Identifying the Important Units of Microbial Diversity with Metagenomics

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Whether or not the vast microbial biodiversity on the planet is organized in discrete units that correspond to ecologically coherent species remains an unresolved issue of major theoretical as well as practical consequence. Recent high-resolution environmental surveys as well as multi-locus sequence data from isolates have implied that a continuum of sequence variants, as opposed to discrete sequence-based clades, typifies most accurately the microbial population structure. However, a major limitation of all these previous studies remains that the organisms compared were typically recovered from different populations and habitats, severely confounding genetic analyses and comparisons. Patterns of genomic variation maintained within natural microbial communities can potentially provide new insights into the previous issues. Such patterns recovered in metagenomic datasets revealed that oceanic planktonic bacteria were frequently, but not always, organized as discrete sequence-based clusters, with the intra-population genomic sequence divergence ranging from ~1% to ~6%. Several lines of evidence indicated that these discrete populations are maintained, at least in part, by genetic exchange (homologous recombination), and that finer levels of ecological or gene-content differentiation within these populations were absent. Therefore, such populations may represent the important units of diversity in the marine environment. A few cases of indiscrete (“fuzzy”) populations were also observed and were attributable to predictable environmental perturbations. Analyses of whole-genome sequences of members of a discrete marine population confirmed that genetic exchange might constitute the cohesive force of the population. These analyses also revealed that bacterial genomic adaptation to environmental fluctuations may be very rapid; much more rapid than previously anticipated. These results underscore the important interrelationship between environmental settings and genetic mechanisms that together shape and sustain microbial population structure.