

Crystallization temperatures of carbonate phases at Kennecott, Alaska based on clumped isotope thermometry

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We measured growth temperatures of eight carbonate phases from the Bonanza Cu-(Ag) mine, Kennecott, Alaska, using the clumped isotope paleothermometer. A comparison of these data with independent geologic constraints, including phase equilibria of hydrothermal silicates and sulfides, suggests measured temperatures reflect carbonate growth conditions (Fig. 1). This method provides a means to document the low-temperature histories of ore bodies and to clarify ambiguous paragenetic positions of unmineralized carbonate phases. Clumped isotope measurements are accompanied by $\delta^{18}\text{O}$ measurements, which together with measured temperatures, are used to calculate $\delta^{18}\text{O}_{\text{water}}$ values for the mineralizing fluids; this helps to constrain the fluid source(s) and genetic model for the Kennecott deposits.

Calcite phases that predate Cu deposition grew at low temperatures (43-71°C); carbonate phases associated with copper deposition are much warmer (89-157°C); postmineral calcite phases are again cool (38-59°C). Limestone wallrock adjacent to the orebodies displays the largest temperature range of any subset (79-164°C) and may reflect burial diagenesis, metamorphism, and/or metasomatism. Premineral baroque dolomite, including zebra dolomite, grew at 102-142°C. Calcite veins containing Cu-sulfides grew at 89-157°C. Synmineral dedolomitization formed in the range 98-109°C. Only one calcite sample crystallized within the stability field of djurleite (<93°C), a volumetrically important component of the ore. Calculated compositions for $\delta^{18}\text{O}_{\text{water}}$ support a fluid mixing model to form the Cu deposits, whereby a 0‰ fluid carrying sulfide mixed with a metamorphogenic, Cu-bearing fluid of 5-8‰ derived from the Nikolai Greenstone.

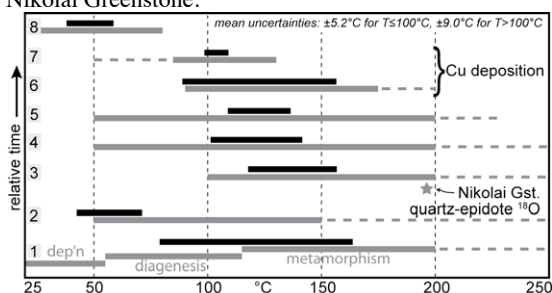


Fig. 1: Independently constrained temperature ranges (grey) and measured temperature ranges from clumped isotope paleothermometry (black) for carbonate phases at Kennecott, Alaska. 1) limestone wallrock, 2) premineral cal. 3) cal. in epidote-quartz veins in Nikolai Greenstone, 4) hydrothermal baroque dol., 5) cal. infilling dol. breccia, 6) Cu-bearing cal. veins, 7) dedolomite selvages, 8) postmineral cal.

Microbial diversity in an arsenic-rich shallow-sea hydrothermal system undergoing phase separation

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Phase separation is a ubiquitous seafloor process in hydrothermal vent systems, yet investigations of how this process affects microbial ecology are rare. We evaluated prokaryotic diversity in arsenic-rich shallow-sea vents off Milos Island (Greece) by comparative analysis of 16S rRNA clone sequences from two vent sites with similar pH and temperature but marked differences in salinity. Clone sequences were also obtained for arsenic functional genes (AFGs) involved in arsenite oxidation (*aioA* -like). Bacteria in the surface sediments (0 to 1.5 cm) at the high salinity site consisted of mainly *Epsilonproteobacteria* (*Arcobacter sp.*), which transitioned to almost exclusively Firmicutes (*Bacillus sp.*) at ~10 cm depth. On the other hand, the low salinity site consisted of Bacteroidetes (Flavobacteria) in the surface and predominantly *Epsilonproteobacteria* (*Arcobacter sp.*) at ~10 cm depth. Archaea in the high salinity surface sediments were dominated by the orders Archaeoglobales and Thermococcales, transitioning to Thermoproteales and Desulfurococcales (*Staphylothermus sp.*) in the deeper sediments. In contrast, the low salinity site was dominated by Thermoplasmatales in the surface and Thermoproteales at depth. The abundance of free and dissolved gases, and other redox couples, were similar at the two sites, suggesting that salinity and/or arsenic concentrations may select for microbial communities that can tolerate these parameters. Many of the archaeal 16S rRNA sequences contained inserts, possibly introns, including members of the Euryarchaeota, something not reported previously. Clones containing *aioA* -like genes affiliated with either *Alpha*- or *Betaproteobacteria*, although most were only distantly related to published representatives. Most clones (93 out of 105) originated from the deeper layer of the low salinity, higher arsenic site, which is also the only sample with overlap in AFG and 16S rRNA gene data, suggesting arsenotrophy as an important metabolism.