

VeGIN Webinar Stakeholder Event

Progress update on Clubroot resistance in Brassica and *Nasonovia ribisnigri* resistance in lettuce

1st December 2021

Graham Teakle

Clubroot

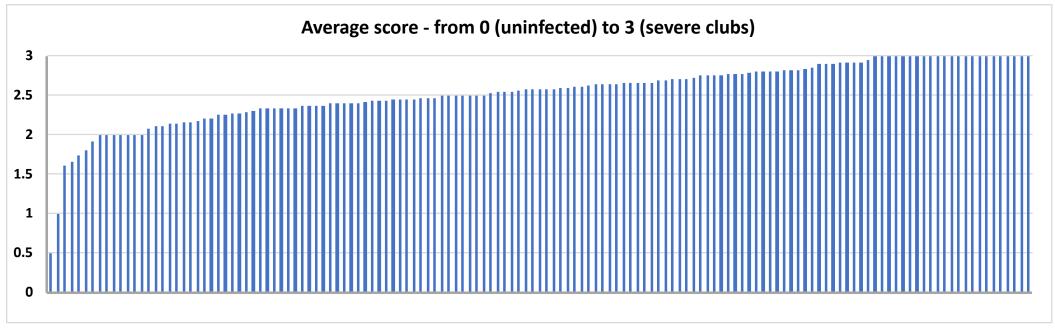
- Caused by soil-borne obligate biotroph Plasmodiophora brassicae
- Affects roots of vegetable brassicas and oilseed rape
- Reduces yield and ultimately kills the plant
- Once a field is infected resting spores survive for years
- There is no effective chemical control
- High pH (liming) reduces pathogenicity
- Genetic resistance has been deployed from Brassica rapa
- There is a new resistance-breaking strain of the pathogen (CN isolate)



2018 VeGIN clubroot field trial

- 4 reps of 3 plants per accession (some had fewer plants)
- Comprises 148 accessions:
 - 70 B. oleracea DFFS accessions
 - 69 wild C genome founder accessions
 - 9 other lines
- Guard = clubroot resistant red cabbage (Lodero F1) provided by Elsoms Seeds

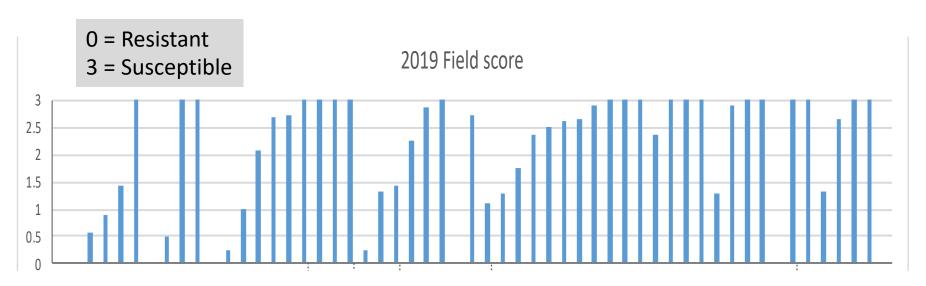


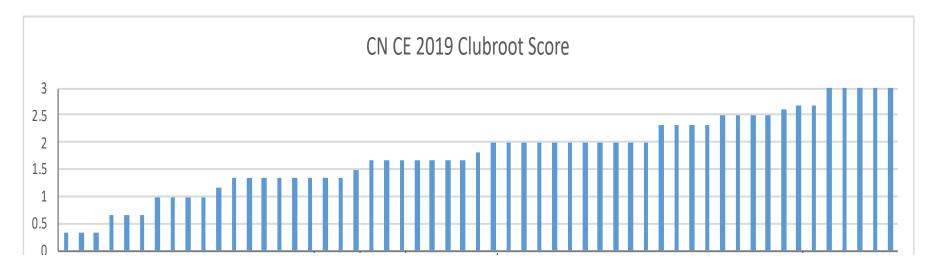


Comparison of 2019 Field Trial with *B. rapa* resistance-breaking isolate

Included:

- Resistant varieties
- Clubroot differential set from National Vegetable Genebank





New strategy for finding resistance

- ➤ Small scale screen of genebank accessions identified in above screens with the CN isolate
- ► Identify accessions that showed variation between individuals and screen a larger number of plants
- ► Genotype the plants to see if we can map resistance loci

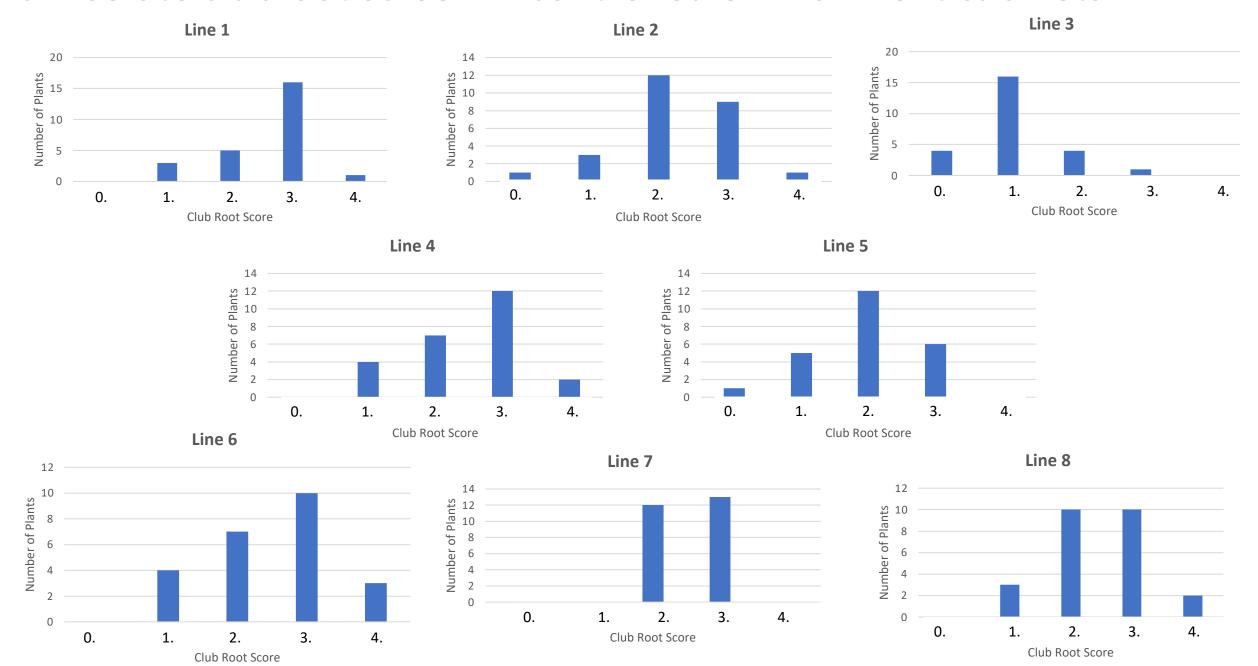
Alternatively make a segregating population by crossing (slow!):







CN isolate clubroot screen in controlled environment cabinets

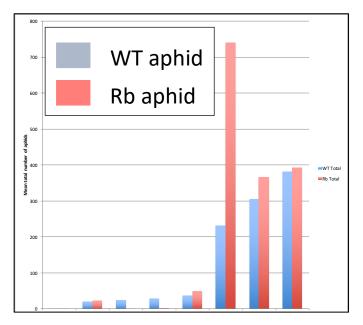


Lettuce-currant aphid (Nasonovia ribisnigri)

- Specialist pest of lettuce (summer host)
- ▶ Difficult to control with pesticides
- ► Nr resistance gene bred into many lettuce vars
- ➤ The Nr:1 resistance-breaking biotype is now becoming a significant pest of UK outdoor lettuce production



Develop new *Nasonovia ribisnigri* resistance resources



Extreme lines selected for crossing

- Performed Resistant x Susceptible crosses
- Confirmed F1 plants were genuine crosses by genotyping
- Generate recombinant inbred line mapping populations to map resistance loci

	S1			S2			S3		
	F1	F2	F3	F1	F2	F3	F1	F2	F3
R1									
R2	16	1 (1	5	3		7	1	
R3	23		$\bigg) \ \overline{\hspace{1cm}}$	1		,			
R4	8			2					
R5			,						





Know your enemy: Nasonovia ribisnigri genetics & genomics

F1 crosses		Resistance-breaking biotype (Nr:1)			
		UK361	Kent Cl		
Susceptible	WT Kent	3	3		
biotype (Nr:0)	Nr 8	0	6		

- ► Each colony was raised from a single fundatrix
- ► All F1s not able to grow on *Nr* lettuce => Rb phenotype is recessive

PhD Student Dion Garrett, RRES

- Genome sequencing
- ► Gene expression
- Population genetics
- ► Alternative host plants
- ► Sampling/modelling

Generation of F2 aphid population

Aphid F1 clone no.	Female	Biotype	Male	Biotype	No. Eggs	Hatched	Surviving colonies
11.3	UK631	Rb	WT Kent	WT	57	5	0
12.2	WT Kent	WT	Kent Cl	Rb	19	2	0
12.4	WT Kent	WT	Kent Cl	Rb	1	0	0
13.1	Nr 8	WT, Insecticide R	UK361	Bb	414	69	2
13.6	Nr 8	WT, Insecticide R	UK631	Rb	0	0	0

Repeating this – another 80 eggs laid so far

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Clubroot work

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Horticultural Services team



Nasonovia ribisnigri work

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