MS10 Protein-carbohydrate interactions

MS10-02

Unveiling the substrate specificity of sulfatases, another important group of carbohydrate active enzymes

M. Dalgaard Mikkelsen [1], T. Barbeyron [2], E. Ficko-Blean [2], A. Naretto [2], R. Larocque [2], S. Genicot [2], T. Roret [3], M. Czjzek [2], A.S. Meyer [1], G. Michel [2]

[1]Protein Chemistry and Enzyme Technology Section, DTU Bioengineering, Department of Biotechnology and Biomedicine, Technical University of Denmark, 2800 Kgs Lyngby, Denmark - Kongens Lyngby (Denmark), [2]Sorbonne Université, CNRS, Integrative Biology of Marine Models, Station Biologique de Roscoff, 29680 Roscoff, France - Roscoff (France), [3]Sorbonne Université, CNRS, FR2424, Station Biologique de Roscoff, 29680 Roscoff, France - Roscoff (France)

Abstract

Sulfated glycans represent an essential part of polysaccharides present in marine environments and mammalian host. Bacterial carbohydrate sulfatases are enzymes that remove sulfate esters from sulfated glycans, and are essential for microbes to utilize sulfated glycans [1-2]. Interestingly, many genomes of marine but also of gut bacteria revealed that polysaccharide degraders contain a surprisingly high number of sulfatases [3-4], many of which have no associated function. Despite their importance, carbohydrate sulfatases are some of the most poorly characterized carbohydrate active enzymes to date. In the context of the explosion of genomic data, the functional annotation of sulfatases is thus particularly prone to flaws and misinterpretations. A recent sulfatase classification system allowing for a better prediction of clades or subfamilies [5], together with intense biochemical characterizations [2,4, 6,7] have shown that, likewise to other enzyme families of the CAZy database, sulfatase clades generally coincide with diversity in substrate specificity. Here we will briefly present the classification of sulfatases and will expose recent examples of sulfatase crystal structures, highlighting how substrate specificity is obtained by subtle sequence variations.

References

1. Tuncil, Y. E. et al. mBio 8, doi:10.1128/mBio.01068-17 (2017).
2. Cartmell, A. et al. PNAS 114, 7037-7042, doi:10.1073/pnas.1704367114 (2017).
3. Barbeyron, T., et al. Environ Microbiol. 18, 4610-4627, doi:10.1111/1462-2920.13584. (2016)
4. Luis, A. S. et al. Nature 598, 332-337, doi:10.1038/s41586-021-03967-5 (2021).
5. Barbeyron, T., et al. PLoS One. 11, e0164846. doi: 10.1371/journal.pone.0164846. (2016)
6. Hettle, A. G. et al. Structure 26, 747-758 e744, doi:10.1016/j.str.2018.03.012 (2018).
7. Mikkelsen, M.D., et al. Sci Rep. 11, 19523. doi: 10.1038/s41598-021-98588-3. (2021)

Active site of a marine fucan-sulfatase