

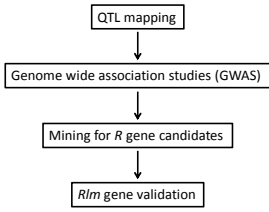

## Brassica genes involved in Blackleg resistance

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## Identification and characterisation of *Rlm* genes in *Brassica napus*


- The Batley Lab is currently working on the identification of *Rlm1*, *Rlm2*, *Rlm3*, *Rlm4*, *Rlm7* and *Rlm9* in *B. napus*

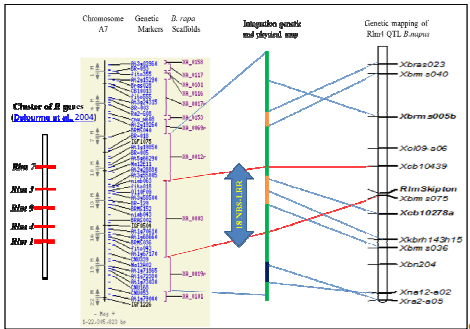

## QTL mapping

Use of previous literature and SSR marker work (Raman, *Rlm4* QTL)

Mapping these to the *B. rapa* (AA) genome and now the *B. napus* (AACC) genome to define the QTL



## QTL mapping to physical map

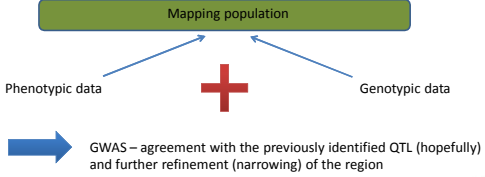




## Genome-wide association studies

Correlation between phenotypic response on juvenile plants (cotyledon score) and the genotype of each individual

Requires a mapping population:

- Skipton x Ag-Spectrum - *Rlm4* (courtesy of NSW DPI)
- Tapidor x Ningyou7 - *Rlm2* (courtesy of Huazhong Agricultural University, Wuhan)





## GWAS *Rlm4* and *Rlm2*

Genotypic data

- 6K and 60K Infinium SNP chip
- Genotyping by sequencing (GBS)

- Rlm4* GWAS study using the 6K infinium assay narrowed the QTL down from ~5.5 Mbp to ~420,000 bp
- Rlm2* GWAS on the Tapidor x Ningyou7 population focused on a region of just over 1 Mbp on A10.
- The *Rlm2* GWAS study using GBS of the mapping population resulted in far greater marker density (440 markers as compared to 21)





## Where are we at?

Chromosome A7 contains 19 potential candidate R genes

**Rlm1**

- 1 candidate gene undergoing LR-PCR and sequencing

**Rlm2**

- 3 candidates, one undergoing transformation while final sequencing is performed

**Rlm4**


- 4 candidate genes undergoing LR-PCR and sequencing
- 2 candidates are undergoing transformation
- Also a region identified by GWAS is being fully amplified

**Rlm9**

- 2 final candidates are now undergoing transformation
- 3 other candidates have been ruled out through sequencing

**Rlm3 and Rlm7**

- No "specific" Rlm3 or 7 candidates as yet



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