

# Characterising soil microbial diversity for conservation and restoration using large scale DNA based methods in New Caledonian ultramafic ecosystems

Fabian CARRICONDE<sup>1</sup>, Laurent MAGGIA<sup>2</sup>, Alexia STOKES<sup>3</sup>, Monique GARDES<sup>4</sup>, Kelly DINH<sup>1</sup>, Nicolas FERNANDEZ<sup>1,5</sup>, Julien DEMENOIS<sup>1,6,7,8</sup>, Pierre-Louis STENGER<sup>1</sup>, Julie RIPOLL<sup>1,9</sup>, Jenifer READ<sup>10</sup> and Pierre MOURNET<sup>2</sup>

<sup>1</sup>*Equipe SolVeg, Institut Agronomique néo-Calédonien (IAC), New Caledonia*

<sup>2</sup>*UMR AGAP, CIRAD, New Caledonia-France*

<sup>3</sup>*UMR AMAP, INRAE, France*

<sup>4</sup>*UMR EDB, Univ. Toulouse III, France*

<sup>5</sup>*UMR*

<sup>6</sup>*AIDA, Univ Montpellier, CIRAD, Montpellier, France*

<sup>7</sup>*CIRAD, UPR AIDA, Turrialba 30501, Costa Rica*

<sup>8</sup>*CATIE, Centro Agronómico Tropical de Investigación y Enseñanza, Turrialba 30501, Costa Rica*

<sup>9</sup>*UMR LIRMM, Univ. Montpellier, France*

<sup>10</sup>*School of Biological Sciences, Monash University, Australia*

## ABSTRACT

Soil microorganisms could be one of the principal lever for conservation and ecological restoration, owing to their crucial role in ecosystems functioning and their ability to rapidly respond to environmental changes.. However, despite their major role, this hidden biodiversity has been widely neglected, particularly in southern hemisphere. New Caledonia is an archipelago located in the southwest Pacific renowned for its exceptional biological diversity, and recognized as a world priority area for conservation and restoration. With one third of its territory covered by soils originated from ultramafic rocks, which contain 20-30% of the global nickel ore reserve, mining has occurred since more than a century and has drastically increased in the past decades. Mining has led to a massive land degradation throughout the entire main island. In this context, we have conducted complementary studies on soil fungal and bacterial communities within diverse ultramafic ecosystems. Their aims were to characterize (i) the taxonomical diversity within these organisms, (ii) the underlying mechanisms that may impact them, as well as (iii) their probable functional roles, and (iv) their potential to be used as monitoring and evaluation tools for restoration. Our investigations relied on different molecular approaches, especially the emergent and revolutionary molecular methods that are next-generation sequencing technologies (NGS). Our results revealed the incredible soil microbial diversity, notably of the symbiotic group of ectomycorrhizal fungi, which may harbour an endemism rate of 87-95%. We highlighted a plant and site effects on both fungal and bacterial communities. Such site effect suggests that each location, or ultramafic massif, displays its own soil microbial community, and could thus represent distinct conservation units. We also showed that microbial composition influence ultramafic soils' susceptibility to erosion. Lately, our findings pointed out the great promise that represent the combination of soil microbial communities and high-throughput amplicon sequencing of environmental DNA (eDNA) to monitor ecosystems recovery. Soil eDNA metabarcoding could then contribute to the identification of suitable symbionts for plant inoculation. Overall, our findings underpin the great interest of considering soil microorganisms and the emergent new sequencing technologies for conservation and restoration.

## KEYWORDS :

Soil microbial communities, high-throughput sequencing, eDNA metabarcoding, biodiversity, monitoring, New Caledonia.

## REFERENCES

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