

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

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Enterohaemorrhagic *Escherichia coli* (EHEC) strains are responsible for food poisoning in humans in developed countries via consumption of vegetal and animal foodstuffs contaminated by ruminant faeces. The clinical conditions vary from undifferentiated diarrhoea to haemorrhagic colitis with, in 10 % of the cases, renal sequelae (Haemolytic Uraemic Syndrome, HUS) that can lead to death. Some EHEC strains belonging to O26, O111, O118 serogroups f.i. are also responsible for undifferentiated diarrhoea in young calves up to 3 months of age.

The aim of this research work is to compare the genomes of O26 EHEC strains by the Whole Genome PCR Scanning (WGPS) method. This technique is based on the amplification of the whole bacterial genome using 579 long range PCR based on the sequence of the human O26:H11 EHEC strain 11368. The differences in the WGPS profiles will identify the genomic diversity in several bovine and human O26 EHEC strains. The regions that seem to be different will be further cloned and sequenced with the aim to identify genes coding for virulence properties that would be specific to bovine or human EHEC strains.

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2. Ogura Y.*et al.* (2006) Complexity of the genomic diversity in enterohemorrhagic *Escherichia coli* O157 revealed by the combinational use of the O157 Sakai OligoDNA microarray and the Whole Genome PCR scanning. *DNA Research* **13**, 3-14.