RESEARCH HIGHLIGHTS

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BACTERIAL PHYSIOLOGY

Remodelling the FtsZ network

In bacteria, the tubulin-related GTPase FtsZ and actin-related FtsA are two components of the Z-ring, a cytoskeletal structure that induces cytokinesis. Although initial models for Z-ring formation suggested that FtsA is a passive membrane anchor, recent data indicate that it influences the organization of FtsZ filaments into large-scale, dynamic cytoskeletal structures. Here, Loose and Mitchison investigate Z-ring formation *in vitro* and uncover a dual role for FtsA in FtsZ network assembly and rearrangement: it first recruits FtsZ filaments to the membrane, and then negatively regulates FtsZ organization.

The authors used fluorescently labelled FtsZ and FtsA proteins, and reconstituted FtsZ polymerization on supported bilayers in vitro. They found that, in the presence of FtsA, GTP (which induces FtsZ polymerization) and ATP (which is required for FtsA-FtsZ interaction), FtsZ filaments attached to the membrane. At low protein concentrations, the authors observed individual, short filaments, which grew at one end and shortened at the opposite end — that is, they showed treadmilling behaviour, similar to actin filaments. At higher protein concentrations, FtsZ filaments formed dynamic filament bundles that self-organized into chirally rotating rings. Although the FtsZ filament network was continuously remodelling itself and seemed to be moving, the authors found that single subunits remained static, which supports the idea that remodelling of the filament network is driven by polymerization dynamics.

Next, the authors asked whether these observed dynamics are an intrinsic feature of FtsZ or whether they emerge from a complex interaction with FtsA. They show that a version of FtsZ that binds autonomously to the membrane also formed a network of filament bundles on the membrane; however, these bundles were stationary. Moreover, FtsZ filaments recruited to the membrane by the alternative membrane-anchor ZipA also assembled into a stationary network, which suggests that the interaction of FtsZ and FtsA is required for rapid and dynamic FtsZ filament reorganization.

So, how does this rapid reorganization of the FtsZ filament network come about? The authors further studied the interaction of FtsA with FtsZ and found that FtsA recruits FtsZ filaments to the membrane but not FtsZ monomers. Moreover, they found that, in contrast to ZipA, FtsA destabilizes the FtsZ network. The underlying mechanism for this remains to be determined, but the authors suggest that fragmentation of FtsZ polymers leads to their detachment from the membrane, as short FtsZ fragments bind only weakly to FtsA, and this enables rapid reorganization of the FtsZ filament network into dynamic structures.

Thus, remodelling of the FtsZ network into dynamic higher-order structures depends on FtsA, and the early stages of Z-ring formation require the coordinated action of many factors. It will be interesting to see whether the mechanism of crosstalk between cytoskeletal regulators has common features with that in other systems.

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ORIGINAL RESEARCH PAPER Loose, M. & Mitchison, T. J. The bacterial cell division proteins FtsA and FtsZ self-organize into dynamic cytoskeletal patterns. *Nature Cell Biol*. <u>http://dx.doi.</u> org/10.1038/ncb2885 (2013)