Stazione Zoologica Anton Dohrn, Naples (Italy)

The Open University, Milton Keynes (UK)

School of Life, Health and Chemical Sciences

Doctor of Philosophy (PhD)

Microbial and Metabolic Dynamics in Sponges under Ocean Acidification

Jana Efremova

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Director of Studies:

Laura Núñez Pons

Stazione Zoologica Anton Dohrn, Italy

Department of Integrative Marine Ecology

Advisor:

Ulisse Cardini

Stazione Zoologica Anton Dohrn, Italy

Department of Integrative Marine Ecology

Internal Supervisor:

Gabriele Procaccini

Stazione Zoologica Anton Dohrn, Italy

Department of Integrative Marine Ecology

External Supervisor:

Jasper de Goeij

Associate Professor of Marine Benthic Ecology

University of Amsterdam, Faculty of Science

Institute for Biodiversity and Ecosystem Dynamics

ABSTRACT

Ocean acidification (OA) poses a significant threat to marine ecosystems, and benthic organisms must develop adaptive strategies. Despite being frequently regarded as 'winner taxa', we lack a comprehensive understanding of how sponges tolerate stress and undergo positive acclimatization. Marine sponges can be categorized as high or low microbial abundance (HMA or LMA) species, which may adopt distinct strategies to maintain homeostasis and fitness under changing conditions. This study investigated adaptive traits of the HMA sponge *Chondrosia reniformis* and the LMA sponge *Spirastrella cunctatrix* by comparing microbial and metabolic shifts in sponge holobionts collected from a natural CO_2 vent system and a control pH site in Ischia, Italy. Microbial diversity and core microbiomes changed for both species in response to OA. Morphologically, *S. cunctatrix* exhibited tissue necrosis accompanied by reduced oscula and water canal sizes, indicating a stress-induced dysbiosis and microbial instability. In contrast, *C. reniformis* appeared to benefit from a highly diverse microbiome with functional redundancy and local microbiome stability, promoting acclimatization to OA. NMR-based metabolomics revealed stable metabolite profiles across sites for *C. reniformis*, indicating metabolic homeostasis, whereas metabolic shifts in *S. cunctatrix* suggested OA interference in several pathways, including osmoregulation and energy metabolism. To expand on organismal acclimatization processes towards biochemical exchanges with the environment, a new *in situ* sampling methodology was developed. The study of inhaled and exhaled water fluxes of filter-feeders was improved using a submarine peristaltic pump, which was tested on *C. reniformis*. The new methodology can be applied to various ecological research topics, such as nutrient cycling, filter-feeding fluxes, plankton dynamics, and seawater metabolomics. This dissertation compares diverse OA acclimatization strategies of two co-occurring Porifera species in a CO_2 vent system based on microbiome and metabolic patterns. Moreover, parallel studies of biochemical exchanges with seawater are crucial to reconstruct these adaptation mechanisms.

Keywords: Ocean Acidification, Microbiome, Metabolomics, Porifera, Climate Change, CO_2 vents, InEx filter feeding fluxes

Graphical Abstract

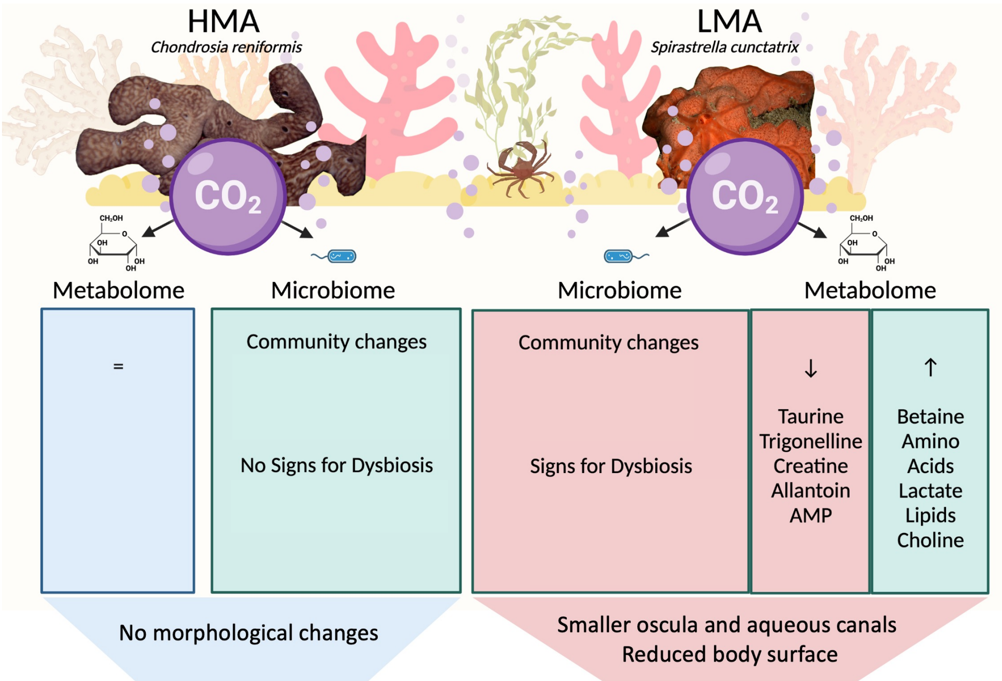

Figure 1: Microbial and metabolic responses in HMA and LMA sponges in response to ocean acidification. The high-microbial abundance (HMA) sponge *Chondrosia reniformis* shows different microbiome and metabolome changes compared to the low-microbial abundance (LMA) counterpart *Spirastrella cunctatrix.* Complex microbial and metabolic responses are correlated to a healthy physiology of the HMA sponge lacking morphological changes. The LMA sponge exhibits smaller oscula, aqueous canals and a reduced body surface, indicating physiological stress.

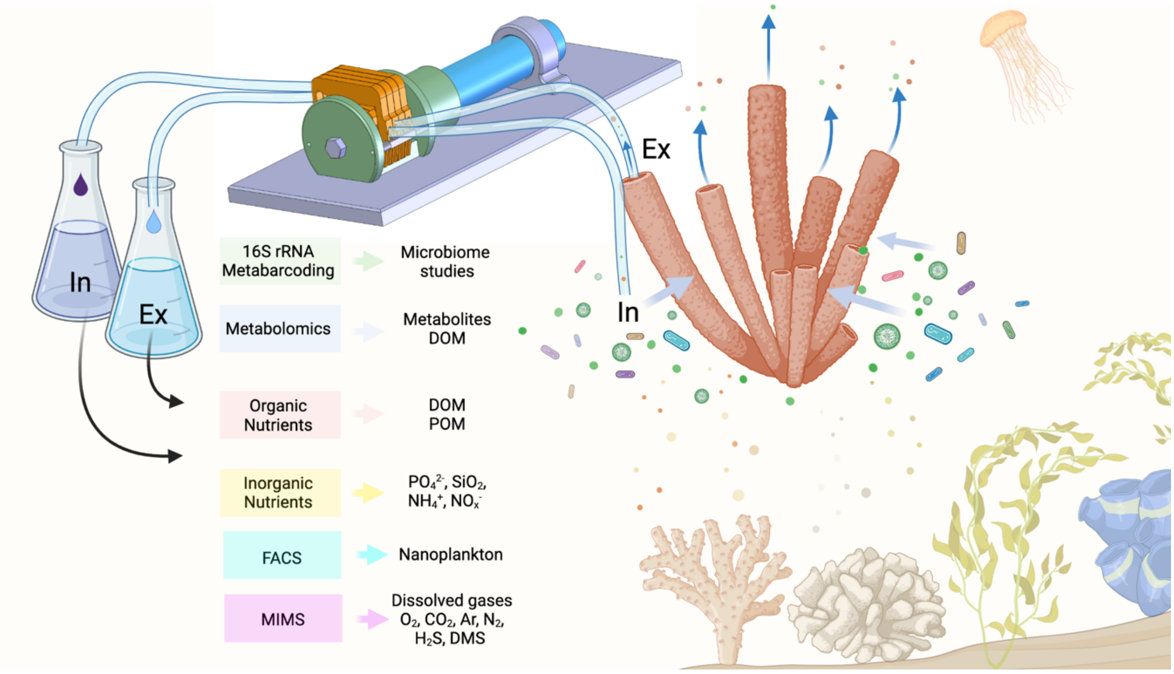

Figure 2: PeriSIP - a new developed methodology to sample inhaled and exhaled water fluxes from filter feeders. In complex reef systems, sponges, corals and algae release dissolved organic matter (DOM) into the water column which are, along with ultra-nanoplanktonic cells and heterotrophic bacteria, inhaled by sponges and metabolized. Exhaled seawater composition is changed and shows a high retention of different trophic cell types (e.g. *Synechococcus,* picoeukaryotes, bacteria), while fertilizing the environment through nutrient recycling processes. PeriSIP sampled seawater allows numerous downstream analyses, including the study of (in)organic nutrients, nano-planktonic cells, microbiome, metabolites, and dissolved gases.