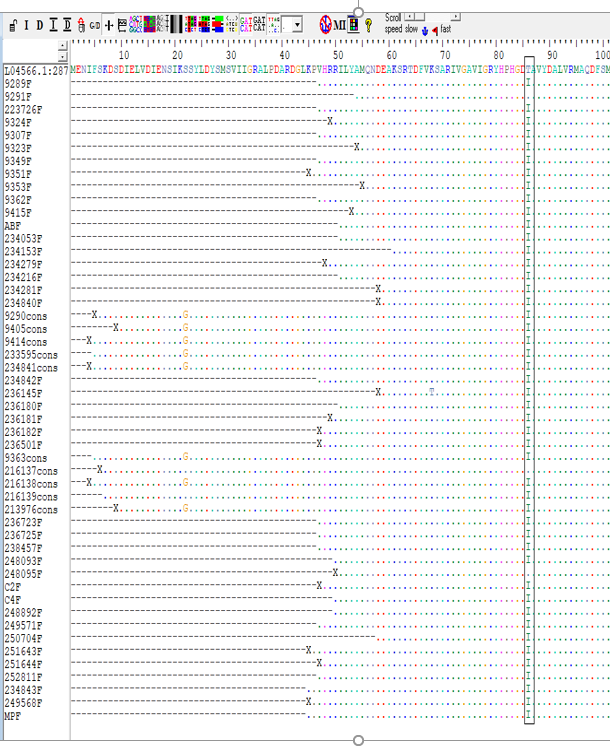
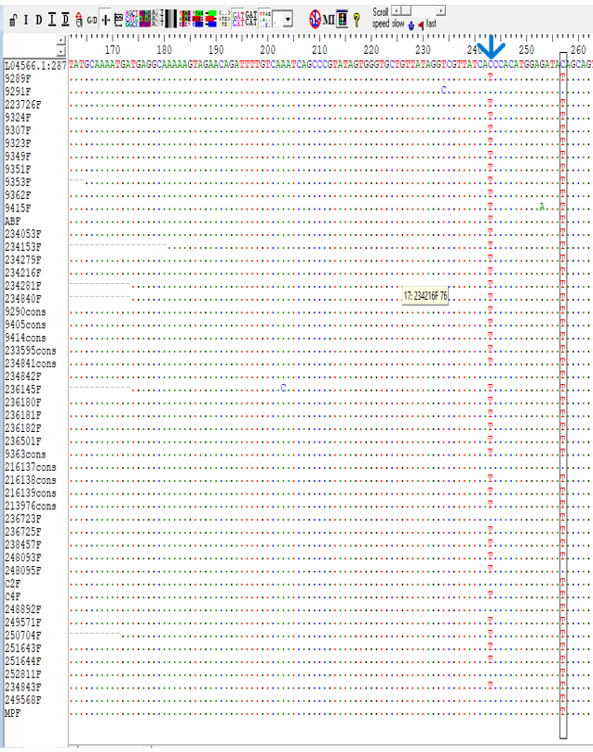
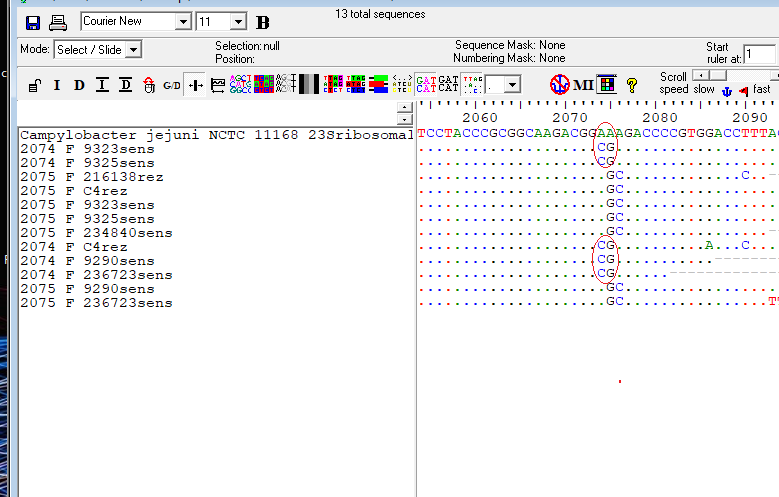
**Fig.1** Alignment of the amino acid sequences of the QRDR region for the *gyr*A gene of *C.jejuni* isolates. The position of the Thr-86-Ile mutation was compared and analyzed with the sequence in the database accession number L04566 for *C.jejuni*.

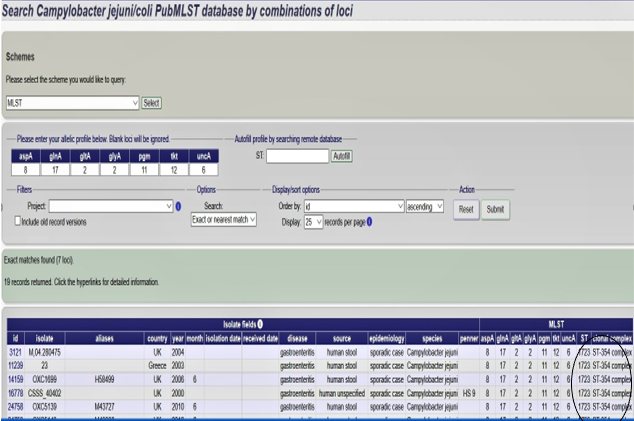


**Fig.2** Alignment of the nucleotide sequences of the QRDR region for the *gyr*A gene. The presence of mutation in position 257 of the ACA to ATA codon and silent mutations in position 243, associated with fluroquinolone resistance of *C.jejuni* isolates.





**Fig.3** The presence of mutations in position 2074 and 2075 in *C.jejuni* strains with increased resistance to erythromycin:-the presence of the double mutation both in position 2074 (A-C) and in position 2075 (A-G); - presence of mutation in position 2075 (A-G).



**Fig. 4**. ST type and clonal complex identified from the MLST database.

**Table S1**. *Campylobacter jejuni* strains analyzed by the MLST (*multilocus sequence typing*).

