Life with No Sugars?

Pedro M. Coutinho, and Bernard Henrissat*

Architecture et Fonction des Macromolécules Biologiques, CNRS-IFR1, 31 Chemin Joseph Aiguier, 13402 Marseille cedex 20, France

Whether hydrolytic or synthetic, glycosyl transfer is, simply in terms of quantity, one of the most important biological reactions on earth. The formation and cleavage of glycosidic bonds are catalysed by glycosyltransferases and glycoside hydrolases which are crucial for a number of biological pathways (biosynthesis and degradation of structural and storage polysaccharides, cellular signalling, host-pathogen interactions, etc.). As complete genomes are becoming available, comparative genomics are emerging and allow complete metabolic pathways to be searched and evaluated (Tatusov et al., 1997). Glycoside hydrolases and glycosyltransferases have been classified in families of related proteins for several years (Henrissat, 1991; Henrissat and Bairoch, 1993; Henrissat and Bairoch, 1996; Campbell et al., 1997). These families can be conveniently accessed through the CAZY server at URL http://afmb.cnrs-mrs.fr/~pedro/CAZY/db.html. This classification system has several advantages, one of which is that one can search complete genomes for these families. We have compiled a library containing these enzymes and related proteins (>4,700 entries). Any genome can be searched for putative glycoside hydrolases and glycosyltransferases by BLASTing (Altschul et al., 1997) its putative coding regions against this library. Glycoside hydrolases and glycosyltransferases frequently display a modular structure with a catalytic domain linked to one or several non-catalytic modules (Gilkes et al., 1991). A given non-catalytic module can be found attached to catalytic modules of different families but also to proteins which are neither glycoside hydrolases nor glycosyltransferases. To avoid «false positive hits» with the non-catalytic modules, we have excised the non-catalytic modules from our putative coding regions against this library. Glycoside hydrolases and glycosyltransferases frequently display a modular structure with a catalytic domain linked to one or several non-catalytic modules (Gilkes et al., 1991). A given non-catalytic module can be found attached to catalytic modules of different families but also to proteins which are neither glycoside hydrolases nor glycosyltransferases. To avoid «false positive hits» with the non-catalytic modules, we have excised the non-catalytic modules from our sequences. We have analyzed the five complete archaean genomes publicly available: *Aeropyrum pernix* (Kawarabayasi et al., 1999), *Archeoglobus fulgidus* (Klenk et al., 1997), *Methanobacterium thermoautotrophicum* (Smith et al., 1997), *Methanococcus jannaschii* (Bult et al., 1996) and *Pyrococcus horikoshii* (Kawarabayasi et al., 1998). Surprisingly, even using permissive thresholds, no similarity with any known glycoside hydrolase was found in three out of these genomes (*A. fulgidus, A. pernix* and *M. thermoautotrophicum*) while the remaining two (*M. jannaschii* and *P. horikoshii*) contained only two and seven respectively (Table 1). On the other hand, the five archaea all appear to contain putative glycosyltransferases (Table 1). For comparison, the genomes of two hyperthermophilic bacteria, *Aquifex aeolicus* (Deckert et al., 1998) and *Thermotoga maritima* (Nelson et al., 1999), and of a mesophilic bacterium, *Escherichia coli* (Blattner et al., 1997), were also searched for glycoside hydrolases and glycosyltransferases (Table 1). While *A. aeolicus* appears to contain only four putative glycoside hydrolases, *T. maritima* and *E. coli* have respectively 39 and 35.

There are two possibilities to explain the apparent total lack of glycoside hydrolase in three out of five archaean genomes: (i) these organisms have glycoside hydrolases completely different (and to be discovered) from those already known, a puzzling hypothesis given the evidence of extensive horizontal transfers between archae and bacteria (Nelson et al., 1999); (ii) these organisms indeed do not require any glycoside hydrolase, perhaps in line with observations that certain sulfur-dependent heterotrophic archaee do not grow on carbohydrates (Grote et al., 1999). The presence of putative glycosyltransferases in genomes apparently devoid of glycoside hydrolase constitutes another surprise as one would expect an organism to be able to degrade the glycosidic bonds it builds.

<table>
<thead>
<tr>
<th>Organism</th>
<th>Number of putative glycoside hydrolases</th>
<th>Number of putative glycosyltransferases*</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Archeoglobus fulgidus</em></td>
<td>2</td>
<td>12</td>
</tr>
<tr>
<td><em>Methanobacterium thermoautotrophicum</em></td>
<td>0</td>
<td>17</td>
</tr>
<tr>
<td><em>Methanococcus jannaschii</em></td>
<td>2</td>
<td>10</td>
</tr>
<tr>
<td><em>Pyrococcus horikoshii</em></td>
<td>7</td>
<td>14</td>
</tr>
<tr>
<td><em>Aquifex aeolicus</em></td>
<td>4</td>
<td>19</td>
</tr>
<tr>
<td><em>Escherichia coli</em></td>
<td>35</td>
<td>54</td>
</tr>
<tr>
<td><em>Thermotoga maritima</em></td>
<td>39</td>
<td>16</td>
</tr>
</tbody>
</table>

*Glycosyltransferases using nucleotide diphospho-sugars, nucleotide monophospho-sugars and sugars-1-phosphate for the synthesis of glycosidic bonds. Pentosyltransferases excluded.

References


Further Reading

Caister Academic Press is a leading academic publisher of advanced texts in microbiology, molecular biology and medical research. Full details of all our publications at caister.com

• MALDI-TOF Mass Spectrometry in Microbiology
  Edited by: M Kostrzewa, S Schubert (2016)
  www.caister.com/malditof

• Aspergillus and Penicillium in the Post-genomic Era
  Edited by: RP Vries, IB Gelber, MR Andersen (2016)
  www.caister.com/aspergillus2

• The Bacteriocins: Current Knowledge and Future Prospects
  Edited by: RL Dorfl, SM Roy, MA Riley (2016)
  www.caister.com/bacteriocins

• Omics in Plant Disease Resistance
  Edited by: V Bhadauria (2016)
  www.caister.com/opdr

• Acidophiles: Life in Extremely Acidic Environments
  Edited by: R Quatrini, DB Johnson (2016)
  www.caister.com/acidophiles

• Climate Change and Microbial Ecology: Current Research and Future Trends
  Edited by: J Marxsen (2016)
  www.caister.com/climate

• Biofilms in Bioremediation: Current Research and Emerging Technologies
  Edited by: G Lear (2016)
  www.caister.com/biorem

• Microalgae: Current Research and Applications
  Edited by: MN Tsakloglou (2016)
  www.caister.com/microalgae

• Gas Plasma Sterilization in Microbiology: Theory, Applications, Pitfalls and New Perspectives
  Edited by: H Shintani, A Sakudo (2016)
  www.caister.com/gasplasma

• Virus Evolution: Current Research and Future Directions
  Edited by: SC Weaver, M Denison, M Roossinck, et al. (2016)
  www.caister.com/virusevol

• Arboviruses: Molecular Biology, Evolution and Control
  Edited by: N Vasilakis, DJ Gubler (2016)
  www.caister.com/arbo

• Shigella: Molecular and Cellular Biology
  Edited by: WD Picking, WL Picking (2016)
  www.caister.com/shigella

• Aquatic Biofilms: Ecology, Water Quality and Wastewater Treatment
  Edited by: AM Romani, H Guasch, MD Balaguer (2016)
  www.caister.com/aquaticbiofilms

• Alphaviruses: Current Biology
  Edited by: S Mahalingam, L Herrero, B Herring (2016)
  www.caister.com/alpha

• Thermophilic Microorganisms
  Edited by: F Li (2015)
  www.caister.com/thermophile

• Flow Cytometry in Microbiology: Technology and Applications
  Edited by: MG Wilkinson (2015)
  www.caister.com/flow

• Probiotics and Prebiotics: Current Research and Future Trends
  Edited by: K Venema, AP Carmo (2015)
  www.caister.com/probiotics

• Epigenetics: Current Research and Emerging Trends
  Edited by: BP Chadwick (2015)
  www.caister.com/epigenetics2015

• Corynebacterium glutamicum: From Systems Biology to Biotechnological Applications
  Edited by: A Burkovski (2015)
  www.caister.com/cory2

• Advanced Vaccine Research Methods for the Decade of Vaccines
  Edited by: F Bagnoli, R Rappuoli (2015)
  www.caister.com/vaccines

• Antifungals: From Genomics to Resistance and the Development of Novel Agents
  Edited by: AT Coste, P Vandeputte (2015)
  www.caister.com/antifungals

• Bacteria-Plant Interactions: Advanced Research and Future Trends
  www.caister.com/bacteria-plant

• Aeromonas
  Edited by: J Graf (2015)
  www.caister.com/aeromonas

• Antibiotics: Current Innovations and Future Trends
  Edited by: S Sánchez, AL Demain (2015)
  www.caister.com/antibiotics

• Leishmania: Current Biology and Control
  Edited by: S Adak, R Datta (2015)
  www.caister.com/leish2

• Acanthamoeba: Biology and Pathogenesis (2nd edition)
  Author: NA Khan (2015)
  www.caister.com/acanthamoeba2

• Microarrays: Current Technology, Innovations and Applications
  Edited by: Z He (2014)
  www.caister.com/microarrays2

• Metagenomics of the Microbial Nitrogen Cycle: Theory, Methods and Applications
  Edited by: D Marco (2014)
  www.caister.com/n2

Order from caister.com/order


