

# Preface

This book provides an overview of the current knowledge on the envelope structures of Gram-positive bacteria, their biosynthesis and assembly, their functions as well as their role as antibacterial targets and in biotechnology applications. This is a concise volume containing eleven chapters, from renowned experts in the field, reviewing recent findings and knowledge on very diverse arguments and at the same time linked to each other. That is the uniqueness behind a book like this and the added value towards a search in literature databases.

The cell envelope of these bacteria includes surface proteins, capsular polysaccharides, peptidoglycan, teichoic acids, and phospholipids. These components play key roles in cell viability, virulence and evasion of host defences. Many virulence factors of pathogenic species reside on the bacterial surface. Surface proteins have very diverse functions (e.g., adhesion, invasion, signalling, conjugation, interaction with the environment and immune-evasion). On the other hand, polysaccharides often play a mechanical protective role for the bacterium and the remarkable structural diversity in capsular polysaccharides favours immune evasion. Peptidoglycan is a well-established target for antibiotics and can undergo modification to decrease susceptibility to the drugs.

Both surface proteins and sugars, being the most exterior components, are also accessible to antibodies and represent important vaccine targets. Certain proteins assemble into complexes forming secretion apparatuses, such as the type VII secretion system, pili (or fimbriae) and flagella. These macromolecular structures have very diverse functions, which include secretion, conjugation, adhesion, bio-film formation and motility. Obviously, different species have different envelope structures and the knowledge on most important species (e.g., *Actinomyces* spp., *Bacillus* spp., *Clostridium* spp., *Enterococcus* spp., *Streptococcus* spp., and *Staphylococcus* spp.) is rapidly increasing.

Given the complexity and breath of the literature behind this argument we decided to write this book in the attempt to give an overview of the current knowledge on the envelope structures of Gram-positive bacteria, their biosynthesis, and functions. Secretion systems, spatial organization of cell wall-anchored proteins and bioinformatic algorithms for predicting subcellular localization of proteins are

explained in a simple but detailed fashion. Assembly mechanisms of structures such as pili and sugar polymers are described along with the recently discovered Type VII secretion system. The latter one has been described in low-GC Gram-positive bacteria and they can show a very complex organization with up to five chromosomal-encoded systems (ESX-1 to ESX-5) in mycobacteria to a much simpler organization in Firmicutes.

Finally, relevant examples of applied science which exploit knowledge on Gram-positive bacteria are also included. Possible targets for new antimicrobials are noted. We highlighted the development of the Twin-arginine protein translocation system (Tat) for the biotechnological secretion of fully folded and co-factor-containing proteins and its potential use as an anti-microbial drug target. The use of these bacteria in biotechnology for the production of heterologous proteins and methodologies for analyzing surface and secreted proteins with a particular emphasis to vaccine antigen discovery are also discussed.

In conclusion, this book is useful to any researcher, clinician or technician who is involved with basic or applied science projects on Gram-positive bacteria.

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