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immunogold electron microscopy and western blotting in bacteria cultured with the colonic cell line. However, deletion of csgA (encoding the putative major subunit of curli) did not appear to affect intestinal colonization. Inclusion of lpfA alleles in the mPCR assay permitted differentiation of EHEC1 and EPEC2 groups, as well as EHEC1 and EHEC2. This methodology resulted in a clinical sensitivity and specificity of 91% and 84%, respectively, when analyzing clinical strains from Argentina.
Conclusions: Further work is needed to more fully examine the link between curli and Lpf production and the specific contribution of each one during colonization and persistence. The use of lpfA alleles in the multiplex PCR assay allowed us to discriminate different classes of pathogenic *E. coli* strains, suggesting this can be used for diagnosis of STEC and EPEC infections.

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Detection of Integrons Class 1 and Class 2 in VTEC Strains Isolated from Pigs

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Introduction and Objectives: In the last 10 years, approximately 500 HUS new annual cases were reported in Argentina, with an incidence of 17/100 000 children under five years old. The production of VT1, VT2 and/or their variants is the primary virulence trait responsible for human disease. VT2e is typically associated with pig edema disease and has been detected only rarely in VTEC of human origin. Some studies have shown that VTEC serotypes have developed resistance to antibiotics used in human and veterinary medicine. Humans may obtain antibiotic-resistant *E. coli* by contact with animals, foods, or environment. The widespread use of antibiotics creates a reservoir of resistant bacteria carrying antibiotic resistance genes. Integrons contain the genetic determinants of the components of a site-specific recombination system which recognize and capture the mobile antibiotic-resistance genes cassette. Integrons include a gene for an integrase (int), an adjacent recombination site (attl), and a strong promoter/s that ensure expression of the integrated cassettes. The aim of this study was to detect integrons in VTEC strains with antibiotic multiresistance.
Material and Methods: Twenty-one VTEC strains isolated from pig faeces from 10 farms (named A to J) from Argentina were analysed to detect integrons (int1 and int2) by PCR.

Table 1: Results

Farm	Toxin subtype	Integron class	Antibiotic resistance
A	vt2e	intl1	S-AMP-TET-CMP-TMP/SMX-DOX-FLOR
B	vt2e	intl2	S-T-CMP-TMP/SMX-DOX-FLOR
B	vt2e	intl2	S-TET-CMP-TMT/SMX-DOX-FLOR
B	vt2e	intl2	TET-DOX-FLOR-CIP-NAL
B	vt2e	intl2	S-TET-CMP-TMP/SMX-DOX-FLOR
C	vt2	intl2	S-TET-TMP/SMX-DOX-FLOR
C	vt2	intl2	S-TET-TMP/SMX-DOX-NAL
D	vt1	intl2	S-TET-DOX-NAL

CIP, Ciprofloxacin; AMP, Ampicillin; TMS, Trimethoprim/Sulfamethaxazole-DOX, Doxycyline; CMP, Choramphenicol; FLOR, Florfenicol; TET, Tetracycline; NAL, Nalidixic acid; S, Streptomycin.

Results: Out of 21 analysed strains, 8 (38%) carried integrons enconding genes. These strains belonged to four different farms. The results of PCR and antibiotic resistance are shown in Table 1.
Conclusions: The use of antibiotics in animal production systems has determined that bacteria could develop resistance mechanisms originating strains with risk for human if entering a food chain. Integrons are not only associated with resistance to antibiotics, but also with the horizontal transference of resistance genes. Some studies have informed of the presence of integrons in Enterobacteriaceae and *Escherichia coli* in samples isolated from pigs, not being registered data in VTEC strains so far. In this study integrons class 1 and class 2 were detected in VTEC strains isolated from pigs showing that inadequate use of antibiotic as therapeutic agents or growing promoter in veterinary, implies a risk for public health because the acquisition and the horizontal transference of integrons among strains.

P-097
Serotypes and Virulence Genes of Shiga Toxin-Producing *Escherichia coli* Isolated from Cattle in Brazil

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Introduction and Objectives: Cattle are the main animal reservoir of Shiga toxin-producing *Escherichia coli* (STEC). The aim of this study was to characterize the serological, phenotypic and virulence genes of STEC isolated from bovine stools at Rio de Janeiro State, Brazil.
Material and Methods: Stool samples of 2402 healthy animals were examined by multiplex PCR (*stx*1, 2 and *eae* genes; China et al, 1996). The *stx*-positive stool samples were then tested for *rfb* O157 gene by PCR (Paton and Paton, 1998). *E. coli* O157 was isolated by immunomagnetic separation followed by plating onto Sorbitol-MacConkey agar plus tellurite (2.5 mg/L) and cefixime (0.05 mg/L). The other STEC serotypes were isolated by colony hybridisation with a radiolabeled stx probe (Feinberg and Vogelstein, 1984) using the PCR product of *E. coli* EDL933 strain as a probe (Paton et al.,1993). *E. coli* serotypes were identified with O1 to O181 and H1 to H56 antisera. The virulence genes EHEC-*hly*A (Paton and Paton, 1998b), *esp*P (Brunder et al., 1999), *saa* (Paton and Paton, 2002), *iha* (Schmidt et al., 2001) and *ast*A (Yamamoto, 2000) were detected by PCR. The haemolytic activity was tested according Beutin et al. (1995) and production of Stx was investigated on Vero cells (Smith and Scotland, 1993). Cell-adherence assay (Cravioto et al.,1979) and fluorescence actin staining (FAS) test (Knutton et al., 1989) were both performed with HEp-2 and Caco-2 cells after 3 h-infection. A negative cell-adhesion or FAS test was repeated after 6 h-infection.
Results: A total of 1562 (65%) animals were positive for *stx* genes. *E. coli* O157 strains were isolated from 27 fecal samples positive for *rfb* O157 gene and eight isolates (42.1%) were identified as STEC (*stx*-positive). Nine hundred and ninety-two non-O157 STEC strains from 33 different serotypes were isolated. All STEC strains were able to induce a cytotoxic effect on Vero cells. STEC serotypes were ascribed to two groups – group I, that occur in human disease (73 strains) and group II, not yet described in human disease (27 strains). The *stx*2 genotype was significantly associated with O157:H7 serotype. However, this genotype occurred among strains from different serotypes in both groups. Most strains in groups I and II, were intimin-negative. Concerning the other virulence genes investigated we did not find differences between serotypes or between O157 and non-O157 strains, with exception of *ast*A, signifi-

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