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Population structure of OXA-48-producing *Klebsiella pneumoniae* ST405 isolates during a hospital outbreak characterised by genomic typing



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ABSTRACT

Objectives: The aim of this study was to investigate the structure of a broad and sustained hospital outbreak of OXA-48-producing *Klebsiella pneumoniae* (KpO48) belonging to sequence type 405 (ST405). *Methods:* Whole-genome sequencing and comparison of ten ST405 KpO48 isolates obtained from clinical samples in our hospital was performed. Using stringent criteria, 36 single nucleotide polymorphisms (SNPs) were detected (range 0–21 in pairwise comparisons), and allele-specific PCR was used to call the SNPs among a larger set of isolates.

Results: Several haplotypes were identified within the population. The haplotypes did not show a spatial structure, but a temporal evolution of sequential haplotype replacements was observed.

Conclusions: The dispersed spatial distribution suggests a reservoir formed by a large pool of colonised patients, and the temporal replacement pattern suggests that the sustained outbreak was composed of several small outbreaks that appeared and rapidly dispersed to several units.

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1. Introduction

OXA-48 and related enzymes are class D β -lactamases that hydrolyse most β -lactam antibiotics, including carbapenems. They are produced by different enterobacterial species and generally appear combined with other antimicrobial resistance mechanisms [1,2]. In most cases the bla_{OXA-48} gene is found in a composite transposon (Tn1999) in a single 62-kb IncL conjugative plasmid that transfers very efficiently within and between species [3,4]. This plasmid has spread during the last years throughout Europe [5–8], most often associated with OXA-48-producing *Klebsiella pneumoniae* (KpO48). In our hospital (Hospital Universitario La Paz, Madrid, Spain), KpO48 were first detected in 2010 [9], simultaneously with its emergence in several other hospitals in Spain [10]. During the first 2 years of the outbreak, most OXA-48-producing isolates were *K. pneumoniae* belonging to multilocus sequence typing (MLST) sequence type 405 (ST405), with a few sporadic *K. pneumoniae* isolates belonging to other MLST types and a few other enterobacterial species. Later on ST11 became the major group [11]. This epidemic has been characterised in our hospital by a sustained and complex pattern of OXA-48-producing isolates

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