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Molecular bases of proteome adaptation to High Pressure in extremophilic Archaea

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Proteome adaptation to high pressure in Archaea is still an open debate. Whole genome comparative studies could not identify a clear adaptation pattern, and HP adaptation is often considered as concomitant to another adaptation, for instance to high or low temperature.

Studies on whole cells of the near isogenic HP-adapted *T. barophilus* (T=85°C, p=400bars, piezophilic) and HP-sensitive *T. kodakarensis* (T=85°C, p=1bar, piezosensitive) highlighted the differences in proteome dynamics between these two species. The observed results are congruent with two major adaptive strategies, either structural differences, which would generate the difference in dynamics of the proteomes, or the existence of a protection mechanism to maintain proteome functionality under pressure stress.

We investigated the first hypothesis using EINS and QENS to unravel the dynamics of the protein *Phosphomannose Isomerase* from the two species. This approach allowed a detailed characterization of the dynamics of the two proteins without the complications of a whole-cell environment. Our results show that the dynamics of the protein from the piezophile is more stable on a time scale of 10-100 ps, and that large side-chain motions are even favoured by HP. In contrast, the protein from the piezosensitive species is destabilized by HP, becomes more rigid and its structure is likely affected. This is the first experimental demonstration of the effect of HP adaptation on the fast dynamics of proteins.

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