

Publication

Thermal acclimation results in persistent phosphoproteome changes in the freshwater planarian Crenobia alpina (Tricladida: Planariidae)

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Mesh terms Animals; Planarians; Acclimatization; Proteome; Phosphoproteins, genetics; Fresh Water Understanding the molecular mechanisms underlying thermal tolerance of aquatic invertebrates can inform predictions about the effects of thermal regime changes on these species. While gene expression and protein abundance changes underlie compensatory responses, little is known about the role of post-translational mod-ifications as thermal tolerance mechanisms. To test the hypothesis that protein phosphorylation changes in response to thermal acclimation, we studied the phosphoproteome of the freshwater planarian Crenobia alpina. This species has a supposedly limited thermal tolerance and is found in cold-stable habitats. We systematically investigated phosphopeptide abundances following 168 h acclimation to 11, 14, 17, and 20 degrees C, using label-free quantitative phosphoproteomics. We provide a comparative analysis of 2115 phosphosites from 1049 phos-phoproteins, whereby little to no differences could be observed between 11, 14, and 17 degrees C. However, more than 130 phosphopeptides were significantly more abundant and 40 were less abundant following acclimation to 20 degrees C. These phosphoproteins were functionally associated with the regulation of neuronal processes, cilia, DNA damage repair, aquaporins, and mitochondrial fission and fusion. These data support the hypothesis that phosphorylation plays a role in thermal acclimation responses, suggesting that PTMs are of significance in invertebrate thermal acclimation. PTMs may therefore offer an alternative route of transient protein adaptation to temperature increase in invertebrates, and should not be neglected when trying to understand how molecular system dynamics in response to elevated temperatures.

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