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Reconstructing ancient enzymes to understand the peculiar consistency of Precambrian carbon isotope biosignatures

BETÜL KAÇAR

University of Arizona

Presenting Author: betulkcr@gmail.com

Life on Earth has generated two main repositories of information with which to reconstruct its past states: first, the genetic diversity of extant organisms, and second, the physical remnants of past life preserved in the geologic record, or biosignatures. By far the most extensive biosignature record — providing the earliest potential evidence of life >3 billion years old - is constructed from $^{13}C/^{12}C$ isotopic compositions of preserved carbonaceous material. These biosignatures preserve the long-term evolution of the microorganism-hosted metabolic machinery responsible for producing deviations in the isotopic compositions of inorganic and organic carbon. Despite billions of years of ecosystem turnover, evolutionary innovation, organismic complexification, and geological events, the organic carbon that is a residuum of the global marine biosphere in the rock record tells an essentially monotonic story: The carbon isotope biosignature (with a few remarkable exceptions) has remained remarkably unchanged over ~3.5 billion years. This peculiar monotony challenges much of what we understand about the dynamism of microbial and molecular evolution. The bulk of this record is conventionally attributed to early-evolved, RuBisCO-mediated CO_2 fixation that, in extant oxygenic phototrophs, produces comparable isotopic effects and dominates modern primary production. However, billions of years of environmental transition, namely in the progressive oxygenation of the Earth atmosphere, would be expected to have accompanied shifts in the predominant carbon metabolisms and enzymatic forms, as well as enzyme-level adaptive responses in RuBisCO CO_2 specificity. These factors would also be expected to result in preserved isotopic signatures deviating from those produced by extant RuBisCO in oxygenic phototrophs. Why does the bulk carbon isotope record not reflect these expected environmental transitions and evolutionary innovations? In this invited talk, I will discuss this apparent discrepancy and highlight the need for greater quantitative understanding of carbon isotope fractionation behavior in extant metabolic pathways. I will present the results of a novel, laboratory-based approach to reconstructing ancestral states of carbon metabolisms and associated enzymes that can constrain isotopic biosignature production in ancient biological systems, applied for the interpretation of the oldest record of life on Earth.