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 School of Molecular and Life Sciences, Curtin University

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 GRDC Curtin University

Sclerotinia stem rot tolerance as a quantitative genetic trait in *Brassica napus*



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Quantity over quality?

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Quantitative trait	Qualitative trait
Controlled by many genes	Controlled by a single gene
Trait takes on a range of values	Trait is either present or absent

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Examples of quantitative and qualitative traits in canola


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QUANTITATIVE

Adult plant *L. maculans* resistance

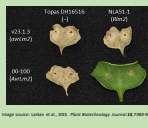


Sclerotinia stem rot resistance



QUALITATIVE

R-gene mediated *L. maculans* resistance



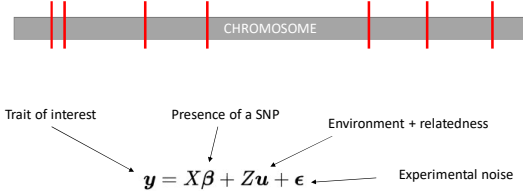
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Identification of 'quantitative trait loci' underlying phenotypes

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$y = X\beta + Zu + \epsilon$

Each SNP considered *individually* for its contribution to the trait.

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Identification of 'quantitative trait loci' underlying phenotypes

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QTL for SSR resistance

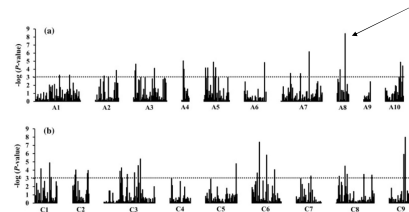


Image source: Gyawali et al., 2016. *Molecular Breeding* 36:72.

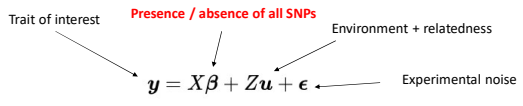
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'Genomic prediction' as an alternative to GWAS for highly complex traits

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$y = X\beta + Zu + \epsilon$

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Genomic prediction requires training and testing

Training population

SNPs and trait values known
Used to test association of SNP content with trait for all SNPs




Image source: CSIRO; <https://blog.csiro.au/omega-corn-3-corn-gets-green-light/>

Testing population

Only SNPs known
Select lines in a breeding cycle based on SNP predictions from the training population




Image source: Wikipedia; https://en.wikipedia.org/wiki/Canola_oil


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Two years of ASSYST screening


Variety A

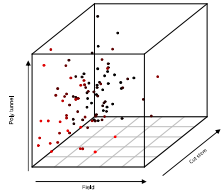
Mean AUDPC = 2594
In vitro (mm) = 41
Field (counts) = 10/150 stems



Variety B

Mean AUDPC = 324
In vitro (mm) = 16
Field (counts) = 0/150 stems



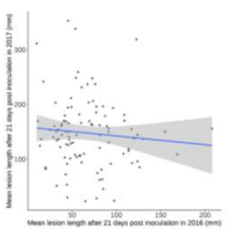
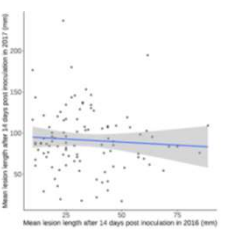


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No correlation between years

Means from 5-10 replicates

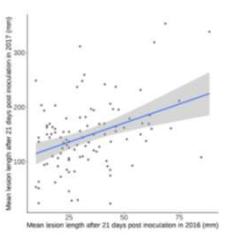
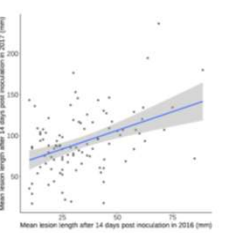



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Correlation if failed infections removed

Means from 5-10 replicates with failed infections removed

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Low R² values but *something* there

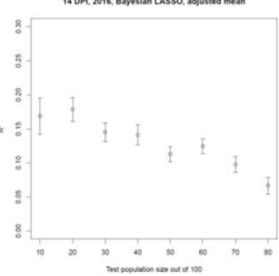
Model	R ² 2016	R ² 2017
Bayesian LASSO	0.18	0.05
Bayesian RR	0.16	0.07
BayesA	0.16	0.08
BayesB	0.16	0.06
BayesB	0.1	0.07

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R² increases with training population size

14 DPI, 2016, Bayesian LASSO, adjusted mean



Extrapolate to a population of 500?

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Conclusions

- Genomic prediction has potential for SSR.
- Requires a larger, more carefully selected population.
- Scope for collaboration:
 - Collaborators: additional populations, statistical expertise.
 - CCDM: infection assay, statistical expertise.

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Title

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THANK YOU

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