

**Diversity of phosphatases in the  
biomineralizing bacterium  
*Ramlibacter tataouinensis*: an *in vitro*  
and *in silico* study**

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The enzymatic activity of microbial phosphatases can trigger the precipitation of metal-phosphate minerals, with global geochemical and environmental implications. An increasing diversity of phosphatases expressed by diverse microorganisms has been evidenced in various environments. However, it is challenging to link this diversity of enzymes, microorganisms with phosphatogenesis capabilities and potential signatures in the produced mineral phases.

Here, we study the phosphatases of a model bacterium, *Ramlibacter tataouinensis* (*Rta*), known to biomineralize Ca-phosphates in the environment and the laboratory. Based on a mineralization assay, we evidence that *Rta* hydrolyses the phosphoester bonds of a wide range of organic P molecules. Accordingly, *Rta* genome has an unexpected diversity of phosphatases: five genes belonging to two non-homologous families (PhoD and PhoX), with diverse genomic organization, regulatory elements and protein structural specificities. Heterologous expression in *E. coli* confirms that these proteins have different profiles of substrate hydrolysis.

The high diversity of phosphatases in *Rta* may favor phosphatogenesis in a range of environments broader than for other species. Moreover, our combined *in silico* and *in vitro* approaches provide a reference framework opening new perspectives for deciphering the enzymatic potential of an ecosystem to induce the precipitation of metal-phosphate minerals.