

## **Hydrothermal Vent Protists: The Missing Piece to the Puzzle**

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Identification of the taxonomic and functional diversity of microbes has played a central role in hydrothermal vent research since the early days of their discovery. From investigations into their roles as engines of biogeochemical cycling in the subsurface biosphere to their contributions as symbionts to megafaunal success, vent microbial research has thrived over the last 40 years. While Bacteria and Archaea have enjoyed much of this attention, the contribution of microbial Eukaryotes (protists) to this ecosystem has been largely overlooked. Little is known about the role of protists in the hydrothermal ecosystem including the most basic questions about species ranges and vent endemism. Using high-throughput DNA sequencing we analyzed protist community 18S rRNA genes from 59 Mariana Arc hydrothermally-influenced and background samples to identify protist groups most likely to contain vent endemic species. Protist sequences, grouped into operation taxonomic units (OTUs) at the species level, were binned according to their distribution across vent and non-vent samples. OTUs from vent fluids were found to have a variety of ranges and specificities, with over half of OTUs occurring only in hydrothermally-influenced samples. Vent and non-vent OTUs were dominated by Alveolate lineages but vent OTUs had greater proportions of Rhizaria and unidentified Eukaryote lineages. Vent OTUs were generally classified to shallower taxonomic depth indicating a high degree of novelty in vent endemic populations. Potential roles of vent-endemic protists in carbon flow and ecosystem function, as well as directions for future research will be discussed.