



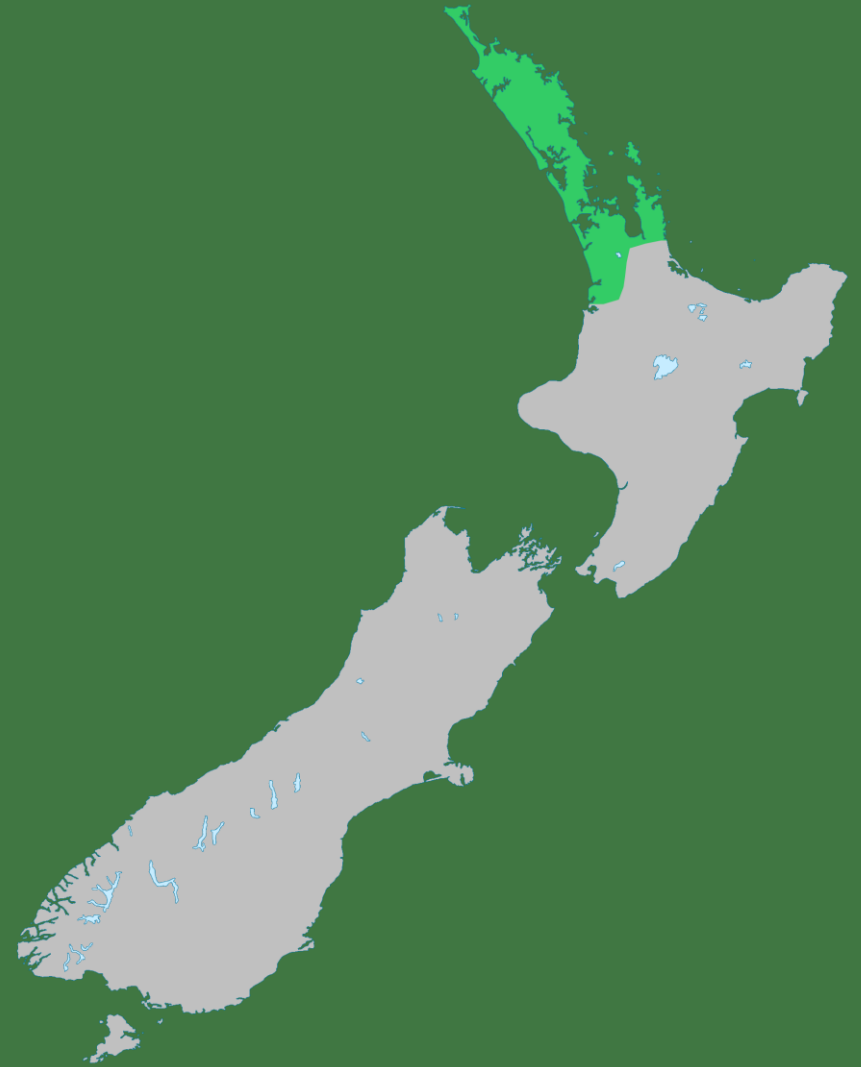
Does kauri dieback disease change soil microbial community structure?

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Auckland University of Technology

Kauri (*Agathis australis*)





Significance of kauri

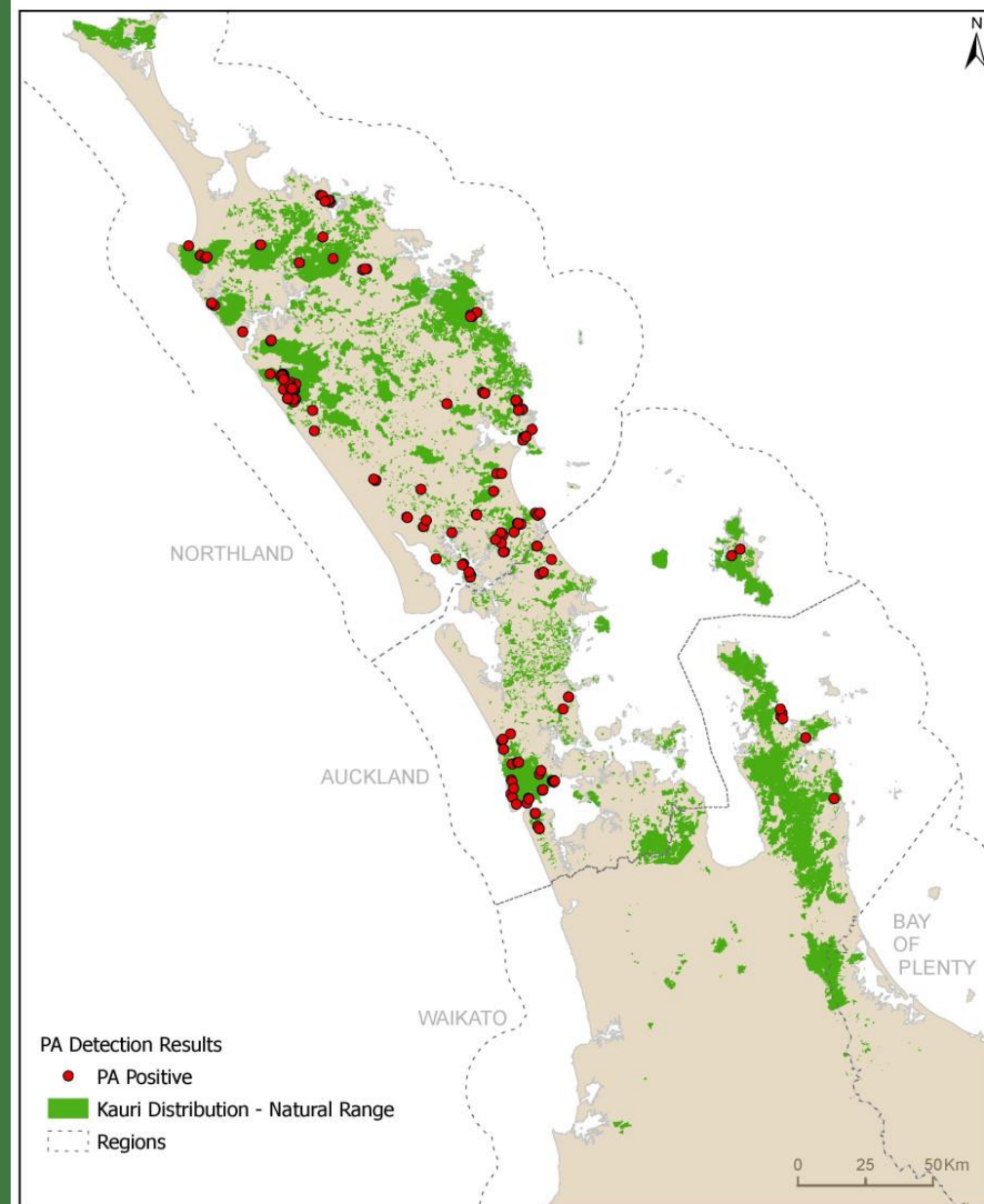
- Cultural
 - Taonga species
 - Creation beliefs
- Economic
 - Kauri timber and gum
 - Tourism
- Ecological
 - Foundation species
 - Carbon storage



Kauri dieback

Phytophthora agathidicida

Distribution of kauri dieback



Kauri Dieback Distribution

Created by the Spatial Intelligence Team
Date: 10/06/20

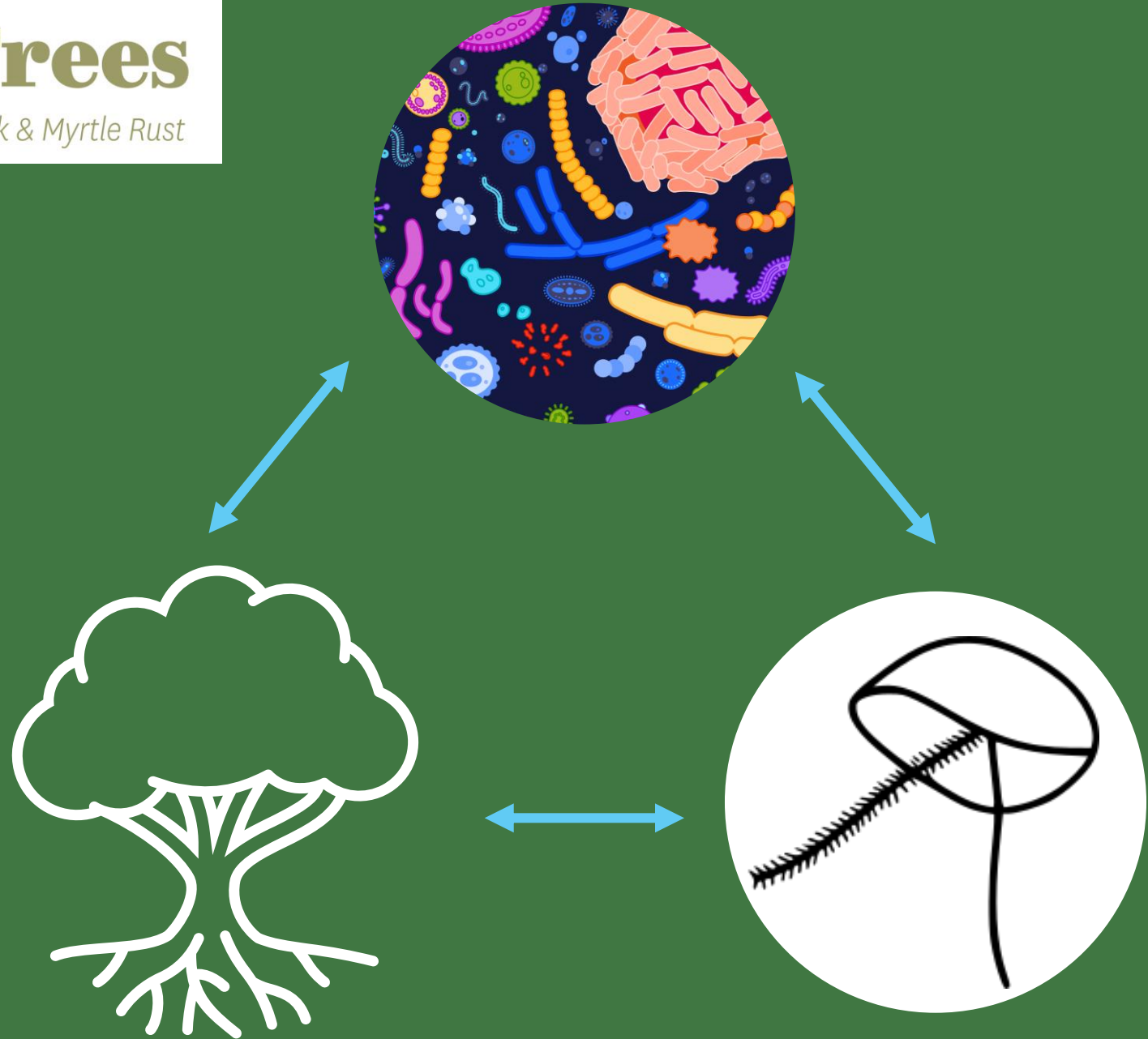
This map and all information accompanying it is intended to be used as a guide only, in conjunction with other data sources and methods, and should only be used for the purpose for which it was developed. The information shown in this Map is based on a summary of data obtained from various sources; it does not yet include some additional field data from the Auckland region, mainly from private land, gathered after 2017. While all reasonable measures have been taken to ensure the accuracy of the Map, MPI: (a) gives no warranty or representation in relation to the accuracy, completeness, reliability or fitness for purpose of the Map; and (b) accepts no liability whatsoever in relation to any loss, damage or other costs relating to any person's use of the Map, including but not limited to any compilations, derivative works or modifications of the Map. Crown copyright ©. This map is subject to Crown copyright administered by Ministry for Primary Industries.

NGĀ RĀKAU TAKETAKE

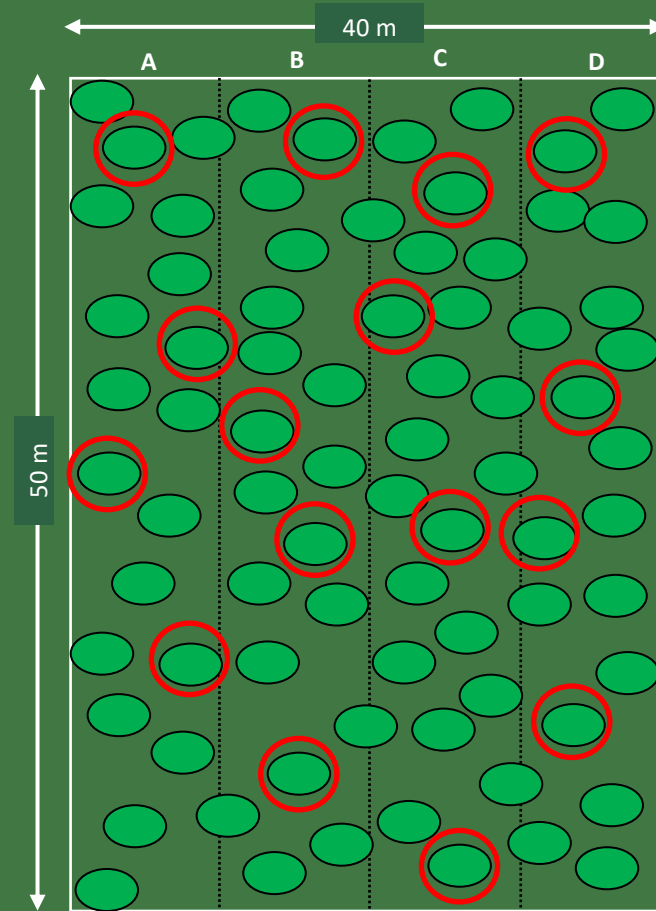
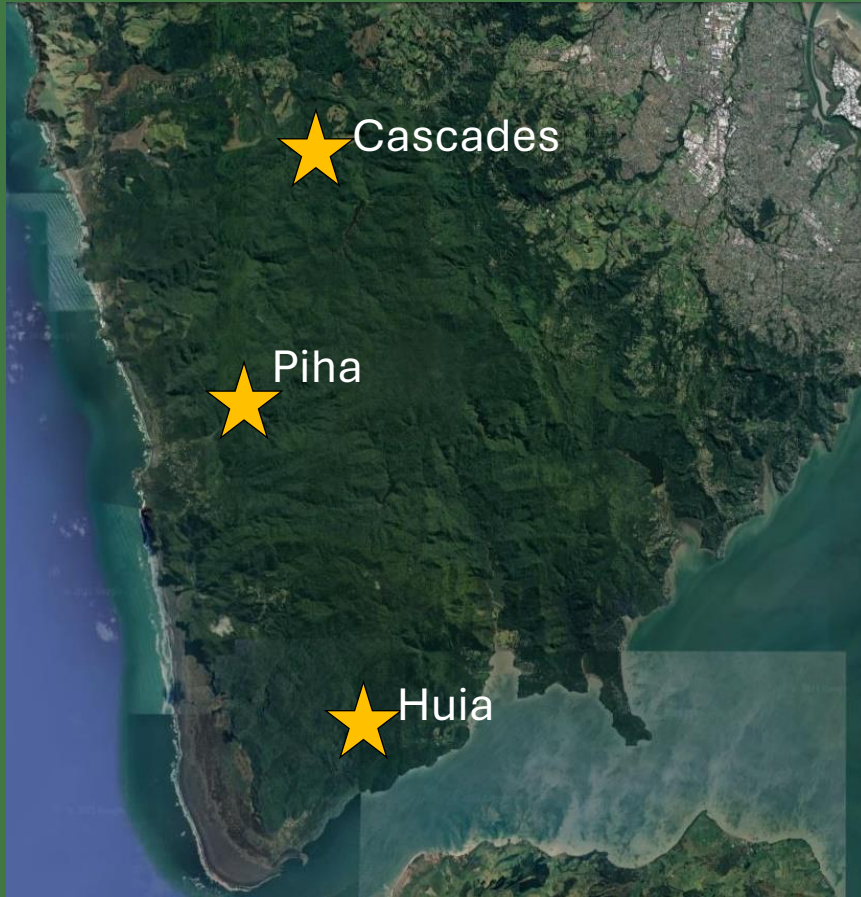
Saving Our Iconic Trees

from Kauri Dieback & Myrtle Rust

- Kauri soil microbial community



Sites and plots

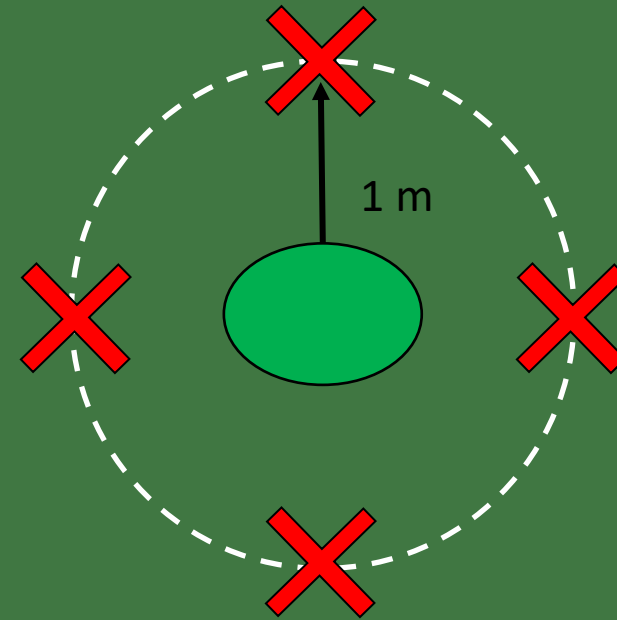




Canopy health classifications

Tree health status	Canopy health score	Trees sampled
Healthy	1 – 2	21
Defoliated	2.5 – 4.5	70
Dead	5	5

Soil sample collection



- 96 kauri trees (16 trees per plot)
- 4 samples per tree
- 384 soil samples total

Amplicon sequencing (16S rRNA gene and ITS gene region)



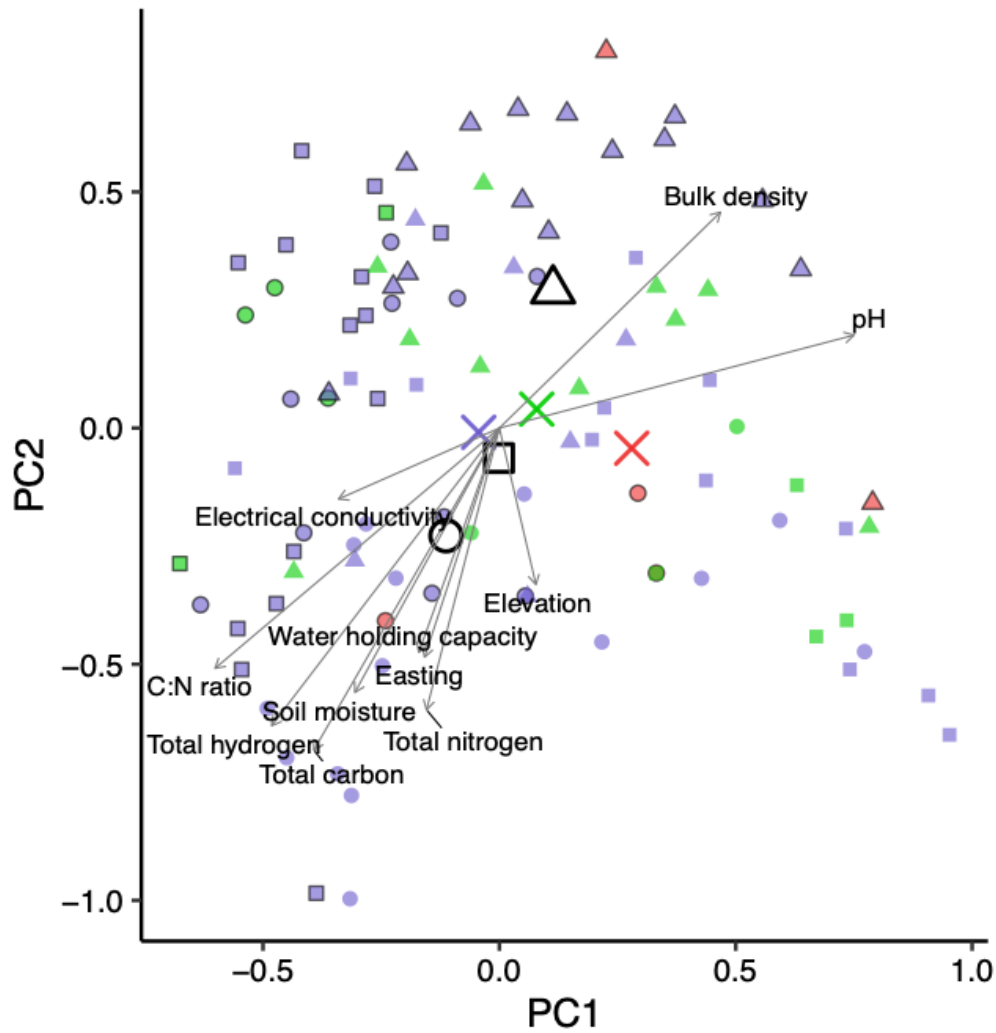
MiSeq Reagent Kit v3
(600-cycle)

Metagenome shotgun sequencing

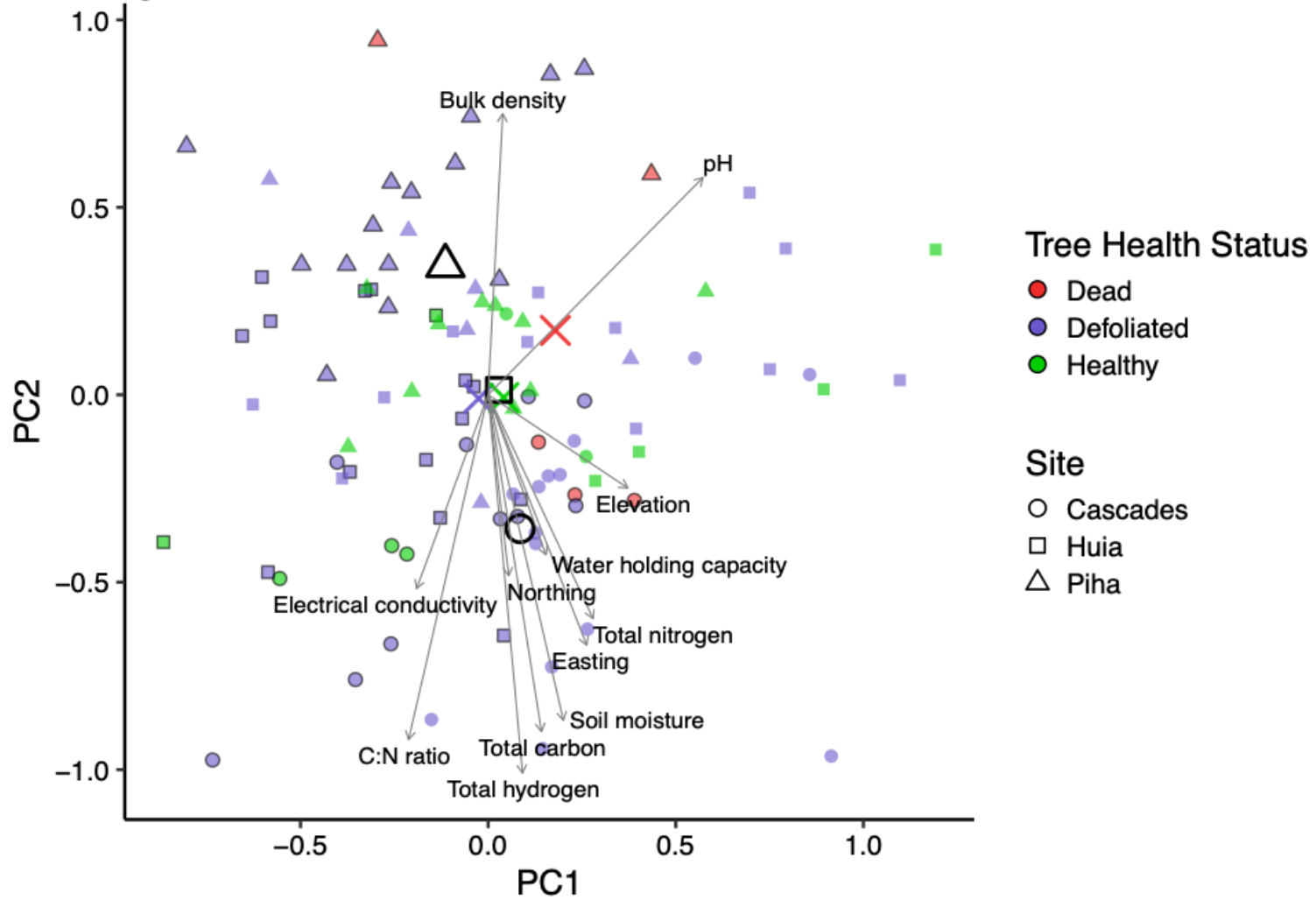


NovaSeq 6000
S4 flowcell

A. Bacteria



B. Fungi



Robust Aitchison principal component analysis of bacterial (A) and fungal (B) community composition

Environmental variables overlaid as vectors using *envfit* R function

Metagenome data processing

Plant



Animalia

Tardigrada



Chordata



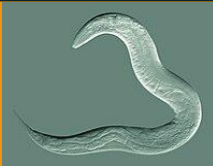
Mollusca



Arthropoda



Nematoda



Annelida



Platyhelminthes



Bacteria

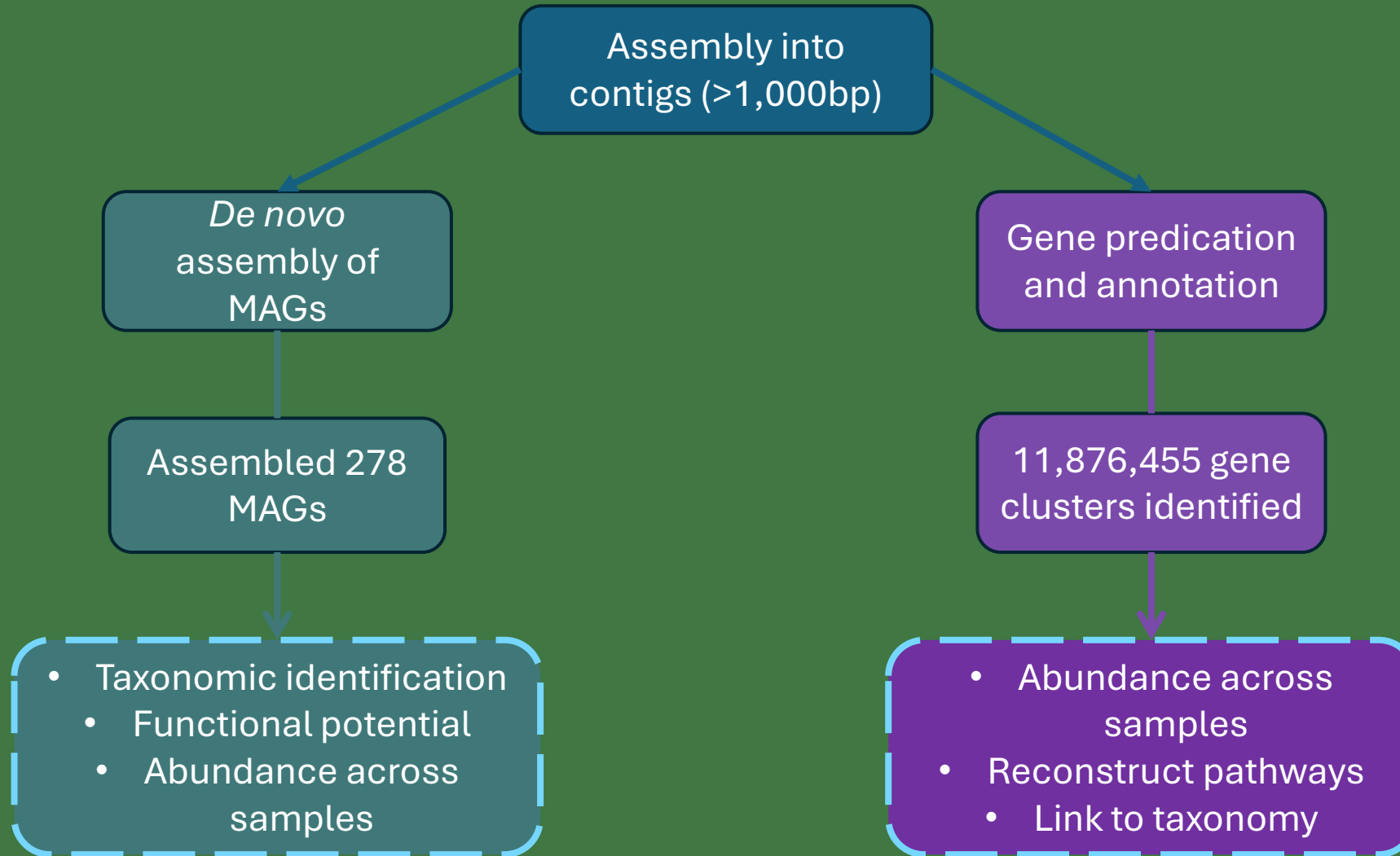
Fungi

Archaea

Oomycota

Viral

Metagenome data progress



Metagenome data progress

Assembly into contigs (>1,000bp)

De novo assembly of MAGs

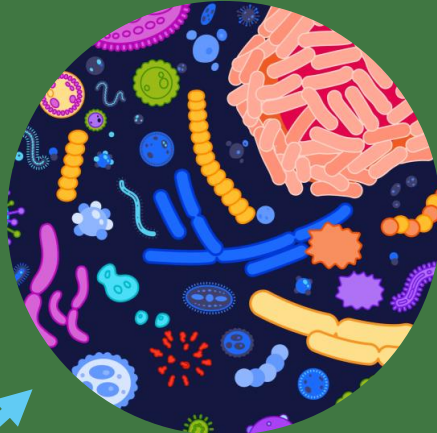
Gene prediction and annotation

Assembled 278 MAGs

11,876,455 gene clusters identified

- Taxonomic identification
- Functional potential
- Abundance across samples

- Abundance across samples
- Reconstruct pathways
- Link to taxonomy



Acknowledgements



Professor Donnabella
Lacap-Bugler



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Buckley



Professor Gavin Lear



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Brent Seale