Bacterial roundabouts determine cell shape

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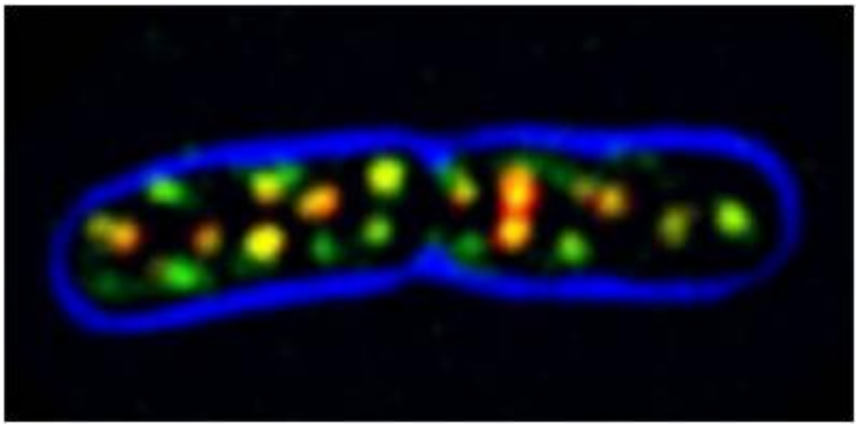

This is a *Bacillus subtilis* cell with several patches of Mbl (MreB-like protein) fused to the green fluorescent protein. Colors represent overlay of images taken by total internal reflection fluorescence microscopy (TIRFM, red), epifluorescence (green) and transmitted light (blue, indicates cell outline). Credit: Roland Wedlich-Söldner / Copyright: MPI for Biochemistry

Almost all bacteria owe their structure to an outer cell wall that interacts closely with the supporting MreB protein inside the cell. As scientists at the Max Planck Institute for Biochemistry and at the French INRA now show, MreB molecules assemble into larger units, but not - as previously believed – into continuous helical structures.

The circular movement of these units along the inside of the bacterial envelope is mediated by cell wall synthesis, which in turn requires the support of MreB. This mutual interaction may be a widespread phenomenon among bacteria and opens up new avenues for therapeutic

intervention. The bacterial cell wall is already a major target for antibiotics. (*Science*, June 3, 2011)

Even single cells have to maintain their shape: In higher organisms, the supporting structures of the cytoskeleton, which include filament networks made of the protein actin, take care of this job. The much smaller bacterial cells possess similar cytoskeletal structures, such as the actin related protein MreB. Up to now, scientists believed that this molecule forms spiral structures on the inside of the cell membrane in non-spherical bacteria, which serve as a scaffold for the assembly of the comparatively rigid cell wall.

Using innovative imaging technologies based on fluorescent microscopy, the scientists in the laboratory of Roland Wedlich-Söldner have now been able to show that MreB proteins do not form such highly ordered structures – and yet are organized in more complex ways than they had previously assumed. "MreB molecules assemble into larger units, or patches. They move in circular paths along the inside of the cell membrane, but without following a preferred direction", explains Julia Domínguez-Escobar, PhD student at the Max Planck Institute of Biochemistry.

A highly unexpected finding of the study was that the movement of MreB patches relies on a functioning cell wall. MreB structures cannot move on their own but are pulled along the bacterial envelope by the newly synthesized cell wall material. The MreB patches are located at the inside, the cell wall at the outside of the cell membrane. Thus, interaction is likely mediated by molecules that span the cell membrane. These molecular adapters link the incorporation of newly synthesized cellular material with the MreB units, which thereby follow the permanently growing cell wall structures.

Many parts of the cell wall are almost universally conserved in bacteria,

making it likely that the newly discovered mechanism is widespread. Hence, the results could play an important role for the further investigation of bacterial cells, but also for medicine: "Cell wall synthesis already is a key target for antibiotics. New insights into the structure of the cell wall could open up urgently needed therapeutic alternatives", hopes Wedlich-Söldner.

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