Plazomicin is Active against Enterobacteriaceae Isolates Producing Extended-Spectrum β -Lactamases, Carbapenemases, and **Aminoglycoside-Modifying Enzymes from United States (US) Hospitals**

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Introduction

- The increasing number of patients with prolonged hospitalization, including those in intensive care or long-term care facilities, immunodeficient patients, and others with malignant conditions, is often associated with growing rates of infections caused by multidrug-resistant (MDR) organisms
- Among MDR Enterobacteriaceae, commonly highlighted isolates produce extended-spectrum β-lactamases (ESBLs), carbapenem-resistant isolates (CRE), and isolates resistant to aminoglycosides that usually carry genes encoding aminoglycoside modifying enzymes (AMEs)
- Plazomicin is a next-generation aminoglycoside synthetically derived from sisomicin that is designed to have stability against most common aminoglycoside resistance mechanisms
- Plazomicin was approved by the US Food and Drug Administration (FDA) to treat complicated urinary tract infections, including acute pyelonephritis
- We evaluated the activity of plazomicin and comparators against US isolates collected in 2017 carrying genes encoding ESBLs, carbapenemases, and AMEs

Materials and Methods

- A total of 2,051 *Enterobacteriaceae* clinical isolates were collected during 2017 from US hospitals participating in the ALERT (Antimicrobial Longitudinal Evaluation and Resistance Trends) Program - Isolates identified as the cause of infection were included in the study and were limited to 1 per patient
- Isolates were susceptibility tested using the reference broth microdilution method described by the Clinical and Laboratory Standards Institute (CLSI)
- Categorical interpretations for all comparator agents were those in the CLSI guidelines (M100, 2019), European Committee on Antimicrobial Susceptibility Testing (EUCAST) website or United States FDA website
- Quality control (QC) was performed according to CLSI guidelines (M07, 2018), and all QC minimal inhibitory concentration (MIC) results were within acceptable ranges as published in CLSI documents
- CRE was defined as any isolate exhibiting doripenem, imipenem, and/or meropenem MIC values at ≥2 µg/mL

 Proteus mirabilis and indole-positive Proteeae were categorized as CRE if doripenem and/or meropenem MIC values were at $\geq 2 \mu g/mL$ due to intrinsically elevated imipenem MIC values

- Whole genome sequencing on a MiSeq (Illumina, San Diego, California, USA) instrument targeting a 30X coverage was performed on 490 selected isolates
- Escherichia coli, Klebsiella spp., Proteus spp., and Enterobacter spp. isolates displaying nonsusceptible MIC values for gentamicin, amikacin, and/or tobramycin according to CLSI criteria were screened for the presence of AMEs, and any *Enterobacteriaceae* isolate with plazomicin MIC values of \geq 128 mg/L was screened for AMEs and 16S rRNA methyltransferase-encoding genes
- CRE and Enterobacteriaceae isolates displaying an ESBL phenotype were screened for the presence of β-lactamases
- Sequences were de novo assembled and genes encoding resistance were searched using a curated library and applying criteria of >94% sequencing identity and 40% minimum length coverage

Results

- Among 168 isolates carrying AME-encoding genes (Figure 1a), the most common genes modifying amikacin, gentamicin, and tobramycin were aac(6')-Ib-cr (73 isolates), aac(3)-Ila (63), and aac(3)-Ild (54) Various other AME genes were also detected
- Plazomicin was active against 96.4% of isolates carrying AME genes (Figure 2)
- Only 16.7% were susceptible to gentamicin and tobramycin, but 94.0% were susceptible to amikacin - Cefepime and piperacillin-tazobactam inhibited only 41.1% and 76.2% of these isolates, respectively
- ESBL-encoding genes were detected among 91 E. coli, 75 K. pneumoniae, and 3 K. oxytoca that were resistant to extended-spectrum cephalosporins (ceftazidime, ceftriaxone, or cefepime) and/or aztreonam and susceptible to carbapenems (Figure 1b)
- The most common gene detected among these isolates was $bla_{CTX-M-15}$ (107/169) that was observed alone in 42 isolates or combined with other genes, most commonly *bla*_{0XA-1} (60 isolates)
- Plazomicin was the most active agent tested against ESBL-producing isolates and inhibited 99.4% of these isolates at the US FDA breakpoint (Figure 2)
- Amikacin, meropenem, and colistin were the most active comparators and 97.6%, 98.8%, and 98.8% of the isolates were susceptible to these agents, respectively
- Among 22 CRE isolates, 18 harbored carbapenemase genes that totaled 11 bla_{kPC-2}, 6 bla_{kPC-3}, and 1 bla_{oxa-232} (Figure 1c)
- Twelve (66.6%) of these isolates were *K. pneumoniae*, but 4 other bacterial species carried these genes: Citrobacter freundii, C. koseri, Enterobacter cloacae, and E. coli

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References

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, colistin, and tigecycline inhibited 94.4%, 100.0%, and 100.0% of these isolates, respectively and were the only agents that inhibited >75% of these isolates

Amikacin and gentamicin inhibited 72.2% and 50.0% of these isolates, respectively

Only 1 K. pneumoniae isolate carried a 16S rRNA methyltransferase, rmtF1, and was resistant to plazomicin and the other aminoglycosides

Conclusions

 Plazomicin was active against 94.4% to 99.4% of this challenge set of Enterobacteriaceae isolates carrying AMEs, ESBLs, and carbapenemases

The activity of plazomicin was greater than the activity of other aminoglycosides against these

Plazomicin seems to be a valuable option to treat these troublesome isolates from US hospitals where the prevalence of 16S rRNA methyltransferases is low

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Figure 1 Distribution of β-lactamases and aminoglycoside resistance mechanisms among isolates submitted to whole genome sequencing



Figure 2 Activity of plazomicin and comparator agents

^a % susceptible based on FDA criteria ^b % susceptible based on CLSI criteria ° % susceptible based on EUCAST criteria