Heavy metal accumulation shaped presence and potential activity of sediment bacteria

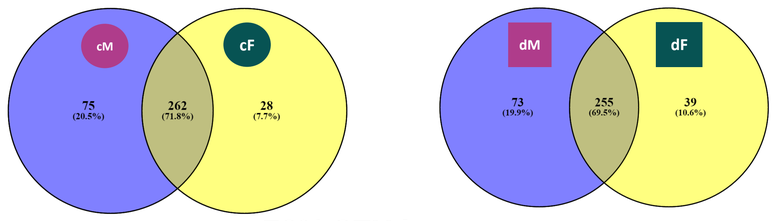
Valentine Cyriaque[1], Samuel Jacquiod[2], Leise Riber[3], Waleed Abu Al-soud[2], Stefan Milani[2],

David C. Gillan[1], Søren J. Sørensen[2], Ruddy Wattiez[1].

Heavy 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 in the **Férin** site (a control site in the Sensée canal). On the basis of a shotgun metaproteogenomic approach, it was found that sediments of the two sites (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® MiSeq® 2x250 bp). The ecological concept of **Functional Response Group** was applied to decipher the tolerance and sensitivity patterns in the microbial community, linked to the long-term pollution (Nunes *et al.*, 2016).



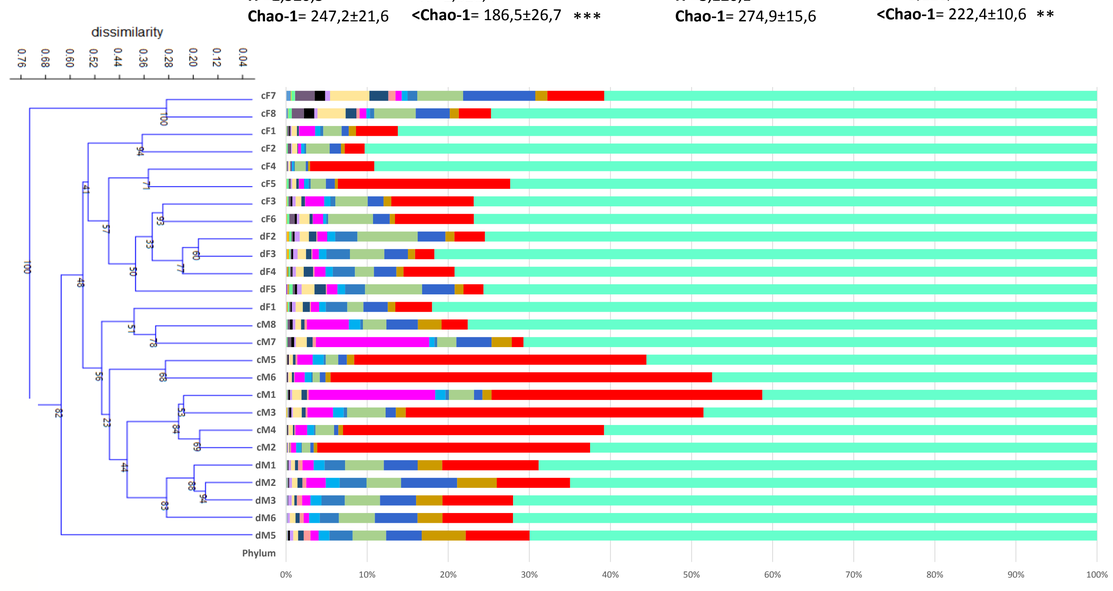
≈70% OTU in common

R= 178±23 | **H'**=2,5±0,3 | **Chao-1**= 247,2±21,6

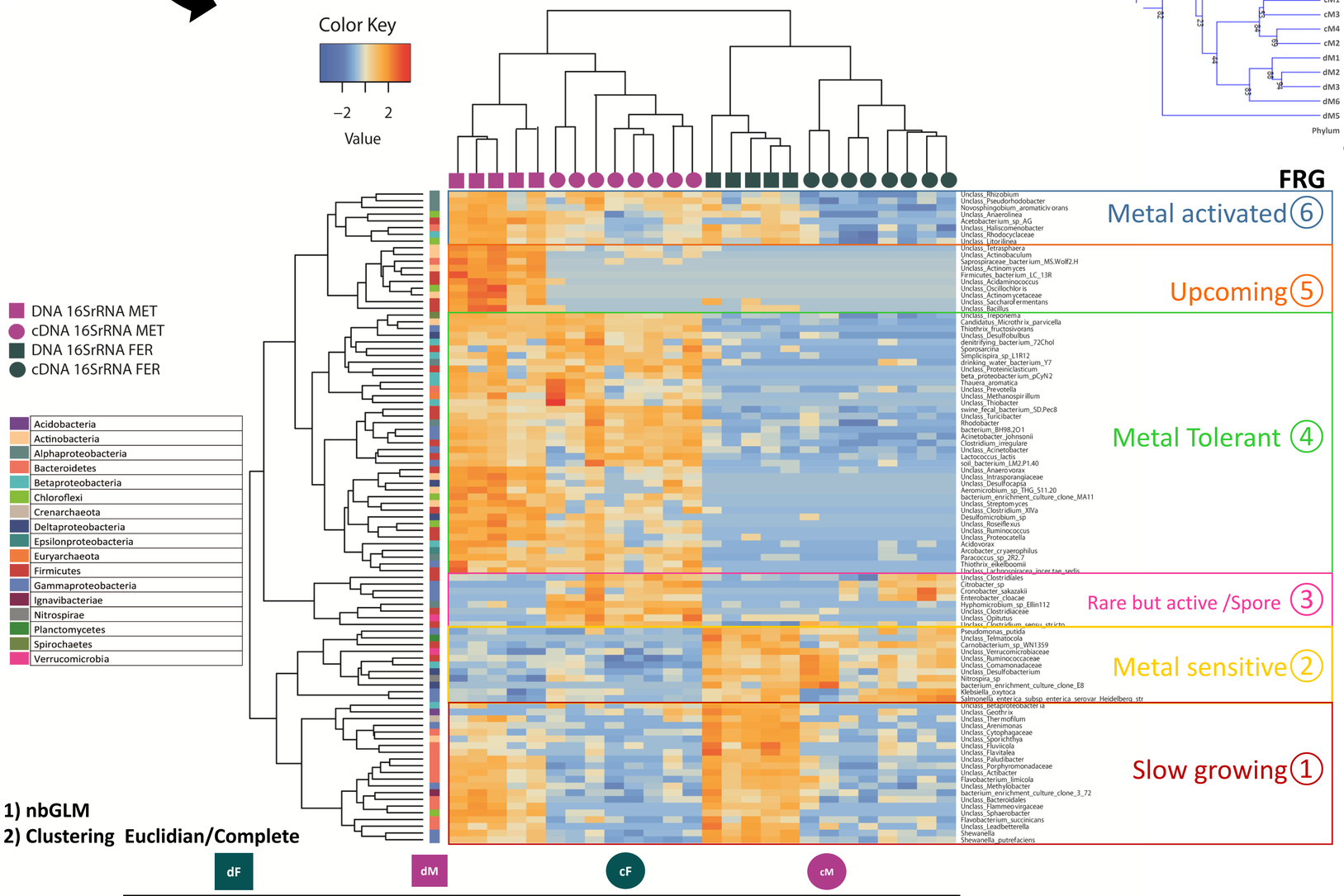
>R=136±23 ** | **H'**=2,5±0,4 | **<Chao-1**= 186,5±26,7 ***

R=235±10 | **H'**=3,2±0,1 | **Chao-1**= 274,9±15,6

>R=184±7 *** | **H'**=3,1±0,2 | **<Chao-1**= 222,4±10,6 **

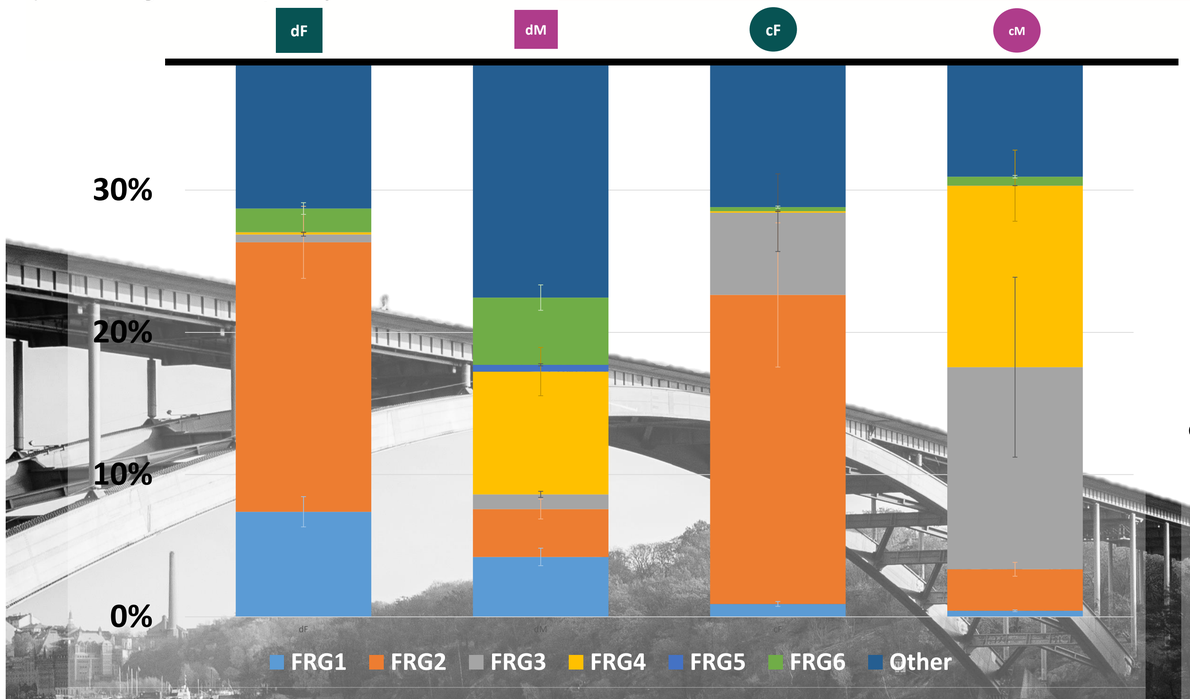


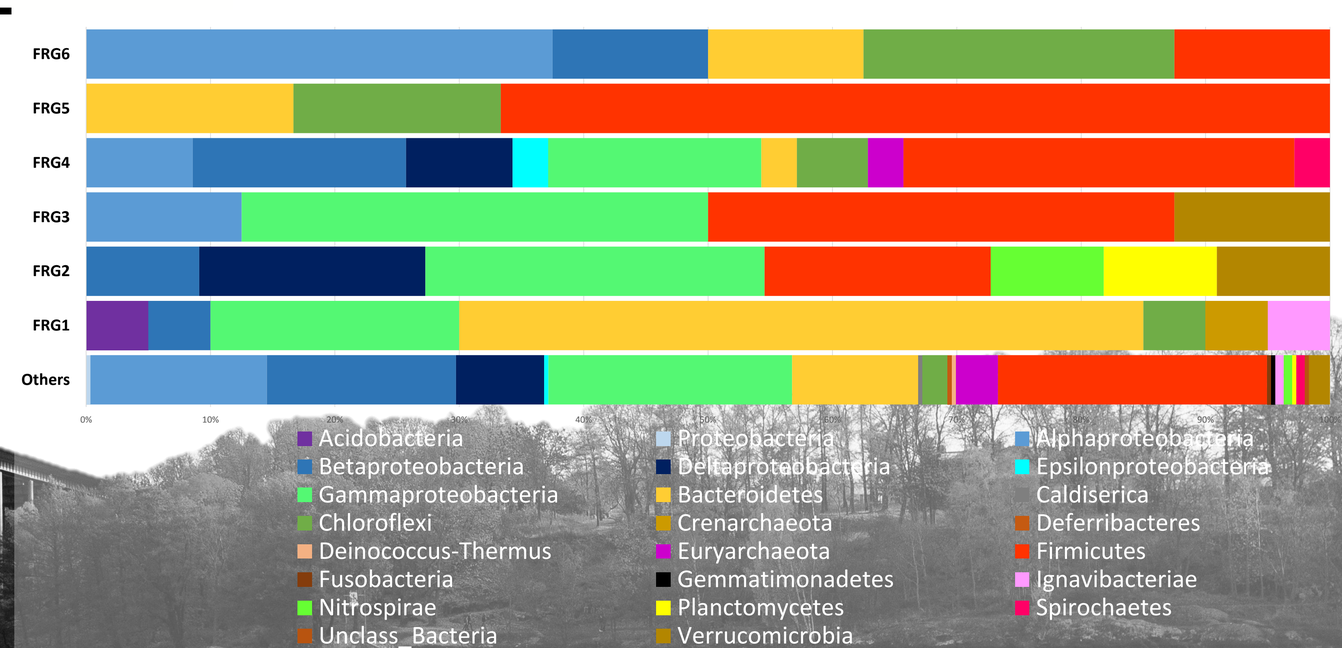
Using nbGLM, 97 OTU were found to respond significantly to metal-contamination and activity pattern



1) nbGLM
2) Clustering Euclidian/Complete

- **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 shaping and activity of the community.
- Anthropogenic metal contamination uncovers rare and very active bacteria (Verrucomicrobia), as well as sporulating/dormant ones (Clostridiaceae)③
- Slow-growing and dormant bacteria constitute a slow genetics **reservoir** ①
- **Metal tolerant** bacteria characterize the contaminated sediments ④. They include diverse Proteobacteria and Firmicutes.





Acknowledgments - This work was supported by a FNRS grant to V.C. and a FNRS grant to D.C.G. and R.W. (PDR Nr 2.4577.12). This work was also partially financed by the FNRS under grant'grand equipement' N°2877824, a Pole d'Attraction Interuniversitaire (PAI) n° P7/25 and the University of Copenhagen.

REFERENCES: D.C. Gillan et *al.*, 2015, *Environmental microbiology* ,17(6); I. Nunes, et *al.*, 2016, *FEMS Microbiology Ecology* 92(11).

Corresponding authors: Valentine Cyriaque[1], Samuel Jacquiod[2]

[1] Proteomics and Microbiology Lab, Research Institute for Biosciences, UMONS, Mons, Belgium

[2]Microbiology section, Department of Biology, University of Copenhagen, Copenhagen, Denmark

[3]Functional genomics section, Department of Biology, University of Copenhagen, Copenhagen, Denmark