



How does the community structure of Sulfate Reducing Bacteria (SRB) shift along the gradient of methane fluxes at Hydrate-Ridge (Cascadia Margin, Oregon, USA)?

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A major effort for microbial ecologists is to link biological community diversity of a habitat with the environmental factors that persist in that habitat. An important first step towards this end is to develop robust methods to assess shifts in community structure of target organisms, such as Sulfate Reducing Bacteria (SRB) at methane seep systems. Hydrate Ridge (Cascadia margin off the coast of Oregon, USA) is characterized by methane venting, high sulfide fluxes caused by some of the highest anaerobic methane oxidation rates found in the marine realm, and the presence of sulfide-reliant faunal communities such as *Calyptogena* clams, *Acharax* bivalves, and *Beggiatoa* bacterial mats. Given the strong geochemical gradients observed spatially across Hydrate Ridge, an open question remains: do SRB community patterns in local microenvironments reflect the levels at which methane and sulfate fluxes shape this ecosystem? Shifts in the SRB community would be investigated by employing fingerprinting methods that are high-throughput and that target a key metabolic gene responsible for the terminal step in sulfate reduction, the dissimilatory (bi)sulfite reductase (*dsrAB*). The linking of patterns of community shifts with their contextual environmental parameters will then bring us closer to the important goal of better understanding the microbial response to strong geochemical gradients.