**Introduction**

Linezolid has been widely prescribed to treat serious infections caused by multidrug-resistant (MDR) Gram-positive pathogens since its clinical introduction as the first oxazolidinone antimicrobial agent now approved by the Food and Drug Administration (FDA) for the treatment of complicated skin and skin structure infections (cSSSI) and complicated urinary tract infections (cUTI) caused by MDR pathogens including MRSA and VRE. The drug is also effective against a number of Gram-negative pathogens, including Pseudomonas aeruginosa (P. aeruginosa) and Acinetobacter baumannii (A. baumannii) [1]. Linezolid is a bacteriostatic agent that inhibits the peptidyl transferase center of the bacterial ribosome, which is critical in the formation and function of the peptidyl transferase center (PTC) of bacterial ribosome on binding of ribosomal targeting agents. The resistance mechanisms are mostly comprised of mutations in the domain V of the 23S rRNA, among which G2576T and C2610T are known to confer linezolid resistance. In addition, several other mechanisms of resistance to linezolid have been described. These include the acquisition of chromosomal modifications of the 23S rRNA, such as the T2211C to A2211V substitution, or the acquisition of plasmid encoding resistance genes [2].

**Methods**

**Antimicrobial susceptibility testing.** Susceptibility testing was performed by broth microdilution method according to the Clinical and Laboratory Standards Institute (CLSI) recommendations (M100-S22. 2012). Validation of the MIC values was performed using a quality control testing kit of CLSI recommended quality control reference strains (Staphylococcus aureus ATCC 29213, Enterococcus faecalis ATCC 29212 and Escherichia coli ATCC 25922). Linezolid-resistant S. sanguinis strains may be susceptible to other antimicrobials, such as chloramphenicol, streptomycin, and teicoplanin [5].

**Screening for linezolid and other resistance mechanisms, and drug-passage testing.** S. sanguinis was screened for the presence of cl, mut and van genes as well as for the presence of vanA or vanB genes.

**Results**

- **Streptococcus sanguinis.** Initial characterization of S. sanguinis revealed a high resistance to clindamycin and tetracycline. S. sanguinis displayed low MICs to doxycycline (8 µg/mL), tiamulin (32 µg/mL), and clindamycin (2 µg/mL) and tigecycline (1 µg/mL). T2211C, T2406C, G2576T and C2610T were observed for L3 and L4. The 23S rRNA modifications, such as T2211C and T2406C, were located more distal and further from the PTC. These modifications are known to be involved in the binding of ribosomal targeting agents. The resistance mechanisms have been extensively characterized. These resistance mechanisms are not commonly reported in the literature. A high number of MICs for linezolid (32 µg/mL), and the resistance in the ribosomal proteins L3, L4 and L22 have also been documented in the literature [3]. S. sanguinis strain demonstrated several mutations in the 23S rRNA, among which G2576T and C2610T are known to confer linezolid resistance. In addition, several other mechanisms of resistance to linezolid have been described. These include the acquisition of chromosomal modifications of the 23S rRNA, such as the T2211C to A2211V substitution, or the acquisition of plasmid encoding resistance genes [5].

**Conclusions**

- The S. sanguinis strain demonstrated multiple mutations in the 23S rRNA, among which G2576T was located within the PTC and known to increase linezolid MIC. The extremely rare detection of a linezolid-resistant S. sanguinis strain causing bacteremia in the United States.

**References**
