A proposal for the naming of N-glycosylation pathway components in Archaea

To the Editor,

In 1976, the long-held opinion that N-glycosylation was a trait restricted to eukaryotes was overturned when the surface-layer glycoprotein from the archaeon *Halobacterium salinarum* was shown to undergo such post-translational modification (Mescher and Strominger, 1976). Largely based on genomic studies, it is now believed that N-glycosylation is a common process in Archaea (Kaminski et al., 2013).

Analysis of the limited number of characterized archaeal N-linked glycan reveals diversity in composition unparalleled in either eukaryal or bacterial N-glycosylation (Schwarz and Aebi, 2011; Eichler, 2013). Such variety is indicative of N-glycosylation in Archaea being largely mediated by different, species-specific pathways. Current biochemical descriptions of archaeal N-glycosylation systems support this claim (Jarrell et al., 2010; Eichler, 2013; Meyer and Albers, 2013). As such, it is essential that workers in the field adhere to a common nomenclature for the genes and proteins involved in the archaeal version of this post-translational modification. Indeed, by adopting an agreed upon naming system, some of the ambiguity plaguing the field of bacterial protein glycosylation might be avoided. For instance, although PglB, PglC, PglD, PglE and PglF all contribute to N-glycosylation in *Campylobacter jejuni* and O-glycosylation in *Neisseria gonorrhoeae*, proteins bearing the same name serve very different roles in each system (Linton et al., 2005; Aas et al., 2007).

In 2006, Chaban *et al.* proposed the use of the abbreviation *agl* (for archaeal glycosylation) to identify genes involved in the archaeal version of N-glycosylation, along the guidelines for naming bacterial genes outlined in Demerec et al. (1966). Studies in *Haloferax volcanii*, *Methanococcus voltae* and *Methanococcus maripaludis* thus annotated proteins serving various N-glycosylation-related roles as AglA to AglZ (for review, see Eichler, 2013). More recently, however, additional genes encoding proteins implicated in *Sulfolobus acidocaldarius* N-glycosylation were annotated and published as *agl1-agl4* and *agl16* (Meyer *et al.*, 2011, 2013). In this case, the nomenclature adopted is similar to that used for naming yeast genes, where a three letter abbreviation is followed by a number (Cherry et al., 2012).

In the absence of an accepted set of rules for naming archaeal genes, we believe that the community would be best served by maintaining use of the *agl*/Agl abbreviation followed by a number for naming new archaeal N-glycosylation genes/proteins, given that all of the letters of the alphabet have already been used in this context. Indeed, given that archaeal N-glycosylation presents aspects of the both its bacterial and eukaryal counterparts (see Calo et al., 2010; Jarrell et al., 2010; Meyer and Albers, 2011), adopting a combination of bacterial and eukaryal nomenclature rules for naming genes involved in the archaeal version of this post-translational modification is fitting.

By adopting an open-ended number-based system for naming novel archaeal N-glycosylation to be identified in the future, the enormous variety of genes/proteins responsible for the diversity seen in archaeal N-glycosylation could be nonetheless linked via the common *agl* abbreviation. At the same time, a shared N-glycosylation-related function would be assigned the same name in all species, as in the case of *aglB*, encoding the archaeal oligosaccharyltransferase. By the same logic, as the precise roles of Agl proteins become clear, components could be renamed with the first letter/number assigned that specific role. While such a naming strategy could result in a given archaeal species containing *agl* genes bearing widely spaced letters and/or numbers, it would allow for easy identification of similarities in N-glycosylation pathways that will likely prove to be otherwise largely species-specific.

As members of the archaeal N-glycosylation research community, we propose that the *agl*-based nomenclature outlined above be adopted for annotating any relevant new genes and proteins identified. To facilitate such efforts, researchers are invited to visit the *agl*genes website (www.bgu.ac.il/aglgenes), where an updated listing of *agl* sequences is provided.

Jerry Eichler*, Ben Gurion University
Ken Jarrell, Queen's University
Sonja Albers, MPI-Marburg

*author for correspondence (jeichler@bgu.ac.il); tel: (+972) 8646 1343; fax: (+972) 8647 9175

References

Aas FE, Vik A, Vedde J, Koomey M, Egge-Jacobsen W. 2007. *Neisseria gonorrhoeae* O-linked pilin glycosylation: functional analyses define both the biosynthetic pathway and glycan structure. *Mol. Microbiol.* 65:607-624.

Calo D, Kaminski L, Eichler J. 2010. Protein glycosylation in Archaea: Sweet and extreme. *Glycobiology* 20:1065–1079.

Chaban B, Voisin S, Kelly J, Logan SM, Jarrell KF. 2006. Identification of genes involved in the biosynthesis and attachment of *Methanococcus voltae* N-linked glycans: insight into N-linked glycosylation pathways in Archaea. *Mol. Microbiol.* 61:259–268.

Cherry JM, Hong EL, Amundsen C, Balakrishnan R, Binkley G, Chan ET, Christie KR, Costanzo MC, Dwight SS, Engel SR, Fisk DG, Hirschman JE, Hitz BC, Karra K, Krieger CJ, Miyasato SR, Nash RS, Park J, Skrzypek MS, Simison M, Weng S, Wong ED. 2012. *Saccharomyces* Genome Database: the genomics resource of budding yeast. *Nucleic Acids Res.* 40:D700–D705.

Demerc M, Adelberg EA, Clark AJ, Hartman PE. 1966. A proposal for a uniform nomenclature in bacterial genetics. *Genetics* 54:61–76.

Eichler J. 2013. Extreme sweetness: Protein Glycosylation in Archaea. *Nat. Rev. Microbiol.* 11:151–156.

Jarrell KF, Jones GM, Nair DB. 2010. Biosynthesis and role of N-linked glycosylation in cell surface structures of archaea with a focus on flagella and S layers. *Int. J. Microbiol.* 2010:470138.

Kaminski L, Lurie-Weinberger MN, Allers T, Gophna U, Eichler J. 2013. Phylogenetic- and genome-derived insight into the evolution of N-glycosylation in Archaea.

Linton D, Dorell N, Hitchen PG, Amber S, Karlyshev AV, Morris HR, Dell A, Valvano MA, Aebi M, Wren BW. 2005. Functional analysis of the *Campylobacter jejuni* N-linked protein glycosylation pathway. *Mol. Microbiol.* 55:1695–1703.

Mescher MF, Strominger JL. 1976. Purification and characterization of a prokaryotic glucoprotein from the cell envelope of *Halobacterium salinarium*. *J. Biol. Chem.* 251:2005–2014.

Meyer BH, Albers SV. 2011. The archaeal cell envelope. *Nat. Rev. Microbiol.* 9:414–426.

Meyer BH, Zolghadr B, Peyfoon E, Pabst M, Panico M, Morris HR, Haslam SM, Messner P, Schaffer C, Dell A, Albers SV. 2011. Sulfoquinovose synthase - an important enzyme in the N-glycosylation pathway of *Sulfolobus acidocaldarius*. *Mol. Microbiol.* 82:1150–1163.

Meyer BH, Peyfoon E, Dietrich C, Hitchen P, Dell A, Albers SV. 2013. Agl16, a thermophilic glycosyltransferase, mediating the last step of the N-glycan biosynthesis in the thermophilic crenarchaeon *Sulfolobus acidocaldarius*. *J. Bacteriol.* In press.

Schwarz F, Aebi M. 2011. Mechanisms and principles of N-linked protein glycosylation. *Curr. Opin. Struct. Biol.* 21:576–582.