Bioremediation of isoproturon and sulfamethazine: linking microbial community composition and structure to degradation capacity

Sylvia Thieffry [1], Julie Aubert [2], Marion Devers [1], Fabrice Martin-Laurent [1], Stéphane Pesce [3], Sana Romdhane [1], Nadine Rouard [1], Mathieu Siol [1], Aymé Spor [1]

[1] *Agroecologie, INRAE, Institut Agro, Université de Bourgogne, Université de Franche-Comté, Dijon, France*
[2] *Université Paris-Saclay, AgroParisTech, INRAE, UMR MIA Paris-Saclay, 92120 Palaiseau, France*
[3] *INRAE, UMR RiverLy, 69625, Villeurbanne, France*

The large use of xenobiotics in current agricultural practices calls for methodological developments aiming at lowering their persistence in soil and aquatic environments. In a bioremediation perspective we need a better understanding of how degrading microorganisms must overcome environmental filtering when introduced into a new environment, and how biotic interactions with the autochthonous microbial communities might shape their colonization trajectories. Here we focused our research on two xenobiotics used in agricultural practices : a recently banned herbicide still frequently retrieved in soil, Isoproturon (IPU), and a veterinary antiobiotics detectable in rivers and sediments, Sulfamethazine (SMZ). We first evaluated the importance of environmental filtering and, promisingly, the extracted degrading microbial communities successfully colonized the environments in which they were introduced and their degrading potential was maintained. We then coupled biocidal treatments with serial dilutions to construct microbial community compositional variants in order to infer associations between specific bacterial OTUs and the two xenobiotic degrading capacities. Different mathematical models were then trained to predict deagradation capacities based solely on community composition. Predictive power of the models was then assessed and significant associations between OTU abundances and mineralisation potentials were detected. Next we looked at community structure and co-occurrence networks, to identify microbial groups and potential interactions - antagonist and cooperative - that play a role in the xenobiotics biodegradation. The structure of cooccurrence networks differ significantly between IPU and SMZ degrading communities, underlying compound-specific interaction patterns potentially shaped by degradation pathways. Upcoming work will evaluate the possibility of mixing degrading communities based on microbial community properties to obtain multi-degrading communities for bioremediation perspective.