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Shiga toxin-encoding *Escherichia coli* from South American Camelids in Germany –prevalence, stx gene subtype distribution and strain characterization

Inhalt

South American camelids (SAC) are popular in Europe, frequently kept with other livestock species and in close contact with humans. They, thus, represent a potential reservoir for transmission of epizootic and zoonotic bacteria to livestock and humans. To investigate the presence of Shiga toxin-encoding *Escherichia coli* (STEC) in SAC, 20 animals each were sampled four times in ten or nine herds. The overall prevalence of stx-positive samples was 32%. This resolved into 6.4%, 18% and 7.5% prevalence for stx1-, stx2- and stx1/stx2-positive samples, respectively. There was no difference in prevalence between alpacas (43%) and llamas (41%). The herd prevalence diverged widely from 0%-95% stx-positive animals. The stx-subtypes determined were primarily stx1c (78%) and stx2b (77%), while a few animals were PCR-positive for stx1a, stx2c, stx2d, stx2e and stx2f. Multiple stx2 subtype signals were detected in multiple samples (13%). In 27 stx2-positive samples, a subtype could not be assigned. So far, 13 isolates were obtained and sequenced. They feature the genoserotypes O5:H19, O55:H12, O76:H19, O87:H16, O128:H2, O151:O118:H16, and O187:H28. The prevalences determined are similar to prevalence ranges published for cattle, small ruminants and camelids. Colonization with STEC differed widely between individual farms and showed no seasonality. More isolates will be required to assess the STEC public health risk. Those identified so far would classify as having low pathogenic potential.

Keywords

Shiga-toxin, *Escherichia coli*, alpaca, llama

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188

Professional Status of the Speaker

Senior Scientist

Junior Scientist Status

No, I am not a Junior Scientist.

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