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„Thermal acclimation in Antarctic eelpout: Transcriptomic profiling of metabolic pathways“

As temperature has a pervasive impact on all biological processes it defines the biogeography of marine ectothermal organisms. The molecular mechanisms defining thermal limits and acclimation capacities have been traditionally studied by describing effects on single proteins or protection mechanisms. Since thermal properties of individual molecules largely exceed the temperature window of whole animals, thermal limits are most likely set at the level of integration of molecules into functional units and networks up to whole organism level. By combining explorative transcriptomic studies with inductive approaches we aim to identify effective mechanisms, defining climate sensitivity and adaptability of cold-stenothermal fish. The Antarctic eelpout *Pachycara brachycephalum* lives circum-polar at water conditions around 0°C. We characterised the liver transcriptome by pyrosequencing of a normalized cDNA library. Based on this the expression of several candidate genes was followed during the time-course of warm acclimation (5°C, 6 weeks). Elevated respiratory chain capacities in liver contrasted with the general picture of cold-induced mitochondrial proliferation in temperate fish. Furthermore, by profiling transcript levels of functional genes in relation to mediative transcription factors large rearrangements of the central energy metabolism became visible, with a shift of the balance from lipid to carbohydrate metabolism. In a canonical correspondence analysis the factors time and temperature divided the incubated animals in two groups and short- and long-term effects could be distinguished. Overall, the data indicate an improvement of metabolic processes upon warm acclimation. The implication of these results will be discussed with respect to the realised ecological niche of the species.