

Whole genome-based characterization of *Salmonella*, STEC, *Campylobacter jejuni* and *Listeria monocytogenes*

Aim:

Using WGS based methods for a) **elucidating population structures, virulence factors and antimicrobial resistance genes** in foodborne pathogens and b) **tracing outbreaks**

1. Population structures, virulence factors and antimicrobial resistance genes

WP1.1: *Salmonella*

A novel lineage of ceftriaxone-resistant *Salmonella* Typhi from India that is closely related to XDR *S. Typhi* found in Pakistan

<https://pubmed.ncbi.nlm.nih.gov/31872221/>

Insight: Two MDR *Salmonella* Typhi isolates from India were found by whole genome sequencing to be closely related to the 2016 XDR *S. Typhi* outbreak strain from Pakistan.

Phylogenomic analysis of *Salmonella enterica* subsp. *enterica* Serovar Bovismorbificans from clinical and food samples

[paper submitted](#)

Genomic analysis of *Salmonella enterica* Serovar Kentucky ST 198 strains isolated over 10 years from clinical cases in Switzerland

[Project ongoing](#)

Salmonella Napoli

[Project ongoing](#)

WP1.2: Shigatoxin-producing *E. coli* (STEC)

Genetic characterization of Shiga toxin producing *Escherichia coli* belonging to the emerging hybrid pathotype O80:H2 isolated from humans 2010-2017 in Switzerland.

<https://www.sciencedirect.com/science/article/pii/S1438422118301887>

Insight: All isolates carried *stx2a* or *stx2d*, the rare *eae* variant *eae-ξ* and at least seven virulence genes associated with pS88, a plasmid that is found in extraintestinal pathogenic *E. coli* (ExPEC). Core genome multi-locus sequence typing (cgMLST) detected two closely related but distinct subclusters with different *stx2* and *iuc/iutA* genotypes. All isolates were multidrug resistant (MDR). STEC/ExPEC hybrid pathotypes such as STEC O80:H2 represent a therapeutic challenge in the event of extraintestinal infection.

Characteristics of Shiga toxin-producing *Escherichia coli* isolated from raw meat-based diets for companion animals

<https://doi.org/10.3390/microorganisms9081556>

Insight: STECs were recovered from 41% of the 59 samples, and strains were subjected to serotyping and virulence gene profiling, using whole genome sequencing (WGS)-based methods. Of 28 strains, 29% carried *stx2a* or *stx2d*, which are linked to STEC with high pathogenic potential. Twenty different serotypes were identified, including STEC O26:H11, O91:H10, O91:H14, O145:H28, O146:H21, and O146:H28, which are within the most common non-O157 serogroups associated with human STEC-related illnesses worldwide.

Distribution of virulence factors, antimicrobial resistance genes and phylogenetic relatedness among Shiga toxin-producing *Escherichia coli* serogroup O91 strains from human infections 2003–2019 in Switzerland.

<https://doi.org/10.1016/j.ijmm.2021.151541>

Insight: The strains belonged to O91:H10, O91:H14, and O91:H21. *stx1a* was the most common Shiga toxin gene subtype among the isolates, followed by *stx2b*, *stx2d* and *stx2a*. All strains were negative for the *eae* gene. STEC O91:H14 were distinguished from STEC O91:H10/H21 by one or more virulence factors found in extraintestinal pathogenic *E. coli* (ExPEC), including *hlyF*, *iucC/iutA*, *kpsE* and *traT* (hybrid STEC).

WP1.3: *Campylobacter jejuni*

Whole genome-based characterization of *Campylobacter jejuni* from human patients with gastroenteritis collected over an 18-year period (2003-2020)

[Project ongoing](#)

WP1.4: *Listeria monocytogenes*

Characteristics of *Listeria monocytogenes* from flowing surface waters in Switzerland.

<https://doi.org/10.1038/s41598-021-88514-y>

Insight: The 25 isolates belonged to major lineages I and II, with the majority assigned to either serotype 1/2a (48%), or 4b (44%). The predominant CCs identified were the hypervirulent serotype 4b clones CC1 and CC4, and the serotype CC412; Two of the isolates belonged to CC6 which is an emerging hypervirulent clone. All isolates contained intact genes associated with invasion and infection, including *inlA/B* and *prfA*. The four CC4 isolates all harbored *Listeria* pathogenicity island 4 (LIPI-4), which confers hypervirulence

2. Tracing (foodborne) outbreaks

Siblings with typhoid fever: an investigation of intrafamilial transmission, clonality, and antibiotic susceptibility.

<https://pubmed.ncbi.nlm.nih.gov/31580900/>

Listeriosis caused by persistence of *Listeria monocytogenes* serotype 4b Sequence Type 6 in cheese production environment.

<https://pubmed.ncbi.nlm.nih.gov/33350924/>