

Enterohaemorrhagic *Escherichia coli* (EHEC) O104:H4: a brief bacteriological introductory profile

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There are many different harmless and pathogenic *E. coli* strains. As far as the current EHEC outbreak event is concerned, the serotype O104:H4 has been clearly identified as the outbreak strain causing the disease. It constitutes in all probability a recombinant of two pathogenic *E. coli* types.

Based on the strain analysis of the serotype O104:H4, BfR believes that it is likely that the transfer of the pathogen to the affected foods could have been caused in the current outbreak event via humans or from humans via the environment. The pathogen can be spread through foods.

For decades, research in disease-causing *Escherichia (E.) coli* has been an important element of infectiology. The first isolates of the *Escherichia coli* serovar O104:H4 Shiga toxin (stx) 2 date back to 2001 and were described by scientists as HUSEC41. The second link to EHEC O104:H4 was discussed in 2006 in scientific journals. The isolation of the pathogen was associated with a woman who contracted HUS in Korea. Further properties, as they are typical, for instance, for EAggEC, were not examined or published at that time.

Only after a DNA sequence analysis, carried out in a strain responsible for the current outbreak, it was determined that the serovar EHEC O104:H4 has essentially more commonalities with the enteroaggregative *E. coli* (EaggEC) than with the conventional Shiga toxin-forming *E. coli* (STEC)/enterohaemorrhagic *E. coli* (EHEC). It is not similar to the known EHEC but has on a sequence level 93 per cent similarity with an EAggEC which has already been characterized. The EHEC-specific feature of this strain is the stx2 gene. It is similar to a human EAggEC strain from Central Africa, whose sequence is known. It is a recombination of two pathogenic *E. coli* types (EHEC eae, stx and EaggEC), but does not carry the eae (attaching and effacing *E. coli*) gene which is typical for classical EHEC.

The reservoir for EaggEC is, in accordance with the current state of knowledge, humans, whereas it is for STEC/EHEC strains animals, mainly ruminants. The National Reference Laboratory for *E. coli* at BfR has so far not detected the pathogen type EaggEC in animals and in foods. Literature studies have likewise not given any indications that the strain occurred so far in foods and animals. However, altogether only a few EHEC O104 strains have been found all over the world.

BfR has no findings according to which the current EHEC outbreak is based on a transmission from humans to humans. . Yet BfR has no findings to suggest that the current EHEC outbreak is based on human-to-human transmission.

The facts suggest that humans could be a source for a possible contamination of foods and the environment. The determination of the underlying causes continues at full speed on all levels.