Editorial
Volume 11:4, 2022

Journal of Medical Microbiology & Diagnosis

ISSN: 2161-0703 Open Access

Cell Regulation Microbial Cell Regulation an Outsider's Perspective

Mark Herman*

Department of Anaerobic Bacteriology, University of Houston, Houston, USA

Editorial

During growth and propagation, a bacterial cell enlarges and subsequently divides its peptidoglycan PG saccules, a continuous mesh-like layer that encases the cell membrane to confer mechanical strength and morphological robustness. The mechanism of saccules growth, how it is regulated and how it is coordinated with other cellular processes is poorly understood [1]. In this article, we will discuss briefly the current knowledge of how cell wall synthesis is regulated, on multiple levels, from both sides of the cytoplasmic membrane. According to the current knowledge, cytosolic scaffolding proteins connect PG synthases with cytoskeletal elements and protein phosphorylation regulates cell wall growth in Gram-positive species. PG-active enzymes engage in multiple protein–protein interactions within PG synthesis multienzyme complexes, and some of the interactions modulate activities [2].

PG synthesis is also regulated by central metabolism and by PG maturation through the action of PG hydrolytic enzymes. Only now are we beginning to appreciate how these multiple levels of regulating PG synthesis enable the cell to propagate robustly with a defined cell shape under different and variable growth conditions. During growth and propagation, a bacterium must regulate macromolecular synthesis in order to replicate precisely [3]. One of the largest macromolecules of the cell is the and morphological robustness. The PG saccules achieves these structural feats through a deceptively simple composition of glycan chains of alternating N-acetylglucosamine and N-acetylmuramic acid residues that are connected by short peptides containing d-amino acid. This basic arrangement is widely conserved across most bacterial species, however, variation in the chemistry of this basic unit, particularly variations in the residues of the peptide stem and secondary modifications in the glycan chains, allow for great diversity in fine structure and architecture. In the well-studied Gram-negative model bacterium Escherichia coli, the newly made peptide has the Dap, meso-diaminopimelic acid.

Many Gram-positive species have d-isogon generated by amidation of d-isogloss at position, l-Lys instead of mesa-Dap at and a peptide branch of amino acids or glycine attached to the side chain of the l-Lys. Substrate for peptide cross-linking enzymes. In Gram negative bacteria, the PG saccules are integrated within a complex cell envelope between the cytoplasmic and outer membranes OM and are mostly a single layer 3–6 nm thick. By contrast, the cell wall of Gram-positive species is thicker 10–40 nm and contains secondary polymers such as teichoic acids and capsular polysaccharides. In addition, many proteins with various functions are covalently anchored to the stem peptides by sortase enzymes. Some Gram-negative species covalently attach an abundant OM-anchored lipoprotein, Braun's lipoprotein, to the mesa-Dap residue of the stem peptide thus tightly connecting the PG and OM.

Bacteria also possess an array of peptidoglycan-binding proteins, some of which play roles in the process of saccules growth. The mechanisms by which bacteria enlarge and divide the PG saccules during cell growth and division are poorly understood. Current model, PG growth is facilitated by dynamic multiprotein complexes containing PG synthases and hydrolases and cell morphogenesis proteins [4]. These complexes are positioned and/or are controlled by cytoskeletal elements to form large cell morphogenesis complexes, the longsome for cell growth in rod-shaped bacteria and the divisive for cell division. The phenotypes of mutant strains, the subcellular localisation of key proteins and the existence of a large number of protein interactions [5]. However, the exact composition of these complexes and how they function in the cell are not known and we presumably do not yet know all of the proteins architecture with distinct domains for catalysis and for interactions regulation.

References

1. Typas, Athanasios, Manuel Banzhaf, Carol A. Gross and Waldemar Vollmer. "From the regulation of peptidoglycan synthesis to bacterial growth and morphology." *Nat Rev Microbiol* 10 (2012): 123-136.
2. Brubaker, Sky W., Kevin S. Bonham, Ivan Zanoni and Jonathan C. Kagan. "Innate immune pattern recognition: a cell biological perspective." *Ann Rev Immunol* 33 (2015): 257-290.
3. Noverr, Mairi C and Gary B. Huffnagle. "Does the microbiota regulate immune responses outside the gut?." *Tre Microbiol* 12 (2004): 562-568.
4. Buchanan, Bob B. "Regulation of CO2 assimilation in oxygenic photosynthesis: the ferredoxin/thioredoxin system: perspective on its discovery, present status, and future development." *Arc Biochemi Biophy* 288 (1991): 1-9.
5. Hett, Erik C and Eric J. Rubin. "Bacterial growth and cell division: a mycobacterial perspective." *Microbio Mol Bio Rev* 72 (2008): 126-156.

***Address for Correspondence:** Mark Herman, Department of Anaerobic Bacteriology, University of Houston, Houston, USA; E-mail: markherman@gmail.com*

Received: 02 April, 2022; Manuscript No. jmmd-22-64945; **Editor Assigned:** 06 April, 2022; PreQC No. P-64945; **Reviewed:** 16 April, 2022; QC No. Q-64945; **Revised:** 19 April, 2022, Manuscript No. R-64945; **Published:** 26 April, 2022, DOI: 10.37421/2161-0703.2022.11.344

How to cite this article: Herman, Mark. "Cell Regulation Microbial Cell Regulation an Outsider's Perspective." J *Med Microb Diagn* 11 (2022): 344.