

Lipid biomarkers record the microbial community and metabolic pathways in Mesoproterozoic ocean

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A large number of molecular fossils were recognized in Xiamaling (XML) Formation in North China Craton. The interactive deposited low mature organic-rich shales, cherts and fine sandy mudstones constitute the primary sedimentary features of this 1.38-Ga-years-old stratum. In consistent with the interactive sedimentary layers, the molecular fossils also described an exquisite figure of XML ocean. Abundant C₂₆~C₃₀ steranes and rearranged steranes, 24-norcholestane, 4-methyl-24-ethyl-cholestane, 24-n-propyl-cholestane were appeared in the lower segment (X₂) and upper segment (X₄) of XML profile, indicating a high degree diversity and differentiation of eukaryote. The ancestors of dinoflagellate and red algae maybe already appeared in Mesoproterozoic ocean. Highly stratified paleoenvironment could be reflected in the middle segment (X₃) of XML profile. Highest productivity during XML was in the lower part of X₃ (X₃¹) with 40 m interactive deposition of cherts and paper-sheet black shales. Scarce eukaryotic molecular fossils and abundant prokaryotic molecular fossils, such as 2-methyl hopane, 3-methyl hopane, C₂₆~C₃₅ hopanes and rearranged hopanes, mean a prokaryotic community with vigorous bacteria and restricted algae in X₃¹. Enter into the middle part of X₃ (X₃²), eukaryotic molecular fossils were appeared and kept in low levels until X₄. However, in the upper part of X₃ (X₃³), both prokaryotic and eukaryotic molecular fossils were scarce in the green fine sandy mudstone, while the 2,3,6-TMAI (trimethyl aryl isoprenoids) from green sulfur bacteria were appeared and kept in high levels, indicating a possible euxinic ocean in X₃³.

The various and frequently alternating of molecular fossils in XML profile illustrated a corresponding change in the Mesoproterozoic ocean chemistry and microbial community. The Mesoproterozoic ocean might be not the bacterial dominated euxinic ocean^[1,2], but a dynamic ocean with complex microbial ecosystems and metabolic pathways at different evolutionary stages.

[1] Brocks, *et al* (2005) *Nature* **437**, 866-870. [2] Martin, *et al* (2012) *Precam Res* **196-197**, 113-127.