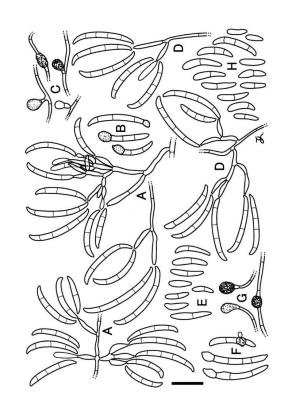
# Updates on Fusarium wilt research: Aerial dispersal and resistance-breaking strains



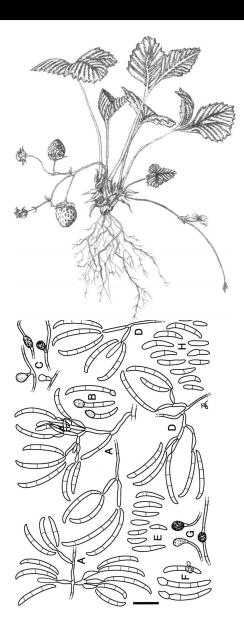
Peter Montgomery Henry, PhD Research Plant Pathologist

Annual Strawberry Production Research Meeting UCCE – Santa Cruz / Monterey Feb 7, 2023





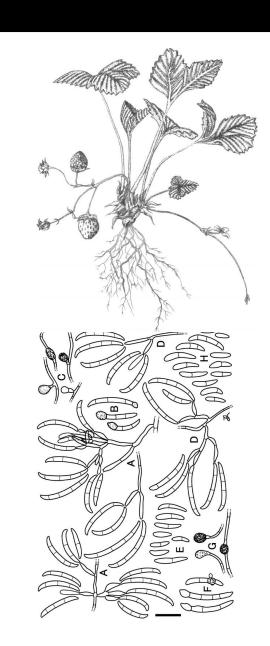
## Overview



Fof has the potential for aerial dispersal

Resistance-breaking Fusarium oxysporum f. sp. fragariae (Fof) race 2 in CA

- Background on Fof races
- Discovery
- Response
- What we know



## Fusarium wilt

Signs: None

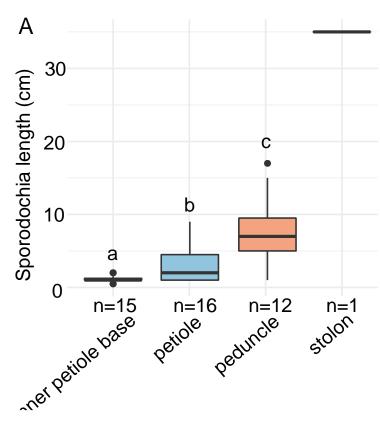


Symptoms: Stunting, chlorosis and deformation of new leaves are early symptoms. Wilting first of outer leaves or sudden collapse of entire plant can also occur.



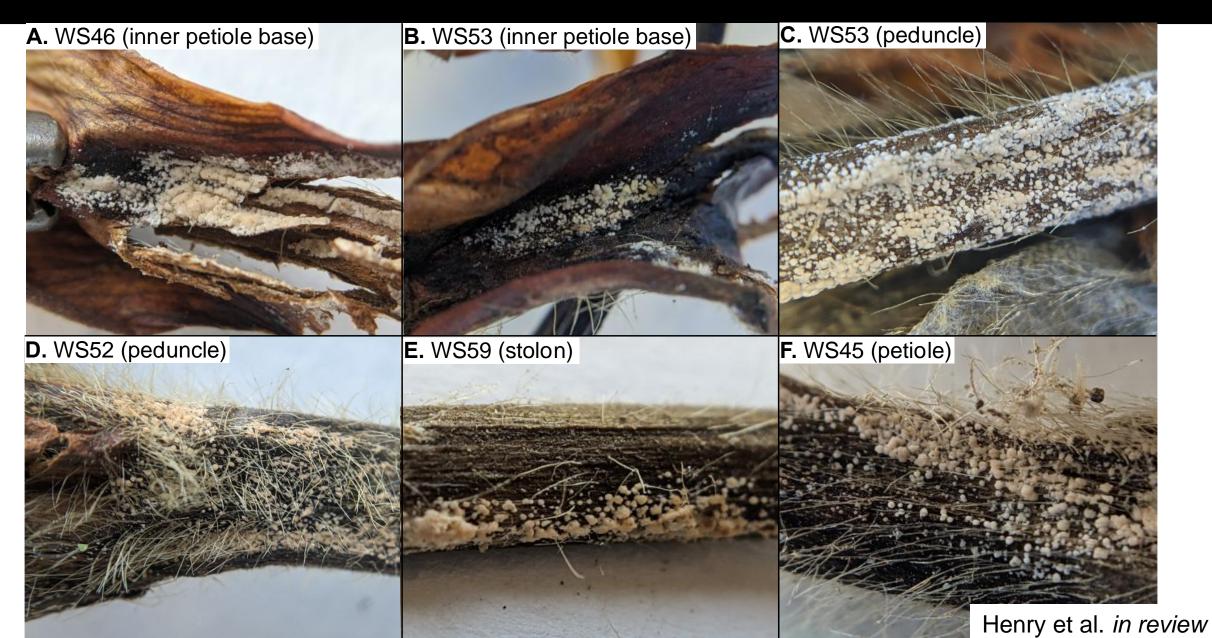
## Sporodochia formed by F.o. fragariae

- Discovered at 87% of Fusarium wilt-afflicted fields (n=24)
- Found on most plants

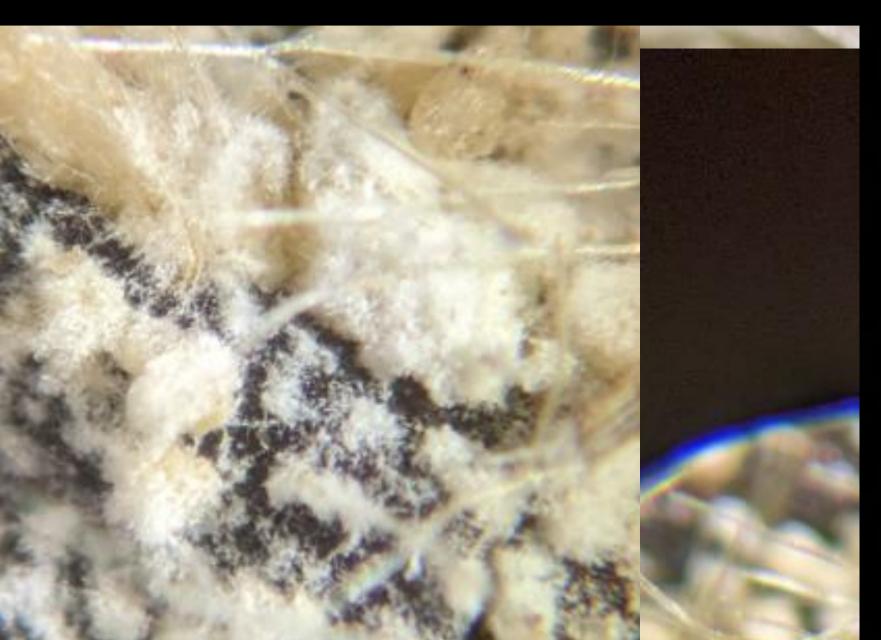




# Sporodochia formed by F.o. fragariae



# Sporodochia formed by F.o. fragariae



## Only macroconidia observed

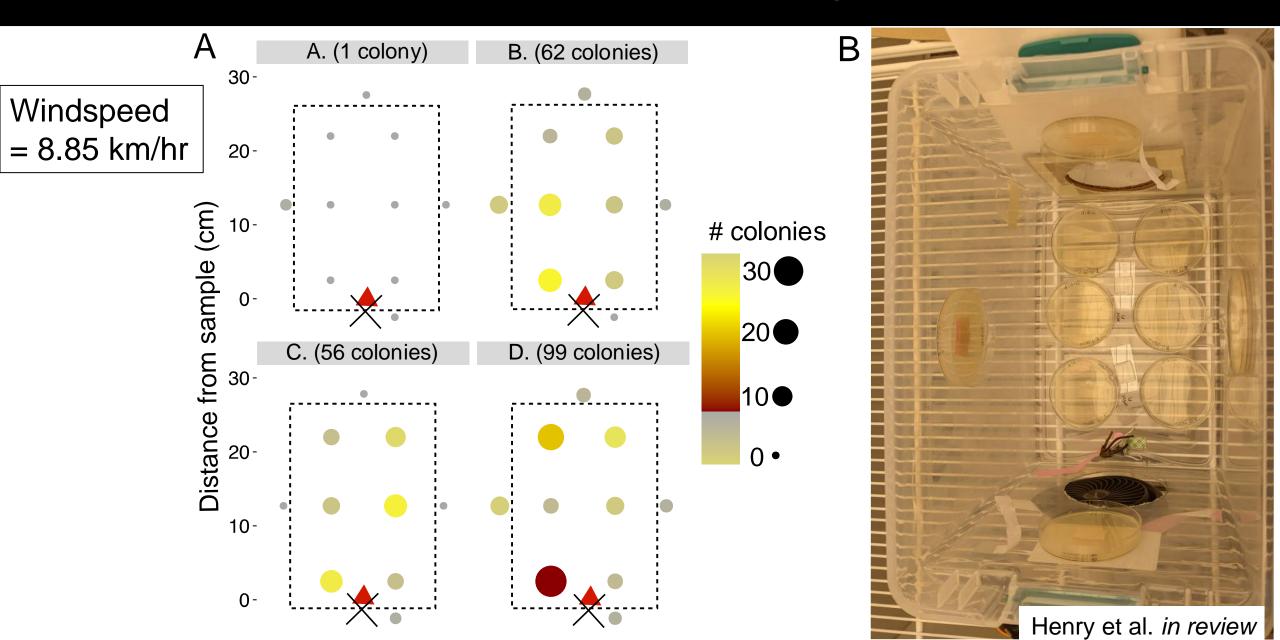


## Short-distance aerial dispersal

Windspeed = 8.85 km/hr



## Short-distance aerial dispersal



## Much higher windspeeds are common

- Bug vacuums are used 1x or 2x per week
- Vacuums generate windspeeds of 7-54 km/hr
- Afternoon windspeeds typically >14 km/hr

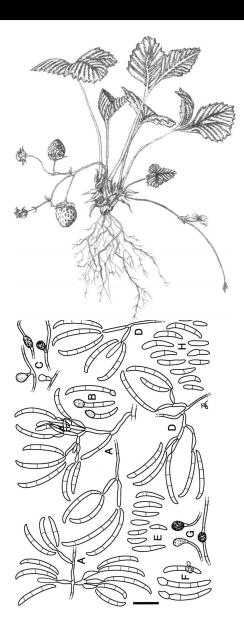


## Takeaways

- Sporodochia are common in Watsonville/Salinas and have been observed near Oxnard
- Aerial dispersal is likely to contribute to field-to-field movement of this pathogen
- Future work:
  - Can aerially dispersed spores cause disease?
  - What is the long-distance range of airborne Fusarium conidia?
  - Can airborne spores account for some cases of ineffective flat fumigation?



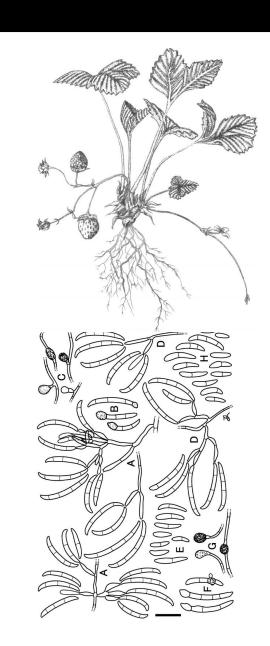
## Overview



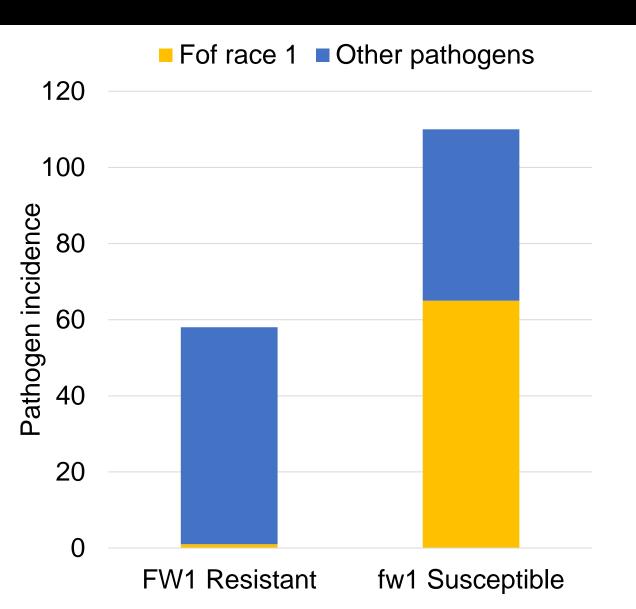
Fof has the potential for aerial dispersal

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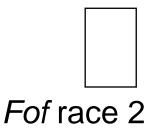
# Genetic resistance is key to managing Fusarium wilt



- In Watsonville/Salinas, Fusarium wilt is the most common disease on susceptible varieties.
- Resistant varieties include:
  - Portola
  - Fronteras
  - San Andreas
  - Victor
  - Moxie

# Gene-for-gene interactions in strawberry

















- FW1 Resistant varieties:
  - Portola
  - Fronteras
  - San Andreas
  - Victor
  - Moxie



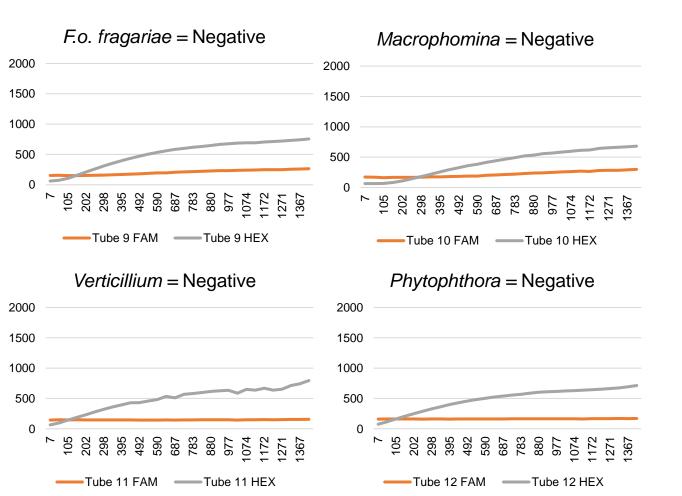
# Fusarium-associated chlorosis





# Inconclusive diagnostics

#### Molecular assays detected no pathogens



### Petioles yielded abundant Fusarium oxysporum



# Pathogenicity test confirms *Fof* race 2

Plants inoculated with pure *F. oxysporum* cultures from Ranch X



susceptible

Gu 2b

FW1 resistant

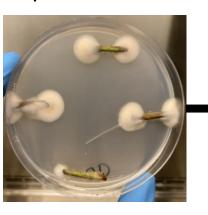


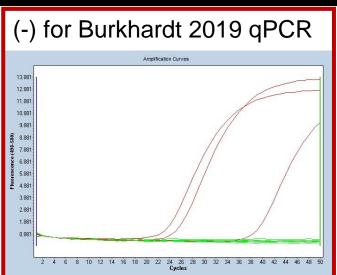
## Early action plan

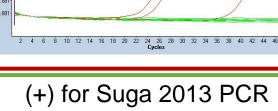
- 1. Survey incidence of *Fof* race 2 at Ranch X
- 2. Survey for *Fof* race 2 at other ranches
  - Ventura
  - Santa Maria
  - Watsonville/Salinas
- 3. Discuss best management practices with any affected grower
- 4. Develop preliminary detection methods

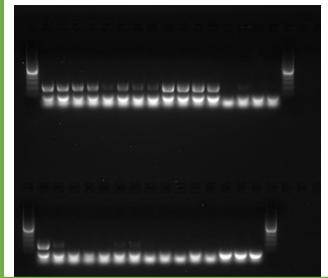
## Current identification methods

Petiole isolations &
Single hyphal tip pure cultures







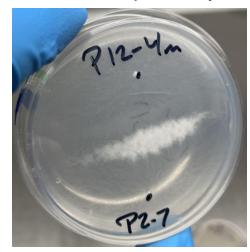


#### Sequence EF-1a gene



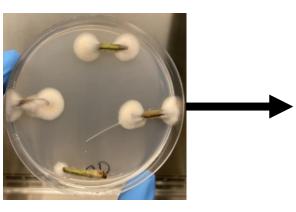
C->T transversion

#### Somatic compatibility test



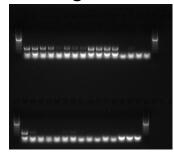
## Current identification methods

Petiole isolations &
Single hyphal tip pure cultures



(-) for Burkhardt 2019 qPCR

(+) for Suga 2013 PCR



(+) for oxr2-TAR1 qPCR

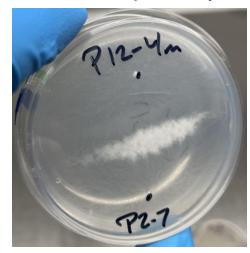
- Assay specific to CA Fof race 2
- Currently in betatesting

#### Sequence EF-1a gene



C->T transversion

#### Somatic compatibility test









Jenny Broome Kelly Ivors Milton Bardmess David Harada



# STRAW SERRY® COMMISSION







Oleg Daugovish

UNIVERSITY OF CALIFORNIA
Agriculture and Natural Resources

**UC Cooperative Extension** 

John Lin
Jason Sharrett
Andrew Molinar
Carolina Lobo Marin
Miriam Mendez
Jasmine Rodriguez



CAL POLY
Strawberry Center

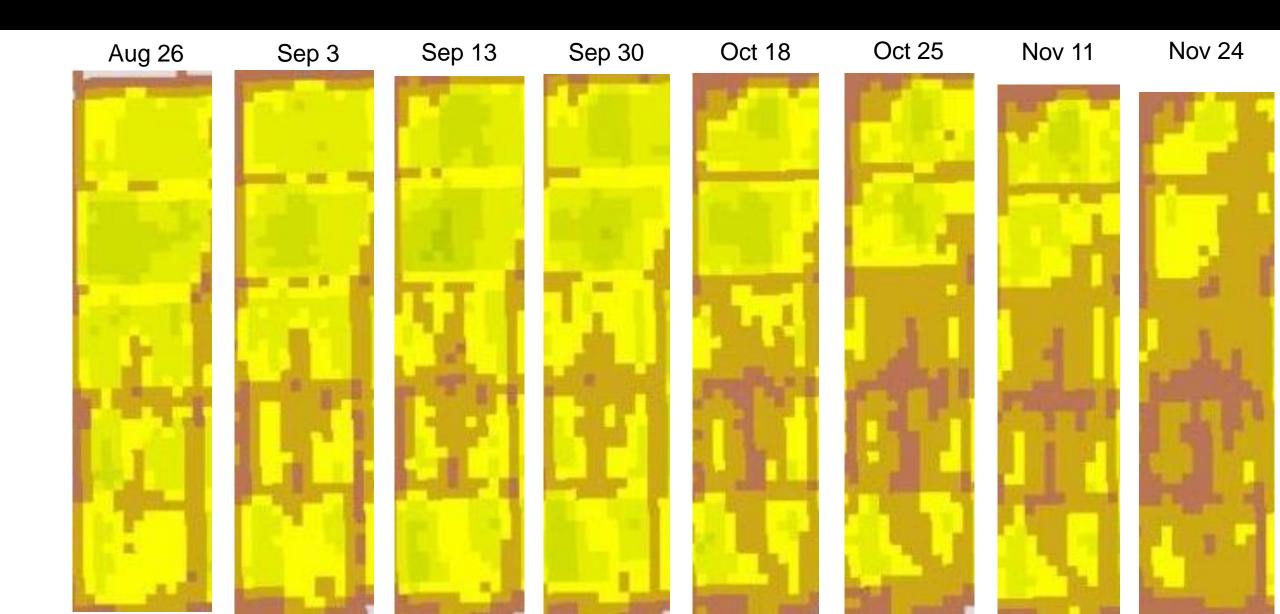
Gerald Holmes Shashika Hewavitharana Mary Steele

# Biosecurity

- Nobody sampled other fields after visiting Ranch X
- New shoe covers and gloves were worn at every site
- Tools were cleaned and soaked in 70% ethanol for >10 minutes after samples collected

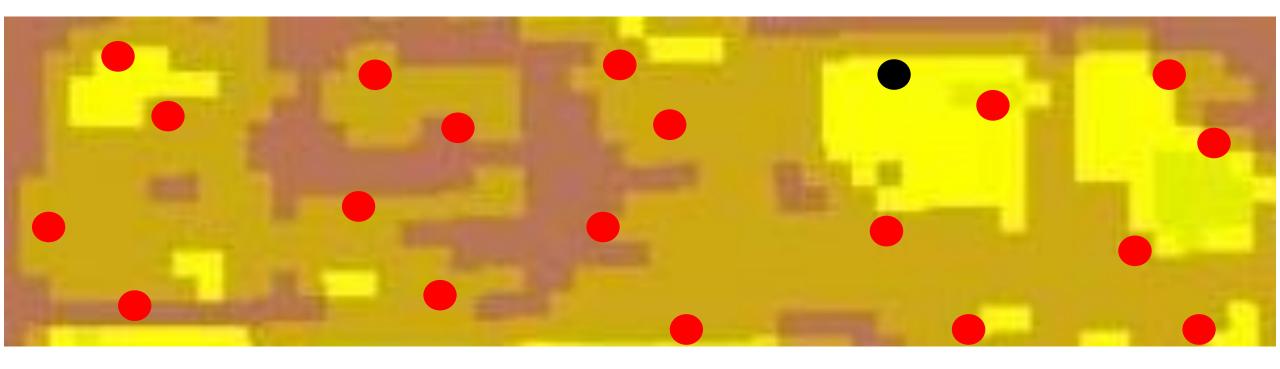


# 1 - Ranch X disease progression - NDVI



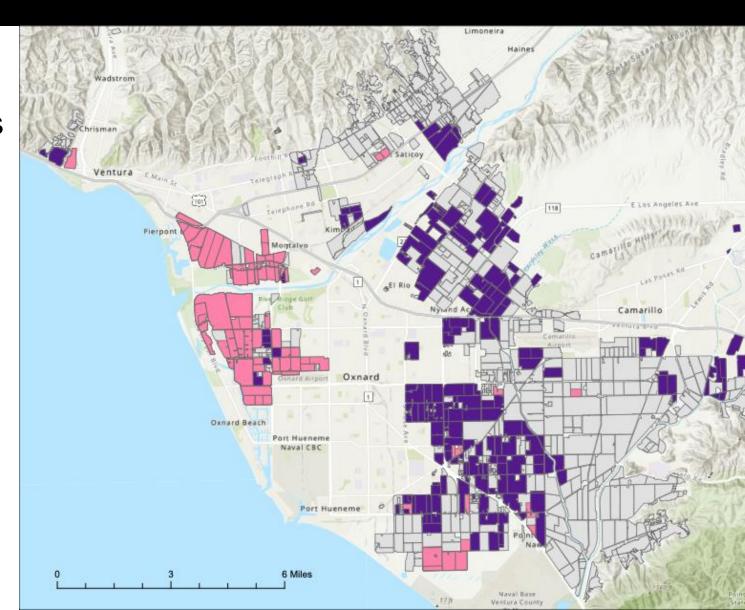
## 1 - Fof race 2 is widespread at Ranch X

- = Fof race 2 detected
- = No Fof race 2 at this location

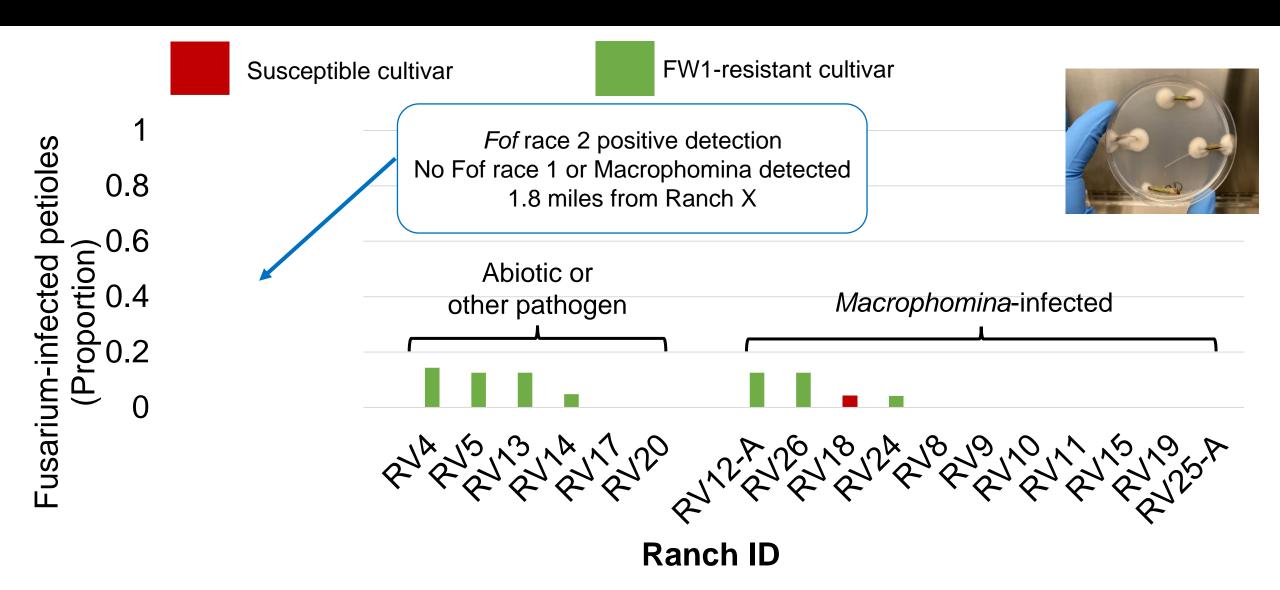


## 2 - Ventura county disease survey for *Fof* race 2

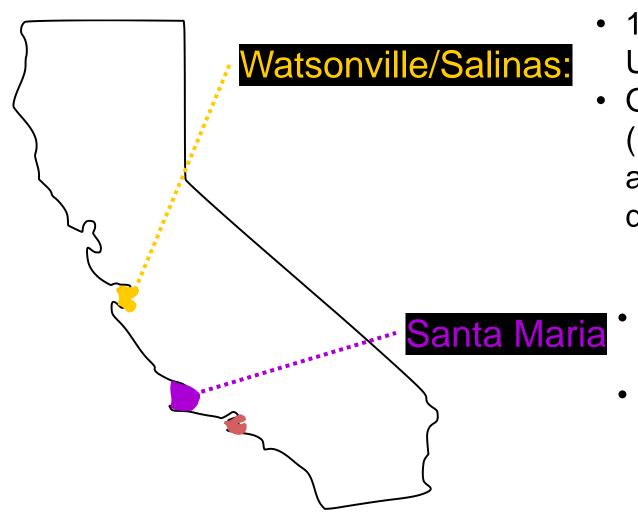
- ~30% of all summer planted fields
- Selected by:
  - Grower recommendation
  - NDVI variation
- Data collected:
  - Molecular assays for Fof race
     1 and Macrophomina
  - Petiole assays selecting for Fusarium oxysporum



# 2 - Ventura county disease survey for *Fof* race 2



# Fof race 2 unlikely to be present in other districts

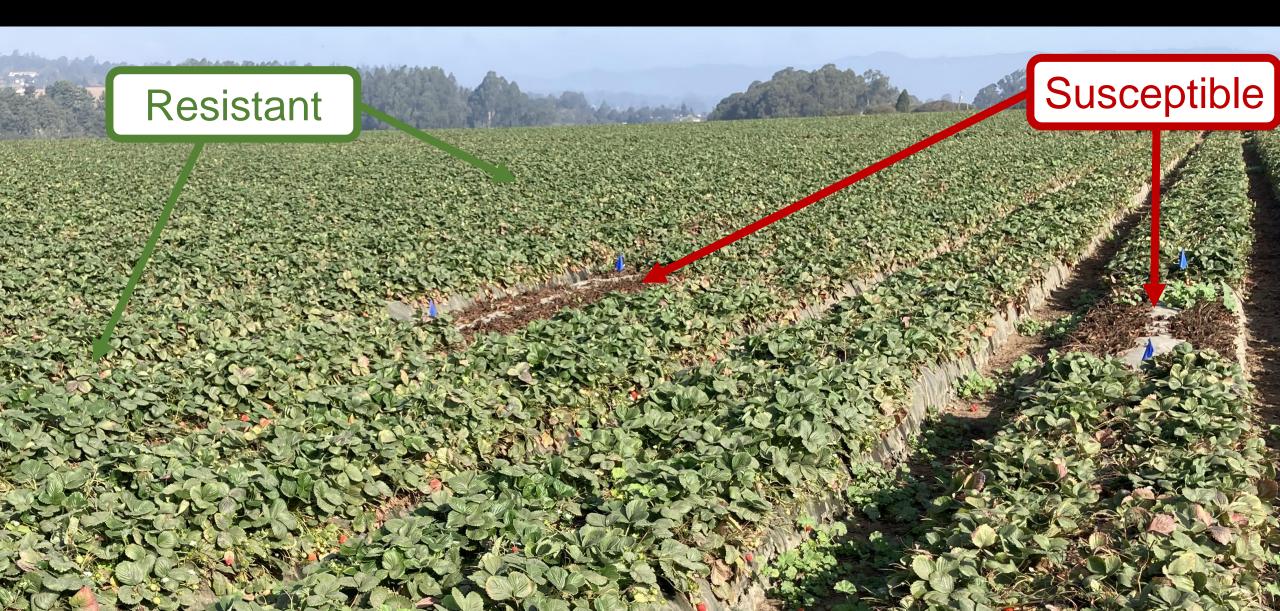


- 146 fields sampled (2021-2022 Cal Poly / USDA)
- Only 3 of these were suspicious (Fusarium-resistant cultivars with ambiguous result and moderate to high disease severity)
  - 100 samples collected from 68 ranches (2022 Cal Poly)
  - Only 3 of these were suspicious (Fusarium-resistant cultivars with ambiguous result and moderate to high disease severity)

## What we know

- 1. Fof race 2 is identified in CA for the first time
  - 1. Widespread at Ranch X
  - 2. Probably originated >1-2 years ago
- 2. Common molecular methods do NOT detect Fof race 2
  - 1. A DNA target specific to Oxnard race 2 has been identified
  - 2. qPCR and RPA assays are designed and in beta-testing.
- 3. Fof race 2 is unlikely to be widespread
  - 1. Likely to be present in 3-4 ranches in Ventura
  - 2. 2021-2022 Disease surveys in Watsonville, Salinas, and Santa Maria suggest it is not present yet in those regions
- 4. The Oxnard race 2 strain is new to science
  - 1. A single race 2 strain has been detected
  - 2. It has not been observed in extensive pathogen diversity surveys across 5 countries.

## FW1-resistance remains effective in most fields



## Acknowledgements

## \*Grower collaborators\*











NIFA Specialty Crops Research Initiative (#2017-51181-26833 and #2022-51181-38328)

## A single strain identified at Ranch X

- "Somatic compatibility"
  - Phenotypic test for clonality
  - Takes 3-4 weeks to complete
  - Diagnostic method
- Single locus sequencing
  - Translation elongation factor 1-alpha
  - A unique single nucleotide polymorphism differentiates these strains



## Oxnard race 2 is new to science

- Genome is distinct from all other known *F. oxysporum* strawberry pathogens
- Appears to have evolved by chromosome transfer between pathogenic and non-pathogenic lineage.
- Local origin is likely

