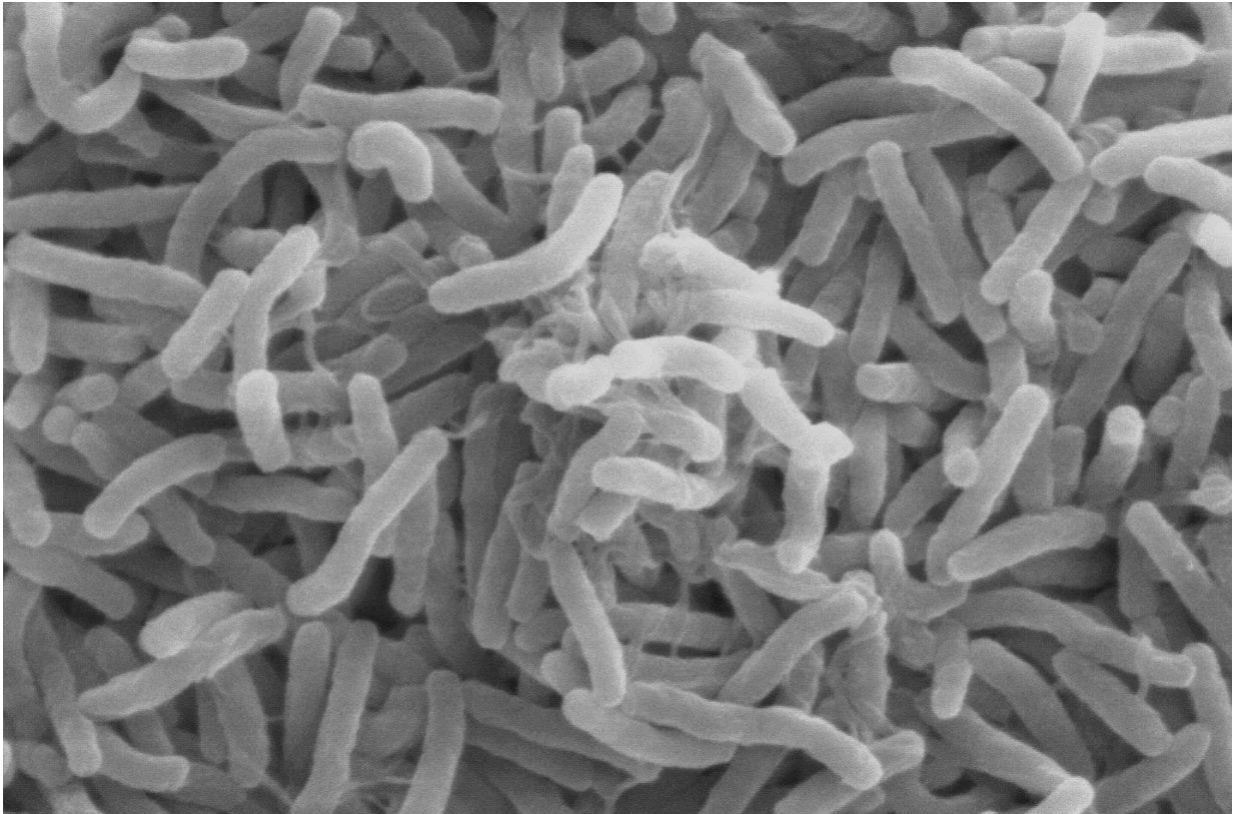


Mystery of Yemen cholera epidemic solved

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Scanning electron microscope image of *Vibrio cholerae*. Credit: Wikipedia

The most likely source of the cholera epidemic in Yemen has been discovered by scientists. Through the use of genomic sequencing, scientists at the Wellcome Sanger Institute and Institut Pasteur estimate the strain of cholera causing the current outbreak in Yemen—the worst cholera outbreak in recorded history—came from Eastern Africa and

entered Yemen with the migration of people in and out of the region.

The results, published today (2 January) in *Nature* show that genomic data and technologies can enable researchers to estimate the risk of future [cholera](#) outbreaks in regions like the Yemen and ultimately be used to better target interventions.

Yemen is facing the worst epidemic of cholera since records began. The disease has affected over 1 million people and caused almost 2,500 deaths. The United Nations estimate that 16 million of the 29 million people in Yemen lack access to safe water and basic sanitation.

The population in Yemen has experienced two outbreaks of cholera; the first occurred between September 2016 and April 2017, and the second began later in April 2017 and has since resulted in more than 1 million suspected cases.

To understand the nature of the strain of bacteria behind these devastating cholera outbreaks, researchers from the Wellcome Sanger Institute, Institut Pasteur and their collaborators sequenced the genomes of *Vibrio cholerae* from cholera samples collected in Yemen and nearby regions.

The team sequenced 42 *V. cholerae* samples from both Yemen outbreaks. To do this samples were collected in Yemen itself and from a Yemeni refugee centre on the Saudi Arabia-Yemen border, along with 74 other cholera samples from South Asia, the Middle East and Eastern and Central Africa.

Researchers compared these genomic sequences to a global collection of over 1000 cholera samples from the current and ongoing pandemic, known as the seventh cholera pandemic, which began in the 1960s and is caused by a single lineage of *V. cholerae*, called 7PET.

Scientists discovered that the cholera strain causing the Yemen epidemic is related to a strain first seen in 2012 in South Asia that has spread globally, but the Yemeni strain did not arrive directly from South Asia or the Middle East. This particular cholera strain was circulating and causing outbreaks in Eastern Africa between 2013 and 2014, prior to appearing in Yemen in 2016.

Professor Nick Thomson, from the Wellcome Sanger Institute and London School of Hygiene and Tropical Medicine, said: "Genomics enabled us to discover that the strain of cholera behind the devastating and ongoing epidemic in Yemen is likely linked to the migration of people from Eastern Africa into Yemen. Knowing how cholera moves globally gives us the opportunity to better prepare for future outbreaks. This information can help inform strategies for more targeted interventions with the ultimate aim of reducing the impact of future epidemics."

Dr. François-Xavier Weill, Head of the Institut Pasteur's Enteric Bacterial Pathogens Unit, said: "Genomic analysis continues to show its power to provide a high resolution, detailed view of the bacteria that causes cholera, *Vibrio cholerae*, which is critical to tackling this devastating disease. Like the other major cholera outbreaks around the world, we discovered that the atypical strain of bacteria behind the Yemeni cholera epidemic is linked to the single lineage called 7PET, which is responsible for the current and ongoing global pandemic. This potentially enables us to focus our research and direct interventions towards this particular lineage of *Vibrio cholerae* to greater effect."

Contrary to previous theories that the two outbreaks of cholera in Yemen were caused by two different strains, this study revealed they were caused by the same strain of the *Vibrio cholerae* bacterium that entered the Yemen in 2016. While most strains of cholera that are causing epidemics are resistant to many antibiotics, the team discovered

the unusual finding that the Yemeni cholera strain was susceptible to many of these antibiotics.

Dr. Daryl Domman, a visiting scientist at the Wellcome Sanger Institute, now based at the Los Alamos National Laboratory in the United States, said: "Surprisingly, we discovered the cholera strain causing the Yemen outbreaks is less resistant to antibiotics than related strains. The strain causing the Yemeni cholera epidemic has deleted four genes responsible for resistance to clinically relevant antibiotics, making itself more vulnerable to treatment."

Dr. Marie-Laure Quilici, a scientist in the Institut Pasteur's Enteric Bacterial Pathogens Unit and Head of the National Reference Center for Vibrios and Cholera, said: "This study illustrates again the key role of genomic microbial surveillance and cross-border collaborations in understanding global cholera spread. All countries need to be aware of this and act accordingly if they are to achieve the targets set by WHO's Global Task Force on Cholera Control, which aims to reduce the cholera death toll by 90 per cent by the year 2030."

More information: François-Xavier Weill et al, Genomic insights into the 2016–2017 cholera epidemic in Yemen, *Nature* (2018). [DOI: 10.1038/s41586-018-0818-3](https://doi.org/10.1038/s41586-018-0818-3)

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