

Identifying potential microbial drivers of community succession and organization near deep sea hydrothermal vents

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The diversity and complexity of microbial communities and presence of higher trophic level organisms adapted to these unique environments increases with each new set of observations. Combining microbial ecology with macrofauna observations can help elucidate the ecological drivers of community composition near vents and uncover a basic set of processes that lay the foundation for the colonization of these higher trophic organisms. In this poster, we attempted to use a basic nonparametric approach to evaluate the relationships between microbial communities and the presence of frequently observed macrofauna in order to discern underlying successional patterns. The results describe a few of the significant positive and negative correlations at the chosen study sites. For example, the presence of the facultative aerobe *Klebsiella* sp. is strongly positively correlated with three deep sea coral genera *Caryophyllia*, *Desmophyllum* and *Madrepora*. On the other hand, a strong negative correlation exists between the microbial mat grazing scale worms in the genus *Branchinotogluma* and the presence of *Thiomicrospira* species. This is not surprising, as *Thiomicrospira* reduces oxygen and increases sulfuric acid concentrations in seawater. We propose that defining these significant correlations can provide more insight into the processes of ecological and physiological adaptation to extreme environments that are shared across similar taxa. Further research using this approach and more comprehensive data sets may begin to reveal how microbial communities at hydrothermal vents lay the groundwork for macrofauna community succession in otherwise inhospitable marine environments.