

## The potential of high-Mg andesites as sources of economic base metals

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Clinopyroxene- and hornblende-bearing andesites of the Cerro San Lucas suite, the eastern equivalent to regional high-Mg andesite (bajaite) lavas [1] of the central Baja Peninsula, are characterized by LILE enrichment, LREE>HREE fractionation, NMORB-like HFSE and Nb-Ta-Ti depletions [2]. Such geochemical signatures are consistent with melts being derived by partial melting of an adakite and aqueous fluid metasomatized mantle, with the principal control on melt chemistry being the extent of adakite contamination and degree of partial melting [2]. Eruption of Cerro San Lucas lavas (11 to 7.7 Ma; [1]) is temporally related to the initial rifting the Santa Rosalía basin, a proto-rift basin to the present-day Gulf of California, and formation of sediment-hosted, stratiform Cu-Co-Zn mineralization that constitute the Boléo deposit [3]. Because mass balance constraints indicate that hydrothermal leaching of basin fill sedimentary units and basement magmatic rocks cannot produce the required quantity of metals, the possibility that metals were transported from aqueous fluids that exsolved from pre-eruptive Cerro San Lucas magmas is being investigated. In addition, a magmatic metal source is being considered because magmatic fluid transport of ore metals requires the removal of metals from the mantle, which is enhanced if the mantle has been oxidized by slab-derived partial melts or supercritical fluids [4]. The  $f_{O_2}$  conditions of the sub-arc mantle source region for Cerro San Lucas magmas is being constrained using Ti-magnetite/ilmenite geothermometry and oxygen barometry [5].

[1] Calmus *et al.*, (2003) *Lithos* **66**, 77-105. [2] Conly *et al.* (2005) *J Volcanol Geotherm Res* **142**, 303-341. [3] Conly *et al.* (2006) *Miner Deposita* **41**, 127-151. [4] Mungall (2002) *Geology* **30**, 915-918. [5] Lepage (2003) *Computer Geosci* **29**, 673-678.

## Tracing the nature of anaerobic methane oxidizing archaeal subgroup partitioning along geochemical gradients

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The anaerobic oxidation of methane (AOM) in marine sediments is a globally important process estimated to consume 384.2 TG of the greenhouse gas methane per year [1]. At least three anaerobic methane oxidizing archaeal (ANME) groups working alongside sulfate reducing bacteria have been implicated in this process. However, none of these organisms have been isolated in pure culture and the ecological and functional dynamics of AOM remain poorly understood. Cultivation-independent genomic and biochemical analyses of several AOM environments have identified a highly expressed homologue of the enzyme Methyl coenzyme M reductase (Mcr) known to catalyze methane formation in methane producing archaea [2, 3]. Based on these and other findings it is thought that ANME groups are capable of oxidizing methane through a process of reverse methanogenesis.

Although small subunit ribosomal DNA is a good proxy for the identification of ANME groups, it is not sufficiently divergent to easily distinguish between ANME subgroups. *mcr*, on the other hand, is divergent enough to resolve fine scale ANME ecotype distributions and, in addition, serves as a functional marker for AOM.

We have developed a suite of primers for use in SYBR green based quantitative PCR assays with the aim of measuring *mcrA* copy number along geochemical gradients. Subgroup specific primers targeting *mcrA* A (ANME-1A,) B (ANME-1B), CD (ANME-2ABC, D (ANME-2C) and EF (ANME-3) isoforms were designed, optimized and tested on sediment cores collected from seep sites along a northeastern pacific transect. Various geochemical measurements including sulfate and methane pore water concentrations from the same cores will be correlated with ANME ecotype abundance. This assay will enable the determination of parameters governing subgroup partitioning along geochemical gradients and provide a robust quantitative framework for inferring the ecological dynamics of methane oxidizing archaeal communities in a wide variety of settings.

[1] Reeburgh (2007) *Chem. Rev.* **107**, 486-513. [2] Hallam *et al.* (2003) *Appl Environ Microbiol.* **69**, 5483-5491. [3] Kruger *et al.* (2003) *Nature.* **426**, 878-881.