"An overview of the 2011 outbreak in Germany: the role of *E.coli* O104:H4"

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INTRODUCTION

Escherichia coli is one of the most studied microorganisms because of its ubiquity and presence in mammals gastrointestinal flora. Despite its profitable features, there are some serotypes of *E.coli* with pathogenic attributes. In the period between 1st may and 4th July 2011 a huge outbreak of *E.coli* infections was declared in Germany. The epidemic comprised almost 4000 cases of acute gastroenteritis, some of them progressing to Hemolytic Uremic Syndrome (HUS). At the beginning of the outbreak, reports wrongly pointed to Spanish vegetables as the vehicles of infection and the media echoed that information with fatal consequences for the economy. Later in the epidemiological investigation the researchers found out sprouted fenugreek seeds, imported from Egypt as the culprits of the epidemic. The causative strain of the outbreak was an Entero-aggregative *E.coli (EAHEC)* of the serotype O104:H4 with a combination of features from different *E.coli* pathotypes that made that hybrid pathogen the worst ever seen in Europe until then. The Shiga toxin-producing phenotype and the aggregative pattern of adhesion to the gut epithelia facilitated EAHEC to cause such high rate of HUS in humans.

OBJECTIVE: The objective of this work is summarize epidemiological information about the German outbreak and describe the virulence attributes of its causal agent.

RESULTS

Data from the German outbreak

- On 1st May, 2011 it was reported the first case of infection with EAHEC O104:H4 of the sequence type 678. The outbreak was officially declared to be ended on July 26 because no additional cases were declared since July 4[1].
- The epidemic comprised 3842 cases, with 855 patients developing HUS and 2987 with acute gastroenteritis. Altogether 53 deaths were reported.
- Adult women were the most affected comprising 68% from HUS cases and 58% of the patients with acute gastroenteritis.
- 125 additional cases were reported in other 13 European countries.

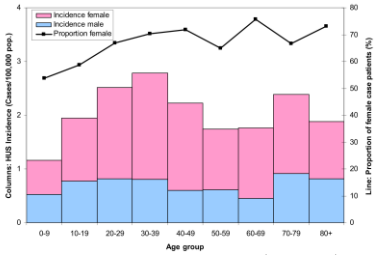


Figure 1: Incidence of HUS sorted by age and gender (left axis) and the average of female affected (right axis) in each age category (n=855 HUS cases). Graphics from Robert Koch Institute final report [1]

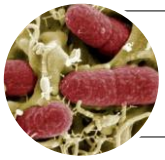
Tracing the sources

· First reports pointed to vegetables as the vehicle of transmission. German authorities banned import of Spanish **cucumbers**.

· Microbiological and statistical analysis showed no significant association with disease.

· Epidemiological investigation pointed to Farm A in Lower Saxony, Germany as the origin of the outbreak. **Fenugreek sprouts** were cultivated in there.

·The origin of contaminated fenugreek seeds was finally reported to be in Egypt.



· Unfortunately, **EAHEC O104:H4** could not be isolated from seeds or fenugreek sprouts.

·The late infections were related with secondary transmission being humans the only known reservoir of EAHEC O104:H4.

Features of Entero-aggregative Hemorraghic *E.coli* O104:H4

EAHEC O104:H4 has genes also present in Shiga toxin-producing *E.coli* (STEC) and Entero-hemorrhagic *E.coli* (EHEC); virulence genes present in Entero-agreggative *E.coli* (EAEC) PAA plasmid and a β-lactamase extended spectrum phenotype codified in another plasmid.

- Genetic analysis showed that EAHEC pathotype probably surged from an EAEC strain by the uptake of Shiga toxin (Stx) lamboid prophage.
- The presence of a powerful pattern of aggregative adhesion facilitates the Shiga toxin-2a adsorption, thus increasing damages in the human gut epithelium.

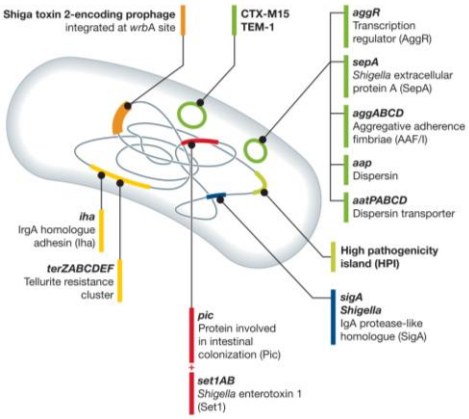


Figure3. Summary of genetic elements present in EAHEC O104:H4 and provenance of each one grouped by color. Green: 2 plasmids, the larger with antibiotic resistance gens and the smaller with genes for aggregative adherence also present in EAEC. Orange: gene for Stx2a encoded in an integrated prophage genome. Yellow: genes also present in STEC chromosome. Red: genes also present in EAEC chromosome. Blue: gene present in *Shigella* sp. From Karch H. *et al.* [2]

Pathology

Shiga toxin has high affinity for small blood vessels that are present, for example in intestine, kidney or lungs.

In the intestine Shiga toxin produces the breakdown of blood vessels and flows through the blood stream infecting other structures. One of the most affected organs is the kidney in where the toxin causes damages in the glomerulus and therefore failure of the filtering function. The consequence is the collapse of the organ, triggering to Hemolytic Uremic Syndrome (HUS).

CONCLUSIONS

- The causative strain, of the German outbreak was an EAHEC of the serotype O104:H4 belonging to the ST678, this hybrid pathogen probably surged from an EAEC strain by the uptake of Stx lamboid prophage.
- The 2011 outbreak in Germany was the worst ever seen because of the high number of HUS cases : the combination of aggregative adherence and production of Shiga-toxin made the new pathotype the most effective causing HUS in humans.
- The differences in gender could be explained by the different food habits between men and women.
- Although fenugreek sprouts were identified as the vehicle of transmission, it was no possible to isolate EAHEC O104:H4 from food, sprouts or seeds: it is still unknown how the EAHEC could colonize seeds or sprouts.
- Secondary transmission from human to human is the most acceptable way of spreading the infection. Humans are the only known reservoir of EAHEC O104:H4 but the possibility of another animal reservoir cannot be discarded.

REFERENCES

[1] Robert Koch-Institute. Final presentation and evaluation of the epidemiological findings in the EHEC O104:H4 outbreak, Germany 2011. September 2011.
[2] Karch H. *et al*. The enemy within us: lessons from the 2011 European Escherichia coli O104:H4 outbreak. 2012. EMBO Molecular Medicine 4, 841-848