potentially resistant in both the field and a greenhouse in Bolivia where new strains of the pathogen may exist.

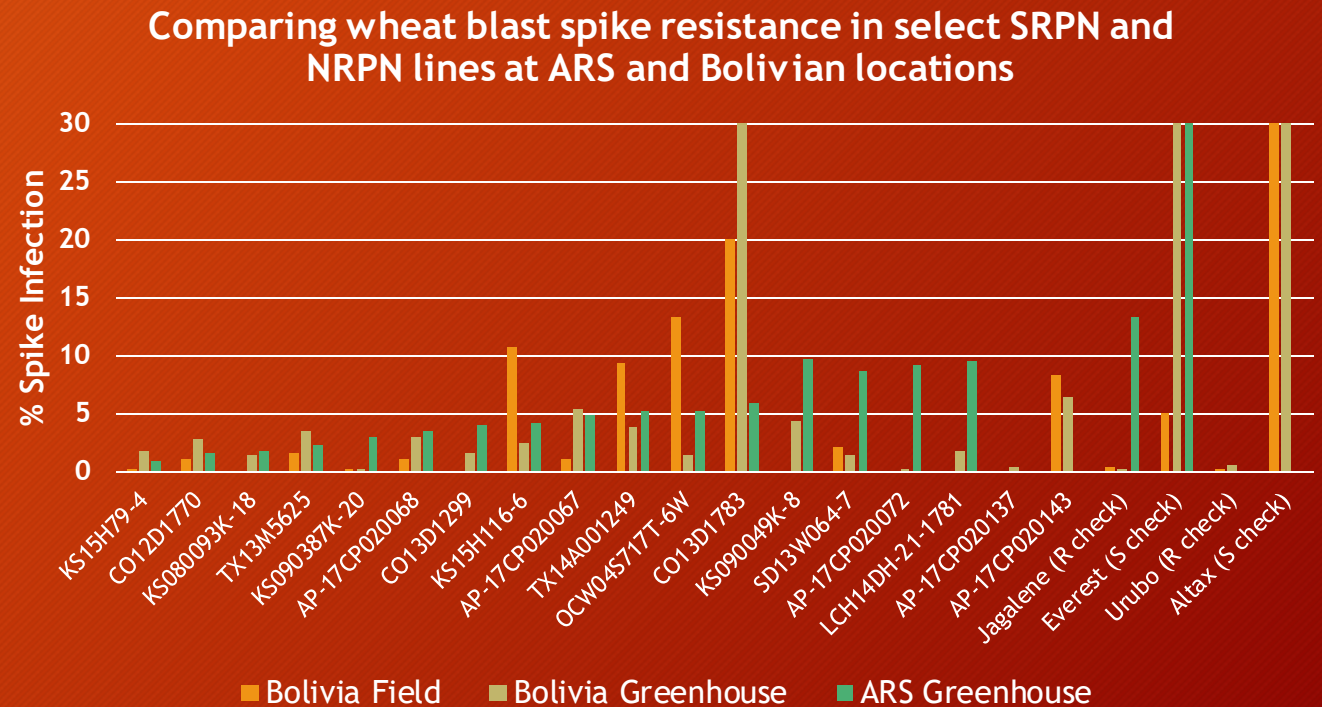
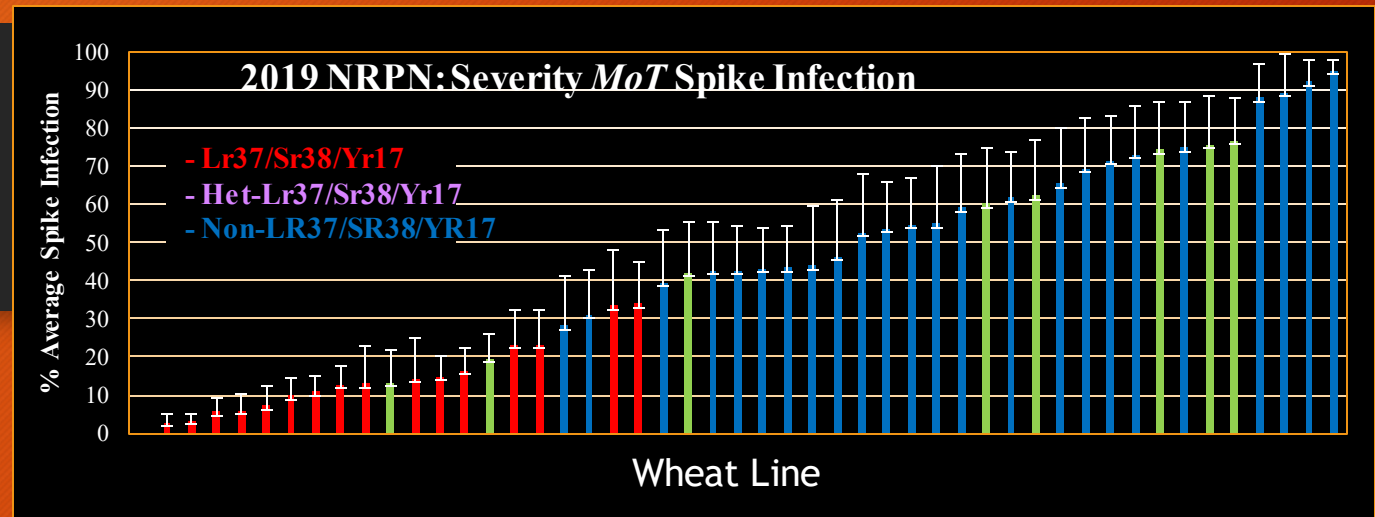


NPDRS: Wheat Blast

Of 93 lines from the U.S. SRPN and 102 NRPN lines tested, a total of 46 lines were shown to be resistant (<10%) to wheat blast at FDWSRU.

Of 38 potentially resistant lines sent to Bolivia, 20 were also resistant in Bolivian greenhouse and field studies.

Seed of 20 lines from SRPN, NRPN, Uniform Southern and Eastern Soft Red Wheat and several BASF lines are currently in Bolivia being prepared for planting this season



National Plant Disease Recovery System (NPDRS)

Tim Widmer, USDA-ARS
(tim.widmer@usda.gov)

<https://www.ars.usda.gov/crop-production-and-protection/plant-diseases/docs/npdrs/>

