

Improving knowledge of *Xylella fastidiosa* vector ecology: modelling vector occurrence and abundance in the wider landscape in Scotland

PHC2020/04 - Policy Summary



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Please cite this report as follows: D. Chapman, S. A'Hara, S. Broadmeadow, R. Cairns, J. Cottrell, E. Fuentes-Montemayor, K. Lester, F. Occhibove, S. Rogerson, S. M. White & K. Park. (2022). Improving knowledge of *Xylella fastidiosa* vector ecology: modelling vector occurrence and abundance in the wider landscape in Scotland: Policy Summary. PHC2020/04. Scotland's Centre of Expertise for Plant Health (PHC). DOI: 10.5281/zenodo.6523478

Available online at: planthealthcentre.scot/publications

Dissemination status: Unrestricted

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Policy Summary

The insect-vector, bacterial plant pathogen *Xylella fastidiosa* is currently absent from Scotland and the wider UK, but if introduced could be a serious threat to trees and other plants. However, there is a lack of knowledge about the ecology and distributions of *Xylella* vectors in Scotland and the potential effects of this on any outbreak of the disease, which this project aimed to address.

Sampling of xylem-feeding potential vector insects (order Hemiptera, Aphrophoridae and Cicadellidae families) was conducted in 2021, including weekly sampling of different habitats at Loch Leven, Fife, and a wider survey across 16 sites in central Scotland.

Key findings were:

- Quadrats were effective for surveying vector nymphs, and nymph identification in the field or through molecular methods were both accurate. Sweep netting was the most effective survey method for adult *Xylella* vectors.
- The principal *Xylella* vector in Europe, the meadow spittlebug (*Philaenus spumarius*), was the dominant species in Scotland.
- Its adult flight period (where disease transmission would occur) lasted approximately three months (mid-July to mid-September) – a similar duration to the *Xylella* outbreak area in Italy.
- Meadow spittlebug densities in the woodland understorey and grassland were similar to those recorded in the Italian outbreak area.
- However, densities in woodland tree canopies were very low. This might limit *Xylella* transmission among woodland trees although an alternative (unconfirmed) potential vector was sampled in tree canopies in good numbers (the alder spittle bug *Aphrophora alni*).
- Unexpectedly, the meadow spittlebug had a clear habitat preference for heathland, with densities *ca* 5 times higher than in other Scottish landscapes and the Italian outbreak area. Heather and other common Scottish heathland shrubs, *e.g.* blaeberry are potential *Xylella* host plants, raising concern about outbreaks in heathland.

To investigate the effects of these results on potential *Xylella* outbreaks in Scotland, an epidemiological model was used to simulate outbreaks in Scottish conditions with a range of vector scenarios and to simulate control efforts based on current EU and UK strategies. Although the modelling is subject to many caveats, key findings were:

- Simulated outbreaks in Scotland grew and spread much more slowly than the outbreak in Italy (due to lower temperatures) and were dominated by asymptomatic hosts (due to lower drought stress).
- High vector densities in heathlands promoted *Xylella* spread in heathland-dominated regions, especially with higher summer temperature and host plant connectivity.
- In simulated eradication efforts, felling known infections and demarcation of buffer zones around them for further surveillance achieved only modest reductions in outbreak growth. Control was hampered by high proportions of asymptomatic host plants which evaded visual surveys.

- Early detection and large initial buffer zones improved control effectiveness.

Overall, this project has produced better understanding of vector phenology, species composition and habitat preferences in Scotland, as well as guidance for sampling vectors and controlling future outbreaks. It highlights a previously unappreciated risk to Scottish heathland, though this should be set in the overall context of a less suitable climate for *Xylella* outbreak growth and impact at present. Better understanding of vector dispersal ranges and of *Xylella* transmission and disease progression in heathland plants under Scottish climatic conditions would further inform on the potential risk of introducing *Xylella* to Scotland.

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