

TITLE: *Klebsiella pneumoniae* ST 3997 HARBOURING bla_{NDM-1} AND $bla_{CTX-M-15}$ ISOLATED FROM HOUSEFLY COLLECTED IN PUBLIC HOSPITAL GARBAGE IN RIO DE JANEIRO, BRAZIL.

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Antimicrobial resistance is a matter of great concern to world health authorities. *Klebsiella pneumoniae* is considered a "trafficker" of resistance genes, acquiring them from environmental and disseminating to pathogenic strains of clinical importance. Muscoid dipterans are highly synanthropic, feeding on and reproducing in decomposing organic matter and open garbage. As such it acts as mechanical vectors of pathogens, including resistant bacteria. From the perspective of One Health concept, in the present study flies were trapped at garbage containers located at a public hospital in Rio de Janeiro, Brazil. The strain *Klebsiella pneumoniae* (LEMEF 23) assigned to ST3997 was recovered from a *Musca domestica* specimen. Bacterial identification was determined by MALDI-TOF/MS. The strain was phenotypically resistant to meropenem, cefepime, ceftazidime, ceftiofur, gentamicin and trimethoprim/sulfamethoxazole at the disk diffusion susceptibility method. Carbapenem Inactivation Method (CIM test) was positive, clearly presenting carbapenemase activity. The BD Phoenix Automated Microbiology System (BD Diagnostics) revealed the follow profiles: meropenem MIC > 32 µg/mL; imipenem MIC > 8 µg/mL; ertapenem MIC > 1 µg/mL; cefepime MIC > 16 µg/mL; ceftiofur MIC > 16 µg/mL; ceftazidime MIC > 16 µg/mL; ceftriaxone MIC > 4 µg/mL and susceptibility to colistin (MIC < 1 µg/mL). The Polymerase Chain Reaction (PCR) screening revealed the presence of bla_{NDM-1} , $bla_{CTX-M-15}$, bla_{TEM-1} and $aac(6')-Ib$ resistance genes. The bla_{NDM-1} gene was flanked by an entire insertion sequence element ISAb125 and the bleomycin resistance gene ble_{MBL} . Southern hybridization with bla_{NDM-1} probe over plasmid membrane and *in vitro* conjugation assays with *Escherichia coli* J53 were unsuccessful, suggesting a non-conjugative plasmid or chromosomal bla_{NDM-1} localization. Whole genome sequence resulted in estimated genome size of 5.663.872 bp with 57,1% of GC content. Resistome analysis revealed the presence of the same resistance genes and also to the following antimicrobials: aminoglycoside [$aac(3)-IIa$, $aph(6)-Id$ and $aph(3'')-Ib$], beta-lactam ($bla_{OKP-B-3}$ and bla_{OXA-1}), fluoroquinolone ($qnrB1$), sulphonamide ($su12$) and trimethoprim ($dfrA14$) with more than 99% of identity. Plasmid Finder identified three plasmids belonging to the IncY, IncFII and IncR. These results present the importance of houseflies in the dissemination of antimicrobial resistance genes outside the hospitals.

Keywords: One Health, antimicrobial resistance, plasmids, molecular epidemiology

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