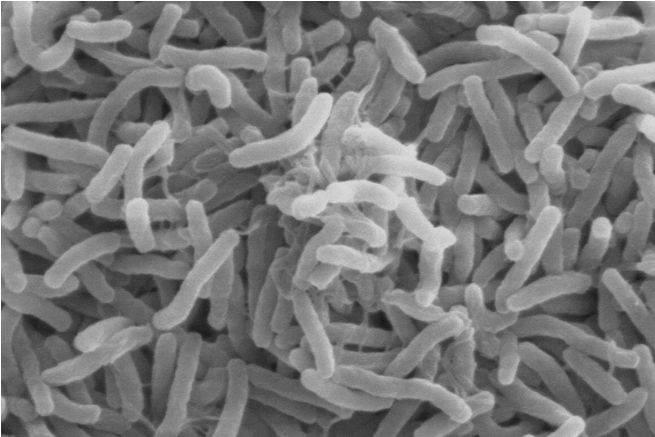


Risk of cholera epidemics estimated with new rule-book

9 November 2017



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

Cholera has repeatedly traveled out of Asia to cause epidemics in Africa and Latin America, an international research team has found. Researchers at the Wellcome Trust Sanger Institute, Institut Pasteur in France, and collaborators from across the world, studied outbreaks in Africa, Latin America and the Caribbean from the last 60 years.

The results of two studies, published today (10 November) in *Science*, present a new 'rule-book' to estimate the risk of different [cholera](#) strains causing an [epidemic](#).

Despite being thought of as an ancient disease, cholera still affects 47 countries world-wide and claims the lives of nearly 100 thousand people a year. Since the 1800s, there have been seven cholera pandemics around the globe, resulting in millions of deaths. The current and ongoing pandemic, which began in the 1960s, is caused by a single lineage of *Vibrio cholerae*, called 7PET.

The largest epidemic in history is ongoing in

Yemen, with the total number of cases quickly approaching 1 million, and the WHO recently announcing a campaign to stop cholera by 2030.

In two new studies, scientists analysed historical cholera samples from across the globe. The team studied genetic data from over 1200 cholera samples, some dating back to the 1950s.

The researchers focused on Africa and Latin America, due to the large epidemics that have occurred in those regions. The seventh pandemic of cholera first came to Africa in 1970, and Africa has since become the continent most affected by the disease. Cholera appeared in Latin America in 1991, after an absence of 100 years.

The team found that 7PET strains from Asia were repeatedly introduced into two main regions of Africa: West Africa and East/Southern Africa.

François-Xavier Weill, first author on the African study and principal investigator from the Institut Pasteur, said: "Our results show that multiple new versions of 7PET bacteria have entered Africa since the 1970s. Once introduced, [cholera outbreaks](#) follow similar paths when spreading across that continent. The results give us a sense of where we can target specific regions of Africa for improved surveillance and control."

Scientists also investigated the evolution of antibiotic resistance in cholera. The team found that all recent introductions of [cholera bacteria](#) into Africa were already resistant to antibiotics. Using the genomic data they were able to track the source of the antibiotic resistance back to South Asia.

In Latin America, the team not only focused on the 7PET strains that cause epidemics, but other strains of *Vibrio cholerae* that cause sporadic low level disease. This allowed the researchers to uncover that different strains of *Vibrio cholerae* can

be assigned different risks for causing large outbreaks. This has significant implications for cholera control efforts world-wide.

Daryl Domman, first author on the Latin American study from the Wellcome Trust Sanger Institute, said: "Our data show that when a 7PET pandemic strain enters into Latin America from elsewhere, it can cause massive epidemics, like those seen in Peru in the 1990s and Haiti in 2010. However, we now know that other [strains](#) already in this region can still make people sick, but seem to not have this epidemic potential. Knowing which strain is which allows for an appropriate public health response from regional or national governments."

Professor Nick Thomson, senior author from the Wellcome Trust Sanger Institute and the London School of Hygiene and Tropical Medicine, said: "These findings have implications for the control of cholera pandemics. We are now getting a real sense of how cholera is moving across the globe, and with that information we can inform improved control strategies as well as basic science to better understand how a simple bacterium continues to pose such a threat to human health."

More information: F.-X. Weill et al., "Genomic history of the seventh pandemic of cholera in Africa," *Science* (2017).

[science.sciencemag.org/cgi/doi ...
1126/science.aad5901](https://science.sciencemag.org/cgi/doi/10.1126/science.aad5901)

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