

## Whole-Genome Sequencing for Genetic Characterization of Antimicrobial Resistance in *Campylobacter jejuni* Isolated from Turkeys in Germany

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### **Abstract:**

*Campylobacter jejuni* is a zoonotic bacterium recognized as the leading cause of bacterial gastroenteritis in humans and several animal species worldwide. The emergence of a high antimicrobial resistance and multidrug resistance were identified in *C. jejuni* isolated from commercial turkey farms in Germany. The Illumina MiSeq<sup>®</sup> technology was used to sequence 66 *Campylobacter jejuni* isolates obtained from commercial meat turkey flocks located in ten German federal states. Phenotypic antimicrobial resistance was determined. Phylogeny, resistome, plasmidome and virulome profiles were analysed using whole-genome sequencing data. Genetic resistance markers were identified with bioinformatics tools (AMRFinder, ResFinder, NCBI and ABRicate) and compared with the phenotypic antimicrobial resistance. The isolates were assigned to 28 different sequence types and 11 clonal complexes. The average pairwise single nucleotide-polymorphisms distance of 14.585 SNPs revealed a high genetic distinction between the isolates. The *wlaN* gene associated with the Guillain–Barré syndrome was detected in nine (13.6%) isolates. The genes for resistance to ampicillin (*bla*<sub>OXA</sub>), tetracycline (*tet*(O)), neomycin (*aph*(3')-IIIa), streptomycin (*aadE*) and streptothricin (*sat4*) were detected in isolated *C. jejuni* using WGS. A gene cluster comprising the genes *sat4*, *aph*(3')-IIIa and *aadE* was present in six isolates. The single point mutation T86I in the housekeeping gene *gyrA* conferring resistance to quinolones was retrieved in 93.6% of phenotypically fluoroquinolone-resistant isolates. Five phenotypically erythromycin-susceptible isolates carried the mutation A103V in the gene for the ribosomal protein L22 inferring macrolide resistance. An assortment of 13  $\beta$ -lactam resistance genes (*bla*<sub>OXA</sub> variants) was detected in 58 *C. jejuni* isolates. Out of 66 sequenced isolates, 28 (42.4%) carried plasmids. Six isolates harboured a pTet-like plasmid which carries the *tet*(O) gene. This study highlighted the potential of whole-genome sequencing to enhance and speculate antimicrobial resistance with a high degree of accuracy. However, resistance gene databases need curation and updates to countermand inaccuracy when using WGS-based analysis pipelines for AMR detection.