The dynamic cytoskeleton in bacterial cell division

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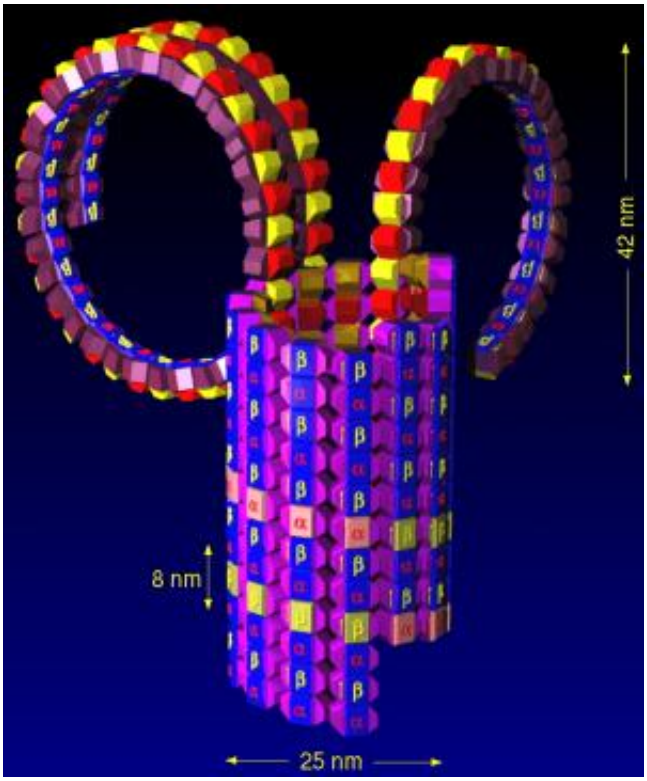

Cytoskeletal Ring Formation. Credit: labs.cellbio.duke.edu

(Phys.org) —The cytoskeletal proteins of eukaryotes polymerize into self-organized patterns even as pure solutions. However, to see more complex dynamics, like filament sliding or rotation, various motor proteins and cofactors usually need to be added to the solution. The ancestral bacterial proteins of actin and tubulin, namely FtsA and FtsZ,

play a key role in bacterial cell division through the formation of a cytoskeletal structure known as the "Z" ring. Researchers Martin Loose and Tim Mitchison have studied these bacterial proteins in solution, along with bits of reconstituted membrane, and found that they support complex dynamics in the absence of any motor proteins. In their recent paper in *Nature Cell Biology*, they describe how these behaviors can spontaneously emerge.

The researchers studied a lipid bilayer preparation in which FtsA protein was readily attached through a special helix found at its carboxy terminus. When GTP was added, they found that the FtsZ was recruited to the membrane region, and was rapidly polymerized. After a critical density was reached, motile streams were seen moving in a single predominate direction, with complex rotating vortices found between them. The structures would persist for tens of minutes and rotated at speed of up to 11 degrees per second.

While their system did not have all the components normally found in bacterial cells, the researchers noted that the vortices were reminiscent of the helical patterns seen during Z-ring assembly in E.coli and Bacillus subtilis. The formation of the patterns required the addition of ATP. The researchers found that no ATPase activity was present, and subsitution with ADP worked just as well. On the other hand, GTP was found to be hydrolyzed in the process, and only static filament bundles were formed when it was prevented.

The researchers observed that the swirls had a preferred directionality. They explained this chirality as a result of polar molecules attaching to a single face of the bilayer, combined with the effects of bundling and treadmilling in curved FtsZ filaments. They also note that the attachment of enzymes to the Z-ring could occur in a spatially organized fashion with the predominate force for inward growth in cell division arising from bond formation during cell wall biosynthesis.

The larger question of asymmetry in cells often escapes everyday notice. Neurons, in particular, are highly polarized with the axon defining a principle direction. Yet very little in terms of neuronal function has been ascribed to any particular handedness. As mentioned previously, one issue which might be further explored in this vein would be orientation specific effects felt beyond the immediate cell, like the direction of glial wrapping, for example.

Other possible effects like rotation of free microtubules as a result of the directed transport of various cargo have scarcely been studied, but could have interesting implications for the organization of cells. Simulation, like one recent model exploring the role of the GTP cap region in microtubule dynamics, will be an important compliment to these kinds of in-vitro experiments. The study of the intrinsic pattern formation capability of more primitive cytoskeletal proteins will lead to greater understanding of the functions of their diverse, and uniquely optimized descendants found today in eukaryotic cells.

More information: The bacterial cell division proteins FtsA and FtsZ self-organize into dynamic cytoskeletal patterns, *Nature Cell Biology* (2013) DOI: 10.1038/ncb2885

Abstract
Bacterial cytokinesis is commonly initiated by the Z-ring, a cytoskeletal structure that assembles at the site of division. Its primary component is FtsZ, a tubulin superfamily GTPase, which is recruited to the membrane by the actin-related protein FtsA. Both proteins are required for the formation of the Z-ring, but if and how they influence each other's assembly dynamics is not known. Here, we reconstituted FtsA-dependent recruitment of FtsZ polymers to supported membranes, where both proteins self-organize into complex patterns, such as fast-moving filament bundles and chirally rotating rings. Using fluorescence microscopy and biochemical perturbations, we found that these large-

scale rearrangements of FtsZ emerge from its polymerization dynamics and a dual, antagonistic role of FtsA: recruitment of FtsZ filaments to the membrane and negative regulation of FtsZ organization. Our findings provide a model for the initial steps of bacterial cell division and illustrate how dynamic polymers can self-organize into large-scale structures.