

THE ENTEROBACTERIA

SECOND EDITION

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To

Marjorie L. Bissett
Chief, Enterics and Special Pathogens Section (Retired)
and
Cathy Powers
Supervisor, Enteric Bacteriology Unit (Retired)
Microbial Diseases Laboratory
California Department of Health Services

Thank you for sharing your knowledge, technical skill, and experience regarding
this fascinating group of bacteria with us
and for your dedication to the field of public health

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PREFACE

In the first edition of *The Enterobacteria*, we stated, “No taxonomically defined group of bacteria has had a greater impact on infectious diseases, medical and clinical microbiology, and public health than the enterobacteria.” With the second edition of this book, this statement has been reinforced over the past 7 years with an increasing body of evidence magnifying both the scope and depth of how the family *Enterobacteriaceae* impacts our daily lives.

There are a number of important changes to the second edition of this book, only a couple of which will be highlighted here. The use of 16S rRNA sequencing both as an aid to the identification of unknown enteric bacteria and to classify taxonomic groups appropriately can be seen throughout the text. Such changes include the reclassification of the oxidase-positive genus *Plesiomonas* as a member of this family (chapter 19). The use of molecular probes to identify specific species or genera is also discussed where appropriate. Also, phylogenetic investigations coupled with molecular studies have increasingly revealed a world of enterobacteria not associated with humans or animals, but intimately connected with

insects as endosymbionts, as plant pathogens, or in specific environmental niches (chapter 2). The number of hosts and environments impacted by the *Enterobacteriaceae* is expanding at logarithmic rates. A second new feature of this book is an appendix, “Differential Biochemical Tables for Enterobacteria.” In this appendix, one can find tables which will help a microbiologist identify an organism from genus to species level or, conversely, can aid a laboratorian in the initial placement of an isolate into the correct genus on the basis of a single trait (e.g., H₂S production) or multiple unusual phenotypes (e.g., negative for lysine decarboxylase, ornithine decarboxylase, and arginine dihydrolase).

It is hoped that this second edition will serve as a reference source for those microbiologists, physicians, infectious disease specialists, pathologists, epidemiologists, infection control practitioners, and scientists who need in-depth information on these bacteria beyond what is covered in the eighth edition of the *Manual of Clinical Microbiology*.

J. Michael Janda
Sharon L. Abbott

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