Impacts of forest pathogens

Predicting the spread of pathogens and risks to forest ecosystems: the case of *Phytophthora*

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Introduction

An increasing number of pests and pathogens are damaging trees and the wider forest ecosystem. In the UK, Chalara dieback of ash and *Phytophthora ramorum* on larch, Rhododendron and understorey Vaccinium are two of the most serious current threats.

One principal recommendation of the recent Tree Health and Plant Biosecurity Taskforce report was the establishment of a UK Plant Health Risk Register. To assess risk we need an ability to horizon scan for potential future threats and know the types of pathogen and their pathways of movement to guide predictions of their likely environmental and economic impacts.

Several current threats to UK tree health involve invasive species of the algal-like Phytophthora group of plant pathogens. Over 120 species have been described but assessing the risks due to these and the as yet un-described species has proved challenging. We present the design and application of a generic *Phytophthora* diagnostic method that is being used to monitor the species active in Scottish Environmental Change Network (ECN) sites to help answer the following key questions:

● Which species are infecting plants in apparently 'healthy' ecosystems?
● What is their ecological function?
● How is their activity affected by environmental change?
● Can we use to method to prevent future incursions?

The data generated will be used to assess the wider risks that *Phytophthora* poses to forest ecosystems.

References
Scibetta S, Schena L, Chimento A, Cacciola SO, Cooke DEL, (2012) A molecular method to assess *Phytophthora* diversity in environmental samples. *Journal of Microbiological Methods* **88**, 356–368.

Methods

Sampling

Water samples (10 l) were collected from streams at four sites at 14-day intervals during 2011–2013. In addition a stream flowing through planted *Larix* infected with Phytophthora ramorum was sampled at a single date. The motile *Phytophthora* zoospores were filtered from the water samples in the field using a knapsack sprayer to pump water through an in-line filter holder.

Sample processing

Filters were freeze-dried and stored for subsequent DNA extraction (methods: Scibetta *et al.*, 2012). Nested PCR using *Phytophthora*-specific primers based on the ITS regions of rDNA was followed by cloning. Eight clones from each Phytophthora-positive sample were sequenced and the data compared to a reference database of previously described species to generate a **catalogue of pathogen diversity**.

Figure 1 Location of sampled streams. ECN sites are shown in orange (http://www.ecn.ac.uk/)

Results

The sampling and detection system proved a very effective means of monitoring *Phytophthora* diversity in these ecosystems. The primers did not cross react with *Pythium*, a closely related ubiquitous group of less pathogenic oomycetes.

● *Phytophthora ramorum* inoculum was detected in streams flowing near an infected larch plantation (Fig 2) indicating the value of the method in monitoring quarantine forest pathogens.
● At the four main sites a broad range of >25 *Phytophthora* species were detected over six months of sampling. In some cases five different species were found in a single 10 litre water sample. Eight groups of sequences did not show any close matches with sequences in GenBank and therefore represent Phytophthora species not yet known to science.
● *Phytophthora* was active throughout the year, with zoospores detected in midwinter even in the upland sites. The diversity of *Phytophthora* species broadly reflected botanical diversity, with a greater diversity of species in more botanically diverse lowland sites with greater disturbance.
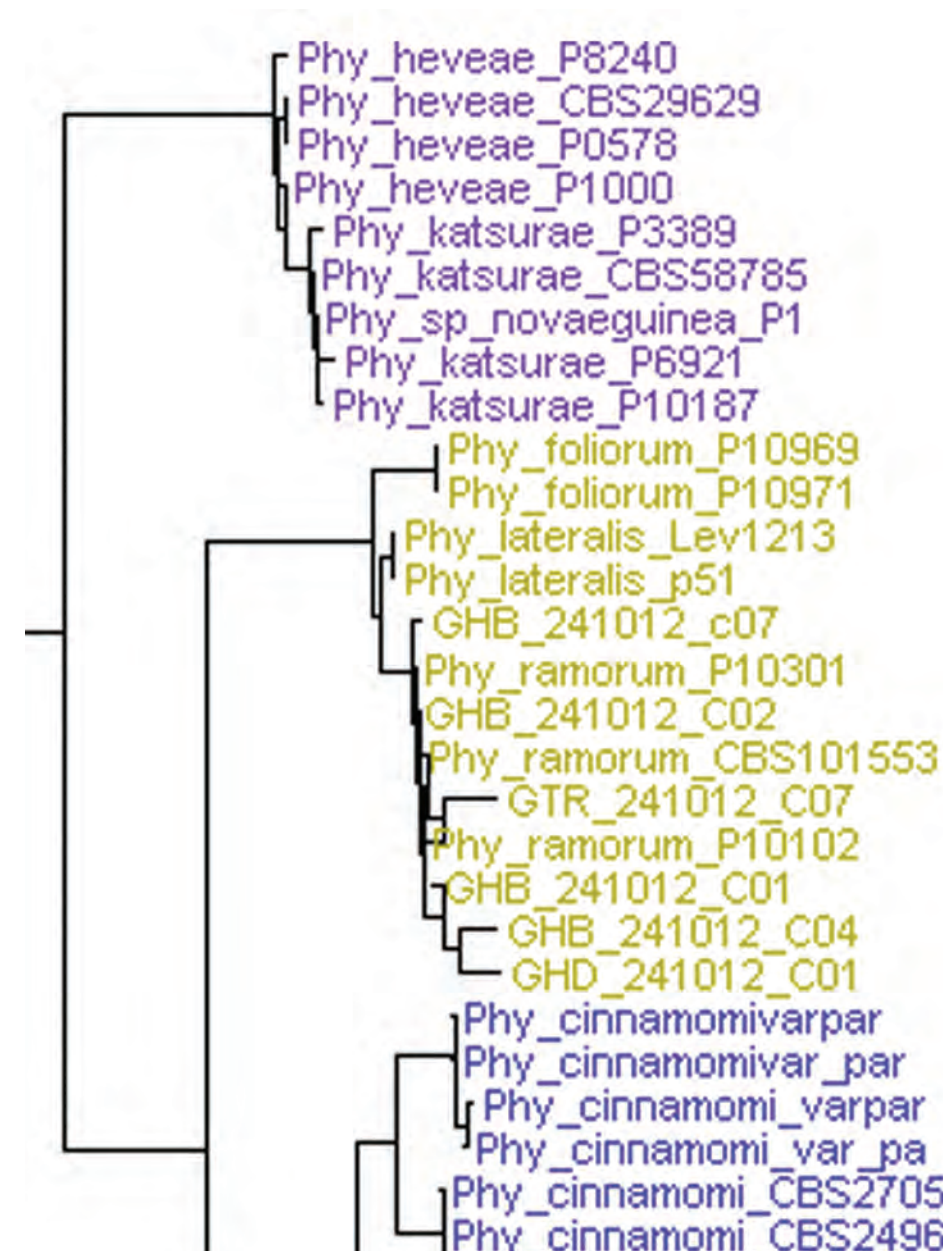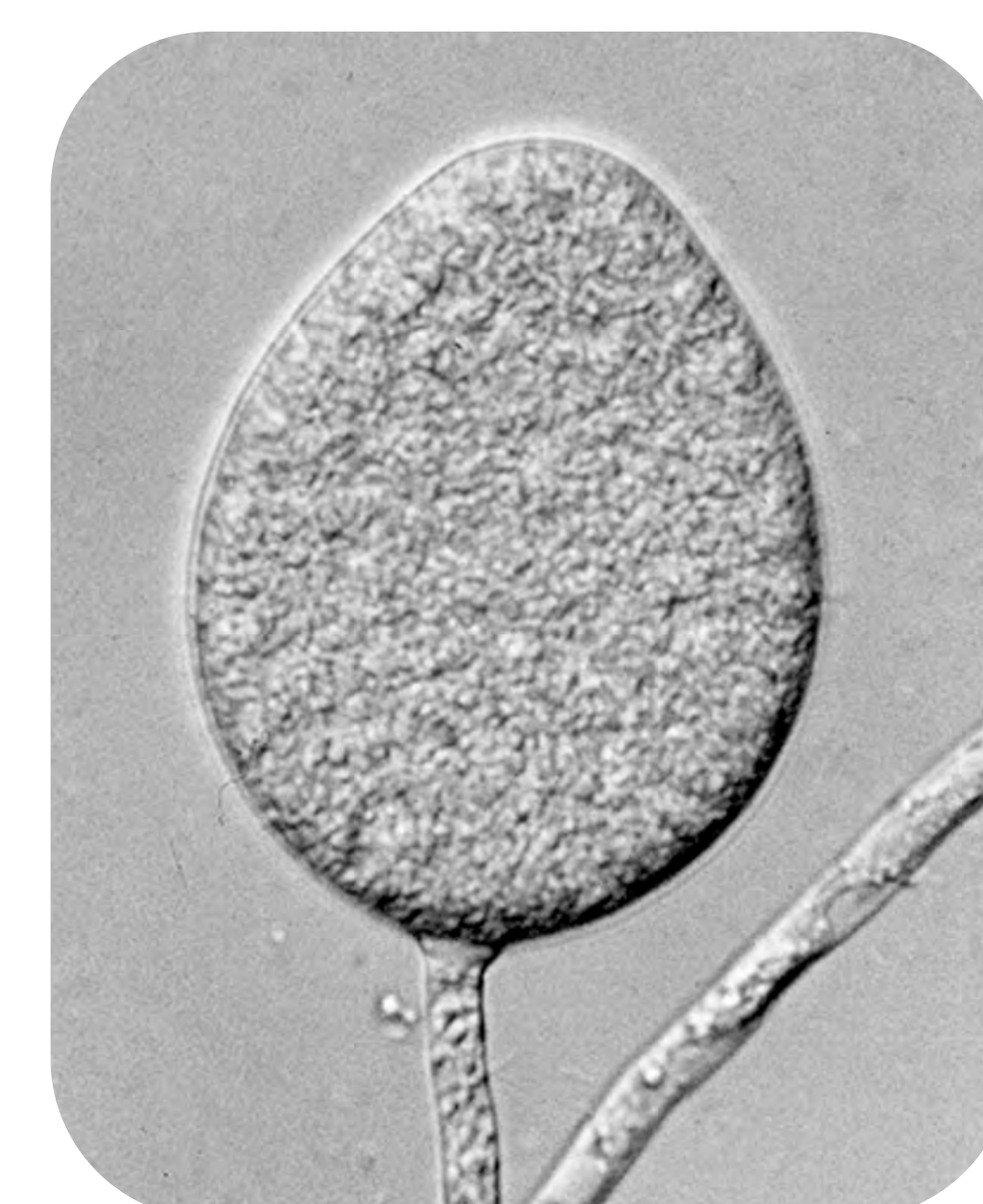

Figure 2 Fragment of output phylogenetic tree indicating *Phytophthora ramorum* reference sequences alongside samples of the same pathogen from streams (GHB, GHD, GTR) in southwest Scotland.

Conclusions

● Generic detection technology for *Phytophthora* pathogens is allowing us to track known pathogens such as *Phytophthora ramorum*
● The method is also providing an insight into the wide range of known and previously unknown pathogen diversity in apparently 'healthy' ecosystems
● Such data is allowing us to assess the risks of new pathogen incursions in the context of existing pathogen diversity
● In combination with our research on wider ecological impacts (**www.hutton.ac.uk**), we are developing robust approaches to assess the nature and risk of environmental impacts of new forest health threats – we offer this expertise in support of a European Forest Risk Facility.