



Multi-gene characterization of endosymbionts associated with two vesicomyid bivalve species co-occurring at a pockmark in the Gulf of Guinea

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In cold-seep ecosystems, vesicomyid bivalves are one of the most abundant and the most diverse members of the symbiont-bearing fauna. Their distribution is influenced by bathymetry or environmental parameters, even at local scale where several species can co-exist. Symbiosis is the most evident adaptation of these bivalves to the highly sulfidic environment. The aim of this study is to understand the distribution of several species along a cold-seep area through a comparative study of their symbionts. On the REGAB pockmark, along the Congo-Angola margin, two vesicomyid species have been observed, forming dense mono- or dual-specific aggregates. "Calyptogena" regab is distributed all over the sampled-sites while Laubiericoncha chuni is only present at the south-western part of the pockmark, exposed to lower methane concentrations. Three aggregates (two mono-specific and one dual-specific) with different environmental conditions, have been sampled on a NE-SW axis along the pockmark. Sequencing of 16S rRNA of both species, combined to fluorescence in situ hybridization highlight a distinct and unique symbiont 16S rRNA phylotype in each species. Further analysis of six symbiont loci (23S, APS, soxA, dsrb, cbb3, COI) however underlines that several gene copies could co-occur in some individuals, or that recombination exists between symbionts of the two vesicomyid species, especially when they live in multi-specific aggregates. Slight differences in the characteristics of the symbiont associated with each host species could explain distinct host distribution on the pockmark. Further analyses, including the density of symbiont in bacteriocytes, will be realized to complete this study.