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Shifts in core bacterial microbiome of gorgonian sea fan related to necrotic-patch disease: Local confinement of pathobiome may facilitate recovery

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Microbiome disruptions triggering disease outbreaks are increasingly threatening corals worldwide. In the Tropical Eastern Pacific, a necrotic-patch disease affecting gorgonian corals (sea fans, *Pacifigorgia* spp.) has been observed in recent years. Massive mortalities of *Pacifigorgia* spp. have also been registered as a consequence of the incidence of this disease. However, the composition of the microbiome and its disease-related disruptions remain unknown in these gorgonian corals. Here, we analysed 16S rRNA gene amplicons from tissues of healthy colonies (n=20) and from symptomatic-asymptomatic tissues of diseased colonies (n=19) of *Pacifigorgia cairnsi* to test for disease-related changes in the bacterial microbiome. We found that potential endosymbionts dominate the core microbiome in healthy colonies. Moreover, healthy tissues differed in community composition and functional profile from those of the symptomatic tissues but did not show differences to asymptomatic tissues of the diseased colonies. Thus, potential endosymbionts in the core microbiome seem to be replaced by a set of more diverse bacteria in the symptomatic tissues. Furthermore, according to a comparative taxonomy-based functional profiling, the taxa that replaces the core microbiome in symptomatic tissues is characterized by heterotrophic, ammonia oxidizer and de-halogenating bacteria, while is depleted in nitrite and sulfate reducers. In conjunction, our results suggest that the bacterial consortium associated with the disease behaves opportunistically. We also conclude that the confinement of the pathobiome to symptomatic tissues may facilitate colony recovery by the potential breakage of affected-necrotic areas, hence contributing to colony resistance to disease and ultimately to the population resilience.

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