Accuracy of Genomic Selection for Resistance to Verticillium Wilt in a Strawberry Population Spanning 165 Years of Breeding

(And some Fusarium updates too!)

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Photos: Thomas (1932); Gordon & Subbarao (2008)
Prior Knowledge

- Despite being a century-old disease and past work, there is still a lot of unknowns when it comes to Verticillium wilt resistance in strawberry.

- Ambiguity across reports regarding resistance or susceptibility to cultivars, and much of the germplasm (varieties) available to breeders lack information altogether.

- Past work suggests a complex resistance.
Global Survey of Verticillium Resistance

68% UCD

Pincot et al. (2020, in review)
1 (Resistant)

9 (Dead)

“Core” Set

$H^2 = 0.76$

$n = 388$

$r = 0.54$

Pincot et al. (2020, in review)
Evolution of Resistance

- Average resistance has decreased over time

Pincot et al. (2020, in review)
• Higher proportion of resistance at higher latitude
  • Likely due to environment that is favorable to Verticillium, leading to higher rates of infection and co-evolution
Resistance is Complex

• Survey of the genome showed no significant DNA markers tied to resistance. This is not unexpected, given past work.

• Genome-informed breeding approaches (eg: genomic prediction) have been used successfully for these types of traits in other economically important crops, like tomato and wheat.
  • These breeding approaches are now options due to the new genomic technologies developed by the breeding program at UC Davis (eg: new SNP array).

Pincot et al. (2020, in review)
Genomic Prediction

Prediction Equation
\[ y = Xb + Zu + e \]

Observed + DNA = Predicted

Expected: Time-Consuming, Expensive, Cost-Efficient, Fast, Free, Super Fast
Genomic Prediction works well!

Disease Score vs. Predicted Score for different years:
- 2017: \( r = 0.41 \)
- 2018: \( r = 0.46 \)
- 2-Year: \( r = 0.49 \)
Takeaways

• Genome-informed selection (genomic prediction) has significant potential in the breeding of accessions more resistant to Verticillium wilt, which is slow, difficult, and expensive to evaluate in the field.

• With genomic prediction, we can breed faster, cheaper, and better.
Progress on Fusarium Wilt Resistance

Photo: Koike and Bolda (2013)
Deploying \( Fw1 \) resistance gene
**Fw2, Fw3...**

**Mapped:**
- *Fw2*: Guardian, USDA Heirloom
- *Fw3*: Wiltguard, UCD Heirloom

Pincot et al. (in preparation)
We hypothesize that many additional and novel resistances exist in heirloom and wild varieties of strawberry.

\[ n = 344 \]
Breeding against future threats

- Sources of resistance against *Fw1*-breaking isolates has been identified and will be targeted in the future.

Henry et al. (in preparation)
Takeaways

• DNA markers have been developed to predict the Fusarium wilt resistance (*Fw1*) in new breeding material.

• Novel sources of resistance against Californian Fusarium wilt have been identified and mapped (*Fw2 & Fw3*), with many more possible options for further investigation.

• Novel sources of resistance against foreign Fusarium wilts have been identified and will be further investigated.

Cobo et al. (in preparation); Pincot et al. (in preparation); Henry et al. (in preparation)