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Emergence of *optrA*-mediated linezolid resistance in *Enterococcus faecalis* clinical isolates from Argentina

03. Bacterial susceptibility & resistance

3a. Resistance surveillance & epidemiology: MRSA, VRE & other Gram-positives

Likely attendance

Onsite

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Background

Linezolid-resistant enterococci are still rare but require strict surveillance to identify emerging resistance mechanisms and the associated clones. Linezolid resistance can result from mutational mechanisms (23S rRNA and/or ribosomal protein mutations) or resistance genes acquisitions (*cftr*, *optrA* and *poxA* genes) often associated with mobile genetic elements.

The aim of this study was to characterize the first linezolid-resistant *E. faecalis* (LRE) clinical isolates from Argentina.

Methods

From 2016 to 2021, 14 LRE were submitted to the National Reference Laboratory from 7 hospitals and three cities in Argentina. Antimicrobial susceptibility was evaluated by disk diffusion and interpreted according CLSI 2021, except tigecycline (FDA). Linezolid resistance was confirmed by Etest, Vitek-2, Phoenix and *optrA* gene PCR. Clonal relation was evaluated by SmaI-PFGE and MLST. All the LRE isolates were whole genome sequenced by Illumina.

Results

Among the 14 LRE, linezolid MICs were between 4 and 16 µg/ml, all showed Oph phenotype of resistance to oxazolidinones and chloramphenicol and carried *optrA* and *fexA* genes. LRE were differentiated in 14 SmaI-PFGE clonal types and 13 sequence-types by MLST.

They were also resistant to tetracycline and minocycline but susceptible to penicillin, ampicillin, vancomycin, teicoplanin and tigecycline. Eight presented high-level resistance to aminoglycosides (gentamicin and/or streptomycin) and five to ciprofloxacin. The genes *cftr* and *poxA* were not detected. In addition, no mutation were found in both 23S rRNA and the ribosomal proteins L3, L4 and L22. Three variants of *optrA* were identified, *optrA*-2 (n=12),

optrA-5 (n=1) and optrA-6 (n=1). All the isolates carried tet genes (*tetM*, *tetL* and/or *tetO*), macrolide, lincosamides, streptogramins resistance *ermB*, *ermA*, *lsaA* and/or *lnu* genes. Aminoglycoside resistant isolates carried *aac(6')*-*aph(2'')*, *ant(6)-Ia*; *ant(9)-Ia*, *aph(3')-III* and/or *str* genes. The five ciprofloxacin resistant LRE presented the same amino acid change in both GyrA (S83I) and ParC (S80I) proteins.

Conclusions

We described, in our knowledge, the first LRE isolates associated with the presence of the optrA gene from Argentina. They were highly diverse and carried multiple resistant determinants. The emergence of LRE with transferable linezolid resistance mechanisms represents a challenge for Public Health.

Keyword 1

Antimicrobial resistance (AMR)

Keyword 2

Bacteria and bacterial infections

Keyword 3

linezolid resistance

Conflicts of interest

Do you have any conflicts of interest to declare?

No