Making sense of the staggering diversity of microbial communities

Dr. Vanja Klepac-Ceraj
Harvard University

Microbial communities are extraordinarily diverse, yet little is known about their composition or mechanisms that structure them. In my research, I explored how many bacterial types co-exist and whether such types form phylogenetically discrete units of potential ecological relevance by investigating bacterial diversity in two complex marine communities (coastal bacterioplankton and sediment sulfate-reducing bacteria). Since most microorganisms remain uncultured, I analyzed the diversity of these communities using sequence data from 16S rRNA gene directly obtained from environmental samples. 16S rRNA gene is commonly used for obtaining a "fingerprint" of individual microbial types. In order to gain unbiased insights into diversity and composition of two distinct marine microbial communities, I sampled two large 16S rRNA gene libraries. One of the most significant findings from this research was that the majority of sequences from the two microbial communities fell into microdiverse clusters containing <1% sequence divergence. This led us to propose that microdiverse clusters are important units of differentiation in natural bacterial communities. We hypothesized that such clusters arise by selective sweeps and contain high diversity because competitive mechanisms are too weak to purge diversity from within them. This finding challenges the current understanding of concepts of microbial diversity and compels investigation to what extent this gene diversity is reflective of ecologically differentiated populations (i.e., groups of microorganisms that responds as a unit to environmental change).