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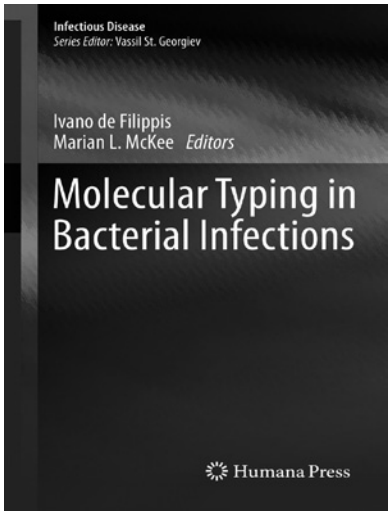

Molecular typing in bacterial infections

Ivano de Filippis, Marian L. McKee (eds)

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New molecular tools taking advantage of DNA-based approaches are highly relevant to epidemiological studies and they have expanded rapidly over the past 20 years. *Molecular typing in bacterial infections*, edited by de Filippis and McKee, is structured into seven parts: (I) General consideration of microorganism typing methods, (II) gastrointestinal pathogens, (III) oral and respiratory pathogens, (IV) urogenital pathogens, (V) vector-borne pathogens, (VI) pathogens causing hospital-associated infections, and (VII) emerging and re-emerging pathogens. Each part discusses the most important microorganisms in each group and the chapters highlight the most frequently used methods for the typing of each of these pathogens. However, the chapters are not unified by a regular format; for example, while some have an introduction and conclusion or concluding remarks, others do not.

In part I, A.E. Seitz and D.R. Prevots define molecular epidemiology and describe its current applications. In part II, Chapter 2, L.M. Teixeira and V.L.C. Merquior discuss the different methods used in the molecular typing of *Enterococcus,* remarking on the absence of a single definitive typing method for this group of bacteria. In Chapter 3, T. J. Ward presents the different phenotypic and genotypic methods used to investigate the epidemiological relationships among *Listeria monocytogenes* strains. He compares the key features of pulse-field gel electrophoresis (PFGE), multilocus sequence typing (MLST), multilocus geno-typing (MLGT), and multiple-locus variable-number tandem repeat analysis (MLVA). Although PFGE remains the gold standard for the discrimination of *L. monocytogenes* strains, further development of DNA-sequence-based subtyping will probably provide the best combination of discriminatory power, epidemiological utility, and efficiency. In Chapter 4, S.L. Foley, A.M. Lynne, and R. Nayak review the different typing methods that comprise restriction-based methods, DNA-amplification-based methods, and DNA sequencing-based methods to discriminate among strains from the most frequently isolated species of Enterobacteriaceae. Here as well, PFGE is the gold standard; however, MLST can be used to gain a better appreciation of the genetic diversity of the population of isolates being examined. A report on molecular methods to type *Vibrio cholera* is provided by T. Ramamurthy, A.K. Mukhopadhyay, R.K. Nandy, and G. Balakrish in Chapter 5. These authors described the most frequently used typing methods but also include a discussion of genetic elements, such as plasmids, insertion sequences, and integrons, as the basis of potential phylogenetic typing systems. This is the first chapter in the book that evaluates the whole genome approach as a powerful tool to understand the origin and relationship of pandemic clones. In Chapters 6 and 7, the typing of two anaerobes (*C. difficile* and *Bacteroidetes*) is introduced. A plethora of different methods have been used to type *C. difficile* because of its clinical importance, with PFGE and MLVA having the highest discriminatory power.

Part III covers oral and respiratory pathogens. L. McGee and B. Beall, in Chapter 8, analyze the three major streptococci (*S. pyogenes, S. agalactiae*, and *S. pneumonia*).

They note that MLST is the most discriminatory tool but also describe the underlying concept of eBURST and its application in exploring patterns of evolutionary descent. In Chapter 9, specific typing of *Streptococcus mutans* is presented. Chapter 10 deals with metagenomic analysis of the oral microbiome and the specific typing of periodontal pathogens. In the authors' view, typing is more informative for therapeutics than for epidemiology. Typing of non-tuberculous mycobacteria is the focus of Chapter 11. The next two chapters address the typing of *Neisseria meningitides* (Chapter 12), and *Haemophilus influenza* (Chapter 13); in both cases, MLST is currently the most commonly used method. Chapters 14–18 cover *Moraxella, Legionella pneumophila,* mycoplasma and ureaplasma, *Corynebacterium diphteriae*, and *Burkholderia.* Overall, the content in these chapters is very heterogeneous; for instance, only seven pages are devoted to *L. pneumophila* while 53 pages are devoted to mycoplasma and ureaplasma. In the chapters on *Moraxella* and *L. pneumophila,* matrix-assisted laser desorption-ionization time-of-light mass spectrometry (MALDI-ToF MS) as a potential typing tool is discussed.

Part IV covers *Treponema* (Chapter 19) and the family Chlamydiaceae (Chapter 20). PCR-based restriction fragment length polymorphism (RFLP) analysis of specific genes is one of the most common techniques used to type these microorganisms. Part V focuses on vector-borne pathogens, i.e., *Borrelia* (Chapter 21) and *Erysipelotrix* (Chapter 22). MLST and PCR-sequencing are viewed as future typing techniques for these microorganisms. Parts VI and VII discuss major nosocomial microorganisms: staphylococci (Chapter 23), *Pseudomonas* (Chapter 24), and *Acinetobacter baumannii* (Chapter 25). In these microorganisms, two routes of investigation can be distinguished: local hospital outbreaks and international population studies, with PFGE and MLST as the most appropriate typing techniques, respectively.

Familiarity with the different methods for the correct typing of microorganisms is important for many fields of medical and microbiological research. This book should be required reading not just for microbiologists, epidemiologists, and infectious disease specialists but also for university students of infectious diseases and clinical microbiology, who while increasingly trained in molecular epidemiology may have a poor understanding of the techniques used in this field.

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