

Two new studies by University of California, Berkeley, scientists highlight the amazing promiscuity of genes, which appear to shuffle frequently between organisms, especially more primitive organisms, and often in packs. Such gene flow, dubbed horizontal gene transfer, has been seen frequently in bacteria, allowing pathogenic bacteria, for example, to share genes conferring resistance to a drug. Recently, two different species of plants were shown to share genes as well. The questions have been: How common is it, and how does it occur?

In a report appearing this week in the Proceedings of the National Academy of Sciences (PNAS), UC Berkeley and Lawrence Berkeley National Laboratory (LBNL) researchers analyzed more than 3,000 different families of genes coding for proteins - families that represent the backbone of proteins in all living creatures - to assess the prevalence of horizontal gene transfer.

They found that more than half of all the most primitive organisms, Archaea, have one or more protein genes acquired by horizontal gene transfer, as compared to 30 to 50 percent of bacteria that have acquired genes this way. Fewer than 10 percent of eukaryotes - plants and animals - have genes acquired via horizontal gene transfer.

In a second report published online by Nature on March 7, two species of bacteria living together in the pink slime of an acidic California mine were found to share large groups of genes. These genes code for proteins that work together, so by acquiring the entire block from another organism, bacteria can gain a new function that helps them adapt more quickly to the same type of environment - in this case, a hot, highly acidic, metal-rich broth.

This is the first observation of exchange of very large genomic blocks between organisms in a natural microbial community, according to UC Berkeley's Jill Banfield, who led the team of researchers from LBNL, Oak Ridge National Laboratory (ORNL), Lawrence Livermore National Laboratory and the U. S. Department of Energy's Joint Genome Institute (JGI).

"One of the key questions being debated is, 'Is horizontal gene transfer extensive and rampant, or is it a relatively rare event?'" said Hong-Hua Kim, professor of chemistry at UC Berkeley and coauthor of the PNAS paper. "This becomes important in classifying organisms and comparing whole genomes to find their relationships.

"Our study shows that gene transfer is fairly common, but the extent in a given organism is fairly low - that is, most organisms have mutated one or more genes from a closely related organism. And while it's very likely that genes are transferred in chunks that are linked genetically, I don't see any way for a group of genes doesn't have value in a new organism. It's not going to stick around."

"This provides important information about the conservation of genetic resources to enable life to survive and thrive," said ORNL's Bob Hattick, a co-author of the Nature paper. "Ultimately, the basic knowledge gained from this research will lead to a greater understanding of genetic diversity in related organisms and should lead to developments in human health and bioremediation."

Though the Nature findings show more than five times the level of horizontal gene transfer, the study's main goal was to identify, with high resolution, which organisms are able to carry out that function within a natural, uncultured microbial community, according to Banfield.

In addition to revealing a history of genetic exchange between two distant organism types in the mine, we show that it is possible to identify large families of the proteins from co-existing organisms and determine which organism most of the proteins comes from, even if the organisms are quite closely related," said Banfield, a professor of earth and planetary science and of environmental microbiology at UC Berkeley.

term study of the community of organisms in mine slimes obtained from the Richmond Mine near Redding, Calif. This microbial biofilm has turned out to be an ideal research subject, Banfield said, because the simple community contains few enough organisms that they can be used as a model system to uncover aspects of how microbes interact with each other and their surroundings in ways that Banfield cannot heretofore have done. Banfield is the senior author of the study, which was published in the journal Nature.

Banfield compares her strategy of ever more detailed studies of a single site to that of Craig Venter, who has been calling the world's attention about his quest, Sequence It, to sample large communities of organisms to survey global diversity. After four years collecting vast amounts of genomic information, he plans to publish some of his analyses next week in the Public Library of Science, or PLoS.

In 2005, the mine was the source of samples for the first fairly comprehensive community genomic, or metagenomic, characterization of a natural microbial consortium. In 2006, Banfield and colleagues presented the first relatively large-scale analysis of the proteins that consortia members make to carry out the various metabolic tasks needed for life underground.

work that revealed information about the machinery used to adapt to the extreme conditions in which they live. More recently, in 2006, research scientist Brett Baker, Banfield and colleagues reported that the biofilms harbor several archaeal organisms that appear to be extremely small compared to other life forms.

"Analysis of these microorganisms required us to think more broadly about the role of exchange of genetic material in adaptation and evolution in response of we are to understand important environmental processes such as acid mine drainage, or even degradation of cellulose for ethanol production by microbial communities," added Banfield.

In their new paper, the researchers combine metagenomics with state-of-the-art techniques to show that different organisms are exchanging large blocks of their genes.

"Who's there and what are they doing are key questions in microbial ecology," said Banfield's colleague Vincent Denard, a post-doctoral researcher at UC Berkeley's Department of Earth and Planetary Science. "Our high-resolution, mass spectrometry-based community proteomics approach answers both at the same time. We can now self-sort apart closely related organisms, which we previously would have grouped as one species, and we can monitor and discriminate their behavior within the same natural community. These abilities will allow us to understand the implications of small differences in genome sequence and content on ecological performance."

