

High-hydrostatic pressure adaptation resolved by combined physiological and biophysical approaches in piezophilic archaea

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HHP, experienced by cells in the deep-sea, has numerous deleterious effects on cellular components. HHP is however required for optimal activity of deep-environment adapted microbes (piezophiles). Experimental evidence on macromolecules shows that HHP has a different impact depending of the biological macromolecule. DNA and lipids are stabilized, while multimeric proteins tend to be destabilized. For these three types of macromolecules, HHP has a similar negative impact on cellular functions.

In thermophilic piezophiles several lines of evidence show that the adaptation of HHP involves the regulation of the transcription of the genome as well as the expression of specific genes under HHP. Using molecular dynamics, we have investigated the protein and membrane structure of *Thermococcus barophilus* to further characterize HHP adaptation at the molecular level. We have direct and indirect evidence for the structural adaptation of the proteome, although the specific signatures at the genome level still remain elusive[1-4]. HHP adaptation also involves the HHP-dependent accumulation of osmolytes to maintain proper protein folding and activity, supporting a view in which the adaptation is both structural and physiological.

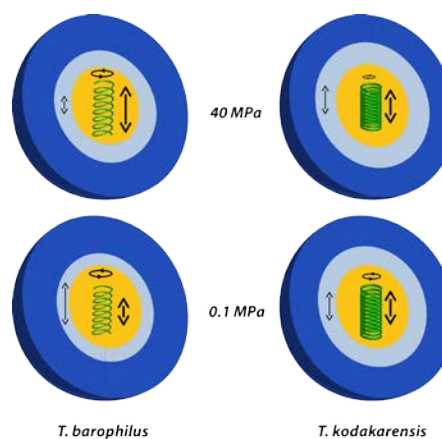


Figure 1. Scheme summarizing the impact of HHP on proteins from a piezophilic hyperthermophile (*Thermococcus barophilus*, left) and a piezosensitive hyperthermophile (*Thermococcus kodakarensis*, right). The dark blue surface represents bulk water, the light blue surface hydration water. The green spring characterizes the proteome and its contributions (translation and rotation) to dynamics. The arrow in the light blue area indicates the dependence of the hydration water dynamics on the system and on pressure.

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