Reading the melt inclusion record of pre-eruptive magmatic volatiles

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Olivine-hosted melt inclusions are one of the most important sources of information on pre-eruptive magmatic volatiles. Although the strength of the olivine largely protects inclusions from decompression and degassing during ascent and eruption, post entrapment processes can affect the concentrations of magmatic volatiles in the included melts. We investigated experimentally the potential for post-entrapment modification of H_2O, CO_2, S, F, Cl and $Fe^{3+}/\Sigma Fe$ in olivine-hosted melt inclusions. Our results demonstrate that diffusion re-equilibrates H_2O and $Fe^{3+}/\Sigma Fe$ in a matter of hours at magmatic temperatures. Pressure drops within the inclusions during diffusive loss of H_2O decrease the solubility of CO_2 – and to a lesser extent S – in the silicate melt. This leads to decreased concentrations in the included melt as CO_2 and S are partitioned into vapor bubbles. The concentrations of F and Cl are not affected by either diffusive loss through the host crystal or partitioning into the vapor phase.

Effects of diffusive re-equilibration were assessed by dehydrating natural inclusion-bearing olivines from Cerro Negro volcano, Nicaragua (initial $H_2O = 3.8 \pm 0.3$ wt%) and Mauna Loa volcano, Hawaii (initial $H_2O = 0.375 \pm 0.006$). Experiments were conducted using both a vertical quenching furnace and a Vernadsky heating stage. Run products were analyzed for major elements by electron microprobe and for H_2O, CO_2, S, F, Cl and D/H ratio by SIMS. $Fe^{3+}/\Sigma Fe$ was determined by μ-XANES.

Our results demonstrate that post entrapment modification may significantly impact the concentrations of H_2O and CO_2 in included melts. The consqeuences of this are far less severe for olivine-hosted melt inclusions with initially low H_2O. In this case the external magma loses very little H_2O during degassing so that a H_2O fugacity gradient does not develop to drive diffusive loss. This is supported by a global compilation of melt inclusion data which show that low-H_2O melt inclusions are capable of recording entrapment pressures consistent with the upper mantle, whereas the internal pressures for melt inclusions with initially high H_2O contents never exceed crustal values.

Microorganisms in flooded underground uranium mines of East Germany

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After the German reunification the Wismut GmbH, formerly the 3rd largest U producer of the world, started to remediate the legacies of their U mining activities. As part of the remediation strategy the pit body was flooded to induce reductive processes. Although flooding of the mines Pöhla and Schlema-Alberoda was already finished about ten years ago, the mine water still contains elevated concentrations of toxic metals such as U, As and Ra. Thus, expensive and long-lasting monitoring and waste water treatment is required. Since microorganisms can influence the toxicity of metals directly or indirectly, one alternative approach is to use them for bioremediation. Here, the diversity of the indigenous microbial community of the mine water from Pöhla and Schlema-Alberoda is reported. *Bacteria* as well as *Archaea* were analyzed by state-of-the-art pyrosequencing of the 16S rRNA gene. Mine water samples were either filtrated or harvested from a flow cell. For the filtrated Pöhla mine water, the Pöhla flow cell, the filtrated Schlema mine water, and the Schlema flow cell 485, 697, 325 and 527 sequences, respectively, were divided into 98, 189, 188 and 89 operational taxonomical units (OTUs), respectively, belonging mainly to *Bacteria*. The bacterial sequences from the Pöhla mine were classified into *Proteobacteria*, *Verrumicrobia*, *Bacteriodetes*, *WS3*, *Chloroflexi*, *Firmicutes*, *Acidobacteria*, *SR1*, *Actinobacteria*, *Spirochaetes* and *OD1*. For the Schlema mine *Proteobacteria*, *Acidobacteria*, *WS3*, *Bacteriodetes*, *Chloroflexi*, *SR1*, *Chlorobi*, *TM7* and *Acinobacteria* were found. The dominant bacterial phylum in all samples are the *Proteobacteria*. Higher bacterial diversities were observed in flow cells in comparison with filtrated waters. A dataset of 15786, 17872, 11404, 7780 sequences revealed 639, 643, 769 and 455 OTUs, respectively, mainly for Archaea of the filtrated Pöhla mine water, the Pöhla flow cell, the filtrated Schlema mine water and the Schlema flow cell, respectively. The archaeal sequences of the Pöhla as well as the Schlema mine water belong to the class of *Methanobacteria*, *Thermoprotei*, *Methanomicrobia*, *Thermoplasmata* and *Halobacteria*.