Molecular signatures of cold-adaptation in the Antarctic eelpout (*Pachycara brachycephalum*)

**Introduction** Adaptation of ectotherm organisms to the key abiotic factor temperature can occur by the development of advantageous traits at different levels of organization [1]. Since all biological processes are subjected to the same physicochemical paradigms (Q10-rule), the composition of biological macromolecules is likely to be affected as well. Hence, proteins and nucleic acids may also contribute to a certain thermal plasticity and tolerance. Antarctic fishes have adapted to constant cold environmental conditions for millions of years and provide therefore excellent study objects to evaluate evolutionary trends of thermal adaptation. Comparative sequence analyses with temperate species shed light on the molecular architecture of biological macromolecules in connection with species habitat temperatures.

**Methods** DNA/RNA sequences as well as their respective translations were compared between the Antarctic eelpout *Pachycara brachycephalum* and its temperate congener, the Northsea Eelpout, *Zoarces viviparus* through analyses of normalized transcriptomic cDNA libraries.

**Results** Functions, differently represented in respective transcriptomes may indicate gene duplication events and distinct metabolic demands. As a "genomic scale", the functional distribution of Gasterosteus aculeatus is indicated by green bars.

**Conclusion** Comparative sequence analyses of zoarcid congeners revealed patterns of a different thermal adaptation at the molecular level although their mean habitat temperature differs only by ~10°C. The compositional biases of cold-adapted proteins and DNA/RNA support an increase of molecule flexibility at the respective levels. These trends promote optimized reaction kinetics at low temperatures trough less stable transition states in reaction processes shaping the thermal plasticity of organisms at a deeper level. Finally, these data highlight another aspect of species’ vulnerability of cold-adapted organisms in the context of the ongoing climate change.

**References**
2. Windisch et al. (2013) BMC Genomics 14, 598.