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Molecular Epidemiology And Antibiotic Resistance Of *Pseudomonas Aeruginosa* Isolates From War Casualties In Ukraine

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Abstract:

Background *Pseudomonas aeruginosa* (Pa) continues to be a major cause of morbidity, affecting combat casualties. The increasing infection rate across evacuation echelons of care can result in the international spread of multi-drug resistant (MDR) strains [1]. Novel data about sequence types harboring antibiotic resistance (AbR) genes, and identifying consistent patterns of Pa

transmission, can help restrict global spread. **Methods** A total of 18 MDR Pa strains isolated from Ukrainian war casualties from 2014 - 2022 were analyzed using whole genome sequencing. Core-genome Multi Locus Sequence Typing identified and tracked through time closely related clusters. Related isolates were subject to additional single nucleotide polymorphism (SNP) phylogenetic analyses. **Results** Isolates were assigned to the following sequence types (ST): ST-235 (6 isolates), ST - 66 (2 isolates), ST - 1047 (3 isolates), ST - 2592 (2 isolates), and 5 isolates belonged to novel STs. Five of the six ST-235 Pa were highly genetically related to each other, differing by just 0-4 SNPs. Notably, these 5 isolates were cultured from three different patients at various times in geographically distant hospitals.

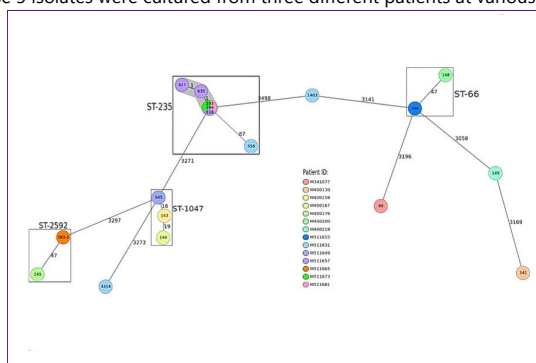


Figure1. The graph shows the relationship between all 18 Pa. Each circle represents a single isolate which is colored based on the individual patient. Sequenced 18 Pa isolates harbored 45 different AbR genes, particularly, carbapenemase genes (*bla_{NDM-1}*, *bla_{IMP-1}*, *bla_{VIM-2}*), an array of genes encoding resistance to aminoglycosides.

The 5 identical ST-235 Pa carry the same complement of AbR genes, including the gene encoding the VIM-2. Three isolates carried *bla_{NDM-1}* along with the *rmt_{B4}*.

Conclusions These results suggest a high likelihood of nosocomial infection, either by patient-to-patient or exposure to a common source, such as an environmental reservoir. The current model of medical care for war-injured patients from Ukraine globally abroad is associated with the peril of the worldwide spread of MDR microorganisms.

Acknowledgments / References:

Zwittink RD, Wielders CC, Notermans DW, et al. Multidrug-resistant organisms in patients from Ukraine in the Netherlands, March to August 2022. Euro Surveill. 2022;27(50):2200896. doi:10.2807/1560-7917.ES.2022.27.50.2200896

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