

Symbiont-related bacteria colonize plant substrates at hydrothermal vents and cold seeps.

Szafranski KM^{1,2*}, Deschamps P³, Cunha MR⁴, Gaudron SM^{1,5}, Duperron S^{1,2,6}

¹Sorbonne Universités, UPMC Université Paris 06, UMR 7208, Adaptation aux Milieux Extrêmes – Paris, France

²UMR MNHN UPMC CNRS IRD UCBN 7208, Biologie des Organismes Aquatiques et Ecosystèmes, 75005 Paris, France

³UMR8079 Unité d'Ecologie, Systématique et Evolution – CNRS Université Paris-Sud 11, Orsay, France

⁴Departamento de Biologia & CESAM, Universidade de Aveiro, Campus de Santiago, Aveiro, Portugal

⁵Present address: UMR8187 Laboratoire d'Océanologie et de Géosciences, Station marine de Wimereux, Wimereux, France

⁶Institut Universitaire de France, Paris, France

*Correspondence: km.szafranski@gmail.com

Chemosynthetic prokaryotes play a crucial role in energy and carbon cycling in the deep-sea. Using the energy of chemical bonds, they are able to convert simple monocarbon compounds into complex organic ones. That is why symbiotic associations with chemosynthetic bacteria allow some metazoans to thrive at hydrothermal vents and cold seeps in the deep ocean. Understanding processes driving bacterial diversity, colonization and dispersal is thus of prime importance for deep-sea ecologists, whereas symbionts themselves are still not well known. To identify and analyze the diversity and distribution of free-living bacterial colonizers, standardized devices filled with wood cubes or alfalfa grass were deployed at four deep-sea sites: in the Norwegian Sea, Mid-Atlantic Ridge, Gulf of Cadiz and in the eastern Mediterranean. These corresponded to either mud volcanoes, hydrothermal vents or cold seeps. Devices were recovered after different periods of deployment ranging from 2 weeks to 3 years. All samples were analyzed by sequencing of 16S pyrotags. We obtained a detailed characterization of bacterial assemblages colonizing plant-derived substrates over a geographic area spanning the North-East Atlantic and Mediterranean. Composition of bacterial communities is influenced more by the region and duration of deployment, than by substrate type, depth or water temperature. We identified numerous bacteria closely related to known bacterial symbionts associated with metazoans, suggesting their abundance at some sites. Their occurrence patterns were similar to those of their respective hosts and only horizontally-transmitted chemosynthetic symbionts could be detected. The significance of these symbiont-related bacteria in the communities is discussed.