



Effects of methane fluxes on the structure of bacterial communities in cold seep sediments

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To better understand how bacterial communities are structured in cold seep sediments with different methane fluxes, we examined the variation of microbial diversity patterns as a function of sediment depth in different habitats at Hydrate Ridge, Cascadia convergent margin. This area is characterised by three typical habitats that consist of mats of filamentous sulfide oxidizing bacteria covering the seafloor surface, and sediments colonized either by *Calyptogena* clams, or by *Acharax* bivalves. Bacterial diversity was determined in cores taken from each habitat by Automated Ribosomal Intergenic Spacer Analysis (ARISA) in 1-cm sediment layers. Geochemical profiles were conjointly measured in each of the cores and multivariate analyses were further used to correlate diversity, geochemistry and spatial distribution. Interestingly, bacterial community structure was significantly different between habitat types and was strongly associated with sediment depth gradients. Moreover, in each core, bacterial community assemblages followed a clear continuum of diversity from surface to deeper sediment layers. Changes in community structures were found to be mostly related to environmental variability associated with methane fluxes and with major biogeochemical reactions occurring in those sediments (e.g., methane oxidation, carbonate precipitation). Furthermore, spatial stratification rather than absolute core depth, significantly contributed to the observed biological variation. These results suggest that methane-related geochemical gradients not only structure macro- and meiofauna as previously observed in the area, but also profoundly shapes the diversity and structure of bacterial communities in extreme environments.