

Utilising samples collected in an existing biodiversity network to identify the presence of potential insect vectors of *Xylella fastidiosa* in the UK

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POLICY SUMMARY

1. The presence of the vector invertebrates has been confirmed in broadleaved and mixed woodlands in a range of settings in central Scotland (The results of the PHC funded project led by Samantha Broadmeadow (PHC2018/04: Risk Mapping for *Xylella* in Scotland, identified this region as higher risk than much of Scotland for entry and survival of *Xylella*).
2. The presence (and abundance) of the invertebrates is related to features of the surrounding landscape, i.e. there is an increased likelihood of the vectors in woodlands located in landscapes with relatively low percentages of broadleaved woodland and other semi-natural habitats. However, this study focussed on woodlands, and little is known about how the abundance of vectors varies between habitats.
3. Molecular detection methods (bar-coding and meta-barcoding) have been refined (e.g. improved primers), confirmed against morphological ID and found not to be generating false positives and will be of value should a suspected outbreak require rapid investigation.
4. Training in invertebrate ID has increased capacity in the Scottish science community to identify key vectors.
5. Understanding of *Xylella* has increased in several partner organisations and has been shared with key stakeholders, contributing to preparedness.

The following key caveats, and in some instance opportunities for further investigation, need to be highlighted.

1. An understanding of how micro-climate varies across the major land-uses/habitat types and how this would determine invertebrate behaviour (e.g. movement into canopy at time of drought; persistence in controlled environments such as polytunnels) would refine the risk mapping and the targeting of surveillance.
2. A wider range of woodland types (including the much valued but potentially vulnerable ancient woodland), landscape settings (e.g. different non-woodland matrix habitats), and sample periods should be examined for patterns of vector occurrence and abundance.
3. The community assemblages within which the vectors are found (as identified in broader scale biodiversity sampling) would indicate the potential collateral losses of flying insects (e.g. loss of rare or protected invertebrates) should *Xylella*-based control regimes (e.g. widespread chemical control) be implemented. Other trapping methods would be required to broaden the biodiversity assessment (e.g. to fully consider ground or canopy dwelling invertebrates).
4. There is insufficient knowledge of spatial distribution (and abundance) of the key host species to allow detailed spread modelling to be reliable and with reduced uncertainty.