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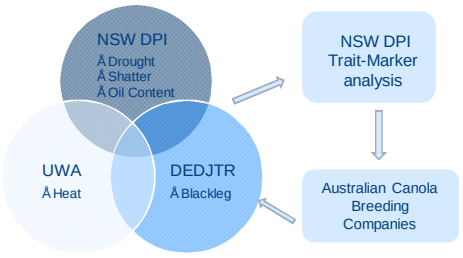
Review of NBGIP traits, and outcomes from the past 5 years

Harsh Raman
National Brassica Germplasm Improvement Program

Current NBGIP research



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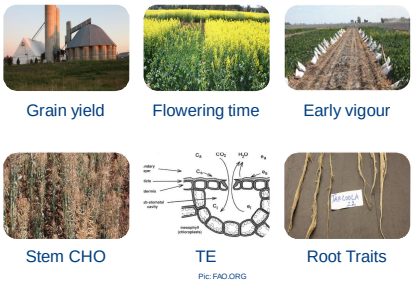
Research on drought tolerance



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Identified QTL and candidate genes for flowering time and grain yield

- Raman et al (2016) Crop & Pasture Science (in press)
- Raman et al (2016). Plant Cell & Environ. doi: 10.1111/pce.12644
- Raman et al (2014). Plant Biotech J. 12(7):851-60
- Zou et al (2014). Theor Appl Genet.127:1593ï 1605
- Raman et al (2013). Theor Appl Genet 126:119-32
- Hou et al (2012) BMC Plant Biol. 12:238
- Zhu et al (2012) PLOS ONE 7(9): e45751
- **Unpublished QTL data for NDVI, biomass & grain yield in 4 Australian DH populations**

BioFirst
A NSW Government Initiative

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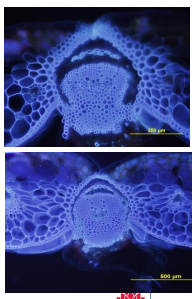
Identified QTL and candidate genes for pod shatter resistance in canola

- Raman et al (2014) PLOS One ***9(7):e101673***
- Liu et al (2016) Frontiers in Plant Sci (Submitted)



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Mapping populations for resistance to blackleg

- Skipton/Ag-Spectrum
- BLN2762/Surpass400
- Maxol/Westar
- Columbus/Westar
- Ag-Castle/Westar
- RP04/Ag-Outback
- Hyola50 populations
- DHC2261/RR05
- DHC2211/RP012*S
- Skipton*2/Ag-Spectrum
- Darmor/Yudal
- Tapidor/Ningyou7
- YW population of *B. carinata*

→ QTL mapping and markers

↓

Canola breeding programs

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Identified loci for blackleg resistance

Qualitative resistance

- *Rlm1* and *Rlm3*
  - Raman et al (2013) Crop & Pasture Sci 63, 1007-17
- *Rlm4*
  - Raman et al (2012) Theor Appl Genet 125;405-18
  - Tollenaere et al (2012) Plant Biotechnology Journal 10:709-715
  - Raman et al (2014) Plant Biotech J 12:851-860
  - Zander et al (2014) Funct & Integ Gen 13(3):295-308
- *LepR3 & Rlm4:*
  - Raman et al (2016) Phytopath (submitted)

Quantitative resistance

- QTL
  - Raman et al (2012) Theor Appl Genet 125;405-18
  - Larkan et al (2016) in preparation
- GWAS
  - Raman et al (2016) in preparation

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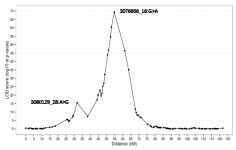
Mapped qualitative and quantitative resistance in RP04/Ag-Outback

- 177 DH lines
- Phenotyping (6 expts)
  - Single spore isolates at Wagga
  - Ascospore shower (2013)
  - Field screening
    - 2013 (2 Expt, Wagga)
    - 2015 (1 Expt, Horsham)
- Genetic map (~2500 markers)
- QTL for resistance on A7, A10 and other chromosomes (LOD of 5)



Qualitative locus for seedling resistance on A7

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Mapped loci for blackleg resistance in Hyola50

- Utilised two DH populations from 11-5107 & 11-5329 crosses
- Phenotyping
  - Qualitative resistance
  - Quantitative resistance (field conditions at several locations)
- Identified closely markers linked with resistance genes

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Mapped a DH population from Darmor/Yudal for quantitative resistance (Wagga Wagga, 2015 trial)

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Validation of qualitative *Rlm* genes-marker associations using differential set in 180 diverse lines of canola

	D2	D3	D4	D5	D6	D7	D8	D9	D10	D13	D14
AvrLm1	Vir	Vir	Vir	Avr	Avr	Avr	Vir	Vir	Vir	Vir	Avr
AvrLm2	Vir	Vir	Vir	Avr	Vir	Vir	Vir	Vir	Vir	Vir	Vir
AvrLm3	Vir	Vir	Vir	Vir	Vir	Avr	Vir	Vir	Vir	Vir	Vir
AvrLm4	Vir	Vir	Avr	Avr	Vir	Vir	Vir	Vir	Vir	Avr	Vir
AvrLm5	Avr	Avr	Avr	Vir	Avr	Avr	Avr	Avr	Avr	nd	Avr
AvrLm6	Avr	Vir	Avr	Vir	Avr	Avr	Vir	Avr	Avr	Avr	Vir
AvrLm7	Vir	Vir	Avr	Avr	Vir	Vir	Avr	Avr	Vir	Avr	Avr
AvrLm8	Avr	Vir	Avr	Vir	Avr	Avr	nd	nd	Avr	nd	nd
AvrLm9	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Avr	Vir	Vir
AvrLmS	Avr	Vir	Avr	Avr	Avr	Avr	Vir	Vir	Avr	Vir	Avr
AvrLepR1	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Vir	Avr
AvrLepR2	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Vir	Vir
AvrLepR4	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr	Avr

Courtesy- Angela

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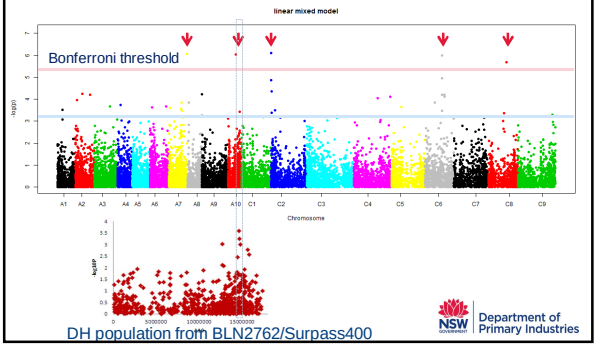
SNP associations were validated with QTL and GWAS (04MGPS021)



DH population from BLN2762/Surpass400

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2015 Season for NBGIP at Wagga

Fodder type *Brassica napus*

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Summary

- NBGIP projects (DAN00117, DAN00208) have made significant progress in
  - Understanding genetics underlying both qualitative and quantitative resistance
  - Mapped loci associated with blackleg resistance
  - Characterized 2 diversity panels for resistance to blackleg
- Further research is required to
  - validate resistance loci under different environments/ populations
  - Identify better isolates to distinguish different *R* genes & investigate *R-Avr* gene interactions

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Acknowledgments

NBGIP-DAN00117/DAN00208

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- Phil Salisbury
- Denise Barbulescu
- Simon Diffey (SAGI)
- **Steve Marcroft**
- **Angela Van de Wouw**

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