

Methane production and evolution within the crystalline basement

O. WARR^{1*}, E. D. YOUNG², I. E. KOHL², J. L. ASH², T. GIUNTA¹, C. J. BALLENTINE³ & B. SHERWOOD LOLLAR¹

¹Dept of Earth Sciences, Univ. of Toronto, Canada

(*correspondence: oliver.warr@utoronto.ca)

²Dept of Earth, Planetary, and Space Sciences, UCLA

³Department of Earth Sciences, Univ. of Oxford UK

CH₄, along with H₂ and other reduced gases, is produced in significant quantities within the Precambrian crystalline basement [1]. However, the mechanisms, rates and temporal evolution of these deep crustal hydrocarbons are poorly constrained. While bulk isotope measurements ($\delta^{13}\text{C}$, $\delta^2\text{H}$) remain a primary tool, multiple abiogenic and biogenic processes can affect and overprint the original signals, challenging interpretations. New developments in high resolution mass spectrometry have allowed measurement of low abundance doubly-substituted methane species (¹³CH₃D & ¹²CH₂D₂) [2]. Through comparison with abundances predicted by a purely stochastic distribution, the degree of ‘clumping’ can be calculated to provide insight into the processes controlling CH₄ in the deep crust [3].

Here we investigated the geochemistry of gases such as CH₄ and N₂ sampled from the 2.7 Ga crystalline basement in the Sudbury Basin in Canada. Gases sampled from this locality are distinctly different in composition, compared to all other gases described to date in Precambrian Shield systems, whether in Canada, South Africa or Fennoscandia. Typically compositions are dominated by N₂ and He (up to 50 % & 30 %) respectively, with much lower H₂, CH₄ and heavier hydrocarbon concentrations than typically found elsewhere [1].

Like other sites examined to date, there is evidence for mixing between abiogenic (Fischer-Troph-type synthesis) and microbial CH₄, but the microbial end-member may be significantly different than the CO₂ reduction-derived CH₄ typically seen at other sites [1]. Recent meta-proteomic and –transcriptomic work has shown that subsurface metabolic networks may be considerably more varied and complex than previously thought, including both microbially mediated methanogenesis and methanotrophy [3]. CH₄ isotopologue signatures at Sudbury share similar characteristics to samples from Kidd Creek interpreted to result from microbial methane cycling in deep fracture water ecosystems [2]. Measurements of doubly-substituted CH₄ isotopologues enable investigation of microbial methane cycling at this new locality.

[1] Sherwood Lollar et al. (2008) *GCA* **72** 4778-4795. [2] Young et al. (2017) *GCA* **203** 235-264. [3] Lau et al. (2016) *PNAS* **113** 7927-7936.