Atmospheric evolution of terrestrial planets constrained by isotopic data: The effects of degassing on Mars

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In order to study the long term evolution of the surface condition of terrestrial planets we need to understand the interactions between inner mechanics and atmospheric history. Here we propose an example of such interaction leading to scenarios for the evolution of the Martian atmosphere we constrain with isotopic ratio data for noble gases.

We model the past state of the Martian atmosphere with a balance between atmospheric loss through escape by non-thermal processes and volatile input by degassing through volcanism. CO_2 is our main subject of study considering it represents the bulk of present and, probably, past atmosphere on Mars. The atmospheric escape model is based on the decreasing Extreme UV flux over the history of Mars and present day escape measurements from the ASPERA instrument. Degassing is estimated from crust production rate models ([1][2][3]) and possible volatile contents of the melted material. It is also confronted to present day observation of the surface of Mars.

Our results show that an eruption rate of 0.01 km^3/y would be needed for the atmospheric CO_2 to be at equilibrium in the present-day situation. We also show that after the early heavy loss of primordial atmosphere during the first billion year, the atmospheric CO_2 pressure variations are relatively small. It is highly unlikely Mars has supported a thick (~1 bar or more) atmosphere during the last few billion years. However periods of higher pressures (like three billion years ago) correspond to the occurrence of fluvial landforms [4]. We also suggest that the present-day Martian atmosphere is composed of a large part of volatiles of volcanic origin and is quite young with possible ages ranging from 1.25 to 1.75 billion years. We finally study the history of water and the evolution of isotopic ratios of C, N and Ar.

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The sulfate-reducing bacterium *Desulfovibrio desulfuricans* ND132 as a model for understanding bacterial mercury methylation

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We propose the use of *Desulfovibrio sp*. ND132 as a model species for understanding the genetics and biochemistry of microbial Hg methylation. ND132 is a dissimilatory sulfate-reducing bacterium (DSRB) that exhibits exceptionally high rates of Hg methylation in culture, but is otherwise a characteristically typical Desulfovibrio strain. The full genome sequence of ND132 will be available soon. ND132 is very similar to other DSRB that are sequenced but do not methylate Hg, allowing comparison for potential methylation genes. Here, we describe the physiological characteristics of the strain, examine its MeHg production capability, and place the strain within the phylogeny of the *Desulfovibrionales* using 16S rRNA. We also examine Hg toxicity and the inducibility of MeHg production amongst the DSRB by comparing ND132 to non-methylating DSRB.

The optimal growth medium for Hg methylation is pyruvate/fumarate, which supports strong respiratory growth without sulfide production. At moderate Hg concentrations (10 ng/ml), and using TiNTA as a reductant, ND132 methylates about 30% of added $HgCl_2$ during batch culture growth on 40 mM pyruvate/fumarate. Under constant culture conditions, MeHg production is an exponential function of Hg concentration, probably reflecting Hg partitioning between aqueous and solid phases. To help understand how Hg is taken up by this organism, we examined the influence of a variety of small thiol-bearing ligands, as well as select amino acids, on methylation by *D. desulfuricans* ND132. All thiol bearing ligands tested affected methylation in similar ways, suggesting that Hg uptake by ND132 is not associated with uptake of a specific amino acid.

To identify enzymes for the methylation activity, a genetic approach is being pursued. Conjugation from *E. coli* donors works well that allows the generation of a transposon library of random ND132 mutants. These mutants will be screened for affects on mercury methylation.