

Bacterial composition and putative functions associated with sponges, sediment and seawater from the Tioman coral reef system, Peninsular Malaysia

ABSTRACT

Microbial communities associated with sponges play important roles in sponge health, defence and nutrient dynamics in coral reef systems. Here, we used a 16S rRNA gene high-throughput sequencing approach in order to test for differences in bacterial composition and predictive functional differences among two LMA (low microbial abundance) (*Stylissa carteri* and *Stylissa massa*), one well-known HMA (high microbial abundance) (*Xestospongia testudinaria*), one putative HMA (*Aaptos lobata*) sponge species, sediment and seawater in a coral reef ecosystem surrounding Tioman Island. Our results showed that biotope (sponge species, sediment and seawater) was a significant predictor of composition and abundance of bacterial communities. Proteobacteria was the dominant phylum in *S. carteri*, seawater, sediment and *A. lobata*, whilst bacterial communities of *S. massa* and *X. testudinaria* were dominated by Cyanobacteria and Chloroflexi, respectively. The predicted metagenome revealed differentially enriched pathways in HMA and LMA sponges. Differentially enriched subcategories in HMA sponges included 'Signaling Molecules and Interaction', 'Carbohydrate Metabolism' and 'Excretory System'. Subcategories enriched in LMA sponges included 'Replication and Repair', 'Energy Metabolism', 'Metabolism of Cofactors and Vitamins' and 'Environmental Adaptation'. Overall, the predicted functional analysis suggests that, although HMA and LMA associated bacterial communities shared core functional features, they use different strategies to defend against pathogens, obtain energy or cope with stress.