

Metabarcoding analysis of *Phytophthora* diversity in spore traps and implications for disease forecasting in the *P. ramorum* management zone

Carolyn Riddell, Sarah Green, Debbie Frederickson-Matika (Forest Research);
Peter Cock, Pete Hedley (Hutton)



Scottish Government
Riaghaltas na h-Alba
gov.scot

Introduction

- Currently around 180 *Phytophthora* species are provisionally named worldwide, many with the potential to be invasive and destructive outside their native range. *Phytophthora ramorum* causes extensive damage and death in larch (*Larix kaempferi*) and spreads to new hosts via windborne transmission.
- To assist forecasting and management of new *P. ramorum* outbreaks a Scottish Forestry-funded project is investigating *P. ramorum* inoculum dispersal distance in relation to abiotic factors using spore trapping and a *P. ramorum*-specific qPCR assay.
- Where qPCR detects single species, metabarcoding reveals species diversity. *Phytophthora* species diversity is often high in UK public amenity gardens and nurseries but knowledge of their wider distribution and abundance in the UK is limited.
- Our PHC-funded project tests the suitability of metabarcoding to both monitor airborne *P. ramorum* and provide early detection of novel *Phytophthora* species that may pose new threats to UK trees and plants.

Objectives

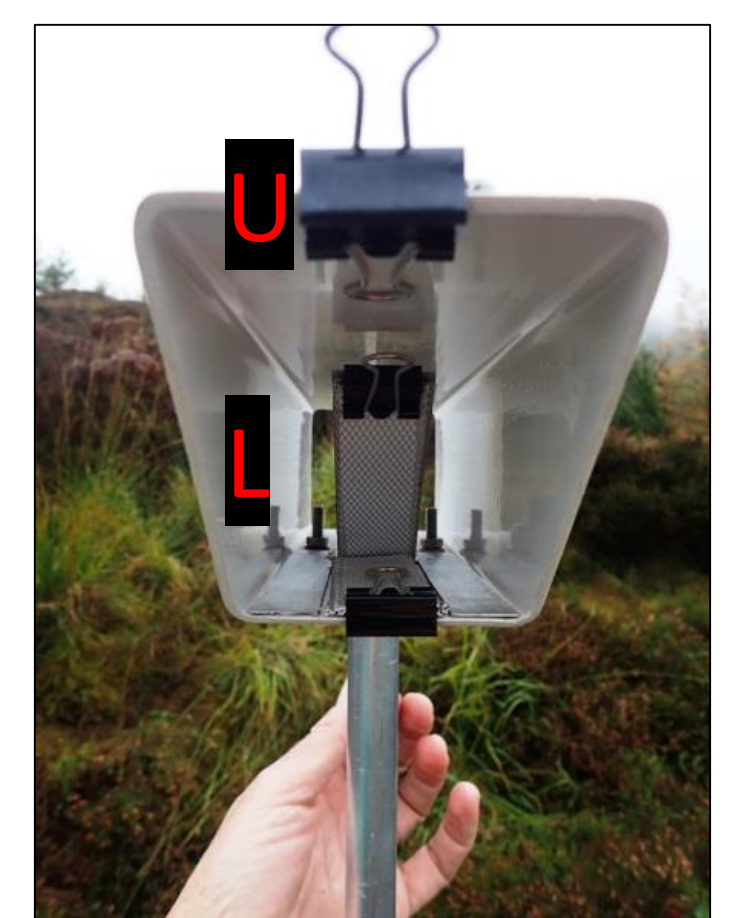
Using spore and rain-trap DNA samples from the Scottish Forestry-funded project we are:

1. Testing whether metabarcoding can detect both *P. ramorum* and other novel *Phytophthora* species that are increasing in prevalence (e.g., *P. pseudosyringae*, *P. foliorum* and *P. kernoviae* in addition to *P. ramorum*)
2. Comparing the sensitivity of metabarcoding to the species-specific *P. ramorum* qPCR assay.
2. Comparing whether different spore-trap methods (wind-vane and Burkhard) capture different *Phytophthora* species.

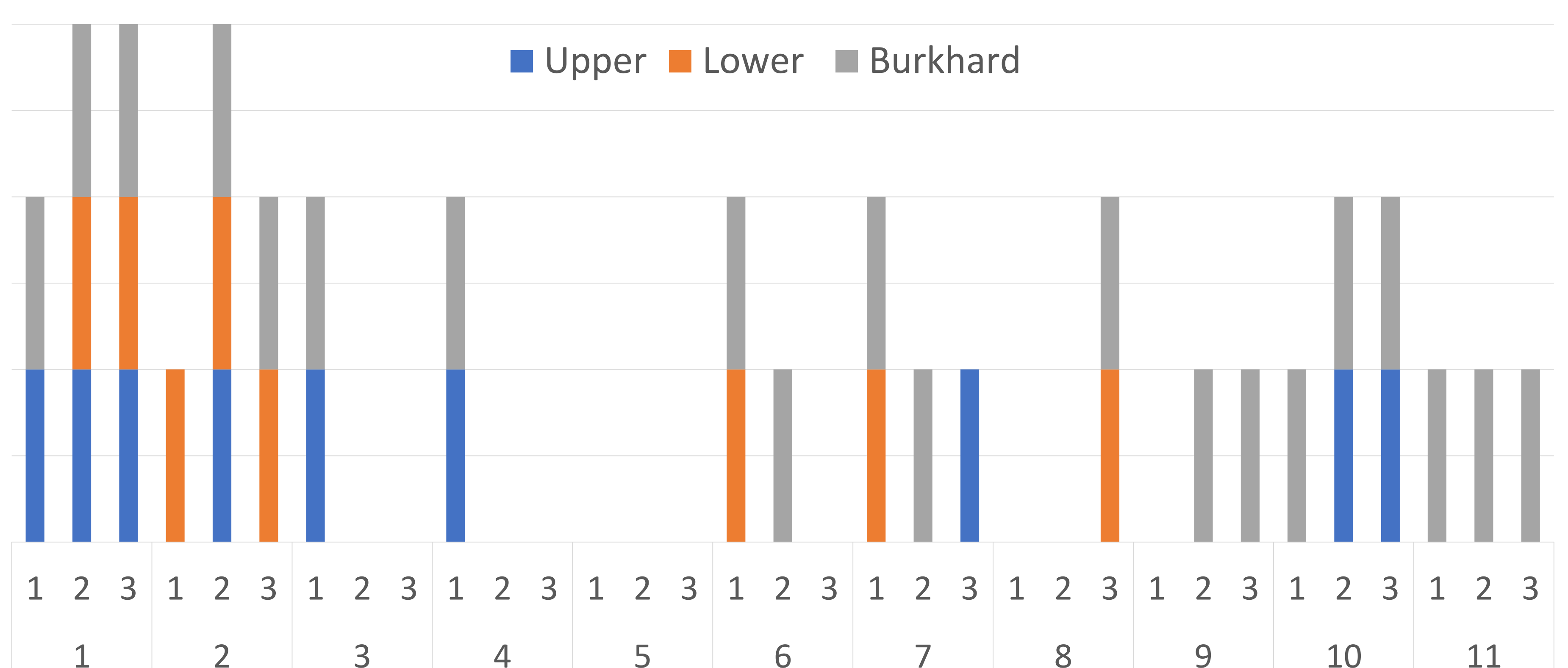


Project outcomes

- So far we have tested 72 of 90 spore-trap DNA samples and identified 38 positive for *Phytophthora* which will be put through metabarcoding to determine species identity.
- Wind-vane and Burkhard spore traps were set-up at <5m, 40m and 100m from a *P. ramorum*-infected stand and collected each week.
- Wind vane and Burkhard traps each produced 50% positives.



Slide positions on wind-vane trap (upper & lower)



Spore traps testing positive for *Phytophthora* at 3 distances from an infected larch stand, over 11 weeks September – December 2019, in wind vanes (in upper & lower slide positions) and Burkhard traps. Species identities in these samples will be determined using metabarcoding.

Key messages

- There is a need to both monitor established windborne *Phytophthora* diseases such as *P. ramorum* and carry out broader *Phytophthora* species surveillance to enable early detection and forecasting of future outbreaks in UK trees and plants.
- Metabarcoding is a good candidate for an alternative *Phytophthora* monitoring and detection method.
- Metabarcoding samples from the Scottish Forestry project will allow us to determine which spore traps capture the greatest variety of *Phytophthora* species.

Acknowledgements

This work was funded by the Scottish Government's Rural and Environment Science and Analytical Services (RESAS) Division through the Centre of Expertise for Plant Health

