

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.

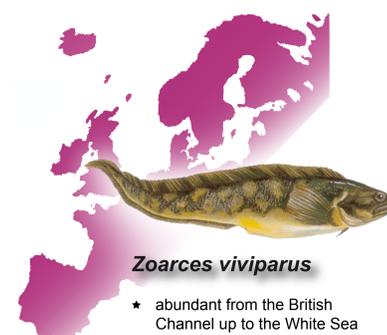


Pachycara brachycephalum

- * abundant around Antarctica at approx. 200 to 1,800 m depth
- * annual water temperatures fluctuate between -1.5 – 2.0°C

overview of cDNA libraries

	<i>Pachycara</i> [2]	<i>Zoarces</i> [3]
reads	reads total	481,802 ~400,000
	in assembly	338,993 349,102
	mean length	321 221
contigs	total	65,565 53,447
annotation	known function	19,460 16,315
orthologs	matching sequence pairs	4,155



Zoarces viviparus

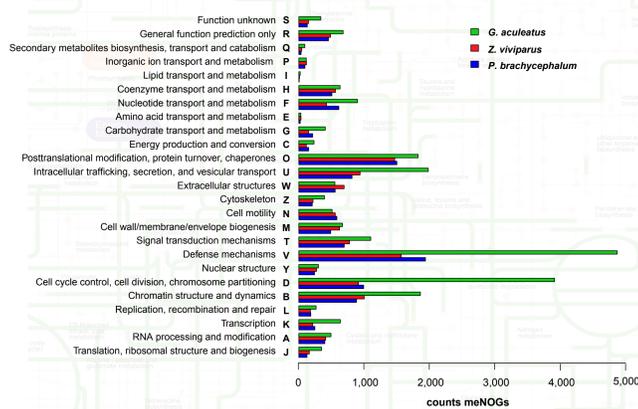
- * abundant from the British Channel up to the White Sea
- * annual water temperatures fluctuate between 4.0 – 21.0°C

Results



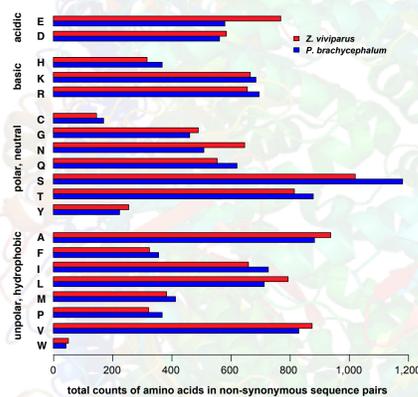
Functional differences

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.



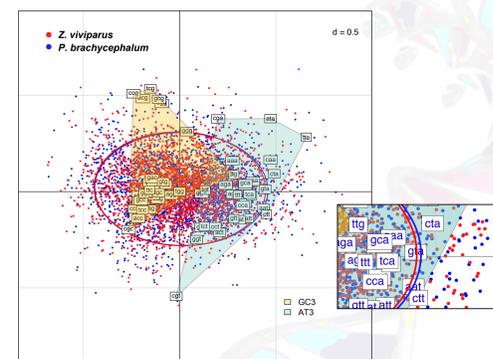
Amino acid usage

Imbalances in the amino acid usage are pronounced by 102 fewer ionic aa in *P. brachycephalum* reducing ionic interactions of proteins. A gain of 117 polar/neutral aa increases protein polarity as well as better solvent-interaction. However, no clear pattern exists within the unpolar/hydrophobic group.



Codon usage

In total 402,219 synonymous codon pairs were analyzed by means of a Within Canonical Analyses (WCA), revealing a trend of a A/T-rich composition of codons on the third codon position in *P. brachycephalum*.



The species-specific codon usage at the wobble position is not random at a significance level of $p = 0.0005$, determined by a Fisher's test. This trend becomes visible in the WCA by a shift between the blue and red ellipse representing respective codon usages.

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 though 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.

