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## **Functional diversity of microbial communities associated with deep-sea hydrothermal deposits**

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Actively forming deep-sea hydrothermal vent sulphide deposits are rapidly colonized by a diversity of microbes. Many of these thermophilic Bacteria and Archaea obtain their energy from the geochemical gradients resulting from the hydrothermal fluid mixing with seawater. The microbial communities can be in part predicted based on the geochemistry of the fluid and the type of deposit [1, 2]. In particular, we have explored the diversity associated with hydrothermal deposits from samples collected from six different vent fields along the Eastern Lau Spreading Center (ELSC) in the Southwestern Pacific. The ELSC was chosen because it provides large and systematic changes in fluid and rock geochemistry, spreading rate, magmatic/tectonic processes, and proximity to the volcanic arc over its relatively short length of 397 km. The individual vent fields therefore provide excellent natural laboratories for exploring, in depth, the factors that influence the diversity and relationships of microbial communities associated with actively forming deep-sea hydrothermal deposits. Using high throughput sequencing of the diagnostic small subunit rRNA gene, significant differences between the communities emerged. For example, the southern andesite-hosted vent field, with low pH, high CO<sub>2</sub>, high Fe vent fluids was dominated by anaerobic Bacteria and Archaea, while the more northern basalt host vent field deposits were characterized with a diversity of microaerophilic to anaerobic thermophiles. To explore the functional relationships within the microbial communities, we assembled the metagenomes of 10 different samples from these sites. All metagenomes confirmed the importance of sulphur cycling in all vent fields, while some samples in the southern vents were clearly more anaerobic. Additionally, the metagenomes have provided insights into the genomes and metabolic role of several previously uncharacterized lineages within the Archaea.

### *References:*

[1] Flores G et al. (2011) Environ. Micro. 13: 2158-2171.

[2] Flores G et al. (2012) Geobiology 10: 333-346 Geobiology 10: 333-346

