

Primeira Sessão: Ecologia e Fisiologia – Comunicações orais

Diel rhythms in coral microbial communities

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Features that vary in a diel pattern are ubiquitous among different organisms. Regarding scleractinian corals, physiological traits are known to change between day and night, but knowledge on oscillations in their associated microbiome is incipient. Currently available data is based on a few species of zooxanthellate corals (i.e. corals that host photosynthetic dinoflagellates), majoritarily from the Pacific Ocean. In an effort to expand the current understanding of the diel variation in coral microbiome, we investigated their composition and abundance during a 72-hour period for four species: the zooxanthellate *Mussismilia hispida* and *Madracis decactis*, and the azooxanthellate *Tubastraea coccinea* and *T. tagusensis*. Samples were taken every four hours for three days (each day corresponding to a replicate) in an experiment set in the Alcatrazes Archipelago (Southwestern Atlantic). After Illumina sequencing of 16S rDNA, DADA2 was used for quality control and taxonomy assignment. Data were rarefied and statistical analyses were performed in R and are still in progress. Alpha diversity (Shannon) was significantly different between *M. decactis* and the other species but not between daytime and nighttime within each species. Beta diversity (Bray-Curtis/PERMANOVA) by species followed a similar pattern, with no difference between day and night or by time. Regarding diel variation, calculated by JTKcycle for each species, significant results (ADJ.P<0.01) were found for one ASV (Amplicon Sequence Variant) in *T. tagusensis*, corresponding to *Pseudoalteromonas* sp. (highest abundance at 4 am). A lack of overall diel variation can suggest that these coral hosts have a greater ability to regulate their microbial communities. ASVs with diel rhythmicity were previously found in a zooxanthellate coral and an azooxanthellate anemone but while none of them belonged to *Pseudoalteromonas*, some belonged to the same class (Gammaproteobacteria). Future analyses should refine our current understanding of variations in the coral microbiome.

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