

RECONSTRUCTING THE PHYLOGENETIC HISTORY OF RUBISCO PROTEINS B. Kacar¹, Z. R. Adam², Z. Zhao³, N. Boekelheide⁴, ¹Harvard University, Organismic and Evolutionary Biology, 26 Oxford Street, Cambridge MA, 02138, kacar@fas.harvard.edu, ²Harvard University, Earth and Planetary Sciences, 26 Oxford Street, Cambridge, MA, 02138, ³Yale University, Ecology and Evolutionary Biology, New Haven, CT 06511 ⁴Colby College, Chemistry, Waterville, ME, 04901

Introduction: Extant organisms (including many in anoxygenic conditions) are from lineages that have likely gone through O₂-rich evolutionary bottlenecks at some point over the last ~500 million years, or have adapted to ephemeral O₂-rich conditions and associated organisms in their microbial consortia. Ribulose 1,5-bisphosphate (RuBP) carboxylase/oxygenase (RuBisCO) catalyses a key reaction by which inorganic carbon is converted into organic carbon. We currently have very limited information regarding the ancient phenotype of RuBisCO; mapping the modern phenotype onto past organisms plays a key role in the biogeochemical interpretation of Precambrian carbon isotope fractionation signals even though the temporal, environmental and organismal limitations of applying this assumption are completely unknown. Here we present the results from the first phase of our study, in which we have reconstructed a phylogenetic tree of the RuBisCO protein family and comparatively analyzed inferred node sequences with extant organismal sequences to extract functional and structural characterization insights into the biochemical role of the ancient RuBisCO sequences.