Probing the Toba super-eruption: Oxygen isotope geochemistry of zoned quartz phenocrysts

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The Toba caldera located in Sumatra (Indonesia) is the source of the largest volcanic eruption in the Quaternary [1]. We present oxygen isotope data for a suite of zoned quartz phenocrysts (n=8) erupted as part of the Young Toba Tuff (YTT), an eruption event of approximately 2800 km^3 some 75 ka ago [1, 2]. Oxygen isotope data has been obtained by SIMS (n=92) in combination with cathodoluminescence (CL) imaging in order to establish the role of shallow level processes such as magmatic fractionation, magma-crust interaction and crystal recycling occurring in the Toba magmatic system. The CL images exhibit defined patterns of magmatic zoning which broadly coincide with fluctuations in $\delta^{18}O$ values in the quartz crystals, allowing correlation of textural and compositional data. Measured $\delta^{18}O_{quartz}$ values range from 6.7 ‰ to 9.4 ‰, independent of position on crystal core or rim. Values for $\delta^{18}O_{magma}$ have been calculated from quartz phenocrysts (assuming $\Delta_{quartz\text{-}magma}$ is 0.7 ‰ at magmatic temperatures). The lowest magma value is 6.0 ‰, apparently reflecting a primitive isotopic signal [3]. The maximum calculated magma value is 8.7 ‰ and the average is 7.2 ‰, indicating multiple sources to the Toba system including a significant crustal component. These new data allow us to unravel the heterogeneous magmatic system at Toba volcano, involving an evolved but dominantly magmatic melt and crustal partial melts reflected in elevated $\delta^{18}O$ crystal zones. Several crystals, however, show gradually lower values towards the rims pointing to either input from a less evolved magma or, more likely, a low-$\delta^{18}O$ contaminant from the shallow volcanic edifice. The crystals therefore record a complex and heterogeneous origin of the YTT magma, comprising an evolved igneous component and several substantial crustal contributions to finally assemble the massive volume of the Toba eruption.

[1] Rose & Chesner (1987) *Geology* **15,** 913-917. [2] Aldiss & Ghazali (1984) *J Geol. Soc. London* **141,** 487-500. [3] Taylor & Sheppard (1986) *Rev. Min.* **16,** 227-271.

Microbial diversity and physiology of Alberta coal seams

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We have begun to map, using 16S pyrosequenicng and traditional enrichment culturing techniques, the microbial diversity and metabolic activities of coal from different Alberta coal zones. Results have implications for optimizing the bioconversion of coal to methane and other products.

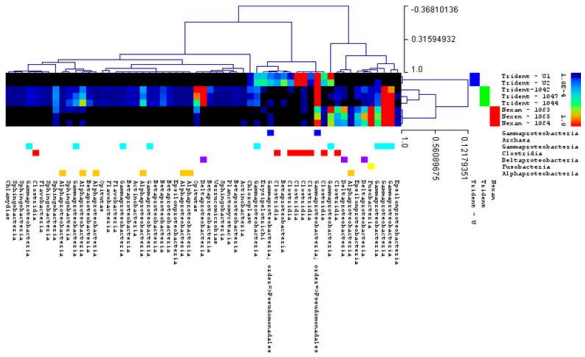

Figure 1: Hierarchical clustering tree (Linear Models for Microarray data significant taxons analysis) of 3 well sites from Mannville coal formation, Alberta.

Culture	μmol CH_4/mL culture
Coal + Tryptone	42.9
Tryptone only	11.7
Coal only	0

Table 1: CH_4 and CO_2 production at 55 days incubation in methanogenic cultures amended with 5 g coal and/or 0.05 g/mL tryptone.

Cluster analysis of microbial DNA sequences shows distinct microbial communities exist in Alberta coal deposits. The geochemical environment (e.g. salinity) likely influences community composition. Anaerobic culturing of the coal with 0.05 g/ml tryptone resulted in significant methane production and sequence reads related to *Methanobacter* increasing up to 30% from less than 1% of the total sequences detected in uncultured coal. GC-MS analysis of culture fluids provides evidence the microbial community uses coal as a carbon substrate in the presence of the nutrient.