Gene's 'selective signature' aids detection of natural selection in microbial evolution

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Scientists at MIT have come up with a mathematical approach for analyzing a protein simultaneously in a set of ecologically distinct species to identify occurrences of natural selection in an organism's evolution.

The new method determines the "selective signature" of a gene, that is, the pattern of fast or slow evolution of that gene across a group of species, and uses that signature to infer gene function or to map changes to ecological shifts.

By reversing the usual order of inquiry—studying an organism, then trying to identify which genes are involved in a particular function—the scientists hope to hasten the understanding of microbial evolution by taking advantage of the nearly 2,500 microbes already sequenced.

"By comparing across species, we looked for changes in genes that reflect natural selection and then asked, 'How does this gene relate to the ecology of the species it occurs in?'" said Eric Alm, the Doherty Assistant Professor of Ocean Utilization in the Department of Civil and Environmental Engineering. "The selective signature method also allows us to focus on a single species and better understand the selective pressures on it."

"Our hope is that other researchers will take this tool and apply it to sets of related species with fully sequenced genomes to understand the genetic basis of that ecological divergence," said graduate student B.

Jesse Shapiro, who co-authored with Alm a paper published in the February issue of *PLoS Genetics*.

Their work also suggests that evolution occurs on functional modules—genes that may not sit together on the genome, but that encode proteins that perform similar functions.

“When we see similar results across all the genes in a pathway, it suggests the genomic landscape may be organized into functional modules even at the level of natural selection,” said Alm. “If that’s true, it may be easier than expected to understand the complex evolutionary pressures on a cell.”

“In a single species, a whole set of genes in the same module tend to change together,” said Shapiro. “Identifying these changes brings us a step closer to understanding the ecological basis of selection in a species and how changes at the genetic level affect the organisms interactions with its environment.”

For example, in Idiomarina loihiensis, a marine bacterium that has adapted to life near sulfurous hydrothermal vents in the ocean floor, the genes involved in metabolizing sugar and the amino acid phenylalanine underwent significant changes (over hundreds of millions of years) that may help the bacterium obtain carbon from amino acids rather than from sugars, a necessity for life in that ecological niche. In one of I. loihiensis’ sister species, Colwellia psychrerythraea, some of those same genes have been lost altogether, an indication that sugar metabolism is no longer important for Colwellia.

Shapiro and Alm focused on 744 protein families among 30 species of gamma-proteobacteria that shared a common ancestor roughly 1 to 2 billion years ago. These bacteria include the laboratory model organism E. coli, as well as intracellular parasites of aphids, pathogens like the

bacteria that cause cholera, and soil and plant bacteria. They mapped the evolutionary distance of each species from the ancestor and incorporated information about the gene family (for instance, important proteins evolve more slowly than less vital ones) and the normal rate of evolution in a particular species' genome in order to determine a gene's selective signature.

"These are experiments we could never perform in a lab," said Alm. "But Mother Nature has put genes into an environment and run an evolutionary experiment over billions of years. What we're doing is mining that data to see if genes that perform a similar function, say motility, evolve at the same rate in different species. To the extent that they differ, it helps us to understand how change in core genes drives functional divergence between species across the tree of life."

Source: Massachusetts Institute of Technology