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TITLE: Patterns of bacteria-host associations suggest different ecological strategies between two reef building cold-water coral species

AUTHOR: ['Anne-Leïla Meistertzheim', 'Franck Lartaud', 'Sophie Arnaud-Haond', 'Dimitri Kalenitchenko', 'Manon Bessalam', 'Nadine Le Bris', 'Pierre E. Galand']

ABSTRACT:

Cold-water corals (CWC) are main ecosystem engineers of the deep sea, and their reefs constitute hot-spots of biodiversity. However, their ecology remains poorly understood, particularly, the nature of the holobiont formed by corals with their associated bacterial communities. Here, we analyzed *Madrepora oculata* and *Lophelia pertusa* samples, collected from one location in a Mediterranean canyon in two different seasons (autumn and spring), in order to test for species specificity and temporal stability of the host-bacteria associations. The 16S rRNA sequencing revealed host-specific patterns of bacterial communities associated with *L. pertusa* and *M. oculata*, both in terms of community composition and diversity. All analyzed *M. oculata* polyps exhibited temporally and spatially similar bacterial communities dominated by haplotypes homologous to the known cnidarians-associated genus *Endozoicomonas*. In contrast, the bacterial communities associated with *L. pertusa* varied among polyps from the same colony, as well as among distinct colonies and between seasons. While the resilient consortium formed by *M. oculata* and its bacterial community fit the definition of holobiont, the versatility of the *L. pertusa* microbiome suggests that this association is more influenced by the environmental conditions or nutritional status. Our results thus highlight distinct host/microbes association strategies for these two closely related Scleractinians sharing the same habitat, suggesting distinct sensitivity to environmental change.

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