

Title of the internship : Bioinformatic study of *Bathyarchaeia* metabolisms in continental wetlands

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Summary (up to 300 words) :

Microorganisms play a crucial role in the production of greenhouse gas (GHG) in continental ecosystems, notably carbon dioxide (CO₂) and methane (CH₄). Yet, in soils, the vast majority of microbial communities encompass recently discovered taxa with unidentified metabolisms. Continental wetlands are waterlogged ecosystems with anoxic conditions in their (sub-)soils. On the one hand, these conditions limit microbial respiration of organic matter and wetlands are efficient CO₂ sinks. On the other hand, they favor specific anaerobic microbial respiration leading to high CH₄ emissions. To better predict the future feedbacks of continental wetlands to a changing climate, it is essential to elucidate how their microbial communities control their carbon cycle and their GHG emissions.

Metagenomic analysis of soils collected in a wetland of the Ploemeur-Guidel critical zone observatory revealed high abundances of a recently-discovered archaeal taxon, *Bathyarchaeia*, in the sub-soils of the wetland. No representative isolate from this highly diversified taxon is available and our knowledge of its metabolism is mostly based on metagenomic-assembled-genomes (MAGs) obtained from marine ecosystems. These studies evidenced a high versatility in the carbon metabolism of *Bathyarchaeia*, including fermentation of high molecular weight compounds, acetogenesis, autotrophy and methylotrophy. This taxon is now recognized as a central player in the anoxic carbon cycle in marine sediments (Zhou et al., 2018). In continental settings, *Bathyarchaeia* are regularly observed in anoxic settings such as wetlands but their metabolisms and role in the carbon cycle has been much less studied (Hou et al., 2023).

The objective of this internship will be to reconstruct *in silico* the carbon and energy metabolisms of *Bathyarchaeia* in the Ploemeur-Guidel wetland. The work will be based on high-quality MAGs already reconstructed from a previous metagenomic analysis and will help to elucidate the ecological role of *Bathyarchaeia* in continental ecosystems.

Other informations :

Insertion within an ongoing research project (yes/no) : yes

Publications on the field of research (up to 3) :

Hou, J., Wang, Y., Zhu, P., Yang, N., Liang, L., Yu, T., Niu, M., Konhauser, K., Woodcroft, B.J., Wang, F., 2023. Taxonomic and carbon metabolic diversification of *Bathyarchaeia* during its coevolution history with early Earth surface environment. *Sci. Adv.* 9, eadf5069.
<https://doi.org/10.1126/sciadv.adf5069>

Zhou, Z., Pan, J., Wang, F., Gu, J.-D., Li, M., 2018. *Bathyarchaeota*: globally distributed metabolic generalists in anoxic environments. *FEMS Microbiol Rev* 42, 639–655.
<https://doi.org/10.1093/femsre/fuy023>