

11TH U.S. SYMPOSIUM ON HARMFUL ALGAE

BACTERIAL CONSORTIA OF CULTURED COOLIA SPECIES EXHIBIT SIMILAR COMMUNITY STRUCTURE AND TEMPORAL OSCILLATIONS

Tropical macrophytes harbor dinoflagellate assemblages that produce complex profiles of bioactive secondary metabolites, some of which can negatively impact both ecosystem and human health. These systems are comprised of thousands of species including bacteria, microalgae, protists, and microfauna all competing for limited space and resources on the surface of the host macrophyte. Close associations between dinoflagellates and bacteria have resulted in interactions between these groups which can have dramatic effects on the physiology and growth of the associated dinoflagellate species. Furthermore, these interactions can promote conservation of functional bacterial consortia associated with specific dinoflagellate taxa.

The dinoflagellate genus *Coolia* is a common constituent of epiphyte communities and a producer of bioactive secondary metabolites speculated to have ecological significance and contribute to ciguatera poisoning. In this study both the free-living (FL) and cell-associated (CA) microbial assemblages of eight cultured strains of *Coolia* including *C. malayensis*, *C. tropicalis*, *C. canariensis*, and *C. palmyrensis* were assessed by 16S rDNA high throughput sequencing. Here we report that some of the most abundant bacterial taxa are highly conserved between strains of *Coolia*, indicating a fundamental bacteria-host relationship. Temporal oscillation in the relative abundances of bacteria revealed both positive and negative relationships between bacterial taxa, indicating potential bacteria-bacteria and/or bacteria-algae interactions. While FL and CA bacterial populations were similar after 24 hours, dramatic changes in the relative abundance of the most abundant taxa were observed in the FL populations between 1 and 12 days while the CA populations remained relatively stable. Together, these results indicate that *Coolia* caters to a specific bacterial microbiome that is tightly coupled to the cell and is likely facilitated by fundamental bacteria-algae interactions.

DEANA ERDNER, GRADUATE STUDENT | UNIVERSITY OF SOUTH ALABAMA AND DAUPHIN ISLAND SEA LAB

Co-Authors:

1,2Alexander K. Leynse, 3Deana L. Erdner, 1,2Alison Robertson

1School of Marine & Environmental Sciences, University of South Alabama, 600 Clinic Drive, Mobile, AL 36688

2Dauphin Island Sea Lab, 101 Bienville Blvd, Dauphin Island, AL 36528

3Marine Sciences Institute, University of Texas at Austin, 750 Channel View Dr, Port Aransas, TX 78373 USA