

Comparison of bovine and human O26 EHEC strains by the Whole Genome PCR Scanning.

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In many industrialized countries, enterohaemorrhagic *Escherichia coli* (EHEC) strains are responsible for food poisoning in humans quite often after consumption of foodstuffs contaminated by ruminant faeces. In humans, the clinical conditions vary from undifferentiated diarrhoea to haemorrhagic colitis with, in 10 % of the cases, renal sequelae that can lead to death. The “reference” EHEC serotype is O157:H7, but EHEC can belong to hundreds of O:H serotypes whose virulence and host-range may differ. In veterinary field, EHEC strains belonging to O26, O111, O118 serogroups f.i. are also responsible for undifferentiated diarrhoea in young calves.

The aim of this study is to compare the genomes of ten O26 EHEC strains (5 bovine and 5 human) by the Whole Genome PCR Scanning (WGPS) method to identify regions of the chromosome that are different between bovine and human strains and may therefore carry host-specific virulence-associated genes. This technique is based on the amplification of the whole bacterial genome using 579 long range PCRs.

After comparison of the WGPS profiles of the 10 EHEC strains, their genomic diversity was studied focusing on regions that give different amplification profiles and may therefore help to differentiate between bovine and human strains. Seven such regions out of the 579 amplified fragments have been so far identified. Therefore, 55 additional strains (O26 EHEC and EPEC strains isolated from bovines or humans) were tested by PCR for these regions to confirm their host specific character. Statistical analyses are currently ongoing.