the cell with critical fitness advantages. Both large and small ncRNAs are structurally diverse, with some of the larger ncRNAs nearly as complex as ribosomes. Their conserved complexity and diversity along with their varied genomic locations suggest that these RNA molecules are involved in a wide range of biologic roles and activities. See Genome Biology (http://genomewebiology.com/2010/11/3/R31) for details.

One of the most surprising recent findings is a cyclic di-guanosyl-5'·monophosphate (c-di-GMP)-binding riboswitch, which is linked to a self-splicing intron. Its host bacterium, Clostridium difficile, appears to harness this apparatus to promote protein production from a downstream pathogenicity gene, according to Breaker. Thus it seems that not all group I self-splicing ribozymes are associated with selfish genetic elements, he says. “Furthermore, because this regulatory region can read both GTP and c-di-GMP concentrations and trigger splicing accordingly, it appears to constitute a two-input gene control system.” Details appear in the 13 August 2010 Science (329:845–848).

Breaker and his collaborators also are investigating a set of ornate large extremophilic (OLE) RNAs produced by Bacillus halodurans. These RNA molecules bind to an OLE-associated protein (OAP), which has several transmembrane domains. “We know that OAP recruits OLE RNA to the cell membrane, suggesting that’s where most of the transcript’s complex structure performs its biochemical function,” Breaker says. Noting that OLEs are not only membrane-bound but also abundant in B. halodurans, he speculates that they enable this extremophile to adapt to its environment. “The newer and faster technologies will most likely reveal a vast number of additional ncRNAs,” he adds, referring to recent improvements in DNA sequencing analysis.

See the January 2011 Molecular Microbiology for details.

“This study shows how inexpensive next-generation sequencing is revolutionizing the field of molecular microbiology,” say Wes Sanders and Alain Laederach at the University of North Carolina in Chapel Hill. “Now it is possible to characterize an entire bacterial transcriptome in a single experiment,” they add. Moreover, says Eric Westhof of the Université de Strasbourg in France, “Until Breaker’s group exploited the power of comparative sequence analysis—combining sophisticated automatic technology with manual intervention—the complex structures of ncRNAs remained hidden in the genome’s ‘dark matter’ long considered nothing more than junk.”


Marcia Stone

Cholera in Haiti Adds to Suffering, Evokes Calls for Drug Treatment and Vaccination Plans

Although the cholera outbreak that began in Haiti during October 2010 is subsiding, its death toll exceeded 1,400 as of late November among more than 60,000 cases, according to officials of the World Health Organization (WHO). Genomic analysis indicates that the outbreak strain was introduced into the country “from a distant geographic source . . . through human activity,” according to Eric Schadt of Pacific Biosciences in Menlo Park, Calif., and his collaborators there and elsewhere, whose findings appear in the January 6, 2011 New England Journal of Medicine (NEJM) (364:33–42). Although rehydration proves a lifesaving therapy for many individuals with cholera, Matthew Waldor of Harvard Medical School in Boston, Massachusetts, and his collaborators recently recommended that the United States stockpile cholera vaccines to deploy at the first signs of outbreaks such as the one in Haiti (see December 9, 2010 NEJM, 363:2279–2282). Meanwhile, David Sack of the Johns Hopkins Bloomberg School of Public Health, Baltimore, Md., and his collaborators, urge that antibiotics also be used judiciously during such outbreaks, noting that appropriate drug therapy “shortens the duration of illness and reduces the shedding of thousands of infectious doses” (January 6, 2011 NEJM, 364:5–7).

Three Crenarchaeotes, All Hyperthermophiles, Form Biofilms

In the absence of other microbial species, three closely related hyperthermophilic crenarchaeotes—Sulfolobus acidocaldarius, S. solfataricus, and S. tokodaii—form biofilms, according to Sonja-Verena Albers and her collaborators at the Max Planck Institute for Terrestrial Microbiology in Marburg, Germany. Although other investigators report finding archaea within bacterial biofilms, these experiments appear to be the first in which archaeal species propagate biofilms on their own, she says. Details appear in the

All three of these acid-loving Sulfolobus species are found in geothermally active environments, and they grow optimally at 75–85°C and in the acidic pH range of 2–3. Earlier, while collaborating with Wolfram Zillig at the Max Planck Institute for Biochemistry in Martinsried, Albers noticed that such Sulfolobus form microcolonies. “This indicated that these strains might be able to form biofilms,” she says.

These archaeal biofilms differ from those that bacteria form, according to Albers and her collaborators. “Bacterial biofilms form carpet-like structures; in contrast, S. acidocaldarius [cells] form tower structures and secrete a large amount of extracellular polysaccharides,” they report. Curiously, the biofilms that these three crenarchaeotes form differ from one another, likely reflecting differences in their responses to localized environments that they encounter in hot springs, according to Albers and her collaborators. “S. solfataricus and S. tokodaii are always isolated from the middle of solfataric hot springs, whereas S. acidocaldarius is mainly found in the crust at the sides of hot springs,” they point out.

Simulating hot-spring conditions in the lab proves challenging, particularly when adapting analytic methods to very high temperatures, according to Albers and her collaborators. For instance, they had to find a way of covering their microliter plates to slow evaporation rates while still allowing enough oxygen through the covering to enable growth of the aerobic strains that they were studying, she says, adding: “Then we had to build a metal container, that we filled with a layer of water at the bottom and which could be sealed for the incubation in the high-temperature oven.”

The researchers from the Max Planck Institute are continuing to analyze proteomic and transcriptomic data gathered while observing two-day-old biofilms of the three Sulfolobus species. “We are most interested in which regulators switch cells to the biofilm mode of growth,” Albers says. “Archaea do not use cyclic-di-GMP, which in bacteria is a main player in this process. Rather, archaea, have to use other mechanisms. Moreover, no quorum sensing molecules have been identified in archaea, and that is again an important issue that has to be addressed.”

“Information about archaeal and/or extremophilic biofilms is very limited,” says microbiologist Gemma Reguera of Michigan State University in East Lansing. “Crenarchaea, in particular, are known to be part of environmental biofilms, yet their ability to form biofilms had not been documented, at least not with this level of detail. This research team optimized every single assay meticulously. The result is a beautifully crafted paper with high-quality, reproducible data, and outstanding microscopy to characterize biofilm components and structure.”

Barry E. DiGregorio
Barry E. DiGregorio is a freelance writer in Middleport, N.Y.

Metabolite from Tooth Decay Bacterium Curbs Yeast Oral Pathogen

A secondary metabolite from Streptococcus mutans can prevent the yeast Candida albicans from becoming pathogenic, according to Robert Cichewicz, a natural products chemist at the University of Oklahoma (UO) in Norman, and his collaborator, Fengxia Qi, a dental researcher at the UO Health Science Center in Oklahoma City. They consider that metabolite, which they call mutanobactin A, a promising lead for agents to treat Candida infections such as thrush, which can erupt in the oral cavity.

Indeed, both microorganisms occupy the human mouth, where S. mutans can be a major contributor to tooth decay. Qi, part of a team that