

The BCPC 9th Disease Review 2023

Theme – Disease Control: Balancing Food Security & Environmental Responsibility

Programme

09.30-10.15 Registration

10.20: Introduction, Chair – Rosie Bryson, CHAP Head of Marketing & Communications

10.30: Uwe Conrath, Professor of Plant Biochemistry and Molecular Biology – Plant defence signalling

11.05: Aoife O’Driscoll, Senior Specialist-Plant Pathology, NIAB – Wheat blends

11.40: Henry Creissen, Applied Plant Pathologist in the Crop Protection, SRUC – Putting a value on IPM

12.15 – PhD Presentations: Morgan Wodring (Fera), Laura Sapelli (Uni of Herts), Elin Falla (Cambridge Uni), Lisa Humbert (Rothamsted)

12.40: Lunch

13.40: Tamara Fitters, ADAS – Disease control and GHG emissions

14.15: Martin Lines – Environmentally responsible disease control

14.50: Discussion

15.30: Closing Remarks

4 BASIS CPD points and 4 NRoSO points have been allocated for attendance at this event

Please note: The following Poster formats have been modified slightly from the original Portrait shape to improve font size for online viewers

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ADAMA



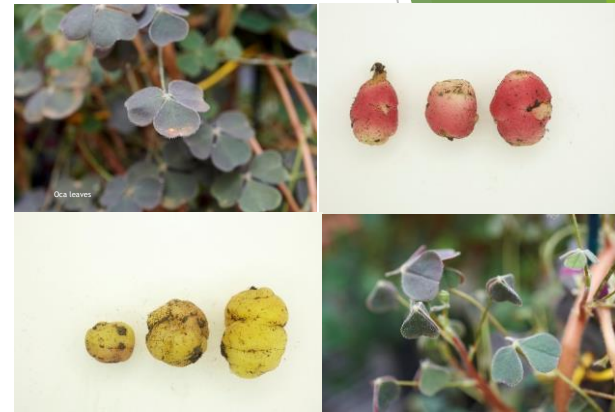
BASF
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syngenta

Introduction and methods

- **Background:** Increased trade volumes have led to an increase of biological invasions¹. In 2021, 73% of consumers on the European continent shopped online, including 91% of people from the United Kingdom, 36% of which was cross-border².
- **Aim:** To use niche tuber crops from the internet as a case study for the risk of unregulated trade in crops via e-Commerce websites.
- **Methods:** French (9) and Polish (27) *Oxalis tuberosa* (oca, shown right) tubers bought on eBay were sequenced with HTS and found to contain six putative novel viruses; two possible Caulimoviruses and likely six viruses belonging to the genera: Nepovirus, Potexvirus, Allexivirus, Capulavirus and Ophiovirus.



Non-native tubers purchased from the internet contained 6 novel virus candidates.

Results

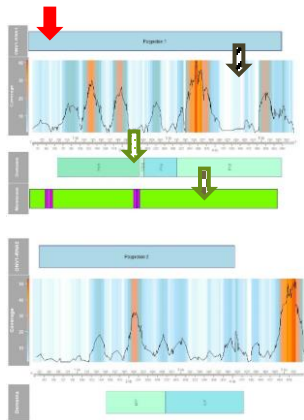


Fig. 1 (top) & 2 (bottom): Generated charts representing the partial genome of one of the novel virus candidates, a Nepovirus (Secoviridae) likely belonging to subgroup C, and tentatively named Oca nepovirus 1 (ONV1). Fig. 1 shows the partial RNA1 sequence; figure 2 the complete coding sequence of RNA2. The layers are as follows:

1. Proposed ORFs generated by ORFik³.
2. A coverage diagram. The line chart and the orange/darker fill both convey deeper read coverage in that portion of the genome.
3. Protein domain matches generated by pfam.
4. Cytoplasmic, non-cytoplasmic and transmembrane domains. ORF2 did not contain these domains according to Phobius and thus this layer is omitted.

Next steps

- This results of sequencing and characterising these viruses will add to existing risk assessments of e-commerce selling plants for planting to consumers cross-border.
- Biological characterisation of the novel Nepovirus is ongoing, focusing on mechanical inoculations and host range.
- Rapid amplification of cDNA ends (RACE) will be performed to obtain the remaining coding sequence & UTRs.

References:

Department for Environment, Food & Rural Affairs, et al. (2023). Plant biosecurity strategy for Great Britain (2023 to 2028).
 Lone, S., et al. (2021). "2021 european e-commerce report."
 Tjeldnes, H., et al. (2021). "ORFik: a comprehensive R toolkit for the analysis of translation." BMC Bioinformatics 22(1).

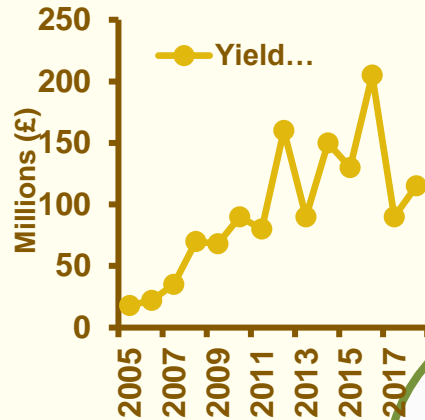


Scan for further information on this study and putative novel viruses.

MUSH-ROOM FOR IMPROVEMENT: STUDYING *PYRENOPEZIZA BRASSICAE* RACES TO MANAGE LIGHT LEAF SPOT IN OILSEED RAPE

BACKGROUND

Light leaf spot disease



RESEARCH

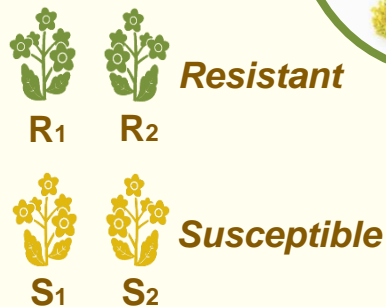
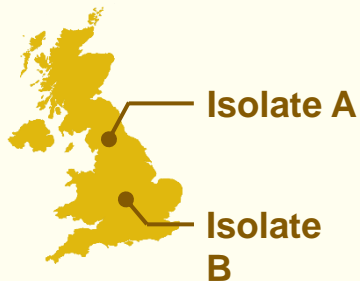
PATHOGEN MUTATIONS

MONITORING SCHEMES

CULTIVAR DEPLOYMENT



QUESTION



Do Pb isolates from different regions cause disease *equally*?

RESULTS



Pb isolates *differ* between geographic regions





Mathematical modelling of non-persistently transmitted plant viruses: the importance of including aphid vector feeding behaviours



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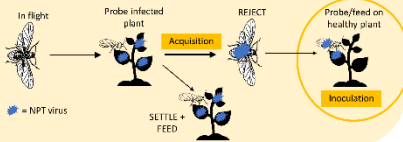
Elin Falla, Nik J. Cunniffe, Department of Plant Sciences, University of Cambridge, UK. Funded by University of Cambridge Department of Plant Sciences and Gonville & Caius College.

Background: aphid feeding and NPT viruses

- Non-persistently transmitted (NPT) plant viruses are characterised by their short retention time (minutes to hours) in the vector
- NPT viruses are horizontally (plant-to-plant) transmitted exclusively by aphid vectors
- Aphids have distinct feeding behaviours that determine virus transmission between plants (see diagram below)

Key features of aphid NPT virus retention:

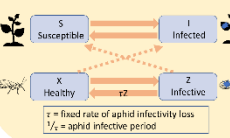
- Aphids can remain infective for probing 1 to ~3 different healthy plants
- Feeding on a plant guarantees the aphid loses the virus



Previous mathematical models

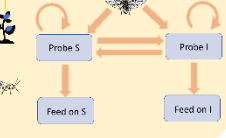
Multiple Infective Probes (MIP) model

- MIP = infective aphids can retain the virus for probes (and inoculations) of multiple plants
- No VRAIL



Variable Rate of Aphid Infectivity Loss (VRAIL) model

- VRAIL = the virus retention time in the aphid changes based on the aphid's feeding behaviour
- No MIP

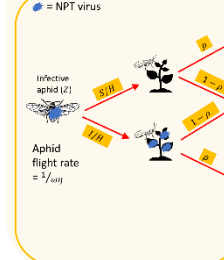


Aim Create an NPT virus mathematical model that is more accurate to aphid feeding behaviour, that includes both VRAIL and MIP features.

Methods

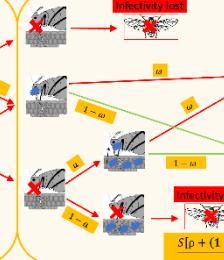
1 - Infective aphid lands on plant

S = number of healthy plants
 I = number of infected plants
 X = total number of aphids
 Z = length of feed on plant



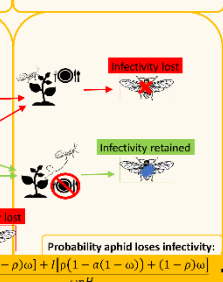
2 - Aphid probes plant

ρ = probability aphid loses infectivity from probing an infected plant
 ω = probability aphid acquires virus probing an infected plant



3 - Aphid feeds on/rejects plant

ω = probability aphid feeds on plant



VRAIL-MIP model structure:

$$\frac{dI}{dt} = \frac{ZbS}{\omega nH} - (c + d)I$$

$$\frac{dZ}{dt} = \frac{XaI}{\omega nH} (1 - \omega) - \tau Z$$

- VRAIL: 'probability aphid loses infectivity' expression based on aphid behaviour replaces fixed RAIL parameter (τ)
- MIP: Expression includes parameter ρ , probability aphid loses infectivity from probing, $0 < \rho \leq 1$

Results

- In our VRAIL-MIP model, the combination of VRAIL and MIP means for $\rho < 1$, the virus retention time in the aphid, and hence the **final epidemic size, is increased compared to VRAIL model** (Figures 1, 3)
- VRAIL-MIP model also has **larger epidemic size than MIP model for $\omega < 0.25$** . This is likely as NPT viruses are usually transmitted by non-colonizing aphids that are likely to reject plants (Figure 2)

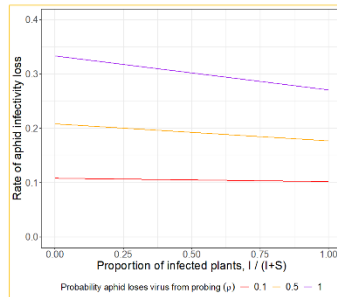


Figure 1: The rate of aphid infectivity loss decreases with (1) increasing $I/(S+I)$ and (2) decreasing probability of infectivity loss from probing (ρ), in VRAIL-MIP model.

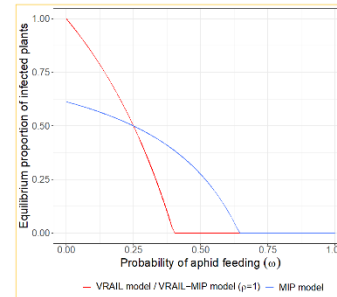


Figure 2: The increase in final epidemic size with decreasing probability of an aphid feeding (after probing) is larger in the models with VRAIL. Model parameters were matched to 0.5 equilibrium I/H . $\rho = 1$ in VRAIL-MIP model.

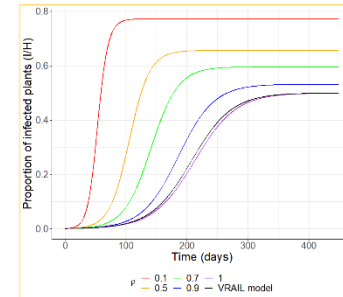


Figure 3: Decreasing ρ (probability of infectivity loss from probing) in VRAIL-MIP model increases final epidemic size. Larger epidemics than VRAIL model with same parameterization.

Conclusions

- Our VRAIL-MIP model is more realistic to aphid behaviour than previous models of NPT virus transmission, with an easily extensible structure
- The VRAIL-MIP model structure often results in larger predictions of epidemic size than previous models

Model	RAIL based on aphid behaviour	Multiple infective probes per aphid	Easily extensible
MIP model		✓	✓
VRAIL model	✓		
VRAIL-MIP model	✓	✓	✓

References: L. V. Madden, M. J. Jeger, and F. van den Bosch. A theoretical assessment of the effects of vector-virus transmission mechanism on plant virus disease epidemics. *Phytopathology*, 90(6):576{594, 2000.
R. Donnelly, N. J. Cunniffe, J. P. Carr, and C. A. Gilligan. Pathogenic modification of plants enhances long-distance dispersal of nonpersistently transmitted viruses to new hosts. *Ecology*, 100(7):e02725, 2019.



1. INTRODUCTION

As the third most important arable crop in the UK, oilseed rape is subject to numerous devastating diseases and pests (Fig. 1). It is estimated that fungal pathogens are responsible for more than £100M of oilseed rape crop yield losses annually.¹ Light leaf spot, caused by the phytopathogen *Pyrenopeziza brassicae* (Fig. 2), is a polycyclic disease presenting several infection cycles through both asexual and sexual sporulation, making it difficult to control.²

Hormone(s), named Sex Factors (SF), produced during *Pyrenopeziza brassicae* sexual reproduction, have been identified to contribute to the switch from asexual to sexual sporulation. Applied to the cultures, in the absence of a compatible mating partner, Sex Factors induce a repression of asexual sporulation and production of sterile sexual structures.³ Used as a disease control agent, SF has exciting potential to contribute to prevent the spread of this epidemics across the crops.

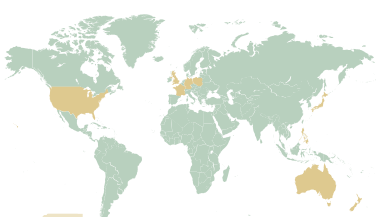
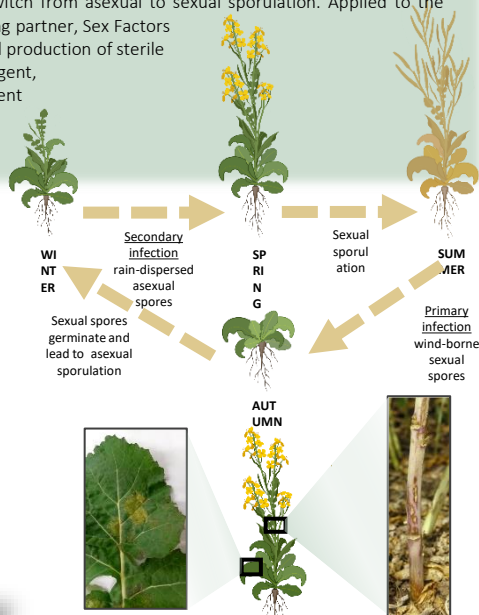


Figure 1: Distribution of Light Leaf Spot (LLS) across the world.⁴

Figure 2: Symptoms of Light leaf spot on leaves and stems of Brassica napus. Images⁵

2. SEX FACTORS INHIBIT ASEQUAL SPORULATION OF P. BRASSICAE

Production of SF from *P. brassicae* sexual crossing

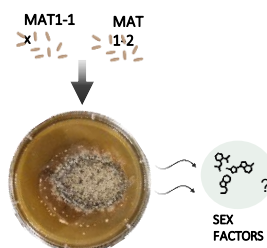


Figure 3: Darkening of *P. brassicae* cultures indicates a repression of asexual sporulation

Activity of SF on *P. brassicae*

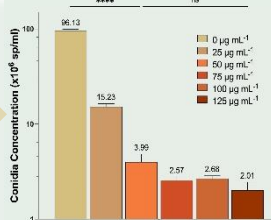
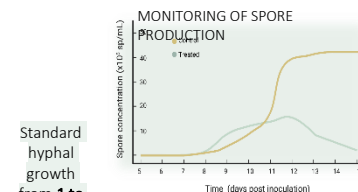
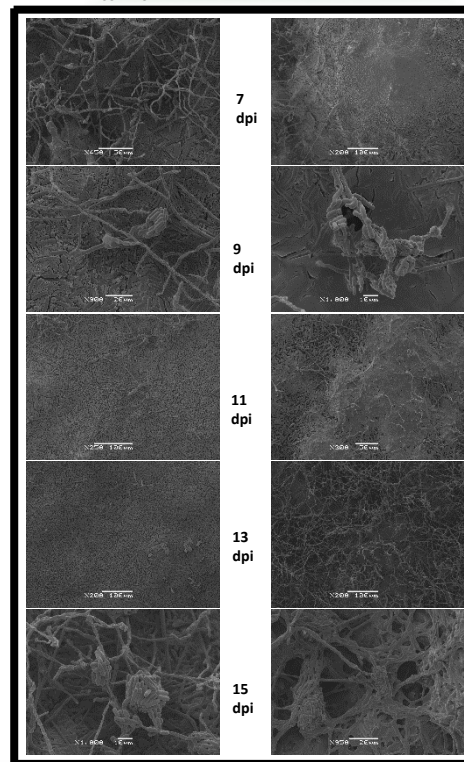
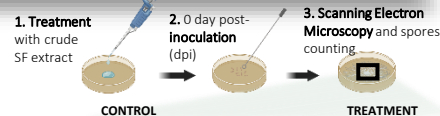


Figure 4: Asexual spores production of *P. brassicae* when treated with different concentrations of SF. Error bars represent SEM

3. MICROSCOPY OBSERVATION OF SF EFFECTS ON P. BRASSICAE DEVELOPMENT



Standard hyphal growth from 1 to 5 dpi
6 dpi: early formation of conidiophore, specialized hyphal branch producing conidia (asexual spores)

7 dpi: from conidiophores to acervuli, asexual fruiting body bearing conidiophores

11 dpi: visual darkening of the cultures (Fig. 5) resulting from the formation of a film, covering the previously produced conidia

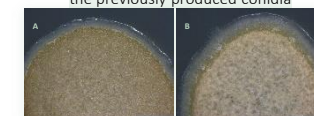


Figure 5: Stereomicroscopy 11 dpi of A. control cultures B. treated cultures

12 dpi: decrease of the concentration of conidia as the film spreads over the culture

13 dpi: a dense mycelium grows over the film

15 dpi: cultures have turned black (Fig.6). 90% inhibition of asexual sporulation observed compared to controls

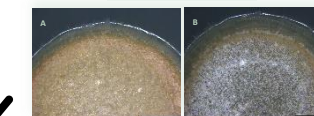


Figure 6: Stereomicroscopy 15 dpi of A. control cultures B. treated cultures

4. DISCUSSION & CONCLUSION

Current work on the identification of Sex Factor(s) using HPLC has narrowed down to a few putative compounds that could be responsible for the repression of asexual sporulation. Full characterisation will be achieved using Nuclear Magnetic Resonance (NMR) coupled with Liquid Chromatography– Mass Spectrometry (LCMS) techniques. Further work is investigating potential genes involved in the biosynthesis of the Sex Factors, while their activity is being assessed on larger scale experiment (i.e plant organs and whole plants).

REFERENCES

¹ Jellis G., Fitt B., 2021. Management of diseases and pests of oilseed rape.
² Gilles, T., Fitt, B., McCartney, H., Papastamati, K., Steed, J., 2001c. Ann. Appl. Biol. 138, 141–152.
³ Siddiq, A., Johnstone, K., Ingram, D., 1990. Mycol. Res. 96, 757–765.

⁴ Carmody, S.M., King K., Ocamb C., Fraaije B., West J., du Toit L., 2020. Plant Path. 69, 518–537.
⁵ Images from Bayer and ADAS Thomas Pearson, PhD thesis, 2021. Fungal sex for disease control and strain improvement.
All illustrations have been created on Biorender. Project funded by the Future Food Beacon