Bacterial community composition and potential driving factors in different reef habitats of the Spermonde Archipelago, Indonesia - DTU Orbit (31/12/2018)

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Coastal eutrophication is a key driver of shifts in bacterial communities on coral reefs. With fringing and patch reefs at varying distances from the coast the Spermonde Archipelago in southern Sulawesi, Indonesia offers ideal conditions to study the effects of coastal eutrophication along a spatially defined gradient. The present study investigated bacterial community composition of three coral reef habitats: the water column, sediments, and mucus of the hard coral genus Fungia, along that cross shelf environmental and water quality gradient. The main research questions were: (1) How do water quality and bacterial community composition change along a coastal shelf gradient? (2) Which water quality parameters influence bacterial community composition? (3) Is there a difference in bacterial community composition among the investigated habitats? For this purpose, a range of key water parameters were measured at eight stations in distances from 2 to 55 km from urban Makassar. This was supplemented by sampling of bacterial communities of important microbial habitats using 454 pyrosequencing. Findings revealed that the population center Makassar had a strong effect on the concentrations of Chlorophyll a, suspended particulate matter (SPM), and transparent exopolymer particles (TEP), which were all significantly elevated at the inshore compared the other seven sites. Shifts in the bacterial communities were specific to each sampled habitat. Two OTUs, belonging to the genera Escherichia/Shigella (Gammaproteobacteria) and Ralstonia (Betaproteobacteria), respectively, both dominated the bacterial community composition of the both size fractions of the water column and coral mucus. The sampled reef sediments were more diverse, and no single OTUs was dominant. There was no gradual shift in bacterial classes or OTUs within the sampled habitats. In addition, we observed very distinct communities between the investigated habitats. Our data show strong changes in the bacterial community composition at the inshore site for water column and sediment samples. Alarmingly, there was generally a high prevalence of potentially pathogenic bacteria across the entire gradient.

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