'SFerOASys' Sponges as Fertilizing agents in Ocean Acidified Systems: Who's in the Loop?

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Project Summary

Darwin's Paradox to explain life in oligotrophic marine habitats lays on organic material recycling. One of the most revealing discoveries disentangling such enigma is the "Sponge Loop". In this process, sponges filter huge volumes of dissolved organic matter (DOM) as exudates and mucus from seaweeds, plants and animals. This DOM is not profitable by other macroorganisms, but is transformed inside the sponge into particulate organic matter (POM), which is released as detritus and can be then assimilated by other benthic components. This process recycles organic material locally, avoiding the loss to the open ocean. Although the specific mechanisms are not clear, it is believed that the sponge associated microbiota is involved in this process. It is predicted that DOM uptake should be higher in high-microbial abundance (HMA) sponges in contrast to low microbial abundance (LMA) species, yet some LMA sponges exhibit significant DOM assimilation, making the role of microbes uncertain. Additionally, there is evidence of distinct incorporation–transformation of algal-derived DOM versus coral-derived DOM by host sponge cells and microbial symbionts. Another unresolved aspect is the trade-off of DOM transformation, into either: detritus, sponge biomass, or secondary metabolites. Most of the studies testing the sponge loop come from tropical reefs, whereas temperate and polar seas have received scarce attention, and similarly no studies have been approached under global warming or ocean acidification (OA) conditions, despite sponges are seen as winners of future climate change scenarios.

The project aims at investigating the sponge loop principles in LMA versus HMA Mediterranean species from Ischia island, Napoli (Italia), where CO2 bubbling vents allow long time scale studies of OA adapted communities. These sponges produce bioactive secondary metabolites, and form predominant assemblages in control and acidified sites. The microbiome of treatment specimens will be altered, and we will evaluate the contribution of sponge microbiota in DOM assimilation from vegetal (*Posidonia oceanica*) versus animal (*Astroides calycularis*) origin, and its transformation to primary metabolites, allelochemicals and POM in distressed versus "normal" holobionts through pulse-chase assays in the lab. Finally, we will test the effect of OA on the sponge loop on naturally adapted communities in the field. The main methods include: 1) HTS (high-throughput sequencing) sequencing for microbial diversity (16S for Bacteria/Archaea, ITS1 for Fungi communities characterization); 2) CSIA (compound specific stable isotope) pulse chase experiments and PLFAs (phospholipid fatty acids) tracing; and 3) LC-MS and/or NMR for secondary metabolites monitoring and quantification.