

Whole-Genome sequencing-based characterization of a metallo-beta-lactamase producing *Pseudomonas* *aeruginosa* isolate from Bulgaria

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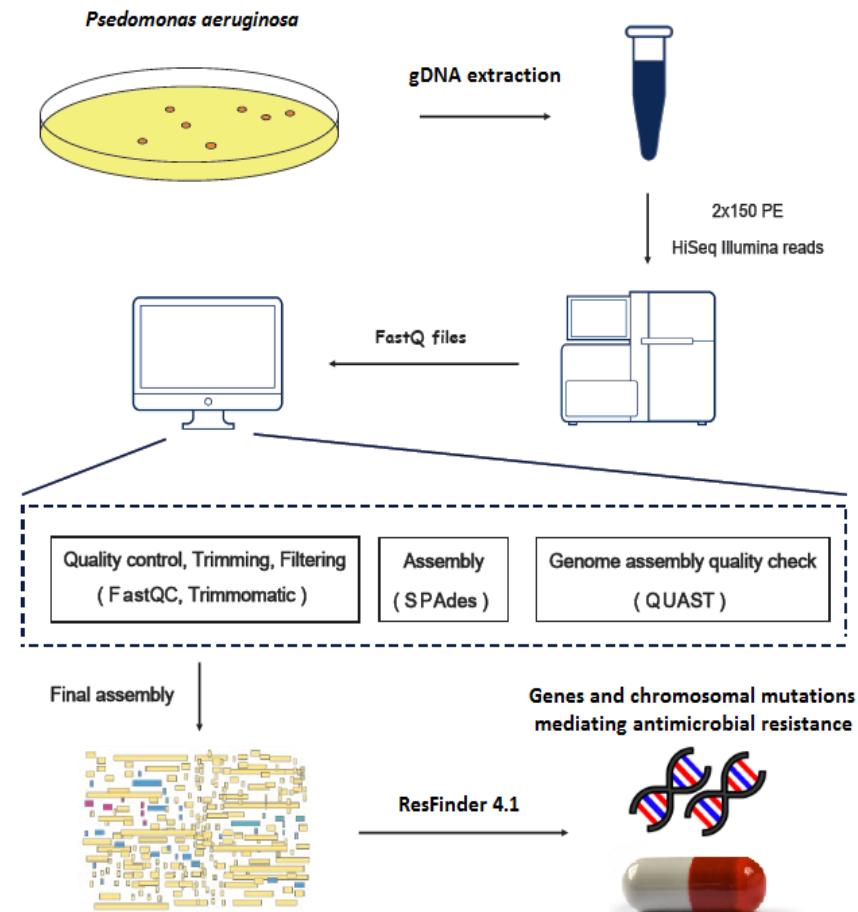
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4- BioInfoTech Laboratory

Abstract

Pseudomonas aeruginosa is one of the leading nosocomial pathogens worldwide. It causes infections that are hard to treat due to the intrinsic resistance of the species and its remarkable ability to acquire additional resistance mechanisms to multiple groups of antimicrobial agents. Therefore, treatment options are narrowed down to only few antibiotics and carbapenems are arguably the most preferred among them. However, carbapenem resistance in *P. aeruginosa* is increasing globally and the major reason for this is the metallo-beta-lactamases (MBLs) production. Here, we report the isolation of a MBL producing *P. aeruginosa* isolate from Bulgaria, which was later subject to a whole-genome sequencing to explore its resistome.

Methodology



Results

Genome assembly quality metrics and antibiotic resistome profile

Statistics without reference	Shovill_on_data
# contigs	90
# contigs (>= 0 bp)	120
# contigs (>= 1000 bp)	78
Largest contig	644 223
Total length	7 162 522
Total length (>= 0 bp)	7 169 178
Total length (>= 1000 bp)	7 153 979
N50	231 855
N75	140 499
L50	10
L75	20
GC (%)	65.75
Mismatches	
# N's	100
# N's per 100 kbp	1.4

GENE	COVERAGE	COVERAGE_MAP	GAPS	%COVERAGE	%IDENTITY	DATABASE	PRODUCT	RESISTANCE
crpP_1	1-198/198	=====	0/0	100	98.48	resfinder	crpP	Ciprofloxacin
catB7_1	1-639/639	=====	0/0	100	99.53	resfinder	catB7	Chloramphenicol
aph(3')-IIb_2	1-807/807	=====	0/0	100	99.26	resfinder	aph(3')-IIb	
blaPAO_1	1-1194/119	=====	0/0	100	99.5	resfinder	blaPAO	
fosA_4	1-408/408	=====	0/0	100	98.53	resfinder	fosA	Fosfomycin
blaOXA-395_1	1-789/789	=====	0/0	100	100	resfinder	blaOXA-395	Amoxicillin;Ampicillin;Meropenem
cmlB1_1	1-1210/126	=====	0/0	95.58	79.5	resfinder	cmlB1	Chloramphenicol
sul1_5	1-867/867	=====	0/0	100	99.89	resfinder	sul1	Sulfamethoxazole
aac(6')-29b_1	1-396/396	=====	0/0	100	100	resfinder	aac(6')-29b	Amikacin;Tobramycin
blaVIM-2_1	1-801/801	=====	0/0	100	100	resfinder	blaVIM-2	Amoxicillin;Amoxicillin+Clavulanic_acid;Ampicillin;Ampicillin+Clavulanic_acid;Cefepime;Cefixime;Cefotaxime;Cefotetan;Ceftazidime;Ertapenem;Imipenem;Meropenem;Piperacillin;Piperacillin+Tazobactam
aac(6')-29b_1	1-396/396	=====	0/0	100	100	resfinder	aac(6')-29b	Amikacin;Tobramycin

QUAST Quality Assessment Tool

ABRicate Mass screening of contigs for antimicrobial and virulence genes Tool

blaVIM-2 - Metallo-beta-lactamase

Accession	ARO:3002272
Definition	VIM-2 is a beta-lactamase found in <i>Pseudomonas</i> spp.
AMR Gene Family	VIM-beta-lactamase
Drug Class	penem, penam, carbapenem, cephamycin, cephalosporin
Resistance Mechanism	antibiotic inactivation
Resistomes with Perfect Matches	<i>Providencia</i> <i>rettgeri</i> ²⁰¹¹ , <i>Pseudomonas aeruginosa</i> ²⁰¹¹ , <i>Pseudomonas putida</i> ²⁰¹¹ , <i>Pseudomonas stutzeri</i> ²⁰¹¹
Resistomes with Sequence Variants	<i>Enterobacter hormaechei</i> ²⁰¹¹ , <i>Klebsiella pneumoniae</i> ²⁰¹¹ , <i>Providencia rettgeri</i> ²⁰¹¹ , <i>Pseudomonas aeruginosa</i> ²⁰¹¹ , <i>Pseudomonas putida</i> ²⁰¹¹ , <i>Pseudomonas stutzeri</i> ²⁰¹¹
Classification	18 ontology terms Show
Parent Term(s)	1 ontology terms Show
Publications	Lee MF, et al. 2008. Int J Antimicrob Agents 32(6): 475-480. Molecular characterisation of the metallo-beta-lactamase genes in imipenem-resistant Gram-negative bacteria from a university hospital in southern Taiwan. (PMID 18804966)

Species	NCBI Chromosome	NCBI Plasmid	NCBI WGS
<i>Enterobacter hormaechei</i>	0%	0%	0.12%
<i>Klebsiella pneumoniae</i>	0%	0%	0.01%
<i>Providencia rettgeri</i>	0%	0%	6.25%
<i>Pseudomonas aeruginosa</i>	4.6%	1.92%	3.95%
<i>Pseudomonas fluorescens</i>	0%	0%	0%
<i>Pseudomonas putida</i>	2.7%	0%	3.12%
<i>Pseudomonas stutzeri</i>	0%	0%	8.33%

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