

Empirically constraining the role of O₂ in the end-Proterozoic diversification of eukaryotes

DANIEL BRADY MILLS¹, RACHEL L. SIMISTER²,
TAYLOR R. SEHEIN³, STEVEN J. HALLAM⁴, ERIK A.
SPERLING⁵ AND SEAN A. CROWE²

¹Ludwig Maximilian University of Munich

²University of British Columbia

³Smith College

⁴The University of British Columbia

⁵Stanford University

Presenting Author: daniel.brady.mills@gmail.com

Microbial eukaryote body fossils, organic biomarker data, and molecular clock analyses all suggest an increase in crown-eukaryote diversity ca. 800 million years ago (Ma), towards the end of the Proterozoic Eon. Certain geochemical redox proxies have also been used to argue for increasing atmospheric oxygen (pO_2) levels at this time, suggesting a positive correlation between O₂ availability and eukaryote diversity. To test this relationship, we collected time-resolved geochemical parameter and sequence information from a model marine oxygen minimum zone spanning a range of dissolved O₂ levels and redox states. Our observations constrain the control of dissolved O₂ concentration on microbial eukaryote diversity, specifically taxonomic richness (that is, alpha diversity), phylogenetic diversity, and evenness. Overall, our results suggest that pO_2 would have only significantly restricted microbial eukaryote diversity in the Proterozoic if it consistently remained below 1% of present atmospheric levels (PAL). Indeed, if pO_2 regularly exceeded 1% PAL before 800 Ma, then the mid-Proterozoic redox landscape already supported the maximum levels of microbial eukaryote diversity observed today and the end-Proterozoic diversification of eukaryotes was necessarily driven by other environmental or internal factors.