

<https://doi.org/10.7124/bc.000B72>

**Ye.V. Filippova¹, N.I. Tashevska¹, L.K. Perstnova¹,
B.O. Vladymyrets², K.M. Shcherba¹**

¹ Laboratory Center of Mechnikov Dnipropetrovsk Regional Clinical Hospital
14, Soborna Sq., Dnipro, Ukraine, 49005

² Institute of Molecular Biology and Genetics, NAS of Ukraine
150, Akademika Zabolotnoho Str., Kyiv, Ukraine, 03143
thashevskaya@gmail.com

INTEGRATED PCR, 16S rRNA PROFILING AND WHOLE-GENOME SEQUENCING IN THE DIAGNOSIS OF COMBAT WOUND INFECTIONS AND SEPSIS

Background. Combat wound infections in servicemen are often driven by multidrug-resistant Gram-negatives that may progress to bacteraemia and sepsis, yet culture underestimates their true diversity. We combined multiplex PCR, 16S rRNA profiling and WGS to map the wound-to-blood pathogen spectrum and its resistome. **Methods.** Paired wound swabs and blood samples from 37 wounded servicemen (2024–2025) were screened by Seegene Magicplex Sepsis multiplex PCR; 16S rRNA sequencing was run on 88 samples and WGS on 11 isolates (Ion Chef/Ion GeneStudio S5). **Results.** PCR detected 20 unique species in wounds (8 Gram-positive, 9 Gram-negative, 3 fungal), dominated by resistant Gram-negatives, with *Klebsiella pneumoniae* and *K. oxytoca* most frequent. In blood the spectrum narrowed to 12 species, again led by *K. pneumoniae* and *K. oxytoca* (35.1% each). 16S profiling recovered 42 genera from wounds versus only 16 after culture; most wounds carried 1–4 dominant taxa, frequently as co-infections. Five core genera were defined – the expected *K. pneumoniae*, *Acinetobacter baumannii* and *Pseudomonas aeruginosa*, plus the unexpected, non-culturable *Elizabethkingia meningoseptica*. Bloodstream penetration (of wound isolates) was high for *K. pneumoniae* (93%), *K. oxytoca* (44%), *Enterobacter cloacae* and *A. baumannii* (41%), reaching 100% for *Serratia marcescens* and 92% for *Escherichia coli* and *E. meningoseptica*, whereas three ESKAPE species (*P. aeruginosa*, *S. aureus*, *E. faecium*) stayed wound-restricted. *E. meningoseptica* is naturally resistant to carbapenems, cephalosporins and colistin and stays invisible without 16S. WGS characterised carbapenem-resistant *K. pneumoniae* (5 strains; 52 resistance genes/markers, 9 plasmids; KPC, NDM, OXA-48), XDR *A. baumannii* ST-2 (OXA-23/-40/-58; 11 genes) and MBL-producing *P. aeruginosa* ST-2592 (32 genes; VIM/IMP/NDM; colistin resistance). **Conclusions.** Integrated diagnostics revealed a broader, more resistant wound microbiota than culture, identified emerging pathogens such as *Elizabethkingia meningoseptica*, and quantified the wound-to-blood transition underlying sepsis. Several carbapenemases and mutations detected by WGS lie outside PCR panels available in Ukraine. Pairing molecular methods with culture enables anticipatory rather than reactive management and can steer bacteriology toward missed co-infecting pathogens.

Keywords: sepsis, combat wound infection, ANR, 16S rRNA sequencing, WGS, NGS.

Received: 06.07.2026; Accepted: 08.09.2026; Published: 29.09.2026

Citation: Filippova Ye.V., Tashevska N.I., Perstnova L.K., Vladymyrets B.O., Shcherba K.M. (2026) Integrated PCR, 16S rRNA profiling and whole-genome sequencing in the diagnosis of combat wound infections and sepsis. *Biopolymers & Cell*, Special issue(42), 55. <https://doi.org/10.7124/bc.000B72>

© Publisher PH "Akademperiodyka" of the NAS of Ukraine, 2026. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted reuse, distribution, and reproduction in any medium, provided the original work is properly cited