Title:
Harnessing a coral model to unravel microbial interactions across kingdoms

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Abstract (300 words maximum): :
Marine reef ecosystems harbor a plethora of microorganisms that engage in intricate microbial interactions. Those interactions are often mediated by chemical cues, which may play roles in warfare, communication or nutrient cycling. Studying the involved chemical cues promises to unravel hidden microbial interactions and may yield novel substances of biotechnological importance.

Intriguingly, an integrated meta'omic analysis of reef-building coral holobionts sampled across 99 Pacific reefs revealed that microbial superproducers for natural products from the phylum Acidobacteriota were the most predictive factor in explaining the variations in coral host gene expression. These findings motivated us to study the only isolated members of marine Acidobacteriota—Acanthopleuribacter pedis and Sulfidibacter corallicola (family: Acanthopleuribacteraceae)—which are known for their biosynthetic potential.

However, the ecological role of Acidobacteriota and the relevance of their biosynthetic potential is yet unknown. This may arise from the impracticability of studying reef ecosystems in remote oceans, or the circumstance that corals are particularly difficult to handle under controlled laboratory conditions. To circumvent those limitations, a laboratory system composed of the sea anemone Exaiptasia—a non-calcifying relative of corals—and Symbiodinaceae algal symbionts is applied as a representative model to study molecular mechanisms of microbial interactions in coral reef ecosystems.

Here, I will present lessons learned from utilizing a coral model to bridge the gap between meta'omic data analysis, hypothesis generation and experimental testing.