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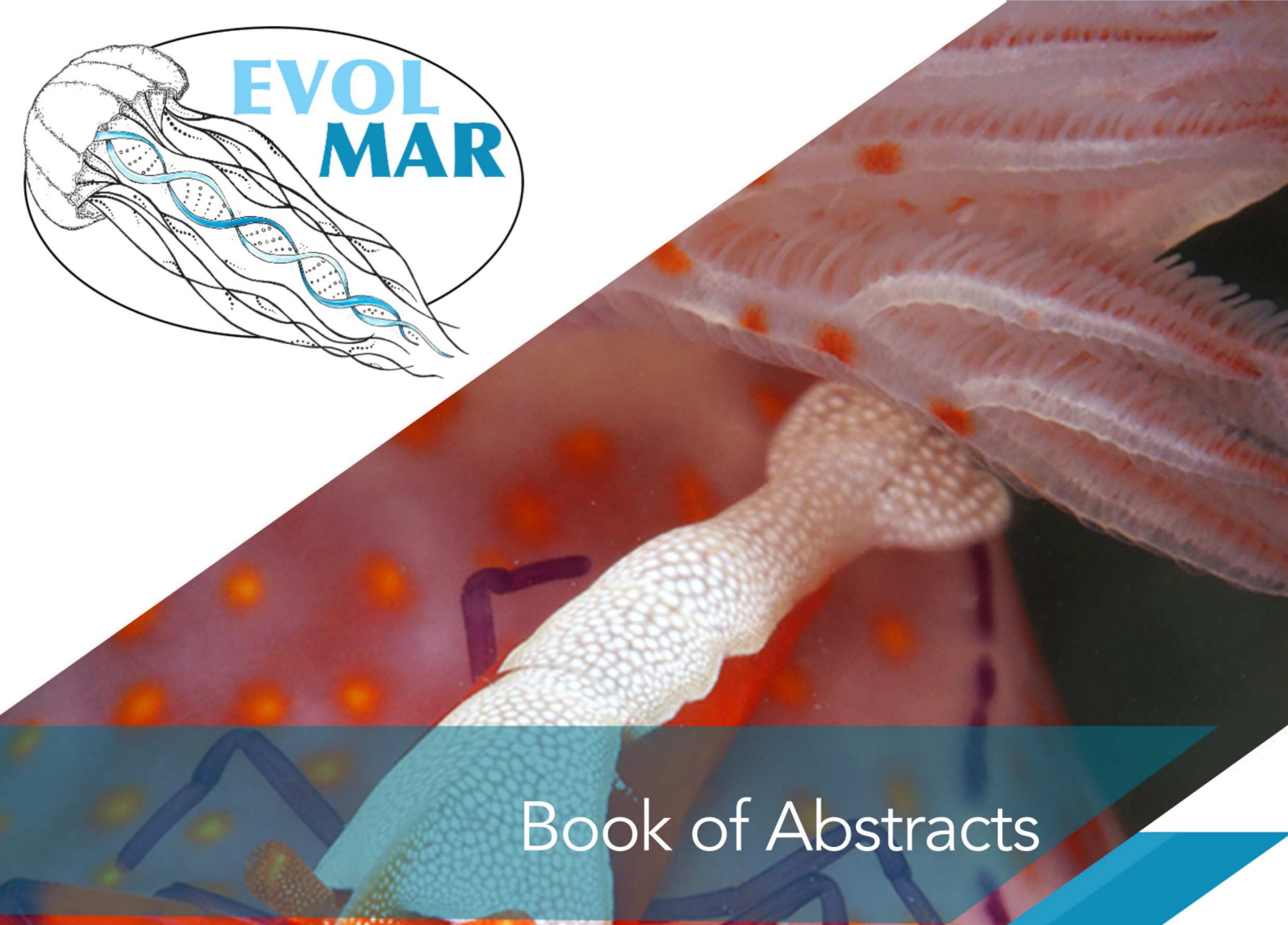

# Book of Abstracts

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# Transcriptomic adaptations of Cryonotothenioidea to the antarctic environment and response to heat stress

*Samuele Greco*[†], *Anastasia S. Gaetano*[†], *Federico Ansaloni*[†§], *Gianfranco Santovito*[‡], *Andrea Miccoli*[*], *Giuseppe Scapigliati*[*], *Alberto Pallavicini*[†], *Piero G. Giulianini*[†], *Marco Gerdol*[†]

† Dipartimento di Scienze della Vita, Università degli Studi di Trieste, Trieste, Italy
‡ Dipartimento di Biologia, Università degli Studi di Padova, Padova, Italy
* Dipartimento di Scienze Ambientali, Università della Tuscia, Viterbo, Italy
§ International School for Advanced Studies, Trieste, Italy

**Aim**

Antarctic fishes adopted a wide set of adaptations that allow them to thrive in the extreme antarctic environment. For example due to the high solubility of gasses in cold waters some *Channichthydae* such as *Chionodraco hamatus* have completely lost hemoglobin and gasses are simply dissolved in their colorless blood.

Although other adaptations, such as an increased activity of carbonic anhydrase activity in gills, have been previously described from a biochemical point of view, these have not been investigated from a genomic perspective.

Here we explore cold adaptations of Cryonotothenioidea at a transcriptomic level in a multi-species comparison. Moreover we investigate the transcriptomic response of *Trematomus bernacchii* to a slight heat stress.

**Methods**

Whole transcriptome sequencing data from 14 fish species were collected from NCBI or generated *de novo*. A bioinformatic approach was used to identify peculiar transcriptomic features of antarctic species compared with species living in temperate environments, and to assess the response of *Trematomus bernacchii* to a slight heat stress in 3 different tissues (brain, gill, muscle).

**Results**

We identified 130 upregulated genes in the gills of Cryonotothenioidea, including two carbonic anhydrases displaying high gill-specificity. Moreover molecular signatures of cobalamin deficiency, which could be linked with the high parasite loads found in these species, were observed.

The heat stress experiment revealed the brain as the most sensible tissue after 20 days of exposure, with most changes affecting protein synthesis, vescicular transport, inflammation and cytoskeleton assembly. Comparatively, the gills and muscle tissues displayed an earlier and weaker transcriptomic response. Interestingly, several hsps were regulated in response to stress both from heat and stabling.

**Main conclusion**

This study allowed us to identify peculiar transcriptomic markers of cold adaptation in Cryonotothenioidea and to understand how the future sea water warming may affect the response of these organisms in the short term.

**Thematic areas**

Adaptation