Anaerobic fungi at great depth in fractured granite

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Recent findings of ^{13}C-depleted carbonate have revealed that sulphate-dependent anaerobic oxidation of methane (AOM) can, in a manner similar to what has been found in marine sediments, occur in oligotrophic crystalline bedrock fractures, down to depths of more than 700 m [1]. The related bacterial sulphate-reduction (BSR) has been traced by S-isotopes in pyrite [2]. In other deep rock environments, such as oceanic igneous crust, records of fossilised fungi [3] indicate that fungi, together with bacteria and archaea, may constitute a significant part of the biomass in the subsurface. Investigations of fungal communities in fracture waters indicate their presence and large diversity under anaerobic conditions at great depth in crystalline rocks [4]. Direct *in situ* observations of fungal communities on fracture walls and their interplay with microorganisms and interaction with minerals are however lacking from this deep environment.

Here we present observations of fungi hyphae from 740 m depth in isolated oligotrophic granite fracture voids in Sweden. SEM and ToF-SIMS studies reveal that the hyphae are undergoing fossilisation (to clay minerals and Fe-oxide) but that significant amounts of organic compounds are still preserved. Microanalytical data (SIMS) of co-genetic carbonate (δ^{13}C) and pyrite (δ^{34}S) reveal that degradation of organic matter by microorganisms, BSR and AOM have occurred in the local fracture system. It is proposed that microbial mats (partly preserved as microfossils) provided nutrients for the fungi and that sulphate reducing bacteria used organic C in the hyphae (pyrite is present on the hyphae). In similarity with deep basalt habitats [3,5] the hyphae have readily dissolved and penetrated secondary zeolites and calcite in the voids.

[1] Drake et al. (2015), *Nature Comm*. **6**, 7020 [2] Drake et al. (2013) *Geochim Cosmochim Acta* **102**, 143-161 [3] Ivarsson et al. (2015) *PLOS* ONE **10**(10) [4] Sohlberg et al. (2015) *Front. Microbiol*. **6**, 573. [5] Bengtson et al. (2014) *Geobiology* **12**, 489-496.