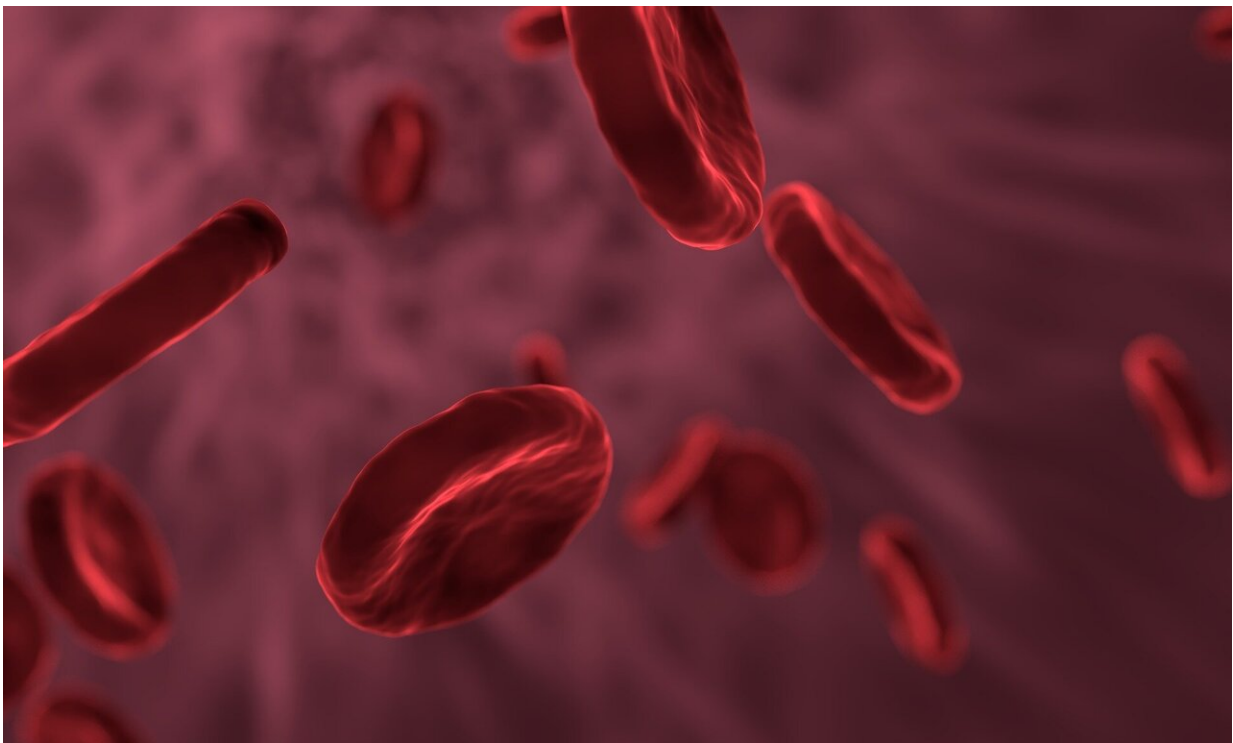


# Metagenomic sequencing outperforms conventional tests to identify antimicrobial resistance in bloodstream infections

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Metagenomic sequencing can provide rapid and actionable antimicrobial resistance predictions to treat bloodstream infections much faster than conventional laboratory tests, and has the potential to save lives and

better manage the use of antibiotics, according to new research being presented at this year's European Congress of Clinical Microbiology & Infectious Diseases (ECCMID) in Copenhagen, Denmark (15-18 April).

The study led by Dr. Kumeren Govender from the John Radcliffe Hospital, University of Oxford, UK, indicates that rapid metagenomics can provide accurate results within just 6 hours of knowing bacteria are growing in a [blood sample](#).

"Antibiotic resistant [bloodstream infections](#) are a leading killer in hospitals, and rapidly starting the right antibiotic saves lives", says Dr. Govender. "Our results suggests that metagenomics is a powerful tool for the rapid and accurate diagnosis of pathogenic organisms and antimicrobial resistance, allowing for effective treatment 18 to 42 hours earlier than would be possible using standard [culture](#) techniques."

Bloodstream infections can rapidly lead to sepsis, multiple organ failure, and even death. Early and appropriate antibiotic therapy is vital for control of the [infection](#).

## **Antimicrobial resistance (AMR) is a major challenge when treating bloodstream**

Infections, causing around 370,000 deaths and associated with nearly 1.5 million deaths in 2019.

The current method used in [clinical settings](#) to identify the pathogen causing the infection is long and laborious, requiring two time-consuming culture and sensitivity tests that take at least 1 to 3 days to complete—first isolating and identifying the pathogen and then performing antimicrobial susceptibility testing (to expose the bacteria to various antibiotics to see exactly which it will respond to, plus the best

route and dose).

In contrast, clinical metagenomics sequences all the [genetic material](#) including infectious pathogens in a sample all at once, so time spent running tests, waiting for results, and running more tests could be reduced.

To find out more, researchers randomly selected 210 positive and 61 negative blood culture specimens for metagenomic sequencing from the Oxford University Hospital's microbiology laboratory between December 2020 and October 2022.

DNA was sequenced using the Oxford Nanopore GridION platform. Sequences were used to identify the species of pathogen causing infections and also to spot [common species](#) that can contaminate blood cultures.

Sequencing was able to identify 99% of infecting pathogens including polymicrobial infections and contaminants, as well as giving negative results in 100% of culture negative samples. In some instances, sequencing detected probable causes of infection missed by routine cultures, and in other instances identified uncultivable species where a result could not be determined.

Sequencing could also be used to detect antibiotic resistance in the ten most common causes of infections. A total of 741 resistant and 4047 sensitive combinations of antibiotics and pathogens were studied. Results of traditional culture-based testing and sequencing agreed 92% of the time. Similar performance could be obtained from raw reads after only two hours of sequencing, overall agreement was 90%.

The average time from sample extraction to sequencing was 4 hours with complete AMR prediction 2 hours later, producing actionable AMR

results 18-42 hours before to the conventional laboratory.

David Eyre, Professor of Infectious Diseases at the University of Oxford, who co-led the study, commented, "This is a really exciting breakthrough that means we will be able to diagnose the cause of patients' infections faster and more completely than has been possible before. We are working hard to continue to overcome some of the remaining barriers to [metagenomic sequencing](#) being used more widely, which include its current high cost, further improving accuracy, and creating improved laboratory expertise in these new technologies and simpler workflows for interpreting results."

**More information:** Direct-from-blood culture metagenomic sequencing provides accurate antimicrobial resistance predictions faster than routine methods, European Congress of Clinical Microbiology & Infectious Diseases (ECCMID), 2023.

Provided by European Society of Clinical Microbiology and Infectious Diseases

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