

Department of Environment and Primary Industries Victoria GRDC Grains Research & Development Corporation



National Brassica Germplasm Improvement Program Trait Development:

Blackleg resistance in *Brassica napus*

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Pathology Workshop February 2014

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Overview

- NBGIP 1 – Past Outcomes
- NBGIP 2 – Horsham node responsibilities
- Horsham Team

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National Brassica Improvement Program 1

- Horsham node research components objectives

- 1) Improved blackleg resistance by identifying, characterising and incorporating resistance genes from European winter canola.
- 2) Identifying and incorporating novel blackleg resistance genes in diploid progenitors and weedy relatives for improvement of canola germplasm.
- 3) Method validation and evaluation of shatter tolerant germplasm.
- 4) Identification and development of germplasm with improved quality traits (low glucosinolates, low saturated fats and high protein & oil content).

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National Brassica Improvement Program 1



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National Brassica Improvement Program 2

VIC DEPI has the sole leading role in the identification and development of germplasm with new resistance to blackleg.

VIC DEPI has a co-lead role with NSW DPI in molecular marker discovery for the new blackleg resistance genes.

Deliverables

1. Germplasm with novel seedling resistance to blackleg developed from diploid progenitors and made available to canola breeders.
2. Developed and validated method for accurate phenotypic assessment and gained understanding of the phenotypic variation for adult plant resistance to blackleg.
3. Identification of loci significantly contributing to the phenotypic variation for resistance to blackleg, both seedling and adult plant resistance – **phenotyping component for NSW DPI**

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Victorian NBGIP team

- **Leadership**
 - Phil Salisbury
 - Tony Slater
- **Germplasm Enhancement Scientists**
 - Denise Barbulescu – pathology, field trials, tissue culture, project management
 - Joshua Koh – phenotyping, self-incompatibility system, molecular biology
- **Skilled technical team and good facilities for large scale phenotyping and genotyping**

