

Factors controlling elemental fractionation in laser ablation ICP-MS zircon geochronology

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Fractionation of elements during laser ablation (LA) is a significant source of error in quantitative and isotope ratio analysis by ICP-MS. It has been demonstrated that phase separation and formation of particles of variable size and composition are the primary cause of laser-induced elemental fractionation [1], and that the element decoupling can be further enhanced by variable aerosol transport and processes in the ICP [2]. Interaction of laser radiation with zircon (ZrSiO₄) typically results in its thermal breakdown to ZrO₂ and SiO₂ and formation of aerosol particles with different composition, size and transport properties [3]. As a result of the preferential partitioning of U+Th and Pb into ZrO₂ and SiO₂ phases, respectively, the decomposition of zircon by transfer of laser heat can efficiently fractionate these geochronologically important trace elements, resulting in erroneous U-Th-Pb ages obtained by LA-ICP-MS dating.

Previous studies have related the laser-induced decoupling of U+Th from Pb in zircon to different element volatilisation temperatures [2], chemical composition of the zircon matrix [4] and radiation damage accumulated since the last closure for annealing in zircon [5]. Recently obtained laser ablation ICP-MS data for a suite of well characterized zircon samples with range of composition and accumulated radiation damage suggest that these factors alone cannot explain the observed variations in the rate of laser-induced elemental fractionation; they may, however, affect the kinetics of the phase separation during the thermal breakdown of zircon. Additional parameters that will be evaluated for effects on laser-induced fractionation include the composition of ambient gas during the ablation and transport properties of aerosol particles formed by laser ablation of zircon.

[1] Kuhn & Günther (2003) *Anal Chem* **75**, 747-753. [2] Guillong & Günther (2002) *JAAS* **17**, 831-837. [3] Kosler *et al.* (2005) *JAAS* **20**, 402-409. [4] Black *et al.* (2004) *Chem Geol* **205**, 115-140. [5] Allen & Campbell (2012) *Chem Geol* **332-333**, 157-165. (* Funding received from Czech Science Foundation - project number P210/12/2114).

Metagenomic insights into the response of indigenous microbial communities in beach sands to the Deepwater Horizon oil spill

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Biodegradation mediated by indigenous microbial communities is the ultimate fate of the majority of hydrocarbons that enter the marine environment. A large amount of oil from the Deepwater Horizon oil spill was transported to and subsequently buried in Gulf of Mexico beaches. The objective of this research is to characterize the *in situ* response of microbial communities in parallel with the fate and chemical changes in oil hydrocarbons. Our time series database encompasses >500 sediment and water samples collected from Pensacola Beach, FL, USA, from 2010 to 2012. Illumina MiSeq and HiSeq platforms were used to obtain an average of 10000 SSU rRNA gene amplicon sequences and 35 million (100bp) paired-end reads on a subset of these samples. A bloom of bacteria was observed in parallel with oxygen consumption rates and the depletion of the majority of highly degradable oil hydrocarbons during the first 4 months after oil came ashore. SSU rRNA gene amplicon and metagenome analysis revealed an initial sharp drop in community diversity after oiling. Moreover, evidence of succession was detected across the time-series, featuring a marked increase in relative abundance of Alcanivorax spp. during the first two months (up to 40% of the community) followed by enrichment in other members of the Gammaproteobacteria (*Parvularcula*, *Hyphomonas*, *Xanthomonadales*) in subsequent months. By July 2011, community diversity had sharply rebounded, and sequences of taxa associated with oligotrophic conditions, such as the Thaumarchaeota (*Nitrosopumilus*) were detectable, whereas phylotypes associated with the oiling event were undetectable. Finally, we observed that genes for central-metabolism functions were enriched in clean samples, while genes related to peripheral metabolism (e.g. aromatics degradation, nitrogen fixation, phosphorus uptake) were enriched in oiled samples, reflecting the community response to a oil-derived carbon source and nutrient depletion. Overall, multiple lines of independent evidence from a time series describe the microbial response to hydrocarbon discharge as a succession dynamics model driven by nutrient availability and hydrocarbon chemistry.