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Authors
Francino, Maria Pilar
Boore, Jeffrey L.

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BACTERIAL PHYLOGENY AND GENOME EVOLUTION

M. Pilar Francino and Jeffrey L. Boore.
DOE Joint Genome Institute and Lawrence Berkeley National Laboratory, 2800 Mitchell Drive, Walnut Creek, CA 94598 USA

Although the number of bacterial genome sequences is ever increasing, species sampling has been very biased towards pathogenic organisms. In contrast, the DOE Joint Genome Institute (JGI) has sequenced the genomes of numerous species based on their environmental relevance and other factors, greatly increasing the taxonomic breadth of sampling. Here we present a phylogeny of 51 bacteria, including 18 species newly sequenced at the JGI, based on the concatenated alignment of ribosomal proteins shared by all bacteria. Using Bayesian phylogenetics, we have obtained the first completely resolved and well-supported global bacterial phylogeny, which recognizes the monophyly of bacterial phyla and unravels branching orders within and among them. We identify the deepest divergence among all nonhyperthermophilic bacteria between, on one hand, Proteobacteria, Chlamydiae, Bacteroidetes and Spirochaetes, and, on the other, Firmicutes, Actinobacteria, Deinococcus-Thermus and Cyanobacteria. We are currently using this phylogeny as a framework on which to trace the evolution of different gene families and genome-level characters.

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