

## The composition of the Archean atmosphere as a tracer of volatile exchange between the mantle, the surface and the outer space

B. MARTY<sup>1</sup>, M. PUJOL<sup>1,2</sup>, R. BURGESS<sup>3</sup>, E. HEBRARD<sup>1</sup>,  
L. ZIMMERMANN<sup>1</sup> AND P. PHILIPPOT<sup>4</sup>

<sup>1</sup>CRPG-CNRS, Université de Lorraine, Vandoeuvre les  
Nancy, France. bmarty@crpg.cnrs-nancy.fr

<sup>2</sup>Present address : Total E&P, Pau, France

<sup>3</sup>Manchester University, UK

<sup>4</sup>IPG Paris, France

The terrestrial atmosphere evolved through time as a result of exchanges of volatile elements with the mantle, the crust, and the outer space. Measurements of noble gases and nitrogen in Archean rocks (barite, hydrothermal quartz, cherts) give insights into the composition of the atmosphere at the time of rock formation. Trapped fluids consist of a mixture of one or several hydrothermal component(s) with an atmospheric end-member, presumably contributed as atmospheric gases dissolved in fresh- or sea-water. The isotopic compositions of Archean neon, argon and krypton appear similar to the present-day ones for radiogenic or fissionogenic isotopes. Compared to extraterrestrial precursors, Archean atmospheric xenon is enriched in its heavy isotopes by 1-2 ‰, and intermediate between chondritic and modern atmospheric [1]. We interpret this difference as resulting from a preferential escape of Xe backwards through time [1,2], due to its increasing photoionization by hard UV light from the young Sun deep into the atmosphere and a more efficient trapping interaction with the primitive organic haze [3]. 3.5 Ga ago, the <sup>40</sup>Ar/<sup>36</sup>Ar ratio was 143±24, which, when integrated into a 3-box (mantle, crust, atmosphere) K-Ar model, is consistent with a significant volume of felsic crust between 30% and 55% of its present-day volume at that time [4]. The partial pressure of atmospheric N<sub>2</sub> was similar to, or lower than, the present-day one, and the Archean N isotopic composition was similar within 2-3‰ to the modern one [5]. These results indicate efficient magnetic shielding of the atmosphere since 3.5 Ga, and, together from estimates of the density of the Archean atmosphere [6], set constraint on the P<sub>CO2</sub> in the Archean atmosphere at <0.7 bar.

[1] M. Pujol *et al.*, *EPSL* **308**, 298 (2011). [2] B. Marty, *EPSL* **313**, 56 (2012). [3] E. Hébrard & B. Marty, AGU Fall meeting (2012). [4] M. Pujol *et al.*, *Nature*, in the press. [5] B. Marty *et al.*, submitted. [6] S.M. Som *et al.*, *Nature* **484**, 359 (2012).

## Ectomycorrhiza-bacterial interactions in weathering

MARUPAKULA S\*, MAHMOOD S AND FINLAY RD

Uppsala BioCenter, Dept Forest Mycology & Pathology,  
Swedish University of Agricultural Sciences, Box 7026,  
Uppsala SE-750 07, Sweden.

(\*srisailam.marupakula@slu.se)

The role of ectomycorrhizal fungi in mobilising nutrients from organic polymers is widely accepted but the function of mycorrhizal fungal mycelia in mobilising and transferring nutrients from mineral substrates to the host trees is less well understood [1]. In addition to increasing the nutrient absorbing surface area of their host plant root systems, the extraradical mycelia of ectomycorrhizal fungi also provides a direct pathway for translocation of photosynthetically derived carbon to microenvironments in the soil. The continuous provision of energy-rich compounds, coupled with the large surface area of the mycelium, suggests that it may constitute an important niche for bacterial growth and colonization, however the role of these microbial interactions in weathering is still poorly understood. It has been shown that different soil horizons harbour different ectomycorrhizal fungi [2] and that the ectomycorrhizal fungi allocate organic acids to mineral substrates. In this study we use high-throughput sequencing to study the distribution of different bacterial and fungal taxa in O, E or B-horizon soil from a podzol collected from Jädraås, Sweden. Bacterial microbiomes from single mycorrhizal root tips colonised by different fungi were also examined to determine whether distinct bacterial communities were associated with particular mycorrhizal fungi.

[1]. Finlay RD, Wallander H, Smits M, Holmström S, van Hees PAW, Lian B, Rosling A. (2009). *Fungal Biology Reviews* 23: 101-106. [2]. Rosling A, Landeweert R, Lindahl BD, Larsson K-H, Kuyper TW, Taylor AFS, Finlay RD. (2003). *New Phytologist* 159: 775-783.