Addiction systems and extended spectrum beta-lactamases in Pediatric Uruguayan Hospital

García V. ¹, Bado I. ¹, Algorta G. ², Vignoli R ¹.

¹Depto. de Bacteriología y Virología, Facultad de Medicina (UDELAR), ²Centro Hospitalario Pereira Rossell (CHPR)

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Introduction

Since 2006, we have observed a change in prevalence of extended spectrum beta-lactamases (ESBL) in our country. In the last seven years, the predominant CTX-M-2 enzyme had begun to be replaced by CTX-M-15 and other CTX-M variants. Toxin-antitoxin addiction systems (AdS) are important for plasmid maintenance that harbor them in different bacterial species. AdS and ESBL association could allow plasmid maintenance independently of antibiotics use.

Objectives

Characterize AdS in clinical enterobacteria harbored ESBL from Pediatric Uruguayan Hospital, and determine if AdS presence could partially explain ESBL predominance.

Methods

We studied 41 clinical isolates of Enterobacteriaceae (2010-2011), unrelated by pulse field gel electrophoresis (PFGE). Conjugation assays were performed for all isolates (Tc) that harbor: CTX-M-15 (13), CTX-M-group 4 (10), CTX-M-2 (7), CTX-M-8 (3), SHV-5 (4), SHV-12 (4). PCR was done to Tc for AdS: pemKI, ccdAB, relBE, parDE, vagCD, hok-sok, pndAC, srnBC.

Results

CTX-M-15 was associated to ccdAB and pemKI; CTX-M-8 to ccdAB and pndAC; and SHV-5 to ccdAB, pndAC and pemKI. Average of AdS of plasmids that harbor ESBL was: 1.3 to CTX-M-8, 1 to CTX-M-15, 0.75 to SHV-5, 0.2 to CTX-M-group-4 and 0 to CTX-M-2 y SHV-12.

Conclusions

We could partially explain that change in ESBL is due to a higher average of AdS in plasmids that harbor CTX-M-15. When association between AdS-ESBL is established, plasmid loss implies bacterial death due to the toxin codified by AdS. For this reason AdS produces a selection pressure independently to the presence of antibiotics.