

## **Deciphering the functional potential of microorganisms for P cycling: a genomics perspective on metal-phosphate biomineralization**

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Microorganisms are involved in the phosphorus (P) cycle, by their ability to actively store and release inorganic phosphate, which then becomes available for the biosphere or trapped by the biomineralization of metal phosphates. Despite the large dataset of currently available microbial genomes, inventory of diversity and evolution of the molecules responsible for these biogeochemical processes is still lacking.

In this study, we selected a set of gene families according to their potential influence on P cycling: non-specific phosphatases, phosphonate hydrolases, Poly-P phosphatases and kinases, P uptake system, transcription factors. We conducted the functional annotation of these genes in the complete microbial genomes available in the NCBI Genome database. We identified specific patterns of gene composition, genomic organization, and transcriptional regulatory sequences, in relation with the taxonomic distribution or the environmental adaptation of microbial genomes.

With constant progress in metagenomics and the possibility to access the whole genomes of numerous microorganisms, it is interesting to investigate how such information might be used to predict the biomineralization capabilities of cells. In particular, we found that bacteria whose genomes have a high number of phosphatase genes are particularly prone to remineralize organic matter, with potential implications for the formation of sedimentary phosphate minerals as well as the development of bioremediation strategies to sequester metal pollutants.

Overall, this study provides high quality reference sequence datasets of genes and regulatory elements from diverse microbial species. These data will be essential for further annotation and combined analysis of metagenomic sequences and geochemical parameters from modern phosphatogenesis environments.