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Overview

- 1) Phenotyping a Brassica napus population for susceptibility to Sclerotinia stem rot (SSR) in collaboration with Prof. Jacqueline Batley lab, UWA
- 2) Susceptibility of hybrid vs open pollinated canola varieties to SSR
- 3) Pathogen genomics
- 4) 'Ground Infection' of canola stems by germinating sclerotia

Phenotyping the ASSYST population

- ⁷ <u>ASS</u>ociative expression and s<u>Y</u>stems analysis of complex <u>T</u>raits in oilseed rape/canola
- [~] Coordinated by Prof. Rod Snowdon, Justus Liebig University, Giessen, Germany
- $\tilde{}$ A genetically diverse set of ~350 winter and spring Brassica napus varieties
- ["] 60K single nucleotide polymorphism (SNP) array
- $\tilde{}\,$ 100 spring varieties phenotyped at the CCDM for SSR susceptibility

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Work for 2017

- " Further testing of plant age hypothesis in glass house
- " Test widely grown hybrid and open pollinated varieties in heavily infested areas

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Background

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GRDC DE

[~] Fungal genome can be used to generate hypotheses about host pathogen interaction

Pathogen genomics

" Previous genome missing ~ 1 Million base pairs with many inaccurate gene annotations









Summary [©] Developed resources and capabilities necessary for robust hypothesis testing

- " Project is gaining momentum
- $\widetilde{}$ 2017 should be a good year for data

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