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High resolution structure of bacterial cell sacculi JOHN DUTCHER, AHMED TOUHAMI, VALERIO MATIAS, ANTHONY CLARKE, University of Guelph, MANFRED JERICHO, Dalhousie University, TERRY BEVERIDGE, University of Guelph — The major structural component of bacterial cell walls is the peptidoglycan sacculus, which is one of nature's strongest and largest macromolecules that allows the cell to maintain a large internal pressure while allowing the transport of molecules into and out of the cell and cell growth. The three-dimensional structure of this unique biopolymer is controversial, and two models have been proposed: the planar model, in which the glycan strands lie in the plane of the cell surface, and the scaffold model, in which the glycan strands lie perpendicular to the cell surface. In this study we have used atomic force microscopy (AFM) to investigate the high resolution structure of isolated, intact sacculi of both Gram-positive and Gram-negative bacterial cells. We have observed a sponge-like structure for both types of sacculi with pore diameters between 5 to 15 nm. Our data for Gram-positive sacculi provide evidence for the validity of the scaffold model, whereas our data for Gram-negative sacculi indicate an orientation along the short axis of the cell which is consistent with the planar model. To further elucidate the structure, we have exposed sacculi to the tAmiB enzyme which cleaves peptide-peptide bonds.

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