

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

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In many industrialized countries (USA, Canada, UK, France, Japan, etc), enterohaemorrhagic *Escherichia coli* (EHEC) strains are responsible for individual cases, or for small to large outbreaks, of food poisoning in humans quite often after consumption of vegetal and animal foodstuffs contaminated by ruminant faeces (mainly cattle), that can be healthy carriers. In humans, 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. The “reference” EHEC serotype is O157:H7, but EHEC can belong to hundreds of O:H serotypes (notably to O26, O111, O103, O145 serogroups) whose virulence and host-range may differ. 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 several O26 EHEC strains 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. The WGPS technique is based on the amplification of the whole bacterial genome using 579 long range PCR using primers based on the sequence of the human O26:H11 EHEC strain 11368. Ten strains were compared: 5 EHEC strains isolated from humans and 5 EHEC strains isolated from bovines.

After comparison of the WGPS profiles of the 10 bovine and the human EHEC strains, the genomic diversity of the strains were 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.

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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.