Comparison of pulsed-field gel electrophoresis (PFGE) and whole-genome sequencing (WGS) for typing of *Campylobacter jejuni*

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INTRODUCTION

Bacteria from the genus *Campylobacter* are the most common cause of gastrointestinal infections in humans in EU. The main causative agent of intestinal campylobacteriosis is *Campylobacter jejuni*, which is naturally present in the intestines of birds, especially from the industrial poultry. For the investigation of *Campylobacter* outbreaks and source attribution, a high-resolution and reliable genotyping method is needed to enable a prompt response of the public health authorities.

Pulsed-field gel electrophoresis (PFGE) has been widely used in the outbreak investigations and has been considered the gold standard for source tracking due to the reported stability of PFGE genotypes. However, whole-genome sequencing (WGS) is becoming the typing method of choice due to its high discriminatory power.

METHODS

- **56 *C. jejuni*** isolates obtained in 2012 (*n*=24) and 2017 (*n*=32) typed by PFGE and WGS to assess their comparability regarding strain discrimination
- **PFGE**: standardised PulseNet protocol (*Sma*I) → BioNumerics v7.6, clusters defined at >90 % similarity
- **WGS**: Illumina paired-end sequencing (2×150 bp) on a NextSeq 500 platform → quality trimming of reads with Cutadapt v1.18 and assembly into contigs with SPAdes v3.13.0 →
  - core-genome multilocus sequence (cgMLST) typing, based on PubMLST scheme comprising 1343 genes, performed with cgMLSTFinder v1.0 (https://cge.cbs.dtu.dk/services/cgMLSTFinder-1.0/)
  - 7-gene MLST typing, enabling classification of *C. jejuni* isolates into sequence types (STs), performed according to PubMLST *Campylobacter* scheme (https://pubmlst.org/campylobacter/)

RESULTS

PFGE: seven *C. jejuni* clusters determined (incidated by specific colours in Fig. 1), but not always congruent with MLST ST → lack of phylogenetic information presented by PFGE

WGS: five major *C. jejuni* clusters, corresponding to individual STs, and one ST3030 isolate

- four clusters (STs 354, 2863, 3157 and 5205) showed <14 allelic differences (AD) → high genetic similarity of isolates belonging to a designated cluster, indicating their epidemiological association, further supported by metadata
- ST905 cluster additionally divided into two subclusters with >34 AD → presence of at least two *C. jejuni* strains; their epidemiological unrelatedness further confirmed by metadata

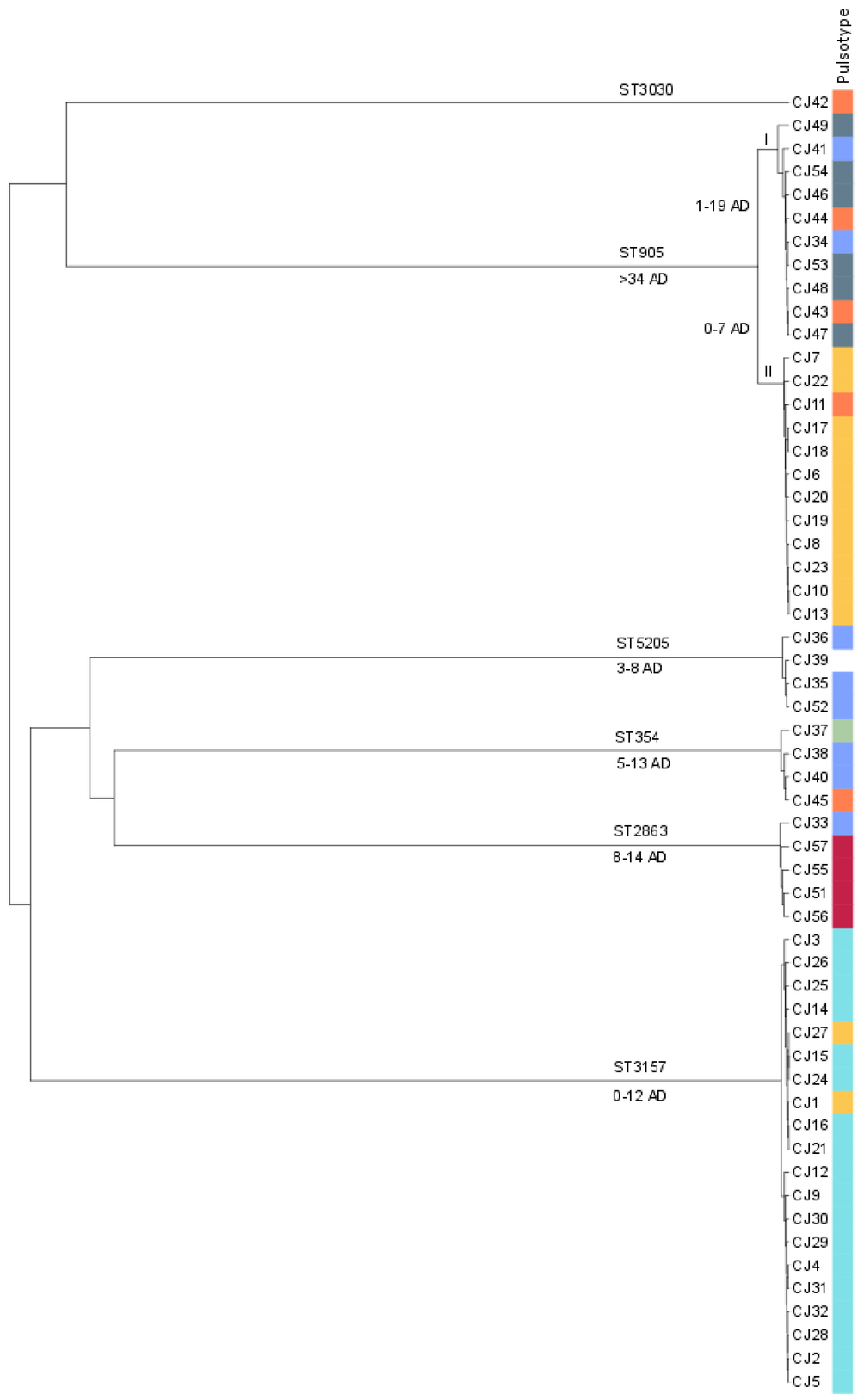

Fig. 1: Dendrogram based on cgMLST analysis.
Sequence types (STs) and allelic differences (AD) are given on the branches. Pulsotypes are indicated by a specific colour.

CONCLUSIONS

Despite the slightly higher number of clusters obtained with PFGE in comparison with WGS, suggesting their comparable discriminatory power, results clearly show that clonal relationship may exist even between strains with different PFGE profiles or that PFGE may lead toward false clustering of phylogenetically very distant isolates. This may result from the weakly clonal nature of *C. jejuni*. Therefore, cgMLST typing should be a method of choice for the epidemiological surveillance of *C. jejuni*, not only in the outbreak investigation but also in the analysis of its population structure.