Barley Yellow Dwarf Virus and Considerations for Future Disease Control

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30th March 2022

Wheat Genetic Improvement Network

Department for Environment Food & Rural Affairs

DFW

UKRI Biotechnology and Biological Sciences Research Council

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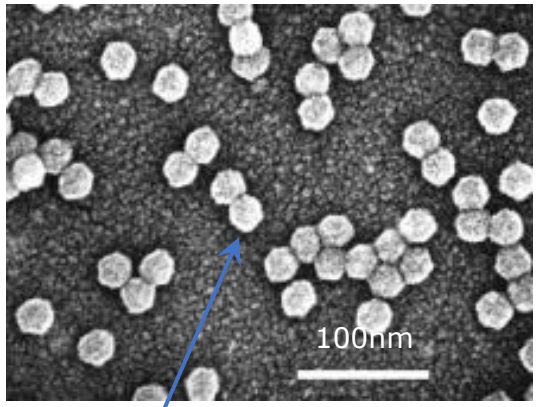
AHDB

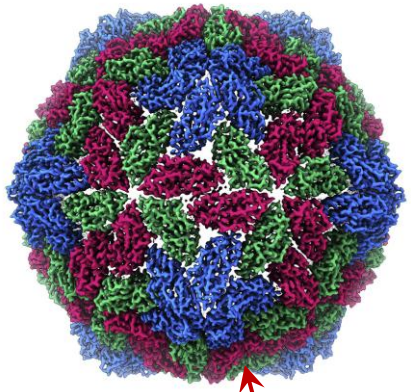
Overview

1. Barley yellow dwarf virus
2. Disease control and associated challenges
3. Improved UK-specific BYDV knowledge and diagnostics

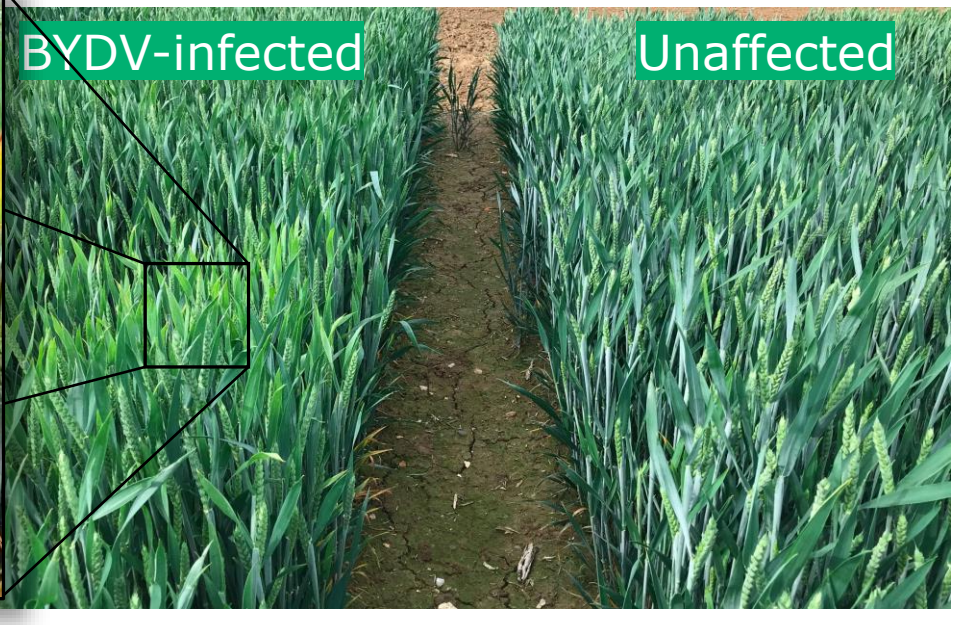
Barley yellow dwarf virus (BYDV)

- Important viral disease affecting wheat
- Harvest yield loss due to natural infection = 11 to 33%[2], upwards of 60%[3]
- Indistinct disease phenotype limits rapid BYDV diagnosis
- No practical virus-focussed chemical control
- Instead, aphid vectors targeted



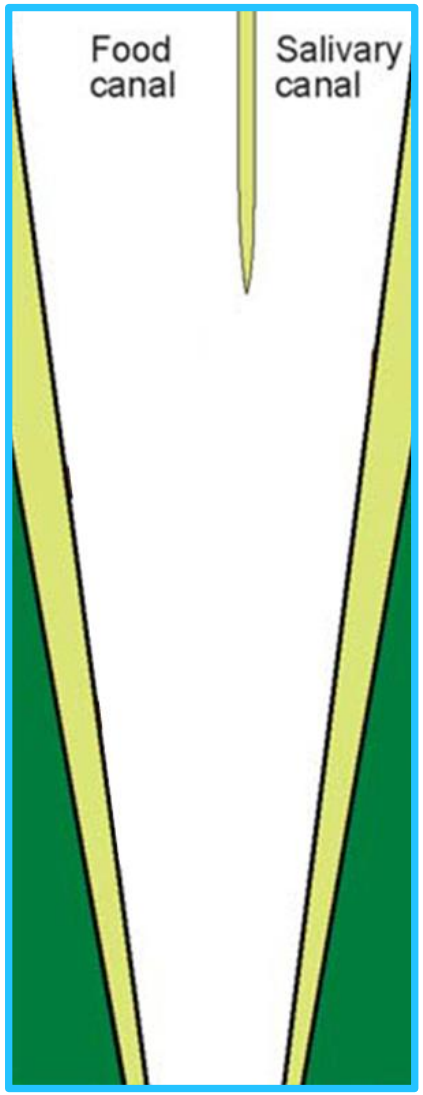


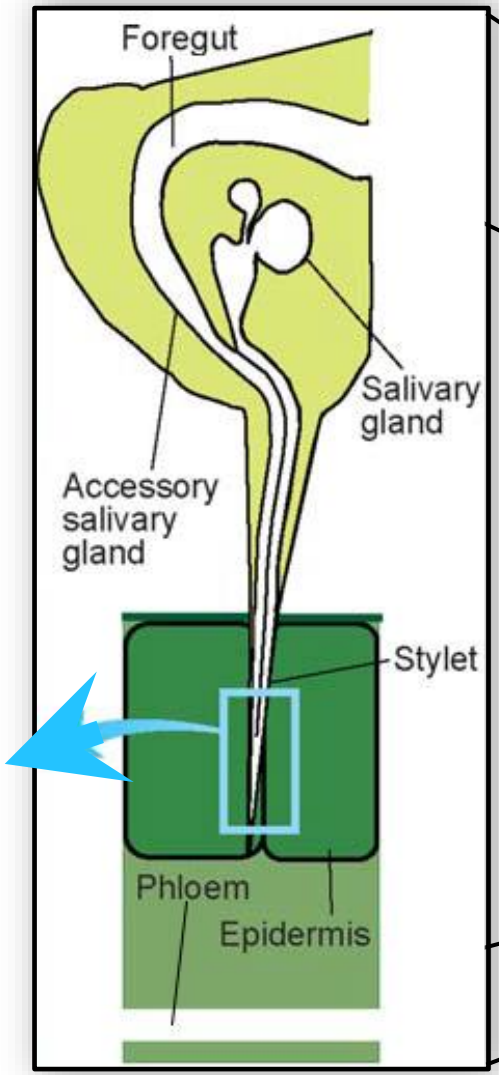
BYDV virion particles and their predicted structure[1]

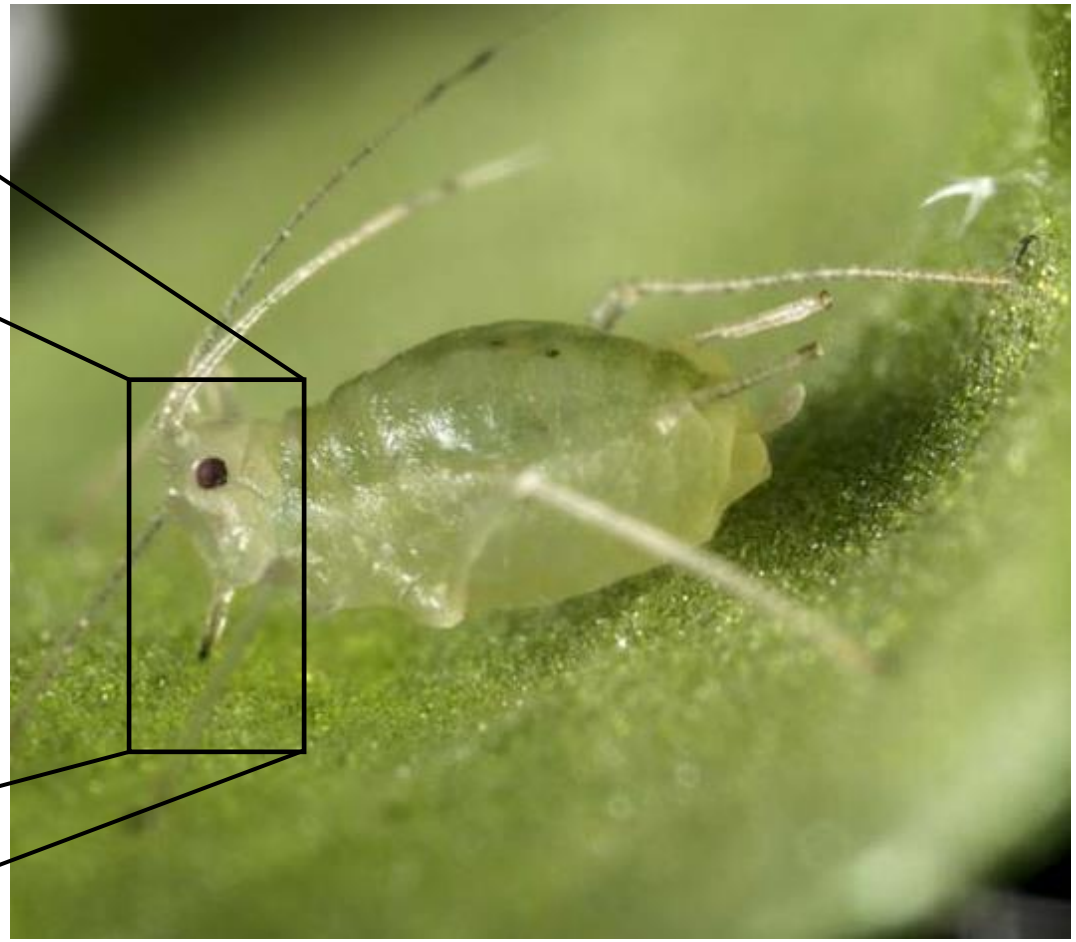


[1]Byrne *et al*., (2019). *Structure*, **27(12),** 1761-1770.
[2]Kaddachi *et al*., (2014). *International Journal of Phytopathology,* **3,** 155-160
[3]Ben Ghanem *et al*., (2018). *Canadian Journal of Plant Science,* **98,** 930-946.

BYDV transmission



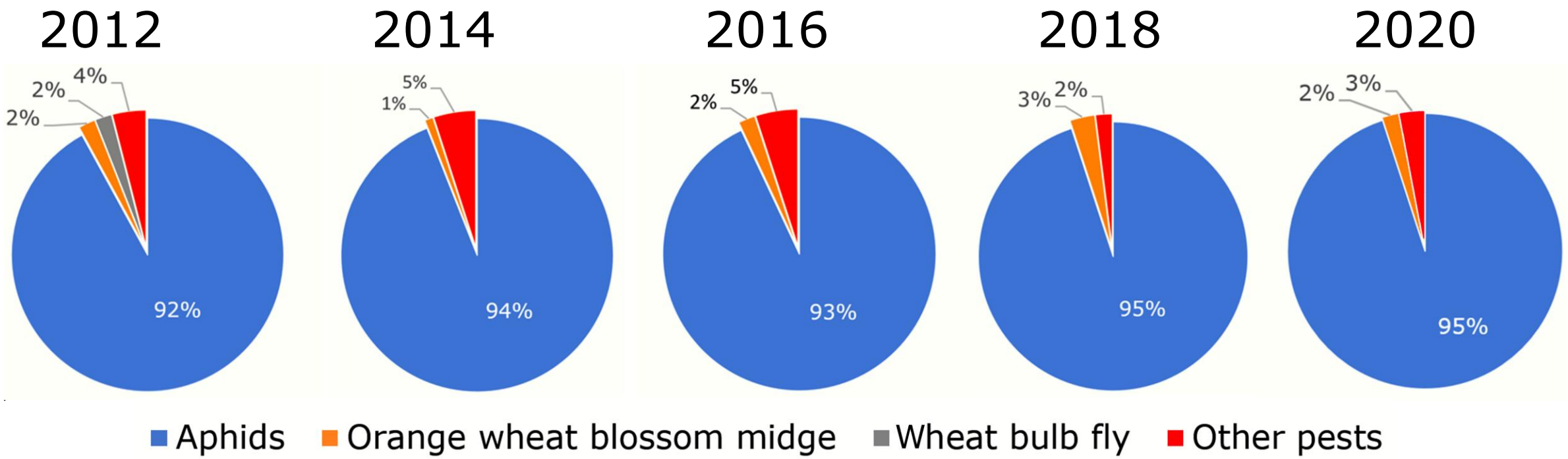




Ng and Perry (2004) *Molecular Plant Pathology*, **5(5),** 505-511.

Historic insecticide use

- Insect targets stated for why foliar insecticides are applied to wheat:

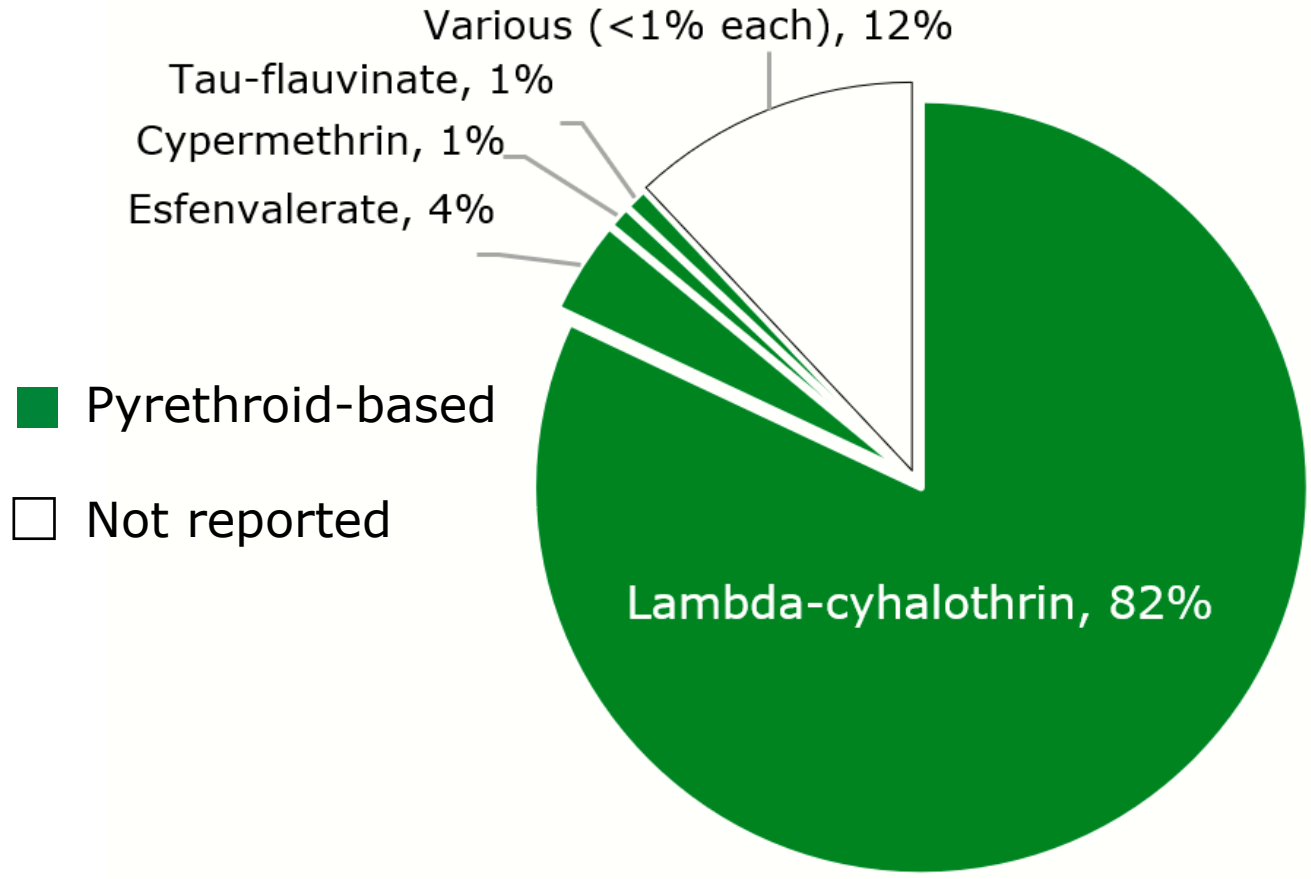


- Aphids (and viruses they vector) are consistent target for pesticides, with significant associated cost and environmental implications

Various Garthwaite *et al.*, UK Pesticide Usage Survey Reports: 250, 263, 271, 284 & 295

Current insecticide use

- Most common formulations (most recent data available, 2020[1]):

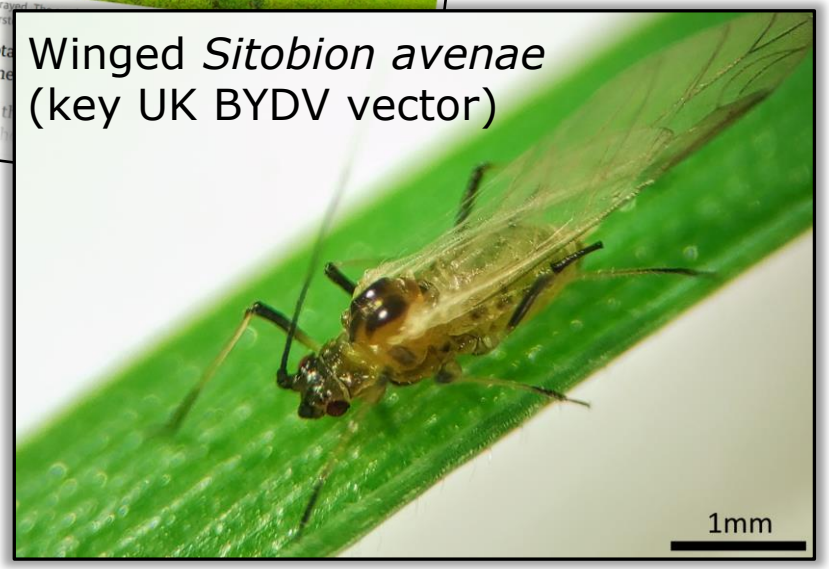


- Moderate pyrethroid resistance widespread across *Sitobion avenae* in UK
- Recent evidence of pyrethroid tolerance in *Rhopalosiphum padi* in Ireland[2]

[1]Garthwaite et al., UK Pesticide Usage Survey Report 295
[2]Walsh et al., (2020). *Outlooks on Pest Management,* **31,** 5-9

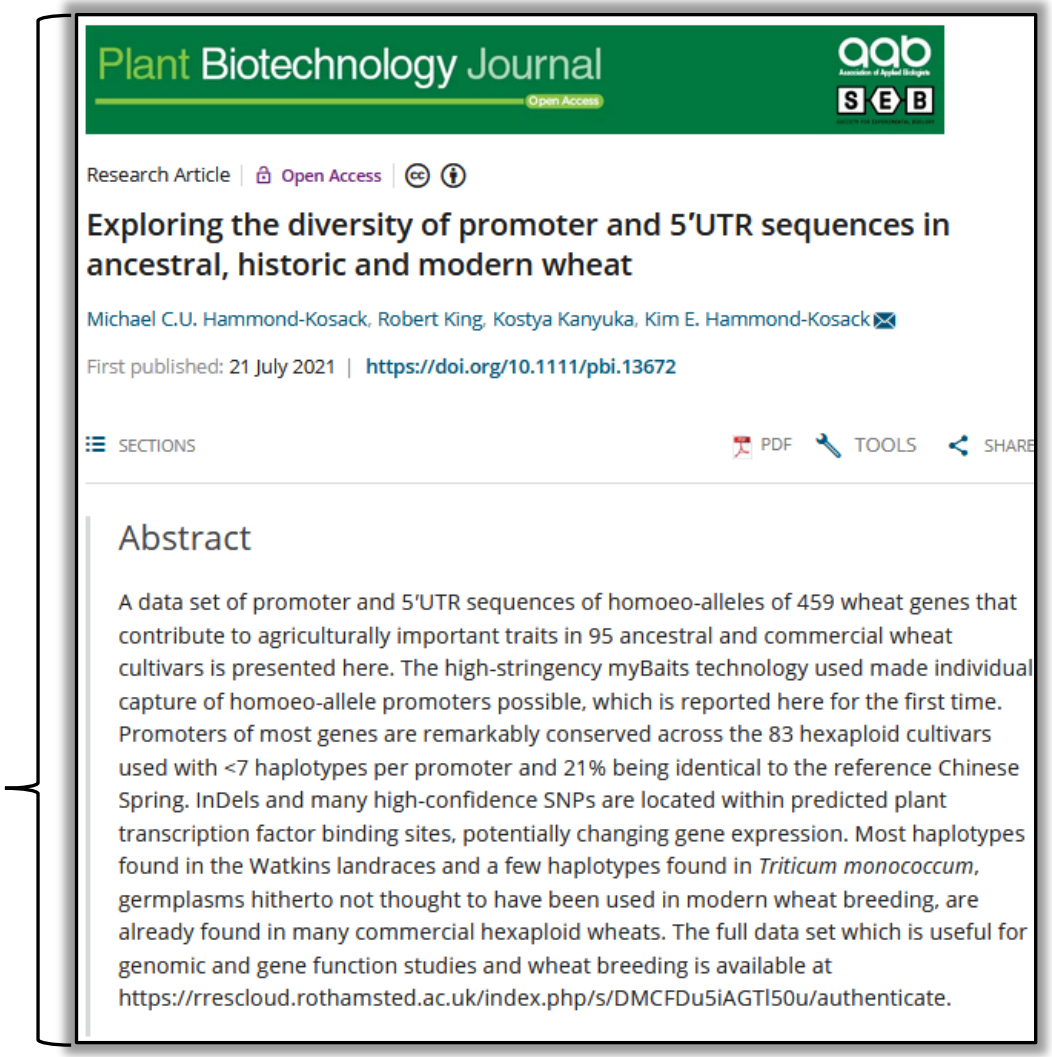
Future insecticide use

- Loss of usable insecticides due to:
  - Targets developing resistance against mode(s)-of-action
  - Regulation changes/restrictions (e.g. neonicotinoids)
- Climate change likely to exacerbate need for aphid/BYDV management strategies
  - Reproductive rate
  - Expansion into new areas
  - Shifts in migration patterns
  - Overwintering survival



Genetic control?

- Genetic BYDV resistances/tolerances exist:
  - Winter barley cv. Amistar (KWS)
  - Winter barley cv. Feeris (KWS)
  - Winter barley cv. Rafaela (LG Seeds)
  - Winter wheat cv. Wolverine (RAGT Seeds)
- Genetic source of aphid resistance being pursued at Rothamsted Research[1,2]
  - Genotyping possible following highly valuable WGIN-funded work (2021 paper)
- UK BYDV strain variation has potential to influence long term effectiveness of BYDV resistance(s), and reliability of diagnostics



Plant Biotechnology Journal

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Exploring the diversity of promoter and 5'UTR sequences in ancestral, historic and modern wheat

Michael C.U. Hammond-Kosack, Robert King, Kostya Kanyuka, Kim E. Hammond-Kosack

First published: 21 July 2021 | https://doi.org/10.1111/pbi.13672

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Abstract

A data set of promoter and 5'UTR sequences of homoeo-alleles of 459 wheat genes that contribute to agriculturally important traits in 95 ancestral and commercial wheat cultivars is presented here. The high-stringency myBaits technology used made individual capture of homoeo-allele promoters possible, which is reported here for the first time. Promoters of most genes are remarkably conserved across the 83 hexaploid cultivars used with <7 haplotypes per promoter and 21% being identical to the reference Chinese Spring. InDels and many high-confidence SNPs are located within predicted plant transcription factor binding sites, potentially changing gene expression. Most haplotypes found in the Watkins landraces and a few haplotypes found in *Triticum monococcum*, germplasms hitherto not thought to have been used in modern wheat breeding, are already found in many commercial hexaploid wheats. The full data set which is useful for genomic and gene function studies and wheat breeding is available at https://rrescloud.rothamsted.ac.uk/index.php/s/DMCFDu5iAGTl50u/authenticate.

[1]Greenslade *et al.,* (2016). *Annals of Applied Biology*, **168(3),** 435-449.
[2]Simon et al., (2021). *Scientific reports*, **11(1),** 1-12.

BYDV strain variation

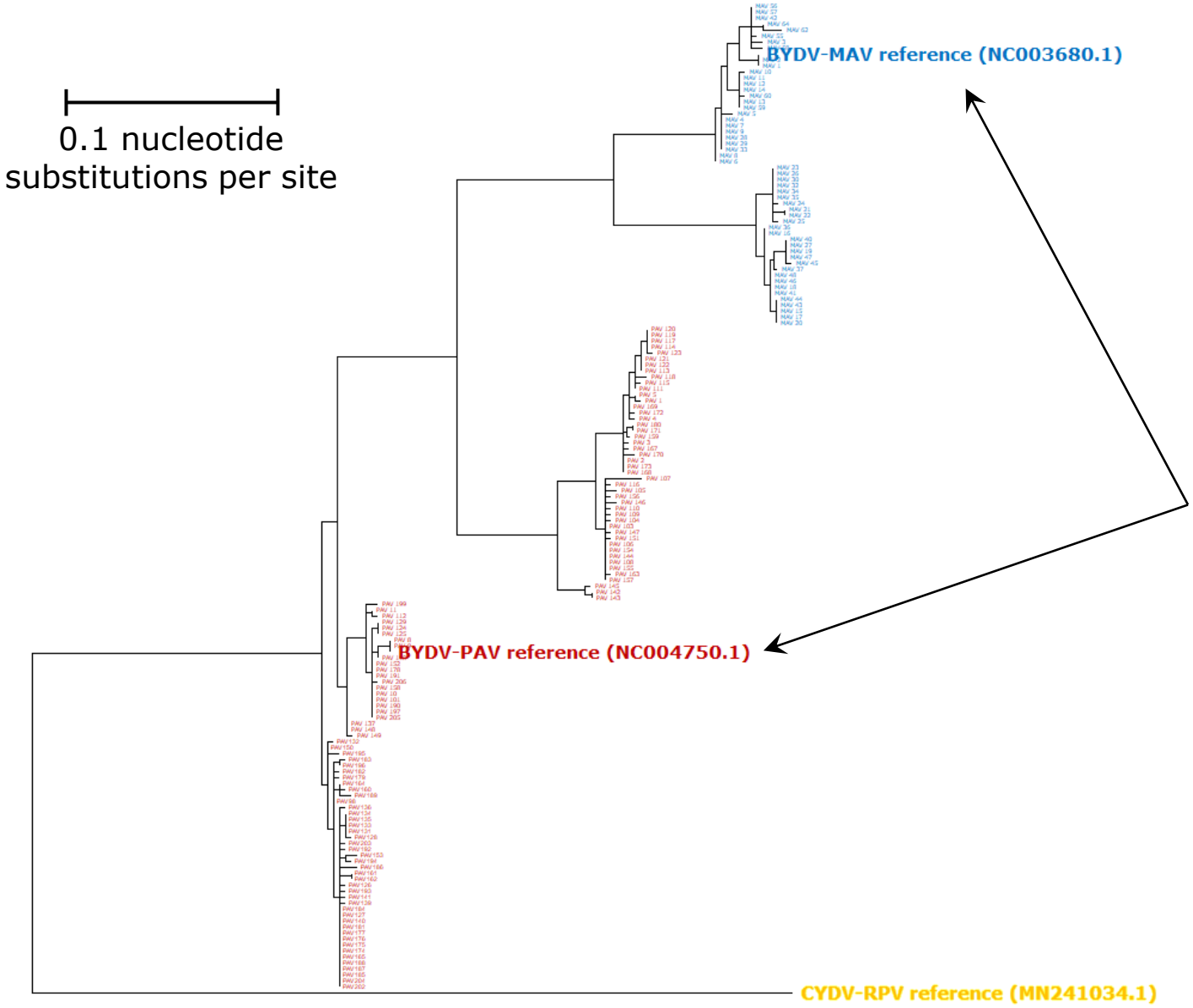
- Worldwide strains and key aphid vectors include:

Genus	Species	Strain	Known aphid vectors
Luteovirus	BYDV	**PAV**	*Rhopalosiphum padi, Sitobion avenae, Metapolophium dirhodum, Schizaphis graminum, Sitobion fragariae*
		MAV	*S. avenae, M. dirhodum, R. padi, S. fragariae*
		PAS	*Rhopalosiphum maidis*
		GAV	*Scizaphis graminum, S. avenae*
Polerovirus	CYDV	**RPV**	*R. padi, S. graminum*

- Most damaging worldwide (high vector abundance and efficiency)
- Potential exists for recombination between strains
- Strain prevalence can rapidly shift

Aradottir and Crespo-Herrera (2021) *Current Opinion in Insect. Science.*, **45,** 59-68

BYDV strain variation



- Phylogenetic analysis for informative subset of global **BYDV-MAV** and **BYDV-PAV** sequencing data from NCBI
- **MAV** and **PAV** substrain variation suggested on global scale
- Majority of molecular BYDV diagnostics based upon discrete references
- Potential for these to be ineffective for viral recombinants, new variants of interest and/or UK-specific BYDV

- BYDV-MAV sequences from NCBI = 53
- BYDV-PAV sequences from NCBI = 110

Challenges for UK BYDV control

- Highly limited UK-specific BYDV sequencing data available

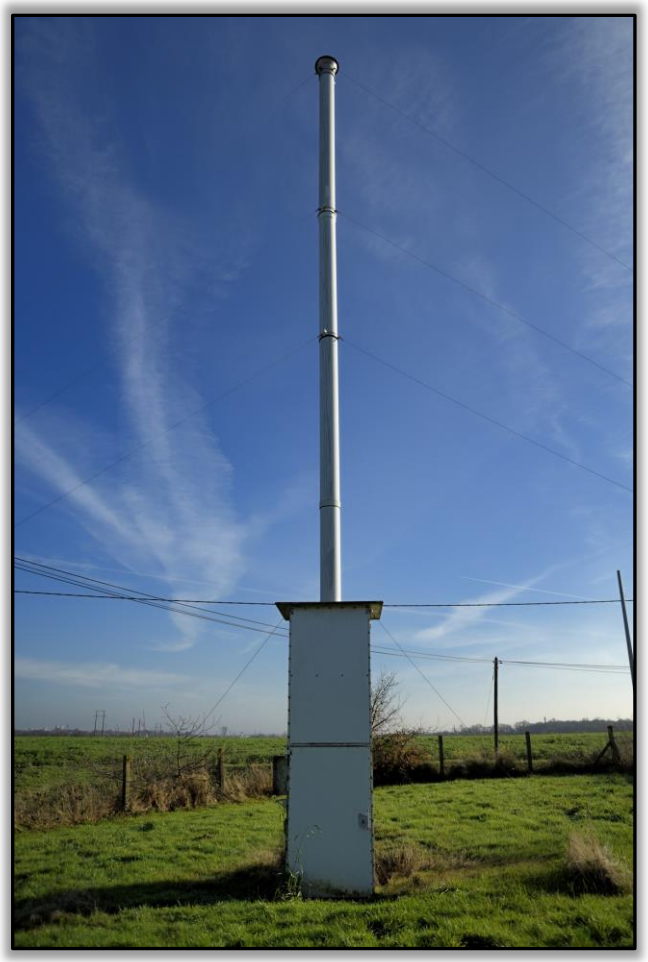
- Current diagnostics not necessarily based on UK-specific data
  - potential for disease misdiagnosis

- No established baseline for UK BYDV variation
  - perhaps fundamental for monitoring of resistance-breaking BYDV

Partial BYDV genome sequencing performed from UK-wide aphid samples collected over 2020 and 2021

Suction trap network

- Rothamsted has access to national insect survey (RIS):



Suction traps (12.2 m)

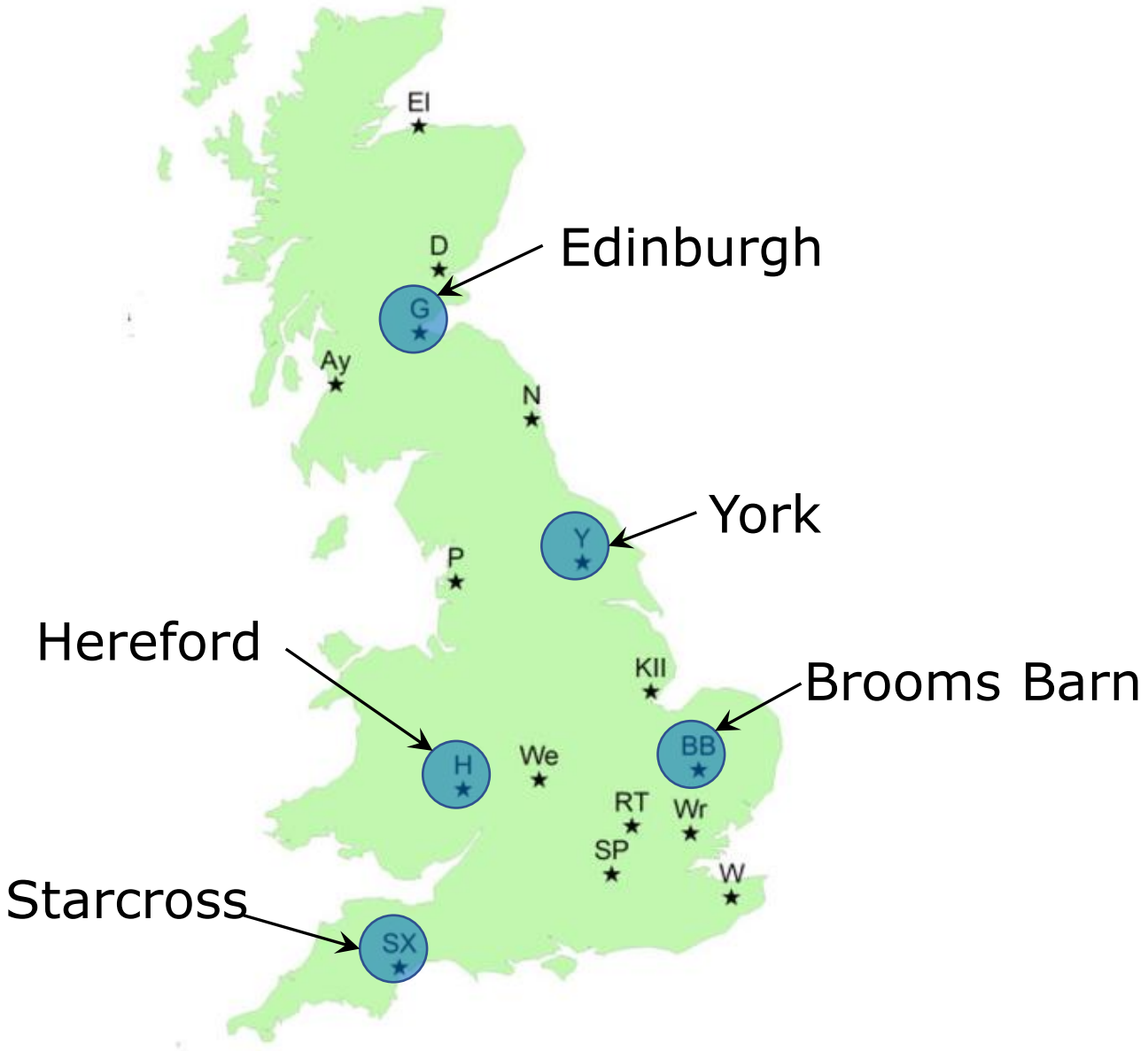
UK-wide locations

El – Elgin
N – Newcastle
BB – Broom's barn
Wr – Writtle
D – Dundee
P – Preston
We – Wellesbourne
SP – Silwood park
G – Gogarbank
Y – York
H – Hereford
W – Wye
Ay – Ayr
K – Kirton
RT – Rothamsted
SX - Starcross

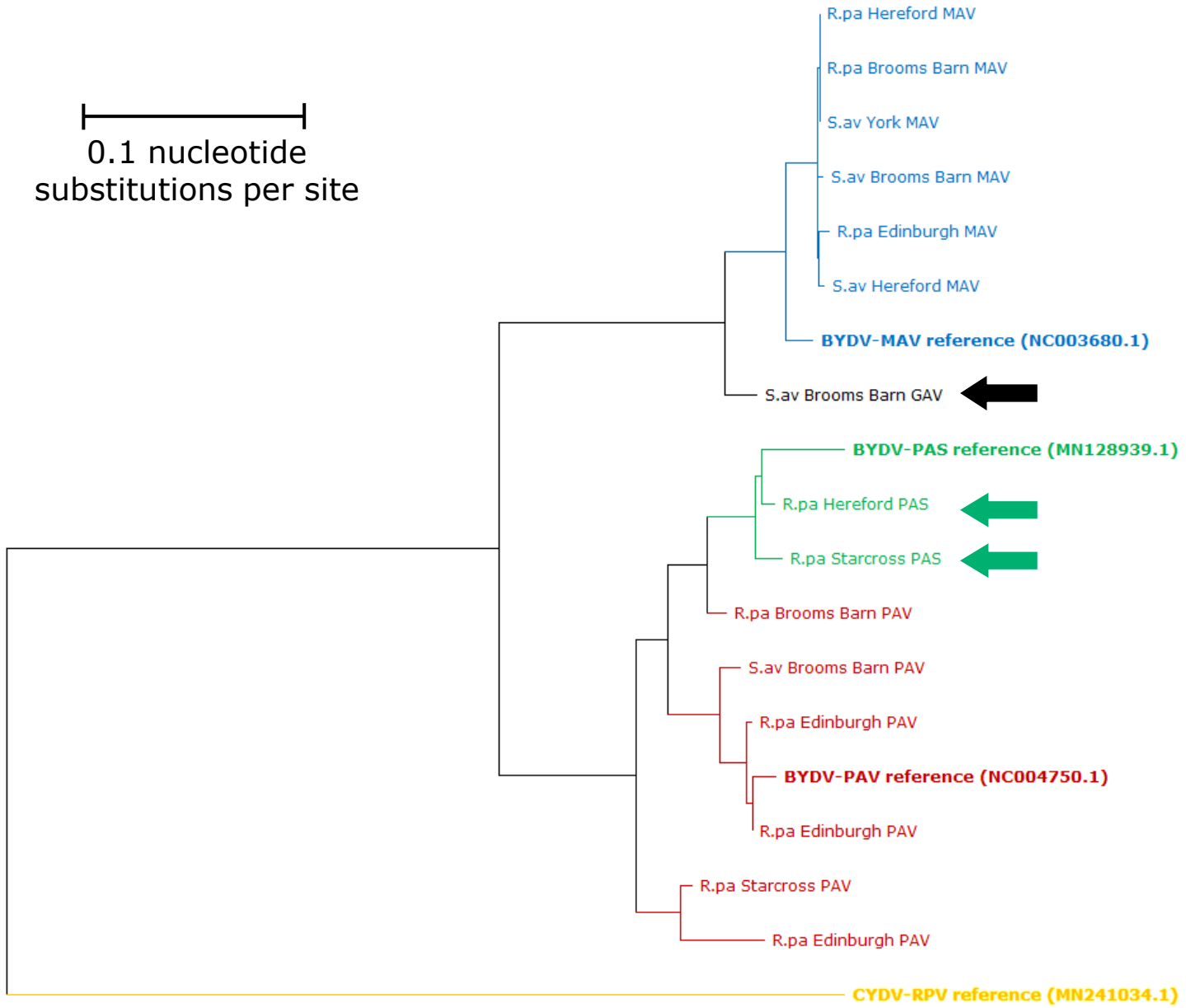
https://www.rothamsted.ac.uk/insect-survey

Suction trap network

- Prioritised aphid samples from:
- Preferentially selected for equal numbers of *R. padi* and *S. avenae*
- All known to be vectoring BYDV
- BYDV coat protein region sequenced as indicator for variation, and for development of improved assays

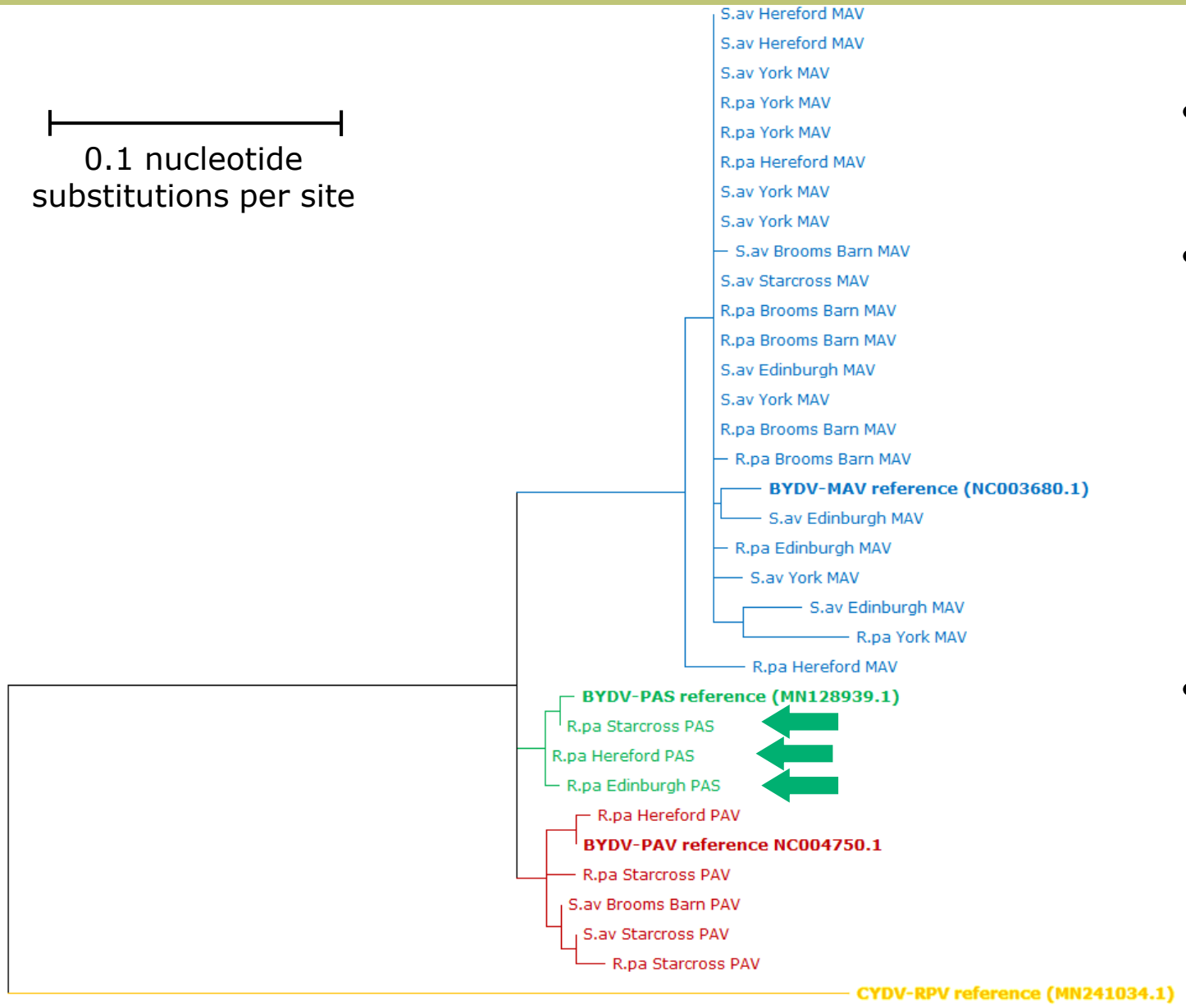


Results from 2020



- Sample IDs = R.pa/S.av _ Location _ strain
- **BYDV-MAV** vectored by both *R. padi* and *S. avenae* across UK with little variation
- Suggestion of **GAV** and **PAS** in UK (both previously unreported)
- **BYDV-PAV** widely distributed, mostly vectored by *R. padi* but with potential mixed infections

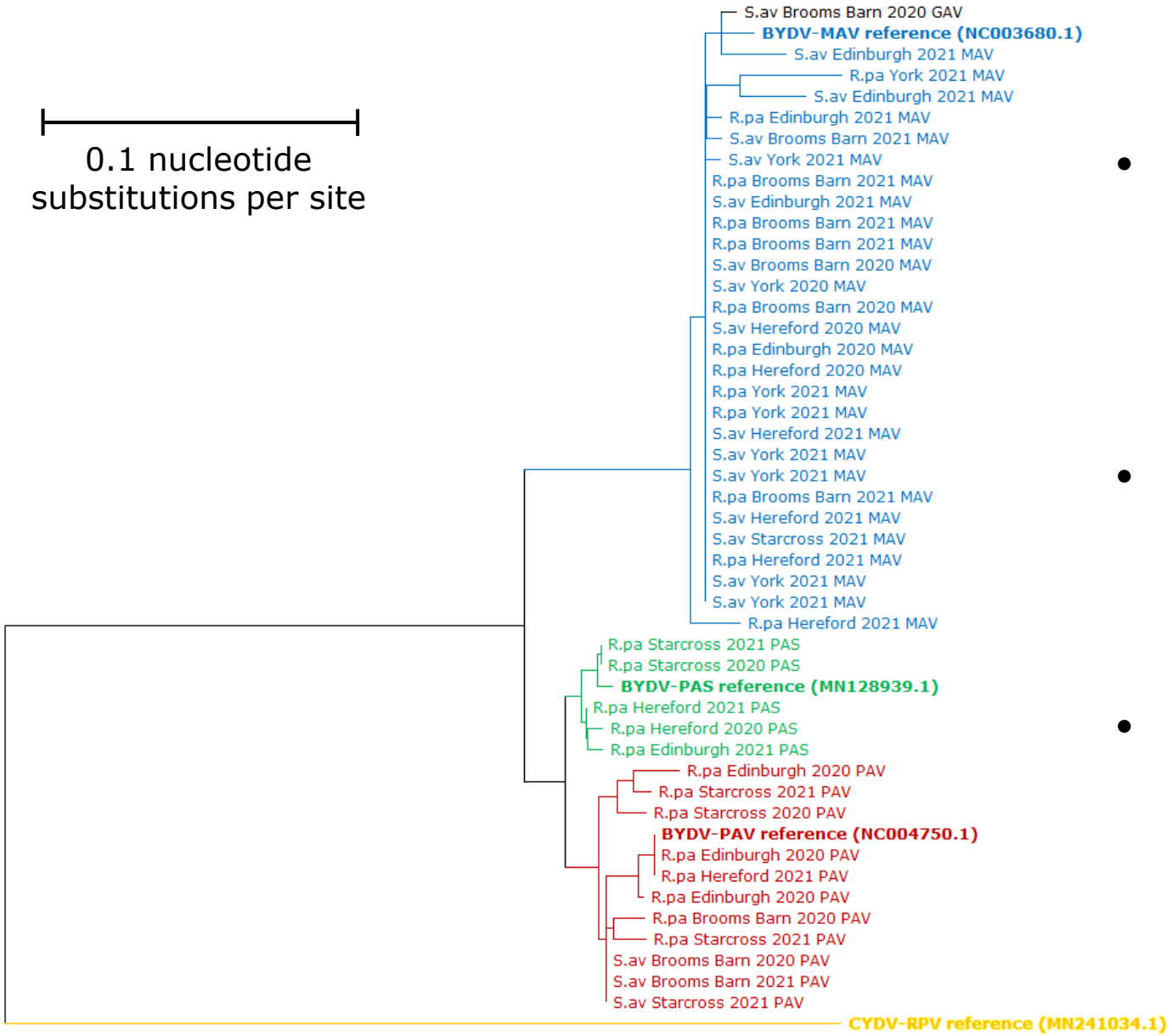
Results from 2021



- Similar trends to 2020
- Further suggestion of **BYDV-PAS** in UK
  - Starcross
  - Hereford
  - Edinburgh

  } **BYDV-PAS** may be present across UK
- Looking to validate this suggestion, and to establish aphid culture with **BYDV-PAS**

Results from 2020 & 2021

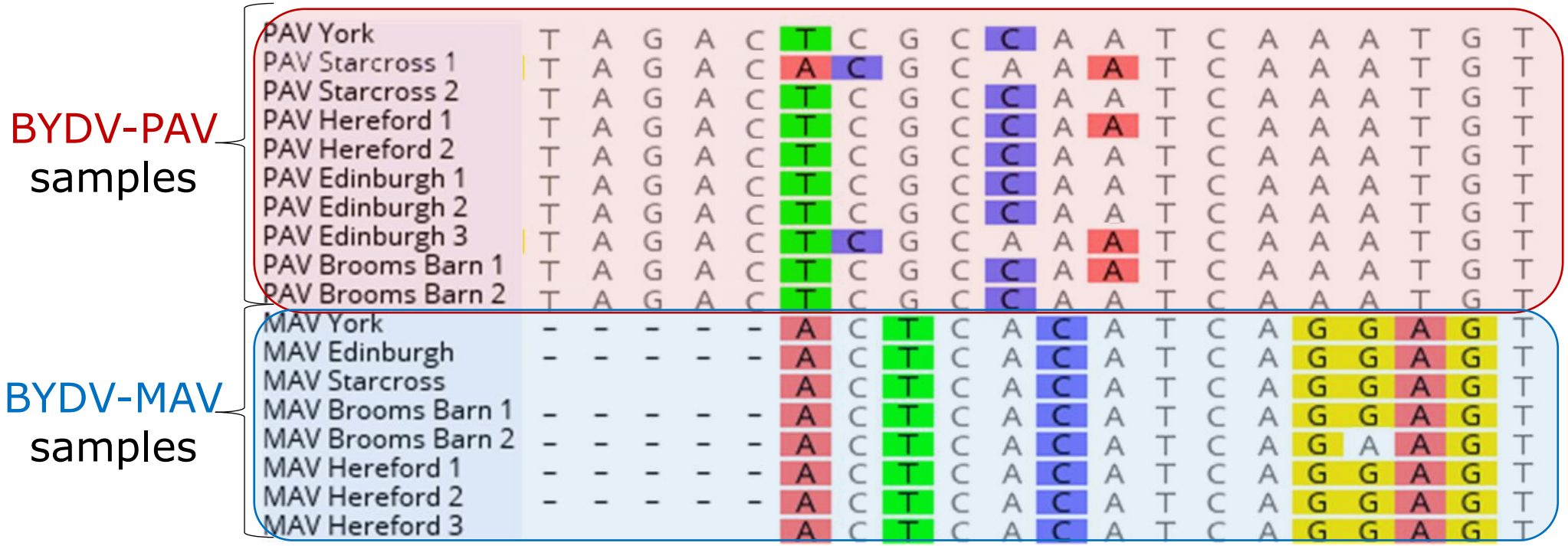


- Merged 2020 and 2021 data suggests that UK BYDV substrain variation is generally maintained
- All data is only an indicator for true UK BYDV variation
- Work pursued as complement to new BYDV assay development

Improved BYDV diagnostics

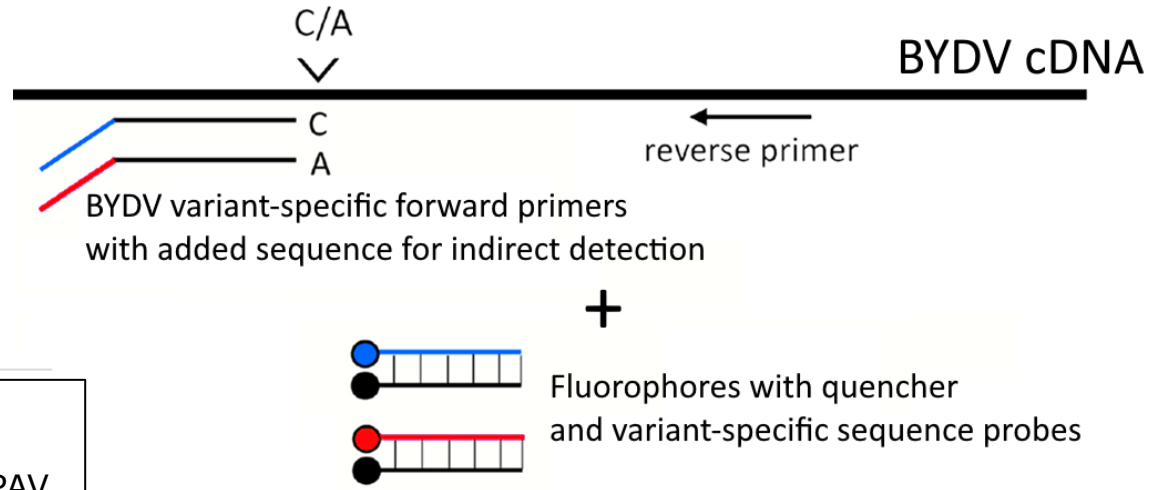
- UK BYDV strain-specific polymorphisms employed for improved BYDV diagnostics

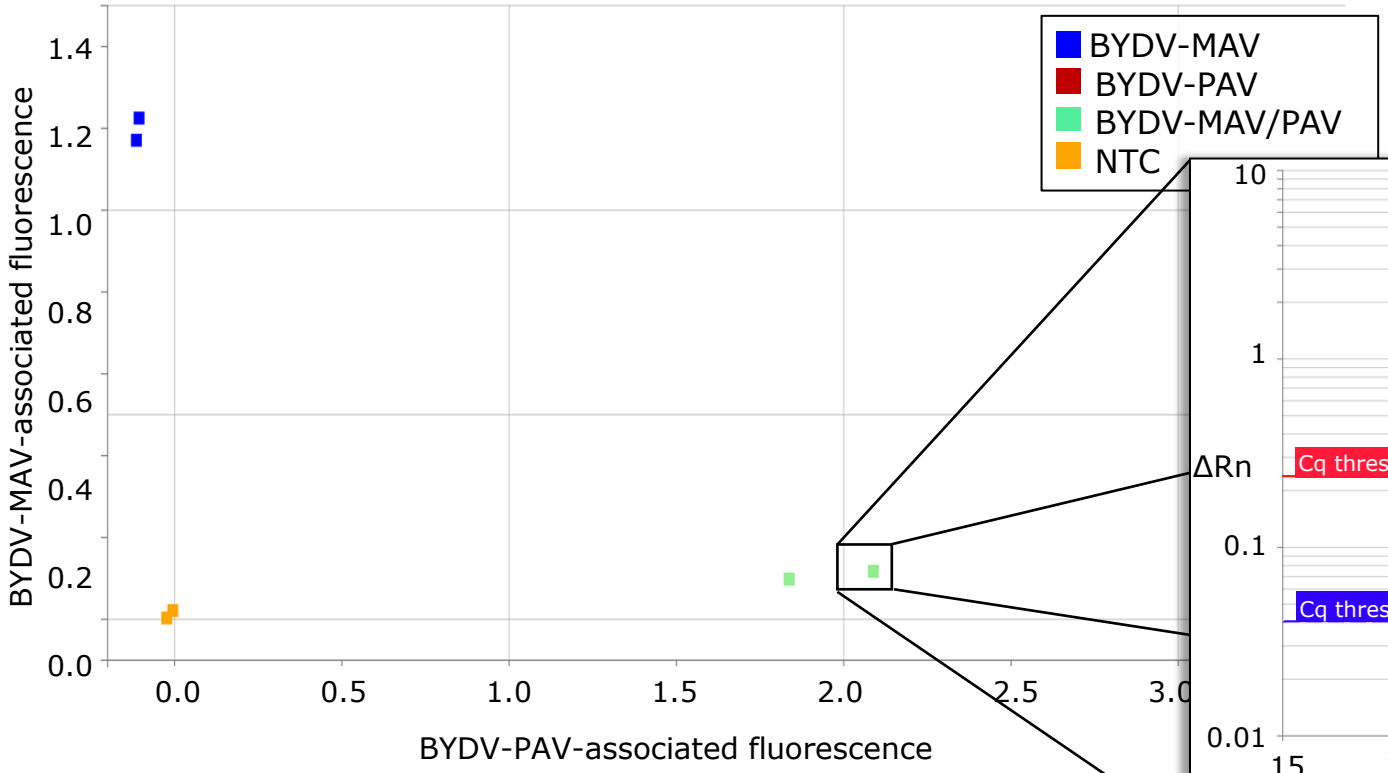
- Representative subset (anonymised):

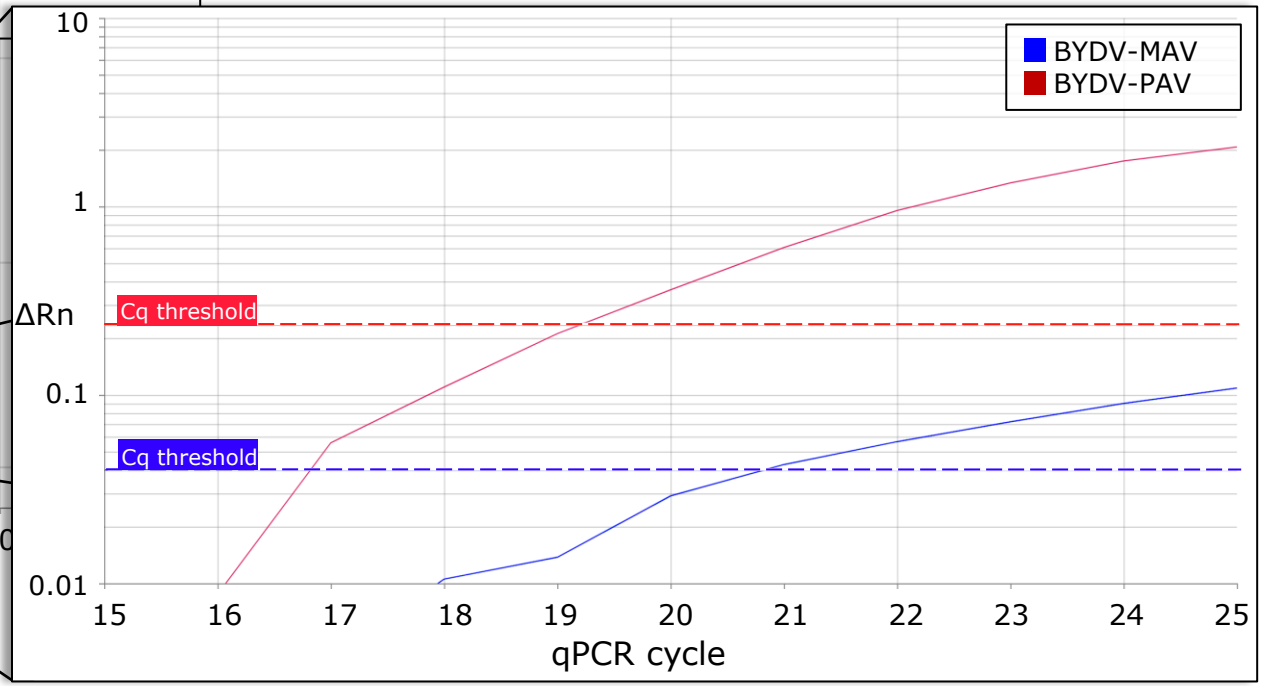


Improved BYDV diagnostics

- KASP genotyping chemistry used
  - more accessible to industry
- Semiquantitative data collection







Summary

- BYDV has notable potential to be of increased concern

- Genetic-based disease control methods exist
  - important to ensure these remain effective long-term

- Recent advancements in knowledge of UK-specific BYDV variation

- Working with industry to optimise assays for wider use
  - need to determine if resistance sources are effective against all or only some BYDV strains

Many thanks to

- RRes Wheat Pathogenomics Team (PI, Kim Hammond-Kosack)
- RRes Aphid-BYDV subgroup, especially Izayana Sandoval-Carvajal (PhD student)
- Martin Williamson and James Bell (RIS sample access)
- Continued assistance from wider wheat community

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