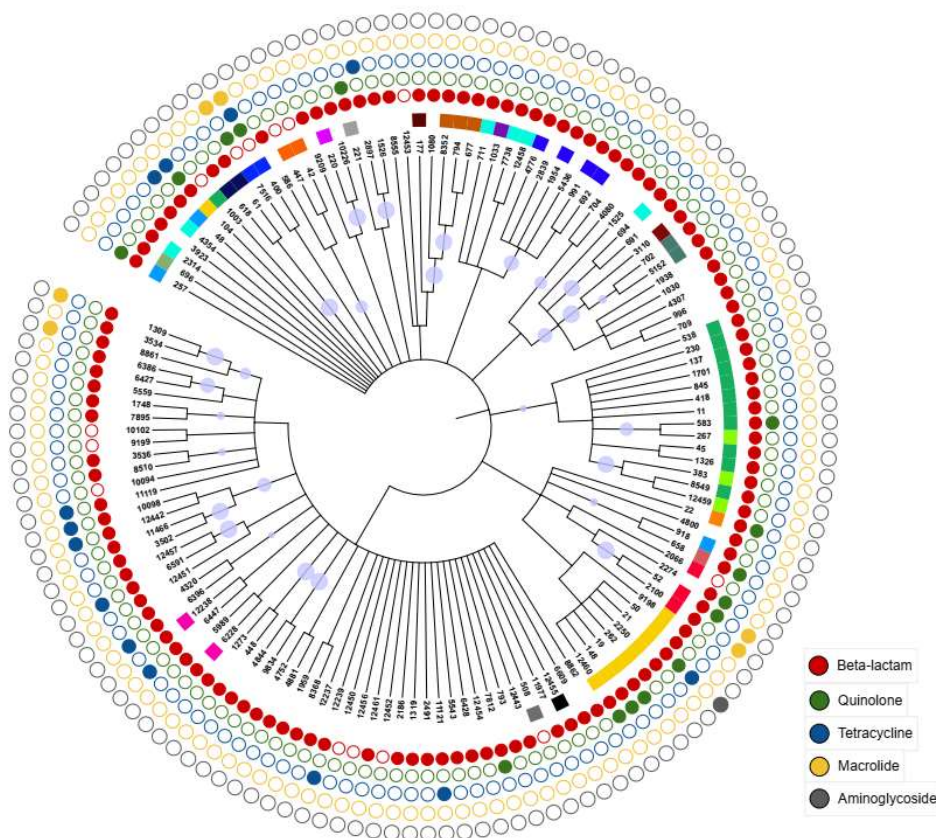# Genomic characterization of antibiotic resistance in *Campylobacter jejuni* isolates from broilers at slaughter in Sweden, 2017-2021

*Campylobacter* is the most common bacterial cause of human gastroenteritis in the world, and chicken is the most important source of *Campylobacter* for human infections. A total of **767 C. jejuni isolates collected from broilers in 2017-2021** were subjected to **whole-genome sequencing** and analyzed for the presence of genes encoding for antibiotic resistance using **AMRFinderplus**.



**Fig. 1** Neighbor-joining tree of 137 STs; bootstrap values >80% are shown as light blue colors on the branches, clonal complexes assigned by PubMLST database shown in different colors in squares, antibiotic classes represented by the presence of genes shown in circles

**Table. 1** List of genes identified for each antibiotic class in the study

| Class | Gene | Count |
|---|---|---|
| Beta-lactam | blaOXA-193 | 376 |
| | blaOXA-184 | 87 |
| | blaOXA-461 | 75 |
| | blaOXA-61 | 31 |
| | blaOXA-447 | 30 |
| | blaOXA-638 | 20 |
| | blaOXA-466 | 18 |
| | blaOXA-603 | 14 |
| | blaOXA-448 | 12 |
| | blaOXA-637 | 12 |
| | blaOXA-785 | 11 |
| | blaOXA-591 | 9 |
| | blaOXA-625 | 5 |
| | blaOXA-623 | 4 |
| | blaOXA-449 | 3 |
| | blaOXA-578 | 3 |
| | blaOXA-615 | 3 |
| | blaOXA-631 | 3 |
| | blaOXA-614 | 2 |
| | blaOXA-636 | 2 |
| | blaOXA-639 | 2 |
| | blaOXA-446 | 1 |
| | blaOXA-452 | 1 |
| | blaOXA-465 | 1 |
| | blaOXA-493 | 1 |
| | blaOXA-617 | 1 |
| | blaOXA-619 | 1 |
| | blaOXA-658 | 1 |
| Quinolone | gyrA_T86I | 156 |
| Tetracycline | Tet(O) | 55 |
| Macrolide | 50S_L22_A103V | 30 |
| Aminoglycoside | aph(3')-IIIa | 1 |
| | rpsL_K88R | 2 |

A total of **743 (96.9%) strains had at least one gene encoding for resistance against antibiotics**. Genes for **beta-lactam resistance were the most prevalent** (**95.3%**), followed by **quinolone (20.5%), tetracycline (7.2%), macrolide (3.9%)** and **aminoglycoside (0.4%)**. For beta-lactams, *blaOXA-193* **was most prevalent**, while it was only *tet(O)*, point mutations in *gyrA* (T86I) and **50S L22 (A103V)** for **tetracycline, quinolone** and **macrolide** resistance, respectively (Table.1). **Forty-one isolates (5.3%) had genes encoding resistance for more than 2 antibiotic classes**, among which the majority had genes for beta-lactam, quinolone and tetracycline resistance. The distribution of genes coding for each antibiotic class (presence or absence) over the sequence types (STs) observed in the study is shown (Fig 1). Further analysis will be done to investigate the distribution of genes within and between farms in relation to the phylogeny and carriage of plasmids as well as the correlation with phenotypic result on the subset of samples.

**Video presentation of the poster!**
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