

Next Generation Sequencing reveals unexplored *Phytophthora* diversity in Australian soils

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The Vegetation Health Survey (VHS) at the Department of the Environment, Western Australia has a *Phytophthora* collection extending back to 1979. Isolates in this collection have been recovered during routine monitoring on natural ecosystems in Western Australia for the presence of *Phytophthora cinnamomi*. Through molecular re-evaluation of this collection we have subsequently described 11 new *Phytophthora* species and the diseases associated with them and additional descriptions are underway. Elsewhere in Australia, however, there is extremely limited information on *Phytophthora* diversity within natural ecosystems. Using modern molecular techniques such as Next Generation Sequencing, it is possible to determine *Phytophthora* species diversity from environmental soil samples. In this study, DNA was extracted from soils obtained from 700 locations around Australia. ITS1 amplicons were generated using *Phytophthora* specific primers (Scibetta et al. 2012) adapted for NGS by Santi Català and sequenced on a Roche Junior GS platform. For 50 samples roots and rhizosphere soil were extracted separately. Results reveal an astonishing diversity, several new species and very different species profiles when comparing roots and rhizosphere soil from the same location. Species described and known only from Western Australia have an Australia-wide distribution raising intriguing questions in regards to origin and movement of species.

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