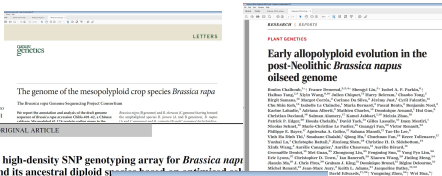


Rlm gene identification

Jacqueline Batley
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 University of Western Australia
 jacqueline.batley@uwa.edu.au

1

Genomic Resources

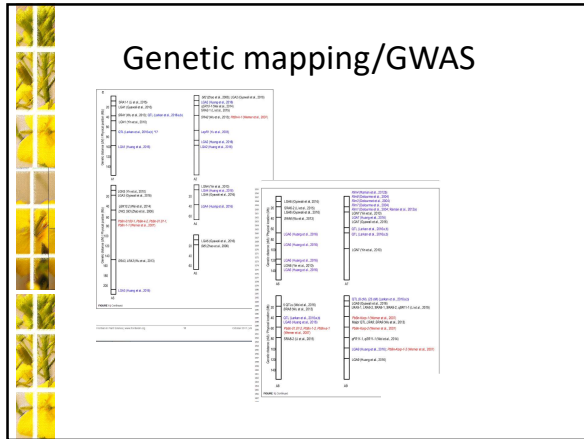


The genome of the mesopolyploid crop species *Brassica napus*

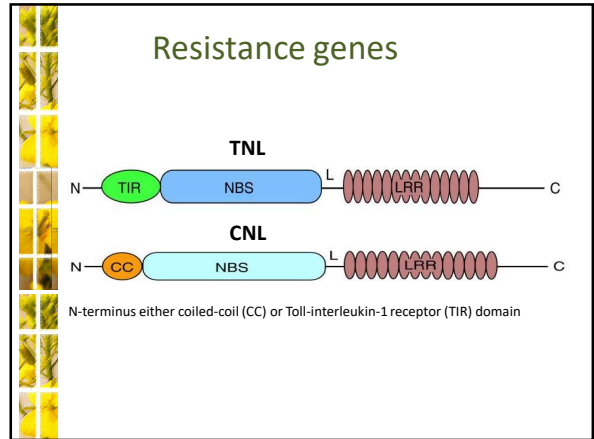
A high-density SNP genotyping array for *Brassica napus* and its ancestral diploid species *B. rapa* and *B. oleracea* using a set of single-locus markers in

Warren E. Clark¹, Felix E. Hitzler¹, Jeroen Jacqueline Batley¹, Steve Edwards¹, Paul Benjamin Lagrè², Wang Chen³, Frederic Benjamin Sleich⁴, Rafal J. Sawolowski⁵, An

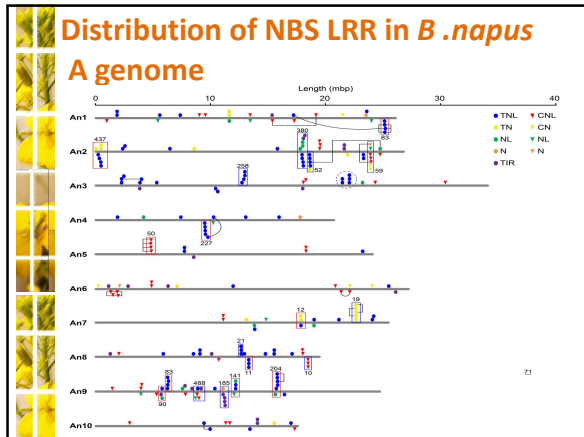
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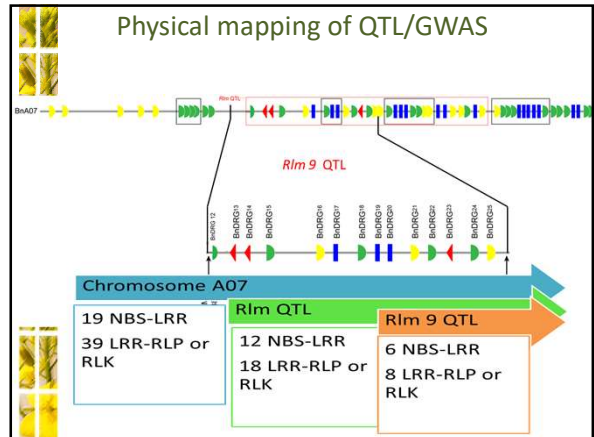
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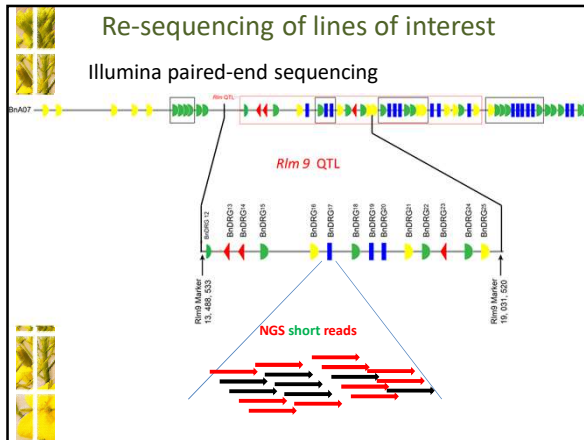
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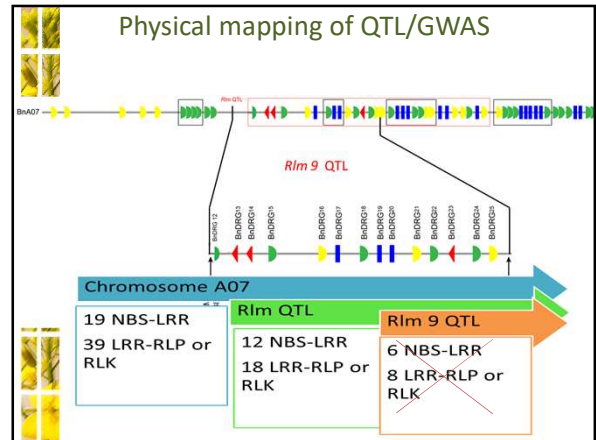
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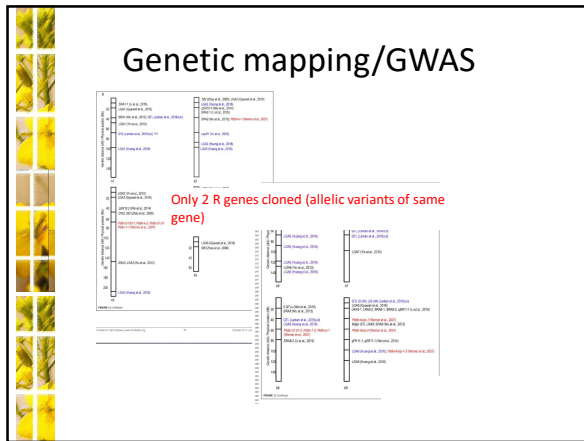
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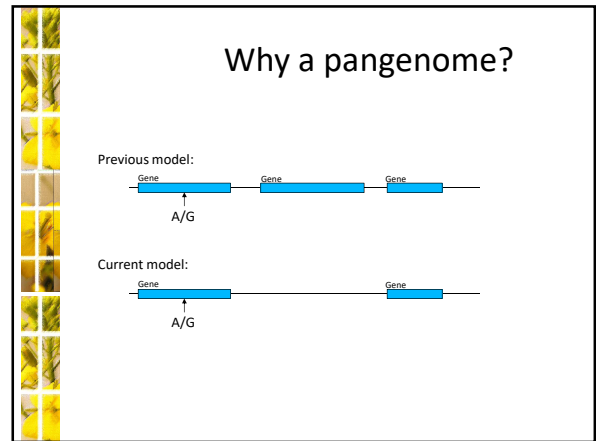
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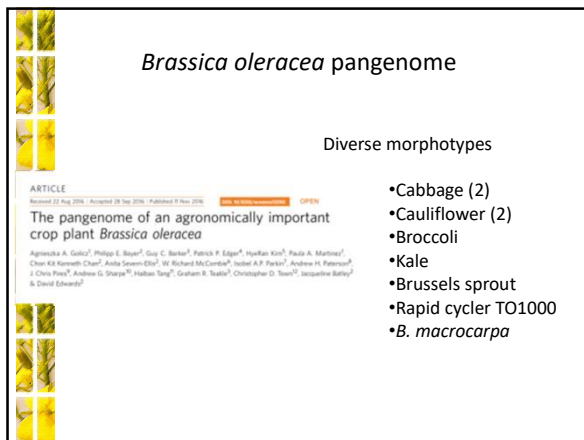
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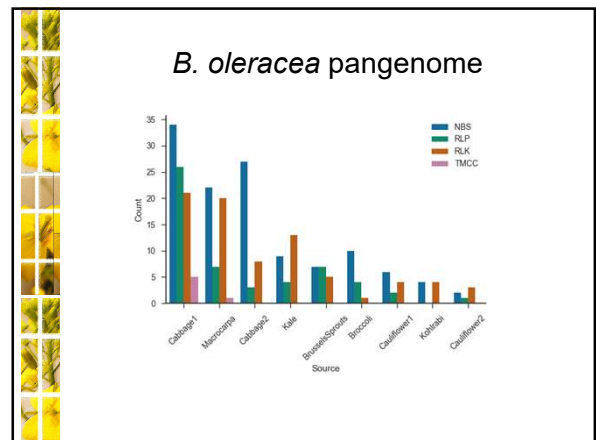
9



10



11



12

R genes in the pan genome

- Almost 70% R genes were variable
- Oilseed types lost more R genes than synthetics

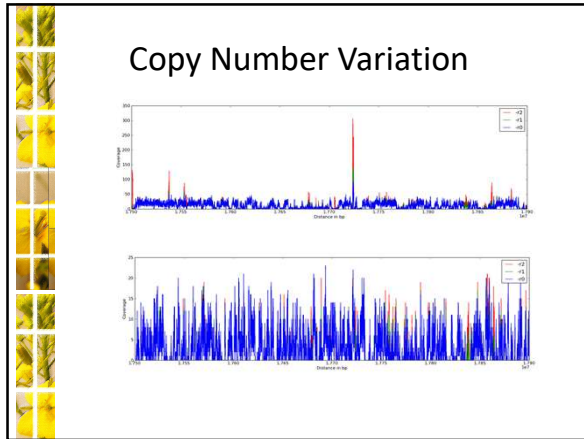
13

Copy number variation

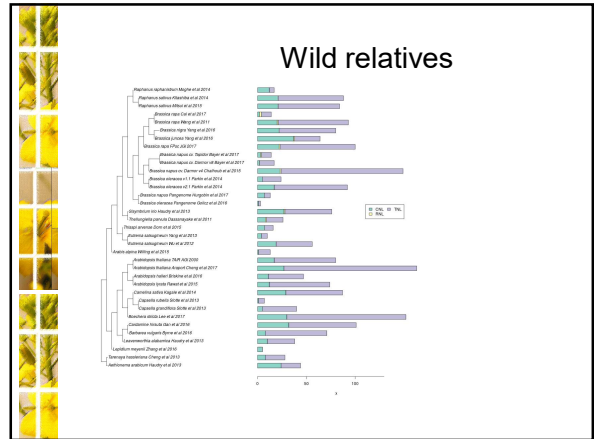
A form of structural variation resulting in the cell having different number of copies of one or more segments of DNA

- Chromosomal deletions
- Insertions
- Duplications

14



15



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Locating candidate region with linked genetic markers

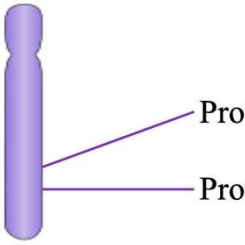
17

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R genes in the candidate region

18

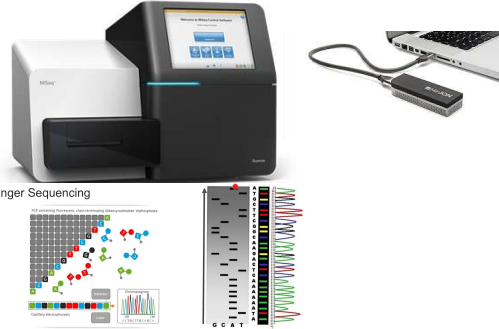
R genes in the candidate region



Functions	
PREDICTED: Brassica napus wall-associated receptor kinase-like 10 (LOC106353392), mRNA	Pro
PREDICTED: Brassica napus serine/threonine-protein kinase BLU51-like (LOC106353395), transcript variant X2, mRNA	

19

Resequencing



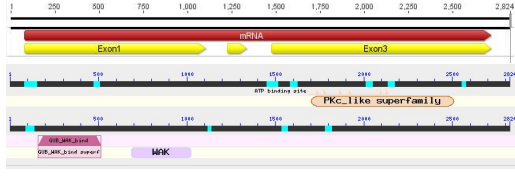
Sanger Sequencing

20

A strong *Rlm4* candidate where all *Rlm4* lines share the same allele and four alleles are identified among resequenced susceptible lines

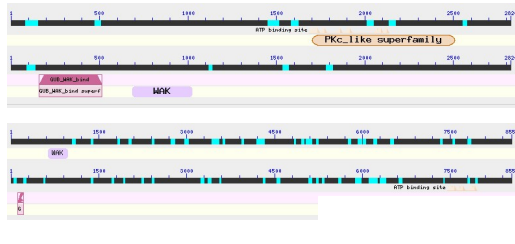
21

The *Rlm4* candidate codes for a typical RLK protein



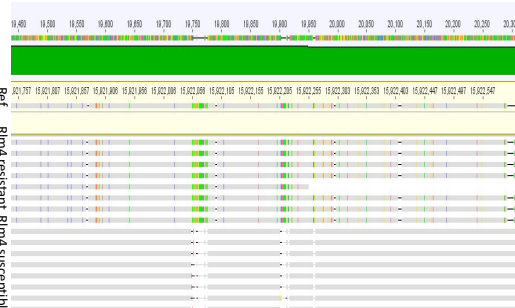
22

6k insertion between the extracellular galacturonan-binding and intracellular kinase domain





23

Polymorphisms consistent with *Rlm4*



24



Future directions

- Candidate gene validation
- Identification of *Rlm7* and *Rlm3* candidate through resequencing

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