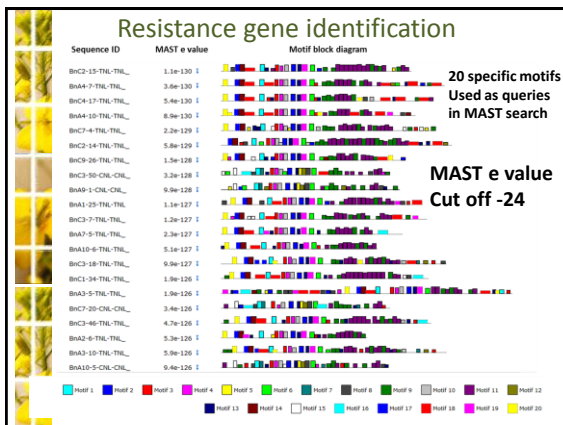
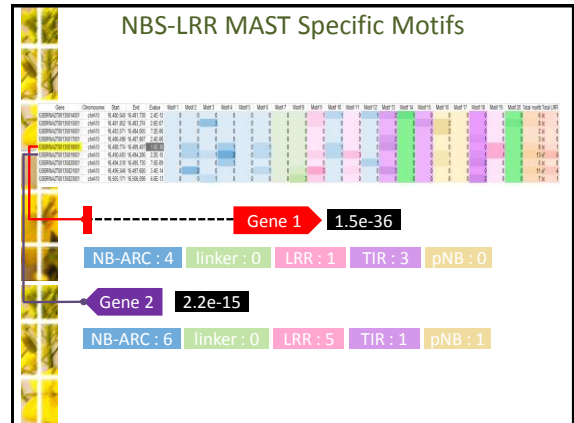
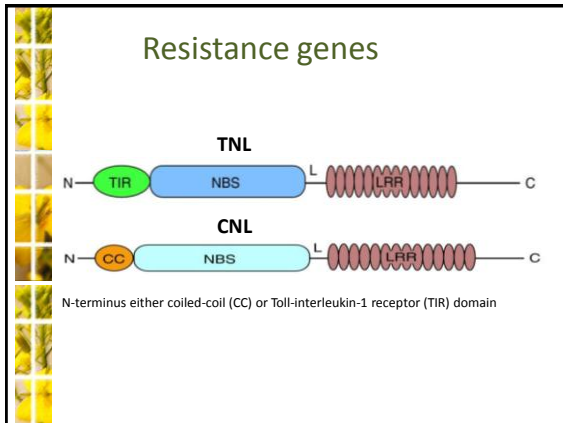


Blackleg resistance gene identification in *Brassica napus*: A pan genome approach

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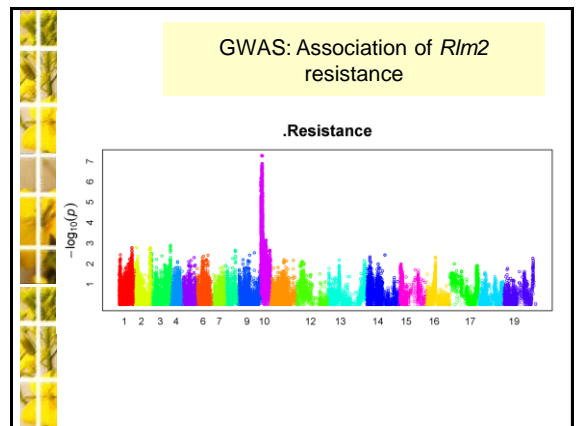
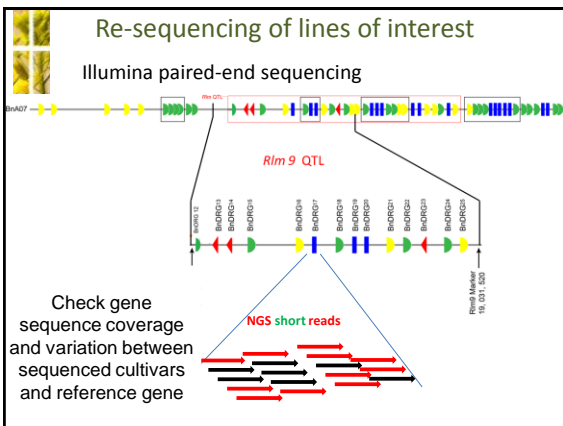
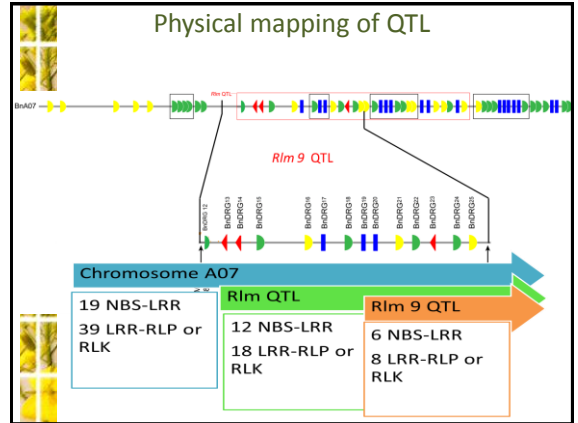
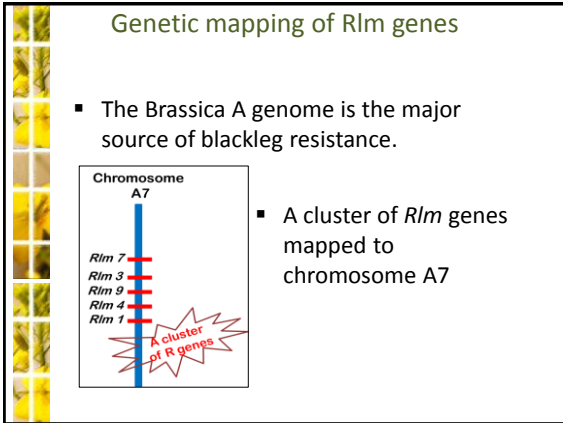
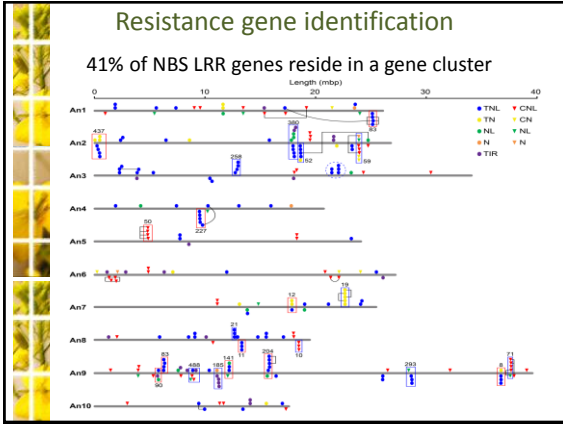
Outline

- Whole genome resistance gene identification
- Candidate gene identification
- Two new approaches for genome analysis
 - Gene loss analysis
 - Presence Absence Variation (PAVs)

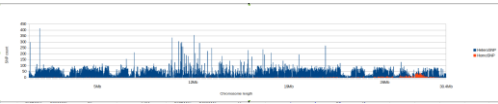


Resistance gene identification

Species	<i>B. napus</i>	<i>B. oleracea</i>	<i>B. rapa</i>
Genome size (Mbp)	1284	650	552
Gene content	111,479	59,225	41,019
Total NBS LRR genes	641	443	248
NBS LRR genes density	0.58%	0.74%	0.60%



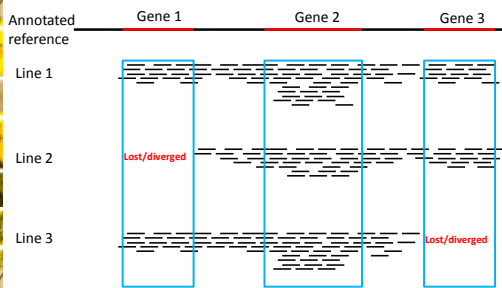
Bulk segregant analysis



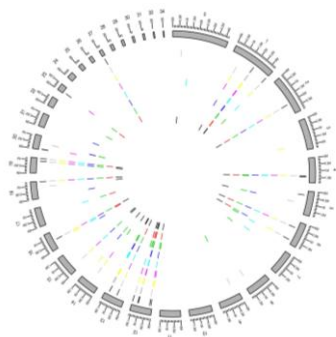
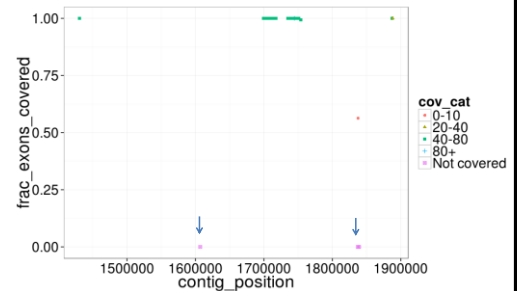
Gene loss analysis

- Analyses sequence read coverage over the annotated genome and reports genes with no sequence coverage i.e. lost genes
- Dependant on correct annotation of reference genome
- Aids understanding of necessary genes vs “disposable” genes
- Potential of discovering new *R* genes by cross-referencing phenotype with lost genes

Gene loss method

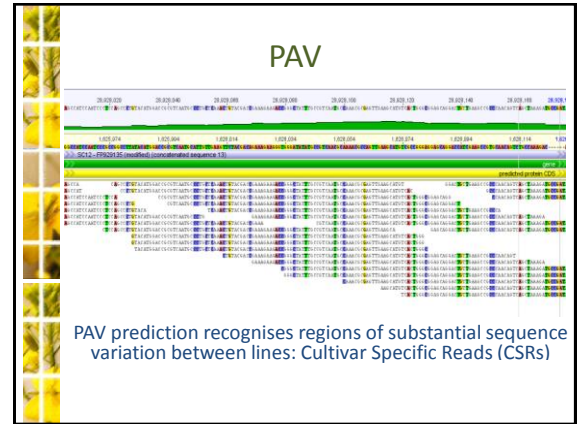
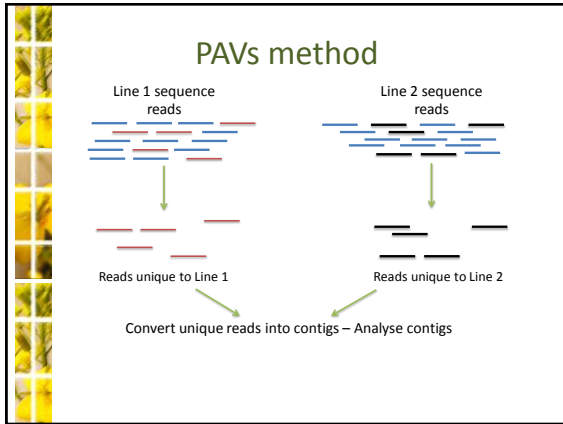


Gene loss



Presence/Absence Variation (PAVs)

- Recognises sequence reads unique to one isolate using a K-mer based approach
- Does not require a reference genome
- Validated in Brassicas



Summary

- Different approaches to gauge which genes are conserved differently across different lines
- Can be used to identify genes of interest
- Next generation sequencing allows rapid identification and validation of candidates