Complete Sequence of a \textit{bla}_{OXA-48}\textsuperscript{-}Harboring \textit{IncL} Plasmid from an \textit{Enterobacter cloacae} Clinical Isolate

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We report a 63,584-bp conjugative \textit{IncL} plasmid (pUR17313-1) from an \textit{Enterobacter cloacae} clinical isolate, containing a \textit{bla}_{OXA-48} gene. The plasmid sequence also carried important mobile genetic elements involved in the spread of antibiotic resistance, namely, the Tn1999.2 composite transposon, which enclosed \textit{bla}_{OXA-48}\textsuperscript{-}, integrase-, and transposase-encoding genes.

Bacterial plasmids are key vectors of horizontal gene transfer, mediating the mobilization of genetic material among bacteria\textsuperscript{(1)}. This study aimed to characterize an \textit{IncL}/\textit{M}-like plasmid containing a \textit{bla}_{OXA-48} gene from an \textit{Enterobacter cloacae} clinical isolate, which constituted the first case of \textit{OXA-48}-producing \textit{Enterobacteriaceae} in Portugal\textsuperscript{(2)}.

Plasmid DNA was extracted from the transconjugant Tc17313-1\textsuperscript{(2)}, using a NucleoBond Xtra Plus kit (Macherey-Nagel) according to the manufacturer’s instructions. Plasmid-Safe ATP-Dependent DNase (Epicentre) was used to eliminate any contamination with chromosomal DNA. The molecular size of the \textit{OXA-48}-carrying plasmid was estimated by using a GeneRuler High Range DNA Ladder (Thermo Scientific). Five hundred nanograms of the plasmid was estimated by using a GeneRuler High Range DNA Ladder (Thermo Scientific).

The plasmid was constructed based on the genetic organization of those plasmids, and the contig neighbors predicted from contig assembly information.

Overall, plasmid pUR17313-1 was 63,584 bp in length with a G + C content of 51.2%. The presence of a Tra region revealed that the plasmid was conjugative. The \textit{bla}_{OXA-48} gene was enclosed on a Tn1999.2 composite transposon. Although this plasmid was not typeable by PCR-based replicon typing\textsuperscript{(2, 4)}, the \textit{incRNA} sequence revealed that pUR17313-1 was an \textit{IncL}\textsuperscript{(7)}. In addition, PHAST analysis predicted one putative incomplete prophage region, from position 3,856 to 17,385 (13,530 bp), consisting of 28 putative coding sequences, including procapsid-like particles and integrase- and transposase-encoding genes, with a 4.32\% G + C content\textsuperscript{(8)}.

We confirmed that the \textit{bla}_{OXA-48} gene was carried by the widespread 63-kb conjugative \textit{IncL} plasmid, which did not encode additional resistance markers but contained other important mobile genetic elements involved in the spread of antibiotic resistance. Given the clinical and epidemiological relevance of these plasmids, its complete sequence is important to understand plasmid evolution and differentiation. In the end, the availability of complete plasmid sequences from different countries supports the global epidemiological surveillance of antibiotic resistance spread.

Nucleotide sequence accession number. The genome sequence of pUR17313-1 has been submitted to GenBank under the accession number KP061858.

ACKNOWLEDGMENTS

V.M. was supported by grant number SFRH/BPD/77486/2011 from Fundação para a Ciência e a Tecnologia, Lisboa, Portugal.

This study was supported financially by the 2015DDI1228 project from National Institute of Health, Portugal.
REFERENCES


