

Beyond the Ring of Life: Applications of Conditioned Reconstruction

Anne B. Simonson

*MCD Biology and Astrobiology Institute
University of California, Los Angeles
Los Angeles, CA 90095-1570
U.S.A.*

asimonso@ucla.edu

Craig W. Herbold

*Molecular Biology Institute
University of California, Los Angeles
U.S.A.*

Jacqueline A. Servin

*Molecular Biology Institute
University of California, Los Angeles
U.S.A.*

Ryan G. Skophammer

*Molecular, Cell and Developmental Biology
University of California, Los Angeles
U.S.A.*

Maria C. Rivera

*IGPP and Astrobiology Institute
University of California, Los Angeles
U.S.A.*

James A. Lake

*MCD Biology, Molecular Biology Institute and Astrobiology Institute
University of California, Los Angeles
U.S.A.*

Understanding the early evolution of organisms on earth is a cornerstone of Astrobiology, as evolution on this planet can serve as a model for understanding and predicting how life might appear and evolve elsewhere in the universe. Our lab is interested in using phylogenomics to describe evolutionary relationships among organisms by combining whole-genome sequence information with phylogenetic methods, however, horizontal gene transfer can confound phylogenetic reconstructions. Conditioned reconstruction (CR) is a new computational method that generates genomic alignments and builds reliable phylogenetic trees even in the presence of significant horizontal gene transfer. When CR was used recently to analyze 6 prokaryotic genomes representing a broad sampling of prokaryotic life, and 2 eukaryotic yeast genomes, the resulting 5 most-probable trees displayed an overlapping pattern consistent with the topology of a single graph. This unique result suggested an underlying cycle graph (ring) rather than a traditional bifurcating tree. Thus, at the deepest levels of eukaryotic evolution, the tree of life appears to be a ring of life. (Rivera and Lake, 2004). We have used CR with new

genomic data sets to further probe the ring of life. Preliminary results using various eukaryotes, and different α -proteobacteria, gram-positive bacteria, and cyanobacteria support the ring of life topology and have garnered new insights into a recently identified phylogenomic reconstruction artifact called big genome attraction.

Rivera, MC and Lake, JA (2004) The ring of life provides evidence for a genome fusion origin of eukaryotes. *Nature*, 431:152-5