

Molecular Adaptations in Bacteria

Author: Lundmark, Cathy

Source: BioScience, 56(10) : 872

Published By: American Institute of Biological Sciences

URL: [https://doi.org/10.1641/0006-3568\(2006\)56\[872:MAIB\]2.0.CO;2](https://doi.org/10.1641/0006-3568(2006)56[872:MAIB]2.0.CO;2)

BioOne Complete (complete.BioOne.org) is a full-text database of 200 subscribed and open-access titles in the biological, ecological, and environmental sciences published by nonprofit societies, associations, museums, institutions, and presses.

Your use of this PDF, the BioOne Complete website, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at www.bioone.org/terms-of-use.

Usage of BioOne Complete content is strictly limited to personal, educational, and non - commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

BioOne sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

Molecular Adaptations in Bacteria

STRUCTURE OF PILI

Bacteria may seem like simple organisms on a cellular level, yet they have evolved elegant molecular machinery that can perform multiple functions. On the surface of gram-negative bacteria (so called because they do not stain blue in the Gram procedure) are fine threadlike structures, called type IV pili, that play critical roles in motility, DNA uptake, colony formation, virulence, and defense against a host's immune response.

Type IV pili are helical polymers of a single subunit known as pilin. Using crystallography and electron microscopy, Lisa Craig of Simon Fraser University and her colleagues at the Scripps Research Institute and the University of Virginia Health Sciences Center have characterized pili from *Neisseria gonorrhoeae* and detailed the qualities that allow this protein filament to carry out its numerous functions. The study, published in the September issue of *Molecular Cell*, has implications not only for treating persistent gonorrheal infections but for combating the bacterial pathogens that cause meningitis (*Neisseria meningitidis*), tularemia (*Francisella tularensis*), and cholera (*Vibrio cholerae*), among others.

Thinner and more numerous than flagella, type IV pili are flexible, strong filaments that are anchored in the bacterial membrane and attach to surfaces somewhat like mooring lines. Once attached, bacteria move along surfaces through dynamic assembly and disassembly of filaments. Type IV pili can bind to cell surfaces directly—antibodies to pilin block bacterial adhesion—and some pili have a tip-associated protein that recognizes specific cell surface receptors of host tissues.

Type IV pili also have a role in interactions between bacterial cells. They adhere to the pili and possibly to the

receptors of other bacteria to form colonies, and they effect bacterial transformation by taking up double-stranded DNA. Craig and colleagues show that the pilin polymer's recessed regions form charged grooves that may be the binding regions for DNA. Pili may then be retracted into the cell, along with bound DNA, through rapid disassembly.

The pilin subunit is a small protein (about 150 to 200 amino acids) shaped like a glob on a stick, containing a hydrophobic alpha-helical stem that anchors the subunit within the filament and a topographically complex head that, in proximity to other subunits in the filament, creates grooves and protrusions on the filament's surface. The protruding regions, which are what antibodies most readily recognize, are hypervariable in sequence, allowing bacteria to evade an immune response and reinfect the host.

It may be possible to create more effective vaccines against gonorrhea by targeting the more highly conserved regions of pilin accessible on the surface of type IV pili. "In addition to vaccines," says Craig, "these results may aid in the identification of antibacterial agents that bind to conserved grooves and can be brought into cells by pilus retraction." Similarities between these and other bacterial pathogens may lead to other valuable vaccines and antibiotics as well.

COASTAL ADAPTATIONS

In a study comparing two strains of the marine cyanobacteria *Synechococcus*, scientists at the Institute for Genomic Research and Scripps Research Institute have cataloged many of the adaptations that distinguish the strain found along the coast from the one living in open ocean waters. The work by Brian Palenik, Ian Paulsen, and others appears in the

5 September issue of the *Proceedings of the National Academy of Sciences*.

By sequencing the genome of the coastal *Synechococcus* strain, CC9311, the scientists found several important ways it differs from the genome of the open-ocean strain, WH8102, that can be linked to environmental differences. They found that CC9311 has almost twice as many sensors and response regulators as WH8102, as might be expected for an organism living in the more variable coastal environment. Yet CC9311 lacks a phosphate sensor-response regulator system commonly found in WH8102 and other bacteria, reflecting the higher phosphate concentrations near the coast—hence CC9311's attenuated need for acquiring phosphate—than in phosphate-limited waters such as the open ocean. Iron and other metals are also found in higher concentrations along the coast, and the study showed that CC9311 has a greater capacity than WH8102 for transporting and storing metals, particularly iron and copper. CC9311 has multiple ammonia transporters that WH8102 lacks, as well, indicative of a more nutrient-rich coastal environment.

The study provides support for the hypothesis that lysogenic phages are more common in nutrient-limited environments. The two strains of *Synechococcus* both contain novel genomic "islands," probably acquired through horizontal gene transfer, but CC9311 lacks the phage genes flanking the islands in WH8102. Some of the islands unique to CC9311 include metal-metabolizing genes, suggesting that some of the adaptations to the coastal environment were acquired relatively recently.

Cathy Lundmark (e-mail: clundmark@aibs.org).