

Phenotypic characterization of quantitative resistance for blackleg in canola

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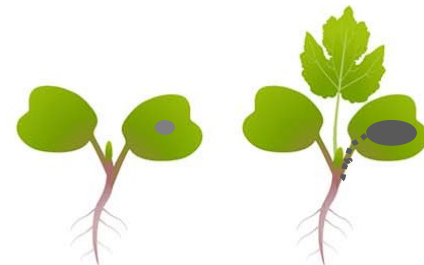
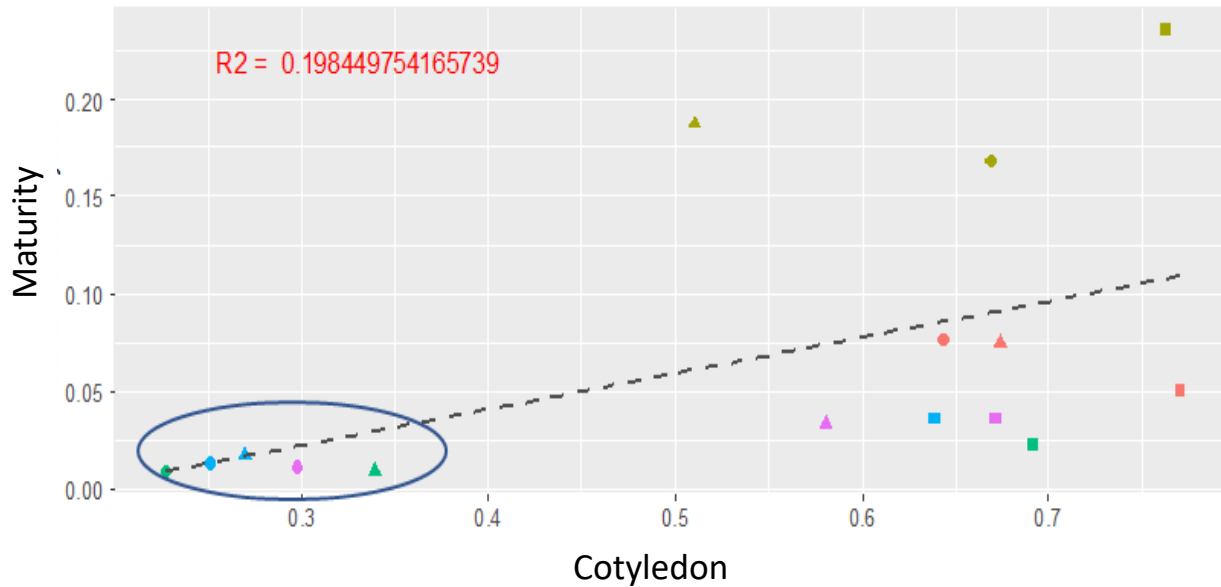
Disease phenotype = Host (G_h) x Environment (E) x Pathogen (G_p) x M





Can phenotyping be done before maturity? YES, but...

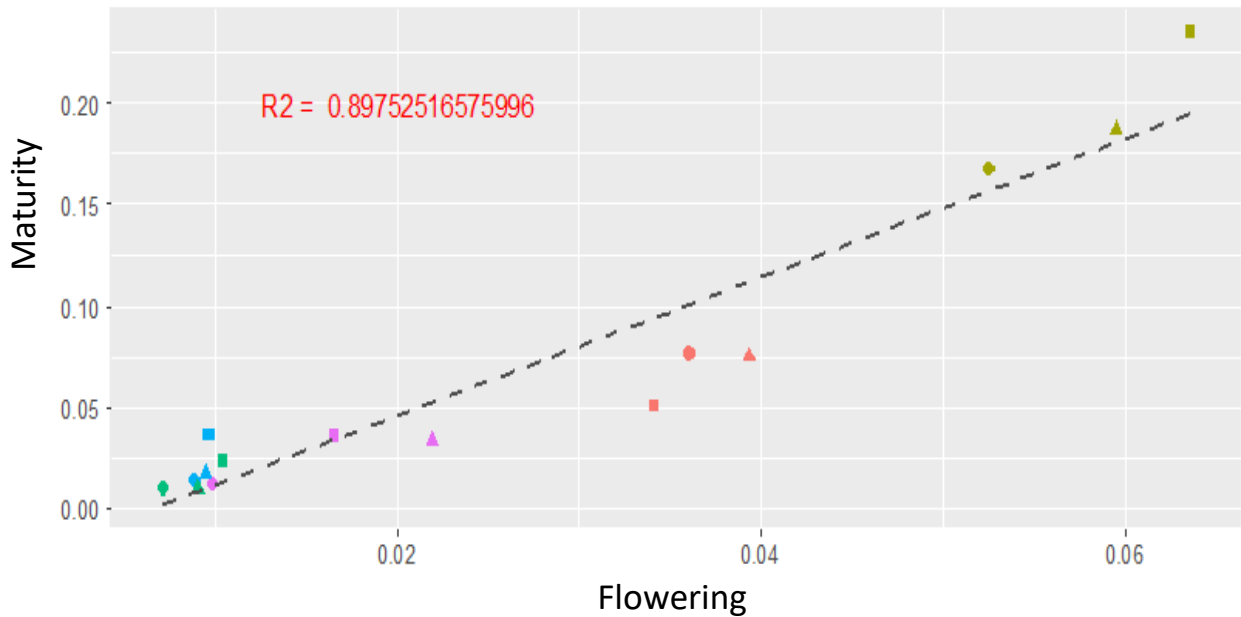
- leaf lesions
- biotrophic phase in petiole





Early crown infection predicts crown canker at maturity

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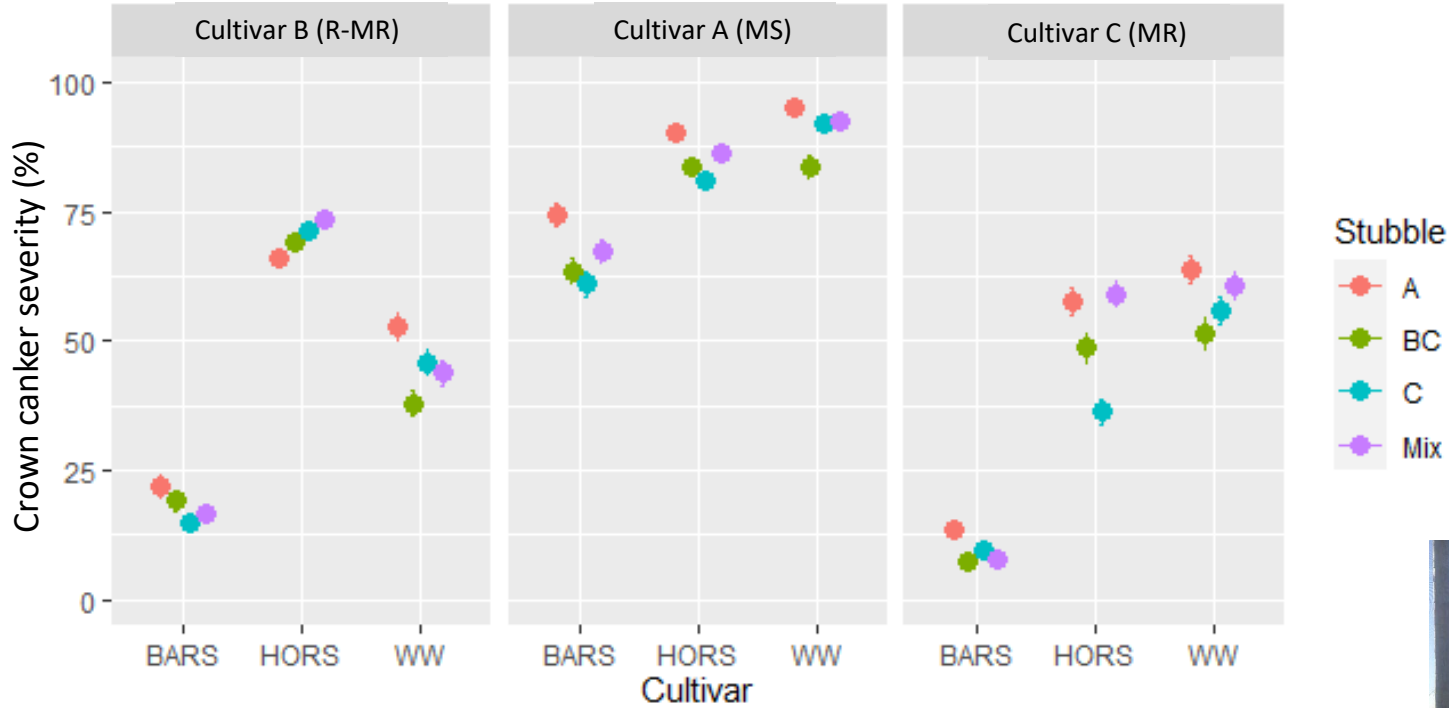
Is pathogen genotype important? YES!

- No partial resistance to all isolates, but instead reacts with individual isolates differently
- Some cultivars are resistant or partially resistant to all isolates, suggesting they have broad QR.
- Rank across all isolates reflects blackleg ratings of the cultivars
- Combinations of QTLs or broadspectrum QTLs?
- Screening with mixed inoculum





How important is the environment? VERY

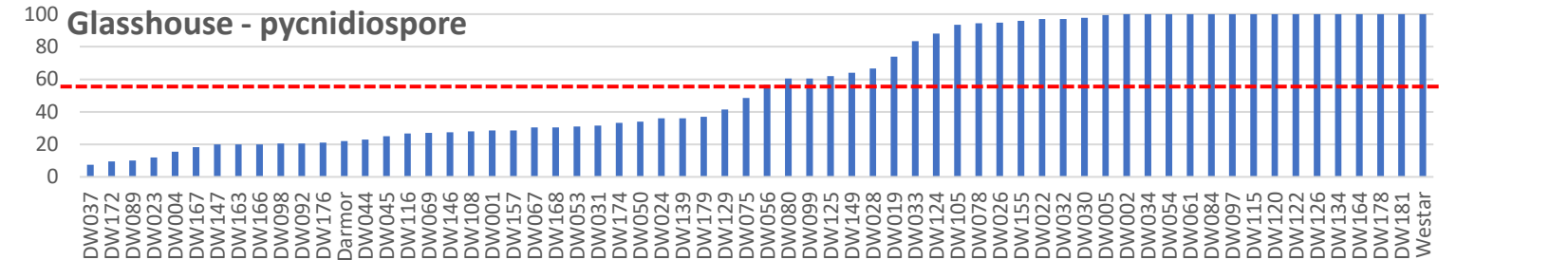
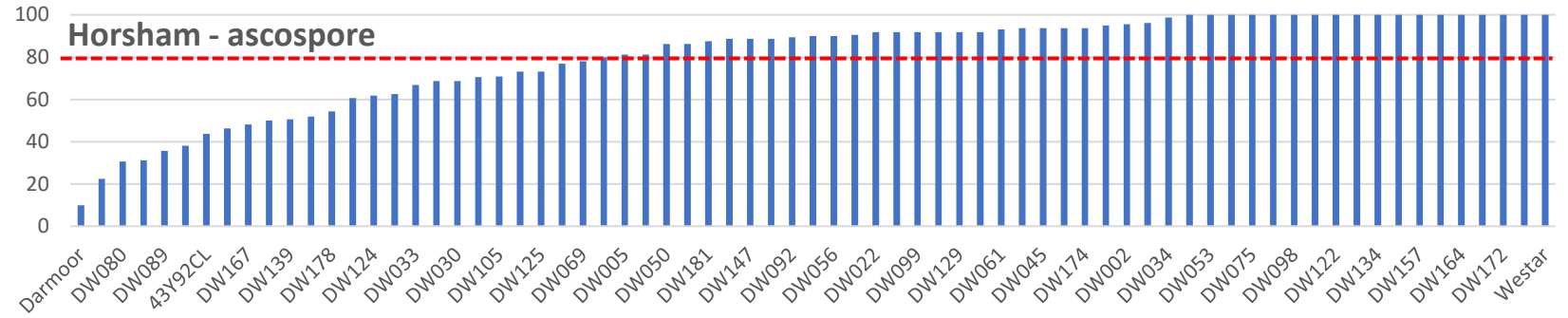
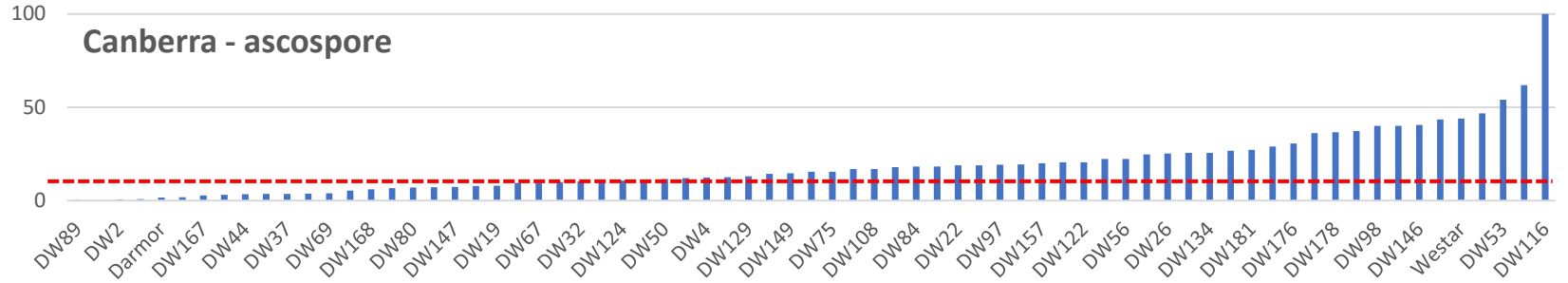




Disease phenotype = Host (G_h) x Pathogen (G_p) x Environment (E) x M

- Darmor-bzh (QR resistant, Rlm9) x Westar (susceptible)
 - subset of 65 DH lines
 - selected for “spring” habit
- 3 environments
 - Canberra and Horsham with same stubble (ascospores)
 - glasshouse with single isolate (pycnidiospores)

Crown canker severity





Summary

- QR expressed in cotyledons and crown, not petioles
- variability not due to mechanism of inoculation - biological
- Blackleg disease phenotype is extremely complex
- Large environmental effect
- Screening with single isolate/population inoculum for detection of QTL's?





Next steps.....

- Phenotyping bottle-neck for breeding
- Improved accuracy to dissect genetics
- Remove subjective human assessment & increase throughput
 - application of machine learning approaches
 - spectral sensors
- QR = broad spectrum and/or combinations of QTL's? Best combinations?
- What are the environmental factors driving blackleg?
 - interrogation of existing datasets