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INTRODUCTION: Argentina has the highest rate of hemolytic uremic syndrome (HUS) in the world. In general, outbreaks and sporadic HUS cases have been associated with Shiga toxin-producing *Escherichia coli* (STEC) O157:H7 of biotype C (dulcitol and rhamnose-fermenter).

OBJETIVE:

The aim of this study was to compare the genetic diversity and to establish the clonal relatedness of *Escherichia coli* O157:H7 strains of biotype B (dulcitol-fermenter and rhamnose non-fermenter), isolated from HUS patients and asymptomatic contacts in Mar del Plata city.

MATERIALS AND METHODS: During February and March 2007, four *E. coli* O157:H7 strains of biotype B were isolated from two HUS patients and two asymptomatic contacts (AC).

HUS#1: girl, 44 months old with symptom onset on February 8, 2007, with good clinical outcome. She lived with her family in Mar del Plata.

HUS#2: girl, 33 months old with symptom onset on February 26, 2007, with involvement of the central nervous system, and convulsions, who died on March 1, 2007.

Asymptomatic contacts living with HUS#2: AC#2-A brother, 5 years old and AC#2-B grandmother, 55 years old. This family was originally from Mar de Ajó city.

The strains were characterized by PCR to amplify *stx*₁, *stx*₂, *rfb*_{O157}, *eae*, *ehxA* and *fliC*_{H7} genes (Pollard et al.(1990), Gannon et al.(1993) and Schmidt et al.(1995) and subtyped by phage-typing (Armed et al. 1987; Khakhria et al. 1990) and pulsed-field gel electrophoresis (*Xba*I-PFGE), following the protocol for *E. coli* O157 described by the CDC. The clonal relatedness among isolates was established using the BioNumerics software version 4.0 (Applied Maths, Kortrijk, Belgium). Besides, the prolonged fecal shedding of the bacteria was also studied.

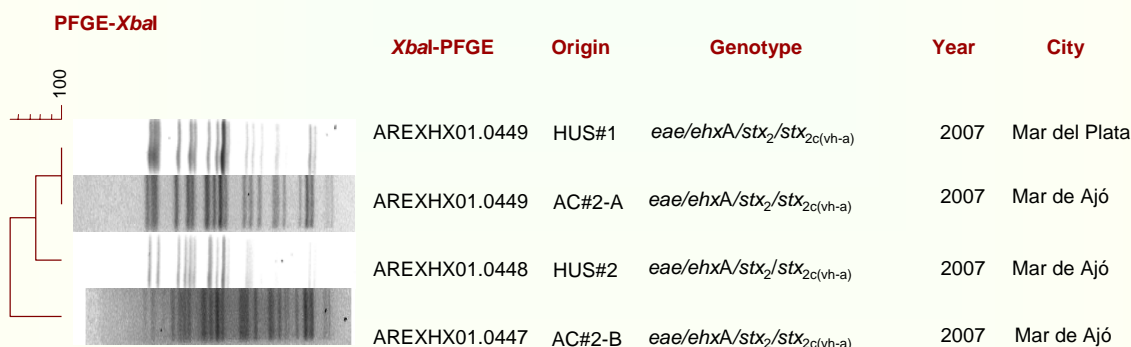
RESULTS:

The four *E. coli* O157 strains of biotype B harbored the *stx*₂, *stx*_{2c(vh-a)}, *eae*, *ehxA* and *fliC*_{H7} genes. They were susceptible to all antimicrobial assayed and belonged to phage type 2.

By *Xba*I-PFGE, three patterns were established: AREXHX01.0447 (AC#2-B), AREXHX01.0448 (HUS#2), AREXHX01.0449 (HUS#1, AC#2-A). AREXHX01.0447 and AREXHX01.0448 patterns showed 95.2% similarity. AREXHX01.0448 and AREXHX01.0449 patterns showed 97.6% homology with one band difference (Figure 1).

Figure 1. CLONAL RELATEDNESS OF *E. coli* O157:H7 STRAINS OF BIOTYPE B

Dice (Opt:1.50%) (Tol 1.5%-1.5%) (H>0.0% S>0.0%) [0.0%-98.3%]



In AC#2-B, an STEC excretion of 20 days was established.

CONCLUSIONS: The identified *Xba*I-PFGE patterns of biotype B strains are new, because they were not previously included in the *E. coli* O157 Database of Argentina. These patterns had a high clonal relationship and therefore are considered to be related to the same event. However the epidemiologic link between both HUS cases could not be established.

As most of *E. coli* O157:H7 strains detected in Argentina, including Mar del Plata, belonged to biotype C, it is important to survey the detection of new clones with potential pathogenic capacity to cause severe diseases.

It is essential the use of molecular epidemiology techniques to improve real-time monitoring of *E. coli* O157, reinforcing the results of the epidemiological investigation in order to apply prevention and control measures .