

Testing Biogeochemical Hypotheses of Microbial Evolution using Time- Calibrated Gene Transfer Phylogenies

GREGORY P. FOURNIER¹, JOANNA WOLFE¹, LILY
MOMPER¹, KELSEY MOORE¹, CARA MAGNABOSCO²

¹Massachusetts Institute of Technology, 77 Massachusetts
Ave, Cambridge, MA, USA.

²Flatiron Institute Center for Computational Biology, Simons
Foundation, New York, NY, USA.

During the course of planetary history, microbial metabolisms have continued to evolve and diversify in the context of changing geochemical systems, substrate availability, and redox couplings. Many of these geochemical changes were driven by microbes themselves, and their evolutionary innovations generating new biological couplings between atmospheric, surface, and aquatic chemistries. The biogeochemical record of our planet provides a rich history of the microbial processes that underlie these changes; however, it is incomplete, and often ambiguous. Observations may be consistent with several hypotheses, both abiogenic and biogenic, and ecological and preservation biases may further complicate the record. Therefore, hypotheses linking the evolution of specific microbial groups and metabolisms to geochemical events within the planetary record can greatly benefit from testing using an independent record: the record preserved within genome sequences of extant organisms across the Tree of Life.

Using this phylogenomic record, we show that time-calibrated phylogenies of biogeochemically important microbial lineages and gene families can, independently, directly inform and evaluate these hypotheses. Avoiding using non-independent biogeochemical dating constraints and instead using horizontal gene transfer events as cross-cutting stratigraphic temporal constraints between lineages greatly improves the utility, accuracy, and precision of this approach.

New molecular age estimates for the evolution of cyanobacteria, sulfate reducing bacteria, sulfur bacteria, and methanogens suggest, in general, a close temporal coupling between the diversification of major microbial lineages and their biogeochemical signatures. Much older age estimates for the origins of these metabolisms further suggest that, analogous to metazoan evolution, a substantial temporal lag generally exists between the evolutionary innovations leading to novel metabolic processes, and their later planetary biogeochemical significance.