

# Tracking the global spread of antimicrobial resistance

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*Escherichia coli*. Credit: Rocky Mountain Laboratories, NIAID, NIH

An international research team has provided valuable new information about what drives the global spread of genes responsible for antimicrobial resistance (AMR) in bacteria.

The collaborative study, led by researchers at the Quadram Institute and the University of East Anglia, brought together experts from France, Canada, Germany and the UK and will provide new information to combat the global challenge of AMR.

By examining the whole genome sequences of around two thousand [resistant bacteria](#), predominantly *Escherichia coli* collected between 2008 and 2016, the team found that different types of AMR [genes](#) varied in their temporal dynamics. For example, some were initially found in North America and spread to Europe, while for others the spread was from Europe to North America.

Not only did the study look at [bacteria](#) from different geographic regions but also from diverse hosts including humans, animals, food (meat) and the environment (wastewater), to define how these separate but interconnected factors influenced the development and spread of AMR. Understanding this interconnectivity embodies the One Health approach and is vital for understanding transmission dynamics and the mechanisms by which [resistance genes](#) are transmitted.

The study, published in the journal *Nature Communications*, was supported by the Joint Programming Initiative on Antimicrobial Resistance (JPIAMR), a global collaboration spanning 29 countries and the European Commission that is tasked with turning the tide on AMR. Without concerted efforts on a global scale, AMR will undoubtedly make millions more people vulnerable to infections from bacteria and other microorganisms that can currently be tackled with antimicrobials.

The team focussed on resistance to one particularly important group of antimicrobials, the Extended-Spectrum Cephalosporins (ESCs). These antimicrobials have been classed as critically important by the World Health Organization because they are a 'last resort' treatment for multidrug resistant bacteria; despite this, since their introduction,

efficacy has declined as bacteria have developed resistance.

Bacteria that are resistant to ESCs achieve this through the production of specific enzymes, called beta-lactamases, that are able to inactivate ESCs.

The instructions for making these enzymes are encoded in genes, particularly two key types of genes: extended-spectrum beta-lactamases (ESBLs), and AmpC beta-lactamases (AmpCs).

These genes may be found on the chromosomes of bacteria where they are passed to progeny during clonal multiplication, or in plasmids, which are small DNA molecules separate to the bacterium's main chromosome. Plasmids are mobile and can move directly between individual bacteria representing an alternative way of exchanging [genetic material](#).

This study identified how some resistance genes proliferated through clonal expansion of particularly successful bacterial subtypes while others were transferred directly on epidemic plasmids across different hosts and countries.

Understanding the flow of genetic information within and between bacterial populations is key to understanding AMR transmission and the global spread of resistance. This knowledge will contribute to the design of vitally needed interventions that can halt AMR in the [real world](#) where bacteria from diverse hosts and environmental niches interact, and where international travel and trade mean that these interactions are not limited by geography.

Professor Alison Mather, group leader at the Quadram Institute and the University of East Anglia, said, "By assembling such a large and diverse collection of genomes, we were able to identify the key genes conferring resistance to these critically important drugs. We were also able to show

that the majority of resistance to extended spectrum cephalosporins is spread by only a limited number of predominant plasmids and bacterial lineages; understanding the mechanisms of transmission is key to the design of interventions to reduce the spread of AMR."

Lead author Dr. Roxana Zamudio said, "Antimicrobial resistance is a global problem, and it is only by working collaboratively with partners in multiple countries that we can get a holistic understanding of where and how AMR is spreading."

**More information:** Dynamics of extended-spectrum cephalosporin resistance genes in *Escherichia coli* from Europe and North America, *Nature Communications* (2022). [DOI: 10.1038/s41467-022-34970-7](https://doi.org/10.1038/s41467-022-34970-7)

Provided by University of East Anglia

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