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The proteomic response of Mytilus galloprovincialis and M. trossulus to acute temperature stress

The Mediterranean blue mussel species *Mytilus galloprovincialis* has invaded southern California at the beginning of the last century and has since replaced the native *M. trossulus* from its southern range. Previous work has shown that *M. galloprovincialis* is the more heat tolerant of the congeners and has suggested that differences in temperature tolerance and increasing temperatures due to climate change drive the range expansion. By comparing the proteomic response of the two congeners in response to heat stress we were aiming to better understand the molecular underpinnings of differences in temperature tolerance and to discover indicators of the metabolic costs of heat stress. After acclimation to 11°C for four weeks we incubated whole mussels gradually to 24°C, 28°C and 32°C for 1 h. Mussels were brought back to 11°C to recover for 24 h. Using two-dimensional gel electrophoresis and tandem mass spectrometry, we separated the proteins of gill tissue and analyzed the resulting gel images to quantify and identify proteins that changed significantly with heat stress. Of the more than 500 protein spots we detected, 28% changed expression in *M. trossulus* but only 14% in *M. galloprovincialis*. Several heat shock protein 70 (Hsp70) and small Hsp isoforms were induced at a lower temperature in the more heat sensitive *M. trossulus*. Changes in a number of metabolic enzymes suggest that gill cells are requiring an increasing amount of reducing equivalents in form of NADH with heat stress, most likely due to the generation of reactive oxygen species. However, the thermal limits of expression of oxidative stress proteins are lower in the heat sensitive *M. trossulus* in comparison to *M. galloprovincialis*, possibly setting the thermal limits to acute heat stress in these two congeners.