Transcriptomic response of *Trematomus bernacchii* to a short to mid term mild heat stress and bias of experimental design

Greco Samuele, Università di Trieste
Gaetano Anastasia Serena, Università di Trieste
Pallavicini Alberto, Università di Trieste
Giulianini Piero Giulio, Università di Trieste
Gerdol Marco, Università di Trieste

Many stenotherm marine species live in the cold and stable environment of the Antarctic Ocean which could be impacted by climate change in the upcoming years. To investigate this issue, gene expression analysis was carried out on *Trematomus bernacchii* specimens caught near Mario Zucchelli Station. Brain, gill and muscle tissues were sampled from naïve animals and from those kept in control (-0.9°C) and experimental (+0.6°C) tanks for six hours, seven and twenty days, post acclimation. RNAseq data showed that the temperature increase mostly affected the brain, with a time dependent response. Immune response was up-regulated at mid-term; protein turnover and energy management were down-regulated and neuronal remodelling related genes were up-regulated at 20 days, where the highest number of differentially expressed genes was observed. Gill tissue showed a mild response after 20 days, mostly involving DNA replication. A great early-starting response to stabling was also observed across the entire experiment in brain and gills, with the latter being the most affected. The expression pattern clustering analysis showed that many synapse-related genes were down-regulated and energy related genes were up-regulated, while several binding processes were up-regulated at the latest time point in brain. The response in gills was milder and mostly involved cytoskeleton and glycolysis. No significant change was observed in muscle. These results identify the brain as the tissue most affected by both heat and stabling, evidencing its great sensitivity to the slightest environmental change, and highlight the importance of a careful experimental design when working with captive wild organisms.