

THE CARRIAGE OF ANTIBIOTIC RESISTANCE GENES IN THE ENVIRONMENT: THE CASE OF CAMPYLOBACTER IN SURFACE WATER AND WILD BIRDS IN LUXEMBOURG.

Main author: Louise Hock (Luxembourg Institute of Science and Technology - LIST)

Co-authors: Cécile Walczak, Juliette Mosser, Maureen Feucherolle, Christian Penny, Catherine Ragimbeau, Henry-Michel Cauchie.

INTRODUCTION

Each new technology brings its own advantages and risks. Even if antibiotics allow us to fight severe bacterial diseases, their unreasonable use increases the selection of resistant bacteria that currently have a negative impact on Public Health. The transmission and widespread prevalence of bacteria carrying antimicrobial resistance (AMR) genes in wildlife and the environment could represent an additional challenge by turning the environment into an AMR hotspot of putative critical epidemiology. Campylobacteriosis is recognised as the principal bacterial gastroenteritis in industrialised countries. Luxembourg presents one of the highest incidence rates of Campylobacter infections in the EU: 103.8 cases per 100,000 inhabitants in 2018 (EFSA and ECDC, 2019). Campylobacter jejuni is implicated in more than 80 % of human cases whereas Campylobacter coli accounts for the majority of the rest. Although campylobacteriosis is usually self-limiting, antimicrobial treatment is necessary in the case of severe infections. Our aim is to assess the prevalence of AMR in *C. jejuni* and *C. coli* strains isolated from surface water and wild birds to obtain a picture of the AMR genes carriage in Luxembourg environment.

METHODOLOGY

An environmental collection (set under the FNR Core Campylomic project 11684203) of 93 *C. coli* and 80 *C. jejuni* isolated from water surface (N=99) and wild bird faeces (N=74) were characterised according their antimicrobial resistances using disk diffusion methods following EUCAST recommendations (EUCAST, 2021). These phenotypic resistance results were compared to “in silico” antibiograms generated from NGS data (Next Generation Sequencing, Illumina technologies) submitted to the ResFinder database.

RESULTS

A total of 6.5 % of the *C. coli* and 21 % of the *C. jejuni* isolates presented at least one antibiotic resistance whereas half of the Campylobacter isolates possessed known AMR genes. The most prevalent resistance observed was to ampicillin and quinolone antibiotics (8 and 5 % of isolates, respectively): nalidixic acid and ciprofloxacin. The single mutation of the DNA gyrase A (C257T) conferring the quinolone resistance was encountered in 4 % of

the collection. No florfenicol (phenol), amoxicillin (beta-lactam) and gentamicin (aminoglycoside) phenotypic resistances were observed whereas aminoglycoside resistance genes were detected in 14 % of the *Campylobacter* isolates. Resistant strains were found in 17.5 and 10 % of the wild bird and surface water samples, respectively. Two *C. jejuni* isolates from water samples were multiresistant (Beta-lactam, Quinolone and Tetracyclin).

DISCUSSION

In Luxembourg, resistance to at least one antibiotic was demonstrated by one in eight *Campylobacter* isolates from wild birds and surface water. Isolates are initially exposed to antibiotics both in animal production systems and in human medicine through drug treatments. Resistant strains emerging from this selection pressure could then reach the environment via faeces and wastewater. Moreover, some wild birds, which are well adapted to anthropogenic environments, come into close contact with livestock, domestic animals and humans. Therefore, they become reservoirs of antimicrobial resistance and contribute to the multi-host spread of AMR. Consequently, the surveillance of resistant bacteria in wild animals and the environment is necessary to guide public health policies to control foodborne illnesses in humans.