Evolving Linezolid Resistance Mechanisms in a Worldwide Collection of Clinical Isolates: Results from the SENTRY Antimicrobial Surveillance Program

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Abstract

Background: Linezolid resistance is critical in vivo for several present and surveillance studies and has reported core and stable resistance rates among Gram- positive clinical isolates. The molecular resistance mechanisms are well known and mostly comprised of G2576T mutations in the 23S rRNA. For nonclinical isolates, the linezolid resistance mechanisms are less known.

Methods: Isolates from the SENTRY Antimicrobial Surveillance Program (2008-2015) were selected based on either the presence of MIC values ≤0.06 or >64 in a panel of antimicrobials. Isolates were analyzed using MALDI-TOF and broth microdilution (CLSI). The remaining isolates were subjected to a proprietary NGS library construction method (B) (USA).

Results: A total of 36 E. faecalis and 62 E. faecium isolates were selected. E. faecalis had linezolid MIC range of 2-16 μg/ml (1%). E. faecium had linezolid MIC range of 4-64 μg/ml (55.6%). A total of 20 isolates (15 E. faecalis and 5 E. faecium) were detected in USA/Thailand and Panama. In contrast, two isolates carrying the cfr-like gene were present in the vicinity E. faecalis (Ampicillin-resistant). In total, E. faecalis isolates originated from the USA (2), Ireland (2), Panama (1) and Malaysia (1). These isolates harbored the cfr-like gene.

Conclusions: Linezolid resistance mechanisms were found in E. faecalis and E. faecium isolates. The cfr-like gene was present in the vicinity of E. faecalis isolates with compromised activity, emphasizing the MDR nature of these isolates. And several other antimicrobial agents had compromised activity, emphasizing the MDR nature of these isolates.

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References


Figure 1. Schematic representation of cfr-like gene chromosomal context in E. faecium. Arrows indicate direction of transcription. Black arrows indicate chromosomal context of selected isolates. These were variable in number and arrangement in different strains.