



Invited paper

Can high throughput sequencing be used in biosecurity? A case study of *Phytophthora* in Australia

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The introduction and subsequent impact of *Phytophthora cinnamomi* within natural vegetation is one of the major conservation issues for biodiversity in Australia. Recently, many new *Phytophthora* species have been described from Australia's natural ecosystems, but their distribution, origin, and potential impact remain unknown. This is concerning because if they are present due to breaches in biosecurity we need to understand the pathways of introduction. Historical bias in *Phytophthora* detection has been toward sites showing symptoms of disease, and traditional isolation methods show variable effectiveness for detecting different *Phytophthora* species. However, new techniques based on the sampling of environmental DNA and metabarcoding are now available through the use of high throughput sequencing (HTS). *Phytophthora* diversity and distribution in Australia has been defined using metabarcoding of soil samples, and the diversity detected using this technique has been compared with that available in curated databases. This study revealed high *Phytophthora* richness within natural vegetation and a difference between land use types (agriculture vs natural ecosystems). The additional HTS records provide a valuable baseline resource for future studies. Many of the *Phytophthora* species now uncovered in Australia's natural ecosystems are newly described. Until more is known the precautionary principle needs to be followed regarding the spread and conservation management of these new species in Australia's unique ecosystems. There are many unanswered questions, but of great importance is evaluation of the invasiveness of different *Phytophthora* species. New technologies can be used to establish baseline databases and then set up monitoring and surveillance protocols for the detection of new pathogen incursions.

