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Oxygen and Early Eukaryote Ecosystems

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It is often assumed that dominantly anoxic oceans during the Proterozoic would have challenged the emergence and diversification of eukaryotes. However, modern anoxic environments host diverse and abundant microbial eukaryotes, many able to thrive via by partnerships with endo- and ectosymbiotic prokaryotes. We propose that at least some, and perhaps many, early eukaryotes were adapted to anoxic or sulfidic settings. This might explain the mismatch between the record of eukaryotic body fossils (>1.6 Ga) and the record of sterane biomarkers (<0.75 Ga), given that eukaryotes in anoxic habitats do not make sterols. An anoxic habitat also makes sense for some long-ranging and widespread taxa that disappear in the late Neoproterozoic around the time oxic habitats become more widespread. To test this hypothesis, we counted species richness and abundance in fossiliferous shale samples from the <775–729 Ma Chuar Group, Grand Canyon, Arizona, that were deposited under oxic or anoxic bottom waters. Preliminary results indicate comparable species richness but different patterns of relative abundance in anoxic vs. oxic samples. Filaments and the colonial form *Synsphaeridium* sp. tended to be more common in oxic samples, as would be expected if they were the remains of benthic cyanobacteria or eukaryotic algae. In contrast, the species *Squamosphaera colonialica,* and *Kaibabia gemmulella*, tended to be more abundant in anoxic samples, while the long-ranging species *Valeria lophostriata* was only found in anoxic samples. These patterns do not correlate with preservational quality or inferred water depth, but are consistent with the hypothesis that anoxic habitats in the Chuar Group supported eukaryotic life.