

TEM-171 in *Proteus mirabilis*, where resistance phenotype does not meet resistance genotype

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Abstract

Introduction: *Proteus* species are opportunistic pathogens of the Enterobacteriaceae family that cause various diseases such as complicated urinary tract infections, wound infections, burns, abscesses, respiratory tract infections and bacteremia.

Materials and Methods: In this study, *Proteus mirabilis* isolates were collected from four UTI patients with cefexime treatment failure. Antibiotic susceptibility of *P. mirabilis* isolates were evaluated by Vitek2. To identify the clonality relatedness, REP-PCR was used. Whole genome sequencing (WGS) Illumina platform, pair-end, for one of isolates was used. The sequence was assembled, annotated and then embedded in Comprehensive Antibiotic Resistance Database and Center for Genomic Epidemiology to find the resistance determinants as well as pathogenicity genes. The respective plasmids were also fully determined.

Results: Based on the results of Vitek2 device, all of four isolates were susceptible to all tested antibiotics. REP-PCR revealed that they were a clone. The WGS contigs submitted and accession number NZ_JABVMA000000000.1 was accepted. Four plasmids were identified. Four resistance genes including TEM-171 (monobactam resistance, cephalosporin), APH(3')-IIa and APH(3')-Ia (aminoglycoside resistance) and sul1 (sulfonamide resistance) as well as various efflux pumps were identified in the bacterium.

Conclusion: According to the MIC results, aforementioned genes did not cause resistance to the tested antibiotics in-vitro. However, outpatient treatment with cefexime was not successful. Patients were treated by ciprofloxacin. Different reactions of TEM-171 under antibiotic stress, i.e. in-vitro and in-vivo, shows the effect of human barriers in front of effective dose of antibiotics in target organ.

Received: June 10, 2022; **Accepted:** June 14, 2022; **Published:** June 18, 2022

Biography

Mr. Himen Salimizand has completed his MSc. from Pasteur Institute of Iran and currently works in Kurdistan University of

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