

**P1736 *Campylobacter*: high resolution phylogenetic surveillance study of a food-borne pathogen over two years in Basel, Switzerland, using whole-genome sequencing (WGS)**

Helena Seth-Smith<sup>\*1 6</sup>, Josiane Reist<sup>1</sup>, Jessica Agnetti<sup>1 6</sup>, Sylvia Gautsch<sup>3</sup>, Daniel Wüthrich<sup>1 6</sup>, Olivier Dubuis<sup>2</sup>, Michael Naegele<sup>2</sup>, Ingrid Steffen<sup>4</sup>, Simon Fuchs<sup>5</sup>, Peter Brodmann<sup>3</sup>, Adrian Egli<sup>1 6</sup>

<sup>1</sup>University Hospital Basel, Clinical Microbiology, Basel, Switzerland, <sup>2</sup>Viollier AG, Allschwil, Switzerland, <sup>3</sup>State Laboratory Basel-City, Basel, Switzerland, <sup>4</sup>Rothen Medizinische Laboratorien, Bacteriology, Basel, Switzerland, <sup>5</sup>Medical Services, Health Department of the Canton Basel-Stadt, Basel, Switzerland, <sup>6</sup>University of Basel, Department of Biomedicine, Basel, Switzerland

**Background:** *Campylobacter jejuni* and *C. coli* are common causes of foodborne disease. Symptoms include bloody diarrhoea and fever, and can lead to complications such as sepsis. Over 7000 cases are reported annually in Switzerland, with peaks in summer and winter seasons. Infection is associated with the food chain, in particular poultry. This is the largest WGS surveillance study to date, aiming to link diarrhoeal and bacteremial isolates to potentially contaminated chicken meat sources.

**Materials/methods:** We collected *Campylobacter* isolates from symptomatic patients in Basel, Switzerland, from November 2015-(prospectively) February 2018, including three Winter seasons and two Summer seasons (n=173 to date). Chicken meat was sampled from butchers in and around Basel, during two Winter seasons (n=82 to date). WGS was performed on an in-house Illumina Miseq, for high-resolution phylogenetic analysis of transmission events. An established core genome MLST (cgMLST) scheme was used to cluster isolates, identify clonal complexes, and indicate sources of cases. Detailed analysis looked within putative transmission clusters, identifying virulence factors and antimicrobial resistance determinants.

**Results:** *Campylobacter* spp. were cultured from approximately 40% of meat samples. Both patient and butcher isolates were found in multiple clonal complexes, and with high diversity, in both *C. jejuni* and *C. coli*. Interim analysis of 119 human and 81 chicken isolates shows clusters containing only patient isolates (no source identified, n=11), only butcher isolates (suggestive of strains with low virulence, n=12), and those containing both butcher and patient isolates, suggestive of transmission (n=7). Some clusters persisted through several seasons, implying a prevailing source of foodborne infection. The isolates from bacteraemic cases are *C. jejuni* and belong to clonal complexes 21 and 48, suggesting a higher virulence of these groups. A genome wide study identified genes associated with transmission and a more invasive clinical course.

**Conclusions:** This comprehensive longitudinal study shows a high diversity of *Campylobacter* in Basel, in both meat and human isolates. Many new clusters have been found, previously unidentified in the cgMLST database. Our data confirms that chicken is an important source of Campylobacteriosis, presumably through undercooking or contamination through the cross-use of cutlery. Other sources remain to be determined.