

Title: Temporal dynamics of prokaryotic communities in the marine sponge *Sarcotragus spinosulus*

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Abstract:

In spite of their putative relevance to host functioning, in-depth knowledge of sponge microbiome stability over time is scarce. This study tackles the temporal maintenance of bacterial and archaeal assemblages in the model host *Sarcotragus spinosulus* along three successive years. Prokaryotic communities were profiled by polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) and 454-pyrosequencing of *S. spinosulus*-derived 16S rRNA gene amplicons. Prevailing bacterial phyla were *Actinobacteria*, *Acidobacteria*, *Proteobacteria*, *Poribacteria*, PAUC34f, *Chloroflexi* and *Bacteroidetes*, with *Bacteroidetes*, *Chloroflexi* and *Poribacteria* showing different abundances over the years. At the approximate species level (operational taxonomic units, OTUs, defined at 97% sequence similarity), no major changes in bacterial richness and composition were found through time. Nearly 50% of all detected bacterial symbionts (96 in 205 OTUs) were recovered from all sampling years, whereas a taxonomically equivalent community of less dominant bacteria characterized the transient sponge microbiota. Despite the evidence for temporal symbiont maintenance, an intriguing cumulative degree of variation between individuals was unravelled, with all the surveyed sponge specimens sharing only 27 bacterial OTUs. Archaeal communities were dominated by one single symbiont of the candidate genus *Nitrosopumilus* (*Thaumarchaeota*), known for its ability to aerobically oxidize ammonia to nitrite. Only few bacterial ammonia oxidizers consistently occurred in *S. spinosulus* across the years as documented by PCR-DGGE fingerprinting. In conclusion, prokaryotic symbionts of *S. spinosulus* display a state of dynamic stability shaped by the interplay between the maintenance of dominant players and turnover of less prevalent community members, in time and across host individuals, with no apparent consequences to holobiont functioning.

Keywords: Ammonia oxidizers, host–microbe interactions, microbial diversity, next-generation sequencing, symbiosis

Financial agency: Portuguese Foundation for Science and Technology (FCT)