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

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South American camelids (SAC) are popular in Europe, frequently kept with other livestock species and in close contact with humans. They represent a potential transmission source of epizootic and zoonotic bacteria to livestock and humans. Therefore, SAC were included as livestock species in the revised European Animal Health Law. However, knowledge on bacterial pathogens in SAC is too sparse for drafting appropriate monitoring and preventive medicine programs. To investigate the presence of Shiga toxin-encoding *Escherichia coli* (STEC) in SAC, 20 animals each were sampled at two different time-points in ten and then nine flocks. The herd prevalence determined was 70% in the first sampling round and 100% in the second. A total of 362 samples from individual animals were tested for stx-gene presence and 21 samples (5.8%) were PCR-positive for stx1, 51 for stx2 (14.1%) and 23 for both genes (6.4%). The intra-flock prevalence fluctuated widely, ranging from 0-53% in the first round and from 6-60% in the second round. The stx-gene subtypes identified were predominantely stx1c (98%; 41/42) and stx2b (63%; 50/80), which are considered as being of low risk for causing severe human disease. A few animals were also PCR-positive for stx1a, stx2c, stx2d, stx2e and stx2f. Multiple stx2 subtype signals were detected in 24% of the samples (19/80). In six stx2-positive samples, a subtype could not be assigned. Current efforts focus on identifying this stx2 subtype and on obtaining isolates.

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Professional Status of the Speaker

Senior Scientist

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No, I am not a Junior Scientist.

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