

Katarina Damjanovic "Coral--associated bacterial communities in early coral life stages: transmission mode and scope for manipulation"

PhD completion seminar

Seminar/Forum

Friday 8 March 2019 11:00am - 12:00pm

G26 Biosciences 1 Tin Alley



[Map](#)

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Global impacts of climate change and other anthropogenic disturbances are causing massive declines in coral reef ecosystems. As reef-forming scleractinian corals provide essential resources to a large part of the population, their degradation has severe ecological and economic consequences. Efforts are therefore urgently needed to assist coral adaptation to our rapidly changing environment. Within this scope, favourably adjusting coral associated microbial communities could greatly benefit the host, as microbial symbionts are known to play critical roles in coral health. Probiotics have already proven efficient in other organisms such as plants to increase crop yields, or humans to treat various bowel conditions. The successful application of probiotics in corals is contingent on the feasibility to manipulate the coral microbiome. Moreover, understanding how corals acquire and maintain their microbial communities is required to evaluate whether probiotics could be retained across generations.

In this study, I investigated the transmission mode of coral--associated bacteria using 16S rRNA gene metabarcoding and fluorescence in situ hybridisation microscopy to gain insights into the stability and acquisition patterns of the coral prokaryotic microbiome. While patterns of vertical transmission were present in a brooder, no evidence of direct vertical transmission was observed in a broadcast spawner. Here, early coral life stages successively associated with different bacterial communities, probably selected from the environmental pool. However, parental colonies may drive the transfer of certain bacteria by releasing them in the water column upon spawning and through the mucus layer coating the gametes. In addition, I explored the possibility of manipulating coral--associated bacterial communities by exposing coral recruits to whole microbiomes as well as to a cocktail comprising a small number of bacterial pure cultures. In the latter approach, the bacterial strains present in the inoculation consortium were enriched in inoculated recruits of the two coral species used in the experiment. Nevertheless, the two species of coral recruits developed a distinct microbiome despite being reared in the same aquaria and being inoculated with the same cocktail, which highlights a role of host factors in shaping bacterial community composition. These results support proof--of--concept for the feasibility of coral microbiome manipulation as a first step towards developing probiotics for coral reef restoration.