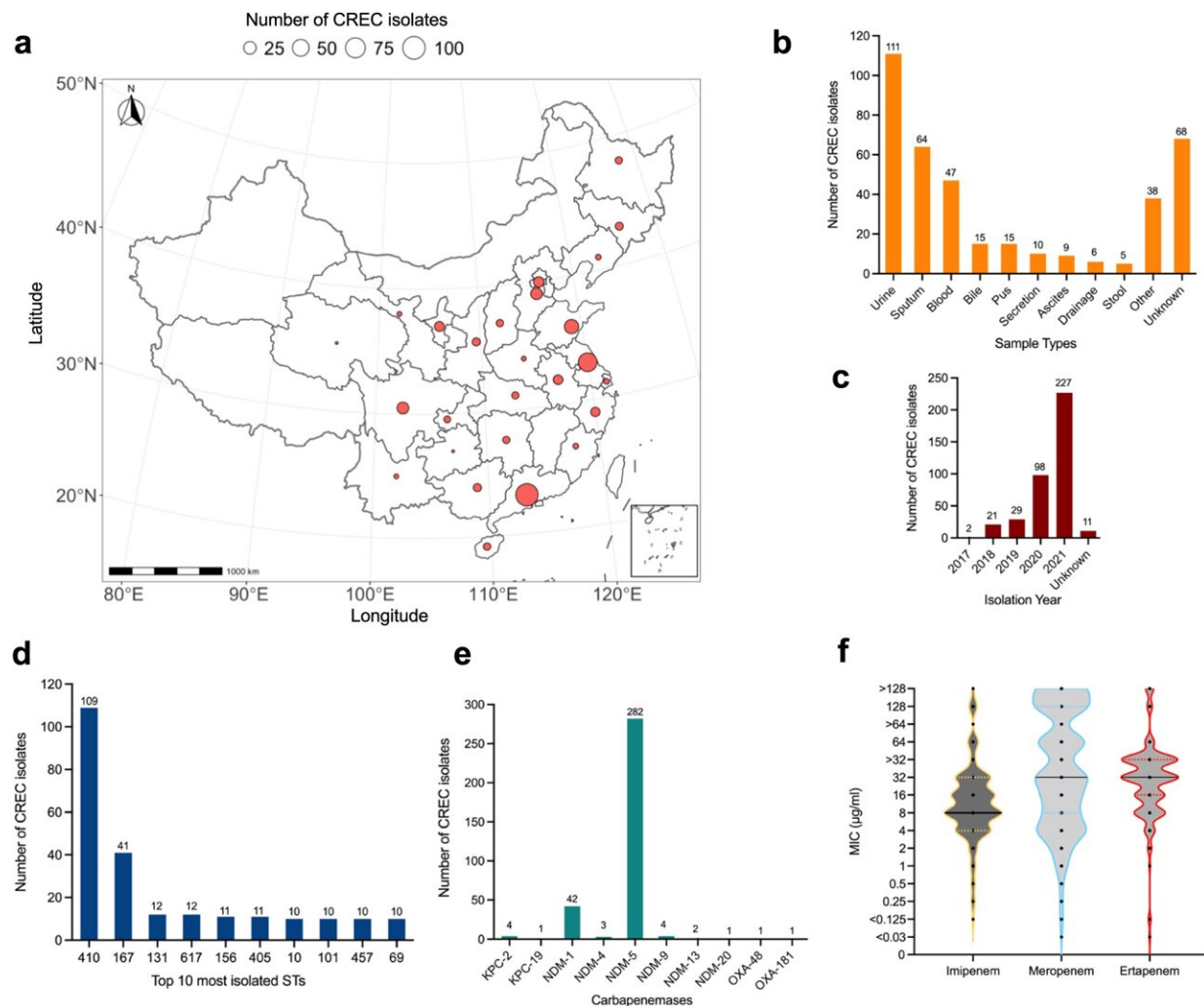


New and highly infectious E. coli strain resistant to powerful antibiotics

January 31 2024



Characteristics of CREC isolates (n = 388) from Chinese hospitals. Credit: *Nature Communications* (2024). DOI: 10.1038/s41467-023-43854-3

A new type of *E. coli* that is both highly infectious and resistant to some antibiotics has been discovered.

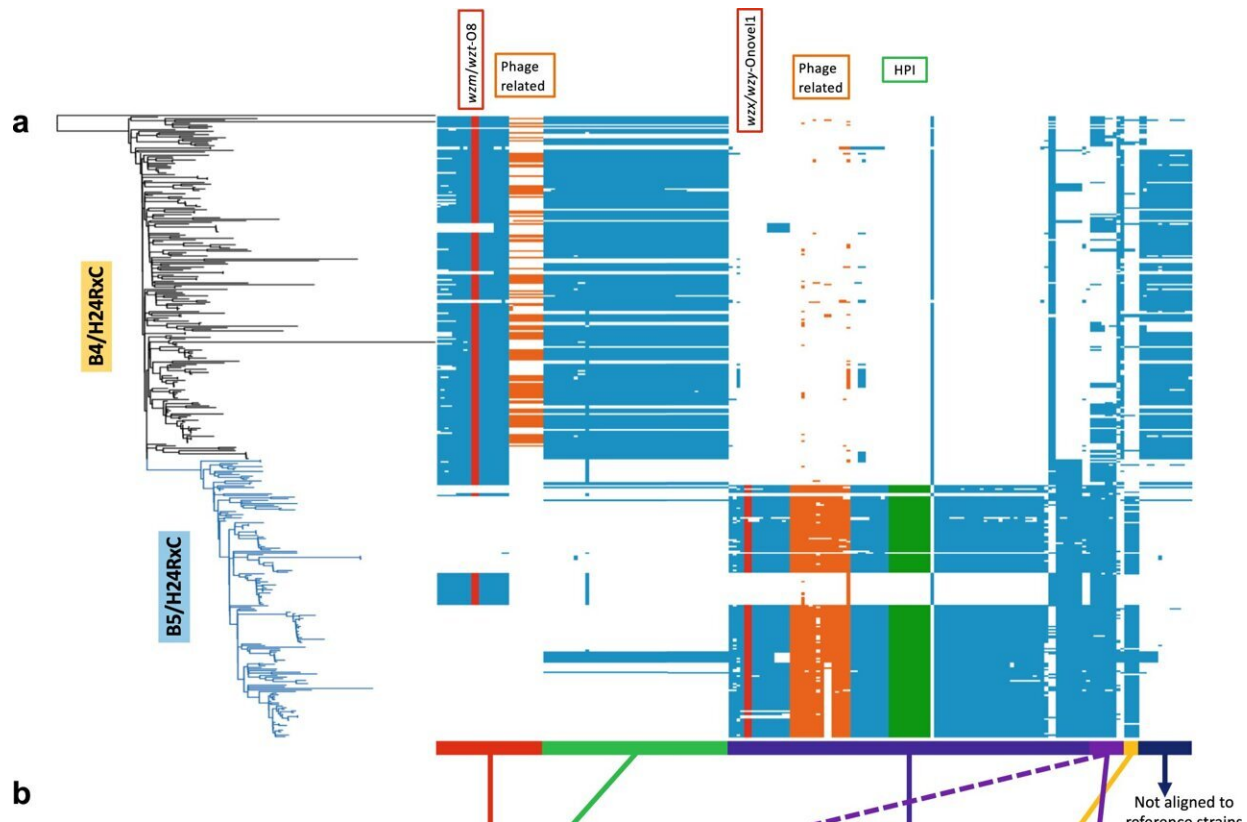
The newly identified mutation of antibiotic-resistant *E. coli* is described in a new paper [published](#) in *Nature Communications*. The team, including Professor Alan McNally from the University of Birmingham suggests that some existing antibiotics called carbapenems will be ineffective against the bacteria.

While scientists have already identified strains of carbapenem-resistant *Escherichia coli* (CREC) and note that is one of the most problematic AMR bacteria in circulation, with the ST410 version becoming the most common resistant *E. coli* in Chinese hospitals between 2017 and 2021. Now, the discovery of a stronger and more infectious version of ST410 CREC, called B5/H24RxC, has been implicated in two outbreaks in a children's hospital in China.

Analysis of the B5/H24RxC strain in a lab showed the bacteria was able to grow faster and was more harmful to living organisms than previous versions.

Professor Alan McNally, Director of Institute of Microbiology and Infection at the University of Birmingham and an author of the study said, "It has often been thought that the *E. coli* that evolve to be most resistant to antibiotics do so at the cost of being able to cause infections in humans. Our incredibly important collaboration with our partners in China ... has allowed us to discover and characterize this new clone of *E. coli* which is becoming both more antimicrobial resistant and more pathogenic.

"This is a worrying new trend and we would now urge surveillance labs across the world to be on the look out for this new clone which we know has spread beyond China."



Core-genome genes associated with the B5/H24RxC MDR clone. a) Presence and absence of the genes positively and negatively associated with the B5/H24RxC clone mapped to the phylogeny. Genes located in phage regions are shaded in orange, genes found in the high pathogenicity island (HPI) are in green and O-group genes are in red. b) Schematic representation of the chromosome and plasmids in the reference strains. Color bars and arrows indicate the location of the genes in the genomes of the reference strains. Credit: *Nature Communications* (2024). DOI: 10.1038/s41467-023-43854-3

Urgent need for collaborative effort

Samples from hospitals across 26 Chinese provinces between 2017 and 2021 were used to examine how widespread antibiotic-resistant *E. coli*

was.

Using a total of 388 CREC isolates from various clinical samples including urine, sputum and blood, the team were able to identify that ST410 was the most common CREC, and given that the highest proportion of samples (111) were taken from urine, that there may be a connection to [urinary tract infections](#).

Dr. Ibrahim Xiaoling Ba, Senior Research Associate in the Department of Veterinary Medicine at the University of Cambridge, and first author of the paper said, "Our study highlights the evolving landscape of antimicrobial resistance within clinically significant pathogens, such as E. coli, emphasizing the urgent need for collaborative efforts to address and mitigate this escalating challenge in global public health."

More information: Xiaoliang Ba et al, Global emergence of a hypervirulent carbapenem-resistant Escherichia coli ST410 clone, *Nature Communications* (2024). [DOI: 10.1038/s41467-023-43854-3](https://doi.org/10.1038/s41467-023-43854-3)

Provided by University of Birmingham

Citation: New and highly infectious E. coli strain resistant to powerful antibiotics (2024, January 31) retrieved 28 April 2024 from <https://phys.org/news/2024-01-highly-infectious-coli-strain-resistant.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.