
Microbial diversity associated with endemic and alien plant species in contrasted fellfield environments in the Sub-Antarctic Kerguelen Islands

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Résumé

Plants evolve in environments rich in micro-organisms colonizing all of their organs, including the rhizosphere, roots, leaves, or seeds. These micro-organisms are transmitted both vertically from generation to generation and recruited horizontally from the pool of micro-organisms in the local environment (*e.g.* air, soil, insects...) and contribute to functions that are crucial for the fitness and adaptation of the plant: hydromineral nutrition, resistance to pathogens, to abiotic stress, etc. Therefore, a plant can be considered as a 'holobiont' made up of the plant and of the micro-organisms that interact with it and modulate its ability to respond to biotic and abiotic stresses. The sub-Antarctic Kerguelen Islands are an ideal open-air laboratory to study these plant-microbiome interactions because they host a very low diversity of native flowering plant species due to their geographical isolation. In these islands, fellfields, rocky and windy areas generally corresponding to former glacial moraines, are one of the ecosystems least affected by anthropic activities and biological invasions, making them an ideal setting in which to investigate patterns of biodiversity in pristine ecosystems. Because some of the endemic flora is probably of pre-glacial origin, the holobiont is the result of thousands of years of evolution in a relatively buffered climate and in complete isolation because of the insular geographical context. Because climate is rapidly changing in the South Indian Ocean islands, with a significant drying trend and increase in mean temperatures, the holobiont probably is and will be affected. To better understand how the holobiont will respond to climate change, it is important to first assess the structure and composition of a baseline holobiont microbial community. We hypothesize that, just like plants, the distinct geographical context of the Kerguelen archipelago has led to low α-diversity in phytomicrobiomes, meaning that plant species (both endemic and introduced) have less micro-organism species to interact with. We also expect climatic and abiotic variabilities along altitudinal gradients to be responsible for a specific pattern in microbial β-diversity, possibly yielding lower diversity at higher altitudes. Finally, coevolution could have led Kerguelen invasives' phytomicrobiome to differ from their native habitat. We investigated shifts in microbial communities in soil and roots of the endemics, *Poa kerguelensis* and *Pringlea antiscorbutica*

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*Intervenant

and the alien *Poa annua* using 16S and ITS DNA metabarcoding with NovaSeq sequencing, across altitudinal transects at three sites in Kerguelen Islands. Additionally, we explored the specificity of these microbiomes using the Earth Microbiome Project database.

Mots-Clés: holobiont, phytomicrobiome, bacteria, fungi, soil, roots, subantarctic, Kerguelen