## Controls on dissolved REE and HFSE in glacial meltwater rivers in southern Iceland

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The chemical composition of river waters in southern Iceland is strongly affected by geological events such as volcanic eruptions (e.g., the Eyjafjallajökull in 2010), due to the input of nanoparticles and colloids from volcanic ashes.

In this study, water samples from twelve rivers and volcanic ashes were sampled twice in 2010, and once in 2011 and 2012 to characterize the geochemistry of glacial melt waters and to investigate the impact of colloids and nanoparticles from volcanic ashes on their chemistry. The REE and other HFSE (e.g., Th, Zr, Nb and Hf) are characterized by low solubilities and high particle-reactivities. In oxic natural waters, therefore, they are not truly dissolved, but typically associated with particulates. In 0.45  $\mu$ m-filtered water samples they are often well-below the lower limit of determi-nation by analytical techniques such as ICPMS. Comparison of the trace element distribution of river particulates (i.e. filter residues) and volcanic ash to that of the respective 0.45µm-filtered glacial meltwater (i.e. sum of truly-dissolved trace elements and those that are bound to colloid-/nano-sized particles <0.45  $\mu$ m) reveals very close similarities.

In 2010, rivers in SW Iceland were affected by the Eyjafjallajökull eruption, while those in the SE were not. La<sub>CN</sub>/Yb<sub>CN</sub> ratios of filter residues in the SW are in a similar range as the Eyjafjallajökull ash (EJ-1: 6.16; EJ-2: 6.58 [1]). River waters, which were sampled in August 2010, show a higher variability in the La<sub>CN</sub>/Yb<sub>CN</sub> ratio and range between 1.46 and 6.96 in the SW and 1.46 and 5.94 in the SE, but the SW rivers, which were sampled 25 days after the Eyjafjallajökull eruptions, show higher La<sub>CN</sub>/Yb<sub>CN</sub> ratios between 7.17 and 9.40. In 2011, an earthquake and a subsequent minor eruption underneath the glacier of Katla volcano caused enhanced glacial flow at the Múlakvísl river, which was accompanied by high trace element concentrations. Its La<sub>CN</sub>/Yb<sub>CN</sub> ratio of 13.5 was significant higher in 2011 than in 2010 (2.64) and 2012 (8.73). Moreover, in 2011, the Zr concentration was 222 ppt, which is several orders of magnitudes higher than in 2010 and in 2012.

These results strongly suggests that natural nanoparticles and colloids of a size <0.45  $\mu$ m control the dissolved REE and HFSE distribution in these rivers.

[1] Sigmarsson et al. (2011), Solid Earth 2, 271-281.

## An improved hot-alkaline DNA extraction method for high cell-lysis efficiency of subseafloor microbial communities

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One of the prerequisite for DNA-based microbial community analysis is the high cell-lysis efficiency –the critical issue has been long ignored or paid very little attention despite of its significance. In fact, using a commonly used DNA extraction kit, ~80% or more of microbial cells in marine sediment are still remained as the intact form (i.e., DNA-stainable cells), indicating that the large DNA fraction of microbial components are initially biased prior to the subsequent molecular analyses.

To address this technical problem, we standardized a new DNA extraction method with alkaline treatment and heating. First, we attempted to destroy all microbial cells in subseafloor sediment samples from different depths by adding 1 M NaOH at 98 °C for 20 minutes, which treatment disrupted more than 98% of the cells in the examined samples. The DNA integrity test showed, however, that such strong alkaline and heat treatment also destroyed DNA molecules into short fragments, which could not be used for PCR-based molecular analyses. Subsequently, we optimized the alkaline and temperature condition to minimize DNA fragmentation with high cell-lysis efficiency: the best condition we standardized resulted in 50-80% of cell disruption with successfully keeping enough DNA integrity for the amplification of complete 16S rRNA gene (i.e., ~1500 bp). Also, the optimized method yielded higher DNA concentrations than those extracted by a conventional kit-based approach in all tested samples. Consequently, using the newly developed hotalkaline method, community structure analysis of the extracted DNA assessed by quantitative real-time PCR and pyrosequencing of 16S rRNA genes showed a clear difference to the result using conventional methods, suggesting the better analytical coverage of subseafloor microbial communities than those by the conventional methods.