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Habitat differentiation by the cold-water coral Lophelia pertusa (Scleractinia) governs bacterial diversity

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Cold-water coral reef ecosystems represent biodiversity hotspots on continental margins, seamounts and mid-ocean ridge features around the world. Framework-building corals such as the cosmopolitan species *Lophelia pertusa* provide three-dimensionally complex structures for a variety of reef-inhabiting organisms. Following the assumption that such pronounced habitat differentiation not only governs faunal but also microbial diversity on various scales in the reef system, our study aimed at characterizing bacterial colonization patterns of several potential microbial habitats associated with *L. pertusa*. It is an unprecedented approach by clearly accounting for fine-scale differences in both habitat and bacterial community structure. Coral specimens collected from *in situ* (fjord slope, Norway) and *ex situ* (maintenance tank) environments were investigated by ARISA, a high-resolution molecular tool targeting differences in bacterial 16S-ITS sequences. The community analyses revealed significant differences in the bacterial signatures associated with each habitat on and around the coral. Coral skeleton surface, coral mucus, ambient seawater and proximal sediment each exhibited distinct community profiles, which strongly suggests specific habitat-bacteria associations. Both coral-generated habitats, i.e. skeleton surface and mucus, displayed a higher diversity than ambient seawater or sediment. This further supports the finding that *L. pertusa* may harbor specific bacterial communities, and also indicates possible coral-bacteria interactions. In addition, it was found that the bacterial patterns obtained from the field shared no similarity with those from the aquarium, thereby demonstrating the limitations of *ex situ* methodology in microbial diversity studies. Further investigations will provide insights into the phylogenetic community composition and putative ecological roles of *L. pertusa*-associated bacteria.