



Disease management in oilseed rape: insights into the *Brassica napus*-*Pyrenopeziza brassicae* pathosystem

Chinthani Karandeni Dewage
c.s.karandeni-dewage@herts.ac.uk

OREGIN Stakeholders' Forum
19 Dec 2024

Light leaf spot disease

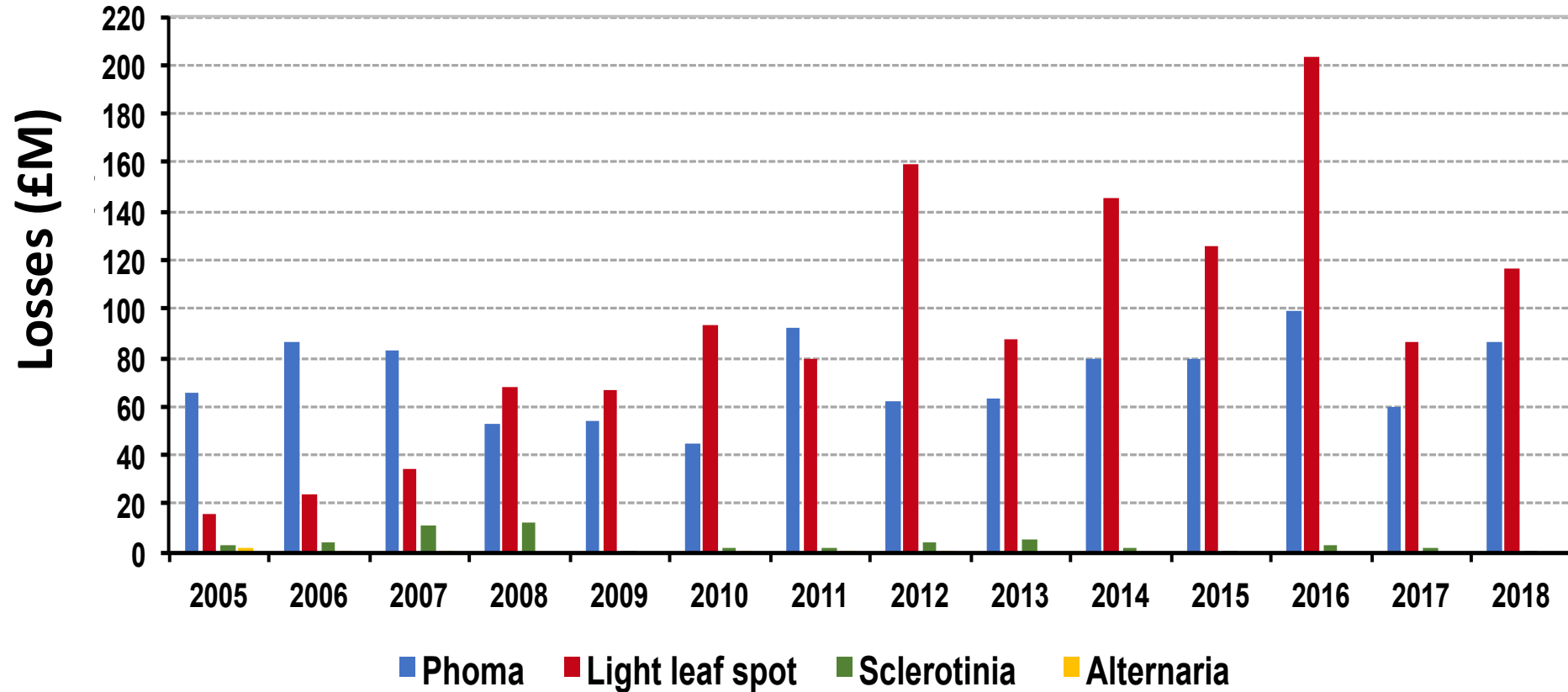
Oilseed rape



Vegetable brassicas

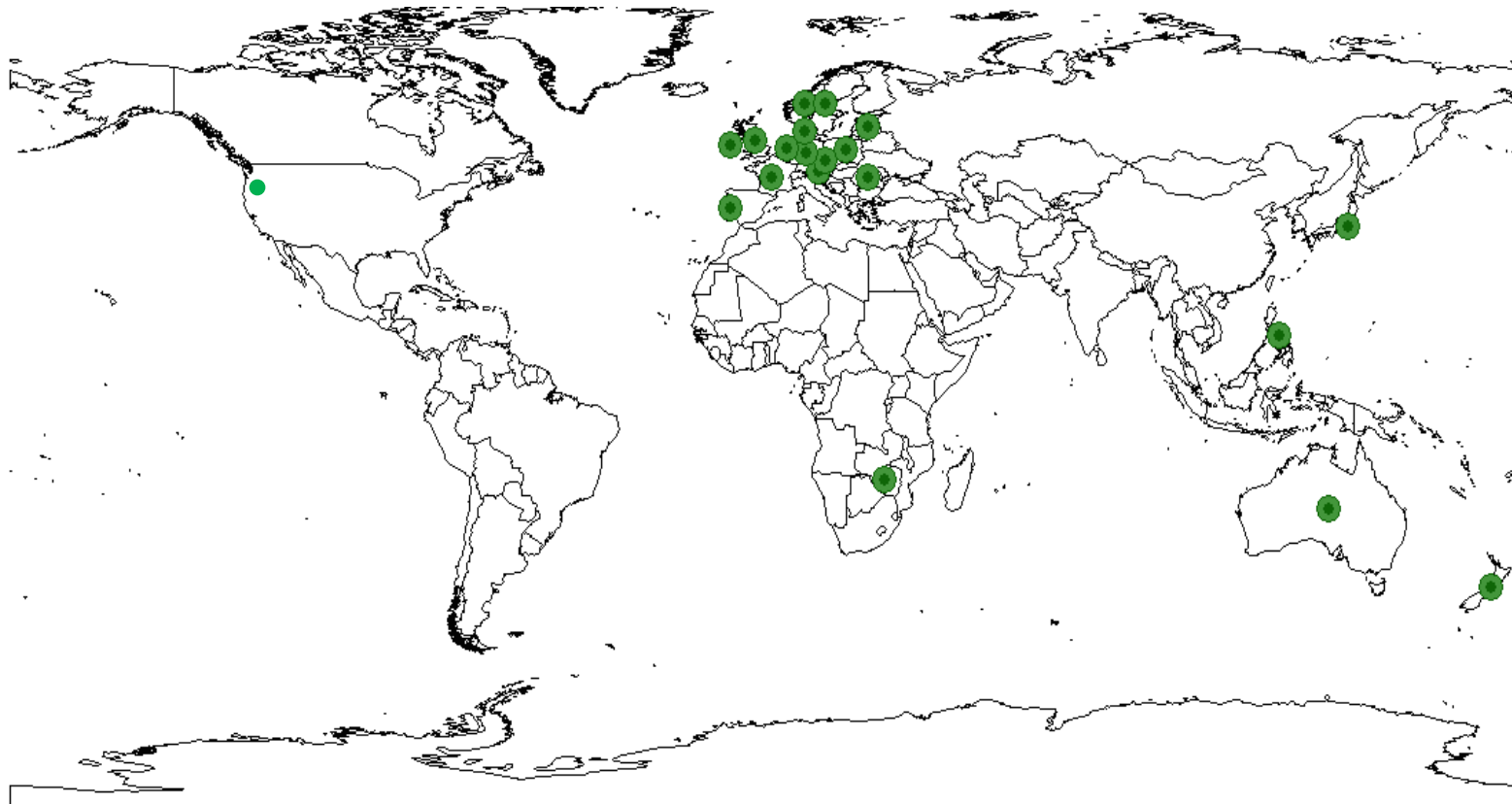


OSR yield losses caused by diseases in England

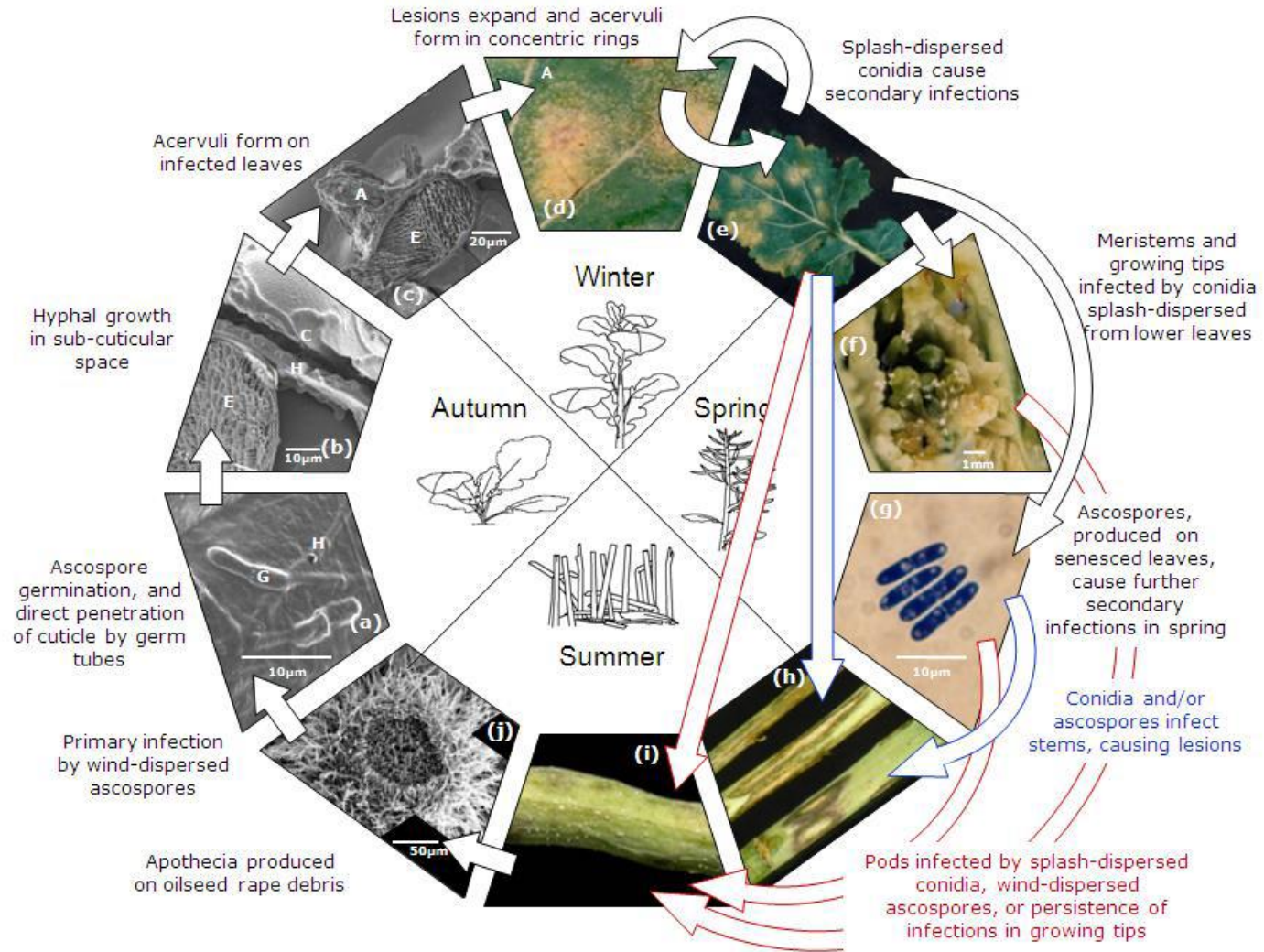


CropMonitor; www.cropmonitor.co.uk, oilseed rape pest and disease

Regional distribution of light leaf spot

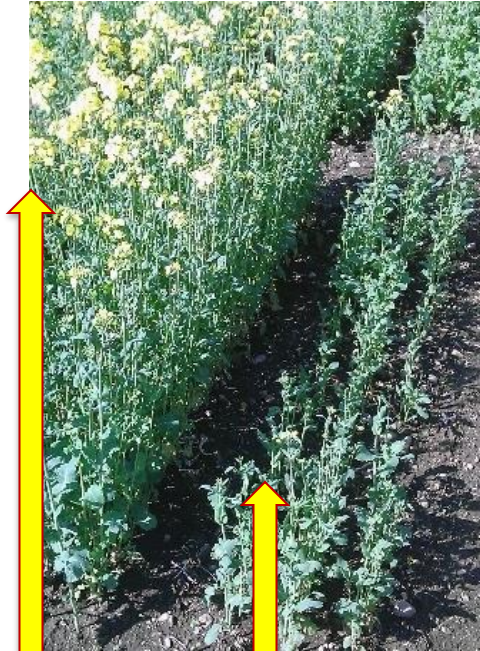


Life cycle of *P. brassicae*

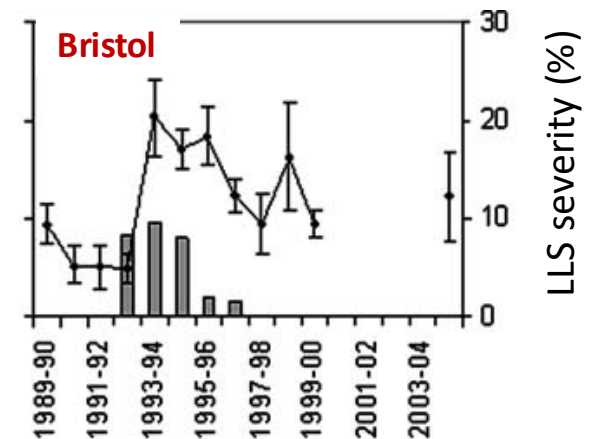
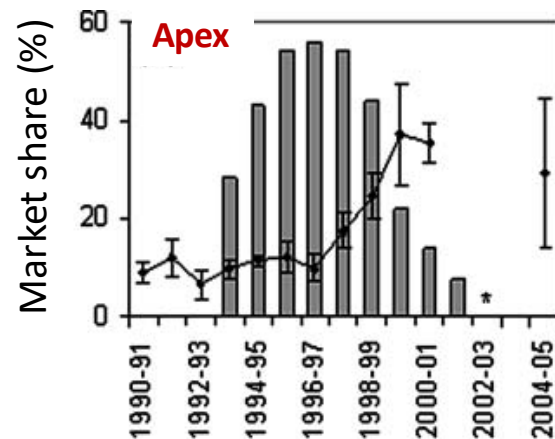
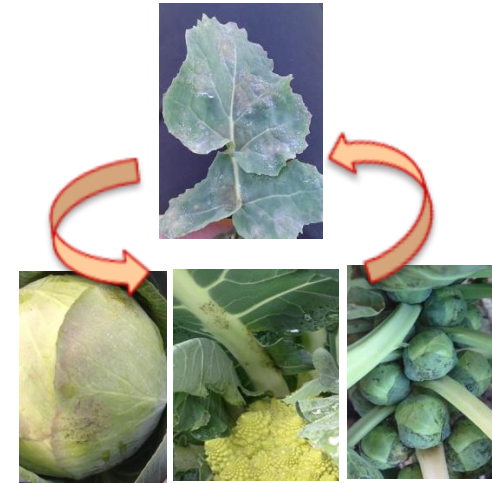


Disease management, issues and knowledge gaps

- Cross-infectivity between different *Brassica* species
- Breakdown of host resistance
- Development of fungicide insensitivity



cv. Cracker with RL resistance rating 8 for the North region



Insights into the *B. napus* - *P. brassicae* pathosystem

- **Resistant and susceptible phenotypes**
- **Differential interactions**
- **Genetic and molecular basis of resistance against *P. brassicae***
- **Identification of new sources of resistance**

Spatial and temporal deployment of different sources of cultivar resistance to increase their durability for an effective management of LLS

Investigation of the phenotype/s of resistance

Leaf deformations - a characteristic feature of light leaf spot

- First sign of the infection
- c. 7 dpi
- Both resistant and susceptible plants

(Petiole elongation)



(Leaf curling)



(Leaf distortion)



Susceptible Cultivar

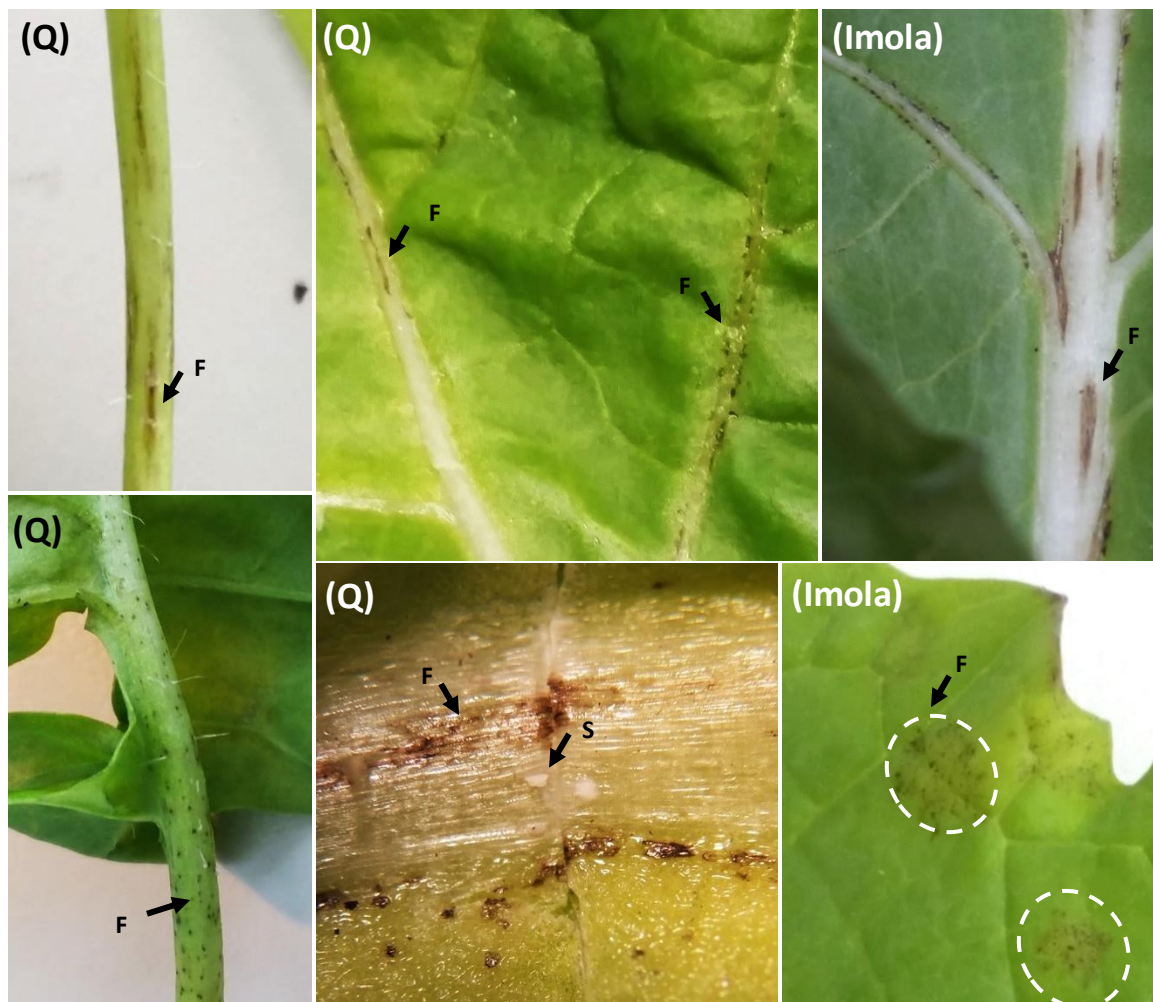


Resistant cultivar

Investigation of the phenotype/s of resistance

Necrotic flecking

- Normally appeared around 9 dpi
- Quantitative
- Amount of sporulation varied depending on the intensity of black flecking
- Concentric ring-like pattern



Mapping of the necrotic flecking phenotype – cv Imola

Biparental (Imola x Line 218-11) DH population

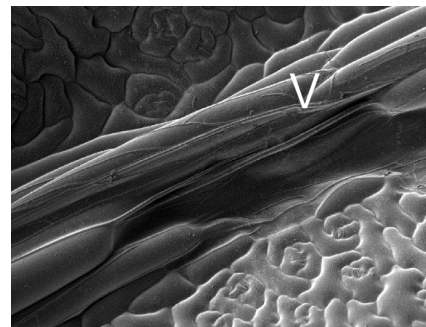


Resistant phenotype

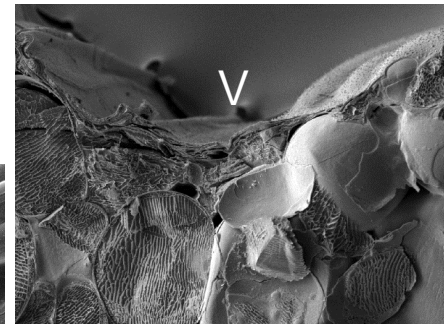


Susceptible phenotype

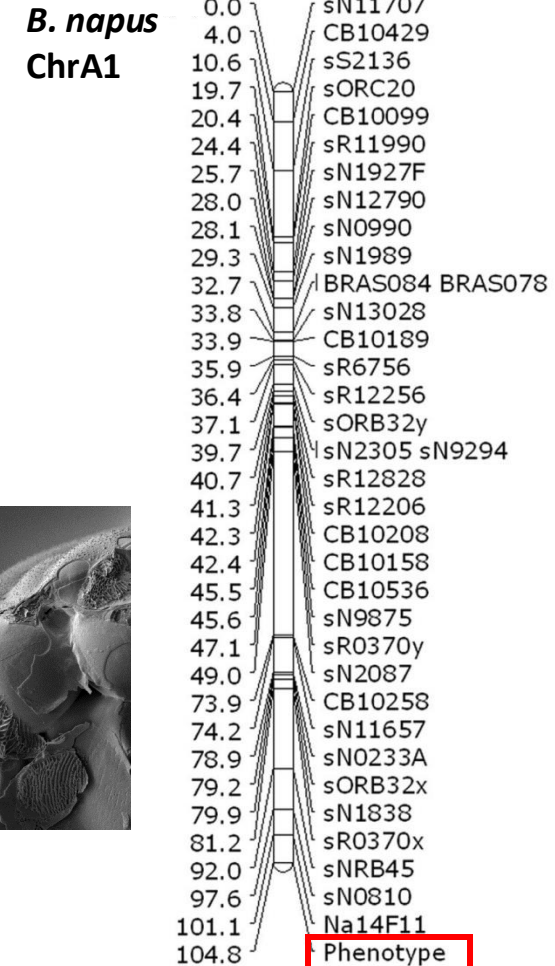
Collapsed epidermal cells
on leaf vein (V)



9 dpi



9 dpi

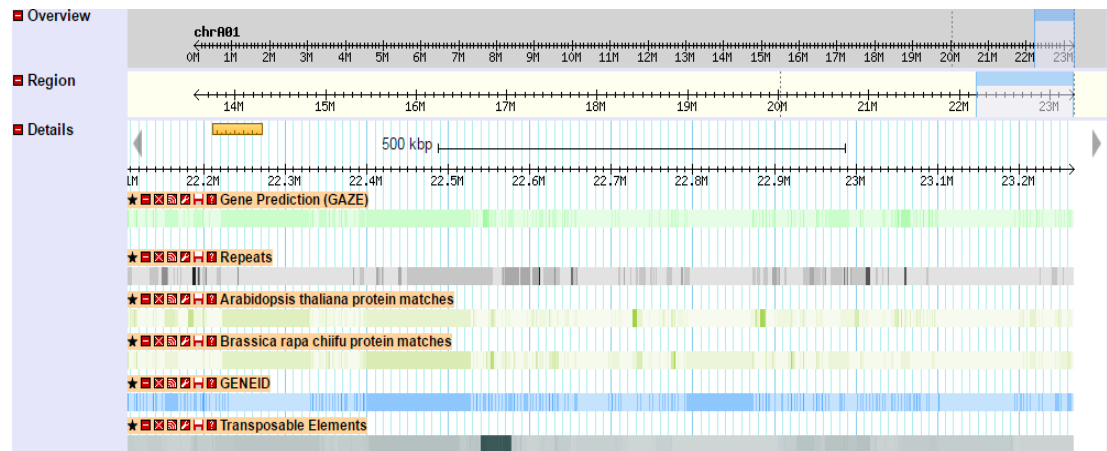
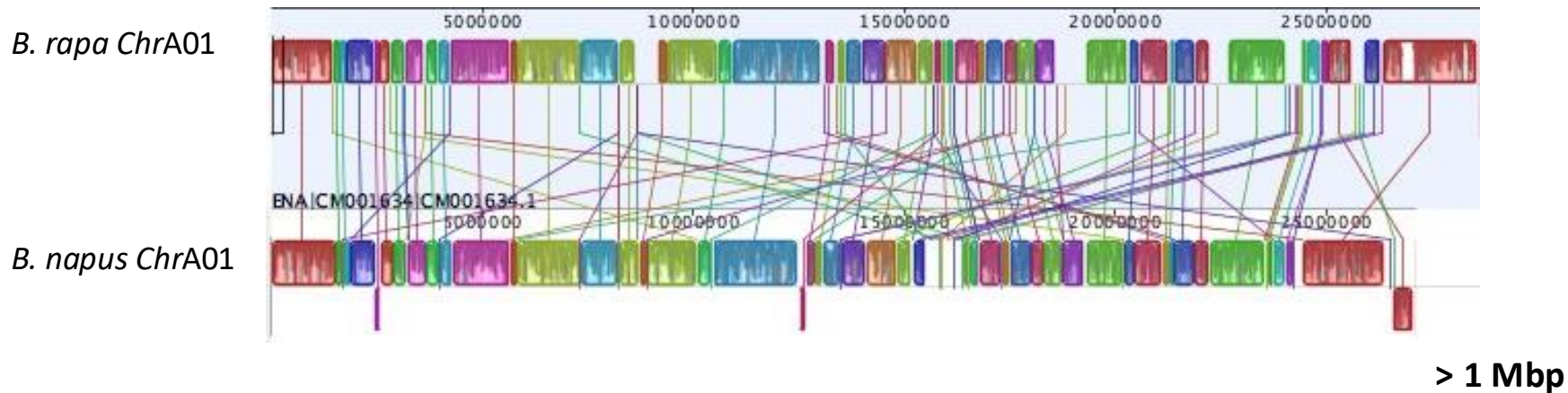


(Boys *et al.* (2012) Plant Pathol.)

Fine mapping of the resistance locus on ChrA1 and identification of candidate resistance genes

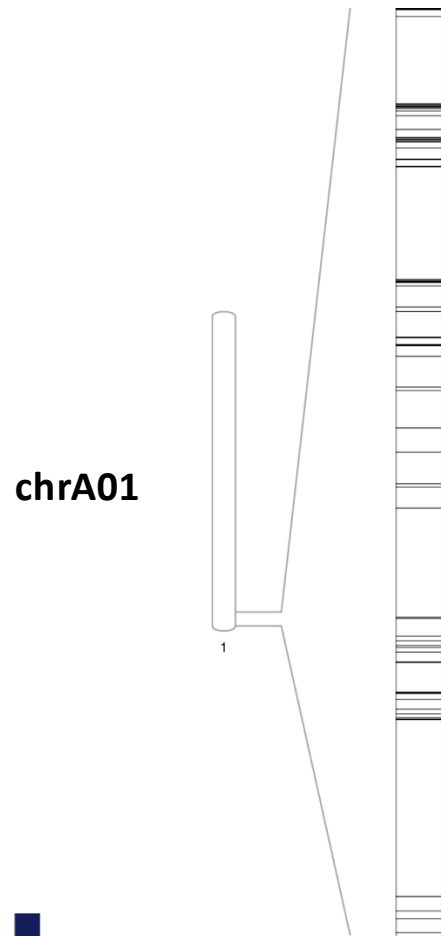
Physical location of the resistance locus on *B. napus* genome

Mauve alignment of the *chrA01* of *B. rapa* (upper line) and *B. napus* (lower line)



Identification of unique SNP loci in chrA01

Bioinformatics workflow was developed to identify single nucleotide polymorphisms (SNP) specific to the corresponding chromosomal region



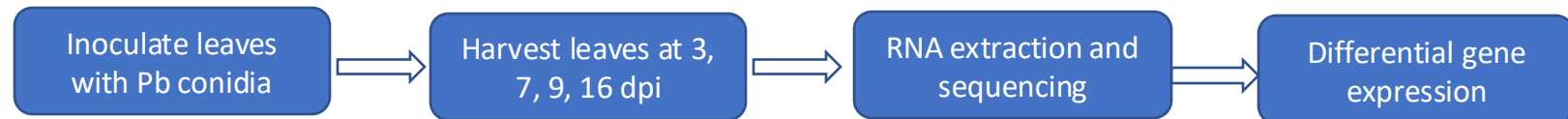
- Based on the SNP information from Snowdon et al. 2015, there are about 3000 putative SNP loci in this chromosomal region
- About 350 specific SNP loci were identified
- KASP (Kompetitive allele specific PCR) markers were developed for a subset of SNPs
- Marker genotyping

Identification of candidate genes

Identification of candidate genes – gene predictions

- Different *Brassica napus* genome sequences and Brassica pan genome to identify gene content in this genomic region
 - Six genes related to resistance against pathogens
 - RLPs, RLKs and NBS-LLRs
 - Genome sequence of Imola

Identification of candidate genes – RNA seq analysis

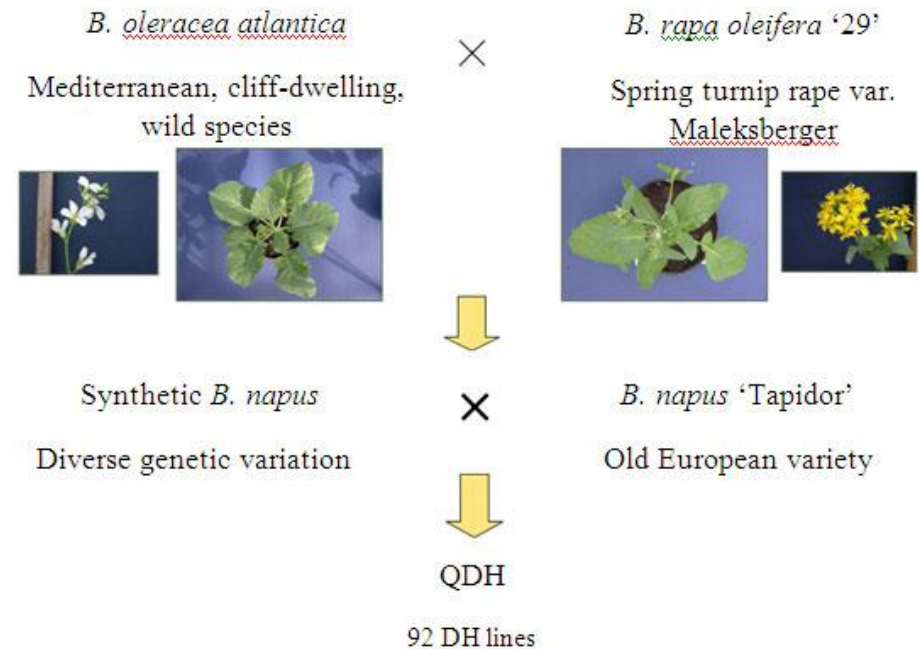


Other sources of host resistance

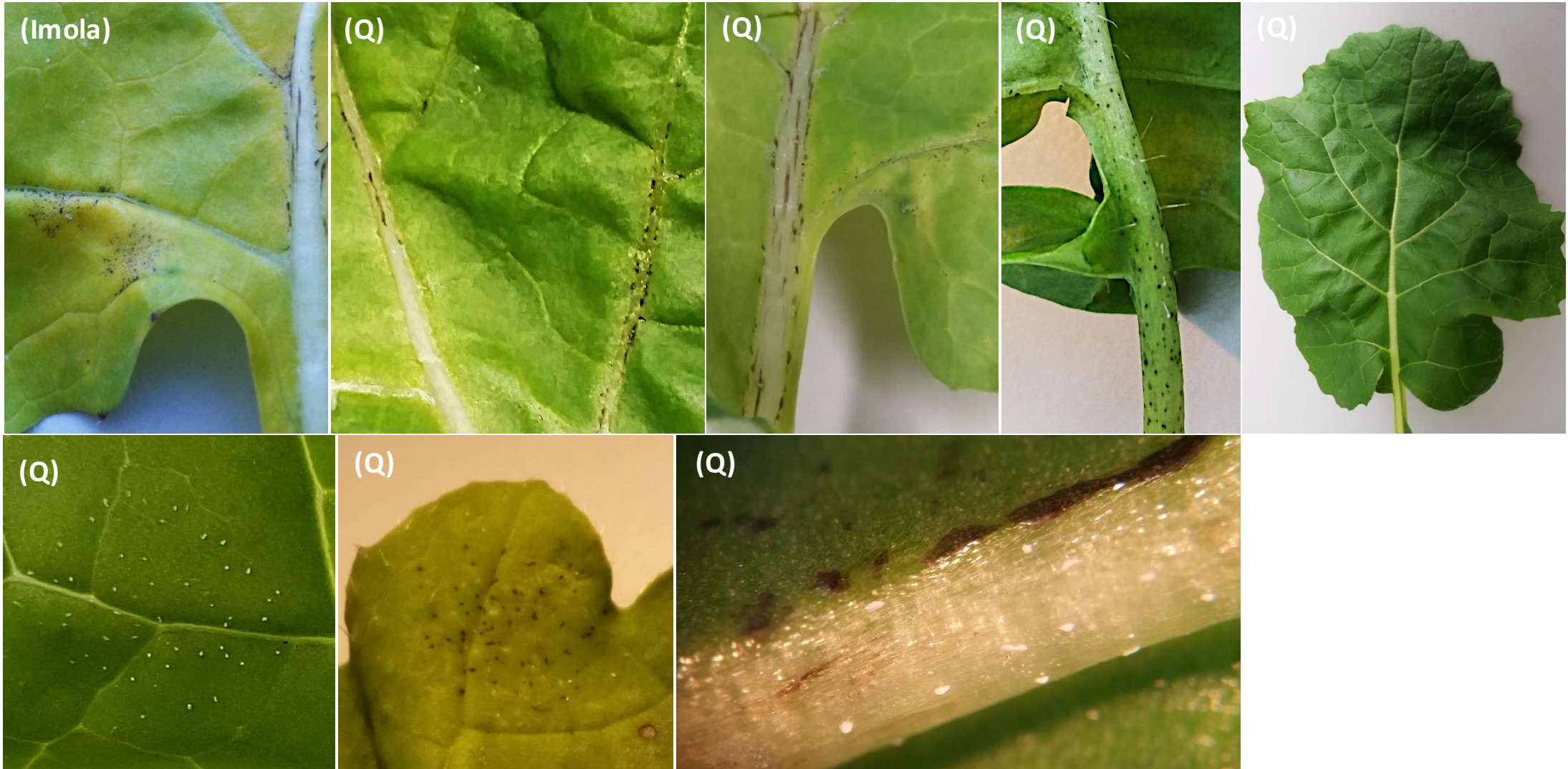
QTL for resistance against *P. brassicae* from *B. napus* secondary gene pool

- Recent origin of the crop (c. 7500 yrs or less), no wild types found in nature
- Bottleneck effect associated with selective breeding
- Low genetic diversity

Q DH (doubled haploid) population

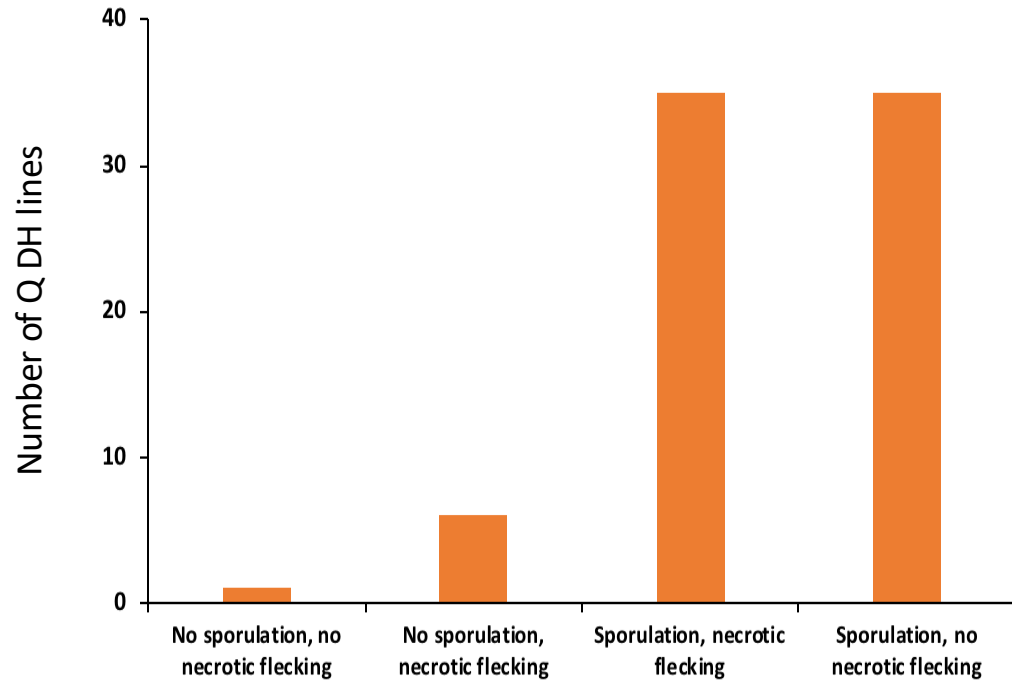


Resistant and susceptible phenotypes observed in the Q DH population

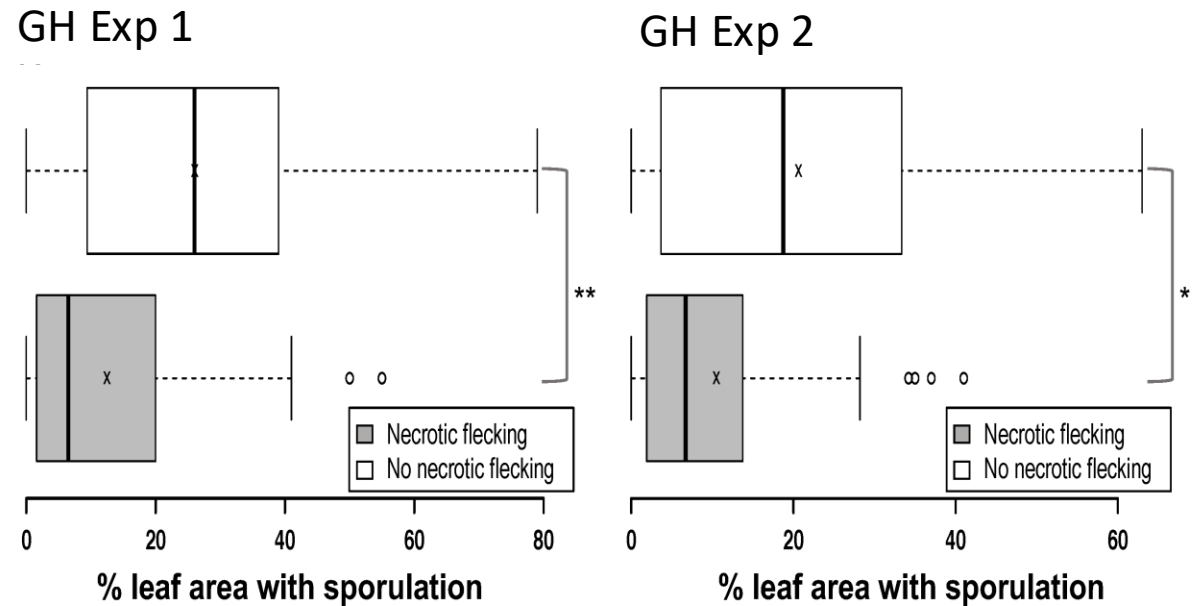


Investigation of the phenotype/s of resistance

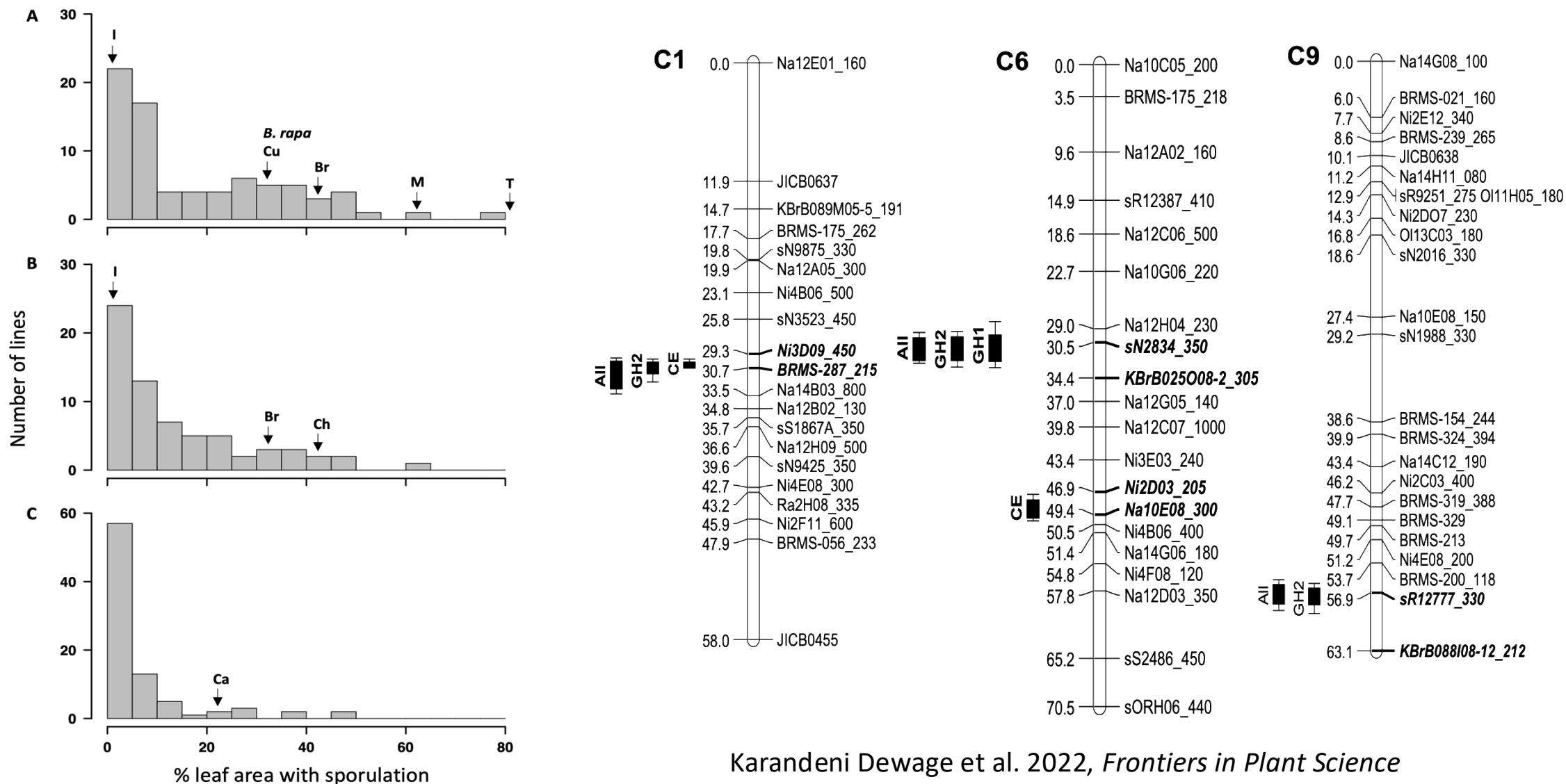
Four different phenotype categories



Light leaf spot severity on lines with or without the presence of a black necrotic flecking

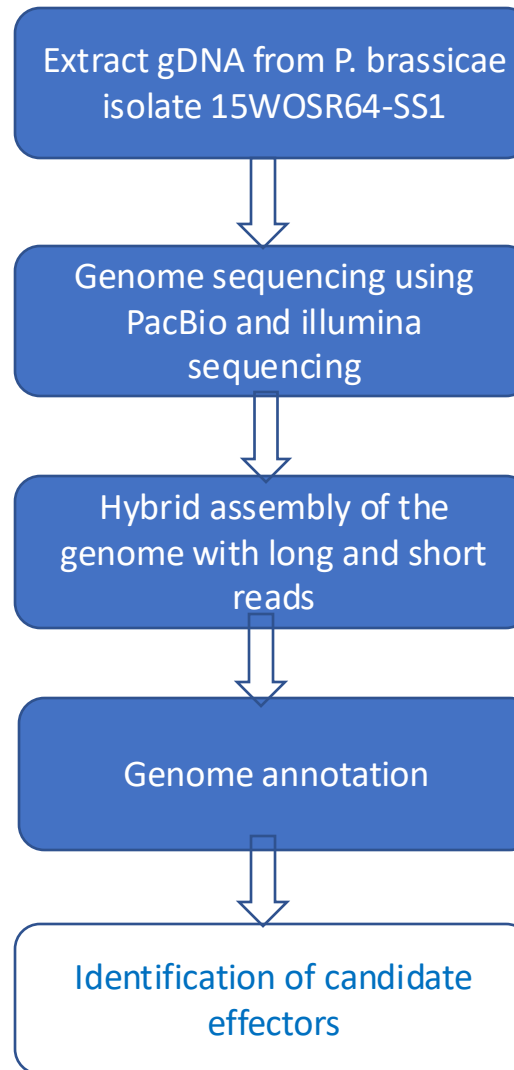


QTL for resistance against *P. brassicae* from *B. napus* secondary gene pool



P. brassicae genome

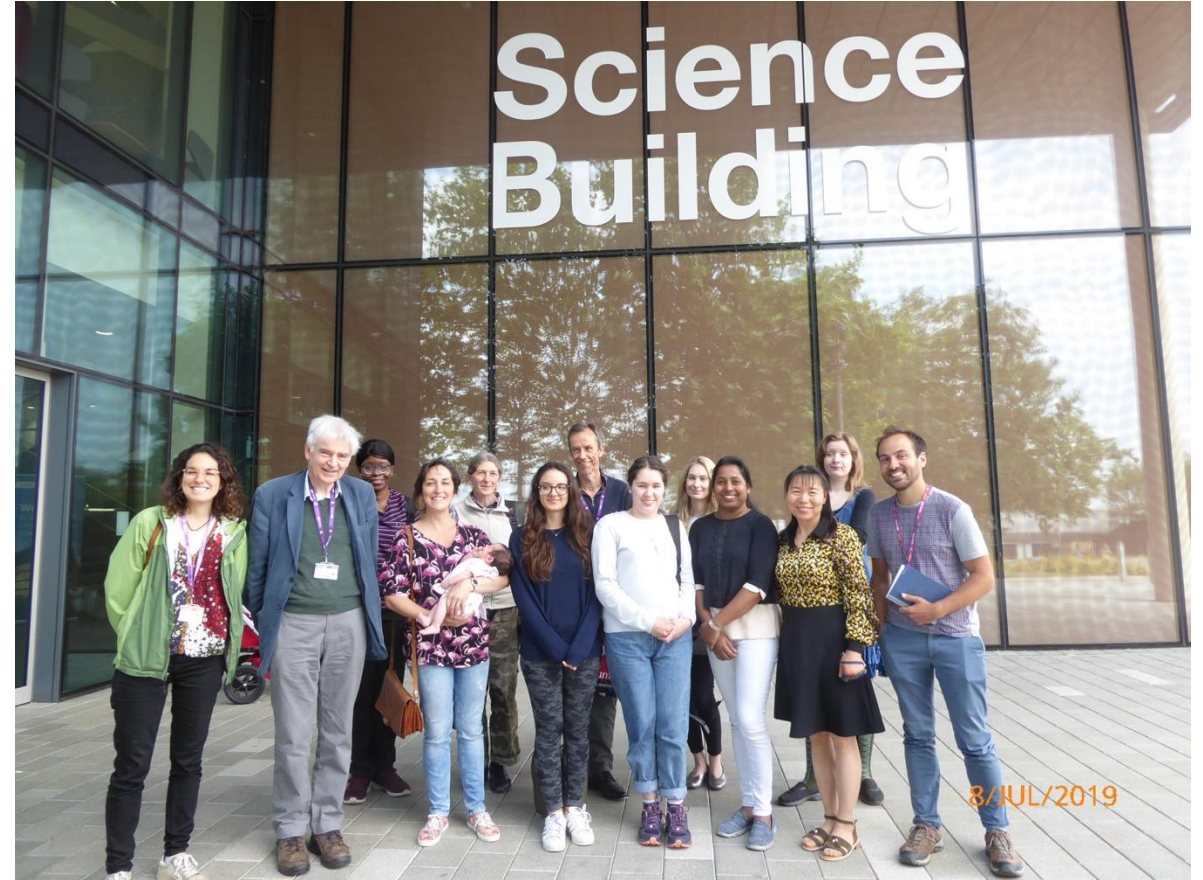
- *De novo* genome assembly of *Pyrenopeziza brassicae*—hybrid approach



P. brassicae genome

- Whole genome re-sequencing to study population variations
 - Isolates from different host species and different geographic locations
 - Re-sequenced 23 isolates in total
 - Host species: oilseed rape, Brussel sprouts, red cabbage, kale
- New DNA markers for isolate characterization
- Comparative genomics analysis between related fungal species (i.e. *Rhynchosporium* spp., *Oculimacula* spp.)

Acknowledgements



Thank you