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Titel der Dissertation: "Antimicrobial resistance and One Health: Occurrence of multiresistant human pathogenic bacteria in food and environment."

Abstract

Throughout evolution, the spectrum of pathogens affecting human health and the thereby associated infectious diseases changed. To decrease dissemination, disease and death, control via constant public health surveillance is essential.

The aim of this project was first, to define the natural reservoirs and sources of pathogenic bacterial organisms. One special focus was on multiresistant strains in the river water environment. Second, the occurrence of the foodborne pathogen *Cronobacter sakazakii*, which is associated with outbreaks of severe infections in infants, was investigated by a European multi-centre study in 2017. Pathogens were analysed in detail determining their antimicrobial resistance- and virulence status as well as characterization and subtyping of pathogenic isolates by whole genome sequencing (WGS).

Overall, the detection of human pathogens is not restricted to hospitals, but antibiotic resistant isolates spill over into the environment. Further, the occurrence of anthropogenic pollution by wastewater treatment plants has been affirmed. Since antibiotics belong to the treatment of choice against bacterial infections, the increasing ineffectiveness is alarming and demands attention and strategies to minimize the spread of multiresistant strains to the environment.

The European *Cronobacter sakazakii* study allowed a comparison of the situation for *Cronobacter* infections across Europe. Species identification turned out to be a major challenge for participating laboratories, contributing to an underestimated prevalence across Europe. The establishment of a typing scheme for outbreak investigations enabled the detection of four previously unpublished historical outbreaks.

Strain typing using WGS data discriminates isolates with the highest possible resolution and is therefore the method of choice for uncovering chains of transmission and outbreak investigations. In addition, WGS data allow the analysis and characterization of genes conferring antibiotic resistance and virulence. The findings corroborate, WGS as the recommended tool for surveillance, outbreak detection and for monitoring the evolution of pathogens.