



ANALYSIS OF MICROBIAL DIVERSITY ASSOCIATED WITH HYDROTHERMAL INVERTEBRATES.

M.A. Cambon-Bonavita (1), M. Zbinden (2), N. Le Bris(3), K. Alain(1), A. Pagé (4),
, F. Lesongeur(1), V. Cueff-Gauchard(1), S.K. Juniper(4), F. Gaill(2) et J.
Querellou(1).

1. LM2E, UMR6197 Ifremer Brest, 29280 Plouzané, France
2. UMR 7138 « Systématique, Adaptation et Evolution », UPMC, 75252 Paris cedex05.
3. DRO/EP Ifremer Brest, 29280 Plouzané, France
4. GEOTOP-UQAM-McGill , (UQAM), Montréal (Canada).

Key words : Microbiology, hydrothermal vents, invertebrates, phylogenetic diversity, interactions.

Deep-sea hydrothermal vents are among the most productive ecosystems on Earth. These environments are characterized by a high hydrostatic pressure and by steep chemical and thermal gradients. At the base of the food web are chemosynthetic micro-organisms fixing carbon dioxide into organic carbon using the energy of the reduced chemical species. These microbial primary producers allow the development of diverse secondary microbial populations and the settlement of a rich fauna such as Polychaete (*Alvinellidae*) on the East Pacific Rise and Juan de Fuca Ridge and shrimps (*Rimicaris exoculata*) on Mid Atlantic ridge. *Alvinella* and *Paralvinella spp.* are present in dense colonies, fixed on the active chimney walls. Microorganisms colonize the animal, both the dorsal integument and the tube or cocoon (inner and outer part of it). The role of these microorganisms is still to be defined. Colonization experiment have been done in order to understand the role of this diverse microflora in invertebrates colonies settlement. Influence of the outer environment has

also been investigated. *Rimicaris exoculata* is particularly abundant, forming dense, motile swarms around the chimney walls. These shrimps have an unusually enlarged gill chamber housing epibiotic bacteria, most abundant on shrimps mouthparts, bacteriophage structures and the inner surface of the gill chamber. A trophic role of these bacteria has largely been discussed, since bacteria have also been found in the gut. The aim of our study, was to determine the molecular phylogenetic diversity, based on the 16S rRNA, of the bacterial populations of the shrimp gut in order to bring information about the type of the microorganisms present in the digestive tract of *Rimicaris exoculata* and their eventual role on the diet. This work has been done on the Fe-rich Rainbow site and will be compared in other geochemical conditions in the next cruise.