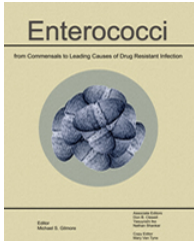




U.S. National Library of Medicine
National Center for Biotechnology Information

NLM Citation: Gilmore MS, Clewell DB, Ike Y, et al., editors. Enterococci: From Commensals to Leading Causes of Drug Resistant Infection [Internet]. Boston: Massachusetts Eye and Ear Infirmary; 2014-. Preface. 2014 Feb 24.
Bookshelf URL: <https://www.ncbi.nlm.nih.gov/books/>



Preface

Created: February 24, 2014.

The enterococci are an ancient genus of microbes that are highly adapted to living in complex environments and surviving harsh conditions. To the extent that we currently understand their native ecology, they inhabit the gastrointestinal tracts of a wide variety of animals, from insects to man. This suggests that they also inhabited the gastrointestinal tracts of our ancient common ancestors. This would place them among the earliest members of a symbiotic consortium, a microbiota that we now appreciate serves roles ranging from facilitating digestion to providing the host with development cues and protecting it from colonization by more antagonistic microbes. It appears that most of the evolutionary refinement of these organisms occurred prior to the advent of humans. However, it is becoming clear that human activities—from urbanization and the domestication of animals to the introduction and broad application of antibiotics—have selected for the convergence of novel combinations of traits in some species, mainly *Enterococcus faecalis* and *E. faecium*, which are now leading causes of multidrug-resistant hospital-acquired infections. Moreover, the enterococci serve as reservoirs for antibiotic resistances that they are spreading to other important pathogens, most notably *Staphylococcus aureus*.

With the advent of genomic technologies, the number of enterococcal species has exploded. It is likely that many of the traits that have emerged in highly adapted hospital lineages of *E. faecalis* and *E. faecium*, including traits that exacerbate infection and even antibiotic resistance, either originate or have passed through some of these species. Our knowledge of the genetic content of the genus is in its infancy. While we are rapidly learning about the genus (in large part through the genomes of its various species), our general knowledge about the ecology and evolution of these species is almost nonexistent. Although several enterococci inhabit humans, it is unlikely that any currently known species evolved in humans as the definitive host (except for the highly hospital adapted *E. faecium* CC17 lineage, which by some measures can legitimately be regarded as a new species). Microbes evolve into new species when introduced into a new and isolated habitat. However, there currently is no real understanding of any particular isolated habitat that gave rise to a specific species of *Enterococcus*. The problem is that, as we discover novel genes in various species of enterococci, we are at a loss to know their precise native function in the ecology in which they evolved. By understanding the traits that have contributed to the host/microbe dynamic in an evolved, natural context, we will be much better positioned to understand their roles when they emerge in hospital lineages that confound human infection.

To advance the understanding of enterococci as leading causes of multidrug resistant infection, to increase our knowledge of the genus and its relation to humans and other forms of life, and to build a collaborative research community, we organized the 1st International ASM Conference on Enterococci in Banff, Canada, February 27–March 2, 2000. That conference produced a recognized need for a comprehensive text that would provide a definitive resource for members of the community, as well as a point of entry for those interested in helping to address this important problem. In response to these issues, *The Enterococci: Pathogenesis, molecular biology, and antibiotic resistance*, published by ASM Press in 2002, was produced by the research community, and has ably served these roles for the past decade.

However, because of the rapid rate of knowledge growth, which has been catalyzed by the introduction of powerful new technologies, it has become increasingly important to reassess the landscape of knowledge of the enterococci. Moreover, new technologies and resources became available that have made it possible to do this in a new way—to generate a living document that can be updated on a regular basis, and to disseminate it instantly and freely on a global scale. Thus, the genesis of *Enterococci: From commensals to leading causes of drug resistant infection*, a compilation of peer reviewed content contributed by many of the leaders in the *Enterococcus* research community, and provided as an open access book on the U.S. National Institutes of Health NCBI Bookshelf. The *Enterococcus* research community once again pulled together to collaboratively author and review chapters that comprehensively span our knowledge of the enterococci, and this document would not have been possible without their effort and a shared interest in advancing the field. Our collective hope is that this document will catalyze progress in solving the important problem of enterococci as leading causes of multidrug-resistant hospital-acquired infections, and will further advance knowledge of this important genus and its place in biology.

Taking this new and democratic approach to publication proved a challenging task, as the path was not clear and there were few examples to draw from. Without the services provided by a commercial publisher, chapters had to be manually parsed for peer review, reviews compiled, chapters revised and edited for scientific content, and content had to be edited for readability. Each of the associate editors contributed much to the process, and this project would not have been possible without their input. After attempting to perform many of the review and revision tasks myself, it became obvious that there was a real need for a professional copy editor. The work of Mary Van Tyne was absolutely instrumental in finally bringing this project to fruition. She worked tirelessly to bring the chapters into a consistent style, to check and automate references, and to interface with NCBI. Finally, this project would not have been possible without the helpful guidance of the leadership and staff at NCBI, including Director David J. Lipman, as well as the NCBI Bookshelf Project Lead, Marilu A. Hoepfner.

Finally, sharing and disseminating this knowledge on a leading public health concern would not have been possible without the support of the National Institutes of Health sponsored Harvard-wide Program on Antibiotic Resistance (AI083214), and support of the Department of Ophthalmology, Harvard Medical School and the Massachusetts Eye and Ear Infirmary. On behalf of all of the editors, we extend our deepest thanks to everyone who contributed in so many ways to production of this volume. As a living document, we also extend our deepest appreciation in advance to everyone who will contribute to its further growth, as it continues to serve the community in the future.

Michael S. Gilmore

Editor in Chief

License

This work is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License. To view a copy of this license, visit <https://creativecommons.org/licenses/by-nc-nd/4.0/>