

Exploiting sources of resistance to Turnip yellows virus (TuYV) for deployment in oilseed rape

The problem

Turnip yellows virus (TuYV), a Polerovirus within the *Luteoviridae* family, is found every year infecting oilseed rape (*Brassica napus*) crops in the UK and across Europe. Although there are rarely clear symptoms, infection can significantly reduce the yield of oilseed rape (up to 26% in UK). The main vector in the UK is believed to be *Myzus persicae*, however, insecticides provide little, or no control when infection pressures are high.

1. The approach

- To identify natural sources of resistance from across the brassica A and C genomes (Fig. 1)
- To characterise resistance sources
- To identify genetic markers for the resistances, to facilitate their introgression into elite oilseed rape lines

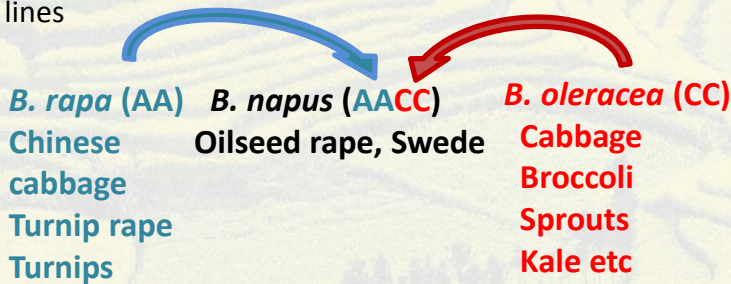


Figure 1: The amphidiploid nature of *B. napus*

2. Progress – Identifying resistance

- A *B. napus* line with quantitative resistance to TuYV has been identified and a QTL accounting for >50% of the observed variation has been identified (Fig. 2)
- Brassica rapa* lines have also been identified that display extreme resistance; one resistance source appears to be recessive
- Brassica oleracea* lines have been identified that display extreme resistance (Fig. 3); the resistances act in a dominant manner. These lines are susceptible to aphid feeding (Fig. 3 inset)

Future plans

A back-crossing strategy is being utilised to generate segregating populations of plants. These populations will be used for fine mapping the genes involved in the different resistance sources using KASPar SNP markers. Resistant plant lines are being tested with further viral isolates to identify the resistance that that is most likely to prove durable. Once the resistance sources have been characterised genetic markers will be identified to allow the rapid introgression of TuYV resistance into commercial oilseed rape varieties.

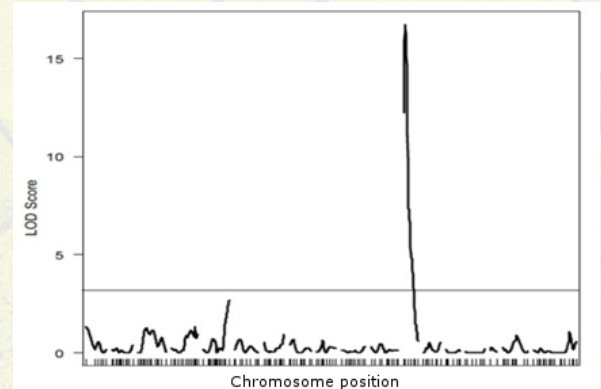


Figure 2: LOD curve showing the QTL identified in the resistant *B. napus* line.

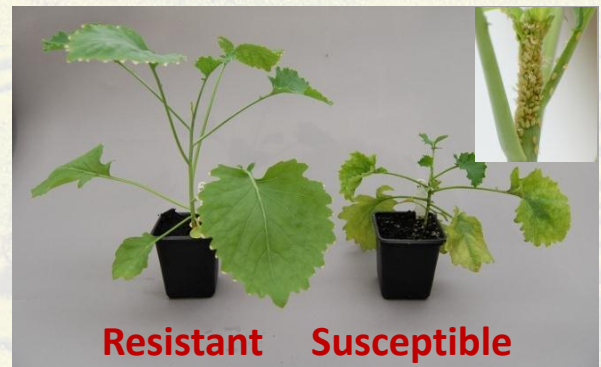


Figure 3: *B. oleracea* following challenge with TuYV. Inset: *Myzus persicae* feeding on resistant *B. oleracea*

3. Progress – Specificity of resistance

- The resistances in *B. napus* and *B. rapa* were effective against TuYV isolates from the two most common phylogenetic groups of the virus (Table 1)
- Resistance in *B. oleracea* has only been tested with a less common group TuYV isolate so far

Table 1: Specificity of TuYV resistances identified

Phylogenetic group of TuYV isolate	Number of resistant plants/number of plants tested				
	<i>B. napus</i>	<i>B. rapa</i> 1	<i>B. rapa</i> 2	<i>B. oleracea</i> 1	<i>B. oleracea</i> 2
Common	4/4	9/9	8/9	n.a.	n.a.
Less common	8/8	7/7	7/7	9/9	9/9

