Corso di Dottorato di Ricerca in Scienze della Vita e dell'Ambiente Ciclo XXXVIII

ToC-ToC - SMART - To Change or not To Change: Assessing Sponge-Microbiome Acclimatization to changing environmental conditions through Reciprocal Transplantation

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INTRODUCTION & AIMS

Porifera represents one of the most successful and functionally relevant taxa colonizing the sea bottoms. The ability of marine sponges to inhabit diverse environmental niches is largely attributed to their symbiotic associations with complex and specialized microbial consortia that enlarge their metabolic arsenal, providing photosynthates, DOM re-cycling products, UV-protectants and chemical defenses.

The aim of this PhD project is to acquire a holistic comprehension of the sponge as an holobiont system, linking hosts ecological traits with microbiome dynamics to better understand the acclimatization potential of Porifera towards changing environmental conditions.

MATERIALS & METHODS

Three sponge species commonly inhabiting Mediterranean hard bottom substrates were selected based on the feasibility for transplants and trophic strategy:

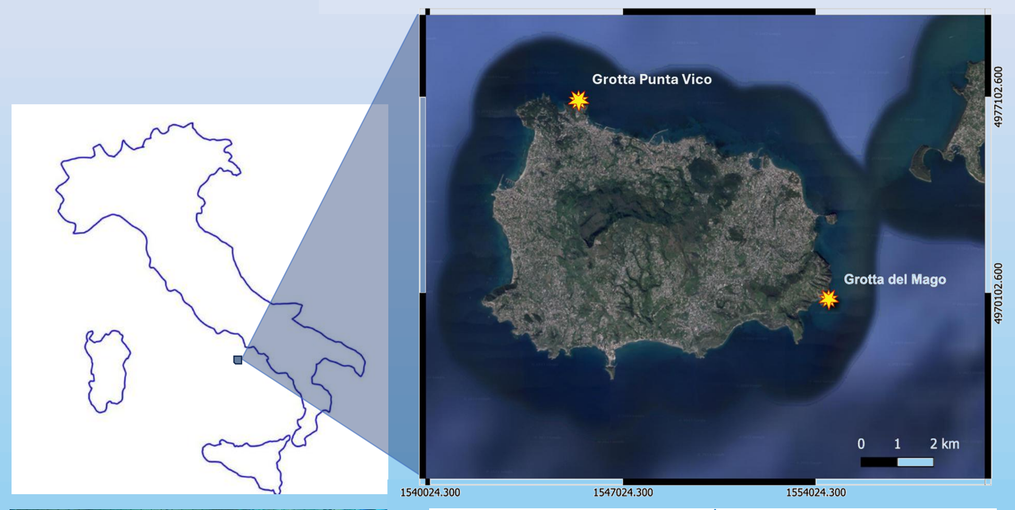
Chondrosia reniformis

Petrosia ficiformis

Chondrilla nucula

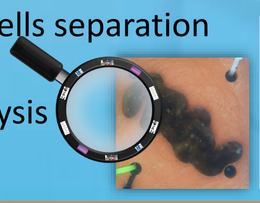
Two study sites and corresponding controls have been selected to assess acclimatization to two paired environmental conditions:

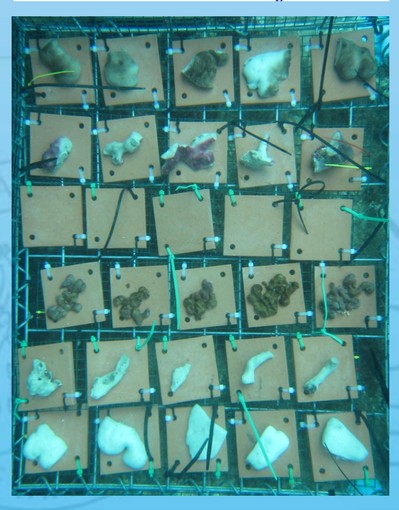
- Acclimatization to OA vs ambient pH – Site Grotta del Mago (Ischia Island, Naples), average pH of ~7.6; control: rocky cave with average pH of ~ 8.1.
- Acclimatization to light vs dark – Site Grotta Punta Vico (Ischia Island, Naples), a semi-submerged rocky cave; control: the illuminated area near the entrance of the cave.

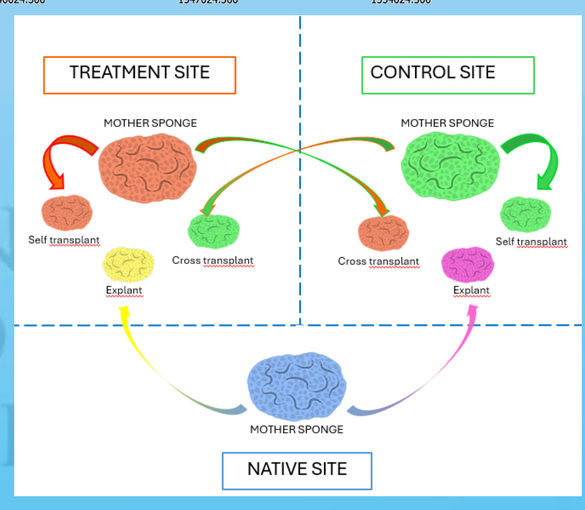


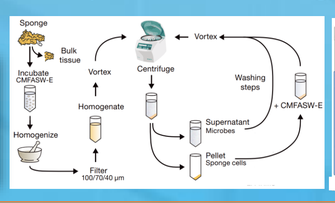
In both the experimental conditions, for *P.ficiformis* and *C.reniformis*, reciprocal transplantation was carried out. Explants of *C.nucula* were instead transplanted from their native site to the different sites. At the beginning of the experiment and after 2.5 months, transplants, wild individuals, and seawater samples were collected for:

- High throughput sequencing of the prokaryotic 16S rRNA gene.
- Sponge-microbial cells separation
- Metabolic profiling
- Stable isotope analysis



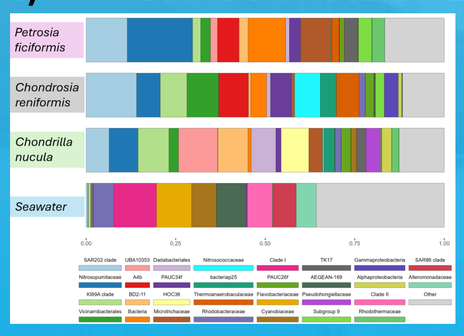


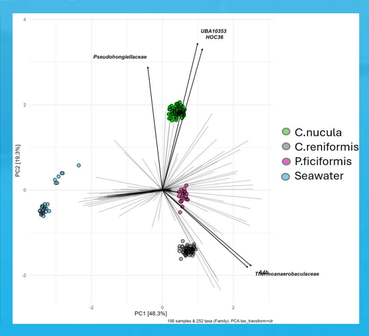




RESULTS & DISCUSSION

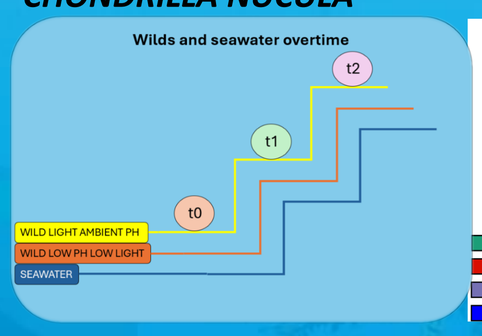
1) MICROBIAL CHARACTERIZATION

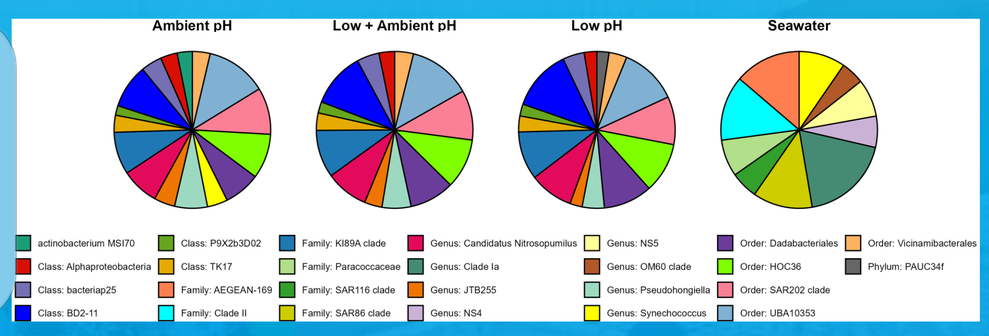




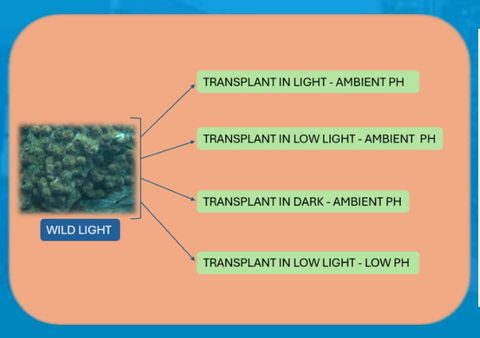
Analysing the whole dataset we found an extremely different microbial composition between the three sponge species and the seawater samples. Microbiome data were clearly divided in four groups: *C.nucula, C.reniformis, P.ficiformis,* and seawater.

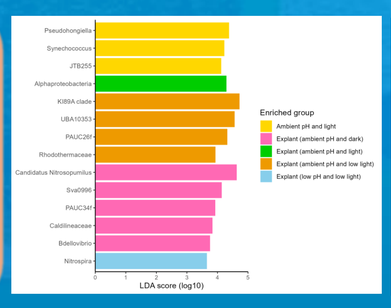
CHONDRILLA NUCULA

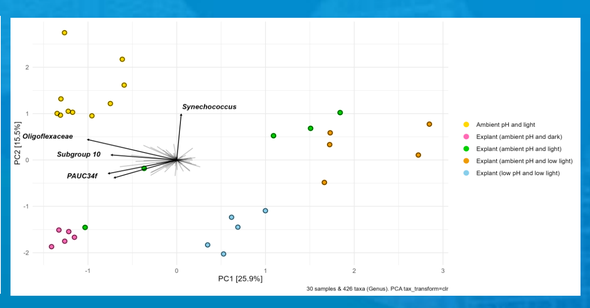




Despite the sponges are filter-feeders and we could expect a microbiome partially similar to that of the seawater, their capacity to actively select bacteria for the symbiosis ensures a differentiated microbiome. The core microbiome remains stable both temporally and across different environmental conditions.





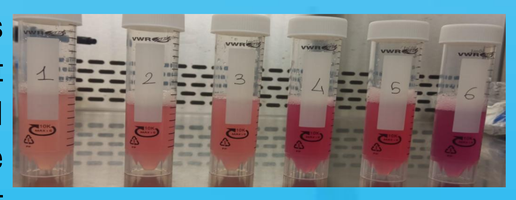


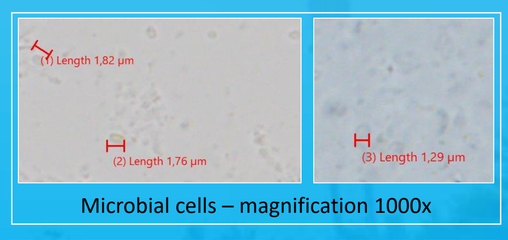
Explants under ambient pH and light, matching wild conditions, showed higher microbial variability. In contrast, explants exposed to altered environmental conditions displayed a more consistent and distinct microbial pattern. This suggests a faster microbiome adaptation in response to environmental stressors. Differential abundance analysis highlighted several key taxa driving these differences.

2) SPONGE-MICROBIAL CELLS SEPARATION

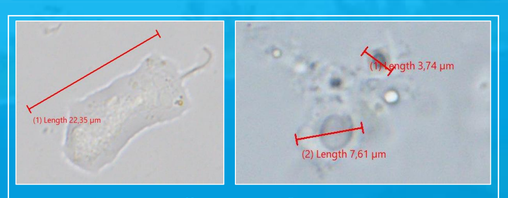
To distinguish the metabolites primarily produced by the host sponge from those produced by associated microbes, we physically separated the host and microbial fractions using a density-based centrifugation protocol. The microbial cells, being smaller and less dense, remained in the supernatant, while sponge cells formed the pellet.

The extracts were used both for metabolomics and stable isotope analysis.



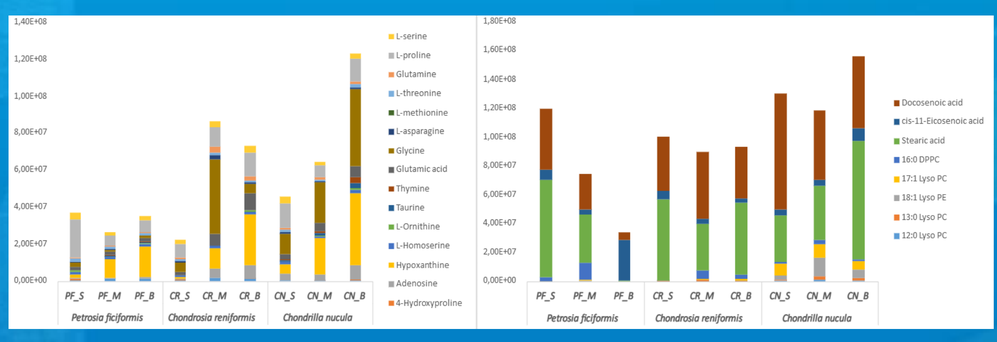


Microbial cells – magnification 1000x



Sponge cells – magnification 1000x

3) METABOLIC PROFILING



An initial, semi-quantitative analysis based on peak areas was performed on bulk, microbial, and sponge fractions. Results indicated no major metabolite loss, supporting the decision to proceed with separate analyses to investigate host–microbe metabolic shifts across treatments.

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REFERENCES: