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Retrospective Analysis of Antibiotic Resistance Genes in *Pseudomonas aeruginosa* Clinical Isolates from a Tertiary Medical Centre

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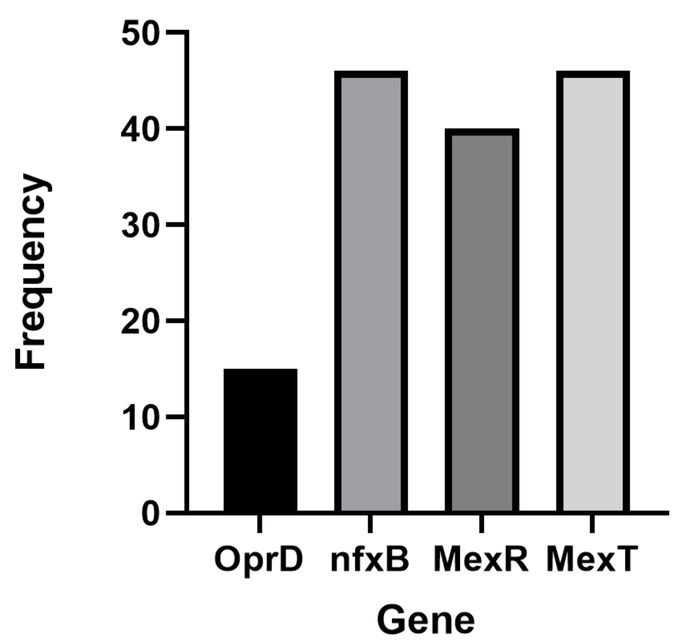
Background

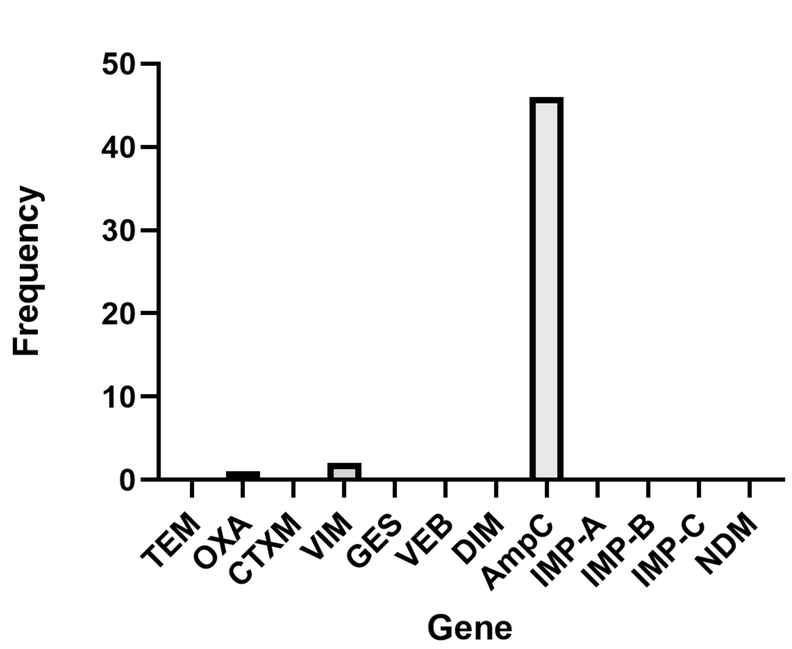
Pseudomonas aeruginosa is a Gram-negative pathogen often associated with healthcare-associated infections, especially in immunocompromised patients. Its capacity to develop resistance complicates treatment. This study aimed to determine the distribution of antibiotic resistance genes in *P. aeruginosa* clinical isolates collected from a tertiary medical centre between April and November 2017.

Methods

Forty-six clinical isolates were collected from the Universiti Malaya Medical Centre in 2017. DNA was extracted and conventional PCR was used to detect 16 resistance genes, including porin (*oprD*), efflux pump regulators (*nfxB*, *mexT*, *mexR*), beta-lactamases (TEM, OXA, CTXM, VIM, GES, VEB, DIM, AmpC), and carbapenemases (IMP-A, IMP-B, IMP-C, NDM). Ethical approval was obtained (MREC ID NO: 2021331-10012).

Results





All 46 isolates (100%) carried *nfxB*, *mexT*, and AmpC. *mexR* and *oprD* were detected in 89.1% (n = 41) and 34.8% (n = 16) of the isolates, respectively. VIM and OXA were found in 4.3%(n = 2) and 2.2% (n = 1), while no isolates harbored TEM, CTX-M, GES, VEB, DIM, or any of the carbapenemase genes tested. One isolate harbored both VIM and OXA resistance genes.

Conclusion

This study provides a molecular overview of the distribution of antibiotic resistance genes in *P. aeruginosa* clinical isolates collected prior to 2019. The high prevalence of intrinsic regulatory genes and AmpC suggests the widespread presence of resistance-related genetic elements before increased surveillance efforts in recent years. Unlike studies published from 2020 onwards, molecular data on *P. aeruginosa* earlier isolates at this centre remain limited. These findings serve as a reference point for tracking evolution of resistance mechanisms in *P. aeruginosa* in Malaysian healthcare settings.

Acknowledgement

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