High rate of carbapenemase and 16S rRNA methylase producers among enterobacterial isolates recovered from hospitalized children, Angola

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Background: Aminoglycosides (AG) play an important role in antimicrobial therapy in severe infections, usually in combination with β-lactam agents. AG resistance usually arises from enzymatic modification of the drug, however another mechanism corresponding to the production of 16S rRNA methylases (RMT) that are mostly plasmid-encoded is currently emerging. We have recently developed the first culture medium for selecting AG pan-resistant bacteria, mainly RMT producers. Our objective was to perform a prospective screening of RMT producers using this novel screening medium.

Materials/methods: Rectal swabs were collected from hospitalized children in a hospital in Angola during a one-week period, January 2017. After an overnight pre-culture in broth, samples were screened for pan-AG Enterobacteriaceae using the selective SuperAminoglycoside medium, supplemented by gentamicin 30 µg/ml and amikacin 30 µg/ml. PCR experiments were performed using primers specific for RMT genes. Genotyping was performed by PFGE analysis and by MLST.

Results: A total of 36 samples were collected from children being 3 months to 13 years-old. A total of 22 pan-AG-resistant Gram-negative isolates were recovered from 20 patients. A total of 16 isolates harboured the rmtB gene (9 Escherichia coli, 5 Klebsiella pneumoniae, 1 Enterobacter cloacae, and 1 Enterobacter aerogenes), five harboured the armA gene (2 K. pneumoniae, 1 E. aerogenes, 1 E. cloacae, and 1 Citrobacter freundii), and a single K. pneumoniae harboured the rmtC gene. All the isolates were resistant to broad-spectrum cephalosporins by production of either CTX-M type enzyme (CTX-M-15 in 15/22 isolates, CTX-M-55 in 2 isolates) or NDM-5 carbapenemase (10 isolates). The rmtB gene was carried either by plasmids belonging to IncFIB, IncL/M, IncN and IncY incompatibility groups and respectively carrying blatem-1, blactx-M-15, blactx-M-55 and blandm-5. The armA gene was carried by an IncA/C plasmid, often associated with the blandm-5 carbapenemase gene. MLST showed a high diversity of genetic backgrounds, either for E. coli and K. pneumoniae isolates.

Conclusions: We report here a high rate of RMT producers, colonizing 55% of the hospitalized children. Worringly, co-association with carbapenemases was often identified, leading to pandrug resistance.