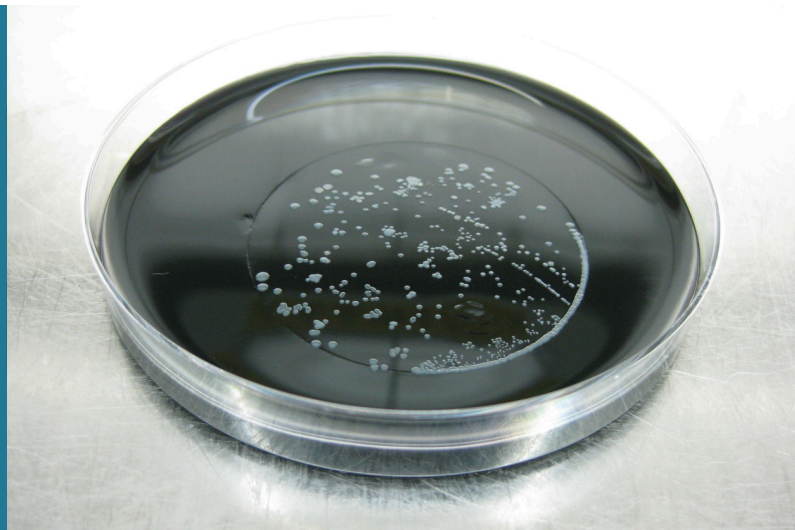


CampylOmic

One Health Genomics study of human recurring *Campylobacter jejuni* in Luxembourg.



Inspiration

According to the World Health Organization, *Campylobacter spp.* is one of four key global causes of bacterial diarrhoeal diseases around the Earth. Luxembourg has one of the highest incidences in the European Union, reaching an incidence rate of 159 per 100,000 inhabitants in 2014 with *Campylobacter jejuni* accounting for 90% of human cases.

Between 2009 and 2013, a collaborative research consortium implicating different food safety administrations in Luxembourg and LIST conducted the research project HypoCamp, primarily focusing on environmental sources of *Campylobacter* infections (CORE C09/BM/09). In an epidemiological source attribution analysis using genetic data, it was shown that most human cases could be attributed to poultry (61.2%), ruminants (33.3%), environmental water (4.9%) and swine (0.6%). Further modelling work showed that surface waters in Luxembourg were mainly contaminated by wild birds (61% of the water isolates). By modifying the existing housekeeping multilocus sequence typing (MLST) scheme to include molecular marker genes *porA* and *gyrA*, an unexpected endemic pattern in the temporal distribution of genotypes was discovered. Almost half of patients were infected by recurring genotypes of which a small subset clustered in time to form micro-epidemics (9% of isolates).

Innovation

In the context of a One Health approach, the Campylomic project aims to conduct two novel pillars of research to complete the picture of the *Campylobacter* population structure in space and time and gain valuable insights on the environmental pathway that might explain the persistence over time of these genotypes. The first focus of the project, for which LIST researchers are mainly involved in, is the carriage of generalist clonal complexes of *C. jejuni* in wild birds, notably through the development of a culture-independent sequencing strategy. In addition to the collection - in collaboration with Natur & Umwelt - of wild bird faecal samples, LIST researchers will detect and isolate *Campylobacter* via culture-dependent methods, identify strains with mass spectrometry tools, as well as characterise them through whole-genome sequencing and bioinformatic analysis.

The second focus of Campylomic is the specific phenotypic traits of endemic strains among humans, in particular their abilities to adhere to inert surfaces, their habituation ability to oxygen and their tolerance to oxidative stress.

Impact

Campylomic will address the occurrence of recurring genotypes isolated over the past 10 years from different sources in Luxembourg, including humans.

A comparative genomic study is currently investigating the occurrence of stable clonally derived genotypes persistent in space and time. Potential links and association between the emergence and persistence of these recurring genotypes and particular phenotypic traits of aerotolerance and biofilm formation capability will therefore be explored.

By assessing the carriage of *C. jejuni* in wild birds, Campylomic will not only contribute to a better understanding of the geographical dispersion of the recurring genotypes, but it will also give keys for a more informed management of *Campylobacter* epidemics. Finally, this project will propose an innovative approach combining culture methods with metagenomics to study the *Campylobacter* diversity.

Partners

Laboratoire national de santé (LU) , Luxembourg Centre for Systems Biomedicine - University of Luxembourg (LU) , SECALIM (FR)

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