

Microbial BioRemediation Database: a comprehensive database of genes involved in microbial bioremediation processes

Presenting author: Silvia Petraro

Silvia Petraro¹, Chiara Tarracchini¹, Leonardo Mancabelli^{2,3}, Gabriele Andrea Lugli^{1,2}, Francesca Turrone^{1,2}, Marco Ventura^{1,2*} and Christian Milani^{1,2*}

1 Laboratory of Probiogenomics, Department of Chemistry, Life Sciences, and Environmental Sustainability, University of Parma, Parma, Italy;

2 Microbiome Research Hub, University of Parma, Parma, Italy;

3 Department of Medicine and Surgery, University of Parma, Parma, Italy.

* These authors contributed equally.

Environmental pollution from a wide range of compounds poses a significant risk to both ecosystems and human health. Although bioremediation is considered a promising strategy for pollutant removal, its broader application remains limited by fragmented genomic resources and an incomplete understanding of microbial biodegradation pathways. To address this limitation, we developed the Microbial BioRemediation (MBR) database, a comprehensive and manually curated repository comprising more than 643,351 bacterial protein sequences associated with the degradation of 564 pollutant compounds across 25 chemical classes. Optimized to support both genomic and metagenomic applications, the MBR database enables high-resolution functional and taxonomic profiling of microbial communities as well as individual bacterial strains. Validation using publicly available genome and metagenome datasets from contaminated environments demonstrated the ability of the database to identify both conserved biodegradation functions and functions specifically associated with distinct environmental contexts. Furthermore, its application to host-associated microbiomes highlighted the potential of MBR for investigating how environmental exposures may shape microbial catabolic capacity across diverse ecological settings. Overall, the MBR database represents a strategic resource for the early identification and prioritization of microbial candidates for bioremediation. By enabling the *in silico* selection of relevant microbial taxa and enzymatic functions, it provides a rational strategy for targeted *in vitro* validation and experimental characterization. This integrative approach may facilitate the development of next-generation, tailored strategies for the remediation of complex polluted ecosystems.