Bacterial cytoskeleton suprastructures and their physical origin

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Bacterial cytoskeletal filamentous proteins, like their eukaryotic counterparts, are key regulators and central organizers of many cellular processes including morphogenesis, cell division, DNA segregation and movement. Such filaments often organize themselves into complex structures within the prokaryotic cell, driven by molecular crowding and cation association, to form bundles (ParM), rings, toroids and helical spirals (FtsZ) or interwoven sheets (MreB). The formation of complex structures is essential for bacterial cytoskeleton function. Here, we highlight the suprastructures of the prokaryotic cytoskeleton that have been observed by high resolution in vitro electron microscopy and set them in perspective with in vivo observations. We discuss the underlying physical principles that lead to complex structure formation.

Ions and water molecules screen charged molecules from each other within a cell. However, the biological polymers that constitute the cytoskeleton associate with counterions that can result in strong electrostatic interactions between the like-charged filaments. In addition, the interior of a cell is about 40% full of various macromolecules, termed molecular crowding. Molecular crowding has been known for almost a half a century to have profound effects on the thermodynamics and kinetics of cellular processes and can enhance the native state of proteins. Due to the excluded volume effect, molecules from each other within a cell.

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Collectively these findings suggest, that the filaments of the bacterial cytoskeleton can adopt specific supramolecular structures in response to the presence of both molecular crowding and cations that make them uniquely suited for the cellular processes in which they participate.

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