# Occurrence of STEC O157 and STEC non-O157 in Belgian slaughter cattle.

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## Introduction :

Shigatoxin producing *Escherichia coli* have been described as the cause of severe food-related clinical cases, such as hemorrhagic colitis and hemolytic uremic syndrome (HUS). Attention is especially given to the well-known STEC O157 strains, however the non-O157 STEC strains, mainly O26, O103, O111 and O145 have been increasingly isolated from human clinical cases. The most important virulence factors are considered to be the shigatoxins 1 and 2. However, there are additional virulence factors such as enterohemolysin and intimin.

The objective of this study was to investigate the occurrence of STEC O157 and STEC non-O157 and to establish the virulence potential of STEC isolates from feces of cattle at slaughterhouse level.

## Material and methods :

Fecal samples (n=399) were obtained randomly in 3 Belgian slaughterhouses. The samples were examined for the presence of STEC non-O157 after enrichment. The selective isolation was achieved by the use of the differential agar medium, described by Possé et al. (2008), by direct plating or after using the immunomagnetic separation technique (IMS) on the enrichment broth. The suspected colonies were transferred to one or more confirmation media. Suspected colonies were confirmed by PCR and examined for the presence of virulence genes by multiplex PCR.

Isolation of STEC O157 was performed by an enrichment during 6 hours of fecal samples (n=228), followed by IMS and plating onto CT-SMAC. Suspected colonies were confirmed by latex agglutination and biochemical tests and molecular methods such as serotype PCR and virulence multiplex PCR.

## Results and discussion :

In the present study 22 of 199 cattle farms (11%) were positive for the STEC non-O157 while STEC O157 was found on 16 out of 72 farms (22%). While emergent non-O157 STEC are being isolated from cattle at the slaughterhouse, the O157 serogroup remains the most dominant.

The screened virulence genes were *eae, hlyA* and *stx1/2*. Shigatoxins were detected in 82.5% of the 40 tested isolates. One quarter of the isolates possessed *stx1* as well as *stx2*. The highly virulent genetic mix, combined presence of *hlyA* and *eae* and *stx1* and/or *stx2*, was present in 65% of the isolates. Only 2 isolates possessed none of the virulence genes.

## References :

Posse, B., L. De Zutter, et al. (2008). "Novel differential and confirmation plating media for Shiga toxin-producing Escherichia coli serotypes O26, O103, O111, O145 and sorbitol-positive and -negative O157." FEMS Microbiol Lett **282**(1): 124-31.