Co-production of 16S ribossomal RNA methyltransferase RmtB with KPC and CTX-M-14 in *Klebsiella pneumoniae* in São Paulo State, Brazil, from 2011 to 2014.

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INTRODUCTION

Acquired 16S rRNA methyltransferases (16S-RMTases) have been described as a novel and high-level resistance mechanism against all aminoglycosides. RmtB is disseminated worldwide. We described RmtD in *P. aeruginosa* and RmtG in *K. pneumoniae* and recently in *P. aeruginosa* isolates in Brazil, most of them co-producing beta-lactamases, ESBL and/or carbapenemases, limiting the therapeutic options.

OBJECTIVES

The aim of this study was to investigate some 16S-RMTase and KPC and CTX-M co-production among aminoglycosides-resistant *Klebsiella pneumoniae* clinical strains belonging to a collection of the Instituto Adolfo Lutz (IAL) of São Paulo City and from a Hospital of São José do Rio Preto City, Brazil. IAL serves as a state reference laboratory and receives multidrug-resistant Gram-negative pathogens on an ongoing basis.

METHODS

During the period of 2011 and 2014, fifty isolates from São Paulo City belonging to a IAL's collection obtained from several hospitals of São Paulo State were selected among a total of 1750 KPC-producing *K. pneumoniae* and fifty isolates from a hospital in São José do Rio Preto City. Resistance profile was analysed and *Klebsiella pneumoniae* isolates with high-level aminoglycoside resistance (MIC ≥ 256 micrograms/mL) and ESBL and KPC producing were tested for the presence of bla_{ESBL} and *rmt* genes by PCR and DNA sequencing. ERIC-PCR and MLST were carried-out to determine the genetic diversity.

RESULTS

PCR and DNA sequencing confirmed the presence of $bla_{CTX\text{-}M\text{-}14}$ and *rmt*B in 2 isolates from different hospitals in São Paulo City. Both were resistant to all beta-lactams, ciprofloxacin and presented high level resistance to amikacin, gentamicin and tobramycin (≥ 256 micrograms/mL) and were sensitive to tigeciclin; polymyxin B were not tested. ERIC-PCR profliles showed that both isolates were strictly related and belonged to ST258 (Table 1).

Table 1. Data obtained from *K. pneumoniae* co-producing KPC, CTX-M-14 and RmtB

Strain number	Patient	Hospital	Source	Disk-diffusion tests					MIC µg/mL					Genes	ERIC-PCR	MLST (ST)
				ATM	FEP	CTX	CAZ	CIP	ETP	MEM	TGC	AK	GN			
SP28	1	A	Urine	R	R	R	R	R	>32	>32	0.38	≥ 256	≥ 256	bla_{KPC}, $bla_{CTX\text{-}M\text{-}14}$, *rmt*B	A1	258
SP36	2	B	Blood	R	R	R	R	R	>32	>32	1	≥ 256	≥ 256	bla_{KPC}, $bla_{CTX\text{-}M\text{-}14}$, *rmt*B	A2	258

CONCLUSIONS

To our knowledge this is the first report of the co-production of KPC and RmtB in *Klebsiella pneumoniae* in Brazil. Multidrug resistance is worrisome, the production of 16S rRNA methyltransferase limits the treatment of the infections caused by these microorganisms.

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