

Possible high diversification of eukaryotic algae in Mesoproterozoic

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As the molecular fossils of eukaryota, though steranes had been identified in Paleoproterozoic or even late Archean sediments, the scarce body fossils were still against the existence of numerous eukaryotic algae [1]. Meanwhile, in some Mesoproterozoic sediments, steranes were in quite low level or even absence. Currently recognized Mesoproterozoic oceanic environment was also seemingly not conducive to the extensive development of eukaryotes [2]. Thus, some scientists considered that eukaryotic algae were still in limited diversification in Mesoproterozoic or older ocean [3].

However, our recently research in the cores of Xiamaling Formation (1.38 Ga) in North China Craton revealed a possible high diversification of eukaryotic algae were already existed in Mesoproterozoic. We used the pure water in drilling to avoid possible contamination. The final results of biomarkers expressed characteristic distribution that was in perfect consistent with the interactive sedimentary layers. This proved that the biomarkers that we identified should be from the raw sediments. In the lower and upper segments of Xiamaling profile, a series of red algae-related biomarkers (C₂₇ steranes), green algae-related biomarkers (C₂₉ steranes), and dinoflagellate-related biomarkers (dinosterane and 4-methyl-24-ethylcholestane) were identified. Meanwhile, some steranes with unclear biological origins, including C₂₈ steranes, 4,23,24-trimethyl cholestane, 24-norcholestanes and triaromatic dinosteranes were also in relative abundance. However, in the middle segment of Xiamaling profile, these eukaryotic algae-related biomarkers were in quite low levels or even absence, insteading with various and abundant prokaryotes-related biomarkers, such as 2-methyl hopane, 3-methyl hopane, C₂₆~C₃₅ hopanes and rearranged hopanes. The precence-absence-presence cycles of eukaryotic algae in Xiamaling profile means that sporadic samples with trace-level steranes could not represent the missing of eukaryotic algae in whole Mesoproterozoic era, but the reflection of microbial community variation in regional ocean.

[1] Schopf, *et al* (2006) *Phil. Trans. R. Soc. B* **361**, 869-885. [2] Planavsky, *et al* (2011) *Nature* **477**, 448-451. [3] Parfrey, *et al* (2011) *PNAS* **108**, 13624-13629.