

Tracking photosynthetic organisms in the Proterozoic fossil record

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The Proterozoic is marked by deep changes of the global Earth system, partly linked with the evolution of Life. During the development and diversification of Life, the emergence of photosynthetic eukaryotes is a major evolutionary step, leading to the complexification of trophic networks and making possible the later colonization of land by plants. However, the successive steps of development and spread of eukaryotic photosynthesis are still poorly defined. Unfortunately, the Proterozoic sedimentary and fossil records being very discontinuous, there is little information to characterize the environmental changes and the major stages in the evolution of living organisms during this period. In addition to being fragmentary, the Proterozoic fossil record is also difficult to interpret due to the often simple morphology of the fossils. It becomes essential to seek new sources of information, in particular through the analysis of geochemical and biological markers, to identify more photosynthetic organisms in the early rock record to better constrain the evolution of eukaryotic photosynthesis through time and its influence on evolution of Life on Earth.

Geoporphyrins are mostly the result of the degradation of chlorophylls during diagenesis and are thermally stable over hundreds of millions of years, thus offering a powerful tool for the detection of photosynthesis. The presence of Ni-tetrapyrrole moieties bound to kerogen and deriving from chlorophyll was recently evidenced in a eukaryotic fossil from the Mbuji-Mayi Supergroup (DR Congo); *Arctacellularia tetragonala*, by using a combination of Synchrotron radiation based X-ray micro- and nano-fluorescence (SR- μ XRF, SR-nanoXRF) and absorption spectroscopy (SR- μ XANES).

Here, we use the same approach on fossils from the Mbuji-Mayi Supergroup (~1 Ga, DR Congo) but also in the Shaler Supergroup (~1 Ga, Canada) and the Atar/El Mreiti Group (~1.1 Ga, Mauritania), three basins with different burial thermal history, different environmental and diagenetic conditions. By identifying the presence of chlorophyll remnants in four other taxa, we show that this methodology allows the direct association