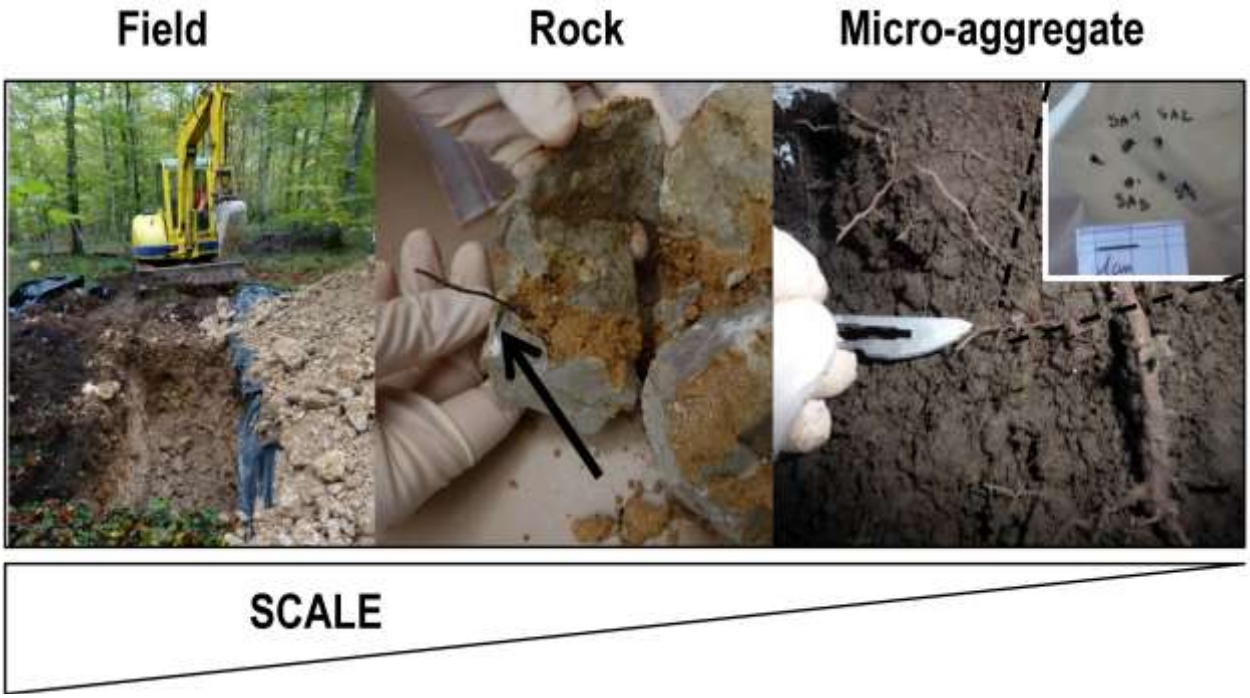
INABACT



Managing different scales

Impact of Nutrient Availability on the diversity, function and functioning of the forest soil BACTerial communities: insights from the soil succession of the forest experimental site of Montiers-sur-Saulx

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Abstract

Understand the functioning of nutrient cycling, how these cycles are maintained in forest soils, how the trees access to the essential nutritive elements required for their growth, where come from these nutrients and how microbial communities are involved in these different processes are all fundamental questions. In the frame of the INBACAT project, we were interested in the relationships between nutrient availability and the bacterial communities in different habitats and at different scales, with a central interest on the mineral weathering ability of bacteria. Whether the implication of soil microorganisms in the release of the nutrients entrapped into the soil minerals is established, the diversity and composition of the communities involved in this process and the factors driving their structure are poorly or not known. In this context, the INABACT project was focused on the experimental site of Montiers, which is characterized by a same land cover dominated by beech (*Fagus sylvatica*) and a toposequence of 3 soil types, and on the experimental site of Breuil-Chenue. In both sites, we combined environmental microbiology, genomics and soil sciences.

The third year of the INABACT project was rich in term of results generated, valorisation of some of them as publication and the writing of research proposals. In term of new results published or recently obtained, we can point out:

- *The analysis of the bacterial communities associated to the beech root in the critical zone,* which revealed a significant

enrichment of effective mineral weathering bacteria at the root/rock interface compared to the other interfaces considered in the Cambisol Calcaric soil. Together our results suggest that the bacterial communities are not structured in the same way in the different interfaces established by beech roots, in the topsoil or in depth, and that nutrient availability play a key role (Nicolitch et al., 2017). These results are original and complementary of the previous ones and suggest that trees may use the nutrients entrapped in the bedrock interface through their depth roots and their microbial associates.

- *The highlight of the mineralosphere effect,* which was performed through the analysis of the distribution of the bacterial communities colonising minerals (apatite, calcite and obsidian). This work evidenced the strong effect of the mineral chemistry and of the soil conditions on the functional and taxonomic structures of the bacterial communities. After only 2.5 year incubation time, the minerals incubated under soil conditions are enriched in specific taxa, demonstrating that minerals represent real microbial habitats et reactive interfaces that need to be considered.

- *The fast effect of a nutritive cation amendment on the bacterial communities*, which was demonstrated using a microcosm approach amended or not with K and Mg (limiting nutrients in the soil considered). Whether the metagenomic approach did not revealed a significant variation of the taxonomic structure, the culture-dependent approach revealed a significant decrease of the effectiveness and frequency of mineral weathering bacteria in the amended treatments compared to the control. These new results highlight that K or Mg have a clear effect on the functioning of the bacterial communities (Nicolitch et al., in prep).

- *The complex and dynamic evolution of Streptomyces bacterial strains isolated from a same micro-aggregate* and their potential role on the structure of the total bacterial communities was demonstrated using a combination of interaction biotests evidencing the production of secondary metabolites and multilocus analyses (MLST). This work demonstrated that the production of these metabolites could differ between *Streptomyces* strains highly-related or clonal as evidenced by MLST analysis, suggesting that evolution was quick enough to generate new variants with different inhibitory capacities among a *Streptomyces* population inhabiting the same microhabitat (Tidjani et al. 2019). Based on the bipartite interaction assays performed (sociomicrobiology), our results suggest that these variable metabolites could act as common goods and be beneficial to the whole population that shared the same micro-habitat. All these results are the subject of a publication currently under writing and enabled to initiate a new Labex project (SexSo) aiming to decipher the bases and the mechanisms underlying this variability of metabolite production.

The results obtained in the frame of the INABACT project improve our understanding of the complex interactions occurring between trees, microorganisms and the edaphic conditions. The approaches performed at different scales provide a new view of the different drivers determining the structure of the bacterial communities, the biotic ones (i.e., root exudates, secondary metabolites) and the abiotic ones (nutrient availability, pH, mineral type). Parts of the results are still under analysis and should be valorised as publications. To conclude, the INABACT project has clearly highlighted the key role of nutritive cations such as K or Mg on the biological functioning of the soil. Several research proposals directly related to the results generated have been submitted (EC2CO programm, INRA, Labex ARBRE) to develop more mechanistic approaches using model bacterial strains and/or synthetic model minerals.

Publications

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-Colloque 'Expérimentation sur le site de Montiers' (Champenoux, France) 20 mars 2015. Relation entre le type de sol et la structure taxonomique et fonctionnelle des communautés bactériennes, S. **Uroz** et al. (Oral)
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