

## Publication

Effects of thermal acclimation on the proteome of the planarian Crenobia alpina from an alpine freshwater spring

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Author(s) Ebner, Joshua Niklas; Wyss, Mirjam Kathrin; Ritz, Danilo; von Fumetti, Stefanie

Author(s) at UniBasel von Fumetti, Stefanie ; Ritz, Danilo ; Ebner, Joshua Niklas ; Wyss, Mirjam ; Year 2022

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Species' acclimation capacity and their ability to maintain molecular homeostasis outside ideal temperature ranges will partly predict their success following climate change-induced thermal regime shifts. Theory predicts that ectothermic organisms from thermally stable environments have muted plasticity, and that these species may be particularly vulnerable to temperature increases. Whether such species retained or lost acclimation capacity remains largely unknown. We studied proteome changes in the planarian Crenobia alpina, a prominent member of cold-stable alpine habitats that is considered to be a cold-adapted stenotherm. We found that the species' critical thermal maximum (CTmax) is above its experienced habitat temperatures and that different populations exhibit differential CTmax acclimation capacity, whereby an alpine population showed reduced plasticity. In a separate experiment, we acclimated C. alpina individuals from the alpine population to 8. 11, 14 or 17 degrees C over the course of 168 h and compared their comprehensively annotated proteomes. Network analyses of 3399 proteins and protein set enrichment showed that while the species' proteome is overall stable across these temperatures, protein sets functioning in oxidative stress response, mitochondria, protein synthesis and turnover are lower in abundance following warm acclimation. Proteins associated with an unfolded protein response, ciliogenesis, tissue damage repair, development and the innate immune system were higher in abundance following warm acclimation. Our findings suggest that this species has not suffered DNA decay (e.g. loss of heat-shock proteins) during evolution in a cold-stable environment and has retained plasticity in response to elevated temperatures, challenging the notion that stable environments necessarily result in muted plasticity.

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