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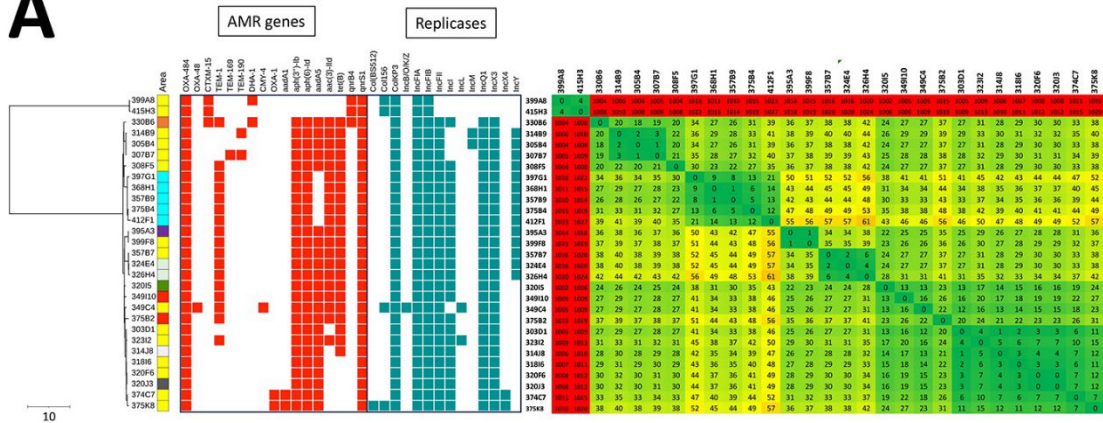
Oxacillinase-484-Producing Enterobacterales, France, 2018–2023

Appendix 2

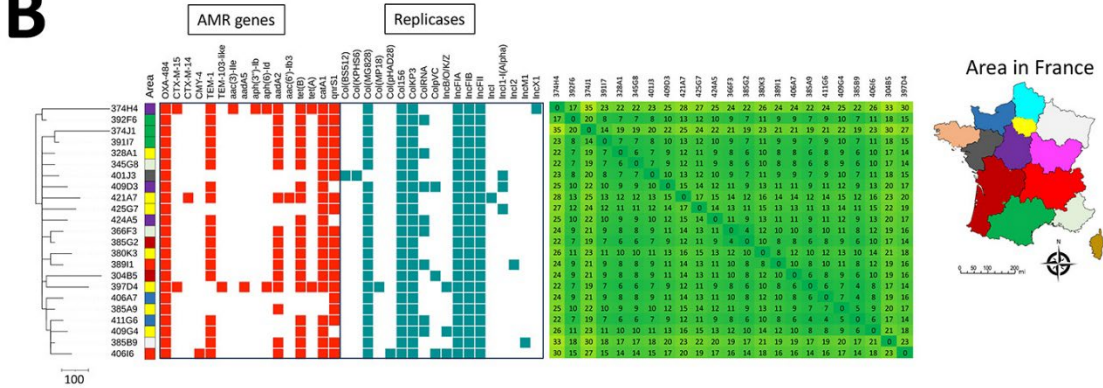
Additional Methods

We conducted short-read next-generation sequencing on the entire set of 64 OXA-484-producing strains by using HiSeq technology (Illumina, <https://www.illumina.com>; BioProject accession no. PRJNA1119420). We assembled reads by using Shovill version 1.1.0 (<https://github.com/tseemann/shovill>) and SPAdes version 3.14.0 (<https://github.com/ablab/spades>). We carried out multilocus sequence typing and resistome analyses by using the pubMLST (<https://pubmlst.org>) and Resfinder 4.5.0 (<http://genepi.food.dtu.dk/resfinder>) databases.

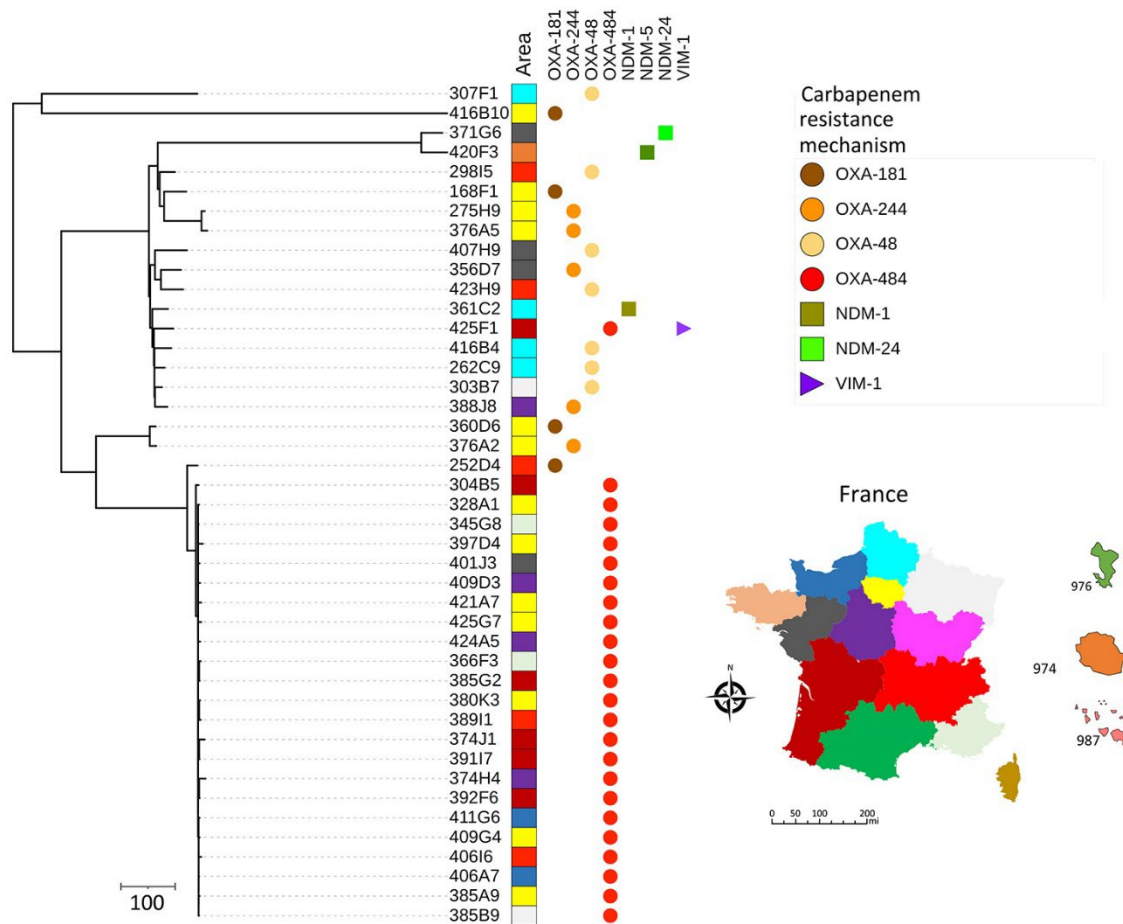
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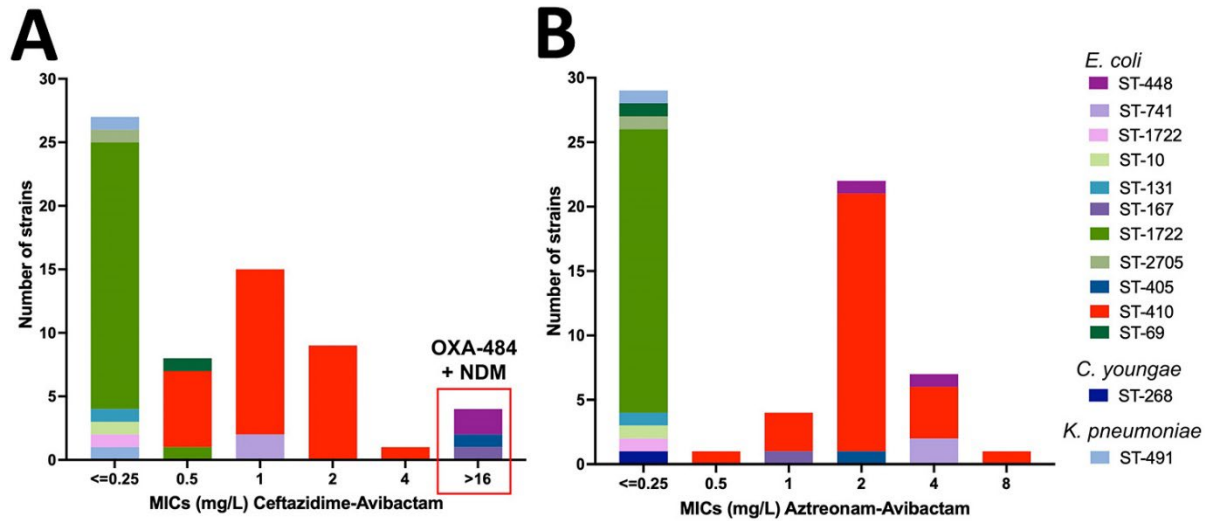
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Appendix 2 Figure 1. Phylogenetic tree with SNPs matrix (single-nucleotide polymorphism) and global characterization (multilocus sequence typing, plasmid, and β -lactamase content) for OXA-484–producing *Escherichia coli* belonging to ST410 (A) and ST1722 (B).



Appendix 2 Figure 2. Phylogenetic tree of ST1722 isolates received at the FNR-C in France from 2012 to 2023. Carbapenemase types are detailed in this figure and OXA-484 producers are indicated with red circles. ST410 strains are indicated by whether there are amino acid insertions (YRIK, YRIN, YRIP, or YTIP motifs) in penicillin-binding-protein 3. We conducted the single-nucleotide polymorphism analysis on a common genome representing 90.15% by using the reference strain 304B5.



Appendix 2 Figure 3. Distribution of minimal inhibitory concentrations (MICs) for ceftazidime-avibactam and aztreonam-avibactam of OXA-484–producing isolates according to their sequence type. NDM, New Delhi metallo- β -lactamase.