Infection and Drug Resistance

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LETTER

Detection of Antibiotic Resistance Genes in *Pseudomonas aeruginosa* by Whole Genome Sequencing [Letter]

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Dear editor

We appreciate the authors who have reported their research results in "Detection of Antibiotic Resistance Genes in *Pseudomonas aeruginosa* by Whole Genome Sequencing" published in Infection and Drug Resistance 2022:15 6703–6709. This is very important information about whole genome sequencing and anti-lamb susceptibility testing for antibiotic resistance using still conventional PCR methods. The purpose of this study itself was to evaluate the genes that were resistant to *Pseudomonas aeruginosa* where the results of the resistance genes were sul1, aac(3)-Ic, blaPAO, blaGES-1, blaGES-5 aph(3')-XV, blaOXA-50, aacA4, catB7, aph (3')-IIb, aadA6, fosA, tet(G), cmlA1, aac(6')Ib-cr, and rmtF.[1]

In this study it was also reported that *Pseudomonas aeruginosa* is resistant to several antibiotics and can be a threat in a society that uses antibiotics irrationally. This is due to the acquisition of enzymes in *Pseudomonas aeruginosa* such as extended-spectrum-lactamase, carbapenemase, and aminoglycoside-converting enzymes. This study also investigated the prevalence of ARG in three *P. aeruginosa* strains using whole genome sequencing where the PCR technique used showed *Pseudomonas aeruginosa* resistance to different antibiotics, such as ceftazidime, cefotaxime, cefepime, piperacillin/tazobactam and imipenem.[2]

Unfortunately, this study has not been able to report in detail the genome sequences that are resistant to *Pseudomonas aeruginosa*. Twelve different dilutions of each antibiotic were required to be tested by the double dilution method (concentrations tested ranged from 1024 µg/mL to 0.5 µg/mL), for example one of the quinolone antibiotics representing four quinolone generations, tested, including nalidixic acid (NAL), which represents the first generation; ciprofloxacin (CIP), norfloxacin (NOR), and ofloxacin (OFL), representing the second generation; levofloxacin (LEV), representing the third generation, and gemifloxacin (GEM) and moxifloxacin (MOX), representing the fourth generation (all from Sigma-Aldrich, USA) using the ATCC27853 code for *P. aeruginosa* to test their quality.[3]

In addition, there is also a method that can be used as a comparison in testing the susceptibility of *Pseudomonas* which can identify down to the species level (ID) and test for antimicrobial susceptibility (AST), using the Becton Dickinson (BD) Phoenix automated system. This method analyzes isolates produced by carbapenemase enzymes using the Modified Carbapenem Inactivation Method (mCIM). The results of this study reported that 110 presumed *Pseudomonas* isolates from the biobank were re-analyzed, 100 of which were found to be *Pseudomonas* and among them *P. aeruginosa* had a resistance rate of 98% and P. putida of 2%. The highest resistance rate was observed to ceftazidime (35%) and the lowest resistance rate was observed to amikacin (2%). Twenty seven isolates were identified as test candidates for carbapenemase enzyme production, where only 3/27 (11%) isolates were detected as carbapenemase enzyme producers.[4]

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Disclosure

The authors report no conflicts of interest in this communication.

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