

Makiola

Characterising plant pathogen communities and their environmental drivers at a national scale

A Makiola^{1,2}, IA Dickie³, RJ Holdaway⁴, JR Wood⁴, KH Orwin⁴, TR Glare², CK Lee⁵

¹ Agroécologie, AgroSup Dijon, INRA, Univ. Bourgogne, Univ. Bourgogne Franche-Comté, F-21000 Dijon, France

² Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand

³ Bio-Protection Research Centre, School of Biological Sciences, University of Canterbury, New Zealand

⁴ Manaaki Whenua – Landcare Research, Lincoln, New Zealand

⁵ Waikato DNA Sequencing Facility, School of Science, University of Waikato, Hamilton, New Zealand

Understanding what drives the dynamics of plant pathogens at the largest scales is crucial for the maintenance of global food security, conservation of natural ecosystems and future resilience and sustainability of ecosystem services in general. Although interactions between plant pathogens, the environment, land use and plants have been described many times, the contribution of these different parameters remain largely unknown. Recent advances in next-generation sequencing (NGS) methods and extended DNA barcode libraries are allowing, for the first time, surveys and the study of entire plant pathogen communities and their interactions across diverse landscapes at national scales. The inference of functional traits from metabarcoding data, such as those associated with plant pathogen status, presents a range of interesting scientific challenges. Here I present what we have learnt from doing this in New Zealand: (1) the advantages and pitfalls of NGS metabarcoding of plant pathogens; (2) the first biomonitoring of fungi, oomycete and bacteria plant pathogens at the national scale of New Zealand; and, (3) the relative importance of environmental factors for plant pathogens and what this likely means for us in face of ever increasing changes in climate and land use.