^{187}Re-^{187}Os geochronology and tracing in sedimentary systems — Applications and limitations of the method

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The ^{187}Re-^{187}Os isotope system is now widely applied in Earth Science, both as a geochronometer and process tracer. High-yield, low-blank chemical separation coupled with precise isotopic analysis of picogram (or femtomolar) quantities of Os is now routine. The geochemical character of Re and Os (chalcophile, siderophile, 'organophile') allows access, with a geochronometer and process tracer, to geochemical pathways not accessible with other isotopic methods. In the sedimentary realm, Re-Os isotopes provide direct age control for shales deposited under suboxic to anoxic conditions – common hydrocarbon source rocks such as black shales. Shales from late Archean to Cretaceous age have been successfully dated using this method in several laboratories, allowing precise, absolute time pins to be placed on hydrocarbon source rocks in basins where biostratigraphic control may be absent or weak, including lacustrine basins. Limitations are also being discovered, including the relative ease of disturbance by post-depositional fluid flow, together with the limited range of Re/Os for some shales, the cause of which remains poorly constrained. Variations in initial ^{187}Os/^{188}Os within the sampled shale interval also limit the method, and in some cases these variations are extermely large, such as the major changes in oceanic Os sources documented during Cretaceous OAEs. Notwithstanding these limitations, Re-Os geochronology adds a new dimension to age control in sedimentary basins, and in some cases precise Re-Os ages are the first reliable ages in thick sequences (>5km) of strata with depositional limits constrained only to a period of hundreds of Myr.

Re and Os occur in most crude oils, together with other redox sensitive metals like Mo, Ni and V. In most crude oils, >90% of Re and Os are present in asphaltene, with high Re and Os contents (up to 250 and 2ppb, respectively). ^{187}Os/^{188}Os measured in oils today correlates positively with source rock age, therefore having significant utility for oil tracing, especially in basins with multiple source rocks of different ages. Migrated hydrocarbons have potential to yield Re-Os oil migration ages, but the method requires further systematic study using both experimental and case study approaches, for full application to petroleum systems.

Spatial patterns in sediment microbial diversity around Gulf of Mexico brine lakes

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Brine lakes along the seafloor are formed when warm salty fluids migrate upward through fault networks and accumulate in depressions on the seafloor. These brines contain three to seven times more salt than seawater and are enriched in energy-rich substrates and nutrients. Sediment samples from several brine lakes along the deep slope of the Gulf of Mexico were collected during an oceanographic expedition on board of the R/V Atlantis on May 2006. Sediment samples were collected at different habitats around the AC601 brine lake, with the objective of characterizing spatial patterns in microbial diversity within a single lake. Geochemical and microbial activity analyses, as well as, 16S rRNA gene-based genetic characterization were carried out. Results show that these deep-sea brine fluids are enriched in DOC (856 to 3812 μM), NH_4^+ (219 to 3957 μM), and CH_4 (178.3 to 2094 μM). At AC601 sites, sulfate reduction (SR) rates were higher in the edge and inner edge of the lake, while anaerobic oxidation of methane (AOM) rates were relatively low, being higher at the outside and edge samples. Rates of methanogenesis were higher at the edge and inner edge samples. Molecular analyses show high bacterial diversity and community richness all around the AC601 brine lake, being higher at the bottom sample. Sequences related to Planctomycetes, Bacteroidetes, and *Gamma-* and *Delta-proteobacteria,* were present at all sites. Sequences related to *Betaproteobacteria* were only identified at the bottom sample. Archaeal diversity was higher at the bottom sample; however, the community richness was higher at the outside sample. An average of 21% of the clones screened were related to methanogens. Work in progress includes the molecular characterization of the microbial communities from other brine lakes (AT340 and MC853) as well as the quantification of functional genes, such as, the ammonia monooxygenase (*amoA*) gene, methyl coenzyme-M reductase (*mcrA*) gene**,** and the dissimilatory sulfite reductase (*dsrAB*) gene.