# Micropaleontology of the lower Mesoproterozoic Roper Group, Australia, and implications for early eukaryotic evolution

E. J. JAVAUX[1] AND A. H. KNOLL[2]

[1]PPP, Department of Geology, University of Liege, 4000 Liège, Belgium (*correspondence: ej.javaux@ulg.ac.be)
[2]Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, Massachusetts 02138, USA

Well-preserved abundant microfossils occur through more than 1000 m of siliciclastic rocks of the 1.5-14 Ga Roper Group, Northern Territory, Australia (Javaux et al., 2001; Javaux & Knoll, in press). Mo abundance and isotope values, and iron-speciation chemistry indicate that surface waters in the Roper seaway were oxic and subsurface waters were anoxic and ferruginous, and at times euxinic (Shen et al., 2003; Planavsky et al., 2011; Arnold et al., 2004; Kendall et al., 2009). The Roper assemblage includes 32 taxa, 6 interpreted unambiguously as eukaryotes, 8 as possible eukaryotes, 6 as possible or probable cyanobacteria, and 12 *Incertae sedis*. Taxonomic richness is highest in inshore facies, and populations interpreted as unambiguous or probable eukaryotes occur most abundantly in coastal and proximal shelf shales. Phylogenetic placement within the Eukarya is difficult, and molecular clock estimates suggest that preserved microfossils may belong to stem group eukaryotes or stem lineages within major clades of the eukaryotic crown group. Despite this, Roper fossils provide direct or inferential evidence for many basic and important features of eukaryotic biology, including a dynamic cytoskeleton and membrane system that enabled cells to change shape, life cycles that include resting cysts coated by decay-resistant biopolymers, reproduction by budding and binary division, osmotrophy, and simple multicellularity.

Roper eukaryotes certainly played a role in completing the marine carbon cycle, as phagotrophs and osmotrophs, possibly in anoxic as well as oxic environments. However, diversification of eukaryotic primary producers might have been limited by fixed nitrogen availability (Anbar and Knoll, 2002; Reinhard et al., 2013), especially in oxic waters above sulfidic water masses (Boyle et al., 2013).

Mesoproterozoic oceans supported diverse prokaryotic and eukaryotic microbial communities. The diversity and ecological importance of these early protists, however, were much lower than in later Neoproterozoic and Phanerozoic ecosystems, a function, at least in part, of ecological constraints involving food web complexity and constraints imposed by marine redox profiles.