Comparative proteomics of stenotopic caddisfly Crunoecia irrorata identifies acclimation strategies to warming

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Species' ecological preferences are often deduced from habitat characteristics thought to represent more or less optimal conditions for physiological functioning. Evolution has led to stenotopic and eurytopic species, the former having decreased niche breadths and lower tolerances to environmental variability. Species inhabiting freshwater springs are often described as being stenotopic specialists, adapted to the stable thermal conditions found in these habitats. Whether due to past local adaptation these species have evolved or have lost intragenerational adaptive mechanisms to cope with increasing thermal variability has, to our knowledge, never been investigated. By studying how the proteome of a stenotopic species changes as a result of increasing temperatures we investigate if the absence or attenuation of molecular mechanisms is indicative of local adaptation to freshwater springs. An understanding of compensatory mechanisms is especially relevant as springspecialists will experience thermal conditions beyond their physiological limits due to climate change. In this study, the stenotopic speciesă Crunoecia irrorata (Trichoptera: Lepidostomatidae, Curtis 1834) was acclimated to 10, 15 and 20 řC for 168 h. We constructed a homologybased database, and via liquid chromatographytandem mass spectrometry (LCMS/MS)based shotgun proteomics identified 1358 proteins. Differentially abundant proteins and protein norms of reaction revealed candidate proteins and molecular mechanisms facilitating compensatory responses such as trehalose metabolism, tracheal system alteration, and heat shock protein regulation. A speciesspecific understanding of compensatory physiologies challenges the characterization of species as having narrow tolerances to environmental variability if that characterization is based on occurrences and habitat characteristics alone.
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