





## Exploring the role of GH3 enzymes in an Antarctic bacterium: evolutionary history and oligosaccharide degradation

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## Abstract:

Polar marine bacteria experience various stressful conditions, such as low temperatures and limited nutrient availability. Glycoside hydrolases (GHs) play a key role in the hydrolysis of glycosidic bonds in oligosaccharides and polysaccharides, which serve as carbon and energy sources for microorganisms. Here we investigated the role of GHs belonging to family 3 in Marinomonas sp. ef1 an Antarctic bacterium able to grow from 4 to 22°C. The genome of this bacterium contains three GH3s, namely M-GH3\_A, M-GH3\_B and M-GH3\_C, which have different architectures and low sequence identity.

M-GH3\_A and M-GH3\_B, show different thermal and structural properties, as well as substrate specificity. M-GH3\_C was produced as an insoluble protein in Escherichia coli cells and its refolding produced a partially folded and inactive protein. Substrate specificity assays indicate that M-GH3\_A is a promiscuous  $\beta$ -glucosidase, which is mainly active on cellobiose and cellotetraose, while M-GH3\_B is a xylanase active on xylan and arabinoxylan.

Overall, this work uncovers the biological role of GH3 enzymes in the degradation pathway of natural polysaccharides in an Antarctic bacterium. Additionally, studying these enzymes helps to decipher the cold adaptation mechanisms of cold-active enzymes.