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CORRELATION BETWEEN THE DETECTION OF BLEMBL AND BLANDM IN KLEBSIELLA PNEUMONIAE AND PSEUDOMONAS AERUGINOSA ISOLATES

Background/Aim. The blaNDM gene is a clinically significant carbapenem resistance determinants, conferring resistance to most β -lactam antibiotics. In many Gram-negative bacteria, it is genetically linked to the bleMBL within the conserved transposon Tn125, where any deviation from the canonical gene order constitutes direct evidence of recombination or transposition. This study aimed to evaluate the correlation between the detection of the bleMBL and blaNDM in *K. pneumoniae* and *P. aeruginosa* isolates using targeted and whole-genome sequencing. **Methods.** Isolates were collected during the treatment of 24 patients. Genomic DNA was analyzed by targeted sequencing and WGS on the Ion S5 platform. The data were analyzed using Torrent Suite and Solu Software. The number of *K. pneumoniae* and *P. aeruginosa* isolates analyzed is specified in the Results section. **Results.** Among *K. pneumoniae* isolates, complete concordance (100%) between the bleMBL and blaNDM was observed; in all cases, both genes were plasmid-borne across 4 distinct plasmid types. Among *P. aeruginosa* isolates ($n = 7$), both genes were exclusively chromosomally located: the bleMBL without the blaNDM was detected in 1 isolate (14.3%), while the blaNDM without the bleMBL was found in 2 isolates (28.6%), with complete gene pair concordance observed in the remaining isolates. **Conclusions.** The 100% concordance between the bleMBL and blaNDM in *K. pneumoniae* confirms high structural stability of the Tn125 module on plasmids, consistent with clonal spread or horizontal transfer of an intact genetic module, and supports the bleMBL as a reliable auxiliary marker for the blaNDM detection. Gene dissociation in *P. aeruginosa* may reflect greater genomic plasticity in this species, potentially driven by active recombination within chromosomal MDR regions and independent integration events of mobile elements, though confirmation is required. Notably, the blaNDM was exclusively chromosomally located in all *P. aeruginosa* isolates, consistent with previously reported chromosomal integration patterns in this species. Taken together, analysis of the bleMBL-blaNDM co-occurrence may serve as an accessible epidemiological tool to differentiate clonal transmission from horizontal gene transfer and to assess the evolutionary dynamics of MDR pathogens, without comparative genomic sequencing.

Keywords: blaNDM, bleMBL, whole-genome sequencing, targeted sequencing, carbapenem resistance, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, mobile genetic elements.

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