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Quest for new sources of resistance to blackleg

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Background

- Australian canola breeding programs (including previous public programs) have been very successful in breeding canola varieties resistant to blackleg
- Selection of resistant varieties relied mostly on field evaluation
- Development of a set of differential isolates facilitated known and new R genes identification
  - Conventional path tests
  - Molecular mapping

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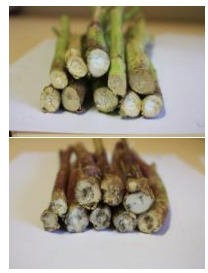
Current NBGIP research on blackleg resistance

- National Brassica Germplasm Improvement Program (NBGIP)
  - NSWDPI (Wagga Wagga)
  - DEDJTR (Horsham)
- Canola Molecular Marker Program (2008-16)



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NBGIP approach

- Evaluate germplasm for resistance
- Phenotyping methodologies
  - Field testing (a valuable breeding tool)
  - Ascospore shower test
  - Single spore isolate
- Germplasm
  - Germplasm collections (*B. rapa*, *B. oleracea*, *B. napus*, *B. carinata* and other subspecies)
  - Mapping populations

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Progress on molecular mapping of blackleg resistance genes (loci)

- NBGIP/CMMP have mapped at least 10 populations of canola for qualitative/quantitative resistance
  - Skipton/Ag-Spectrum
  - Maxol/Westar
  - Columbus/Westar
  - BLN2762/Surpass400
  - Ag-Castle/Westar
  - RP04/Ag-Outback
  - Tapidor/Ningyou7
  - Darmor/Yudal
  - Hyola50 populations (11-5107 & 11-5329)
  - YW population of *B. carinata*

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Genome-wide association mapping for blackleg resistance

- Bi-parental mapping populations
  - Sample only two segregating alleles
  - Mapping populations may not be relevant to genetic improvement programs
  - Trait-marker associations may be specific to pop.
    - Long time-lag to marker assisted breeding
- Genome-wide association approach overcomes above limitations
  - Utilise diverse breeding germplasm

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Experiment plan for GWAS

1. Diversity panel of 175 *B. napus* genotypes
2. Phenotyped with isolate 04MGPS021 (NSW DPI, Wagga)
3. Genotyped a diversity panel with 18804 SNPs markers (MAF> 0.05)
4. Trait-marker association using GAPIT, Mixed model and parsimonious multi-QTL model

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Stubble sources used for phenotyping for blackleg resistance in a diversity panel

Resistance Group	Source of Stubble
A	Av-Garnet
B	CrusherTT
C	CB Jardee HT
D	Hyola50
E	Monola 76 TT

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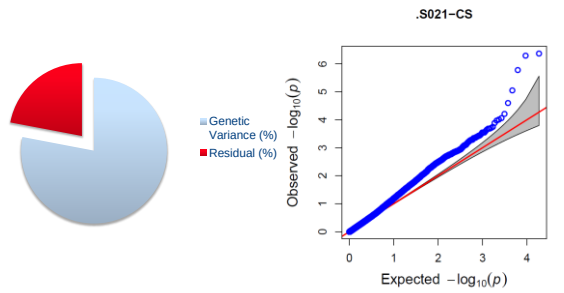
Association between blackleg resistance and marker data



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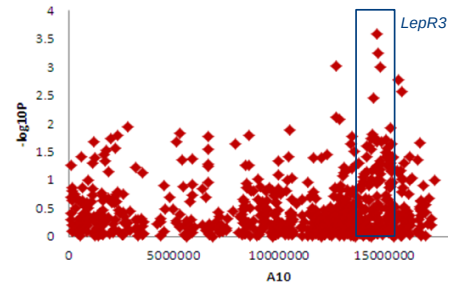
GWA & locations of markers linked with blackleg resistance in *B. napus*



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Conclusions

- GWA analyses validated known *R* genes and known QTL identified in *B. napus* populations.
- GWA analyses also detected new associations for resistance to blackleg
  - Presence of new loci (genes) was also validated in bi-parental populations
  - Novel favourable alleles are of great interest to canola breeders
  - Some of novel alleles were also traced back to ancestors of *B. napus*

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