

P1178 **Prevalence of aminoglycoside resistance 16S rRNA methyltransferase in Korea**

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Background: Exogenously acquired 16S ribosomal RNA methyltransferases (16S RMTases) have emerged as a major mechanism of high-level resistance to most clinically important aminoglycosides in Gram-negative pathogens. 16S RMTase-producing bacteria are becoming prevalent in Korea and highlight the need for continued surveillance to investigate the overall trend of aminoglycoside resistance among clinically important pathogens. In this study, we investigated the prevalence of 16S RMTases in Korea from our data and from previously published literature.

Materials/methods: A total of 222 amikacin resistant gram-negative clinical isolates from patient specimens was collected between 1999 and 2015 from three hospital banks across Korea. The susceptibility of the isolates to amikacin was evaluated using the Etest. We screened the amikacin-resistant isolates using polymerase chain reaction to detect the known 16S RMTase genes *armA*, *rmtA* through *rmtH*. To further investigate whether aminoglycoside resistance was transferable, plasmids from clinical isolates demonstrating high-level resistance to amikacin (> 256 µg/ml) were prepared using the alkaline lysis method and were electro-transformed into *E. coli* TOP10 competent cells (Invitrogen, USA). To investigate overall trends over time of 16S RMTases from clinical isolates in Korea, we reviewed 419 articles using the keywords “16S rRNA methyltransferase” or “16S methyltransferase” or “Korea” in PubMed for articles published from 1974 to 2017. A total of 10 papers related to 16S RMTases from clinical isolates were published in Korea from 2006 to 2017.

Results: Among all of the isolated microorganisms, *armA* and *rmtB* were the two most common 16S RMTases. The most prevalent was *armA* in *K. pneumoniae* (57.8%), and *A. baumannii*/*Acinetobacter* spp.(56%). The other Gram-negative pathogens producing *armA* were *E. coli* (10.6%), *C. freundii* (12.3%), *E. cloacae* (29.0%), *S. marcescens* (22.8%), and *P. aeruginosa* (7.0%). The RmtB-producing microorganisms were *K. pneumoniae* (15.2%), *E. coli* (6.6%) and *C. freundii* (5.5%). Only one *P. aeruginosa* isolate with *rmtA* was reported in 2006.

Conclusions: This study provides recent information regarding the 16S RMTase genes responsible for aminoglycoside-resistant isolates circulating in Korean community settings. *armA* and *rmtB* were the predominant 16S RMTase genes, and one *rmtA*-producing isolate was detected back in 2006 but not since then.