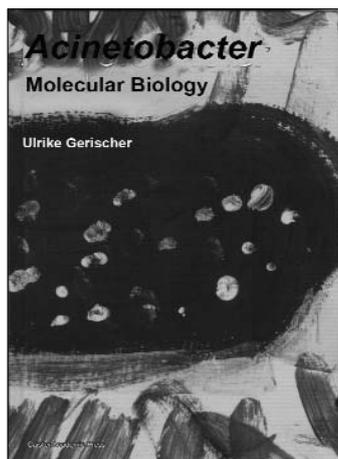


# BOOK REVIEWS

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## *Acinetobacter*. Molecular biology

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In 1911, Martinus W. Beijerinck (1851–1931) described an organism that had been isolated from soil by enrichment cultivation on calcium acetate mineral medium. This organism was named *Micrococcus calcoaceticus*. In the following decades, similar organisms were described independently and assigned different genus and species names, such as *Bacterium anitratum*, *Herellea vaginicola*, and *Mima polymorpha*. In 1968, Paul Baumann, Roger Y. Stanier (1916–1982), and Michael Doudoroff (1911–1975) published a detailed study in which they concluded that these organisms represented a single genus, for which they proposed the name *Acinetobacter*.

The ubiquity, nutritional versatility, and pathogenicity of many *Acinetobacter* species make the genus a worthy subject of investigation. In *Acinetobacter–molecular biology*, state-of-the-art information about these recent investigations is presented. *Acinetobacter* is a group of gram-negative, non-motile, and non-fermentative bacteria belonging to the family Moraxellaceae of the  $\gamma$ -proteobacteria. They are commonly present in soil and water, but most isolates have come from clinical sources. A heterogeneous group of organisms, they comprise at least 32 different species, 17 of which have been assigned valid species names, with 14 unnamed species as a “genomic group”. Biochemical identification at the species level has proven difficult; instead, molecular methods (based on nucleotide sequence) are expected to be a useful tool for correct identification. However, their successful application requires the availability of libraries containing sequences of strains of all described genomic species, and for each species the sequences should cover the intra-species diversity. Molecular characterization has been further complicated by several problems, including that fact that 16S rRNA gene sequences have been submitted to GenBank under erroneous

names. Thus, the taxonomy of *Acinetobacter* is very confusing to those not familiar with the genus. Chapters 1, 2 and 6 of *Acinetobacter–molecular biology* address the diversity, taxonomy and genetics of members of the genus.

Horizontal gene flow is a driving force in bacterial adaptation and has been shown to have a tremendous impact on the evolution of bacterial genomes. *Acinetobacter baylyi* strain ADP1 has a high competence for natural transformation—a trait that differentiates *A. baylyi* from all other *Acinetobacter* species. The unique features of the natural transformation system and the widespread distribution of *A. baylyi* strain ADP1 in different environments have stimulated analyses of recombinant DNA spread and horizontal gene transfer in natural environments (Chapter 5). *Acinetobacter* strains isolated from the environment are capable of degrading many types of aromatic compounds. The  $\beta$ -keto adipate pathway serves as the main route through which aromatic compounds enter central metabolism. While other genera, such as *Pseudomonas*, *Sphingomonas*, *Ralstonia*, have a broad range of catabolic substrates, including natural and synthetic compounds, *Acinetobacter* seems to be a catabolically more conservative genus, with its growth substrates mainly limited to naturally occurring compounds, either of plant origin or derived from oil reserves (Chapters 4 and 8). Most catabolic pathways in bacteria are controlled with respect to expression of the enzymes making up the respective pathway. Those organisms that most efficiently regulate gene expression are likely to be well positioned in terms of competition with others (Chapter 8). Lys R-type transcriptional regulators (LTTRs) make up the largest family of homologous regulators in prokaryotes. Chapter 7 explores their function in *Acinetobacter* strains to improve our understanding of metabolic regulation (aromatic compounds catabolism), pathogenicity, and drug resistance.

Many of the characteristics of *Acinetobacter* ecology, taxonomy, physiology, and genetics point to the possibility of exploiting the unique features of this genus for biotechnological applications. *Acinetobacter* strains are often ubiquitous and exhibit metabolic versatility as well as high transformability, all of which are important in the design of bacterial systems for modern molecular genetic manipulation and subsequent product engineering. These characteristics are being exploited in biodegradation and bioremediation, novel lipid and peptide production, enzyme engineering, biosurfactant and biopolymer production, and the engineering of novel derivatives of these products, among others. It is anticipated that progress in these fields will broaden the range of biotechnological applications of *Acinetobacter* (Chapter 9).

Members of the *Acinetobacter* genus play an important role in nosocomial infections and have attracted particular attention in severe cases involving ICU patients. *Acinetobacter baumannii* is the most relevant human pathogen within the *Acinetobacter* genus. Outbreaks of nosocomial infections caused by this microorganism include urinary tract infections, secondary meningitis, wound and burn infections, and, particularly, pneumonia. *Acinetobacter* virulence is mediated by fimbriae, exopolysaccharide, lipopolysaccharide (Chapter 3), and extracellular enzymes. The molecular nature of these potential virulence factors and their role in pathogenesis remain to be investigated (Chapter 10).

*Acinetobacters* are widely distributed in hospitals, and contaminated surfaces serve as an indirect source of *A. baumannii* infection. Up to 27% of hospital sink traps; 20% of hospital floor swabs; 11% of beds, bed curtains, tables, monitors, charts; and 29% of the hands of medical personnel have yielded isolates of *Acinetobacter*. The capability of *A. baumannii* to survive on inanimate surfaces for an extended period of time has been implicated in the persistence of endemic strains, particularly in the ICU. Environmental surveys have shown that *A. baumannii* can be found on a multitude of patient-near surfaces, from where these organisms may be

inadvertently transferred to other patients either directly or via the hands of hospital personnel (Chapter 11). Some of the challenges in the prevention and treatment of infections caused by *A. baumannii* are the bacterium's remarkable widespread resistance to antibiotics and its persistence in nosocomial environments and medical devices, even under conditions that inhibit other bacterial pathogens, such as methicillin-resistant *Staphylococcus aureus* to "switch" its genetic structure may explain the unmatched speed at which it captures resistance markers under antibacterial selection pressure.

Therefore, this useful book is especially recommended for advanced students in the field, senior researchers, and physicians; but all microbiologists will find in the book an exceptional opportunity to extend their understanding of an unusual and unique microbial group.

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