Progress toward understanding Sclerotinia pathogenicity and plant resistance to Sclerotinia diseases

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Sclerotinia diseases of sunflower



Basal Stalk Rot / Wilt

Mid-stalk Rot

Head Rot

Sclerotia













Pathology program goals for Sclerotinia

- Characterize relevant diversity within the pathogen populationand use information on differential aggressiveness to identify virulence determinants.
- Use comparative genomics and functional studies with the plant model plant system *Arabidopsis* to identify genetic factors and defense mechanisms contributing to *Sclerotinia* resistance.

AIM – Unravel complexity to facilitate improvement of sunflower resistance



Topics



 Progress on understanding mechanisms of plant resistance to Sclerotinia sclerotiorum.

• Update on identifying genes controlling aggressiveness of *Sclerotinia* isolates.

• Sclerotinia field disease nurseries: issues and challenges.

Progress on understanding mechanisms of plant resistance to Sclerotinia sclerotiorum.

- Leveraging Arabidopsis genomic and functional resources -

Past year:

- Acquired 360 accession Arabidopsis diversity panel.
- Phenotyped 315 accessions for *Sclerotinia* resistance upon spot inoculation of leaves with mycelia of *Sclerotinia* isolate 1980 (sequenced reference isolate).
- Performed genome-wide association mapping to identify candidate genes contributing to resistance.
- Phenotyping with a second, less aggressive *Sclerotinia* isolate is ongoing.

Arabidopsis diversity panel phenotyping

• Leaves spotted with suspension of ground mycelium.

• Resistance scored at 4 dpi and 7 dpi using a 0-9 rating scale.

0 – No visible lesion 1 – lesion confined to inoculation site 2 - < 25% leaf area 3 – 25-50% leaf area 4 – 50-75% leaf area

5 – Entire leaf 6 - < 25% plant area 7 – 25-50% plant area 8 – 50-75% plant area 9 – 75-100% plant area







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Genome-wide association

Mixed model to control for population structure, SNPs with minor allele frequency > 5% considered.

Bonferroni



• At Bonferroni cutoff (stringent), over 30 significant associations observed. At more lenient 5% FDR, large number of putative associations.

Genome-wide association

Some common themes of interest:





Ongoing work



- Phenotyping and GWA with a second *Sclerotinia* isolate.
- Functional validation of subset of candidate genes using insertional mutant lines.

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Potential Implications for Sunflower

May be worth considering breaking down *Sclerotinia* resistance into potentially easier to phenotype defense physiology components: phytoalexin (scopolin, ayapin) accumulation, JA/ET signaling readout(s), etc.

Potential impacts on agronomic traits (yield) should be evaluated.

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• Sclerotinia field disease nurseries: issues and challenges.

Identifying genetic factors contributing to differential aggressiveness of the pathogen (virulence factors)



DNA extraction from isolate collection Phenotyping virulence of isolate collection (~250 isolates) on multiple sunflower inbred lines SNP marker discovery (genotyping-by sequencing) Association mapping for SNPs correlated with aggressiveness Identification of candidate genes from sequenced reference *Sclerotinia* genome Validation of candidate genes (targeted knock-out & HIGS) Functional studies of virulence factors

Sclerotinia sclerotiorum isolate collection Aggressiveness on Sunflower inbred line HA 207









Sclerotinia sclerotiorum isolate collection Aggressiveness on Sunflower inbred line HA 207





-0.20

-0.40

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Improving field screening of sunflower materials

- 2017 Field Nurseries for the Pathology Program:
 - Stalk Rot: ~5500 rows at two sites (NDSU Carrington-REC, Carrington, ND and Central Lakes College Ag & Energy Center, Staples, MN)
 - Head Rot: ~1000 rows in mist nurseries at the same locations





Improving field screening of sunflower materials





Staples site very difficult for stalk rot



Ongoing and Future Work



- Complete phenotyping of *Arabidopsis* diversity panel with second *Sclerotinia* isolate.
- Evaluate subset of candidate genes via insertional mutants to verify *Arabidopsis* GWAS results.
- Complete phenotyping of *Sclerotinia* isolates on HA441, complete association mapping, evaluate candidate genes.
- Greenhouse-based stalk rot phenotyping for late-maturing AB populations (w/ Lili).
- Isolate collection for *Phomopsis* genetic and pathogenic diversity project.

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THANK YOU

QUESTIONS?

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