The invading Mediterranean blue mussel species *Mytilus galloprovincialis* requires higher salinity levels than the more hypo-saline tolerant and native *M. trossulus*, which it replaced from its southern range in California, possibly due to climate change. Hypo-salinity, due to an increase in extreme precipitation events, has been hypothesized to limit the expansion of the invader. By comparing the proteomic responses of the congeners to acute hypo-saline stress we were trying to identify the interspecific differences that set limits to hypo-saline stress and assess their contribution to the range shifts. We exposed mussels to acute hypo-saline (100%, 85% and 70% salinity) stress for 4h followed by a 0h and 24h recovery period while the shells were forced to stay open. We used gill tissue to separate proteins with 2D gel electrophoresis and identify protein expression patterns (two-way ANOVA, p<0.02). About a third of the proteins (and the same total number) showed a time-dependent response to different salinities (interaction effects) in both species. A similar proportion showed time and salinity-dependent patterns (main effect) in *M. galloprovincialis*. Differing slightly, *M. trossulus* showed more of a time-independent response to hypo-saline stress. The results suggest that although there are broad similarities in the responses of the two congeners, *M. trossulus* may be responding faster to hypo-saline stress, which in turn may limit the invaders range expansion. Proteins identified with tandem mass spectrometry include proteins involved in cytoskeletal modifications, molecular chaperones, proteasome, oxidative stress proteins and proteins involved in energy metabolism.