The prokaryote contributed source rocks in Mesoproterozoic OMZ

X M WANG[1], S C ZHANG[1*], H J WANG[1], D E CANFIELD[2]

[1]Key Laboratory of Petroleum Geochemistry, RIPED, CNPC, 100083, Beijing, China

[2]Institute of Biology and Nordic Center for Earth Evolution, University of Southern Denmark, 5230 Odense M, Denmark

(sczhang@petrochina.com.cn)

The Mesoproterozoic Eon (1600 to 1000 million years ago, Ma) is emerging as a key interval in Earth history, with a unique geochemical history that might have influenced the course of biological evolution on Earth, thus shales with high total organic carbon (TOC) formed.

The high-TOC shales are enriched in the redox-sensitive elements molybdenum (Mo) and uranium (U), but are either depleted or unenriched in vanadium (V). Thus, an oxygen minimum zones (OMZs) where anoxic waters overlay sediments was deduced. And the chemical environment of the Xiamaling Formation is further constrained by the abundance of 2,3,6-trimethylarylisoprenoids (2,3,6-TMAI).

The concentration of terpanes, including hopanes, rearranged hopane, 2-methylhopanoids (2-MeH) and 3-methylhopanoids (3-MeH) are all high in the whole OMZ samples. So absolutely dominated prokaryotic biomarkers in this high TOC sediments confirmed the prokaryote contribution. The disappear of eukaryotes suggests the occurrence of a catastrophic transition or environmental perturbation for the eukaryotic biomass in a Mesoproterozoic OMZ setting, which provides a favourable environment for the prosperity of different prokaryotic organisms.

So these trace elements and biomarkers could provide intriguing glimpses into the biological and ecological patterns in the Mesoproterozoic Ocean, and hints derived from biomarkers in the organic-rich Xiamaling sediments could display microbial communities in an old OMZ set.