

Title: PHC2019/08 – Metabarcoding analysis of *Phytophthora* diversity in spore traps and implications for disease forecasting in the *P. ramorum* management zone.

Background: The oomycete *Phytophthora ramorum* has caused substantial losses of Scottish forests in recent years due to widespread mortality of European larch trees (*Larix decidua*). Since 2009, legislation and policies have been implemented to control *P. ramorum* outbreaks on larch including the use of a 250 m larch 'fire-break', although it is unclear whether this distance is optimal for disease control. A project funded by Scottish Forestry is using a *P. ramorum*-specific qPCR assay to compare several spore trapping techniques for quantifying wind- and rain-borne inoculum and to better estimate inoculum dispersal distance. This project will add value to that of the Scottish Forestry-commissioned work, through evaluation of metabarcoding as an alternative method to both monitor *P. ramorum* inoculum dispersal and detect a broader range of aerially dispersed *Phytophthora* species. A second objective is to determine the lineage composition of *P. ramorum* inoculum throughout the observed peak sporulation period.

Impact: Timely management and prioritisation of policy to manage *P. ramorum* and facilitate early forecasting of other *Phytophthora* outbreaks.

Objectives and research required for this call: Using spore and rain-trap DNA samples from a Scottish Forestry-funded project determine: (i) whether metabarcoding can detect both *P. ramorum* and other novel *Phytophthora* species; (ii) the sensitivity of metabarcoding compared to the species-specific *P. ramorum* assay and (iii) whether different spore-trap methods capture different *Phytophthora* species.

Outputs required:

- Apply DNA metabarcoding to samples generated from Scottish Forestry funded *P. ramorum* project.
- Bioinformatic analysis of metabarcoding data carried out to compare *P. ramorum* abundance and comparison of *Phytophthora* species diversity.
- Analyse the lineage composition of airborne inoculum.
- Final report with 1-2 page policy summary

Key Milestones:

- Project start by 6th January 2020
- Project start-up meeting with PHC Directorate
- Metabarcoding and bioinformatic analysis
- Testing lineage-specific qPCR primers
- Data Analysis

Project Duration: 3 months

Date all work needs to be completed by: 31st March 2020

Project type: Call down - collaborative

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