One Health Symposium
Challenges in a rapidly changing environment
2025
13. – 15.10. | Berlin

ID der Kurzfassung : **263**

# Combining Short- and Long-Read Sequencing to Investigate a Ralstonia pickettii Outbreak Linked to Contaminated Saline Solutions

## Inhalt

In December 2023, the WHO reported a Ralstonia pickettii outbreak in Australia linked to contaminated saline solutions. Concurrently, German surveillance detected an increase in nosocomial R. pickettii bacteremia cases, prompting a national outbreak investigation.

From August 2023 to June 2024, 15 patient isolates were sequenced using Illumina whole genome sequencing. Five of these were additionally sequenced using Oxford Nanopore Technology (ONT). Combining short- and long-read data enabled the reconstruction of complete genomes. Similarities to publicly available data were assessed with core genome multilocus sequence typing (cgMLST), using a newly created scheme.

Six isolates from patients in three hospitals across different federal states clustered within ≤6 allele differences. German and Australian outbreak clusters differed by at least 43 alleles, requiring further investigation into their potential link.

Rapid genomic investigation enabled cluster identification and assessment of relatedness to the other outbreaks, supporting epidemiological investigation. The absence of a standardized cgMLST scheme, limited public data, and sparse documentation of analyses in prior studies posed key challenges. Although, ONT allowed the recovery of complete genomes and plasmids, its increased error rates inflated cgMLST distances, highlighting the usefulness of combined long- and short-read data for bacterial outbreak investigations.

## Keywords

Ralstonia pickettii, cgMLST, Public Health, Outbreak, Genomic Epidemiology

## Registration ID

111

## Professional Status of the Speaker

Senior Scientist

## Junior Scientist Status

No, I am not a Junior Scientist.

**Track Klassifizierung:** Genomics &amp; Proteomics

**Typ des Beitrags:** Oral presentation