



FINNISH FOOD AUTHORITY

Ruokavirasto • Livsmedelsverket



FINNISH FOOD
AUTHORITY
Ruokavirasto • Livsmedelsverket

Population genetics of antibiotic-resistant *Campylobacter jejuni* in broilers in Finland – Vertical transmission, fact or fiction?

Anniina Jaakkonen & Satu Olkkola

EURL-Campylobacter workshop

NRL-Finland

30 Sep 2025

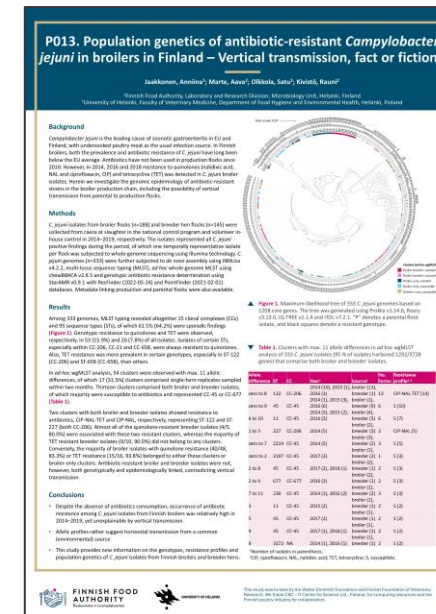
Joint research study



- University of Helsinki
 - Aava Marte, BVM (Master's Thesis in Veterinary Medicine)
 - Docent Rauni Kivistö
- Finnish Food Authority, NRL-Finland
 - Anniina Jaakkonen, PhD, MSc (Tech)
 - Satu Olkkola, PhD, DVM
- External advisors
 - Päivikki Perko-Mäkelä, PhD, DVM (Atria Oy)
 - Hannele Nauholz, DVM (Animal Health ETT)



Master's Thesis (in Finnish):
<http://hdl.handle.net/10138/596233>





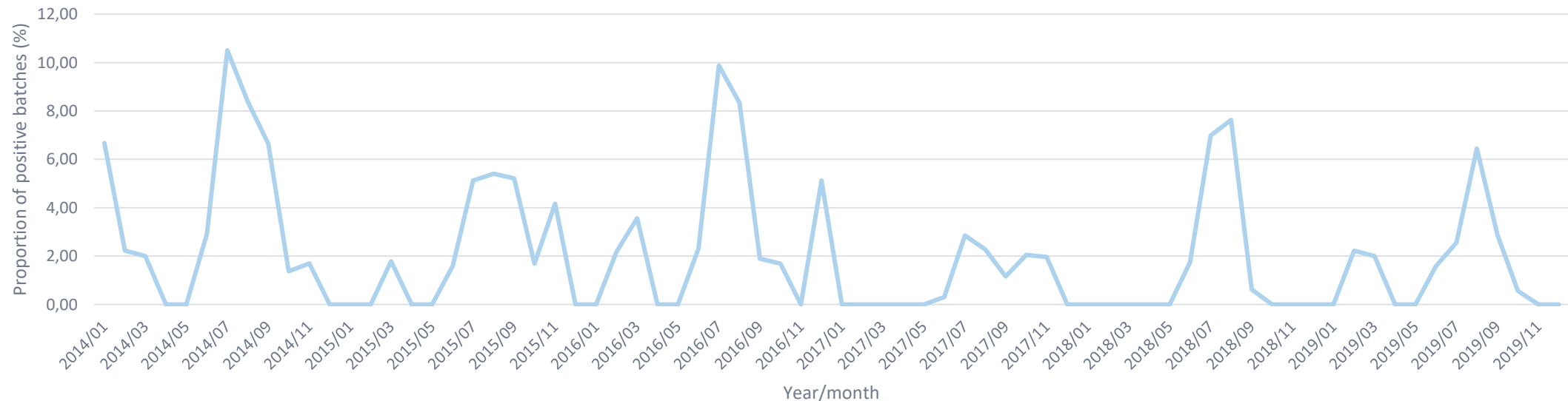
**FINNISH FOOD
AUTHORITY**
Ruokavirasto • Livsmedelsverket

Background: thermotolerant *Campylobacter* sp. in broilers in Finland

Prevalence of *Campylobacter* sp. in broilers (caeca) at slaughter



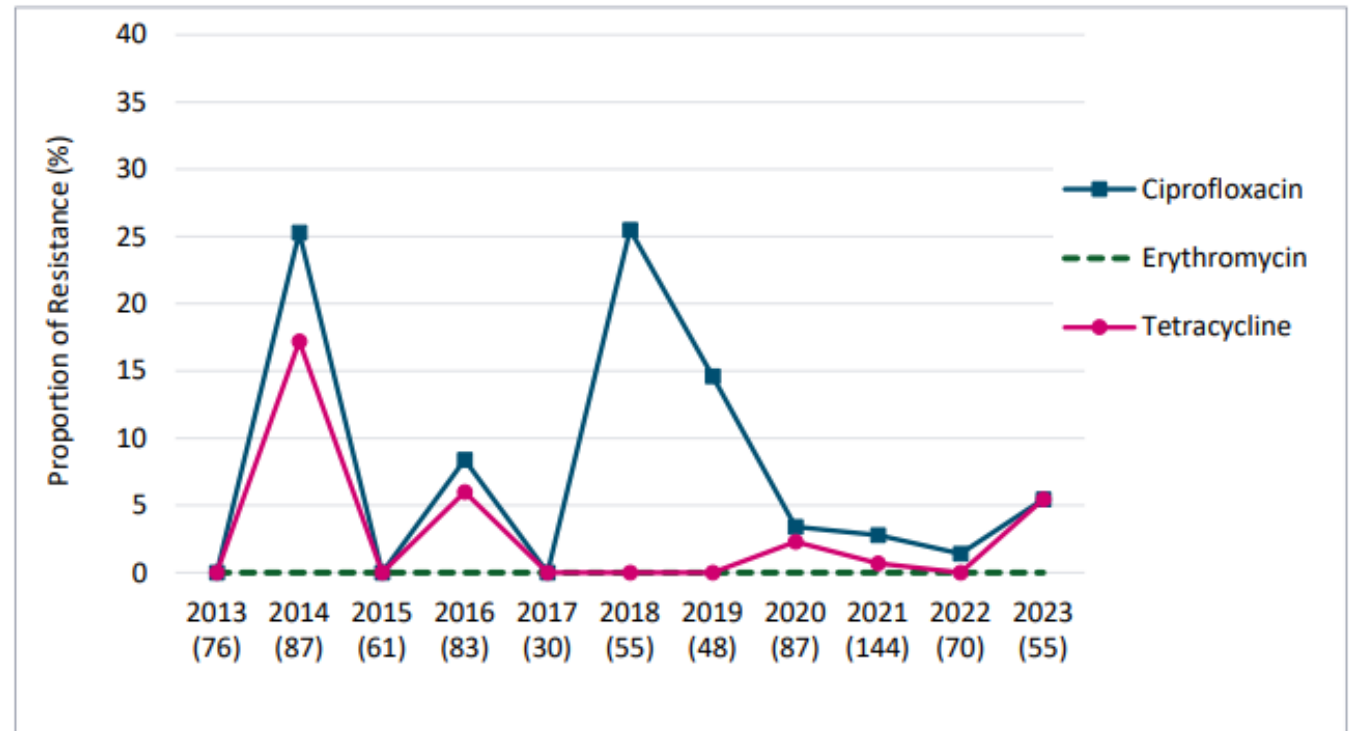
- National control program (since 2004)
 - Every slaughtered batch tested for *Campylobacter* (ISO 10272-1) in June–Oct, sample in Nov–May
 - Combined caecal sample of 10 birds per slaughtered batch/flock
 - Phenotypic antibiotic resistance tested on one isolate per each positive flock on MIC panels (FINRES-Vet)
 - On average, 6.5% of slaughtered broiler batches positive for *Campylobacter* sp. in June–Oct (92.1% *C. jejuni*)
 - Highest prevalence in July–Aug (10.5%)





Proportion of antibiotic-resistant *C. jejuni* isolates from broilers at slaughter

- Antibiotic resistance has long been below the EU average
 - Production flocks have not been treated since 2010 (ETT.fi)
- Before 2013, less than 4% of the isolates were resistant to quinolones or tetracycline (TET)
- After 2013, quinolone (CIP) and TET resistance peaked in certain years



The number of isolates tested each year are in brackets.

Source: FINRES-Vet, 2024.



Breeder hens (parental flocks)

- Annually, 3–20% of the parental flocks had been treated with antibiotics, highest proportion in 2014 (ETT.fi)
 - Penicillin, but also amoxicillin and oxytetracycline
 - Quinolones had not been used
- Also in 2013, the import practises and origin countries of grandparental flocks changed
- Voluntary own-check sampling of every slaughtered batch until 2023
 - Almost all flocks positive for *Campylobacter*
 - No (phenotypic) antibiotic resistance testing



**FINNISH FOOD
AUTHORITY**
Ruokavirasto • Livsmedelsverket

The study



Aims

- Genotypes, resistance profiles and population genetics of *C. jejuni* from Finnish broilers and breeder hens
- Whether the antibiotic-resistant *C. jejuni* could have transmitted vertically from parental to production flocks or not



Materials

- *C. jejuni* isolates (n=333) from broiler production flocks (n=188) and parental flocks (n=145) in 2014–2019
 - One temporally representative isolate per flock
 - Represented annually 34–74% of *Campylobacter* positive production flocks
 - Represented all positive parental flocks
- Metadata linking production and parental flocks



Methods

- Whole-genome sequencing (Illumina)
- Genome assembly and quality control, MLST
 - INNUca v4.2.2
- *Ad hoc* whole genome MLST
 - chewBBACA v2.8.5
- Genotypic antibiotic resistance determination
 - StarAMR v0.9.1 with ResFinder (2022-05-24) and PointFinder (2021-02-01) databases



Antimicrobial susceptibility results

- Higher resistance rates to quinolones among broiler than breeder isolates
- Tetracycline resistance evenly in both generations
- No genotypic resistance to other tested antibiotics

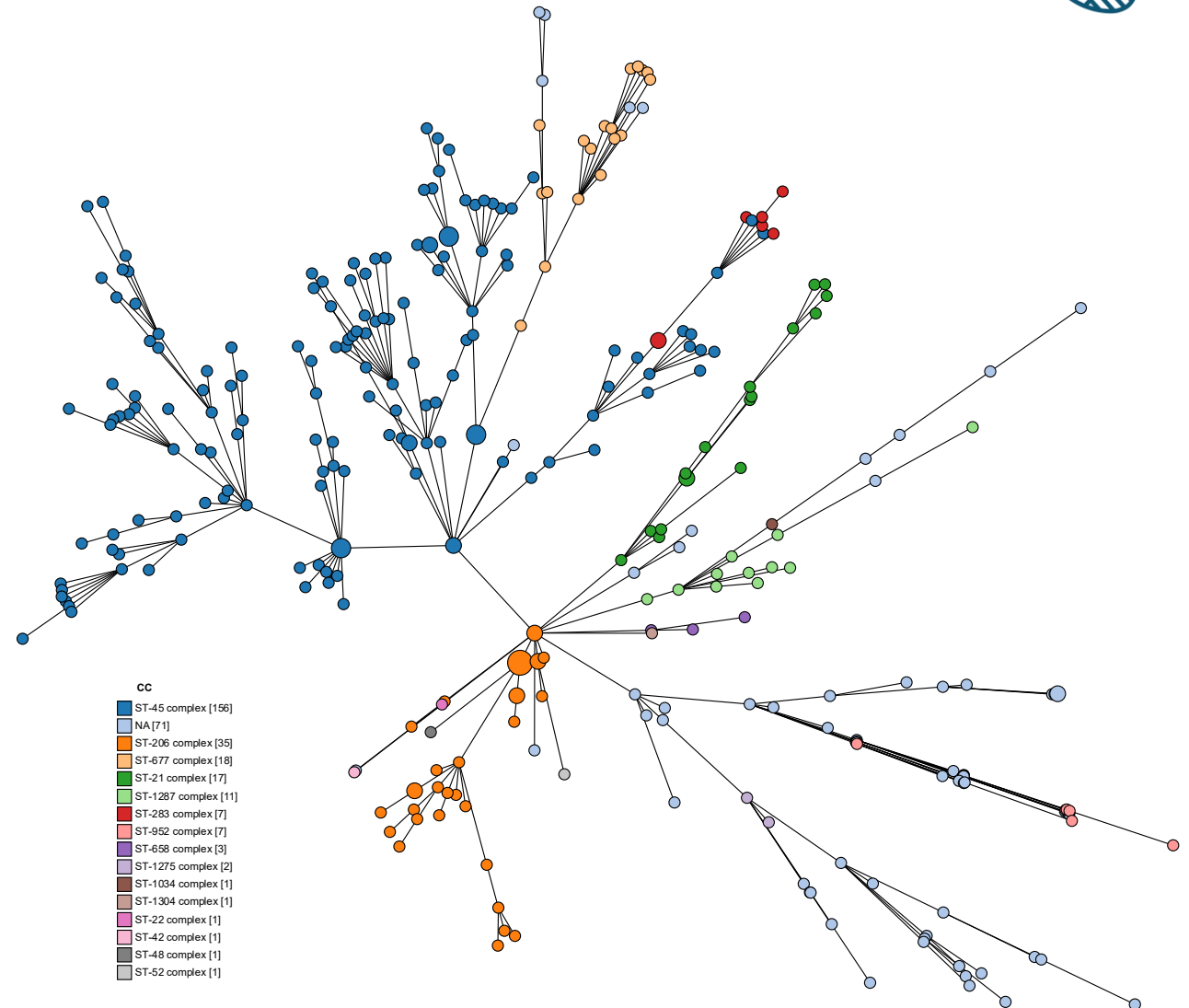
	Broiler isolates, phenotypic resistance	Broiler isolates, genotypic resistance ¹	Breeder isolates, genotypic resistance
Ciprofloxacin (Quinolones)	44/185 (23.8%)		
Nalidixic Acid (Quinolones)	52/185 (28.1%)		
Tetracycline	15/185 (8.1%)		
<i>gyrA</i> T86I or T86A (Quinolones)		48/188 (25.5%)	5/145 (3.4%)
<i>tet(O)</i> or <i>tet(O/32/O)</i> (Tetracycline)		16/188 (8.5%)	10/145 (6.9%)

¹97.7%–100.0% concordance with the phenotypic results



Population structure

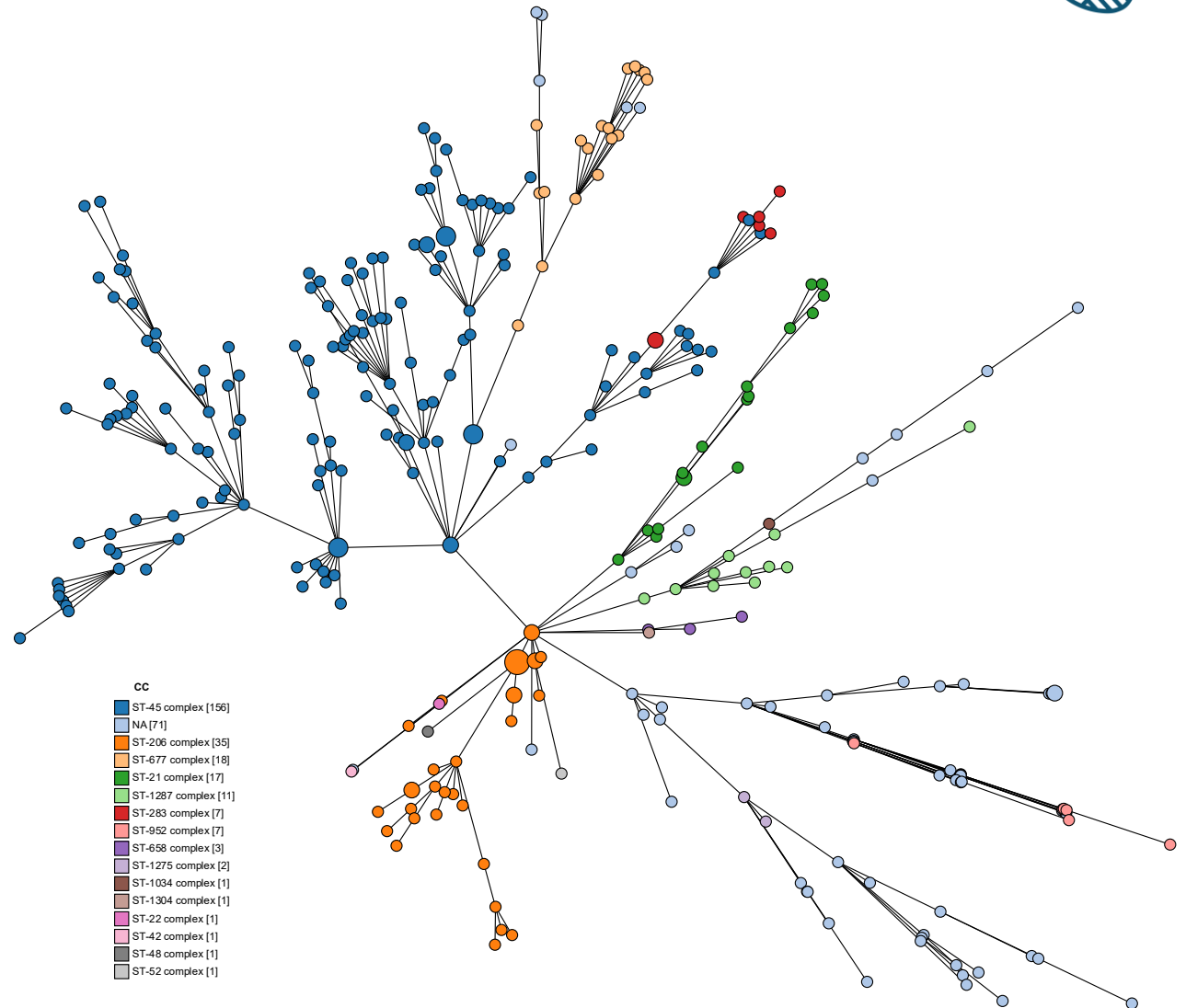
- 95 sequence types (STs) and 15 clonal complexes (CCs)
- 61 STs (64.2%) represented by single isolates
- Same STs between broiler (57.5%) and breeder (61.5%) isolates





Population structure

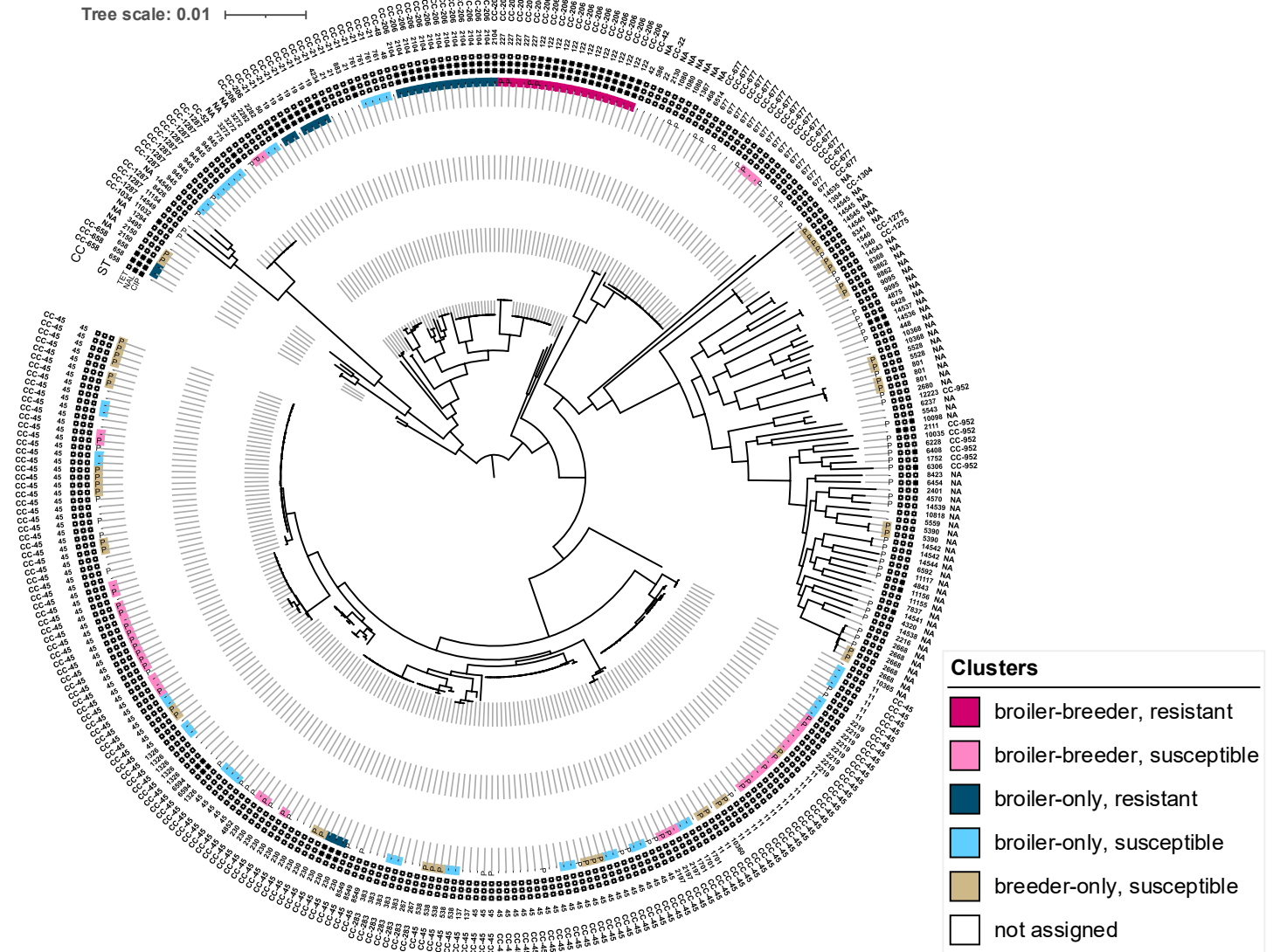
- CC-45 was the most prevalent CC
 - 51.0% of breeder isolates and 43.6% of broiler isolates
 - Only CC isolated every year in both generations
 - Mainly susceptible genotype
- ST-45 also the most prevalent ST in human infections in Finland for several years





Population structure

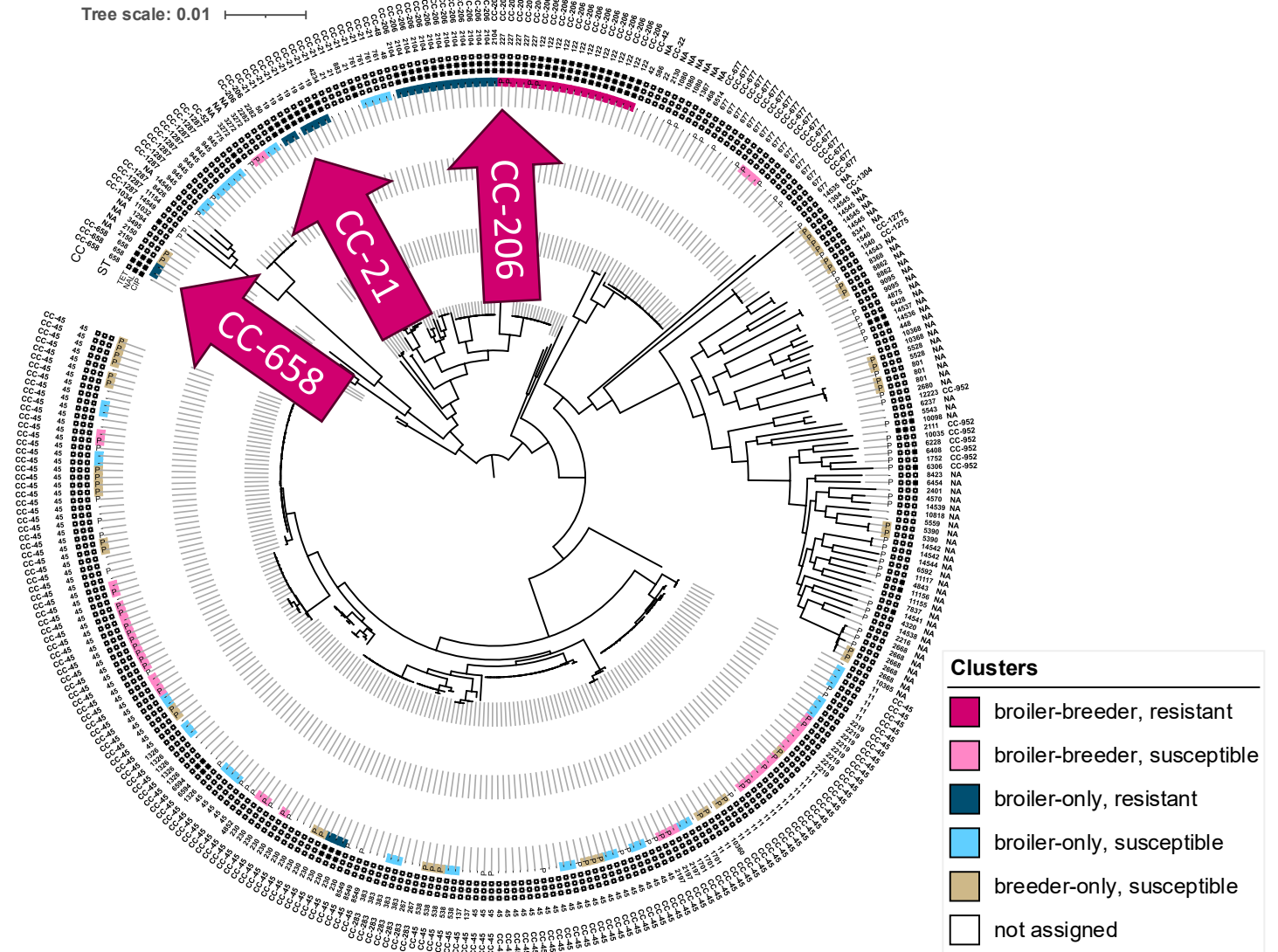
- Antibiotic resistance was associated with certain sequence types
 - Quinolone resistance: CC-206, CC-21, CC-658
 - Tetracycline resistance: CC-206, CC-658





Population structure

- Antibiotic resistance was associated with certain sequence types
 - Quinolone resistance: CC-206, CC-21, CC-658
 - Tetracycline resistance: CC-206, CC-658





Clusters (*ad hoc* wgMLST)

- With max. 11 allelic differences, 54 clusters (2–14 isolates in each cluster)
 - 31.5% single-farm replicates sampled within a two-month period
 - Often same *C. jejuni* clone in different rearing halls of the same farm
- 13 clusters comprised both broiler and breeder isolates
 - 2 resistant clusters (CC-206): CIP-NAL-TET (14 isolates) and CIP-NAL (5 isolates)
 - 80.0% of quinolone-resistant breeder isolates were associated with these resistant clusters, whereas 90.0% of TET-resistant breeder isolates were sporadic findings
 - 83.3% of quinolone-resistant broiler isolates and 93.8% of TET-resistant broiler isolates belonged to these clusters or broiler-only clusters



Resistant clusters

Clusters with max. 11 allelic differences in *ad hoc* wgMLST analysis of 333 *C. jejuni* isolates (95 % of isolates harbored 1292/3728 genes) that comprise antibiotic-resistant isolates

No.	Allele difference	ST	CC	Year ¹	Source ¹	Resistance profile ¹	No. farms	Distance of farms ²
1	zero to 2	2104	CC-206	2018 (13), 2019 (1)	broiler (14)	CIP-NAL (14)	6	Within 50 km
2	zero to 8	122	CC-206	2014 (10), 2015 (1), 2016 (3)	broiler (13), breeder (1)	CIP-NAL-TET (14)	13	Within 60 km. Same region ³ and partly same farms as in cluster 1
3	1 to 5	227	CC-206	2014 (5)	broiler (2), breeder (3)	CIP-NAL (5)	2	40 km
4	6 to 11	19	CC-21	2019 (4)	broiler (4)	CIP-NAL (4)	2	12 km
5	1 to 6	230	CC-45	2016 (3)	broiler (3)	CIP-NAL (3)	2	200 km. One farm in the region of clusters 1 and 2
6	2	19	CC-21	2019 (2)	broiler (2)	CIP-NAL (2)	1	Same farm as in cluster 2
7	4	658	CC-658	2016 (2)	broiler (2)	CIP-NAL-TET (2)	1	Same farm as in cluster 1

¹Number of isolates in parenthesis.

²All farms located within 310 km.

³Region of Finland where animal production is concentrated: broilers, cattle, fur animals.



Vertical transmission

- No epidemiological linkage was observed between antibiotic-resistant broiler and breeder isolates
- Some uncertainty remains
 - Most broiler flocks had animals originating from several parental flocks
 - Metadata was missing for many of the broiler flocks
 - Only one temporally representative isolate per flock was sequenced → representative of the whole diversity?



Conclusions

- Genotypically diverse *C. jejuni* populations with overlaps between broiler and breeder isolates
- Unlikely vertical transmission of antibiotic-resistant *C. jejuni* → rather horizontal transmission from a common (unknown) environmental source

ACKNOWLEDGMENTS



ICT Solutions for Brilliant Minds



WALTER EHRSTRÖMIN SÄÄTIÖ



**Suomen
eläinlääketieteen
säätiö**



QUESTIONS?

anniina.jaakkonen@ruokavirasto.fi

satu.olkkola@ruokavirasto.fi

FINNISH FOOD AUTHORITY

Ruokavirasto • Livsmedelsverket

