Short Communications

Editorial Process: Submission:01/02/2026 Acceptance:07/08/2026 Published:07/27/2026

Identification and GenBank Registration of Two Novel Bloodstream Bacterial Strains from Oncology Patients: *Escherichia Coli* OncoEval 1 and *Pseudomonas Aeruginosa* OncoEval 2

Bassam Abdul Rasool Hassan[1]*, Watheq Mohammed AL-Jewari[2], Ali Haider Mohammed[3], Ahmed Zuhair Abdulhameed Alsammarraie[4], Mohammed Kamil Al Qayyim[5], Abu Bakar Abdul Majeed[2], Muhamad Faiz Othman[6], Musaab Kadhim Alabboodi[7]

Abstract

Objective: Bloodstream infections are a significant complication in cancer patients and play an important role in morbidity and mortality, especially in immunocompromised populations. It is crucial that clinically derived bacterial strains be molecularly documented to aid infection surveillance and future translational research in oncology practice. **Methods:** This brief communication describes the identification and National Center for Biotechnology Information (NCBI) GenBank registration of two bacterial strains isolated from bloodstream infections in oncology patients. Partial 16S ribosomal RNA gene sequencing was used for molecular identification. **Results:** One isolate was identified as *Escherichia coli* strain OncoEval 1, and the second as *Pseudomonas aeruginosa* strain OncoEval 2. Validated and quality-screened sequences of both were deposited in the GenBank database to provide public genomic references derived from cancer-associated bloodstream infections. **Conclusion:** The registration of these strains broadens the molecular resource base for pathogens isolated from oncology patients and drives continued studies in infection surveillance and research in the setting of cancer care.

Keywords: Bloodstream infection- Oncology patients- *Escherichia coli*- *Pseudomonas aeruginosa*- 16S rRNA gene

Asian Pac J Cancer Prev, **27 (7)**, 2359-2362

Introduction

Bloodstream infections (BSIs) are one of the leading causes of morbidity and mortality in patients with cancer, especially those with chemotherapy, radiotherapy, or other immunosuppressive treatments. Neutropenia, mucosal barrier injury, and prolonged hospitalisation increase susceptibility to invasive bacterial infections, which makes BSIs a serious complication in oncology care [1, 2]. Thus, early and proper diagnosis of the causative pathogen is crucial for informing efficacious antimicrobial therapy and enhancing the clinical management. Among the Gram-negative pathogens, *Escherichia coli* and *Pseudomonas aeruginosa* have consistently been listed as the top two causes of BSIs in patients presenting with oncology. *E. coli* is mainly recognized for gastrointestinal translocation and healthcare-associated infections, whereas P. aeruginosa is of the greatest concern owing to its intrinsic resistance processes as well as accumulation of various antimicrobial resistance characteristics [3, 4]. Infections from these organisms are related with prolonged hospitalization, higher health care costs, and excess mortality in cancer patients [5]. Importantly, bloodstream isolates derived from oncology patients represent a distinct clinical and ecological subset compared with isolates from general hospitalized populations. Cancer patients are frequently exposed to repeated cycles of broad-spectrum antimicrobials, central venous catheters, cytotoxic

*[1]Faculty of Pharmacy, Al Rafidain University, 10001, Baghdad, Iraq. [2]Department of Pharmacology and Life Sciences, Faculty of Pharmacy, Universiti Teknologi MARA, 42300 Bandar Puncak Alam, Selangor, Malaysia. [3]School of Pharmacy, Monash University Malaysia, Jalan Lagoon Selatan, 47500 Bandar Sunway, Subang Jaya, Selangor, Malaysia. [4]Medical Oncology Department, Oncology Teaching Hospital Baghdad, Baghdad, Iraq. [5]Department of Haematology, Medical city complex, Haematology and Transplant centre, Baghdad, Iraq. [6]Department of Pharmacy Practice and Clinical Pharmacy, Faculty of Pharmacy, Universiti Teknologi MARA, 42300 Bandar Puncak Alam, Selangor, Malaysia. [7]Medical Oncology Department, Alamal National Hospital for Cancer Treatment, Baghdad, Iraq. *For Correspondence: bassamsunny@yahoo.com*

chemotherapy, and prolonged hospitalisation, all of which create unique selective pressures that may shape pathogen diversity and strain-level characteristics. Profound or recurrent immunosuppression further alters host–pathogen interactions, increasing the likelihood of invasive disease and recurrent bloodstream infections. Therefore, molecular documentation of isolates specifically originating from oncology settings is particularly relevant for understanding pathogen evolution and infection dynamics within this vulnerable population. Molecular characterisation of bacterial isolates is vital to understanding pathogen diversity and infection surveillance. Clinically derived bacterial strains can be sequenced, then publicly deposited, which enables geographic and population comparison of bacterial strains, as well as future research on the mechanism of pathogenicity and antimicrobial resistance [6]. Bacterial isolates derived exclusively from oncology patients are however underrepresented in public genomic databases, and especially in bloodstream infections in general. This brief message summarizes the discovery and registration by National Center for Biotechnology Information (NCBI) GenBank of two new bacterial strains isolated from bloodstream infections in oncology patients, *Escherichia coli* strain OncoEval 1 and *Pseudomonas aeruginosa* strain OncoEval 2. These sequences are published in an accessible manner, thus providing molecular evidences of clinically important pathogens in cancer care and supporting current investigations on infection surveillance and translational oncology.

Materials and Methods

Design and clinical isolates

This brief communication presents final reports on laboratory work on the molecular identification and public registration of two bacterial isolates recovered from bloodstream infections in oncology patients. The isolates were obtained from blood cultures taken from hospitalised cancer patients during routine clinical care in September 2024.

Bacterial identification and DNA sequencing

Initial bacterial identification was done according to standard microbiological procedures. Molecular confirmation was carried out by partial sequencing of the 16S ribosomal RNA (rRNA) gene, now widely accepted for bacterial taxonomy. Genomic DNA was isolated from pure bacterial cultures and 16S rRNA gene fragments were amplified and sequenced by Sanger dideoxy sequencing technology.

Quality control and validation of sequences

All generated sequences were screened for chimeras before submission to the database to ensure the integrity and reliability of our output sequences. Chimera diagnostics and sequence quality assessment were carried out using Geneious software (version 11.1) in accordance with established validation protocol for 16S rRNA gene analysis [7].

GenBank submission and accession numbers

Sequences that were validated were sent to the NCBI GenBank database. The *Escherichia coli* isolate was classified as strain OncoEval 1 with accession number PQ661370.1, and the *Pseudomonas aeruginosa* isolate was identified as strain OncoEval 2 with accession number PQ661371.1. Submission metadata for the submitted organism was source of isolation (blood), host (human), collection date and DNA sequencing method, as set forth in the GenBank submission requirements [8-10].

Results

Two bacterial isolates recovered from bloodstream infections in oncology patients were successfully identified and molecularly characterised using partial 16S ribosomal RNA gene sequencing. Sequence analysis confirmed the taxonomic identity of the isolates as *Escherichia coli* and *Pseudomonas aeruginosa*, respectively. The *Escherichia coli* isolate was designated strain OncoEval 1. A partial 16S rRNA gene sequence of 1,348 base pairs was obtained, validated, and deposited in the National Center for Biotechnology Information (NCBI) GenBank database under accession number PQ661370.1. The isolate originated from a human blood sample collected in September 2024. The second isolate was identified as *Pseudomonas aeruginosa* and designated strain OncoEval 2. A partial 16S rRNA gene sequence of 1,399 base pairs was generated and deposited in GenBank under accession number PQ661371.1. This strain was also isolated from a bloodstream infection in an oncology patient during the same study period. Key characteristics of both bacterial strains, including species identification, clinical source, sequence length, and GenBank accession numbers, are summarised in Table 1. Both sequences passed quality control and chimera screening prior to submission, confirming their validity as publicly accessible genomic references derived from cancer-associated bloodstream infections.

Discussion

In oncology the burden of bloodstream infection with Gram-negative bacteria continues to be a major clinical concern, which is amplified with immunosuppression and frequent healthcare visits resulting in increased susceptibility to severe and recurrent infection. In this regard, molecular registration of clinically relevant pathogens is a valuable tool within infection surveillance and future translational studies. We report in this short

Table 1. Characteristics of Bacterial Strains Isolated from Oncology Patients

Strain	Species	Sample source	16S rRNA length (bp)	GenBank accession
OncoEval 1	*E. coli*	Blood	1348	PQ661370.1
OncoEval 2	*P. aeruginosa*	Blood	1399	PQ661371.1

communication, identification and registration of two bacterial strains isolated from bloodstream infections in oncology patients, broadening the genomic profile of cancer-associated bacterial isolates. *Escherichia coli* and *Pseudomonas aeruginosa* have been identified as the most common causes of bloodstream infection among patients with malignancies and are associated with adverse results particularly in the presence of antimicrobial resistance [1, 3]. While these organisms are fully identified, diversity at the strain level is less explored within the oncology community, especially low- and middle-income populations. Accordingly, identifying *E. coli* strain OncoEval 1 and P. aeruginosa strain OncoEval 2 gives useful information for the reference material, which has been obtained directly from patients of cancer who are suffering from bloodstream infections. Publishing validated 16S rRNA gene sequences in the National Center for Biotechnology Information (NCBI) GenBank database can facilitate access and reproducibility of this information, and enables comparative and phylogenetic studies across geographic regions and clinical contexts [11]. In addition, the availability of these oncology-derived sequences may support future regional molecular surveillance initiatives, enable comparative phylogenetic mapping of bloodstream isolates across cancer centres, and facilitate integration with antimicrobial-resistance investigations specific to oncology care settings. These genomic resources are critical in strengthening molecular epidemiology frameworks, and in advancing further knowledge of pathogen diversity of susceptible patient populations. Although the present study cannot evaluate antimicrobial resistance mechanisms or clinical outcomes, the availability of those registered strains serves as a stepping stone towards further investigations involving genomic, phenotypic, and clinical data. In oncology practice, where early pathogen identification and directed therapy prove essential, further molecular identification of bloodstream isolates serves as a key component of interventions for infection prevention and control [12].

In conclusion, this brief report details the identification and GenBank registration of *Escherichia coli* OncoEval 1 and *Pseudomonas aeruginosa* OncoEval 2, bacterial strains isolated from bloodstream infections in oncology patients. The availability of these validated 16S rRNA gene sequences in the public domain adds to the scarcity of genomic resources resulting from cancer-associated bloodstream infections. This work contributes to the understanding of clinically relevant strains from an oncology context, paving the way for further molecular surveillance, comparative analyses, and translational studies of infection management in at-risk communities in cancer.

Author Contribution Statement

Conceptualization: AHM; BARH. Data curation: AHM, LJY, LJS, LJE, LJX. Formal analysis: AHM, LJY, LJS, LJE, LJX. Investigation: AHM, LJY, LJS, LJE, LJX. Methodology: AHM, LJY, LJS, LJE, LJX. Project administration: AHM, LJY, LJS, LJE, LJX. Resources: AHM, LJY, LJS, LJE, LJX. Software: AHM, LJY, LJS, LJE, LJX. Supervision: AHM; DSR. Validation: AHM; AB;AL;BARH. Visualisation: AHM. Writing - original draft: LJY, LJS, LJE, LJX; AHM. Writing - review & editing: all authors.

Acknowledgements

The authors thank the expert panels who provided feedback on the items and participants who participated in the content validation of the KP-AMS-OC-Q.

Ethics approval and consent to participate

The Ministry of Health, Center of Training & Human Development Committee approved this study (46119/41247). The research was conducted in accordance with the ethical standards of the Declaration of Helsinki. The researcher thoroughly explained the objectives and benefits of the study to the participants, in which they were given an explanatory statement and informed consent was obtained. The anonymity and confidentiality was maintained by assuring that no identifying demographic information was collected.

Consent to Participate

Informed consent was obtained from all individual participants included in the study.

Consent to Publish

Participants provided informed consent regarding the publication of their de-identified data.

Availability of Data and Materials

Data and other materials are available upon request from the corresponding authors.

Availability of data and materials

Data and other materials are available upon request from the corresponding authors.

Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

References

1. Gudiol C, Aguado JM, Carratalà J. Bloodstream infections in patients with solid tumors. Virulence. 2016;7(3):298-308. https://doi.org/10.1080/21505594.2016.1141161.
2. Nesher L, Rolston KV. The current spectrum of infection in cancer patients with chemotherapy related neutropenia. Infection. 2014;42(1):5-13. https://doi.org/10.1007/s15010-013-0525-9.
3. Trecarichi EM, Tumbarello M. Antimicrobial-resistant gram-negative bacteria in febrile neutropenic patients with cancer: Current epidemiology and clinical impact. Curr Opin Infect Dis. 2014;27(2):200-10. https://doi.org/10.1097/qco.0000000000000038.
4. Moradali MF, Ghods S, Rehm BH. *Pseudomonas aeruginosa* lifestyle: A paradigm for adaptation, survival, and persistence. Front Cell Infect Microbiol. 2017;7:39. https://doi.org/10.3389/fcimb.2017.00039.
5. Liu C, Rosen EA, Stohs EJ, Imlay H, Nigo M, Gottesdiener

LS, So M, Tverdek F, Dadwal S, Gudiol C, Satlin MJ. Tackling antimicrobial resistance in people who are immunocompromised: leveraging diagnostic and antimicrobial stewardship. The Lancet Infectious Diseases. 2026 Jan 1;26(1):e30-48.
6. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, et al. Ncbi prokaryotic genome annotation pipeline. Nucleic Acids Res. 2016;44(14):6614-24. https://doi.org/10.1093/nar/gkw569.
7. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, et al. Geneious basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 2012;28(12):1647-9. https://doi.org/10.1093/bioinformatics/bts199.
8. National center for biotechnology information (ncbi). Genbank: The nih genetic sequence database. Nucleic acids res. 2024;52(d1):D92–d96.
9. Hassan BA, AL-Jewari WM, Mohammed AH, Alsammarraie AZ, Al-Qayyim MK, Al-Saadi FS, et al. Escherichia coli strain OncoEval 1 16S ribosomal RNA gene, partial sequence. GenBank [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2024 [cited 2026 Feb 8]. Available from: https://www.ncbi.nlm.nih.gov/nuccore/2863140916
10. Hassan BA, AL-Jewari WM, Mohammed AH, Alsammarraie AZ, Al-Qayyim MK, Al-Saadi FS, et al. Pseudomonas aeruginosa strain OncoEval 2 16S ribosomal RNA gene, partial sequence. GenBank [Internet]. Bethesda (MD): National Center for Biotechnology Information (US); 2024 [cited 2026 Feb 8]. Available from: https://www.ncbi.nlm.nih.gov/nuccore/2863140917.
11. Gudiol C, Aguado JM, Carratalà J. Bloodstream infections in patients with solid tumors. Virulence. 2016 Apr 2;7(3):298-308.
12. Gudiol C, Tubau F, Calatayud L, Garcia-Vidal C, Cisnal M, Sánchez-Ortega I, et al. Bacteraemia due to multidrug-resistant gram-negative bacilli in cancer patients: Risk factors, antibiotic therapy and outcomes. J Antimicrob Chemother. 2011;66(3):657-63. https://doi.org/10.1093/jac/dkq494.