

# 'Superbug gene' found in one of the most remote places on Earth

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Credit: Newcastle University

Antibiotic-Resistant Genes (ARGs) that were first detected in urban

India have been found 8,000 miles away in one of the last 'pristine' places on earth, a new study has shown.

Soil samples taken in the Kongsfjorden region of Svalbard have now confirmed the spread of blaNDM-1 into the High Arctic—an ARG originally found in Indian clinical settings, which conditionally provides [multidrug resistance](#) (MDR) in microorganisms.

Worldwide spread of blaNDM-1 and other MDR genes is a growing concern because they often target "last resort" classes of [antibiotics](#), including Carbapenems.

Carried in the gut of animals and people, the research team, led by Newcastle University's Professor David Graham, say that blaNDM-1 and other medically-important ARGs were found in Arctic soils that were likely spread in the faecal matter of birds, other wildlife and human visitors to the area.

"Polar regions are among the last presumed pristine ecosystems on Earth, providing a platform for characterizing pre-antibiotic era background [resistance](#) against which we could understand rates of progression of AR 'pollution'," says Professor Graham, an [environmental engineer](#) at Newcastle University who has spent 15 years studying the environmental transmission of antibiotic resistance around the world.

"But less than three years after the first detection of the blaNDM-1 gene in the surface waters of urban India we are finding them thousands of miles away in an area where there has been minimal human impact.

"Encroachment into areas like the Arctic reinforces how rapid and far-reaching the spread of antibiotic resistance has become, confirming solutions to AR must be viewed in global rather than just local terms."

## **Concern over the spread of Antibiotic-Resistant (AR) genes**

Increasing antibiotic resistance is a global health crisis. An example is NDM-1, which is a protein that can confer resistance in a range of bacteria. NDM-1 was first identified in New Delhi and coded by the resistant gene blaNDM-1.

Strains that carry blaNDM-1 were first found in clinical settings in 2008, but by 2010 blaNDM-1 was found in surface waters in Delhi. Since then, the resistant gene has been found in over 100 countries, including new variants.

There are currently few antibiotics to combat bacteria that are resistant to Carbapenems—still a last-resort antibiotic class—and worldwide spread of blaNDM-1 and related ARGs is a concern.

"What humans have done through excess use of antibiotics on global scales is accelerate the rate of evolution, creating a new world of resistant strains that never existed before," explains Graham.

"Through the overuse of antibiotics, faecal releases and contamination of drinking water, we have consequentially speeded-up the rate at which superbugs might evolve.

"For example, when a new drug is developed, natural bacteria can rapidly adapt and can become resistant; therefore very few new drugs are in the pipeline because it simply isn't cost-effective to make them."

## **Benchmark for tracking resistance**

Published today in the academic journal *Environmental International*, this latest research was carried out by an international team of experts from the Universities of Newcastle, York and Kansas and the Chinese

Academy of Science in Xiamen, and was funded by the UK Natural Environmental Research Council and other agencies.

Analysing the extracted DNA from forty soil cores at eight locations along Kongsfjorden, a total of 131 ARGs were detected.

"The resistance genes detected were associated with nine major antibiotic classes, including aminoglycosides, macrolides and  $\beta$ -lactams, which are used to treat many infections. As an example, a gene that confers MDR in Tuberculosis was found in all cores, whereas blaNDM-1 was detected in more than 60% of the soil cores in the study.

"This finding has huge implications for global AR spread," warns Graham. "A clinically important ARG originating from South Asia is clearly not 'local' to the Arctic."

"Identifying an ARG 'gradient' across the study landscape, which varies as a function of human and wildlife impact, shows there are still isolated Polar locations where ARG levels are so low they might provide nature's baseline of antimicrobial resistance," Graham says.

"The gradient of resistance [genes](#) closely reflects corresponding indicators of wastes in the geochemistry, which suggests a novel basis for identifying sites for further AMR research" adds lead author, Dr. Clare McCann, of Newcastle University.

"The only way we are going to win this fight is to understand all pathways that lead to antibiotic resistance.

Clearly, improved antibiotic stewardship in medicine and agriculture is crucial, but understanding how resistance transmission occurs through water and soils is also critical. We contend that improved waste management and water quality on a global scale is a key step."

**More information:** 'Understanding drivers of antibiotic resistance genes in High Arctic soil ecosystems' Clare McCann, Beate Christgen, Jennifer Roberts, Jian-Qiang Su, Kathryn Arnold, Neil Gray, Yong-Guan Zhu and David Graham. *Environment International*

Provided by Newcastle University

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