Enterococcus research: recent developments and clinical challenges

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Over the last two decades, awareness of enterococci as important multidrug-resistant (MDR) nosocomial pathogens has increased [1,2]. Enterococci are now among the leading healthcare-associated pathogens worldwide [3–7]. Enterococcus faecalis and Enterococcus faecium remain the dominant species in clinical infections, although their relative contributions have changed over the years. The ratio of E. faecalis to E. faecium in systemic infections has now approached 1:1 in many countries [3–5]. Importantly, the absolute and relative increase in E. faecium infections has been associated with acquired resistance to important anti-enterococcal agents such as ampicillin, aminoglycosides and vancomycin [3,8]. Molecular epidemiological studies and population structure analyses suggest that the emergence of E. faecalis and E. faecium as major nosocomial pathogens has resulted from the evolutionary development of specific hospital-associated lineages or clonal complexes in which antimicrobial resistance and virulence determinants have accumulated [9–11].

During the last decade, risk factors for colonization and bacteraemia have been identified and include underlying diseases, antibiotic use, noncompliance with infection control measures and colonization pressure [12–14]. Moreover, molecular evidence with respect to how gastrointestinal colonization with MDR enterococci can be promoted by antibiotic-induced mucosal innate immunity deficits has recently been provided [15]. Notably, early and appropriate antimicrobial therapy of bacteraemia caused by MDR enterococci improves patient survival [14]. Thus, the changing epidemiology of enterococcal infections remains a true challenge in clinical diagnostic microbiology, both for infection control and antimicrobial treatment.

This special theme section on enterococcal infections has been stimulated by the collaborative efforts of many co-authoring researchers during the ongoing ACE (Approaches to Control multi-resistant Enterococci) project, funded by the Sixth Framework Programme of the European Union (http://www.aceproject.eu/project_outline.php). In this special section, the mechanisms that may have promoted the transition of enterococci from human gastrointestinal commensals to major nosocomial pathogens are reviewed, as well as the latest insights concerning anti-enterococcal therapy. Recent genomic insights into the evolution of E. faecalis and E. faecium are reviewed by van Schaik and Willems [16]. Whole-genome sequencing and comparative genomic analysis have revealed large intra-species diversity also within clonally related strains. Until recently, there has been a relative lack of genome information in enterococci compared to other human pathogens. However, in 2009, more than 20 draft genome sequences of E. faecalis and E. faecium were deposited in public databases, providing new opportunities for refining our understanding of Enterococcus. Sava et al. [17] summarize our current knowledge of putative virulence factors in E. faecalis and E. faecium and the identification of targets of protective immune responses. Subsequently, Hegstad and co-workers provide an update on mobile genetic elements in enterococci and their contribution to the spread of antimicrobial resistance and associated virulence determinants [18]. Recent developments in the molecular epidemiology and typing of enterococcal plasmids are also addressed. Finally, Arias et al. [19] review the clinical challenges faced with respect to antimicrobial treatment of infections by MDR enterococci. Current therapeutic alternatives of severe MDR enterococcal infections remain to be based on empirical observations and extrapolation from in vitro and animal data, emphasizing the critical need for clinical studies that evaluate new therapies.

Transparency Declaration

The authors state that they have no conflicts of interest.

References