

NOVEL STERANE BIOMARKERS SOURCED FROM SPONGES SUPPORTS THE EVIDENCE FOR NEOPROTEROZOIC ANIMALS

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Lipid biomarker assemblages suggest that Mesoproterozoic (1000 Ma and older) marine communities were dominated by bacteria as revealed by a dearth of syngenetic sterane biomarkers relative to hopanes in both rock bitumens and kerogens. The ecological expansion of marine eukaryotic phytoplankton is conservatively first recorded by steranes in lipid biomarker assemblages from 740-800 Ma sedimentary strata (Brocks et al., 2015), which were deposited prior to the onset of the Sturtian glaciation event. Sterane carbon number abundance patterns within the C₂₇ to C₃₀ range can constrain the taxonomic affinity of the major eukaryotic source organisms, such as green versus red algal clades, and have captured early evidence of Neoproterozoic animal life from unusual C₂₈ and C₃₀ sponge-derived steranes (Love et al., 2009; Brocks et al., 2015).

We have used multiple reaction monitoring (MRM)-GCMS of rock extracts and kerogen-bound products from a suite of carefully selected and thermally well-preserved Neoproterozoic sedimentary rocks and oils from Eastern Siberia, India, Oman, Sweden and USA to characterize the diverse and abundant polycyclic biomarker alkane assemblages. Utilizing analytical methodology and self-consistency checks on ancient rocks that largely eliminate contamination from younger hydrocarbons (see French et al., 2015), including analysis of the kerogen-bound biomarker pool using hydrogen pyrolysis (HyPy), we have successfully resolved a variety of C₃₀ sterane compounds. These include C₃₀ sterane series not reported before in the literature as well as the diagenetic breakdown products of naturally occurring sterols produced exclusively by extant demosponges which co-occur with the established 24-isopropylcholestane sponge biomarkers in rocks from South Oman (Love et al., 2009).

We have confirmed the structural identification of our new ancient sterane series by co-elution of steranes produced from the reductive conversion of distinctive sponge sterols using HyPy. Our findings support the notion that sponges had evolved and were abundant in productive marine shelf settings during the late Neoproterozoic, consistent with the latest molecular clock predictions of animal divergence long before the Cambrian explosion. Our overall biomarker findings provide a new perspective on Neoproterozoic eukaryotic evolution, diversification and ecological expansion.

References

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