Heavy metal accumulation shaped presence and potential activity of sediment bacteria

Valentine Cyriaque\(^1\), Samuel Jacquiod\(^2\), Leise Riber\(^3\), Waleed Abu Al-soud\(^2\), Stefan Milani\(^2\), David C. Gillan\(^1\), Søren J. Sørensen\(^2\), Ruddy Wattiez\(^1\).

Anthropogenic metal contamination of sediments poses serious biotoxicity and bioaccumulation issues. Besides important ecological roles such as organic matter mineralization, bacteria play a key role in metal speciation. The MetalEurop foundry released zinc, copper, cadmium and lead in the “Deûle” river (France) during a century, resulting in present-day metal concentrations in sediments up to 30-fold higher than upstream (Férin, control site in the Sensée canal). On the basis of a shotgun metaproteogenomic approach, it was found that sediments (MetalEurop & Férin) harbored phylogenetically analogous microbial communities (Gillan et al., 2015).

But what about bacterial activity?

This study compares taxonomic profiles of the complete (DNA) and the potentially active (RNA) fraction of the sediment prokaryotic communities present in MetalEurop and Férin via 16S rRNA gene amplicon sequencing (Illumina\(^\text{®}\) MiSeq\(^\text{®}\) 2x250 bp). The ecological concept of Functional Response Group was applied to highlight the tolerance and sensitivity levels in the microbial community, linked to the long-term metal pollution (Nunes et al., 2016).

Using nbGLM, we found OTUs responding significantly to metal-contamination and activity pattern

Acknowledgments: This work was supported by a FNS grant to V.C. and a FNS grant to S.J.S. and R.W. (2014-2017). This work was also partially financed by the FNRS under grant E. N. 2877824, a Pole d’Attraction Interuniversitaire, provided by the Brussels-Capital Region, and the P7/25 and the University of Copenhagen.

REFERENCES:

This work was supported by a FNS grant to V.C. and a FNS grant to S.J.S. and R.W. (2014-2017).

Similar communities dominated by Gammaproteobacteria and Firmicutes.

Richness and Firmicutes activity increased in the metal-stressed community.

The arrival of new bacteria (from upstream or the river banks) combined to the in situ metal selection seems to drive the structure and activity of the community.

Anthropogenic metal contamination removes dominant bacteria permitting specialist/slow growing bacteria to thrive better as Verrucomicrobia, Alphaproteobacteria, Acidobacteria.

Some species can act as "public good" thanks to metal precipitation contributing to the overall community richness.

In MetalEurop, the increasing richness but similar genetic diversity imply that other mechanisms could explain the previously reported metaproteogenomic functional differences as Horizontal Gene Transfer.