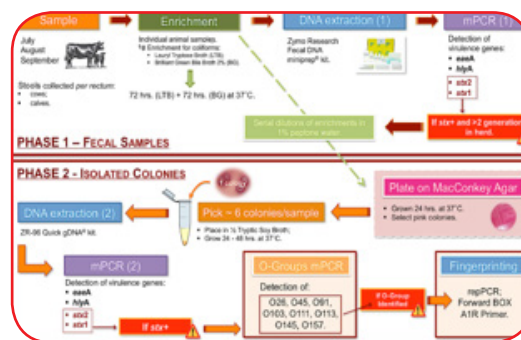


5th World Congress on
MICROBIAL BIOTECHNOLOGY & VACCINE DESIGN
September 17-18, 2018 Lisbon, Portugal

Shiga toxin-producing *Escherichia coli* distribution and characterization in a pasture-based cow-calf production system

Patricia Baltasar, François Elvinger, Monica Ponder, William Swecker and Korine Kolivras
Virginia Tech, USA

Escherichia coli is part of the normal gastrointestinal microbiota of many animals, especially cattle. While most strains are commensal, Shiga toxin-producing *E. coli* (STEC) can cause severe human illness. Persistent carriers and environmental contamination may be responsible for maintenance of STEC in cattle. Prevalence and distribution of *E. coli* virulence genes (stx1, stx2, hlyA and eaeA) were assessed in a cow-calf pasture-based system. Angus cows (n=90) and their calves (n=90) were kept in three on-farm locations and fecal samples were collected at three consecutive time-points (July through September, 2011). After enrichment, sample detection of stx1, stx2, eaeA and hlyA was done by multiplex PCR (mPCR). Fecal samples positive for stx genes were obtained from 93.3% (84/90) of dams and 95.6% (86/90) of calves. Age class (dam, calf) and spatial distribution of cattle and sampling time-point influenced prevalence and distribution of virulence genes. Of 293 stx-positive fecal samples, 744 *E. coli* colonies were isolated. Virulence patterns of isolates were determined through mPCR: stx1 was present in 41.9% (312/744) of isolates, stx2 in 6.5% (48/744), eaeA in 4.2% (31/744) and hlyA in 2.4% (18/744). Prevalence of non-O157 STEC was high among isolates: 33.8% (112/331) were O121, 3.6% (12/331) were O103, 1.8% (6/331) were O113. One isolate (0.3%) was identified as serotype O157. Repetitive element sequence based-PCR (rep-PCR) fingerprinting was used to study genetic diversity of stx-positive isolates. Rep-PCR fingerprints were highly similar, supporting the hypothesis that strains are transmitted between animals, but not necessarily from a dam to its calf. Highly similar STEC isolates were obtained at each sampling time-point, but isolates from dams were more diverse than those from calves, suggesting that strain-to-strain differences in transfer may exist. Furthermore, fingerprints from O121 isolates closely resembled those of test isolates from in human outbreaks.



Biography

Patricia Baltasar has an impressive background in veterinary medicine, public health and research. Her excellent analytical, communication, people skills, coupled with a strong command of epidemiology have been critical in consistently reflecting the highest academic standards. She has a solid record of publications and presentations and has established a sound trajectory towards a career focused in the “One Health” concept.

patbaltasar@gmail.com

Notes: