

Mantle to microbe to mollusc and more: The role of chemosynthetic symbioses in matter and energy flux in chemosynthetic ecosystems

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Since the discovery of animal-microbial symbioses, numerous studies have focused on the physiological and biochemical adaptations that enable animal hosts to harbor and support billions of chemoautotrophic bacterial symbionts. Many studies have also focused on the symbionts' biochemistry, to better understand their metabolic capacity. We have learned much about how these partners each contribute to supporting net chemoautotrophy. However, there is a paucity of data on the metabolic rates of many species, and what factor(s) govern their productivity. The technical challenges associated with studying live vent symbioses (whether in situ or ex situ) has hindered making "environmentally relevant" rate measurements, and our understanding of how these associations respond to environmental perturbations. Many of these symbioses are considered foundation species, yet we remain woefully unaware of how their metabolic activity might further influence the ecology (and evolution) of associated microflora and fauna. Our lab has focuses on addressing such questions by conducting "omics-informed" high-pressure experiments to measure metabolic activity (including carbon, sulfur and nitrogen metabolism) among a variety of associations. We have developed tools to study patterns of host and symbiont gene expression in different microhabitats, as well as tools to make in situ geo-referenced geochemical measurements around these associations. The resulting data has re-shaped our thinking about these associations, the nature and extent of their geochemical transformations, and, ultimately, their role in shaping vent ecosystems. Here we present our recent and ongoing research, and our latest ideas about how these symbioses govern matter/energy flux throughout the vent ecosystem.