

# ASSESSING ADAPTIVE ABILITIES OF THE MEDITERRANEAN RED CORAL *CORALLIUM RUBRUM* IN AN HIGHLY VARIABLE ENVIRONMENT USING COMMON GARDEN AND RNA-SEQ APPROACHS.

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## Abstract

To understand the underlying mechanisms of adaptation to thermal stress in the mediterranean red coral, *Corallium rubrum*, we studied two populations: a shallow one living at the edge of the specie's range (5 m depth), and a deeper one living in more stable thermal environment (40 m). A common garden experiment in aquaria showed different molecular phenotypes depending on the depth of origin of the individuals and of their thermal history. The transcriptome of individuals sampled in situ at 5 m or 40 m depth is currently under analysis, with more than 10<sup>8</sup> sequences for both populations. Our study will offer consistent elements to discuss the hot topic "plasticity vs local adaptation" in a context of climate change, and our results emphasize the conservation value of marginal populations.

Keywords: Cnidaria, Global change, Genetics, North-Western Mediterranean

Mediterranean benthic ecosystems, including Mediterranean red coral *Corallium rubrum*, have been deeply impacted by thermal anomalies during the last decades [1]. Adaptive capacities for marine species facing climate change can be understood at two different levels, at the individual level (i.e. phenotypic plasticity) and at the population level (i.e. selection). The Mediterranean red coral, *Corallium rubrum*, is well suited to study adaptative evolution in heterogenous environment. This sessile species is present in contrasted environments with a strong genetic structure [2], and differences of response to thermal stress between populations. To understand the underlying mechanisms of adaptation to thermal stress in this species, we studied three *C. rubrum* populations from different depths (5 m, 20 m and 40 m depth) and therefore different thermal regimes in the same area. We submitted red coral colonies to different heat shocks in aquaria that mimicked in situ stresses in common garden conditions. We measured the expression levels of several candidate genes by real-time PCR. Heat Shock Protein 70 (HSP 70), considered as a real molecular phenotype [4], showed significant differences of expression depending on the depth of origin of the individuals and of their thermal history.

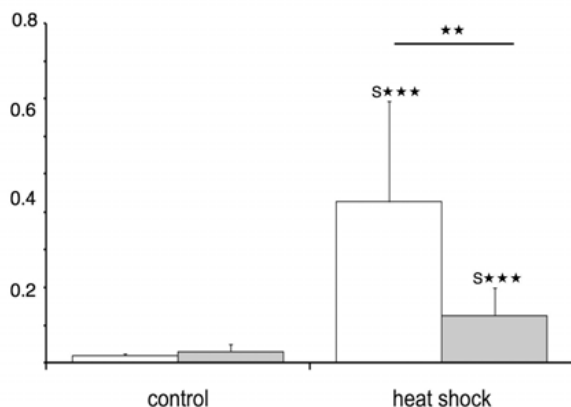


Fig. 1. HSP 70 induction after heat shock for 5 m population (white bars) and 40 m population (grey bars). HSP 70 mRNA expression was calculated using COI as reference gene. Results are represented as mean  $\pm$  SD. Stars indicates significant differences (3 stars  $p < 0.008$ , 2 stars  $p < 0.016$ ). S indicates significant differences between control and stress condition in the same population.

A RNA-seq experiment (Illumina technology) performed on individuals sampled *in situ* at 5 m and 40 m depth is currently under analysis, with more than 10<sup>8</sup> sequences for both populations. This analysis will provide usefull data to look for potential genomic basis for red coral adaptation to climate change. Our study will offer consistent elements to discuss the hot topic "plasticity vs local adaptation" in a context of climate change, and emphasizes the conservation value of marginal populations [5].

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