

# Environmental dynamics of *Campylobacter jejuni* genotypes circulating in Luxembourg: WHAT IS THE ROLE OF WILD BIRDS?

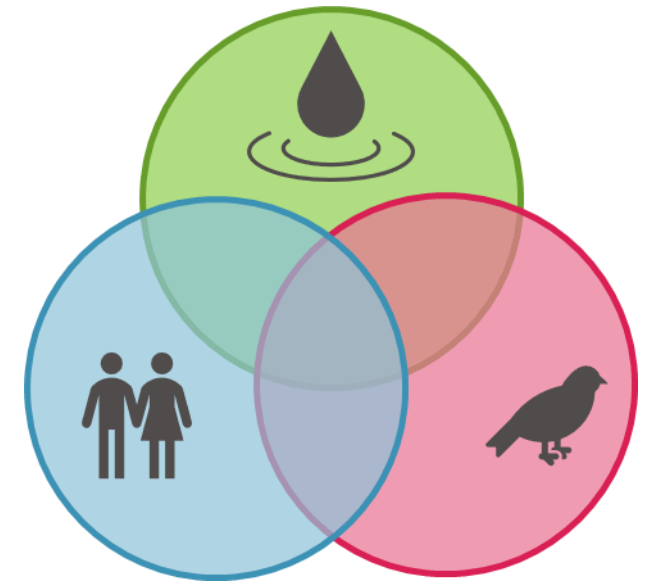
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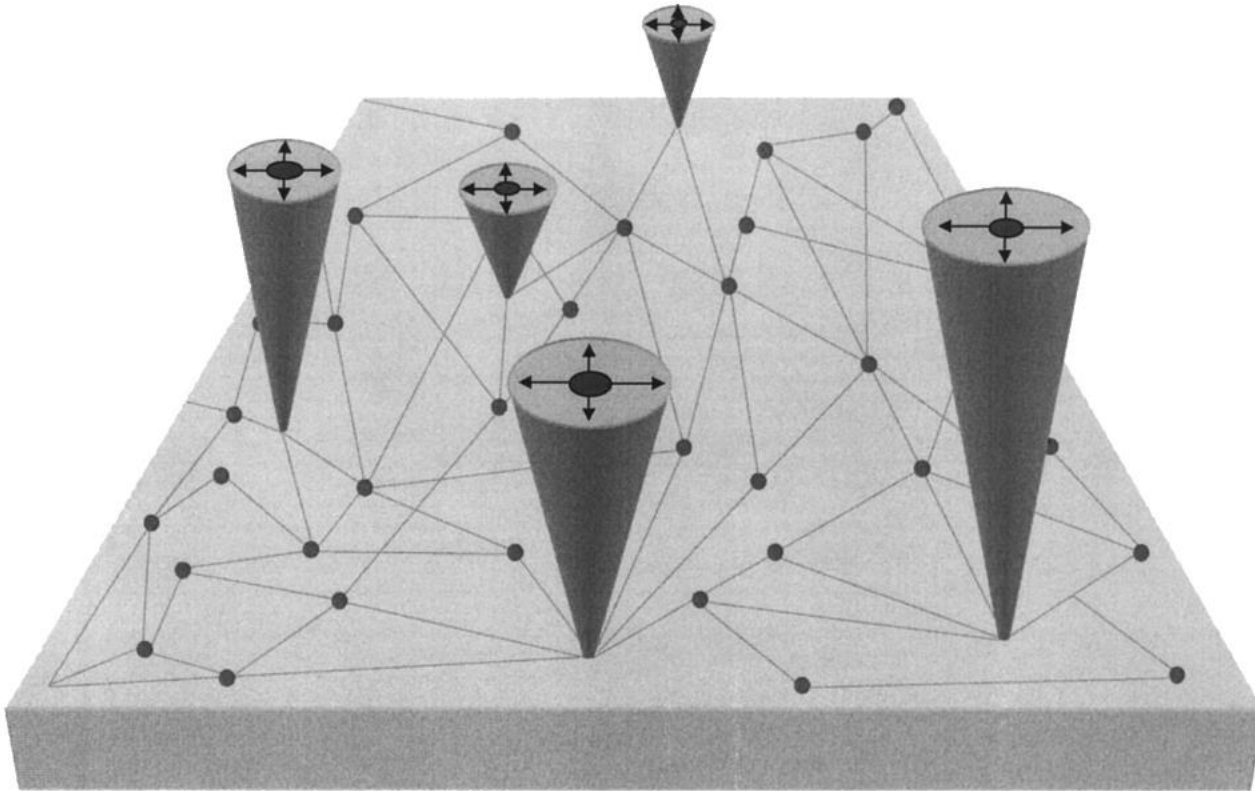
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## Population structure of *C. jejuni*.

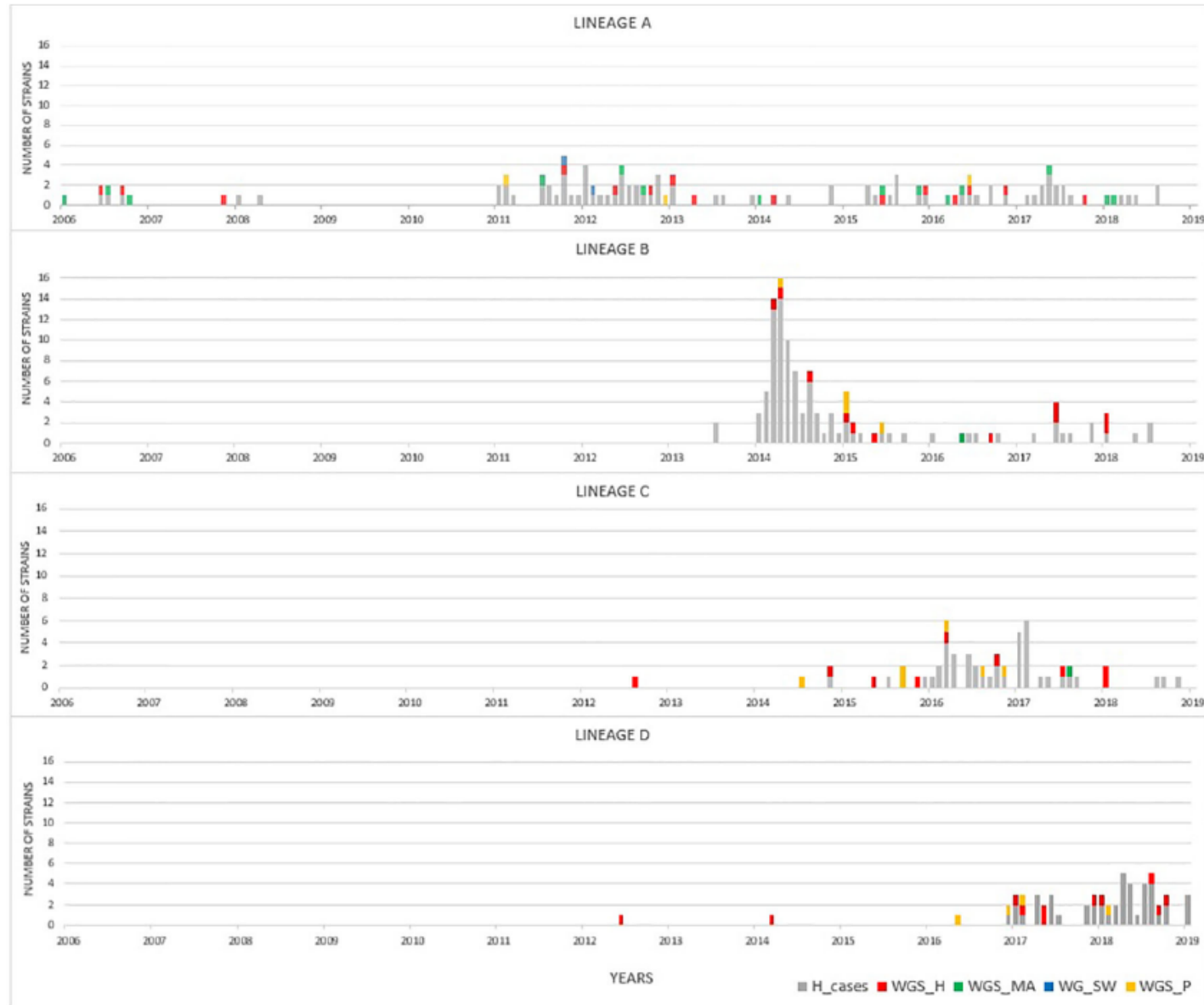


### **Background population (network):**

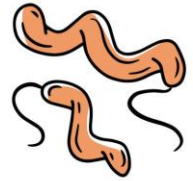
- Rare and unrelated genotypes
- High genetic diversity
- High recombination rate

### **Clonal complexes (clones):**

- Frequent genotypes
- Clusters or closely related genotypes
- A single, highly adaptive, ancestral genotype
- Persist for decades



**FIGURE 1** | Distribution of strains occurrence for lineages A to D over time. Clinical strains of the laboratory collection are displayed in gray (extended MLST typing). Colors represent to source of selected isolates that were analyzed by WGS: human (red), cattle and sheep (green), poultry (yellow), and surface water (blue) samples.



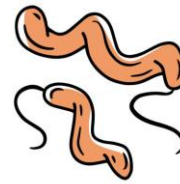
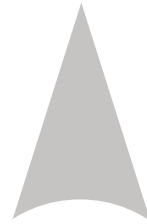
**Genotype** = Complex Type (CT) – Sequence Type (ST) – *gyrA* – *porA*

cgMLST Seqsphere  
(637 loci)

(7 loci)



2018-2021:  
1712 cases of campylobacteriosis



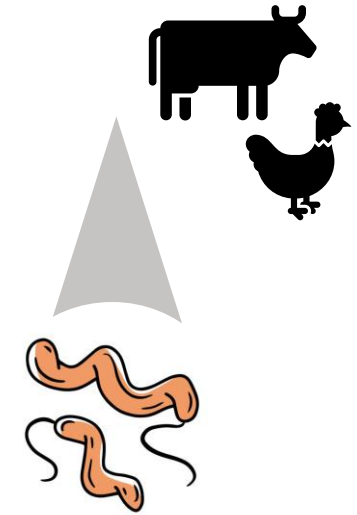
1131 *C. jejuni* isolates  
593 genotypes



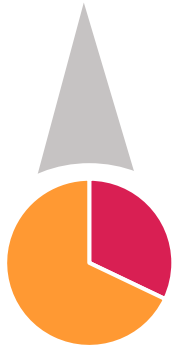
59 Recurring  
genotypes (41%)



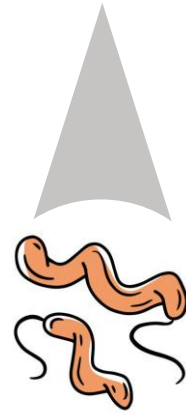
2018-2021:  
1712 cases of campylobacteriosis



240 *C. jejuni* isolates  
158 genotypes



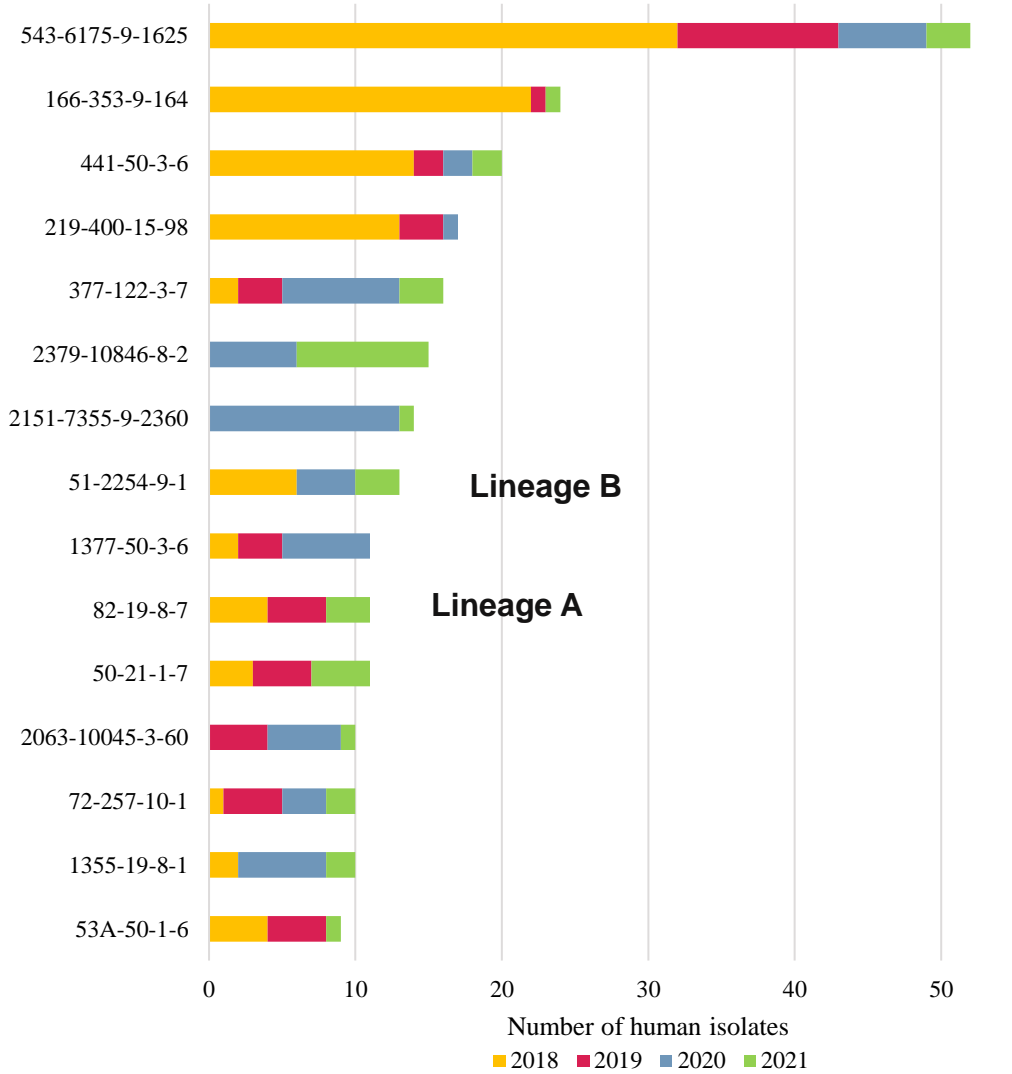
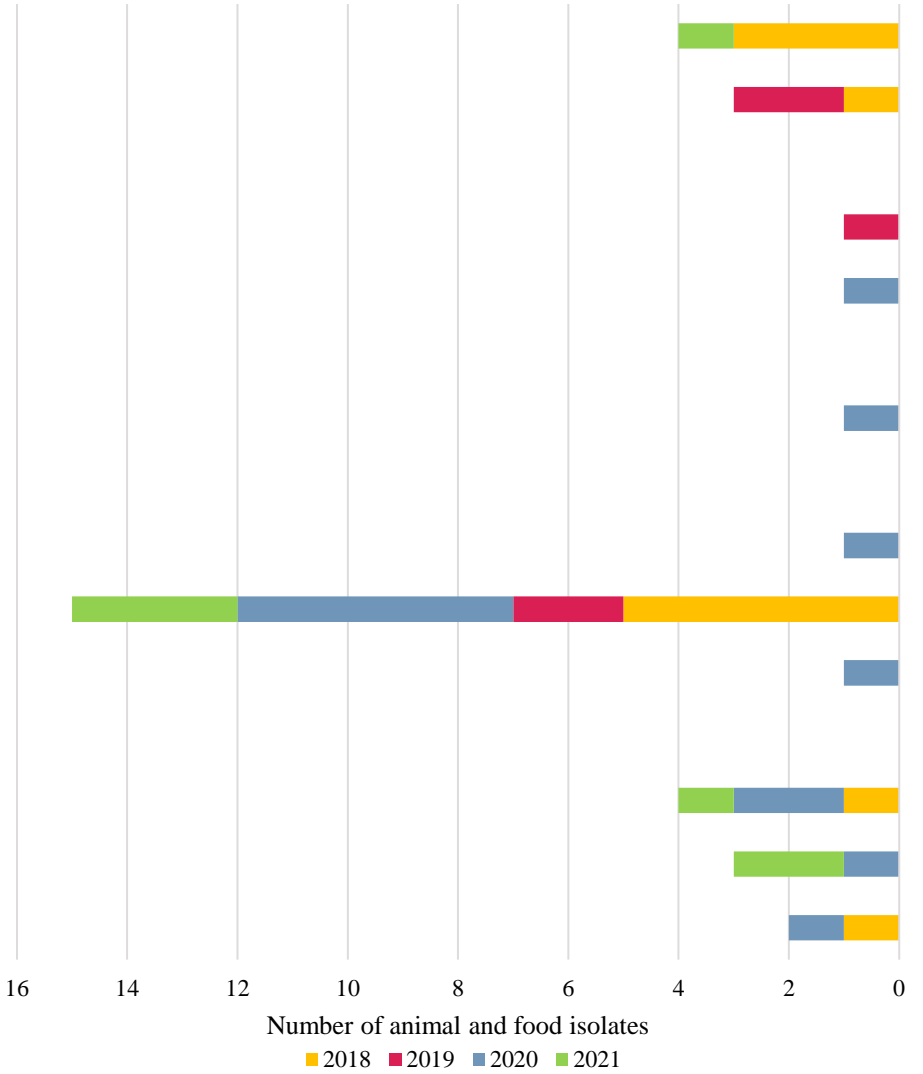
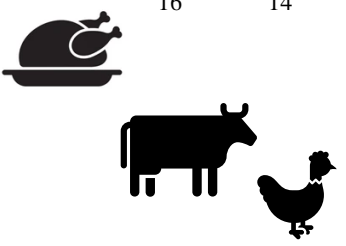
27 Recurring  
genotypes (35%)



1131 *C. jejuni* isolates  
593 genotypes



59 Recurring  
genotypes (41%)



**Lineage D**

**Lineage B**

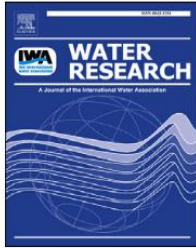
**Lineage A**





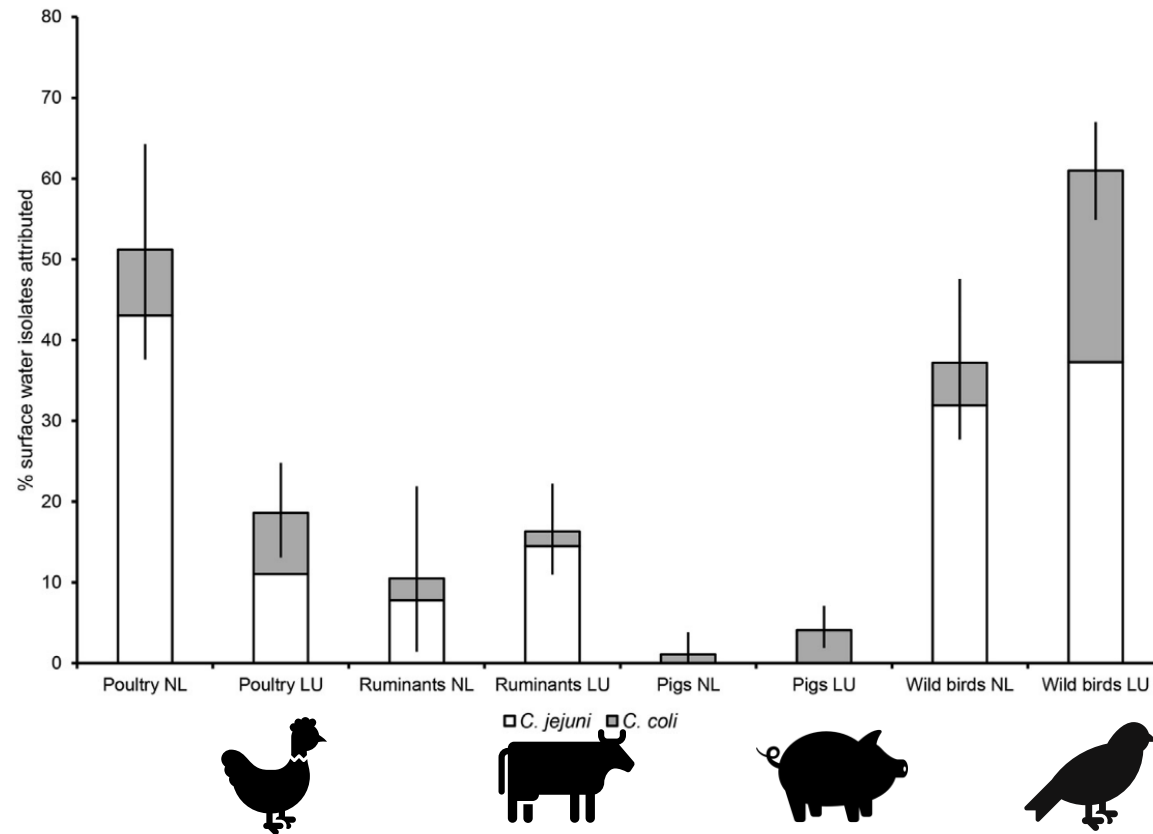
Optimal temperature for *C. jejuni* growth

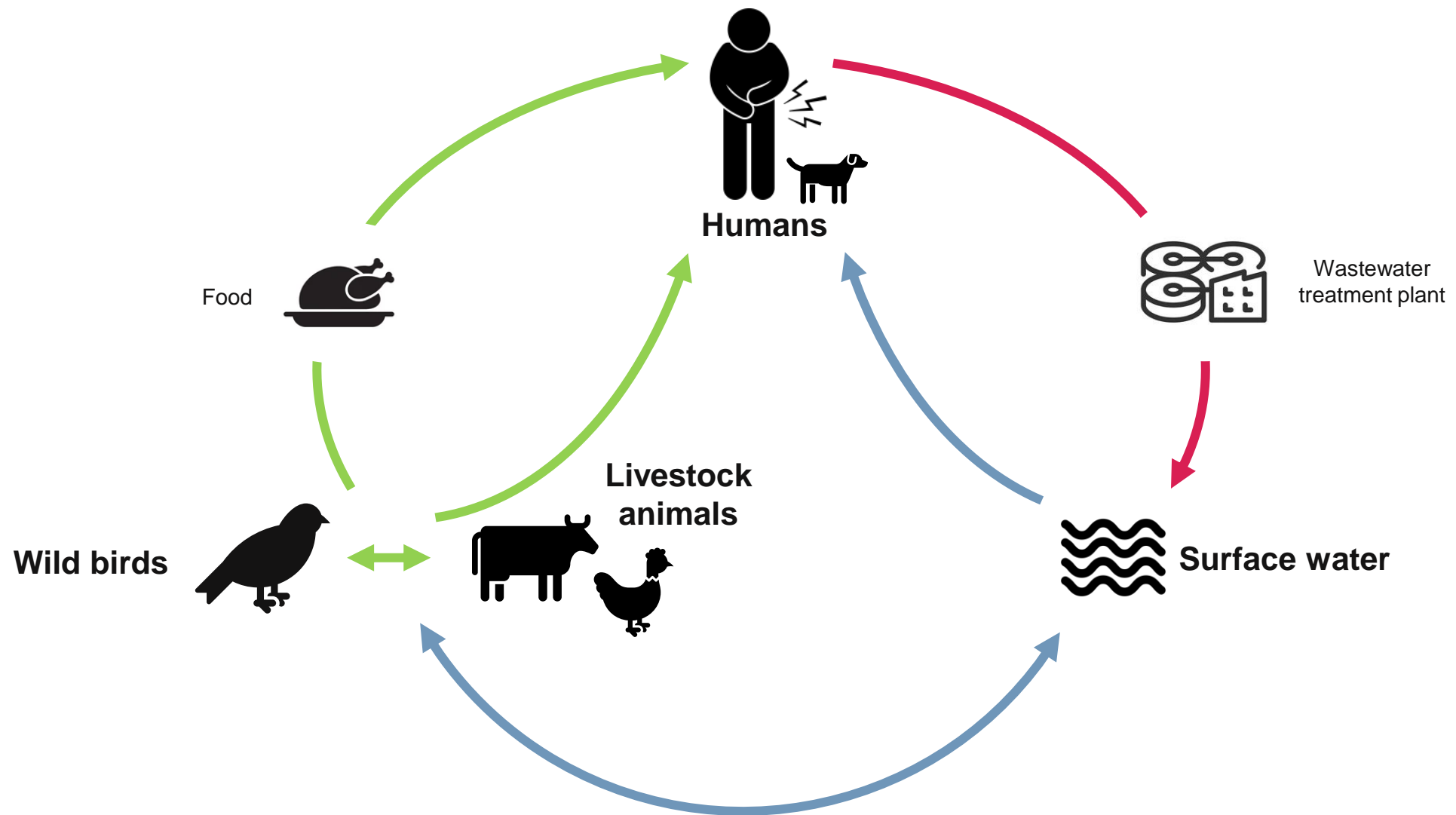




## Quantifying potential sources of surface water contamination with *Campylobacter jejuni* and *Campylobacter coli*

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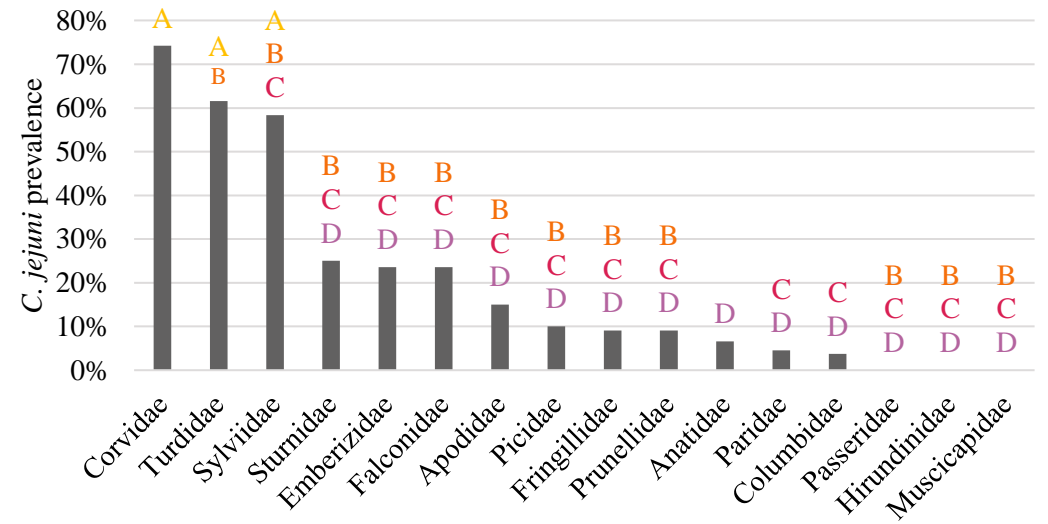
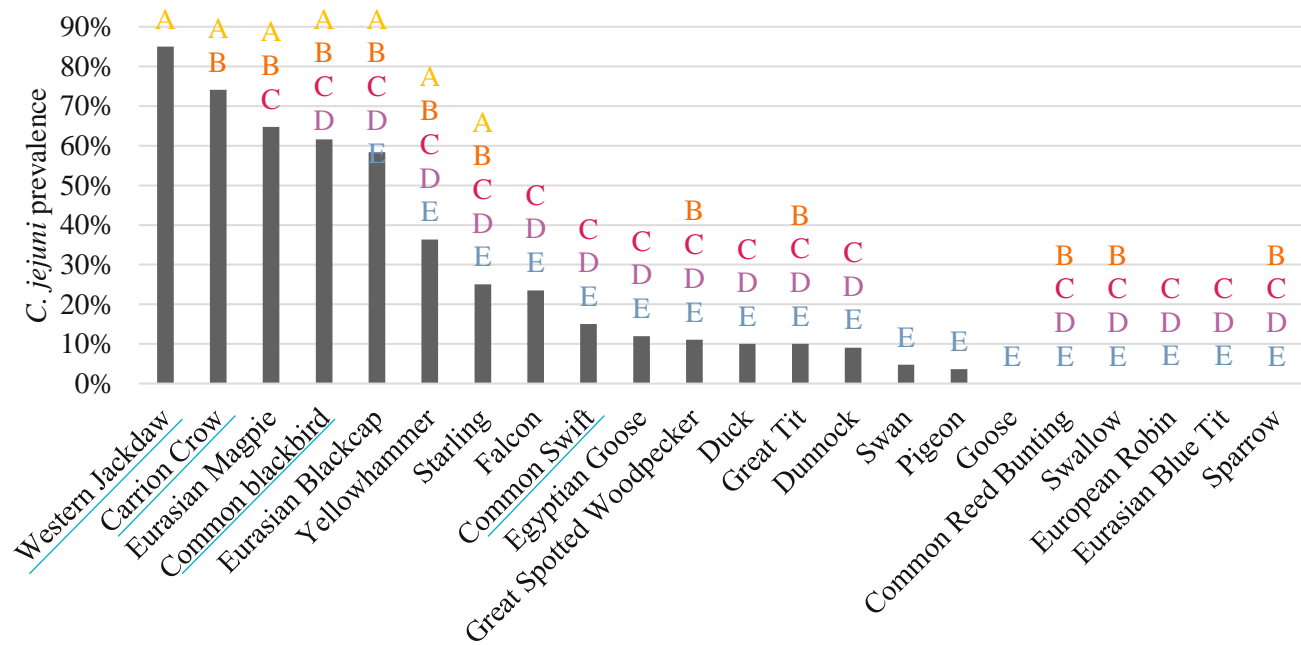


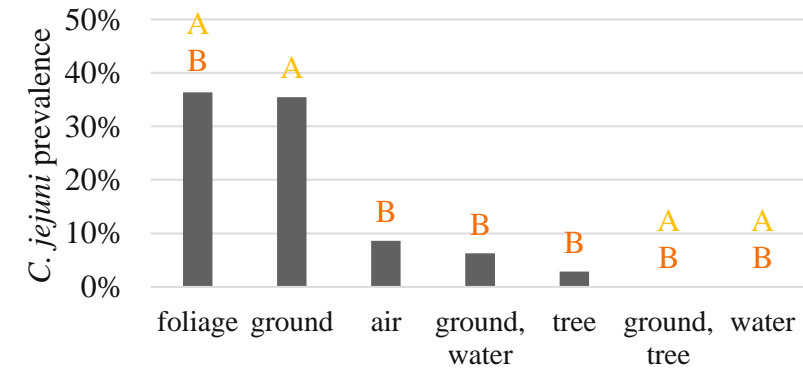
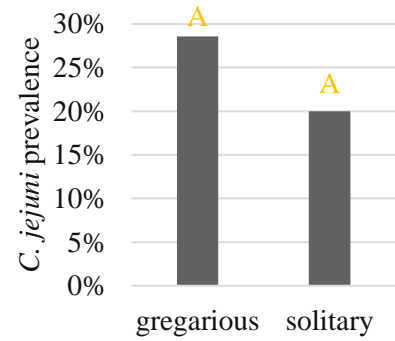
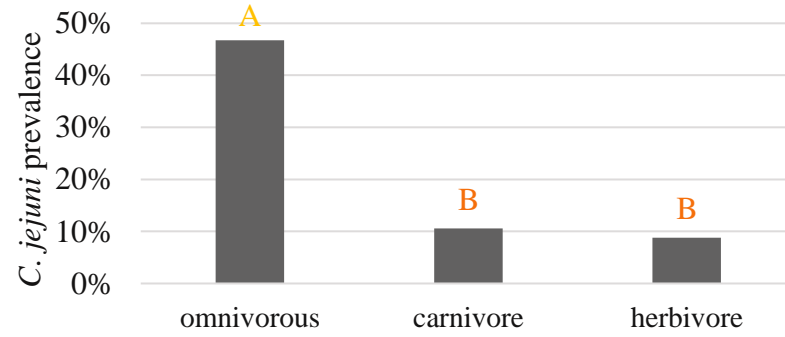
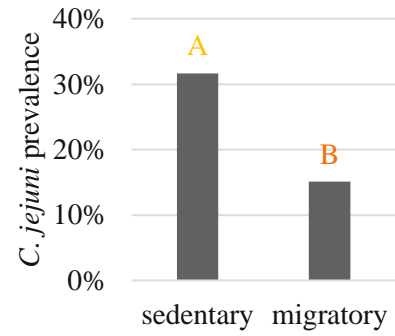


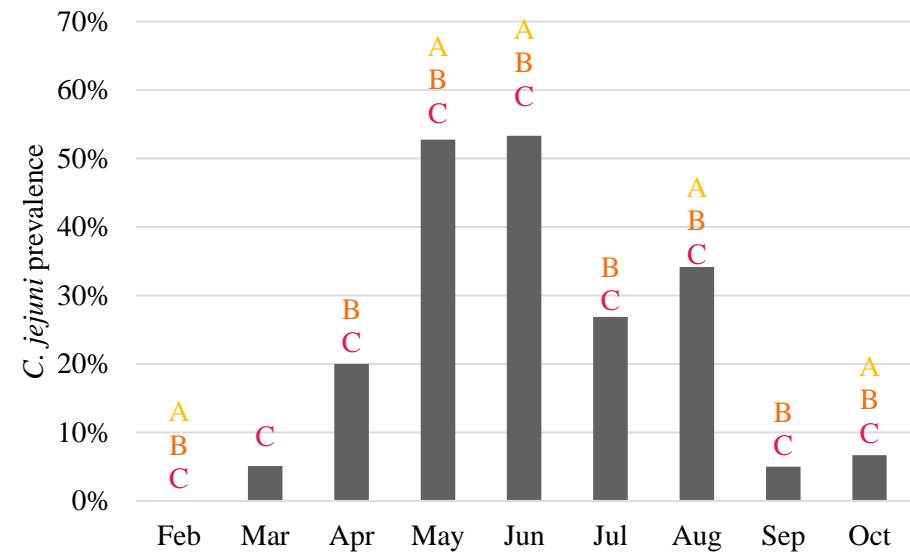
362 wild bird faeces samples



*C. jejuni* positive samples (27%)

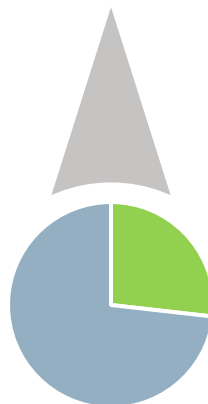




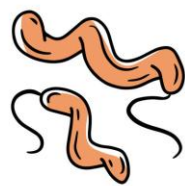




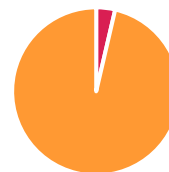
362 wild bird faeces samples



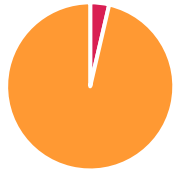
*C. jejuni* positive samples (27%)



110 *C. jejuni* isolates  
80 genotypes



3 Recurring genotypes (4%)



3 Recurring genotypes (4%)

Lineage A

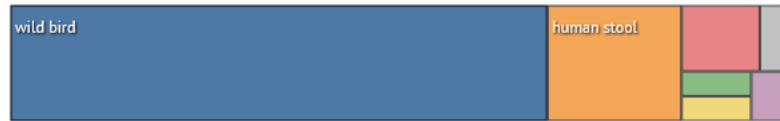
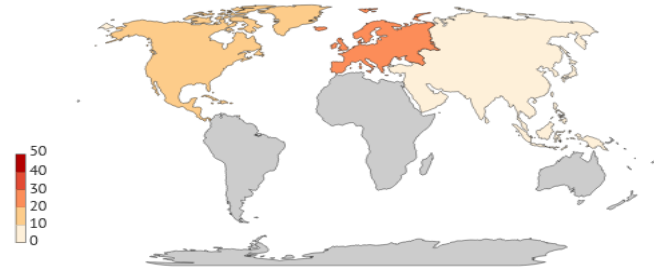
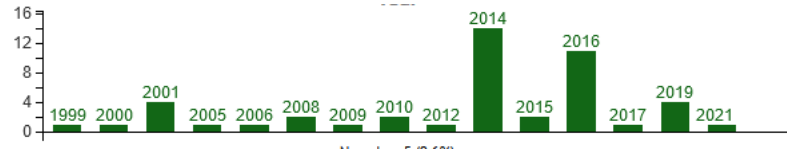
Genotypes	Bird species (no. of isolates)	Sampling period in wild birds	No. of isolates in humans				No. of isolates in animals and food (bovine-turkey- chicken)			
			2018	2019	2020	2021	2018	2019	2020	2021
82-19-8-7	Great spotted woodpecker (1)	June 2021	4	4	0	3	5-0-0	2-0-0	4-1-0	2-0-0
84-1044-27-25	Common swift (1)	July 2020	2	2	0	1	0-0-0	0-0-0	0-0-0	0-0-0
	Eurasian magpie (1)	June 2021								
827-475-5-67	Common swift (1)	July 2019	4	1	0	0	0-0-0	1-0-0	0-1-1	0-0-0



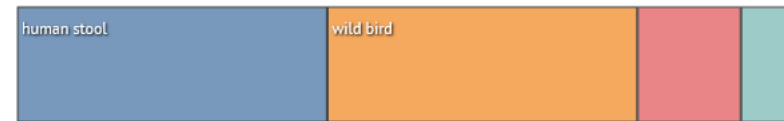
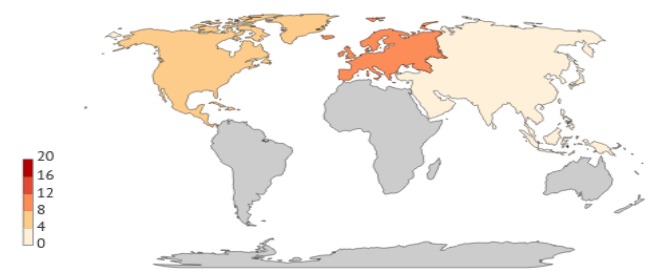
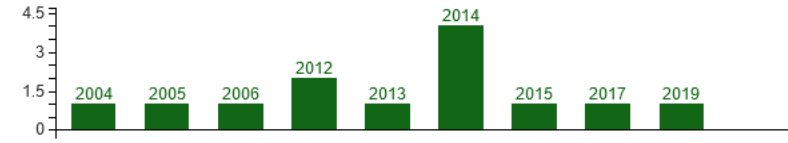
Migratory bird species  
Eat insects  
Transmission during summer



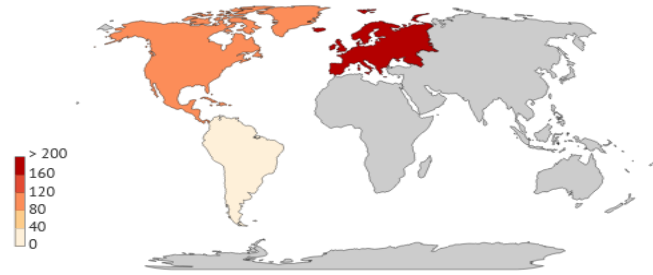
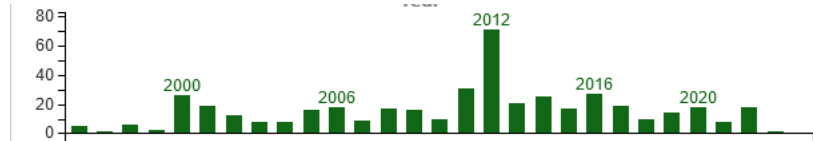
### ST448



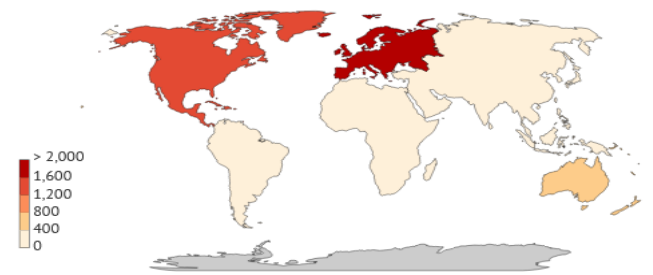
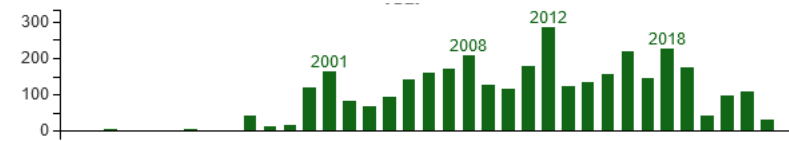
### ST1540



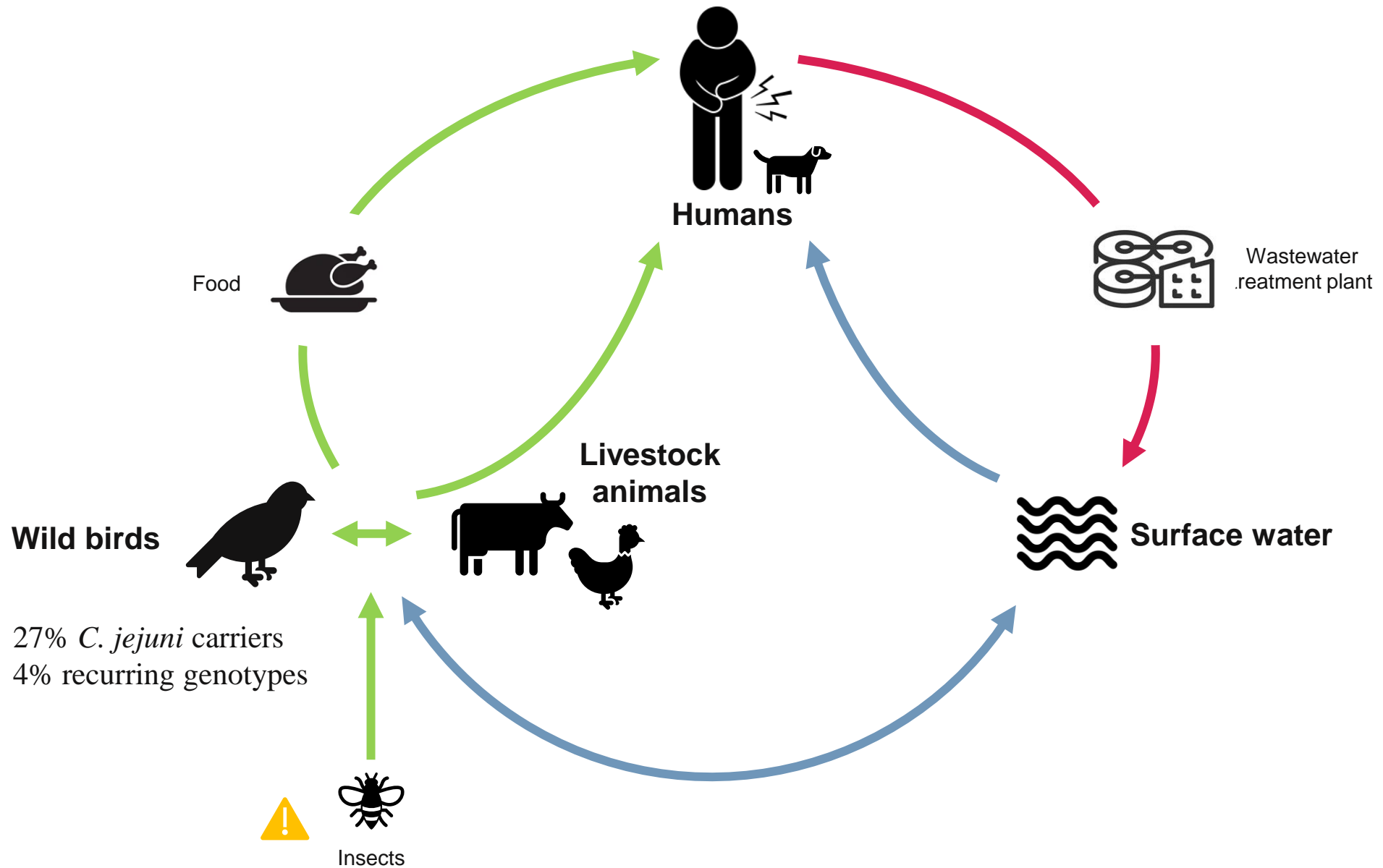
### ST267



### ST45



40% of clinical isolates link to recurrent genotypes





## Environmental dynamics of *Campylobacter jejuni* genotypes circulating in Luxembourg: what is the role of wild birds?

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### Abstract

*Campylobacter jejuni* is the leading cause of bacterial gastroenteritis worldwide, but, unlike other foodborne pathogens, is not commonly reported as causing outbreaks. The population structure of the species is characterized by a high degree of genetic diversity, but the presence of stable clonally derived genotypes persisting in space and time, and potentially leading to diffuse outbreaks, has recently been identified. The spread of these recurring genotypes could be enhanced by wild birds, suspected to act as vectors for a wide range of microorganisms that can be transmissible to other animals or humans. This study assessed the genetic diversity of *C. jejuni* carriage in wild birds and surface waters to explore a potential link between these environments and the persistence over years of recurring lineages infecting humans in Luxembourg. These lineages corresponded to over 40% of clinical isolates over a 4 year period from 2018 to 2021. While mainly exotic genotypes were recovered from environmental samples, 4% of *C. jejuni* from wild birds corresponded to human recurring genotypes. Among them, a human clinical endemic lineage, occurring for over a decade in Luxembourg, was detected in one bird species, suggesting a possible contribution to the persistence of this clone and its multi-host feature. Whereas 27% of wild birds were carriers of *C. jejuni*, confirming their role as spreader or reservoir, only three out of 59 genotypes overlapped with recurring human strains. While direct transmission of *C. jejuni* infection through wild birds remains questionable, they may play a key role in the environmental spreading of stable clones to livestock, and this issue merits further investigation.