Too small and numerous to count: Better ways to estimate the diversity of unseen life on and in our bodies

7 February 2013

(Phys.org)—Ecologists often rely on the twin standards of the variety and numbers of species to describe a given region's diversity. But scaling down the size also scales up the numbers: On and in our bodies is a community with ten times as many microbes as there are cells of a human host, which makes counting species and comparing diversity an intractable problem.

Santa Fe Institute Omidyar Fellow James O'Dwyer, SFI External Professor Jessica Green of the University of Oregon's Microbial Ecology and Theory of Animals Center for Systems Biology (META), and Steven Kembel at the University of Quebec at Montreal have developed a new approach, which they detailed December 20 in the journal *PLOS Computational Biology*.

Using a gene that codes for a scaffolding used in building proteins – whose crucial role in a fundamental process means its sequence has changed little over millennia – they bypassed the ambiguous step of species identification and compared organisms by looking at the degree of change in that gene. In the resulting tree of relatedness, the longer the branch, the more changes in the gene and the less the organisms are related.

"Traditionally, we look at biodiversity in terms of total number of species, and whether they're rare or abundant," explains O'Dwyer. "Sequence data lets us go beyond that."

The new idea is looking at and predicting phylogenetic diversity, which takes into account relatedness within community. "Phylogenetic diversity is more tightly correlated with functional diversity – what a community is doing and why – than species diversity alone, and is therefore more informative," he says.

At the center of their new approach is what they call the Edge-length Abundance Distribution, where "edge" refers to the branch length determined by the gene's similarity between species. This quantifies the contribution of different clades – an ancestor and all of its descendents – to phylogenetic diversity.

They tested the approach on a subject with a huge range of habitats: the human body. One round of sampling the subjects' foreheads, forearms, elbows, knees, mouths, noses (both on and in) and guts yielded millions of sequences.

The team found that a habitat's diversity increased with its size according to a power law, and that this boost in diversity in turn arises from an unexpected power law scaling in the Edge-length Abundance Distribution with clade size.

With these findings and techniques in hand, O'Dwyer wants to characterize microbial communities on plants, fish, and in the indoor environment, and find the sweet spot of sufficient information to extrapolate trends in diversity from samples to entire communities.

Read the paper in PLOS Computational Biology (December 20, 2012).

Provided by Santa Fe Institute