



Are diversity and evolution of bacterial symbioses driven by environmental constraints in deep-sea mytilids ?

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Large mussels of the genus *Bathymodiolus* thrive at hydrothermal vents and cold seeps worldwide thanks to their sulfide- and methane-oxidizing bacterial symbionts. These mussels have been the subject of numerous studies focusing on their adaptation to harsh environmental conditions such as high variability of physico chemical parameters, toxicity of fluids, or distance between suitable habitats. Despite recent evidence showing that smaller mussels like *Idas* are actual representatives of evolutionary intermediates between symbiont-free mussels and deep-sea, symbiont-bearing mussels, very few data is available regarding their symbioses.

Focusing on symbiont diversity and distribution in *Idas* species from cold seeps and sunken woods, our work aims at understanding how mussels deal with the peculiar constraints of these environments, and whether they are different from *Bathymodiolus* species. We discovered an unexpected diversity of 6 bacterial endosymbionts in an *Idas* sp. from cold seeps of the eastern Mediterranean, and mostly sulfide oxidizing bacteria associated with several other *Idas* species from sunken woods of the Pacific ocean. Because of the relatedness between *Idas* species and *Bathymodiolus*, these results shed light on the evolution of symbiosis in deep sea mytilids: during evolutionary time, mussels might have been capable of establishing symbiosis with a variety of environmental bacteria depending on their specific needs, resulting in a highly flexible system.

Besides comparison between species, we also aim at understanding whether symbiont diversity and density vary within a given host species depending on local conditions.

For this, we use Fluorescence *in situ* techniques coupled with 3D image reconstruction and analysis in order to quantify bacteria and compare between specimens exposed to different environmental conditions. Associated with accurate description of the environment using *in situ* tools, these techniques will help to understand the coupling between variable environmental parameters and symbiont dynamics.