

Gene discovered in Georgia water a possible global threat

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A gene that causes bacteria to be resistant to one of the world's most important antibiotics, colistin, has been detected in sewer water in Georgia. The presence of the MCR-9 gene is a major concern for public health because it causes antimicrobial resistance, a problem that the

World Health Organization has declared "one of the top 10 global public health threats facing humanity."

Researchers from the University of Georgia's Center for Food Safety (CFS) collected sewage water from an urban setting in Georgia to test for the MCR gene in naturally present bacteria. Led by College of Agricultural and Environmental Sciences assistant professor Issmat Kassem, whose research focuses on MCR's presence around the world, the team was surprised at how quickly they detected MCR—they found evidence of the gene in the first sample they took.

Kassem said that demonstrates that the gene is becoming established in the U.S.

The bacteria where the gene was found, *Morganella morganii*, added further concern for Kassem. This marked the first time that MCR was found in *M. morganii*, which is problematic because it is a bacteria not often tested by researchers. This means that the problem could be considerably more widespread than initially thought.

The spread of MCR in agriculture, imports, travel

It was previously believed that agriculture was a driving factor in the spread of MCR. Nations such as China and India use the colistin antibiotic in livestock. Colistin is considered a "last resort" antibiotic because it can kill infections that other antibiotics cannot. Its frequent use means that some bacteria are becoming resistant to it. This means that if people or animals contract a strain of colistin-resistant bacteria, there are potentially no medications that can treat their infection. They face extreme, invasive health measures and possible death.

Colistin is banned in the U.S. for use in food animals and it was previously thought that this measure would help slow the spread of

antimicrobial resistance to colistin in the country. However, MCR can be spread through global travel and the import of foods from other countries. Results of the CFS study prove that the U.S. is no less susceptible to the threat than other nations around the world.

Further complicating the issue is the way that the gene is spread. It transmits in plasmids, which are strands of DNA found inside cells that can replicate on their own, independent of the cell. A plasmid with antimicrobial resistance found in one type of bacteria can transmit to other types of bacteria. This means that bacteria like *E. coli* and *Salmonella* that commonly cause outbreaks in humans can potentially carry MCR, turning them from treatable illnesses to potentially deadly infections.

How worried should we be about the MCR-9 gene?

Kassem said that taken all together, the global threat of antimicrobial resistance, the presence of MCR in Georgia, that it was found inside a bacterium that is often overlooked, and that it occurred even without the use of colistin in U.S. agriculture is a serious problem that requires immediate action on the part of many industries including research, healthcare and government to work together toward a solution.

"If we don't tackle it right now, we are jeopardizing human and animal medicine as we know it and that can have huge repercussions on health and the economy," Kassem said. "It's a dangerous problem that requires attention from multiple sectors for us to be able to tackle it properly."

Because of this urgency, findings from the research were printed in short format manuscript out now in the *Journal of Global Antimicrobial Resistance*. It was funded through a CFS grant and other researchers involved were Jouman Hassan, David Mann, Shaoting Li and Xiangyu Deng.

More information: Jouman Hassan et al, First report of the mobile colistin resistance gene mcr-9.1 in *Morganella morganii* isolated from sewage in Georgia, USA, *Journal of Global Antimicrobial Resistance* (2021). [DOI: 10.1016/j.jgar.2021.11.013](https://doi.org/10.1016/j.jgar.2021.11.013)

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