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# ST5136 is a multi-drug resistant and the largest vertically expanding UK wide clone of *Campylobacter jejuni*

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**Introduction:** *Campylobacter jejuni* and *Campylobacter coli* are the most common causes of bacterial gastroenteritis in the developed world. The aim of this study was to understand how antibiotics in the farm environment select for antibiotic resistant clones of *Campylobacter*. The diversity of tetracycline resistant determinants and quinolone resistances conferred by *gyrA* mutations in *Campylobacter* isolated from different host reservoirs was assessed.

**Materials & Methods:** DNA from pure cultures of *Campylobacter* spp. from chicken, cattle, sheep and humans in Grampian region of Scotland was extracted and whole genome sequencing was done using an Illumina HiSeq 2000 sequencer with 100 base paired-end sequencing and the FASTQ paired-end reads were assembled using Velvet. The genomes (4000) were assessed for purity and submitted to the Bacterial Isolate Genome Sequence Database (BIGSdb), where alleles were tagged and the presence of the tetracycline resistance determinant CAMP1698 and the C257T *gyrA* mutation were identified.

**Results:** Whole genome multilocus sequence typing (MLST) analysis using 136 representative strains isolated from UK identified that ST5136 is a UK wide clone, having emerged from ST464 through substantial genetic recombination. ST5136 was exclusively associated with chicken, turkey and humans and was the most prevalent strain harbouring the *tet(O/32/O)* 7-like determinant. The most common tetracycline resistant alleles were *tet(O/32/O)*7 and *tet(O/32/O)*8, 13. The *tet(O/32/O)*-7 variant was chromosomally associated in ST5136. 99% (207/209) of CC464 strains were ciprofloxacin resistant and had the C257T *gyrA* mutation.

**Conclusion:** The *tet(O)* [ $\Phi$ -m46.1] and *tet(O)*-like variants in *Campylobacter* were closely related. The *tet(O/32/O)* from human gut bacteria and *Campylobacter* were also similar in sequence, suggesting the potential for *Campylobacter* and other species to rapidly evolve through common DNA transfer systems. The increase in resistance to ciprofloxacin and tetracycline in clonally expanding populations of *Campylobacter* and the usage of these antibiotics in agriculture will be discussed.

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