

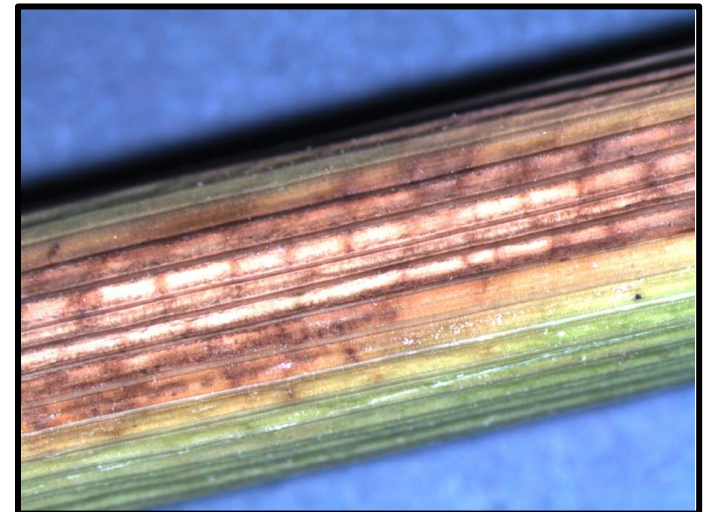
New Insights Into Narrow Brown Leaf Spot of Rice

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Narrow Brown Leaf Spot

- *Cercospora janseana*
- Narrow brown lesions on leaf tissue
- Net blotch pattern on sheath/stem
- Late-season disease
 - Earlier plantings, less disease
 - Ratoon impact
- Yield losses up to 40%
- Fungicide applications
- Host resistance is a viable strategy

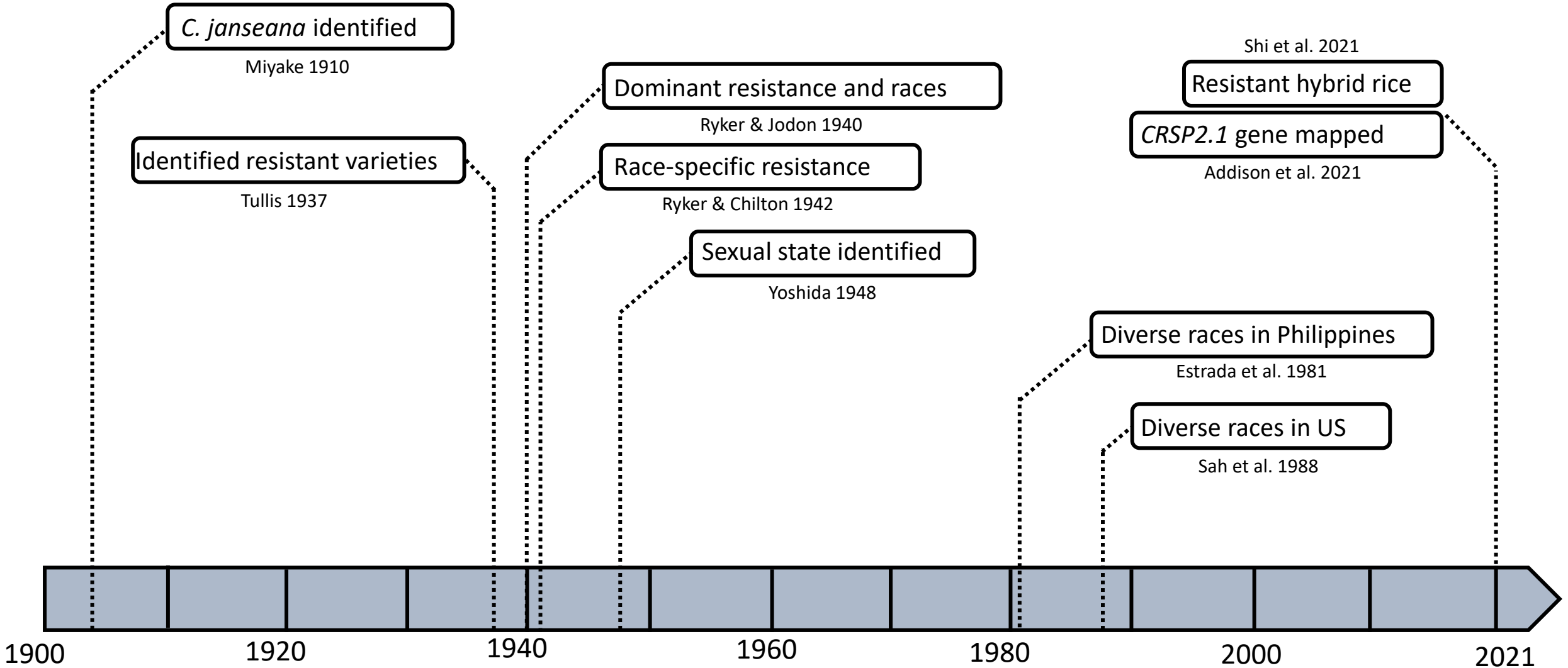


The problem(s)

- What is the genetic architecture of host resistance to NBLS?
- Are leaf and sheath symptoms under different genetic control?
- Can quantitative resistance be incorporated into elite lines?
 - Stacking with major genes can prevent resistance gene defeat
- Can *C. janseana* migrate between production regions and sexually reproduce?
- Are *C. janseana* populations resistant to fungicides?

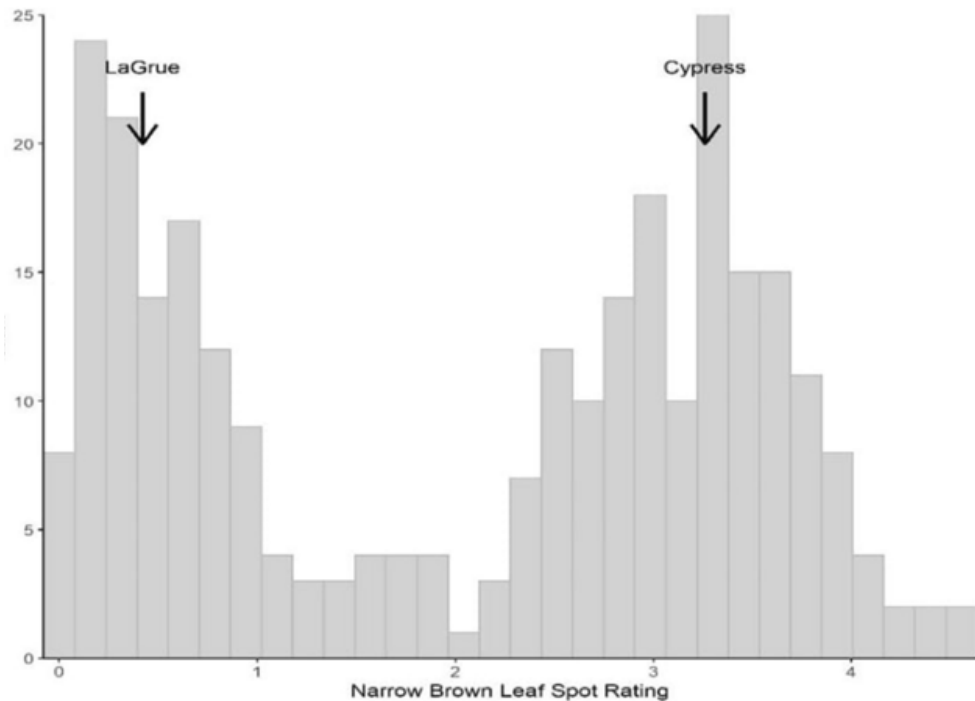
Applied and basic approaches to understand disease resistance/management

A brief history of NBLS research



CRSP2.1 Major Resistance Gene

- Originally identified/mapped by Addison et al. (Famoso lab)
- Major effect resistance
- Leaf tissue nearly immune



Addison et al. 2021



***CRSP2.1* +**

***CRSP2.1* -**

CRSP2.1 Major Resistance Gene

- Identification of the *CRSP2.1* gene
- Fine mapping approach
 - Genotyped ~10,000 individuals
 - Phenotyped in greenhouse
 - Comparative genomics

Finding gene can aid deployment and understand/identify other forms of resistance

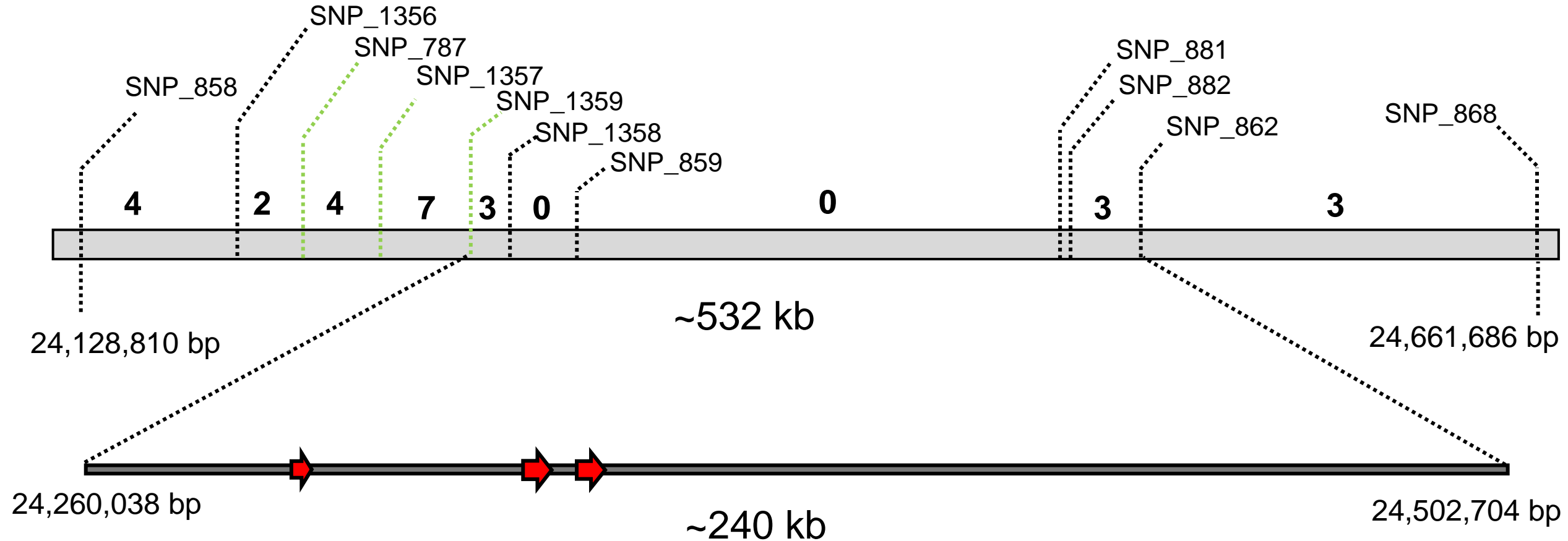


***CRSP2.1* +**

***CRSP2.1* -**

Three candidate receptor-like kinase genes

Chromosome 2



Which gene is it? Currently functionally validating candidates

Stem/sheath symptoms are 'different'

- *CRSP2.1* provides broad spectrum resistance in leaf tissue
- Lines with *CRSP2.1* may develop stem/sheath symptoms (PVL03)
 - Differences in gene expression?
- Do different genes control resistance in sheath/stem?
- Are different races involved?
- Need to look for symptoms beyond the leaf
- Currently phenotyping in GH
 - Identify sheath/stem resistance

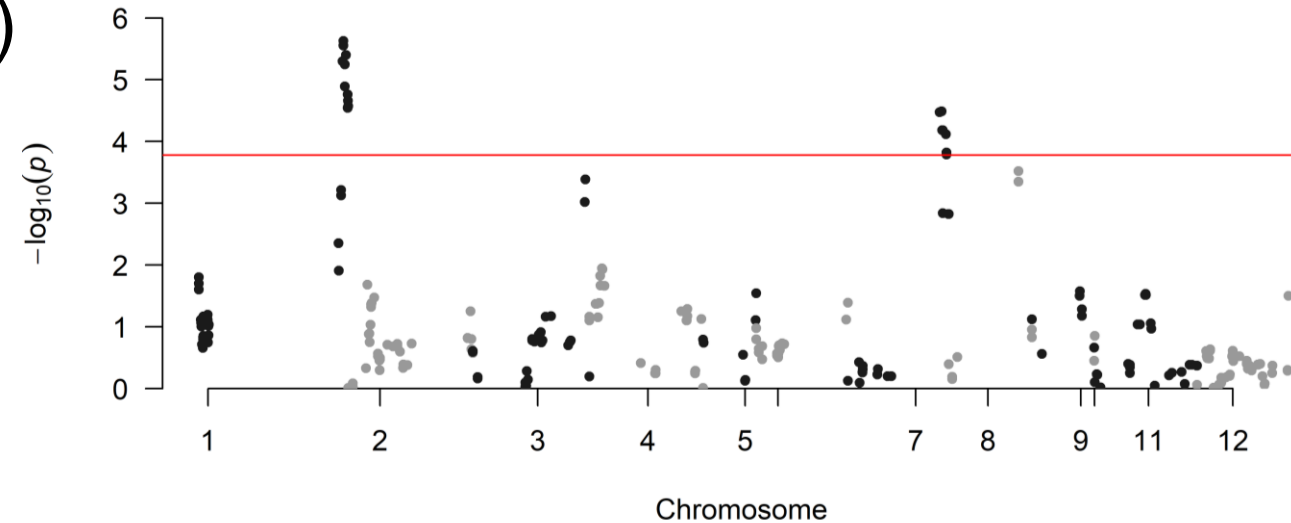


CRSP2.1 -

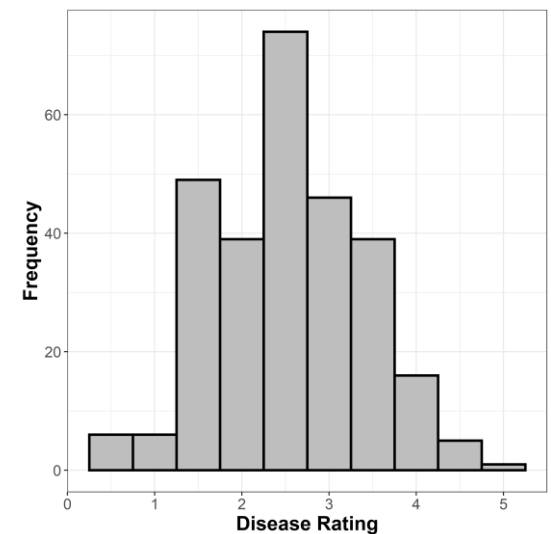
CRSP2.1 -

Quantitative NBLS Resistance

- MPC population (Cypress x CL172)
 - Neither parent has *CRSP2.1*
- Normal distribution of phenotypes
- Quantitative resistance detected (small effect, ~8-10%)
- Preliminary predictions were promising (0.54)
- Evaluation in field and GH in 2023



Are quantitative resistance loci stable across years?
Can genomic prediction be used to make genetic gains?



Now, what is the pathogen doing?

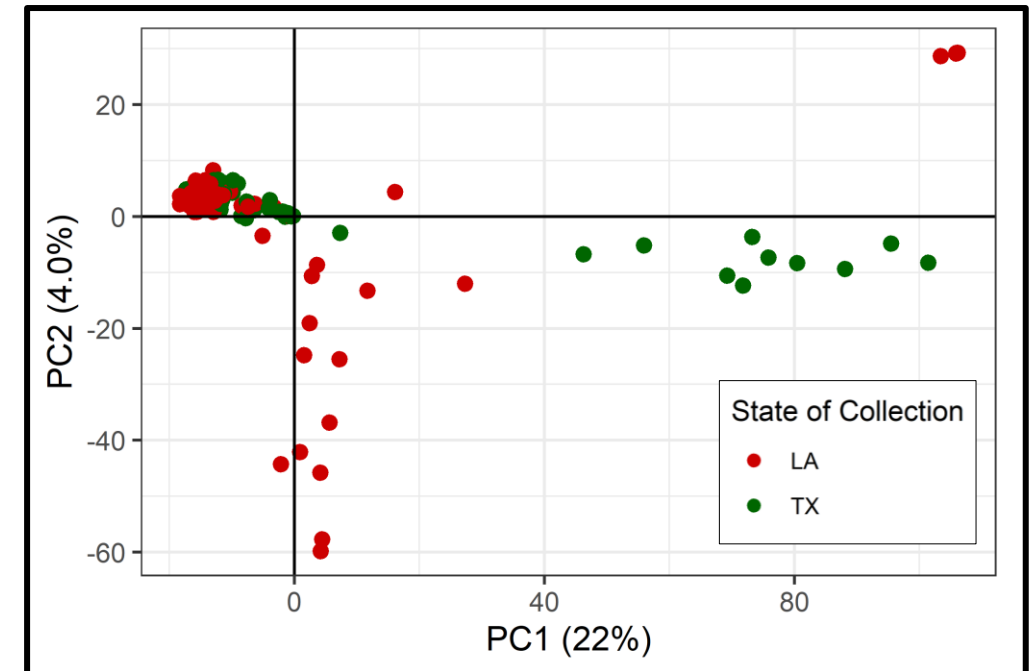
Genetic diversity of *C. janseana*

- High genetic diversity in LA populations
- Migration to/from Texas
- Evidence for sexual recombination
 - New virulent race formation

Idiomorph	# of Individuals
MAT1-1	69
MAT1-2	70
Total	139

$\chi^2 = 0.007$, p-value = 0.93241

Sampling Population	Location	Date	Isolates Collected	Isolates Sequenced
1	Crowley, LA	09/2019	118	32
2	Beaumont, TX	10/2019	181	27
3	Crowley, LA	08/2020	84	27
4	Beaumont, TX	10/2020	62	28
5	Crowley, LA	10/2020	19	16



Assess virulence of *C. janseana* in LA

- Previous studies indicated high virulence diversity
- **How many races exist/are prevalent?**



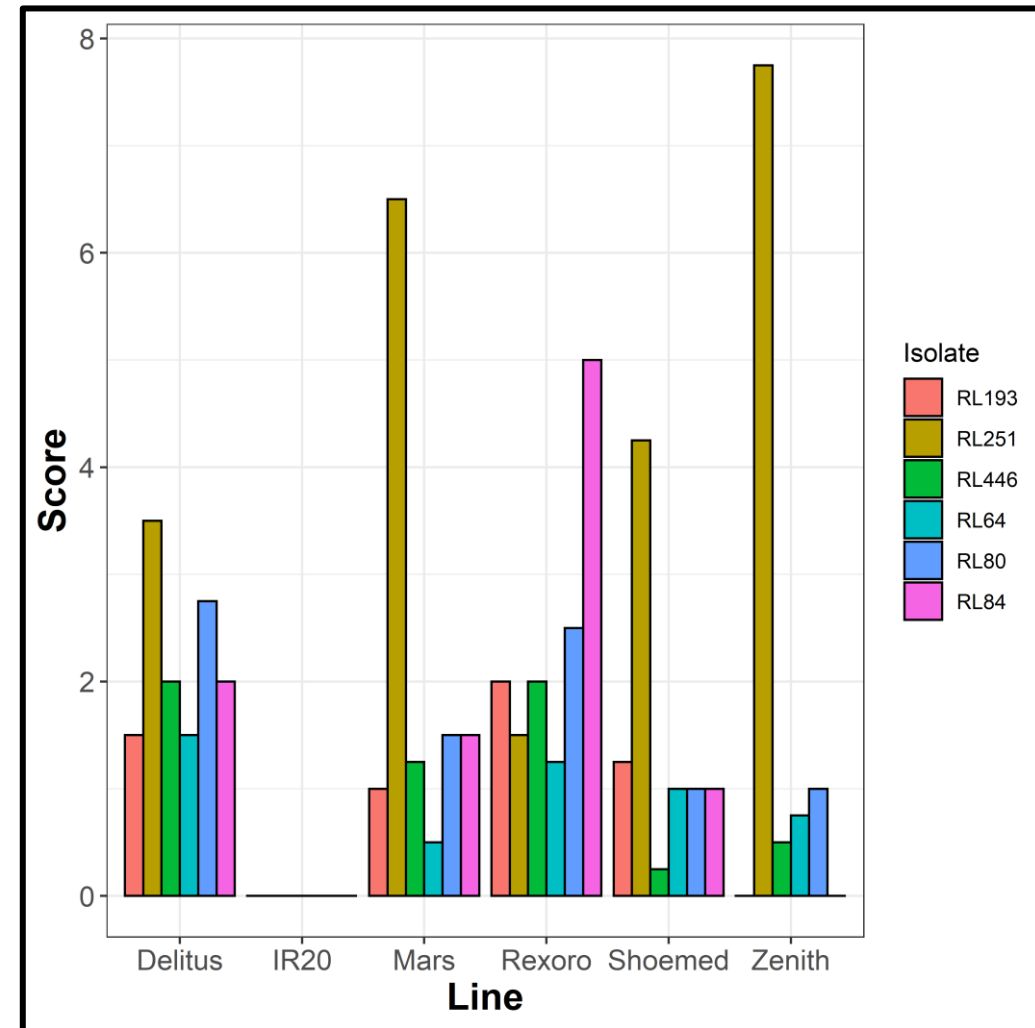
Cypress (Susceptible)



Delitus (Resistant)

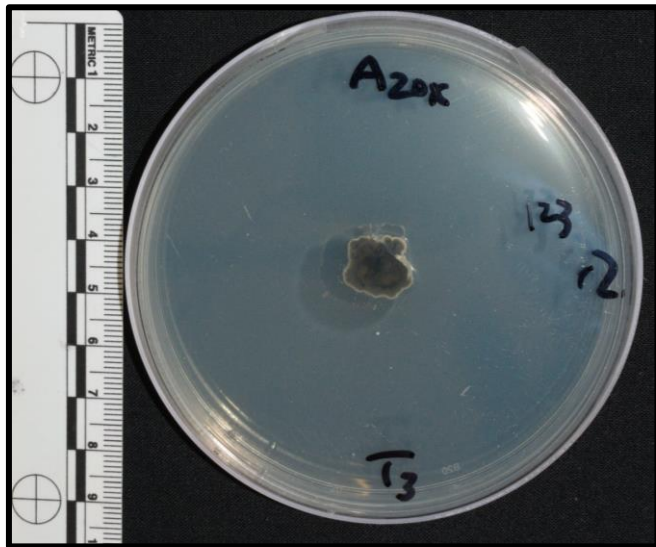


Zenith (Susceptible)

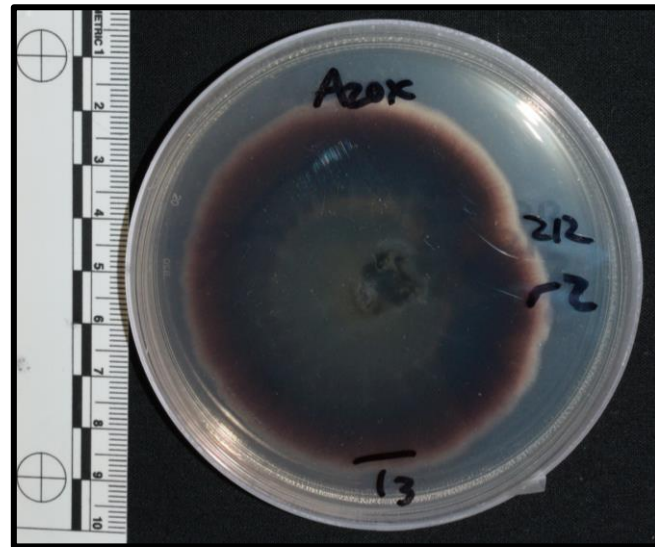


Fungicide resistance in *C. janseana*

- *In vitro* fungicide sensitivity assays (azoxystrobin and propiconazole)
- ~75% of isolates have G143 mutation
 - Reflect low QoI effectiveness
 - Confirmed with *in vitro* assay
- No substantial differences in propiconazole sensitivity

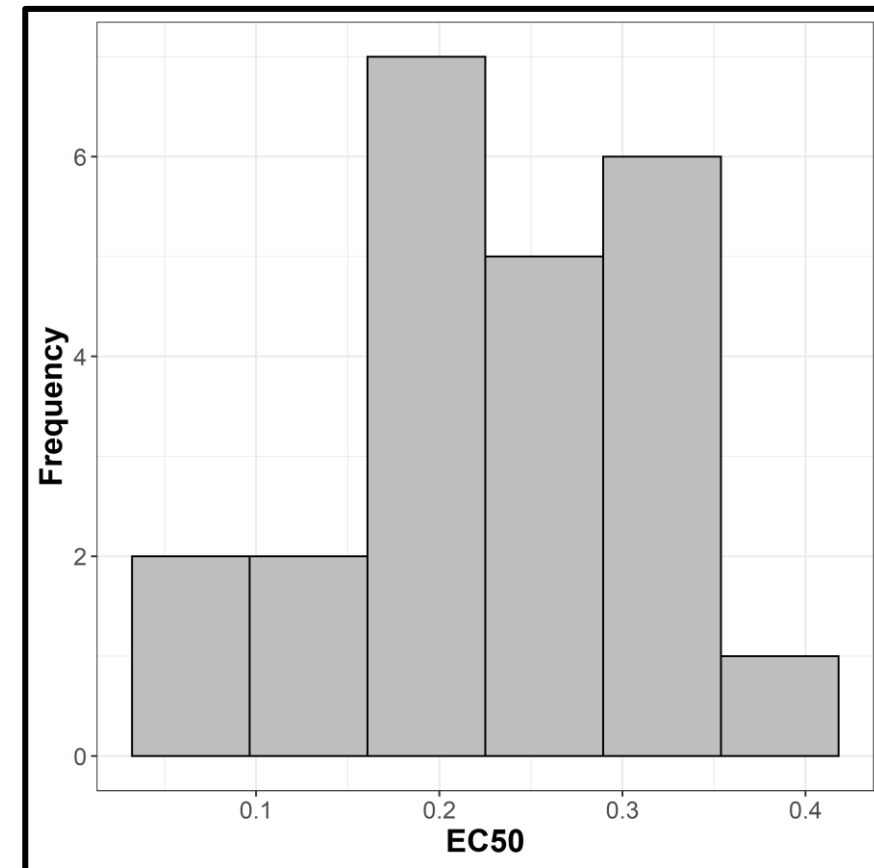


Sensitive



Resistant (G143A)

Propiconazole EC50



Conclusions and future work

- *CRSP2.1* provides robust NBLS resistance in leaves
- Symptoms may form on sheaths/stems of *CRSP2.1+* lines
- Quantitative resistance has been identified
- *C. janseana* has potential to migrate and form novel races
- Multiple races present in LA
- QoI resistance is widespread

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