

A salty tale: New bacterial genome sequenced from ancient salterns

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Tourists in Spain often stop to ogle the country's many saltwater lagoons, used to produce salt since Roman times. Scientists, too, admire these saltern crystallizers--and even more so, the microbes that manage to survive in such briny environs. Now, reporting in the November 28-December 2 early online edition of the Proceedings of the National Academy of Sciences, researchers at The Institute for Genomic Research and collaborators reveal the genome of one bacterium at home in the salty Spanish ponds.

The bacterium is *Salinibacter ruber*, a bright red, rod-shaped organism. Several years ago, scientists first isolated *S. ruber* from saltern crystallizer ponds in Alicante and Mallorca, Spain. Although extreme-loving microbes called archaea were known to eke out life in the ponds, scientists were surprised to discover ordinary bacteria also thriving in such a physically demanding environment, at salt concentrations up to 30 percent. How could these microbes--which normally prefer milder environments--thrive in such high salt?

To find out, TIGR researchers Emmanuel Mongodin and Karen Nelson, working with Canadian and Spanish colleagues, set out to sequence *S. ruber*'s genome. In doing so, the scientists discovered evidence that the resourceful bacterium independently evolved some salt-surviving biochemistry. More surprising, *S. ruber* apparently also borrowed some genes from neighboring archaeal species, in an unusual example of cross-domain lateral gene transfer.

"Scientists are increasingly learning how microbes adapt to harsh environments," remarks Mongodin, first author on the PNAS study, funded by a grant from the National Science Foundation and United States Department of Agriculture. "*S. ruber* illustrates that even in a really extreme environment, bacteria can do what it takes to survive, including exchanging genes with other microbial species that we might not expect."

Normally, high-salt environments denature bacterial proteins. To survive, *S. ruber* must maintain a high concentration of potassium inside its cytoplasm, keeping an osmotic balance against the high sodium chloride concentration outside. That's where evolutionary strategy comes in.

Analyzing the bacterium's genome, researchers found that *S. ruber*'s proteins are typically rich in acidic amino acids and relatively poor in hydrophobic (water-repellent) amino acids, making them soluble and highly stable at such salt concentrations. Researchers recognized this biochemical adaptation: it's the same one used by archaea also living in the salterns.

That wasn't the only similarity. Scientists also found two types of rhodopsin genes: one variety typical for bacteria, and another previously recognized in archaea. A photosynthetic protein, rhodopsin works as a proton pump, capturing light energy and using it to move protons across the membrane and out of the cell. In doing so, the protein maintains a balance of ions inside and outside the cell.

"It's very unusual to find the two different types of rhodopsin in the same organism," Mongodin says. "*S. ruber* may have independently evolved one type of rhodopsin and acquired the other through lateral gene transfer from the archaeal species also living in the salterns." This study is the first to document bacteria adopting the archaeal-type

rhodopsin. The two systems may work at different wavelengths, expanding *S. ruber*'s ability to thrive in this environment. Alternatively, Mongodin says, the double system may be redundant, a kind of biological back-up.

Because *S. ruber* grows in high salt, its enzymes are strikingly stable. And that means the bacterium may hold promise for industrial applications. Meanwhile, TIGR's collaborators are pursuing studies of Spain's salterns, testing the ponds to find out what other microbes call the briny waters home. "How much diversity is there?" Mongodin asks. "We'll all be interested to learn."

Source: The Institute for Genomic Research

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