

Knowledge of bacteria's origin and spread can prevent disease

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Salmonella Typhimurium DT104 is an aggressive type of bacteria, which is particularly problematic because it has developed resistance to a number of antimicrobials and has been able to quickly spread throughout the world. Using new technology the National Food Institute, Technical University of Denmark, has been able to trace the bacteria back to its origin and work out when it developed resistance. The technology can likely be used to monitor new bacterial strains, prevent and not least understand infectious diseases.

Salmonella is one of the foodborne bacteria which causes the greatest number of foodborne illnesses globally. The variant S. Typhimurium DT104 is one of the most studied variants because it is very aggressive and has quickly spread around the world. Yet until very recently it was not known when it originated or how it has spread.

Just like when the police suddenly solve a cold case with the help of [new technology](#), researchers from the National Food Institute have used whole genome sequencing and found out both when DT104 originated and when the bacteria developed resistance to common antimicrobials. In whole genome sequencing a disease-causing microorganism's entire DNA profile is mapped simultaneously.

The bacteria's family tree

A total of 315 samples from both humans and animals were analyzed in the study. The samples have been collected between 1969 and 2012 in 21 different countries on six continents. By detecting the mutations that have occurred over time in the DNA, scientists have constructed the bacteria's [family tree](#) – a so-called [phylogenetic tree](#).

From the phylogenetic tree the researchers have estimated that DT104 originated in 1948 from an unidentified source and in 1972 it developed resistance to a number of antimicrobials. The

analysis has also revealed the [bacteria's](#) global transmission routes and how it has spread both between animal species and to humans.

Evidence for the eradication in pigs

In 1996 in a bid to eradicate DT104 in Danish pig herds Denmark introduced a sanitation programme for herds infected with DT104. The programme required that the animals had to be removed and the buildings had to be thoroughly cleaned and disinfected before being repopulated with pigs free from DT104.

The sanitation programme was stopped in 2000 as there was no evidence that it was working. The National Food Institute's study can however show that the prevalence of DT104 in pigs fell sharply in 1999 and 2000, and thereby confirm that the programme had the great and desired effect.

Surveillance and prevention

Using the study results the researchers can refute several hypotheses on the evolution of DT104. They are advocating that whole [genome sequencing](#) is used to help us better understand the past, so that this knowledge can be used to tackle the current problems with antimicrobial resistance, and that the technology be used to monitor new bacterial variants in order to prevent new [infectious diseases](#).

More information: Pimlapas Leekitcharoenphon et al. Global genomic epidemiology of Typhimurium DT104, *Applied and Environmental Microbiology* (2016). [DOI: 10.1128/AEM.03821-15](https://doi.org/10.1128/AEM.03821-15)

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