

### O0338 Emergence of linezolid-resistant enterococci in France

Mohamed Sassi<sup>1</sup>, François Guérin<sup>2</sup>, Asma Zouari<sup>3</sup>, Michel Auzou<sup>2</sup>, Marguerite Fines-Guyon<sup>2</sup>, Sophie Potrel<sup>5</sup>, Anaïs Collet<sup>5</sup>, Gabriel Auger<sup>5</sup>, Richard Bonnet<sup>4</sup>, Vincent Cattoir<sup>\*1 5</sup>

<sup>1</sup>Université de Rennes 1, Inserm unit U1230, Rennes, France, <sup>2</sup>CHU de Caen, Microbiology, Caen, France, <sup>3</sup>CHU de Rennes, National Reference Center for Enterococci, Rennes, France, <sup>4</sup>CHU de Clermont-Ferrand, Microbiology, Clermont-Ferrand, <sup>5</sup>CHU de Rennes, Microbiology and National Reference Center for Enterococci, Rennes, France

**Background:** Linezolid is an important option for the treatment of infections caused by vancomycin-resistant enterococci (VRE). Although resistance to linezolid was mainly due to chromosomal mutations in rRNA 23S and ribosomal proteins, plasmid-mediated resistance has recently emerged with the spread of *cf*r-like and *op*trA genes. The aim of the study was to describe the epidemiological trend of linezolid-resistant enterococci (LRE) collected in France and to extensively characterize LRE isolates.

**Materials/methods:** The National Reference Center for Enterococci (NRC-Enc) received isolates suspected to be VRE and/or LRE from all French hospitals between 2006 and 2016. LRE isolates were phenotypically characterized (MALDI-TOF, disk diffusion, MIC microdilution). Genomes of LRE isolates were sequenced by Miseq (Illumina) and bioinformatic analysis was done using the CLC Genomics Workbench software (Qiagen) and the ResFinder server. Transfer of linezolid resistance to *Enterococcus faecium* (EFM) BM4107 and *Enterococcus faecalis* (EFS) JH2-2 was attempted by filter mating experiments.

**Results:** From 2006 to 2016, 3,974 clinical isolates of enterococci were received at the NRC-Enc. Of them, 9 (0.2%) were resistant to linezolid (MICs from 8 to >32 mg/L). These strains were epidemiologically unrelated, and were isolated in 2010 (1 EFM), 2013 (1 EFM), 2014 (1 EFM), 2015 (2 EFM) and 2016 (1 EFM and 3 EFS). All LRE isolated before 2016 were EFM VRE (*vanA*) whereas strains isolated in 2016 were susceptible to vancomycin. All strains were susceptible to daptomycin and tigecycline. Except for the strain isolated in 2010, all LRE were positive for *op*trA that was mainly plasmid borne (6/8). Note that *op*trA and *vanA* were not carried by the same plasmid. The four first strains also harbored G2576T mutations in 23S rRNA (4-5 mutated alleles/6) while no mutations were found in L3, L4 and L22 ribosomal proteins. Conjugation experiments were successful for 3 LRE harboring a plasmid-mediated *op*trA (2 EFM and 1 EFS).

**Conclusions:** There is a significant increase of the prevalence of linezolid resistance among enterococci in France over time, which is due to the spread of *op*trA. It may be related to higher consumption of linezolid in France since it has been a generic drug in 2015.