
Multiscale analysis of the coral holobiont thermotolerance under contrasted thermal environment

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Abstract

In the context of global change, corals are being submitted to an increase in sea surface temperatures that is reaching values they never experienced in their lifetime. In order to better predict the future of these animals of great ecological importance facing this unusual thermal stress, we started an integrative approach to better understand acclimation as well as adaptive response potential. In this work, we performed a multiscale comparative thermotolerance experiment for two coral species: *Pocillopora damicornis*, a tropical scleractinian coral, and *Corallium rubrum*, a temperate coral from the Mediterranean Sea. For each of these species, we compared the response to thermal stress for two populations that have experienced in their life history contrasted thermal regimes (high or low annual thermal variations), and for distinct individual genotypes of each population. We considered the holobiont coral entity, *i.e.* the cnidarian itself, its associated microbial community and the symbiotic zooxanthellae (for *P. damicornis*). We followed the transcriptomic response of the cnidarian host using RNAseq, and the dynamic of the microbiota (using 16S metabarcoding) as well as the zooxanthellae (using ITS barcoding) until the upper limit of thermotolerance and for the different species / populations / genotypes. These comparative, multiscale analyses of the thermal stress response of the coral holobiont will allow us to identify potential convergent molecular mechanisms existing between these two ecologically and phylogenetically distant species, as well as specific pathways within the same species between populations experiencing different thermal regimes.

Keywords: Coral, *Pocillopora damicornis*, *Corallium rubrum*, Symbiodinium, microbiota, thermotolerance, holobiont, RNAseq, metabarcoding, zooxanthellae

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