

Whole genome characterization of Shiga toxin-producing *Escherichia coli* in Free-ranging Red Deer from Italian Central Alps.

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Free-ranging red deer (*Cervus elaphus*) in Stelvio National Park (Italian Alps) have been suggested as potential carriers for LEE-negative, *subAB* positive Shiga toxin-producing *Escherichia coli* (STEC), which have been reported in human diseases. This work describes the genomic characterization of such isolates in order to define the zoonotic potential of wildlife-associated STEC.

Whole genome analysis of 9 STEC isolates collected in the Stelvio National Park during the winter season 2016-2017 from feces of culled free-ranging red deer was performed.

One STEC isolate harbored *stx1* and *stx2* genes, whereas 5 and 3 possessed *stx2* and *stx1* only, respectively. Subtype *stx1a* was carried by three strains and *stx1c* was observed in one isolate. Only subtype *stx2b* was observed in the six *stx2* positive strains. No STEC isolate possessed the *eaeA* gene. The serogroups identified included O146, O91, O113 and O174. Seven isolates of serogroups O146, O91 or O113 possessed the *subAB* locus. The core genome MLST analysis of the four O146:H28 showed that the strains' genomes fell within the 37-95 alleles differences.

Our results strengthen the hypothesis that red deer may represent carriers for LEE-negative, *subAB* positive STEC strains. Such strains display features similar to those causing illness to humans. The similarity in the genome of O146 STEC strains suggests that a population of these STEC isolates is circulating in the area. Our findings underline the zoonotic potential of STEC strains isolated from wild ruminants, including free-ranging deer.