

**MICROBIAL DIVERSITY AND COMMUNITY STRUCTURE
DETERMINATIONS THROUGH ANALYSES OF SSU rRNA GENE
DISTRIBUTIONS AND PHYLOGENY**

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ABSTRACT

The majority of this study focused on the analysis of diversity and community structure through an examination of small-subunit (SSU) rRNA genes from the microbial mat assemblage located at an active, hydrothermal vent system, Loihi Seamount, Hawaii. The habitat studied was Pele's Vents, a deep-sea hydrothermal ecosystem located near the summit of Loihi. Through a restriction fragment length polymorphism (RFLP) distribution analysis of a SSU rDNA clone library generated by the polymerase chain reaction (PCR), it was determined that two operational taxonomic units (OTUs) dominated the bacterial assemblage of the mat community. These two OTUs together accounted for ~73% of the bacterial SSU rDNA clone library examined, with ten OTUs accounting for the remaining ~27%. A technique, analogous to rarefaction, was developed to determine that diversity had been sufficiently described by the clones examined. SSU rDNA fingerprinting of clones belonging to each OTU was conducted to confirm OTU specificity and SSU rDNA identity.

The phylogenetic diversity of the bacterial OTUs discovered at Pele's Vents (abbreviated PVB, for Pele's Vents *Bacteria*) was also described. Two dominant phylotypes were found that included more than a single OTU, and therefore comprised a cluster of phylogenetically related taxa. The most abundant phylotype was the PVB OTU 2 cluster, which was comprised of PVB OTUs 2, 3, 6, and 8. The PVB OTU 2 cluster accounted for ~61% of the bacterial clone library and had a lineage contained in the ϵ -*Proteobacteria* subclass and a *Thiovulum*-like phylogeny. The second dominant

phylotype was the PVB OTU 1 cluster, which consisted of PVB OTUs 1 and 11 and accounted for ~27% of the bacterial clone library. The PVB OTU 1 cluster had a lineage within the γ -*Proteobacteria* subclass and a *Xanthomonas*-like phylogeny. The remaining five PVB OTUs, each determined by a single clone, were represented by a wide variety of phylotypes spanning the domain *Bacteria*.

The phylogenetic diversity of the archaeal OTUs discovered at Pele's Vents (abbreviated PVA, for Pele's Vents *Archaea*) were also described. The archaeal clones were dominated by the PVA OTU 2 cluster (comprised of PVA OTUs 2, 3, and 4), which was phylogenetically contained in the *Crenarchaeota*, whereas PVA OTU 1 was contained in the *Euryarcheota*. Both of these lineages were phylogenetically affiliated with recently discovered cosmopolitan marine archaeoplankton.