



Brucella: Molecular Microbiology and Genomics

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Brucella is a genus of Gram-negative, facultative, intracellular bacteria that are highly pathogenic for a variety of mammals, including humans. Recently, the World Health Organization cited brucellosis to be the world's most widespread zoonosis. An important feature of the pathogenicity of these organisms is their ability to survive and replicate within the host macrophages. However, the mechanism for this is unclear. In addition, none of the classical bacterial virulence factors found in other bacterial pathogens have been found in the genomes of the 40 Brucella species and biovars analyzed to date. Nevertheless, the application of systems biology approaches in recent years has transformed research, permitting fascinating new insights into Brucella molecular biology and genomics. Written by highly acclaimed Brucella scientists, this book comprehensively reviews the most important advances in the field. The opening chapters focus on genetic diversity within Brucella, covering both classical and new species. Particular emphasis is given to how comparative genomics has led to advances in molecular diagnostics, taxonomy, and phylogeny. Additional chapters cover proteomic analysis, transcriptomic analysis, the VirB type IV secretion system, signaling complexes - e.g. the BvrR/BvrS two-component regulatory system and quorum sensing. These chapters highlight the intricate interplay between factors involved in virulence. Another chapter discusses the role of the Brucella cell envelope in bacterial virulence and evasion of host defenses, and the final two chapters review the current strategies for the development of novel antibacterial agents and improved vaccines. This volume is essential reading for everyone with an interest in Brucella and brucellosis. It is also recommended for cellular microbiologists and immunologists, and vaccine development scientists, as well as a wider body of scientists, veterinarians, and MDs with an interest in microbial diagnostics, microbial pathogenesis, and host-parasite interactions.

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