

Abstract

Bacteria of the genus *Enterococcus* are categorised among common nosocomial pathogens. They are a significant reservoir of resistance genes to a majority of antibiotics and exhibit an intrinsic resistance to low levels of beta-lactams, glycopeptides, aminoglycosides, streptogramins and lincosamides. The aim of this paper is to review the main resistance genes and other mechanisms involved in the resistance of bacteria of this genus to antibiotics. The paper is mainly focused on the resistance to beta-lactam antibiotics, which is provided by the expression and mutations of low-affinity PBPs, the individual van resistance types mediating resistance to vancomycin, and the expression of enzymes capable of modifying the functional groups of aminoglycoside antibiotics. The paper also describes the resistance to newer antibiotics that are used to treat vancomycin-resistant isolates. The resistance to individual antibiotics can arise from the coding of their own chromosomal genes or entire signaling pathways leading to a reduction in the effect of antibiotics, the acquisition of genetic mutations, and especially the spread of new resistance genes by horizontal transfer.