

N-GLYCOSYLATION IN ARCHAEA – EXTREMELY SWEET

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Today, it is clear that N-glycosylation takes place across evolution. Still, N-glycosylation in Archaea remains far less well characterized than the parallel processes in Eukarya and Bacteria. Indeed, not only have few pathways of archaeal N-glycosylation been delineated, the reasons for the enormous diversity seen in archaeal N-linked glycan composition and architecture also remain unclear. At the same time, the importance of N-glycosylation in Archaea is only starting to be understood. As with numerous aspects of archaeal biology, roles currently assigned to N-glycosylation in Archaea may be unique to this domain of life or have yet to be reported elsewhere. Moreover, the relation between archaeal N-linked glycan composition and the impact this has on the different aspects of archaeal cell physiology affected by N-glycosylation remains poorly defined. Better understanding of the roles played by N-glycosylation in Archaea and how changing the makeup of N-linked glycans decorating archaeal glycoproteins impacts these roles requires a model species for which the pathway used for such protein processing is known and for which an appropriate molecular toolkit exists. With a sequenced genome, developed genetic and biochemical tools, simple growth conditions and a relatively well-defined N-glycosylation pathway, the halophile (“salt-loving”) *Halobacterium salinarum* is one such species. In my talk, I will consider N-glycosylation in *Hbt. salinarum* and how modifying the composition of an N-linked glycan decorating *Hbt. salinarum* glycoproteins impacts different roles served by this post-translational modification, an emerging aspect of glycobiology and cell biology research.