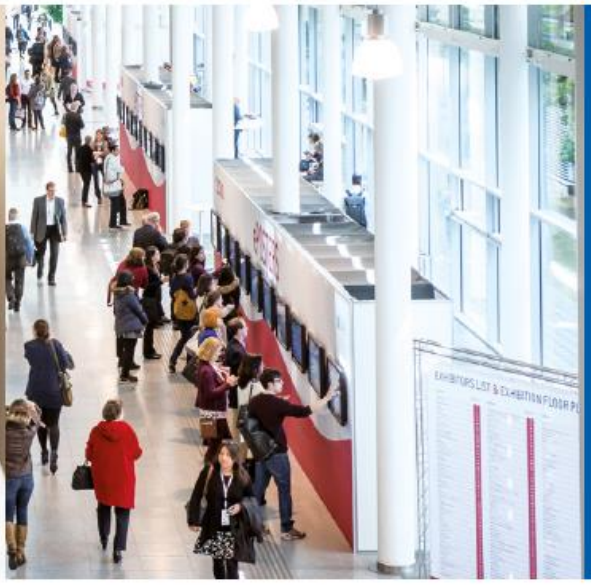
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Aminoglycoside resistance mechanisms in invasive *Klebsiella pneumoniae* and *Escherichia coli*: a threat of rmtC mediated resistance

Iffet Uzun*[1], Tugce Celik[1], Burak Aksu[1], Nurver Ulger Toprak[1], M.Ufuk Hasdemir[1]

[1]*Marmara University School of Medicine, Istanbul, Turkey*

Background: Aminoglycosides (Ags) are often used in combination with other antibiotics and provide a valuable therapeutic option for treating multidrug resistant bacterial infections. Aminoglycoside resistance (AgR) due to 16S ribosomal methyltransferases (RMTs) seems to emerge as real threat that limit the use of these antibiotics for salvage therapy. In this study, we aimed to investigate genetic determinants of RMTs together with aminoglycoside modification enzymes (AgMEs) in invasive *Klebsiella pneumoniae* and *Escherichia coli*.

Materials/methods: Fifty *K. pneumoniae* and 49 *E. coli*, isolated throughout the year 2016 and exhibited resistance to at least amikacin or gentamicin in routine susceptibility testing (VITEK® 2 Compact, BioMérieux, France) were included in the study. Amikacin, gentamicin, tobramycin, and netilmicin MICs of the isolates were determined by standard broth microdilution method (BMD) in the study isolates. Genetic determinants of RMTs (*armA*, *rmtA*, *rmtB*, *rmtC*, *rmtD*, *rmtE*, *rmtF*, *rmtG*, *rmtH*, *npmA*) and AgMEs [*aac(3)-II, aac(3)-I, aac(6')-Ib, ant(2")-I*] were investigated by PCR.

Results: Twelve of 50 (24%) *K. pneumoniae* isolates exhibited high level resistance (>256 mg/L) to all Ags tested in BMD. High level aminoglycoside resistance was not detected in any of the *E. coli* isolates. *rmtC* was the most common (13/50) RMT gene followed by *armA* (2/50) in *K. pnuemoniae* (Table 1). *aac(3)-II* was found together with *aac(6')-Ib* in 64% of *K. pneumoniae* and 32.7% of *E. coli* isolates.

Conclusions: *rmtC* encoded high level aminoglycoside resistance seems to be a threat in *K. pneumoniae* in our hospital, especially considering high risk of multidrug resistance in such isolates.

Table 1. Distribution of aminoglycoside resistance genes in *Klebsiella pneumoniae* and *Escherichia coli* isolates exhibiting resistance to amikacin and/or gentamicin

	Number of isolates (%)	
AgR[a] genes	*K.pneumoniae*	*E.coli*
aac(3)-II	9 (18)	23 (46.9)
aac(3)-II + rmtC	1 (2)	0
aac(6')-Ib	4 (8)	9 (18.4)
aac(6')-Ib + rmtC	3 (6)	0
aac(3)-II + aac(6')-Ib	20 (40)	15 (30.6)
aac(3)-II + aac(6')-Ib + rmtC	9 (18)	0
aac(3)-II + aac(6')-Ib + armA	2 (4)	0
aac(3)-II + ant(2")-I	1 (2)	1 (2)
aac(3)-II + aac(6')-Ib + ant(2")-I	1 (2)	1 (2)

[a]AgR, aminoglycoside resistance

Presenter email address: iffetcavusoglu@gmail.com