Ce projet est soutenu par le Laboratoire d'Excellence OSUG@2020 (ANR10 LABX56) financé par le programme d'Investissements d'Avenir lancé par l'Etat et mis en oeuvre par l'ANR.

Titre du projet : ice-communities. Community dynamics in response to glacial retreat

Volet : ***Recherche***

Porteur du projet : Gentile Francesco Ficetola

Laboratoires impliqués : ***LECA, LGGE***

Bilan du projet pour la période

Bilan d'activité

Glaciers show a pattern of retreat at the global scale. Increasing areas are exposed and colonized by multiple organisms, but lack of global studies hampers a complete understanding of the future of recently deglaciated terrains. The aim of the Ice-communities project was a more comprehensive reconstruction of the dynamics of communities and of species assemblages after glacial retreat, through environmental DNA (eDNA) metabarcoding. To achieve this task, we investigated chronosequences ranging from recently deglaciated terrains to late successional stages of soil pedogenesis (areas deglaciated >300 years ago). First, we performed an analysis of the literature and of satellite images to identify the appropriate glaciers. In 2015, we performed a 2-weeks field mission, during which we sampled four chronosequences in two distinct areas of the tropical Andes. In Ecuador, we investigated the forelands of the Antisana and of the Carahuirazo glaciers. In Bolivia, we sampled the forelands of the Charquini and of the Zongo glaciers (Fig. 1).

For each glacier foreland, we considered terrains deglaciated between ~350 and 8 years before sampling. For each glacier and each deglaciation age, we collected 5 replicated soil samples (total: 125 soil samples collected). Samples were immediately dried using silica-gel and brought back to France. eDNA was extracted at LECA, following standard protocols (see Ficetola et al. 2015 Mol Ecol Resources). For each sample, eDNA was amplified using six primers (following Taberlet et al. 2018): Bact01 (amplifying bacteria); Euka02 (eukaryotes); Sper01 (vascular plants); Olig01 (earthworms); Inse01 (insects); Coll01 (springtails). For each sample and each primer pair, we performed four PCR reactions. Including extraction controls and blanks, overall we performed 4608 PCR reactions. Amplified DNA was sequenced using next generation sequencing (Illumina Hiseq / Miseq) and the sequencing results have been analysed with bioinformatics tools (ObiTools; Boyer et al. 2016 Mol Ecol Resources). DNA sequences have been compared to reference databases (GenBank), in order to reconstruct communities. Furthermore, we analysed soil features (pH, loss on ignition (LOI), XRF and color), to understand relationships between soil evolution and biotic colonization.

Metabarcoding analyses showed a coherent pattern of increase of biodiversity through colonization. For each sample, we detected up to 70 molecular taxonomic units (OTUs). Within eukaryotes, the highest diversity was detected for protists and fungi (Figs 2-4). For animals and plants, biodiversity clearly increased in terrains with higher age of de-glaciation. For instance, for animals (Metazoa) in recently deglaciated terrains we generally detected less than 5 OTUs per sample, while in late successional stages diversity was up to five times higher. The pattern of biodiversity was clearly different with protists, as the diversity of protists did not increase with age of deglaciation (Figs 2-4).

Our analyses also showed a functional shift of communities (Fig. 5). For instance, in the Zongo foreland, 8 years after deglaciation, the communities of animals only included bacterivoros and decompositors. At late successional stages, we observed an increase of both functional and taxonomic biodiversity, as we detected more functional groups (bacterivorous, decompositors, grazers, parasites, predators).

Overall, the results of this project open new avenues for the study of the impact of glacial retreat at the global scale. This project provided the baseline information for a project (''Reconstructing community dynamics and ecosystem functioning after glacial retreat''; ERC action 772284) that is going to be funded by the European Research Council (expected starting date: spring 2018).

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Illustrations - avec légende et crédit *(à envoyer également séparément)*

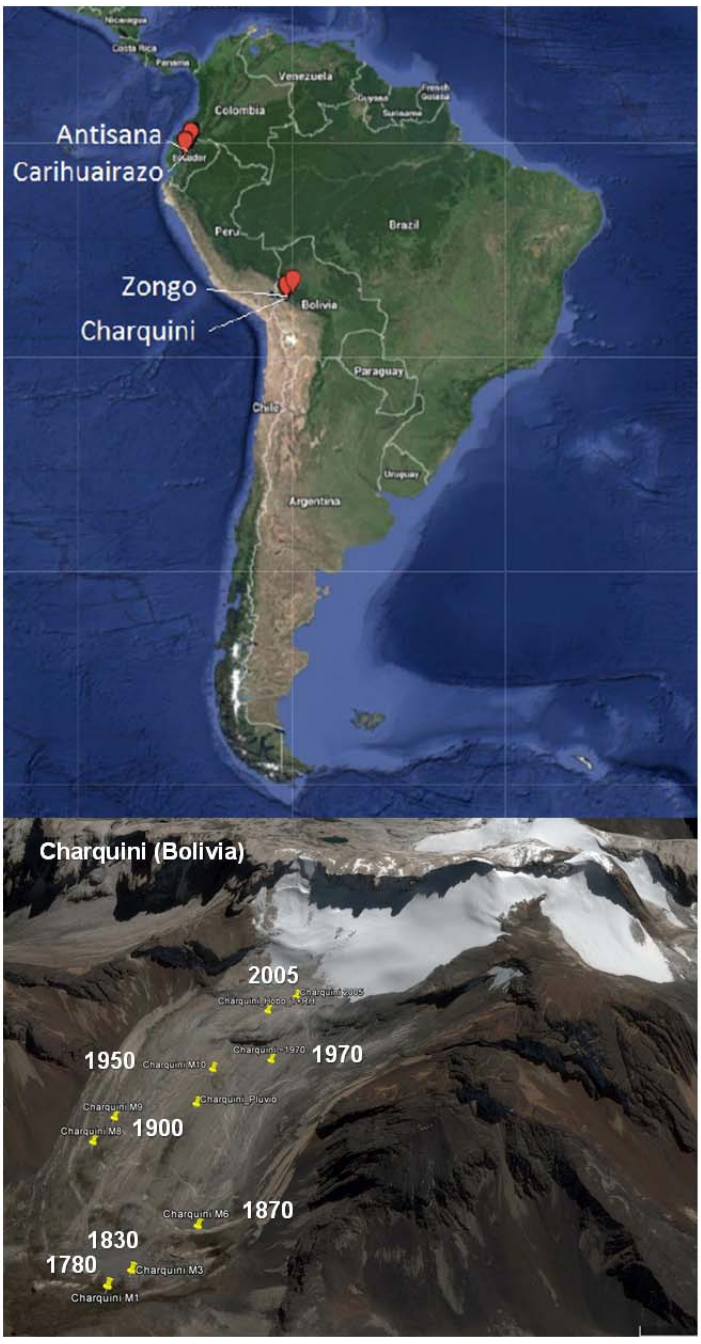

Figure 1. The four sampled glaciers, and the location of samples collected for the Charquini glacier (Bolivia) Source: Google Earth (TM)

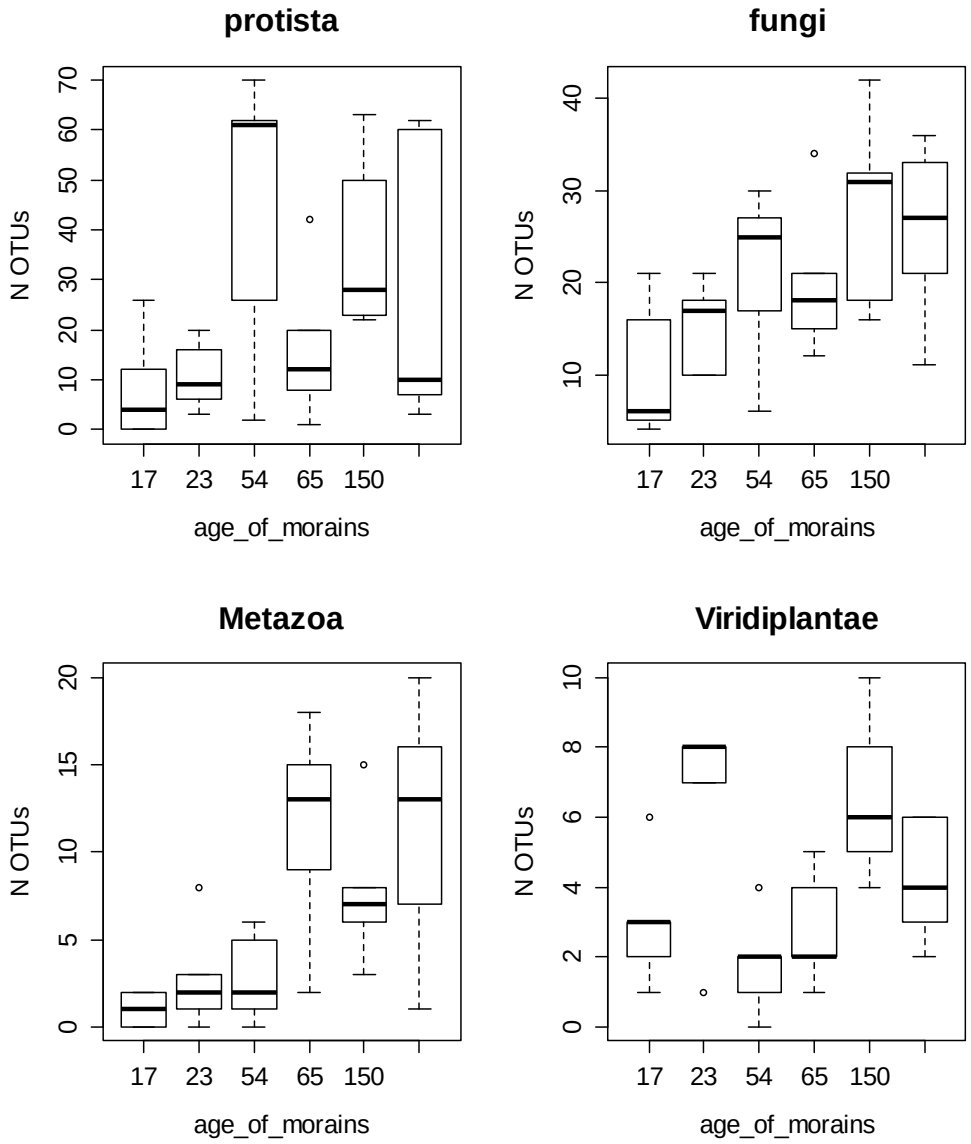

Figure 2. Relationship between age of de-glaciation and biodiversity (number of taxonomic units, N OTUs) in four taxonomic groups for the Antisana Glacier (Ecuador). Image by G.F.F.

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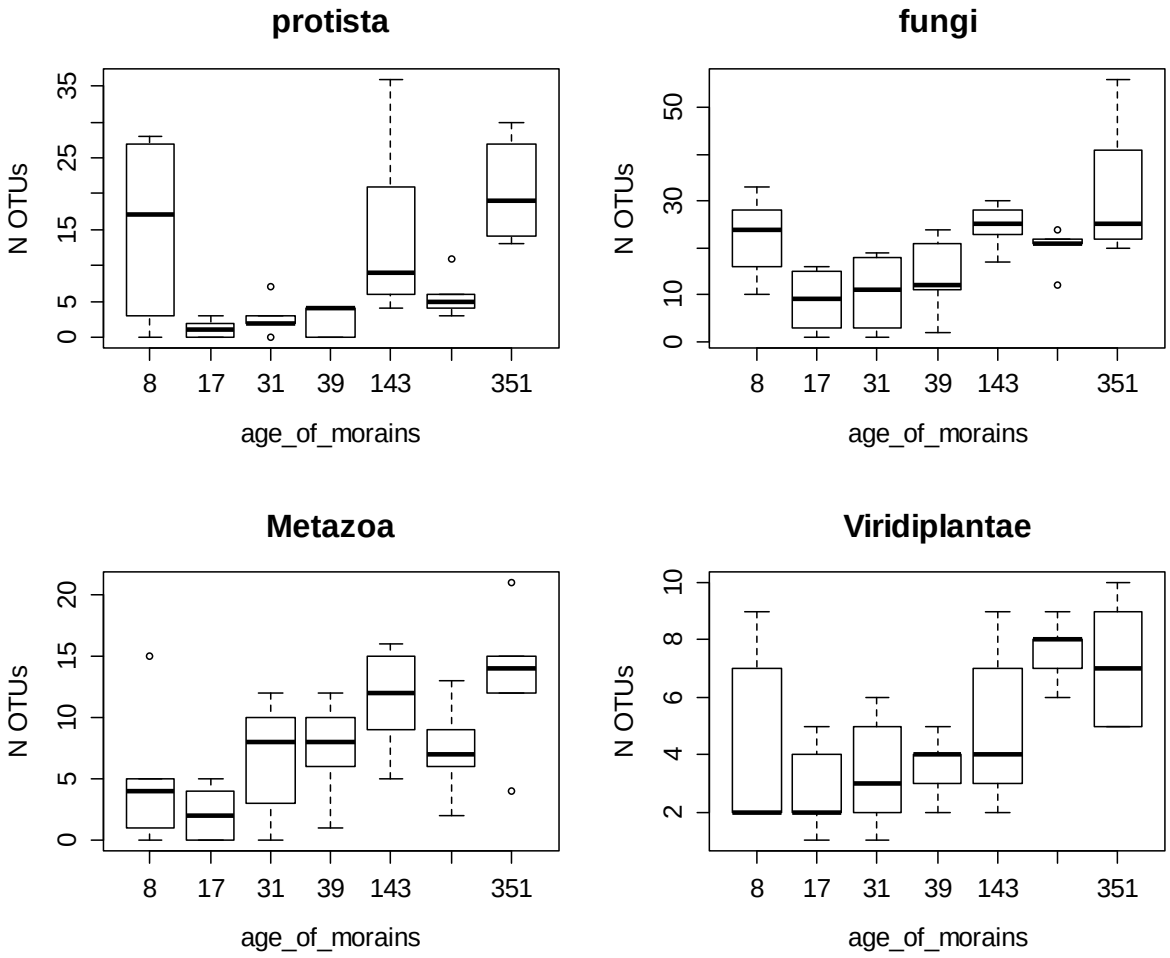

Figure 3. Relationship between age of de-glaciation and biodiversity (number of taxonomic units, N OTUs) in four taxonomic groups for the Zongo Glacier (Bolivia). Image by G.F.F.

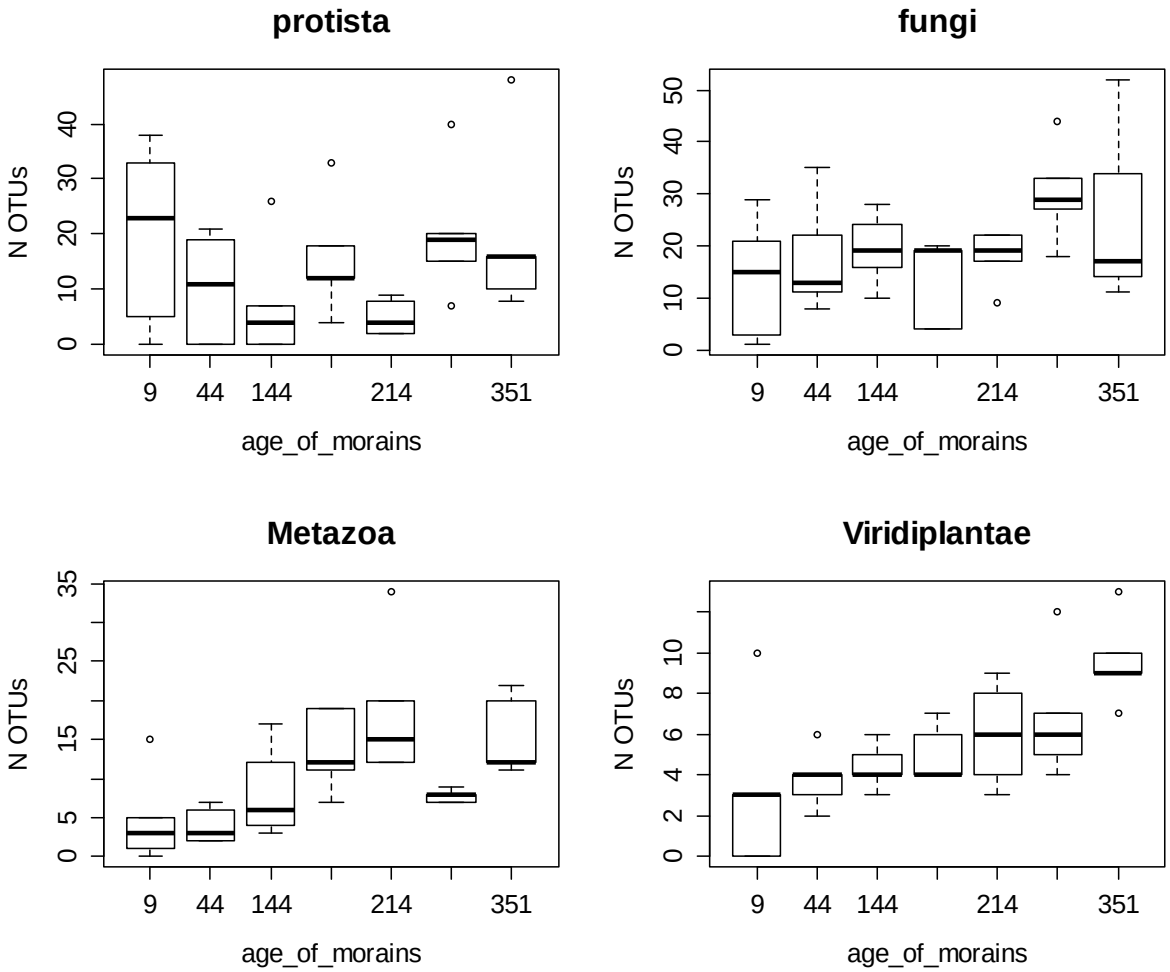

Figure 4. Relationship between age of de-glaciation and biodiversity (number of taxonomic units, N OTUs) in four taxonomic groups for the Charquini Glacier (Bolivia). Image by G.F.F.

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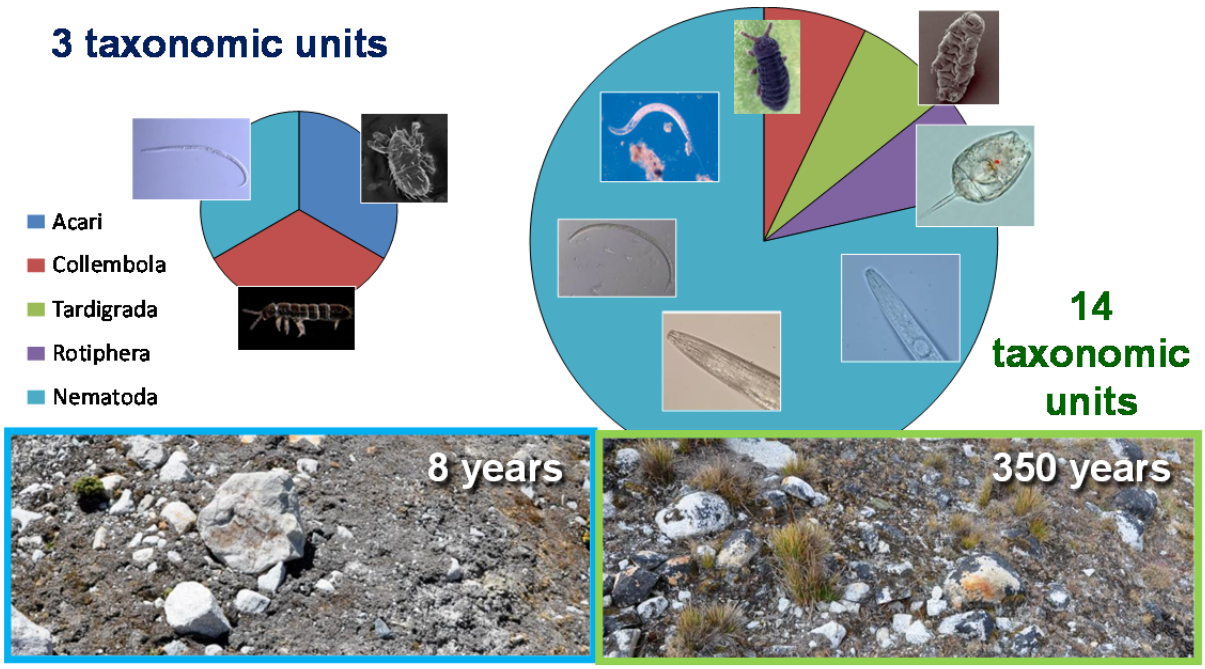

Figure 5. Biodiversity in terrains with different age of deglaciation. The example reports the taxa found for the Zongo Glacier (Bolivia). Image by G.F.F.

Production scientifique

The next steps of the project are going to be funded by the European Research Council (ERC action 772284), therefore the publication of these results we will be integrated with the global results of the ERC. The preliminary results have been presented at the following congresses:

Ficetola, G.F., 2015. Environmental dna and metabarcoding: new genetic tools for biodiversity studies, In International workshop "The next generation of biodiversity research: theory, traits and methods", Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany.

Ficetola, G.F. 2018. Reconstructing community dynamics and ecosystem functioning after glacial retreat. National Congress of Parasitology, Milan, Italy.

Furthermore, the data collected with the project have been a basis of the following publication:

Ficetola, G.F., Taberlet, P., Coissac, E., 2016. How to limit false positives in environmental DNA and metabarcoding? Molecular Ecology Resources 16, 604-607.

Bilan financier succinct

Activity	Expenses
Field mission in Ecuador and Bolivia (2 people)	3400 €
DNA extraction and amplification	13110 €
Sequencing	4500 €
TOTAL	21010 €

The Ice-Communities project received 8,000 €. The remaining part of the budget has been funded by other financements by the PI and by project collaborators (AquaDNA).

Annexes si besoin ou lien sur des sites existants et pérennes jusqu'à la fin du Labex (2020)