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ACCESSIBLE GENOMIC SURVEILLANCE WORKFLOW FOR MONITORING ANTIMICROBIAL RESISTANCE IN WAR-RELATED HOSPITAL INFECTIONS IN UKRAINE

Aim. The ongoing war in Ukraine has increased the burden of antimicrobial resistance (AMR). *Acinetobacter baumannii*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* are among most common Gram-negative pathogens causing severe infections and are often resistant to multiple antibiotics. Genomic surveillance is therefore essential for epidemiological monitoring and informed treatment decisions. The aim of this study was to develop an accessible bioinformatics methodology for hospital-based genomic surveillance and apply it to isolates obtained from wounded military personnel in Ukraine. **Methods.** We developed a lightweight, assembly-based workflow for routine surveillance in resource-limited settings. Pipeline can be executed on standard PCs and incorporates agent-assisted automation, reducing the requirement for advanced bioinformatics expertise while maintaining controlled semi-automation. The workflow includes assembly quality assessment, species identification, AMR profiling, virulence factor and plasmid identification. The pipeline was applied to 87 WGS isolates from hospitals in Odesa, Vinnytsia, and Dnipro, including *K. pneumoniae* (n = 35), *P. aeruginosa* (n = 33), and *A. baumannii* (n = 19). **Results.** The identified AMR profiles were consistent with previous reports on resistant Gram-negative pathogens. We detected 47 resistance determinants in *A. baumannii*, 64 in *P. aeruginosa*, and 101 in *K. pneumoniae*, including widespread carbapenemase genes. To assess the applicability of the proposed methodology for local surveillance, we compared resistance gene compositions across hospitals. Although statistical significance was not reached, likely due to limited sample sizes, several genes showed notable regional variation (*aph(3')-Ia*, *armA* in *A. baumannii*; *aph(3')-Ib*, *aac(6')-Ib*, *qacE* in *P. aeruginosa*; *armA* in *K. pneumoniae*), suggesting that local AMR profiles may differ between healthcare institutions and highlighting the importance of hospital-level monitoring. **Conclusions.** The proposed workflow provides an accessible framework for genomic surveillance that can support infection control within hospitals and contribute to future nationwide AMR monitoring in Ukraine. The observed trends in resistance gene frequencies emphasize the value of local surveillance for controlling the spread of resistant pathogens.

Keywords: antimicrobial resistance, genomic surveillance, WGS, hospital epidemiology, Ukraine.

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