that have been around for 3 billion years, and have adapted to survive under the most extreme condition, will always overcome whatever we decide to throw at them.”

Marcia Stone is a freelance science writer based in New York City.

RESEARCH ADVANCES

Transferred Microbial Genes Enable Eukaryote To Cope with Extremes

Marcia Stone

The single-cell eukaryote Galdieria sulphuraria has acquired at least 75 separate gene families, amounting to about 5% of its genome, from extremophilic bacteria and archaea—enabling it to occupy a niche that eukaryotes typically shun and thus thrive in some of the hottest, most toxic places on earth, according to Gerald Schönknecht at Oklahoma State University in Stillwater and his collaborators. Details appeared March 8, 2013 in Science (339: 1207–1219).

“It’s well known that single cells are genetically promiscuous, but finding a eukaryote that can adapt to new, very hostile environments through extensive horizontal gene transfer (HGT) from other domains is surprising,” says Schönknecht who, along with Andreas P. M. Weber at Heinrich-Heine-Universität in Düsseldorf, Germany, led an international team of 18 French, German, and U.S. scientists from 15 separate research centers in an effort to sequence the 13.7-Mb G. sulphuraria genome.

While the group found evidence for gene transfers from a broad range of extremophilic microbes, the most significant sources were bacteria. For example, genes that encode sodium-excreting pumps, and thus account for salt tolerance, trace to halophilic cyanobacteria. In addition, the G. sulphuraria genome contains transporter genes of bacterial origin whose products help them cope with toxic metals—for instance, their two intransless arsenic pumping genes known as ArsB. “The sequences most similar to G. sulphuraria’s ArsB are from thermoacidophilic bacteria, once again indicating a central role for HGT in extremophilic adaption to hostile environments,” Weber says.

“Genes of bacterial origin in G. sulphuraria have fewer introns and atypical sequence compositions, suggesting ongoing adaption to the genome,” comments Eduardo P. C. Rocha at the Institut Pasteur in Paris, France, who was not involved in this research. The dynamics of this process await exploration, he points out.

Genes encoding the two largest protein families in G. sulphuraria appear to descend from an archaeal ATPase gene that duplicated and diversified. This special class of soluble archaeal ATPases is not found in other eukaryotes, and Schönknecht speculates that they contribute to G. sulphuraria’s ability to withstand heat. “These blue-green members of the Phylum Rhodophyta, commonly known as ‘red’ algae, dominate sulfur springs and volcanic soils, frequently making up more than 90% of the total biomass, something they’ve probably done for hundreds of millions of years,” Schönknecht says.

“Its ability to neutralize biohazardous metals could make G. sulphuraria very useful algae,” Schönknecht and his collaborators note. “It’s also important to determine if G. sulphuraria is as radiation-resistant as Deinococcus, or ro-

MINTOPIC

Tidbits on Fungi: Trees, Forests, Bats, Brains

Recent developments involving research on fungi include:

• The 31.5-Mb genome of Ophiostoma ulmi, the fungus responsible for Dutch elm disease, apparently encodes 8,639 genes, based on its sequence analysis, according to Alan Moses of the University of Toronto in Toronto, Ontario, Canada, and his collaborators. Details appeared March 12, 2013 in BMC Genomics (doi: 10.1186/1471-2164-14-162).

• As much as 70% of the carbon stored in boreal forests is associated with fungi, called mycorrhizal mycelium, that associate with tree roots—a realization that should be taken into account when modeling global carbon balances, according to Karina Clemmensen of Swedish University of Agricultural Sciences in Uppsala, Sweden, and her collaborators. Details appeared March 29, 2013 in Science (doi: 10.1126/science.1231923).

• A DNA-based test is now available for identifying Geomyces destructans, the fungus responsible for white nose syndrome in bats, making it easier to discern this pathogen from other related species, according to David Blehert of the U.S. Geological Survey in Madison, Wisc., and his collaborators. Details appear in the February 2013 Mycologia (doi: 10.3852/12-242).

• Cryptococcus neoformans, a fungus that can cause meningitis and which is particularly problematic among AIDS patients, maintains virulence within macrophage cells of mice by detoxifying copper in two ways—making proteins that bind the metal and others that interfere with the host supplying more of it to macrophage cells, according to Dennis J. Thiele at Duke University in Durham, N.C., and his collaborators. Details appeared March 13, 2013 in Cell Host & Microbe (doi: 10.1016/j.chom.2013.02.002).
tifers, and some fungi, which, at the moment, are ranked at the top for most efficient DNA repair following gamma radiation,” says Michael J. Daly at the Uniformed Services University of the Health Sciences in Bethesda, Md. “I expect these algae use manganese complexes to protect their enzymes from oxidative damage and other forms of stress. Small-molecule Mn (II) antioxidants are becoming increasingly evident in all branches of life, and the remarkable metabolic repertoire of G. sulphuraria likely will expand the list.” (See Microbe, April 2009, p. 164.)

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